UNIVERSITY OF BIRMINGHAM

"Manipulating the frequency and distribution of genetic crossovers during meiosis in barley."

A thesis submitted by

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This project is a CASE studentship carried out under the supervision of Dr Sue Armstrong and Prof F.C.H Franklin at the University of Birmingham, in partnership with Dr Luke Ramsay and Prof Robbie Waugh of the James Hutton Institute, and Anne-Marie Bochard and Thomas Jolliffe of LIMAGRAIN UK.

Abstract

In commercial barley cultivars meiotic crossover (CO) distribution is skewed to the distal regions of the paired chromosomes. This restricts recombination to these regions thereby reducing the potential genetic variation that can be exploited in plant breeding programs. The aim of this project was to develop experimental strategies that will enable the frequency and distribution of meiotic crossovers to be modified in order to generate progeny with novel gene combinations.

Preliminary studies were carried out to develop a procedure that would enable chemicals to be administered to the meiocytes at the appropriate developmental stage via the transpiration stream. This was carried out by using a hypodermic syringe to inject the chemical directly into the region of the stem harbouring the spikes (sites of meiosis). As the first step, the administration of the thymidine analogue bromodeoxyuridine (BrdU) enabled a meiotic time course to be established, as BrdU is incorporated into the meiocytes during meiotic S-phase.

Using this method, an investigation was carried out to determine the possible mechanism(s) by which the telomeres pair and cluster to form the classical 'bouquet' structure, which is traditionally observed in zygotene. The microtubule destabilising drug, colchicine, was found to disrupt the clustering together of the paired telomeres to form the 'bouquet' but did not prevent the pairing of the homologous chromosomes. This result suggests that the pairing of the homologous chromosomes and the clustering of the paired telomeres to form the 'bouquet' structure, may be controlled by two distinct mechanisms or even be two steps of the same process.

In addition, treatment with the histone deacetylase inhibitor trichostatin A, led to significant modifications in crossover frequency in a concentration-dependent manner with lower concentrations not greatly impacting fertility, and allowing for the extraction of fertile seeds. The genetic screening of a treated marker population carried out at The James Hutton Institute

(JHI), demonstrated subtle but significant shifts in the distribution of meiotic recombination, indicating that modifying recombination through chemicals applied via the transpiration stream is indeed feasible in barley and hence, possibly in other cereals.

The cytological study of a barley desynpatic mutant *des8* in collaboration with JHI revealed that synapsis is normal despite reduced chiasma frequency. Genetic mapping studies are in progress to identify the mutant gene responsible for this phenotype which will help us to improve our current knowledge of meiosis in barley.

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I would like to dedicate this PhD to my late Grandfather Ajit Singh Sandhu and late uncle Abdul Ghani Khan. Finally, I would like to thank my parents for their continued support and encouragement over the years, to help me stay focused throughout the course of my PhD. I would also like to thank my friends for inspiring me to fulfil my potential, and for their support and motivation.

Table of Contents

List of Figures

List of Tables

List of Abbreviations

AE ..... **Axial element**

ASP ..... **Asparagine**

ASY1 ..... **ASYNAPTIC 1**

At ..... **Arabidopsis thaliana**

Bd ..... **Brachypodium**

BIO ..... **Biotin**

BrdU ..... **Bromodeoxyuridine**

BSA ..... **Bovine Serum Albumen**

Cdk ..... **Cyclin-dependant Kinase**

cM ..... **Centimorgan**

Col-0 ..... **Columbia-0 Ecotype**

CRISPR ..... **Clustered Regularly Interspaced Short Palindromic Repeats**

CVI ..... **Cape Verde Islands Ecotype**

DAPI ..... **4',6-diamidino-2-phenylindole**

des ..... **desynaptic**

DHJ ..... **Double Holliday junction**

DIG ..... **Digoxigenin**

DMC1 ..... **Disruption of meiotic control 1**

DSB ..... **DNA Double strand break**

EM ..... **Electron microscopy**

EMCs.....**Embryo sack mother cells**

EMS..... **Ethylmethanesulfonate**

Fei-0..... **Santa Marı´a de Feira**

FISH..... **Fluorescence *in situ* hybridisation**

GISH..... **Genomic *in situ* hybridisation**

HATs..... **Histone acetyltransferases**

HIS..... **Histidine**

Hv.....**Hordeum vulgare**

JHI.....**The James Hutton Institute**

LIM.....**Limagrain UK**

LN.....**Late nodule**

Mb..... **Megabases**

MCC1.....**MEIOTIC CONTROL OF CROSSOVERS1**

MET1.....**Methyltransferase 1**

MLH1..... **MutL homolog 1**

MLH3..... **MutL homolog 3**

MRE11..... **Meiotic recombination 11**

MSH4.....**MutS homolog 4**

MSH5.....**MutS homolog 5**

MUS81.....**MMS and UV sensitive 81**

NASA.....**National Aeronautics and Space Administration**

NGS ..... **Next-generation sequencing**

NHEJ ..... **Nonhomologous end-joining**

NILs ..... **Near isogenic lines**

NOR ..... **Nucleolus organising region**

NTR ..... **Non-transcribing repeat**

OPA ..... **Oligo Pool Assay**

PBS ..... **Phosphate buffered saline**

PCR ..... **Polymerase chain reaction**

Ph1 ..... **Pairing homoeologous 1**

PMC ..... **Pollen mother cells**

POT1 ..... **Protection of telomeres 1**

QTL ..... **Quantitative trait loci**

RPA ..... **Replication protein A**

RPM ..... **Rapid prophase movements**

SC ..... **Synaptonemal complex**

SDW ..... **Sterile distilled water**

Sb ..... **Sorghum**

SDS-PAGE ..... **Sodium-dodecyl-sulfate polyacrylamide gel electrophoresis**

SEI ..... **Single-end invasion**

SMC ..... **Structural maintenance of chromosomes**

SNPs ..... **Single nucleotide polymorphisms**

SPO11.....**Sporulation specific protein 11**

SSC.....**Saline sodium citrate**

SS DNA.....**Single stranded DNA**

SUMO.....**Small ubiquitin-like modifier**

TEBP.....**Telomere end-binding protein**

TF.....**Transverse filament**

TIN2.....**TRF interacting factor 2**

TRF.....**Telomere repeat-binding factor**

TSA.....**TrichostatinA**

UoB.....**The University of Birmingham**

VRS1.....**Six-Rowed spike 1**

WS.....**Wassilewskija Ecotype**

CHAPTER 1

INTRODUCTION

1.1 General introduction

Current world population projections have estimated that by 2050, the world population could reach 9 billion and in conjunction with the environmental stresses of climate change and changes in cultural attitutes to food consumption, there will be an increase in the need for food production (Royal Society, London, 2009). It was initially proposed that by 2030, food production should be increased by a target of 50% in the House of Commons by the former Labour Secretary of State for Environment, Food and Rural Affairs, Hilary Benn (Benn, 2009), alongside overwhelming agreement with the aforementioned target (Benn, 2009) by the opposing conservative party leader David Cameron at the 2008 National Farmers Union convention (Cameron, 2008). Later studies revised this target suggesting the probable need to increase food production by 100% (Godfray *et al*., 2010). It has been claimed that economic success will the driver for the vast majority of increased global urbanisation being accounted for in developing countries (**Figure 1.1**, United Nations, 2006) such that over 70% of the global population is predicted to be urbanised by 2050 (FAO, 2009). Also, infrastructural constraints are a key factor (Godfray *et al*., 2010) because even though the Southeast Asian peninsula is so close to sources of irrigation (**Figure 1.2,** Maplecroft, 2012), the mean annual rice yield gap is 40% (Cassman, 1999).

Various field trials have shown that it may be possible to educate and train farmers in third world countries such as Syria, Morocco and Tunisia, to be able to contribute to global barley breeding programs (Ceccarelli *et al*., 2001). Such a strategy could be useful in helping central Asia (Syria and other countries within the subcontinent) (Ceccarelli *et al*., 2001) and the vast majority of countries in Africa where food security is most problematic (**Figure 1.3**, Maplecroft, 2012).

A higher demand will have to be met by improving crop yield by different methods, one of them being the use of the control of meiotic recombination patterns to unlock roughly 30% of

the genes in barley and wheat, which occupy recombination redundant regions (Erayman *et al*., 2004; Mayer *et al*., 2011), which may provide a greater genetic variety of crops that the crop breeder will be able to utilise. Manipulation of meiotic recombination could make a significant contribution but is only one approach to the problem (Osman *et al*., 2011). So far, genetically modified (GM) crops have been a feasible means of tackling the issue of food security, which was inititated by the pioneering experiment in which the kanamycin gene was successfully transferred into tobacco protoplasts (Paszkowski *et al*., 1988), which later, made way for the generation of commercially viable GM crops such as Golden Rice in which the genes required for the beta-carotene biosynthetic pathway, were cloned into Carotenoid-Free rice (Ye *et al*., 2000). Recently, the clustered regularly interspaced short palindromic repeats (CRISPR) system has been piloted to carry out genome targetting, which utilises the endonuclease Cas9 found in bacteria. The sites of DNA double strand break induction and subsequent genome editing can be targeted by altering the sequence of the Cas9 associated chimeric RNA, such that it is complimentary to a specific target genomic sequence, allowing for the insertion of a desired gene using an appropriate vector. Such an approach holds the promise of directed genome editing in plants (reviewed by Puchta and Fauser, 2013).

The improved harnessing of the available genetic diversity in wild crop relatives as well as that which occupies recombination backwaters in already established elite lines, via a better understanding of meiosis is the key to successful crop improvements as it is this gene pool which may provide a means of potential resistance against disease and adverse abiotic stresses which occur as a result of climate change. This will become increasingly important due to the effect of global warming, creating a harsher environment, presenting a challenge to crop survival.

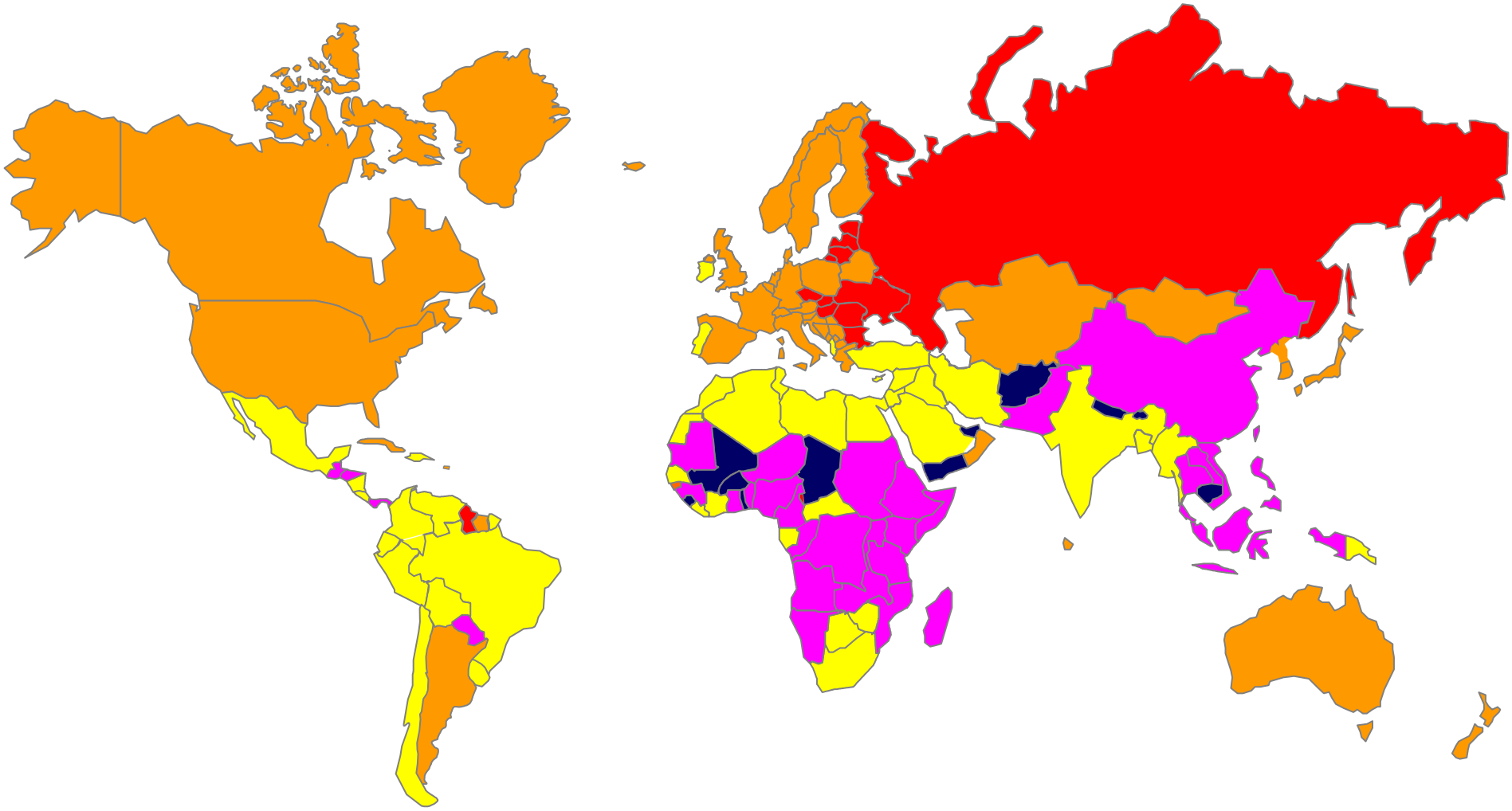
The study of meiosis in *Arabidopsis thaliana* has been pivotal in elucidating the factors that are involved in the control of meiotic recombination. The choice for this species was due in part to

the small size of its genome and its short life cycle, establishing it as a model **plant** species for the study of meiosis (Meyerowitz, 1987). Even though *Arabidopsis* has no commercial value, the knowledge of Angiosperm meiotic recombination that has been gained by the study of this species can be applied to more commercially viable crops such as barley (*Hordeum vulgare* L.), wheat (*Triticum spp*.), rice (*Oryza sativa*) and the Brassicas (which are a close crop relative of *Arabidopsis*).

Figure 1.1

World urbanisation index

Adapted from United Nations, Department of Economic and Social Affairs, Population Division (2006)

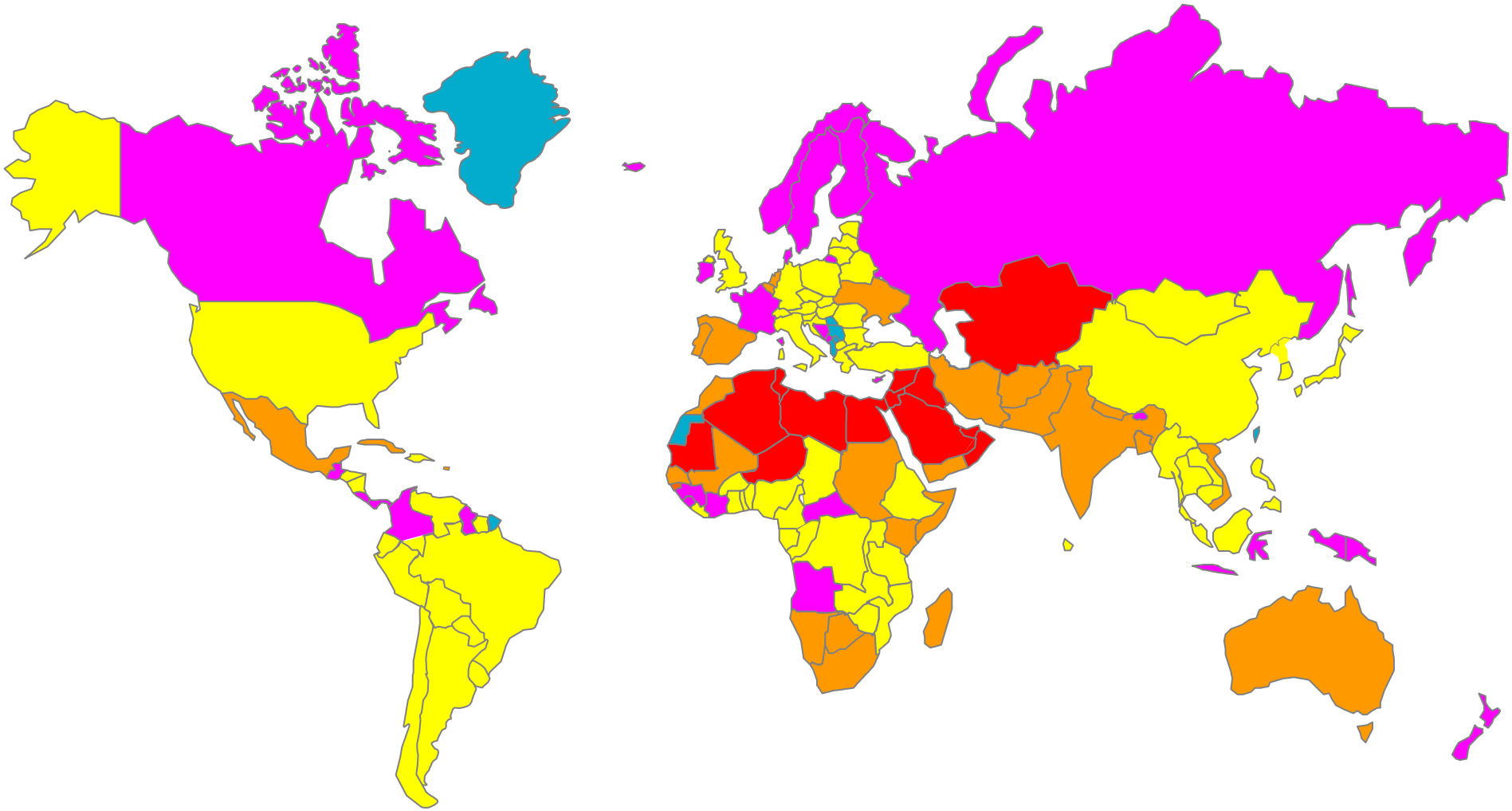


World map courtesy of www.presentationmagazine.com

Figure 1.2

World water security index

Adapted from Maplecroft

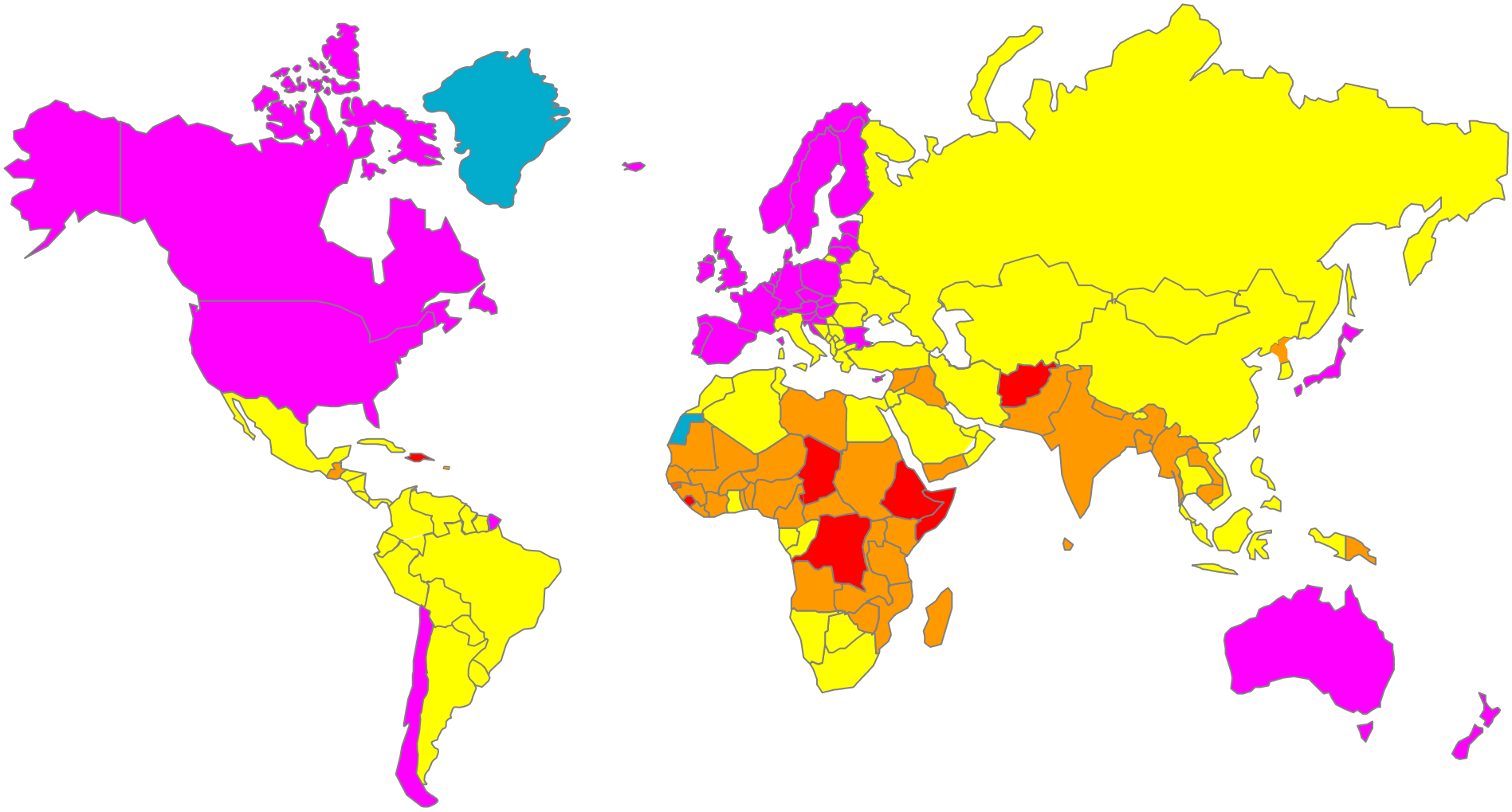


World map courtesy of www.presentationmagazine.com

Figure 1.3

World Food security index

Adapted from Maplecroft



World map courtesy of www.presentationmagazine.com

1.2 The importance of barley

Barley (*Hodeum vulgare* L.) has been ranked the fifth crop in food production in the world (FAOSTAT, 2007; http://faostat.fao.org/), and is used in the production of beer. In addition, it is a vital ingredient in animal feeding and is grown on over 57 million hectares of farm land world-wide (FAOSTAT, 2010; http://www.fao.org/faostat).

Barley is a member of the grass family Poaceae, and originally existed as wild barley (*Hordeum vulgare subsp*. *spontaneum*). The genus *Hordeum* belongs to the tribe Triticeae, which in turn, belongs to the Poaceae family. *H spontaneum* has a brittle spike that allows for the dispersal of its seeds however, domesticated barley consists of spikes that do not shatter, and the mature seeds can be harvested (Zohary and Hopf, 2000). The non-shattering phenotype was caused by the recessive mutation of two linked genes, Bt_1 and Bt_2. Then the selection of the non-shattering phenotype in homozygous mutants when humans began harvesting the seeds, gave rise to new cultivars (Zohary and Hopf, 2000).

The general structure of barley consists of a central spike (rachis), which is surrounded by groups of spikelets that are organised as a triplet. Generally, only the rachis is fertile in cultivars that consist of two rows of spikelets. The naturally occuring two-rowed cultivars are Barke, Betzes and Bowman (**Figure 1.4**). A mutation in the gene, *SIX-ROWED SPIKE 1 (VRS1),* gave rise to six-row barley (the naturally occuring cultivars Morex and Bere) (**Figure 1.4**) in which the lateral spikes are also fertile (Komatsuda *et al*., 2006).

Barley is a diploid (2n = 14), self-fertilising, seed based crop with a genome size of 5.3×10^9 bp/1C (Bennett and Smith, 1976). The seven chromosomes of barley have been allocated the abbreviations Hv1 to Hv7. In the past, restriction fragment length polymorphism (RFLP) linkage maps have been devised. This information made it possible to generate a synteny with all of the wheat genomes (Dubcovskey *et al*., 1996).

The emergence of fluorescence *in situ* hybridization (FISH) methods have allowed the investigation of the relationship between physical and genetic distances on chromosomes (Schwarzacher, 2003b) and the mapping of low and single copy genes in barley by FISH revealed that there is a greatly reduced recombination frequency in the inner half of the chromosome arms (Pedersen *et al*., 1995).

Figure 1.4: A Two-rowed barley ear from a Bowman background (left) and a six-rowed barley ear from a Morex background (right). Bar = 1 cm

1.3. Early attempts of crop improvement

The process of plant breeding initially involves the generation of a library of crops with novel gene combinations, which leads to the generation of new crop varieties with desired characteristics by crossing and selection.

Plant breeding first emerged thousands of years ago as a simple process of farmers selecting seeds from a plant with a desired characteristic, called **selective breeding**, allowing the production of subsequent generations of crops that were in demand by consumers. This process is sometimes called **domestication**. However, it must be taken into account that domestication sometimes leads to a condition known as domestication syndrome, where the domesticated crop is no longer able to survive in the wild and requires human intervention for its survival and reproduction, as it loses its natural ability of seed dispersal, resistance to natural toxins and increased morphological variation in the part of the plant that its extracted for use by humans (Pickersgill, 2007). The loss of a plants dispersal mechanism is usually due to the loss of its abscission zone within an inflorescence, which induces the shattering of the inflorescence to release the seeds. This effect has occurred in various cultivars of maize and rice (Mao *et al*., 2000).

The earliest records of domestication trace back to 11,050 BC, when pre-Neolithic populations attempted to domesticate rye in Syria (Hillman *et al*., 2001). Before the emergence of ceramics, *Lagenaria siceraria*, was domesticated and used as a container as far back as 10,000 BC. This bottle gourd reached as far as the Americas by 8,000 BC, as a result of a possible migration of populations from Asia to America (Erickson *et al*., 2005).

1.4 Introduction to meiosis:

Meiosis is a specialised pathway of nuclear division that is involved in the production of gametes. This process consists of crucial steps in gamete synthesis, one of which involves the halving of the diploid chromosome number to form haploid gametes which after successful fertilisation will restore the diploid chromosome number in the resulting progeny (Roeder, 1997). Meiosis leads to *re-assortment* of genes by the recombination of genes between homologous chromosomes, and the random assortment of chromosomes.

1.5 Summary of chromosome behaviour during male meiosis in plants:

Gametes are only formed from cells that are programmed to undergo meiosis. As briefly mentioned in **Section 1.4**, the role of meiosis is to produce haploid gametes and this process consists of a number of distinct stages/substages (Roeder, 1997). The first is S phase, when each chromosome undergoes replication to form two sister chromatids. They are held together along their length by the cohesin complex. The next stage is called prophase I, where each chromosome pairs up with its corresponding homologue followed by a tight association by a process called synapsis along the entire length of the paired chromosome arms, which is brought about by the formation of a tripartite structure called the synaptonemal complex (SC) until complete synapsis is achieved at pachytene (Roeder, 1997). The SC begins to disassemble from diplotene onwards, through diakinesis followed by chromatin condensation until metaphase. Each pair is held together by at least one crossover (Jones, 1984). Next, the exchange of chromosome arms occurs between the homologous chromosomes in a process called recombination. Subsequently, the homologue pairs line up on the spindle fibres at equator of the metaphase plate during metaphase I (reviewed by Schwarzacher, 2003). At anaphase I, the homologues separate, and each chromosome of every pair migrates towards

opposite poles of the spindle. In the final step of the first meiotic division, the chromosomes group together at opposite poles to form a dyad, with two distinct nuclei, telophase I.

The second meiotic division begins with metaphase II, where each chromosome lines up at the spindle equator. This is followed by the separation of the sister chromatids towards each pole of the spindle, at anaphase II. The final stage of meiosis is telophase II, in which four haploid nuclei form around each polar groups of chromatids to form a tetrad.

1.6 The sub-stages of Prophase I in *Arabidopsis* and barley:

Prophase I consists of five distinct sub-stages, which have been identified using light microscopy. This method was used to devise an atlas of meiosis in *Arabidopsis* (2n=10) (Ross *et al*., 1996) and barley (2n=14). Prior to entry into meiosis, the chromatin is uncondensed at premeiotic interphase (**Figure 1.5(a)** and **Figure 1.6(a)**). The first sub-stage is leptotene where chromatin starts becoming visible as thread-like structures indicating the inititation of synapsis (**Figure 1.5(b)** and **Figure 1.6(b)**). The progression to the next sub-stage leads to the increasing synapsed regions, at zygotene (**Figure 1.6(c))**. This is followed by pachytene where there is complete synapsis of the homologous chromosomes (**Figure 1.5(c)** and **Figure 1.6(d)**). Next, the paired bivalents begin to separate at diplotene (**Figure 1.5(d)** and **Figure 1.6(e) and (f)**), followed by the final sub-stage, diakinesis, where the homologous chromosome pairs undergo further compaction and the homologues move apart but are held together at chiasmata to form five visible bivalents in *Arabidopsis* (**Figure 1.5(e)**) and seven bivalents in barley (**Figure 1.6(g)**). Recombination occurs at the sites of chiasmata. At metaphase I the bivalents align at the spindle equator (**Figure 1.5(f) and Figure 1.6(h)**) before separating towards opposite poles (**Figure 1.6(i)**) to form two daughter cells (the sister chromatids remain held together at the centromere). At metaphase II the sister chromatids align at the equator of the

metaphase plate (**Figure 1.5(g) and Figure 1.6(j)**) before separating at anaphase II (**Figure 1.5(h) and Figure 1.6(k)**) to form four tetrads (**Figure 1.5(i) and Figure 1.6(l)**).

The duration of meiosis in wheat (~24 h), rye (~51 hr) and Triticale (~21 h) was determined in the early 1970's by tracking tritiated thymidine that was incorporated into DNA at pre-meiotic S-phase (Bennett *et al*., 1971). Later studies showed that prophase I occupies a large proportion of the meiotic pathway. For example, its duration was determined by sampling Bromodeoxyuridine (BrdU) pulse labelled meiotic *Arabidopsis* buds to examine their progress through meiosis (Armstrong *et al*., 2003). It was found that the duration of meiosis, at 18.5°C, from the end of meiotic S-phase to the appearance of tetrads, was 33 h. The duration of leptotene was found to be 6 h, zygotene/pachytene lasted 15.3 hrs and diplotene to tetrads lasted 2.7 h (Armstrong *et al*., 2003). The same technique demonstrated that the duration of the meiotic pathway in barley is 43 h under similar growth conditions (of which prophase I occupies ~40 h: Higgins *et al*., 2012).

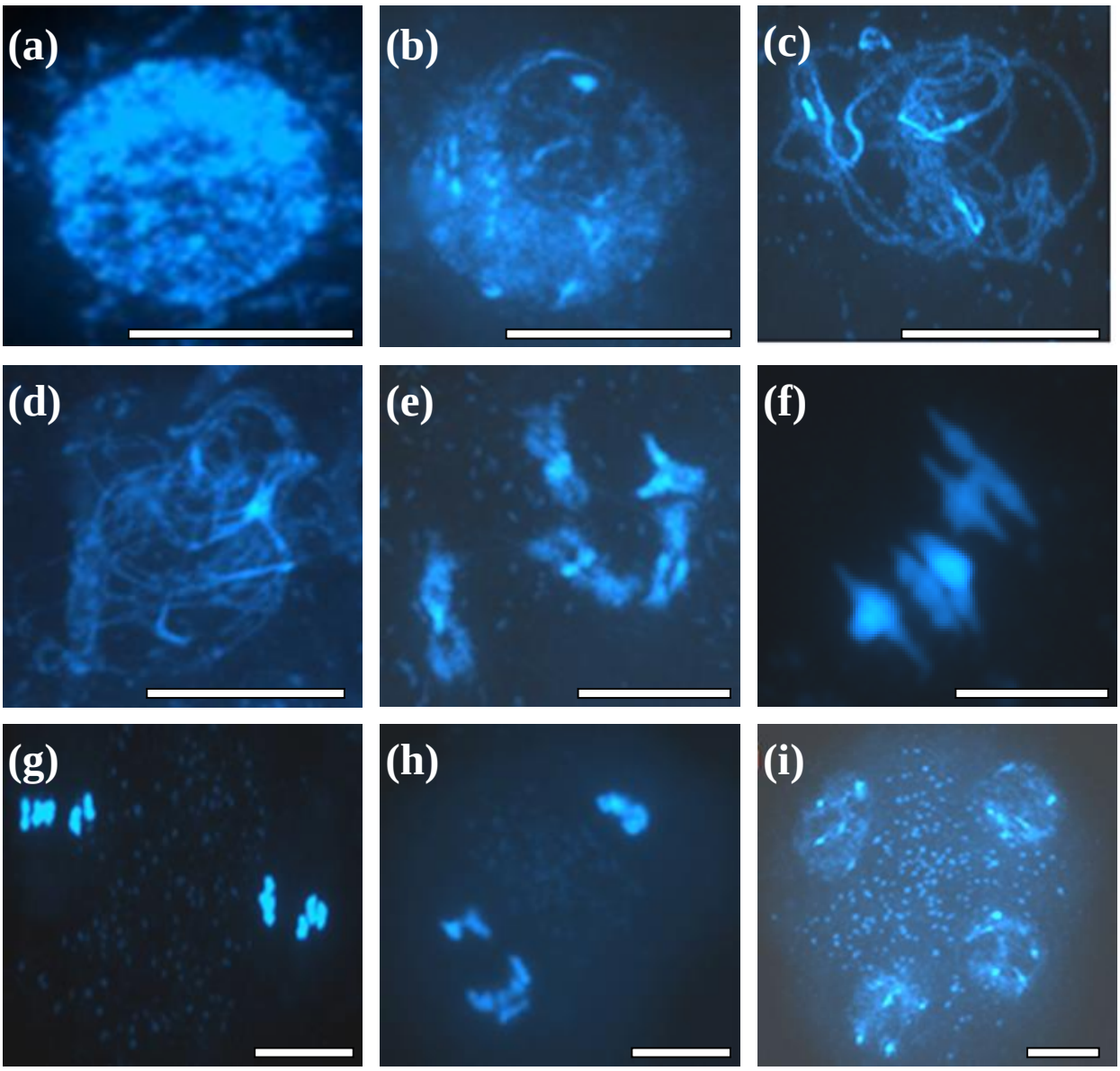


Figure 1.5: A meiotic atlas of DAPI (blue) stained *Arabidopsis* (Col-0) meiotic nuclei. (a) Premeiotic interphase: uncondensed chromatin. (b) Leptotene: regions of chromatin begin condensing and are visible as thread-like structures, which is followed by entry into zygotene. (c) Pachytene: Complete synapsis of the whole length of chromatin. (d) Diplotene: Desynapsis, allowing the separation of the groups of paired homologues which are held together by at least one chiasma. (e) Diakinesis: the condensed bivalents become discrete. (f) Metaphase I: five bivalents line up at the spindle equator and separate at anaphase I. (g) Metaphase II: each chromosome lines up at the spindle equator. (h) Anaphase II: separation of the sister chromatids towards each pole. (l) Tetrad stage: sister chromatids group together to form four haploids. Bar = 10 µm

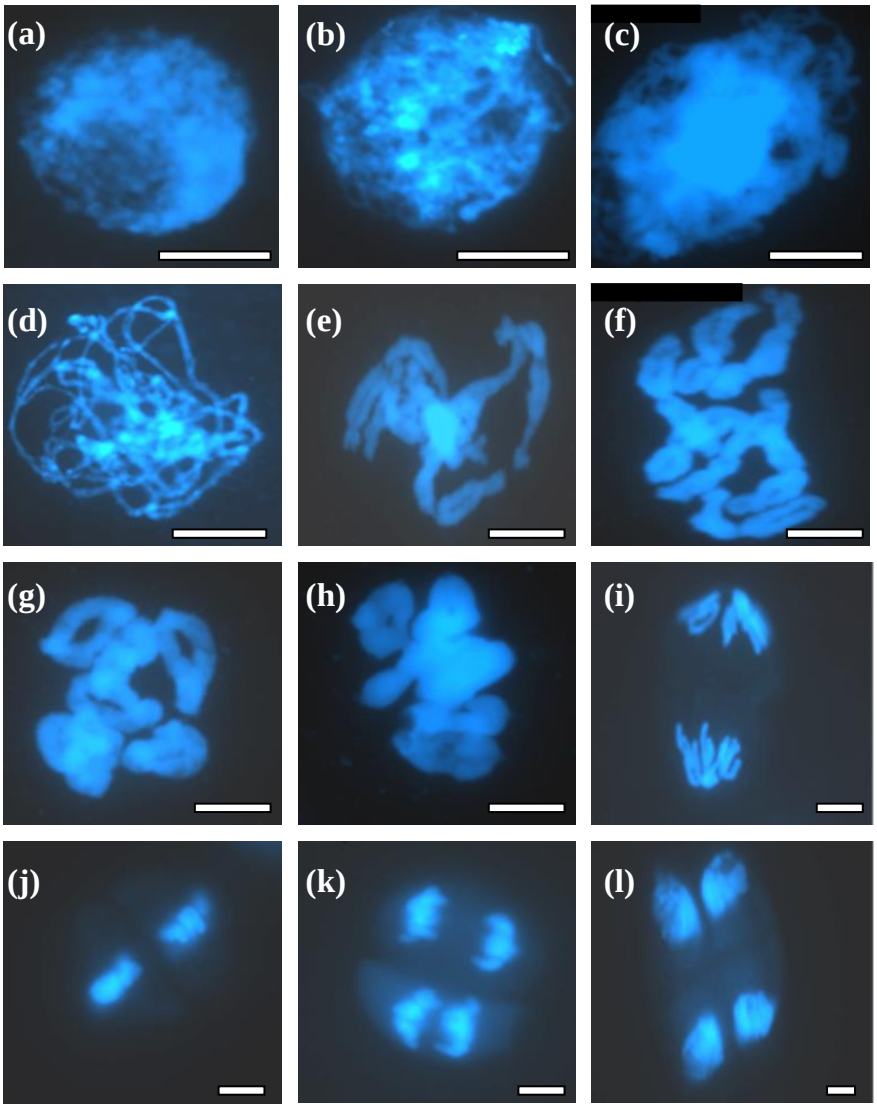


Figure 1.6: A meiotic atlas of DAPI (blue) stained barley (Morex). (a) Premeiotic interphase: uncondensed chromatin. (b) Leptotene: regions of chromatin begin condensing and are visible as thread-like structures. (c) Zygotene: synapsis progresses (regions of condensed and uncondensed chromatin). (d) Pachytene: Complete synapsis of the whole length of chromatin. (e) Diplotene: Desynapsis, allowing the separation of the groups of paired homologues which are held together by at least one chiasma. (f) Late diplotene: further separation of the paired homologues. (g) Diakinesis: the condensed bivalents become discrete. (h) Metaphase I: seven bivalents line up at the spindle equator. (i) Anaphase I: the homologues separate towards opposite poles to form a dyad. (j) Metaphase II: each chromosome lines up at the spindle equator. (k) Anaphase II: separation of the sister chromatids towards each pole. (l) Tetrad stage: sister chromatids group together to form four haploids. Bar = 10 µm

1.7 The events involved in the control of recombination

1.7.1 Early recombination events; DNA double strand break formation

The initial event in crossover formation, is the formation of programmed DNA double strand breaks (DSBs) in one chromosome of each homologous pair at leptotene, which triggers the initiation of meiotic recombination (Reviewed by Mehta and Haber, 2014). A topoisomerase type II transferase enzyme, SPO11, which is homologous to the subunit A of the type II topoisomerase, TOP6A found in the archea bacterium *Sulpholobus shibatae* (Bergerat *et al*., 1997), is directly involved in the generation of DSBs and has been found to be highly conserved amongst a wide variety of organisms (Keeney, 2001) such as fungi, nematodes, flies, mammals and plants (reviewed by Lam and Keeney, 2014).

Studies have shown that the *Arabidopsis* genome encodes three *SPO11* paralogues (*AtSPO11-1*, *AtSPO11-2* and *AtSPO11-3*) however, only *AtSPO11-1* and *AtSPO11-2* have a meiotic function (Hartung and Puchta, 2000; Grelon *et al*., 2001; Stacey *et al*., 2006). SPO11-3 was demonstrated to have a role in endoreduplication in somatic cells, required for normal plant development as *Atspo11-3* lines exhibited significantly reduced endoreduplication (Hartung *et al*., 2002). It was also shown that *Arabidopsis* harboured a homologue of the subunit B of topoisomerase 6 (AtTOP6B) (Hartung and Puchta, 2001). Studies on rice revealed the existance of proteins OsTop6A1, OsTop6A2, OsTop6A3 and OsTop6B, which are related to AtSpo11-1, AtSpo11-2, AtSpo11-3 and AtTopVIB, respectively (Jain *et al*., 2006). Later investigations with rice identified a further two Spo11/TopVIA homologues (OsSpo11-4 and OsSpo11-5) (An *et al*., 2011).

The importance of SPO11 in meiotic recombination was demonstrated by the use of *spo11-1* mutants that were obtained by the screening of a *Versailles* collection of T-DNA-transformed lines, including lines that were mutagenised by the use of ethyl-methane sulfonate (Grelon *et*

al., 2001). It was found that homozygous mutants exhibited normal growth just as the wild-type. There was a reduction in seed formation to an average of 2 seeds per silique in comparison to the wild-type, where an average of 40 to 50 seeds per silique are produced. To study the effect of the *AtSPO11* mutation on the recombination frequency, lines of the ecotype *Wassilewskija* (*WS*) which were heterozygous for the *spo11-1-1* mutation, were crossed with a *Columbia* (Col-0) line. The recombination frequencies of two microsatellite markers, nga280 and nga111, were determined in the F2 generation and it was found that the calculated map distance of both markers was 10 times lower than that of the wild-type (Grelon *et al*., 2001), indicating a significant decrease in recombination frequency which was depicted by a decrease in bivalent formation.

Subsequently, it was demonstrated that AtSPO11-2 is required for the correct segregation of chromosomes as the analysis of *Atspo11-2* progeny by flow cytometry, revealed the presence of spores with a DNA content that was greater than that of the haploid complement and hence, subsequent aneuploidy which was observable due to a sterile phenotype (Hartung *et al*., 2007).

DSB formation in budding yeast has been found to require a multi-protein complex where a minimum of nine other proteins (Mre11, Rad50, Xrs2, Ski8, Rec102, Rec104, Rec114, Mei4 and Mer2) act in association with SPO11 in DSB formation (Cole *et al*., 2010). However, it must be noted that the function of the homologues across species has not been conserved, as the SKI8 orthologue in *Arabidopsis* does not have a meiotic function, and AtMRE11 and AtRAD50 are not involved in the formation of DSBs (Jolivet *et al*., 2006).

AtPRD1, AtPRD2 and AtPRD3 are required for AtSPO11-1/AtSPO11-2, mediated DSB formation, where it has been shown that AtPRD1 has a similar sequence to MEI1, which is a protein involved in DSB formation in mammals (Libby *et al*., 2003). The same study revealed that AtPRD1 and AtSPO11 interact and could function together in DSB formation. AtPRD2

may be an ortholoque of MEI4 in budding yeast and mouse (Kumar *et al*., 2010), and *AtPRD3* is homologous to the rice *OsPAIR1* gene (Nonomura *et al*., 2004).

The phosphorylation of histone H2AX at leptotene in the male mouse was found to be an accurate marker for SPO11-dependant DSB formation, as phosphorylation occurs at the sites of DSB formation (Chicheportiche *et al*., 2007). A subsequent time-course study revealed a delay between the association of AtSPO11-1 with the chromatin, and DSB formation and hence, subsequent AtH2AX phosphorylation, providing evidence in supporting the theory that DSB formation is delayed when SPO11 associates with DNA (Keeney, 2001).

SPO11 forms DSBs using a nucleophilic mechanism, to produce a 3' hydroxyl break. This 3' end remains covalantly bonded to SPO11 (**Figure 1.7**) at the 5' end of the DNA break (Keeney, 2001). It was determined that a tyrosine-135 residue of yeast SPO11, has a catalytic function in the formation of DSBs (Diaz *et al*., 2002). Later studies found that both AtSPO11-1 and AtSPO11-2, harbour vital catalytically active tyrosine-103 and tyrosine-124 residues respectively, and may function as a heterodimer in the formation of DSBs in *Arabidopsis* (Hartung *et al*., 2007). A primer directed mutagenesis in which tyrosine (Tyr) was replaced by phenylalanine (Phe) in both proteins, led to a reduction in complementation (Hartung *et al*., 2007), and evidence in support of the multimeric association of SPO11 heterodimers before the formation of DSBs was found in studies involving yeast (Maleki *et al*., 2007).

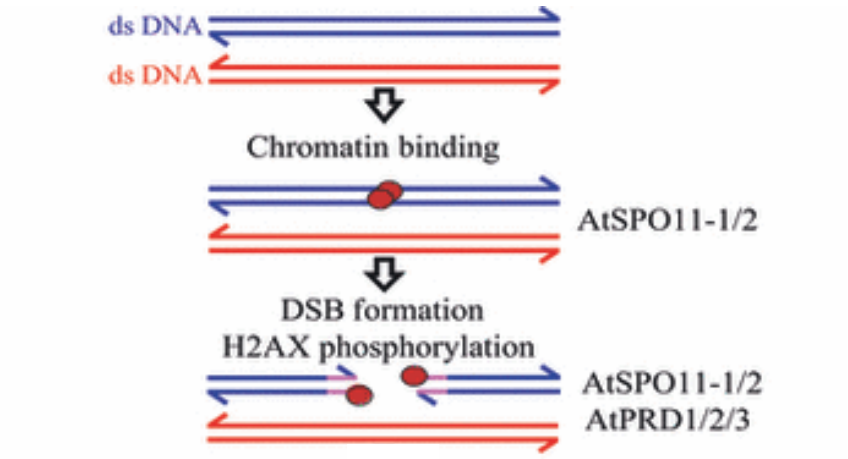


Figure 1.7: The binding of AtSPO11 to ds DNA and the formation of DSBs, the sites of which are marked by H2AX phosphorylation (taken from Osman *et al*., 2011).

1.7.2 DSB repair and removal of SPO11

Once formed, the 5' end of the DSB undergoes further processing steps, leading to strand resection which yields a 3' single stranded DNA (ssDNA). This processing step also removes protein SPO11 (**Figure 1.8**).

Both processes are carried out by the interaction of two highly conserved multi-protein complexes, MRX/MRN and SAE2 (budding yeast)/CtIP (human)/COM1 (*Arabidopsis*). It is thought that the MRX/MRN complex is involved in the regulation of DNA end processing, whereas SAE2/CtIP/COM1 functions in partnership with the MRX complex to activate (Mimitou and Symington, 2009) the 3'-5' exonuclease activity of MRE11 (Trujillo and Sung, 2001), to trim the ends of the DSBs.

The second step may involve a redundant complex, which excises long sequences of DNA to form 3' single-stranded DNA. It is thought that this step is dependant on two possible pathways in yeast. One is a pathway involving the helicase Sgs1 and the nuclease Dna2, whereas the other pathway involves the exonuclease EXO1 (reviwed by Mimitou and Symington, 2009).

Initially, the covalently bound SPO11 must be cleaved off the DSB end to allow processing by 5'-3' resection. The generation of a separation-of-function *RAD50* and *MRE11* alleles in yeast, led to a significant accumulation of unresected DSBs that were still bound to SPO11. This suggested that MRE11 and RAD50 function in partnership (**Figure 1.8**). Rad50 belongs to the structural maintenance of chromosomes (SMC) family of proteins (de Jager *et al*., 2001). Further, a proposed MRE11-Rad50-XRS2/NBS1 (MRX/MRN) multi-protein complex, is involved in the processing of meiotic DSBs (Alani *et al*., 1990; Cao *et al*., 1990; Tsubouchi *et al*., 1998; Nairz and Klein, 1997) in which RAD50 and XRS2/NBS1, complement the exonuclease activity of MRE11 (Carney *et al*., 1998; Desai-Mehta *et al*., 2001). The human orthologue of yeast XRS2 is NBS1 (Mimitou and Symington, 2009) and the *Arabidopsis* homologue is AtNBS1 (Tsukamoto *et al*., 2005).

Further research was carried out into the *Arabidopsis* homologues, AtMRE11 and AtRAD50 which are involved in the repair of somatic DNA (Puizina *et al*., 2004), and it was observed that *Atmre11* and *Atrad50* mutants exhibited chromosomal asynapsis during meiosis (Puizina *et al*., 2004). Earlier in vitro studies showed that AtMRE11 and AtRAD50 interact (Daoudal-Cotterell *et al*., 2002).

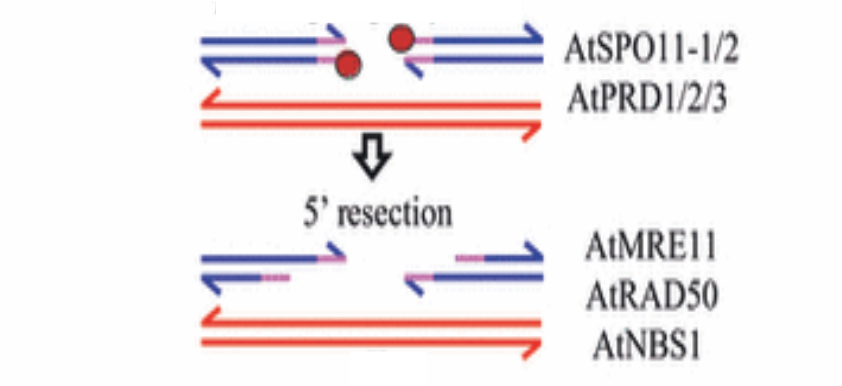


Figure 1.8: The processing of the DSBs, the removal of AtSPO11 and single-strand end resection (taken from Osman *et al*., 2011).

1.7.3 The initiation of strand exchange

The completion of DBS processing to form 3'-SSDNA tails, is followed by the sequential formation of a strand exchange multi-protein complex. The formation of this multi-protien complex involves the loading of RecA-related recombinases, forming a presynaptic nucleoprotein "scaffold" (Osman *et al*., 2011), which goes on to invade the double stranded DNA of the homologue to carry out a search for homologous sequences.

It is thought that two recombinases, RAD51 (Keeney, 2001) and DMC1 (Neale and Keeney, 2006) working as interacting partners, are responsible for the progression of meiotic recombination (**Figure 1.9**). In most Eukaryotes, RAD51 and DMC1 are orthologs of the bacterial protein, RECA, however RAD51 is involved in both mitosis, where it controls strand invasion amongst sister chromatids and in meiosis, where it functions in association with DMC1, to control recombination between homologues (Bishop *et al*., 1992; Neale and Keeney, 2006). DMC1 only exhibits a meiotic function which mediates inter-homologue recombination (Bishop *et al*., 1992).

Studies reported that *Arabidopsis* harbours one *DMC1* gene, *AtDMC1*, which was initially amplified using degenerate primers based on the yeast *DMC1* gene and sequenced (Klimyuk and Jones, 1997). It was found that the *AtDMC1* gene contains 15 exons and 14 introns, and RNA *in situ* hybridisation showed that it is exclusively expressed in the pollen mother cells (PMCs) in the anthers and embryo sac mother cells (EMCs) (Klimyuk and Jones, 1997). The significance of the meiotic role of AtDMC1 was confirmed in mutants lacking AtDMC1, which were void of COs and exhibited random chromosomal segregation (Couteau *et al*., 1999).

In stark contrast, it was found that *Arabidopsis* possesses six *RAD51* paralogues (*AtRAD51*, *AtRAD51B*, *AtRAD51C*, *AtRAD51D*, *AtXRCC2* and *AtXRCC3*). However, studies investigating the DNA repair response in T-DNA insertion mutant lines in response to DNA damage, found

that only *AtRAD51*, *AtRAD51C* and *AtXRRC3* are involved in meiosis (Bleuyard *et al*., 2005). In addition, studies showed that there is an interaction between AtRAD51C and AtXRCC3, including an interaction between AtRAD51 and AtRCC3 (Osakabe *et al*., 2002), demonstrating that they may function as a complex as further analysis demonstrated that the mutation of *AtRAD51* or *AtXRCC3*, resulted in an accumulation of un-repaired AtSPO11-induced DSBs (Bleuyard *et al*., 2004). The barley homologs HvRAD51 and HvDMC1 share a 92% and 53% polypeptide sequence match with AtRAD51 and AtDMC1, respectively, and localise onto mature regions of the chromatin axis to mediate downsteam recombination events (Higgins *et al*., 2012; discussed in **Section 1.15**).

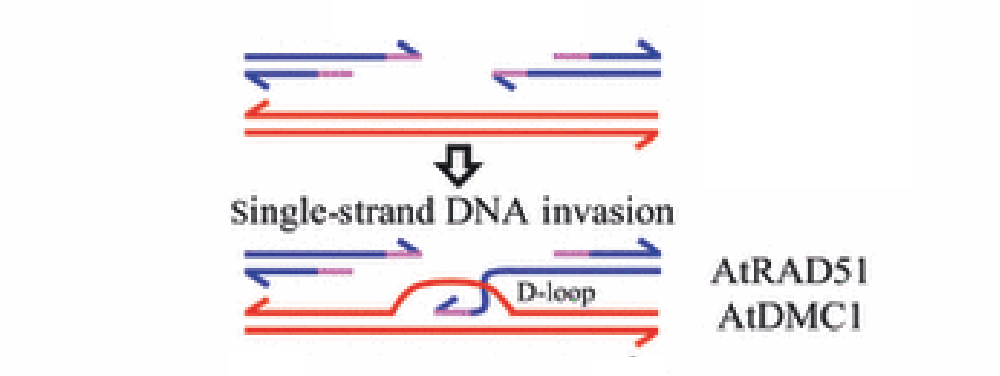


Figure 1.9: AtDMC1 and AtRAD51 mediated single-strand DNA invasion (taken from Osman *et al*., 2011).

1.7.4 The initiation of strand exchange: the role of Replication protein A

The ssDNA binding heterotrimeric protein, replication protein A (RPA) binds to the ssDNA and influences the activity of the strand exchange proteins. This protein is highly conserved and its largest subunit has been shown to be encoded by the gene, *RFA1*, in *S. cerevisiae* whereas in mammals, it is encoded by the gene, *RPA1*. The *Arabidopsis* genome encodes five paralogues of *RPA1*, including two paralogues of *RPA2* (which encodes a second subunit of RPA) (Shultz *et al*., 2007). The rice genome encodes three copies of *RPA1* (Ishibashi *et al*., 2006).

Studies in *S. cerevisiae* have demonstrated that RPA controls the step-wise accumulation of RAD51 filaments on ssDNA (San Filippo *et al*., 2008). It was shown to promote the step-wise assembly of the presynaptic filaments by removing secondary DNA structures and sequestering the ssDNA strands (Sugiyama *et al*., 1997). A stoichiometric analysis showed that RPA mediates RAD51 filament formation at an optimum level where there are 20 to 30 nucleotides of ssDNA per RPA heterotrimer (Sugiyama *et al*., 1997). However, it must be noted that due to the high affinity of RPA for ssDNA, there is a competition with the recombinases that form the presynaptic filament, leading to empedement of filament formation (Haruta *et al*., 2006).

Several recombination mediators have been identified that overcome the inhibitory function of RPA, allowing the completion of filament formation. An investigation was carried out into the function of the *RAD52* group of genes (*RAD50*, *RAD51*, *RAD52*, *RAD54*, *RDH54*/*TID1*, *RAD55*, *RAD57*, *RAD59*, *MRE11*, and *XRS2*). Most of the genes were required for repairing ionising-radiation-induced DNA damage in *S. cerevisiae*. However, the *RAD55* and *RAD52* gene products associate to form a heterodimer which acts as a mediator and has been shown to overcome RPA mediated inhibition, by promoting RAD51-mediated strand invasion (Sung, 1997). A confirmatory investigation showed that when ssDNA was incubated *in vitro* with RAD51 and RPA, there was a decrease in the efficiency of strand exchange however, the

addition of RAD52 protein (purified from *S. cerevisiae*), restored the efficiency of RAD51-mediated strand exchange (Sung , 1997).

In addition, another group of accessory proteins, RAD54 and RDH54/TID1 function in conjunction with the RAD52 epistasis group (RAD52, RAD55 and RAD57) in increasing the efficiency of RAD51 mediated stranded exchange. RAD54 and RDH54/TID1 belong to the SWI2/SNF2 superfamily of proteins. This group of proteins is characterized by dsDNA-dependant ATPase, DNA super-coiling, DNA translocase and chromatin modifying activities (Symington, 2002). The *Arabidopsis* genome encodes a *SW12*/*SNF2* family, which includes a *RAD54*-like gene (*AtRAD54*) (Shaked et al., 2006) which is an orthologue of the *S. cerevisiae RAD54* gene (Klutstein *et al*., 2008).

Confirmatory studies in *S. cerevisiae*, showed that the RDH54/TID1 complex has a role in the mediation of inter-homologue recombination as *rdh54* and *rad54 rdh54* double mutants, failed to produce viable budding products when the tetrads were analysed (Shinohara *et al*., 2003). The same investigation showed that RDH54/TID1 may be involved in the DMC1-dependant pathway (Shinohara *et al*., 2003).

In most Eukaryotes, RAD51 and DMC1 are orthologs of the bacterial protein, RecA, however RAD51 is involved in both mitosis, where it controls strand invasion amongst sister chromatids and in meiosis, where it functions in association with DMC1, to control recombination between homologues (mentioned earlier in **Section 1.7.3**: Neale and Keeney, 2006). Further studies in *S. cerevisae* have shown that proteins HOP1, MEK1 and RED1, form a complex which has a role in "influencing" recombination between homologues by reducing the mitotic function of intersister repair by RAD51 (Hollingsworth and Ponte, 1997). Further investigations showed that RAD51 functions by interacting with DMC1, to initiate recombination between homologues (Neale and Keeney, 2006).

1.7.5 The role of ASY1 in strand exchange

In *Arabidopsi*s the protein ASY1, comprises a HORMA domain that is homologous to the HORMA domain found in yeast HOP1 (Caryl *et al*., 2000). This domain was found to be located near to the N-terminal domain using a BLAST database search (Hollingsworth *et al*., 1990). Investigations using immunolocalisation techniques have been used to visualise the spatial and temporal arrangement of ASY1 during meiosis in *Arabidopsi*s (Armstrong *et al*., 2002), barley (Higgins *et al*., 2012) and wheat (Martin *et al*., 2014). The analysis of *Arabidopsis* and barley meiocytes revealed that ASY1 is present as distinct foci at meiotic interphase (G2) along the chromatin structure. The distribution of ASY1 became more continuous at leptotene and at zygotene, the signal spanned the full length of the chromatin (Armstrong *et al*., 2002; Higgins *et al*., 2012). As meiosis progressed and the homologous chromosomes began to desynapse, the ASY1 signal began to disappear. At diplotene, the signal disappeared in *Arabidopsis* (Armstrong *et al*., 2002) but persisted as very faint short stretches in barley (Higgins *et al*., 2012). In addition, *Brassica oleracea* also expresses a protein which is homologous to ASY1 which is found in *Arabidopsis.* The antibody that was used to detect ASY1 in *Arabidopsis* was successfully used to detect ASY1 in *B. oleracea*, and when the genes *AtASY1* and *BoASY1* were compared, it was found that the cDNA was 87% identical (Armstrong *et al*., 2002).

ASY1 is required for the successful synthesis of the synpatonemal complex as *ASY1* null mutant *Arabidopsis* lines, displayed asynapsis and a reduction in the frequency of chiasmata formation (Ross *et al*., 1997). Further confirmatory tests regarding the function of ASY1 showed that the localisation of ASY1 was independent of DSB formation (Sanchez-Moran *et al*., 2007). An immunolocalisation technique was used to visualise AtSPO11-1 in mutant *asy1 Arabidopsis* meiocytes, and it found that the distribution of AtSPO11-1 was the same as that in the wild-type. In addition, the treatment of *asy1* lines with the DSB inducing drug cisplatin, did

not result in an increased crossover frequency, showing that DSB formation was not affected in *asy1* (Sanchez-Moran *et al*., 2007). Further analysis showed that although DSB formation took place normally in *asy1*, there was a reduction in the chiasma frequency at metaphase I (Sanchez-Moran *et al*., 2007). This conclusion was achieved by using anti-DMC1 and anti-RAD51 antibodies to decipher the location of the proteins DMC1 and RAD51, respectively. The treatment of wild-type nuclei 12hrs after a BrdU pulse-labelling, showed a signal compromising over fifty foci for every meiocyte. However, no foci were present in *asy1* at the same time point (Sanchez-Moran *et al*., 2007). This result showed that ASY1 is has an essential role in the formation of crossovers in meiosis. It was initially thought that ASY1 was a component of the axial and lateral elements however, further investigations utilising electron microscopy revealed that it is only associated with chromatin that is adjacent to the axial/lateral elements (Armstrong *et al*., 2002).

After the strand exchange protein complex is established, it begins a 'search' for a homologous base sequence along the length of one chromatid of the homologous chromosome and then 'invades' that region of the sequence via complementary base pairing (reviewed by Gerton and Hawley, 2005). This leads to the formation of a region of DNA, where the invading ssDNA strand is base paired with a complementary sequence of the ssDNA strand of the donor strand, leading to an exchange of strands between the homologues. The exchange of strands leaves the end of the donor strand in a 'displaced' configuration, which goes on to form a signature structure called a 'D-loop'. This 'D-loop' undergoes stabilisation by the helicase MER3 to form a single end intermediate (SEI), allowing DNA synthesis to occur at the invading ends to 'replenish' the original bases that were lost during the nucleolytic processing stage (Hunter and Kleckner, 2001). This step also leads to a ligation between the replenishing 3' ends and the 5' ends, leading to the second strand exchange event, forming a double Holliday junction (DHJ). Each Holliday junction acts as a site where crossing over occurs.

1.7.6 The meiotic role of ASY3

In *Arabidopsis* a pilot studied revealed the expression of an 88 KDa protein (AtASY3) exclusively in the meiotic tissue. Upon further investigation it was found that the proteins C-terminal coiled-coil domain shared a 26.6 % homology to that of the meiotic gene *PAIR3* product in rice, suggesting that it may have a functional role in meiosis (Ferdous *et al*., 2012).

To elucidate the function of AtASY3, immunolocalisation studies were undertaken using a T-DNA insertion mutant (*Atasy3-1*) and it was found that no foci appeared on the meiotic chromatin spread. Analysis of the localisation of ASY1 at late G2 and leptotene was indistinguishable from wild-type however, upon studying subsequent stages the ASY1 foci failed to linearise. To the contrary, the localisation of AtASY3 was identical to that observed in wild-type. The same result was observed in yeast where HOP1 loading is dependant on RED1, however the reverse is not so (Smith and Roeder, 1997). In addition to this, cytological analysis revealed that RED1 and HOP1 co-localise to un-synapsed regions of chromatin and hence, precede ZYP1 loading, with alternating regions of low/high abundance of RED1/HOP1 at pachytene (Borner *at al*., 2008). Previous to this, studies on *red1* knockout mutants showed that HOP1 only localised to chromatin in the presence of RED1 and co-localised with RED1 in wild-type (Smith and Roeder, 1997).

A co-immunoprecipiation study in *Brassica* gave evidence in support of BoASY1 and BoASY3 existing as complex and hence interacting. Further evidence in support of this theory that was carried in an experiment showing that both proteins directly interact by co-expressing both proteins as cDNA fusion constructs in yeast and under high levels of nutrient stress, only yeast harbouring both cDNA's exhibited growth (Ferdous *et al*., 2012).

1.8 The existence of two crossover pathways: the role of the ZMM group of proteins

Generally, COs exhibit a nonrandom distribution where multiple COs on the same chromosome are regularly spaced. This is known as CO interference, where one CO interferes with and reduces the probability that another CO will form in an adjacent region (Jones and Franklin, 2006), giving rise to the class I pathway of meiotic recombination. Further, genetic studies have provided evidence in support of a second pathway of meiotic recombination, where the COs do not exhibit interference or maintain the obligate CO. This is called the class II pathway (Higgins *et al.*, 2004).

Studies in *S. cerevisiae* have revealed the existence of a group of proteins that are vital for the progression of the class I pathway of meiotic recombination, called the ZMM group of proteins (ZIP1, ZIP2, ZIP3, ZIP4, MSH4, MSH5 and MER3) (Borner *et al.*, 2004). Studies in *S. cerevisiae* mutants that lacked proteins of the ZMM group were analysed and it was found that crossover and SC formation was defective (Borner *et al.*, 2004). Subsequent investigations in *Arabidopsis*, led to the discovery of the ZMM homologues *AtMER3/RCK, AtMSH4/AtMSH5, AtZIP3, AtZIP4* and *AtZYP1a/AtZYP1b* (reviewed by Luo *et al*., 2014).

Further studies were conducted to elucidate the functions of the meiosis-specific proteins, MSH4 and MSH5, which have a role in crossover formation in Eukaryotes (Ross-Macdonald and Roeder, 1994). Both proteins are homologs of MutS, which has been found to have a central role mismatch repair in *Escherichia coli* (Ross-Macdonald and Roeder, 1994). MutS acts as a subunit of the mismatch repair (MMR) pathway by binding to mismatched nucleotides. However, both MSH4 and MSH5, are not involved in this pathway. Studies have shown that both proteins are involved in the recombination pathway, as studies of MSH4 mutations in mice, exhibited chromosome asynapsis, and MSH4 mutations in yeast exhibited a reduced crossover frequency (Ross-Macdonald and Roeder, 1994). Investigations with an *Arabidopsis* homolog, AtMSH4 (Higgins *et al*., 2004), utilised a T-DNA insertional mutant

(*AtMSH4*) and it was found that the crossover frequency was reduced to approximately fifteen percent compared to that of the wild type, including greatly reduced fertility. This investigation also helped to "temporally" place the function of AtMSH4 because, despite the fact that the later meiotic stages were abnormal in *Atmsh4*, DSB formation occurred normally, placing the function of AtMSH4 after DSB formation. Immunolocalisation studies also showed that AtMSH4, initially localised as discrete foci with meiotic chromosomes at leptotene and then disappeared at late pachytene (Higgins *et al*., 2004). The same investigation also provided evidence in support of two crossover pathways in *Arabidopsis* as the *Atmsh4* mutants exhibited residual chiasmata formation. But, the chiasmata were randomly distributed and this put forward evidence in support of a chiasma formation pathway that is independent of AtMSH4. Confirmatory investigation in *S. cerevisiae*, elucidated two possible pathways, the class I and class II recombination pathways. In the class I event, crossovers show interference and are controlled by a MSH4/5 heterodimer, however in the class II event, crossovers do not show interference and are controlled by a complex comprised of MMS4/MUS81 (de Los Santos *et al*., 2003). Recently it was found that AtMSH5, another homologue of the MutS family works in partnership with AtMSH4 in the class I crossover pathway (Higgins *et al*., 2008). Immunolocalisation studies revealed that AtMSH5 and HvMSH5 initially appear as discrete foci at leptotene, which are present through zygotene and pachytene in *Arabidopsis* and barley, respectively (Higgins *et al*., 2008; Higgins *et al*., 2012). The foci completely disappear at late pachytene (Higgins *et al*., 2008). Also, HvMSH4 and HvMSH5 share a polypeptide sequence match with AtMSH4 and AtMSH5, respectively (Higgins *et al*., 2012). To investigate the inter-dependance of AtMSH4 and AtMSH5, co-immunolocalisation studies were carried out on both of the wild-type proteins in both *Atmsh5* and *Atmsh4* mutants. The cytological study of both mutants revealed that none of the wild-type proteins were detected (Higgins *et al*., 2008), supporting the theory that the loading of both AtMSH5 and AtMSH4 is dependent on each

other and that they are functional as a heterodimer, mimicking a sliding clamp that holds the homologues together (Snowden *et al*., 2004). The cytological study of meiocytes harbouring *Atmsh5-1* and *Atmsh5-2*, led to the finding that the later stages of meiosis (after pachytene) were defective. For example, there was a significant decrease in the frequency of chiasma at metaphase I, as exhibited by the presence of univalents.

Studies have shown that MER3 in *S. cerevisae*, is a DExH-box-type DNA helicase that unwinds DNA in the 3′ to 5′ direction (Nakagawa *et al.*, 2001). The *in vitro* analysis of MER3 protein purified from *S. cerevisiae*, showed that it had ATPase activity when it was incubated with single stranded or double stranded DNA. However, MER3 only exhibited this ATPase activity in the presence of RPA, emphasising its role in meiosis (Nakagawa *et al.*, 2001). Further *in vitro* studies showed that DNA synthesis in the invading strand of the D-loop is greatly reduced in *mer3* mutants (Terasawa *et al.*, 2007). In this study, wild-type and *mer3*Δ cells were subjected to a BrdU pulse after which the DNA was then purified and then incubated with anti-BrdU antibody. The detection of BrdU labeled DNA showed that long DNA tracts were present in *WT* but absent in *mer3*Δ (Terasawa *et al.*, 2007).

The *Arabidopsis* homologue, AtMER3 (sometimes called ROCK-N-ROLLERS [RCK]), exhibits a 51% similarity to MER3 in *S. cerevisae*, and the study of T-DNA insertional mutants of this gene resulted in a significant reduction in fertility, coupled with a reduction of bivalent formation at diakinesis (Chen *et al.*, 2005). The same study also showed that the gene is mostly expressed in the meiocytes.

1.8.1 An introduction to the role of the ZIP proteins in chromatin synapsis

The synapsis of homologous chromosomes during *prophase* of the first meiotic division, is initiated and completed by the step-wise alignment of a structure called the synaptonemal complex (SC). Early studies using electron microscopy (Watson, 1952) yielded evidence in

support of paired filament like structures along the length of the chromosomes in the spermatocytes of crayfish and grasshopper. Additional tests conducted on crayfish spermatocytes suggested that this structure runs perpendicular to the chromatin axis (Moses, 1956) and later investigations using the same technique in the same year confirmed the existence of the SC in vertebrae spermatocytes (cats, humans and pigeons) as a highly dense central structure, with the centre of this structure interlaced with parallel light and dark bands perpendicular to the length of the dense central structure (Fawcett, 1956).

Later investigations in yeast suggested that ZIP1 is a structural component of the transverse filament as mutations that increase the length of the coiled-coil domain of ZIP1, lead to an increased width of the SC (Sym and Roeder 1995). Later, confirmation of the role of ZYP1 in plants was demonstrated by AtZYP1 in *Arabidopsis* (Higgins *et al.*, 2005), ZEP1 in rice (Wang *et al*., 2010), ZmZYP1 in maize (Golubovskaya *et al*., 2011) TaZYP1 in wheat (Khoo *et al*., 2012) and HvZYP1 in barley (Barakate *et al*., 2014). Homologs of this protein have also been observed in *C. elegans* (SYP1) as demonstrated by the screening of *ZIP1* mutant lines which lacked SC formation (Sym *et al*., 1993). In *Drosophila*, C(3)G (crossover suppressor on 3 of Gowan) has been established as a homolog. The analysis of *C(3)G* strains led to the observance of failed SC formation and later studies in barley duplicated this phenotype by the analysis of *ZYP1* RNAi lines (Barakate *et al*., 2014). Furthermore, the analysis of the structure of the protein encoded by the C(3)G gene in *Drosophila* showed that it is similar to SC proteins in mammals and yeast. Furthermore, immunolocalisation studies of the protein showed that the protein aligns itself transversely along the length of the synapsed chromosomes (Page and Hawley, 2001) in agreement with previous studies conducted in yeast (Sym and Roeder 1995). Finally, the mammalian equivalent of ZIP1 is called SCP1. Studies have revealed a high level of amino acid sequence conservation amongst SCP1 proteins across mammalian species. The cDNA encoding rat SCP1 (Meuwissen *et al*., 1997) was isolated and it was found that the

resulting polypeptide (rnSCP1) shared a 75% sequence homology to that for the human homologue (hsSCP1).

Even though there is a high level of polypeptide sequence homology amongst mammals, this is not the case between species despite the fact that they share identical structural/function properties. For example, there was a high degree of sequence conservation of the predicted amino acid sequence of TaZYP1 in wheat with ZEP1 in rice (80%) and ZmZYP1 in maize (75.9%), both of which are close relatives of wheat, but this sequence conservation was greatly reduced in both AtZYP1b and AtZYP1a in *Arabidopsis* (40% and 39%, respectively) (Khoo *et al*., 2012).

Antibodies complimentary to specific domains of ZIP1 were used and it was found that the N-terminal domains positioned themselves along the centre of the SC in contrast to the C-terminal domains, which tethered themselves along the length of the lateral element (Dong and Roeder, 2000). Previous to this, studies carried out on mutations that increased/decreased the length of the coiled coil polypeptide chain of Zip1, resulted in a respective increase/decrease in thickness of the SC. This suggests that each ZIP1 molecule is positioned perpendicular to the axial elements (Tung and Roeder, 1998). The orientation of the ZIP1 molecules in the SC were determined by mapping the protein three domains using immunogold labelling. Anti-ZIP1-N antibodies localized at the centre long the length of the SC, and the anti-ZIP1-C antibodies localised along the length of the lateral elements. Anti-ZIP1-coil antibodies localized in between the central and lateral elements. This suggests that the ZIP1 molecules traverse the length of the SC, lying side-by-side (Dong and Roeder, 2000). The arrangement of the monomers in register was confirmed with truncated ZIP1 lacking the C-terminus and it was observed that the dimer appeared as a rod with a single globular structure at only one end, instead of a structure with globular structure at both ends which would be indicative of and antiparallel arrangement. In addition to this, it was found that purified ZIP1 proteins formed

dimers and tetramers in vitro suggesting that dimerisation is the mechanism by which adjacent lengths of polymerised ZIP1 align themselves along the length of chromatin (Dong and Roeder, 2000).

The investigation of an RNA interference (RNAi) line for ZYP1a and ZYP1b in *Arabidopsis* led to a reduction in fertility and a 6 hour delay in the meiotic pathway, including incomplete synapsis at pachytene. In both cases however, AE formation occurred as in *wild-type* allowing from the alignment of homologous chromatin axes. Even though there was a reduction in chiasma frequency at metaphase I, there was also the appearance of multivalents which consisted of homologous and non-homologous chromosome pairing (Higgins *et al.*, 2005). To decipher if a loss of or down-regulation of ZYP1 affected the recombination pathway, MLH1 was studied and it was found that there was a significant reduction in the number of foci compared that in the *wild-type* even though it loaded normally along the chromatin showing that the ZIP1 mutation does not block the progression of meiosis but instead as previously mentioned, caused a delay (Higgins *et al.*, 2005).

Immunolocalisation studies In *Arabidopsis* (Higgins *et al.*, 2005) and barley (Higgins *et al.*, 2012) have demonstrated that ZYP1 localises onto chromatin as discrete foci at leptotene. As meiosis progresses through to the onset of early zygotene, the foci begin to linearise until at pachytene, a complete linear signal spanning the entire length of the chromatin is observed, marking complete synapsis (Higgins *et al.*, 2005; Higgins *et al.*, 2012).

The step-wise alignment of the axial elements which leads to synapsis is caused by the formation of transverse filaments (TFs) until complete synapsis is achieved at pachytene. The join between the TFs forms a linear structure called the central element as synapsis progresses and the three structures (TFs, AEs and central element) together, form what is called a tripartite structure. At the beginning of diplotene, the SC depolymerises, allowing for the separation of the paired homologous chromosomes.

In *S. cerevisiae*, ZIP3 is a small ubiquitin-like modifier (SUMO) ligase protein, that controls the step-wise polymerisation of ZIP1 to form the transverse element of the SC. Studies have shown that it works in partnership with a proline isomerase protein, Fp3 (MacQueen and Roeder, 2009). Interestingly, it was found that the presence of either the *fpr3* or *zip3* mutation, led to antagonistic effects on SC formation, where the *fpr3* mutation led to a reduction in SC formation among the centromeric regions, whereas the *zip3* mutation promoted SC formation (MacQueen and Roeder, 2009). This puts forward evidence in support of a checkpoint, where meiotic recombination can only occur between homologues, as the investigation demonstrated that the combined absence of Fpr3, and ZIP3, led to SC formation on chromosomes even when non-homologues were paired.

In *S. cerevisiae*, ZIP2 and ZIP4, act downstream of Fpr3 and ZIP3, to promote the polymerization of ZIP1 along the length of the chromosomes (Tsubouchi *et al.*, 2006). In *zip4* null mutants, ZIP1 fails to polymerize along the length of the chromosomes. In *wild-type*, green fluorescent protein (GFP) tagged ZIP1 initially appears as discrete foci on chromosomes from leptotene, before SC polymerization to early zygotene and becomes increasingly continuous in appearance as zygotene progresses due to polymerization, until the signal is completely continuous at pachytene bringing the homologues into close proximity (Borner *et al.*, 2004). However, in *zip4*, it was observed that ZIP1 initially localizes as discrete foci just as in the *wild-type*, but the signal remains punctuate (Tsubouchi *et al.*, 2006). Studies using the same mutants showed that ZIP2 and ZIP4 are interdependent on each other and may function as a complex. An additional observation led to the finding that ZIP3 localises onto the chromosomes in the presence of either, *zip4 and zip2, or both*, showing that ZIP2 and ZIP4 function downstream of ZIP3. Furthermore, the failure of ZIP2 and ZIP4 to co-localise in *zip3* mutants, showed that the ZIP3 is required to promote the association of the ZIP2/ZIP4 complex with chromosomes (Tsubouchi *et al.*, 2006). A T-DNA insertional screen in meiotic mutants

led to the identification of the *Arabidopsis ZIP4* homologue, *AtZIP4*, however, further analysis found that unlike *S. cerevisiae*, ZIP1 polymerisation was not abrogated in *Atzip4* mutants (Chelysheva *et al.*, 2007).

Further analysis in *Arabidopsis* has shown that at leptotene, AtZYP1 loading occurred at the same time as AtMSH4/AtMSH5 before the formation of the SC, suggesting that it may have a role in recombination (Higgins *et al.*, 2005). Furthermore, the analysis of mutants of the rice orthologue *ZEP1*, led to an increase in chiasma frequency (Wang *et al.*, 2010; mentioned later in **Section *1.17.3***).

1.8.2 The role of MLH3 in the meiotic pathway

Traditionally, the scoring and localisation of CO has been undertaken by counting the number of chiasmata, counting the late recombination nodules (LNs) or the immunofluorescence tagging of constituents proteins of the LNs. The scoring of chiasmata at metaphase I using light microscopy has been used often in species with large genomes however this method is less amenable in organisms with comparatively smaller genomes, leading to potential underestimation of the CO frequencies. Early findings in *Drosophila* demonstrated that recombination nodules are closely associated with the SC at pachytene and that their distribution and abundance correlated closely that that of the distribution and abundance of crossovers (Carpenter, 1975), hence it was postulated that these structures may have a functional role in the control of chiasma formation. In addition, it was found that if two nodules localised on the same chromosome arm, they localised far apart in support of the theory of positive chiasma interference (Carpenter, 1975). Recombination events are carried out by various proteins in the recombination nodules (RNs), which are comprised of early nodules which are associated with chromatin from leptotene to pachytene and late nodules (LNs) which are associated from pachytene to diplotene (Anderson and Stack, 2005). Later

studies demonstrated that roughly 70% of LNs in tomato were immuno-labelled with MLH1 (Lhuissier *et al*., 2007) and that the foci were evenly distributed supporting the notion that the LNs that are labelled, exhibit intereference and hence belong to the class I recombination pathway and the non-labelled LNs belonged to the class II pathway, which displayed a less evenly spaced distribution of LNs. It is assumed that unlike class I crossovers, class II crossovers don't diplay interference (de los Santos *et al*., 2003). The highly ordered and even distribution, and presence of obligate COs have been demonstrated to be part of the same class I mechanism of CO formation as all three consequences are absent in the case of any defects in the class I pathway (Hillers, 2004), and such COs were only associated with MHL1 foci. Similarly in *Arabidopsis*, MHL1 foci have been found in association with chromatin at late prophase in studies in conjunction with ZYP1 detection to mark CO sites (Higgins *et al*., 2005).

1.8.3 MLH1 positive and MLH1 negative late nodules

The prokaryotic mismatch repair (MMR) MutHLS system is involved in post-replication DNA repair during mitosis (Dion *et al.,* 2007). It was initially studied in *Escherichia coli*, when it was given the term MutHLS because it comprises three main constituent proteins: MutH, MutL and MutS, where MutS and MutL function as dimers (Ban and Yang, 1998b).

The eukaryotic MutL homologues (MLH) have an important role in meiotic recombination. In humans, four proteins comprise this homologous system (MLH1, MLH3, PMS1 and PMS2) to form heterodimers which are coordinated around a monomeric MLH1, which acts as a molecular anchor (Lipkin *et al.,* 2000). The proteins always associate in the following combination: MLH1/PMS2, MLH1/PMS1 and MLH1/MLH3 (Marti *et al.,* 2002). The *Arabidopsis* homologues, AtMLH1 and AtMLH3 are involved in meiosis (Dion *et al.,* 2007). But, AtPMS1 is involved in DNA MMR and the reduction of recombination between

homologous sequences in somatic cells (Li *et al.*, 2009). The study of *Atmlh3* mutants also revealed that AtMLH1 fails to localise on chromosomes, leading to a significant reduction in chiasma formation (Franklin *et al.*, 2006).

Evidence so far has led to the suggestion of the existance of MHL1 (class I) and non-MLH1 (class II) LNs and experiments in yeast have pointed to the existance of class I COs corresponding to MLH1-positive COs (Argueso *et al*., 2004). In this study, various knockdown mutants revealed the role of MUS81/MMS4 complex in the class II meiotic pathway, and the two separate complexes MSH4/MSH5 and MLH1/MLH3 occupying the class I pathway. So far previous investigations have shown that the knockout of MSH4 leads to reduction in fertility and reduced CO frequency leading to unbalanced chromosome segregation (Ross-MacDonald and Roeder, 1994). Tests involving the search for mutant genes in exhibiting various defects in the meiotic pathway yielded the identification of MSH5 which phenocopied the the deliterious effects of *msh4* (Ross-MacDonald and Roeder, 1994) and studies using *msh4/msh5* double knock-outs revelead that both genes are epistatic to one another (Hollingsworth *et al*., 1995). Secondly, an *MLH1* knockout in yeast has shown a defect in CO formation and mis-match DNA repair. This result was phenocopied in either *msh4*/*msh5* knockout strains and when *mlh1*/*msh4* double mutants were analysed, the same phenomenon was observed, including a loss of intereference (Argueso *et al*., 2004). This suggests that MLH1 and MSH4/MSH5 belong to the same functional (class I recombination) pathway (Hunter and Borts, 1997). In addition, it has been shown that MLH1 and MLH3 act together to promote CO formation. An MLH3 mutant exhibited a significant reduction in the mean CO frequency in yeast and co-immunoprecipitated with MHL1, including a failure of MLH1 localisation to the chromatin when mutant lines of both proteins were studied. The study also showed that MLH1 co-precipitated with and hence, possibly interacted with MLH2 amd PMS1 (Wang *et al*., 1999). Recombination between the *HIS4:LEU* markers was examined in tetrads

in each or both *mlh1* and *mlh3* mutants and it was found that there was a marked reduction in the map distance in both the *mlh1* and *mlh3* mutants and marked reduction in chiasma frequency, which supports the possibilty that MLH1 and MLH3 function as a heterodimer and have a crucial role in the control of CO formation. In support of this, it was previously shown that *mlh1* knockout mice were void of DNA mismatch repair and homozygous males failed to generate viable sperm due to the pausation of the meiotic pathway at pachytene (Edelmann *et al*., 1996).

PCR analysis in *Arabidopsis* indicated that MLH1 is present in all tissue whereas MLH3 is exclusively expressed in the buds (Jackson *et al*., 2006). Secondly, PMCs at various stages of the meiotic pathway were isolated and subjected to immunolocalisation studies and discrete MLH3 foci colocalise with MLH1 and initially appear at zygotene and gradually become most abundant at pachytene, represented by a mean number of 9.4 foci which is in agreement to previous studies which confirmed the the mean chiasma frequency as 9.86 in previous studies in the same species (Jackson *et al*., 2006). Hence, this information is in support of MLH1/MLH3 being a marker of the sites of chiasma formation during meiosis. The foci persist through diplotene/diakinesis and disappear at Metaphase I. The role of AtMLH3 in meiosis was determined by the study of to T-DNA insertion mutant lines (*Atmlh3-1* and *Atmlh3-2*) and there was a significant reduction in the mean number of seeds per silique when compared to the wild-type and cytological analysis revealed a significant reduction in chiasma frequency (univalents and hence, subsequent aneuploidy (Jackson *et al*., 2006).

Similar studies in Barley showed that the MLH3 mRNA transcript is highly abundant in the inflorescence (Phillips *et al*., 2013) and based on previous immunolocalisation studies in *Arabidopsis* (Jackson *et al*., 2006), MLH3 foci also appear at zygotene and become most abundant at pachytene however, the difference in this case is exhibited by a decrease in the number of foci at the onset of diplotene, followed by a complete loss of foci entering

diakinesis. The mean number of MHL3 foci per pachytene nuclei for the cultivar Bowman (14.2) (Phillips *et al*., 2013) as previously demonstrated in studies on *Arabidopsis* (Higgins *et al*., 2004, Jackson *et al*., 2006), also related to the mean chiasma frequency of 13.2 (Phillips *et al*., 2013).

1.8.4 The pachytene checkpoint

In the vast majority of Eukaryotes, the synapses of homologous chromosomes at pachytene, exhibits a checkpoint. For example, if *Drosophila melanogaster* meiocytes harbour any defects in the recombination or synaptic pathway, the meiotic pathway is halted at pachytene (the "*pachytene checkpoint*": Ghabrial *et al*., 1999). The gene *PCH2* in *S. cerevisiae*, encodes an AAA-ATPase that is involved in this checkpoint, and is crucial for the completion of the meiotic pathway (Segundo and Roeder, 1999). Recent studies in mice led to the discovery of the ortholog *Trip13*, as mice that lacked the product of this gene displayed the arrest of spermatogenesis at pachytene and a significant decrease in viable oocytes at the time of birth (Li and Schimenti, 2007).

1.9 The existence of two crossover pathways: the class II pathway of meiotic recombination

The formation of non-interfering COs occur via the class II pathway of meiotic recombination and account for roughly 15% of the type of crossovers that occur in *S. cerevisiae* (de los Santos *et al.*, 2003), and are dependent on the Mus81–Mms4 system. However, studies have shown that fission yeast is dependent on the Mus81-Eme1 system (de los Santos *et al.*, 2003).

Initially, the analysis of *Arabidopsis* genetic data suggested that atleast two possible meiotic recombination pathways to produce COs may exist (Copenhaver *et al.*, 2002). It was found that the crossover distribution in the tetrads of *Arabidopsis* differed from what was observed in

Drosophila and *Neurospora, and the* chi-square distribution could only fit the data if it was assumed that *Arabidopsis* had two separate pathways of meiotic recombination, where one of them seemed to exhibit no interference (Copenhaver *et al*., 2002).

Further evidence in support of this theory was the surprising observation of residual COs that formed in *Atmsh4* mutants, which were initially not expected to form. However, it was found that their numerical distribution fitted a Poisson distribution, which is consistent with a non-interference model (Higgins *et al.*, 2004).

The cytological analysis of AtMUS81 using an AtMUS81 antibody, showed that protein loading was dependent on DSB formation as discrete foci on class I recombination sites. However, in contrast to AtMLH1/3, which only associates with sites that progress via the class I recombination pathway, AtMUS81 also associated with other sites that appeared to progress via an non-class I recombination pathway (Higgins *et al.*, 2008).

Additional, Studies in *S. pombe* showed that the mutation of *MUS81* and the RecQ family helicase *SGS1*, led to cell death (Bastin-Shanower *et al.*, 2003), and later experiments showed that the same mutant phenotypes displayed an accumulation of recombination intermediates (Oh *et al.*, 2008). This put forward a theory that SGS1 is involved in the removal of such intermediates and may act as a 'fail-safe' mechanism if the Mus81–Mms4 pathway fails (Oh *et al.*, 2008), where SGS1 operates via a class II pathway to repair 'incorrectly' joint molecules that were formed via the class I pathway.

1.10 The classical role of telomeres

The telomere is a modified region at the end of all eukaryotic chromosomes comprised of tandem DNA repeat sequences associated with proteins, which functions to protect chromatin from degradation by distinguishing the ends of the chromosomes from DSBs hence, playing a vital role in maintaining the stability of the genome (Shakirov *et al*., 2004). The basic telomere structure comprises a G-rich sequence of repeats with a single stranded overhang at the 3'end (McEachern *et al*., 2000).

As a possible origin of telomeres, it is thought that the endocytosis of a Eubacterium into an Archeabacterium and the introduction of the invading group II introns into the hosts genome, led to the generation of introns and subsequent nucleus formation (Koonin, 2006). The group II introns are retroelements which gave rise to introns involved in post-transcriptional splicing, and non-long terminal repeat (non-LTR) retrotransposons (Sharp, 1985). It is postulated that high levels of breakage and resulting linearisation of the circular genome, led to the utilisation of the DNA repair machinery. The subsequent repair of non-LTR retrotransposons with G/C rich sequences caused capping of the DSB's, forming "proto-telomeres" (Villasante *et al*., 2007).

The consensus sequence for the repeats in vertebrates is TTAGGG (Meyne *et al*., 1989). The appearance and evolutionary conservation of the sequence was determined using a tagged RNA consisting of the sequence cloned from human DNA, which was subsequently used to screen 91 different species of vertebrates (Meyne *et al*., 1989). It was found that all representative samples of species harbour this consensus sequence and hence, it is assumed that it is conserved amongst all vertebrates. The sequence doesn't hybridise with insect and plant DNA, indicating an evolutionary "split" amongst the eukaryotes at the point of the appearance of the animal kingdom which would also coincide with the same time point for the change in telomere repeat sequence (Meyne *et al*., 1989). By taking into account that

evolutionary shifts in DNA sequences of 0.25 to 1.25% can occur once every million years (Britten, 1986), the TTAGGG sequence may have emerged from a common ancestral origin dating back a little over 400 million years. Furthermore, it was discovered that the telomere repeat sequence was TTACAG in fission yeast and humans, suggesting a divergence from the above mentioned consensus sequence but both shared common telomere binging proteins (such as POT1) associating with the ends of the chromosomes. In contrast, budding yeast exhibited the consensus sequence ((TG)1-4 G2-3) and an association of a member of the Cdc13 family of proteins with the ends of the chromosomes, suggesting a possible divergence of the budding yeast consensus sequence from that of fission yeast, including a divergence of the function of telomere binding proteins (Hiraoka et al., 1998, Kanoh and Ishikawa, 2003). Various theories to explain the cause of telomere repeat divergence have been put forward. One, being cause by "template slippage" which was observed in investigations using telomerase extracted from the ciliate *Tetrahymena thermophila*, within a region of G/C repeats, leading to the emergance of poly(dG) repeats (Collins, 1999). A second theory states that some organisms display a high level of incorrect nucleotide incorporation during replication, such as *Paramecium tetraurelia* (McCormick-Graham *et al*., 1997). The low degree of telomere repeat sequence variance in the related ciliate *Paramecium caudatum* was disrupted when telomerase RNA from *P. tetraurelia* was transferred to *P. caudatum* nuclei, leading to single points of nucleotide mis-incorporation. The third theory puts forward the possibility of "abortive reverse transcription" which may occur as as result of a conformational change which is induced when the RNA template binds to the substrate. This in turn, could expose certain sequences of bases which may in turn, act as template for reverse transcriptase activity (Forstemann and Lingner, 2001).

The telomere repeat TTTAGGG is common amongst plants (Fuchs *et al*., 1995) with the exception of the Asparagales (TTAGGG), probably due to a higher error rate occuring during telomerase mediated repeat sequence synthesis (Sýkorová *et al*., 2003), but does vary across

the spectrum of the plant kingdom in length with 2 to 5 kb for the *Arabidopsis* ecotype Columbia (Richards and Ausubel, 1988) to 150 kb in *Nicotiana tabacum* (Fajkus *et al*., 1995). In addition to this, telomere length may differ amongst different ecotypes of the same species. Taking *Arabidopsis* as an example, telomere lengths vary from 2 to 5 kb however, telomere lengths are longer in the Wassilewskija (Ws) ecotype ranging in length from 2 to 9 kb (Shakirov *et al*., 2004).

Telomere integrity is maintained by the reverse transcriptase (RT) telomerase which is involved in the synthesis of G-rich DNA sequences. It functions by utilising its own RNA subunit as a template and its 3' end as a primer (Blackburn, 1992). Early studies involving the cloning of short telomere sequences from yeast to linear *Tetrahymena* DNA without the requirement of DNA polymerase-like activity which always requires a template hence, suggesting that there is a different form of activity that is acting on the terminal regions of the chromosomes to generate telomeres repeats (Shampay *et al*., 1984). Further studies on *Tetrahymena* were conducted and it was found that using a G-rich single-stranded oligonucleotide primer corresponding to the telomere repeats in this species, there was a generation of the *Tetrahymena* telomere repeat sequence. However, the process was not inactivated by DNA polymerase specific inhibitors (Greider and Blackburn, 1985). Furthermore, the addition of RNase to nuclear extracts led to an inactivation of telomere synthesis and attempts to isolate the possible catalytic protein responsible for telomere repeat syntheis yielded a protein which which co-purified with RNAs, suggesting the possible role of a ribonucleoprotein in telomere repeat sequence syntheis (Greider and Blackburn, 1987). Attempts to clone the RNA moiety of this telomerase led to the discovery of an RNA which was 159 nucleotides long, which harboured the sequence CAACCCCAA (complimentary to the TTGGGG telomere sequence) (Greider and Blackburn, 1989). Subsequent treatment of cell extracts with an RNase led to the inactivation of the telomerase suggesting that the RNA

moiety may act as a template for telomere synthesis. For organisms with unique telomere sequences, there also exhists a telomerase with a corresponding RNA moiety. This was shown to be the case for the related ciliate *Euplotes crassus*.

Futher attempts to elucidate the remaining structural components of the telomerases has led to the identification of the catalytic moiety referred to as the telomerase reverse transcriptase (TERT). The TERT subunit from *Euplotes aediculatus* was purified and sequenced and it was revealed that it harboured an amino acid sequence typical to that found in reverse trancriptases and when mutant forms of the *S. cerevisiae* homologue were analysed, it was found that there was a shortening in telomere lengths suggesting that telomerases function via a reverse transcriptase mechanism (Lingner *et al*., 1997). Later the *Arabidopsis* TERT gene (*AtTERT*) was cloned and T-DNA insertion mutant analysis found that telomerase activity was impeded, leading to a shortening of telomere lengths by 500 bp for every succesive generation (Fitzgerald *et al*., 1999). Similar studies were also carried out in *Oryza sativa* which led to the identification of the OsTERT subunit (Heller-Uszynska *et al*., 2002).

1.10.1 Telomere binding proteins

The majority of Eukaryotic telomeres exhibit the ability to form a classical T-loop structure as first discovered in chromosomes purified from mouse liver cells (Griffith *et al*., 1999). It has been postulated that various telomere binding proteins function as a capping (shelterin) complex to prevent the degradation of the telomeric single-stranded overhang by altering its conformation to form the T-loop (reviewed by de Lange, 2005). The telomeric overhangs in *Oxytricha* are bound to telomere end-binding protein (TEBP) which masks the telomeric ends from degradation (Horvath *et al*., 1998).

The telomere capping process in *S. cerevisiae* proceeds via a recruitment process in which the DNA binding motif of the protein Cdc13 binds to the ssDNA overhang, which then recruits

Stn1p (Pennock *et al*., 2001). Later, it was found that Ten1p interacts with the Cdc13/Stn1 complex (Grandin *et al*., 2001) and the study of a range of *ten1* mutants revealed an accumulation of uncapped telomeric ends, suggesting that Ten1 acts downstream of Cdc13/Stn1, to complete the capping process (Xu *et al*., 2009). The suggested homologue of TEBP and Cdc13 in *S. pombe* and humans is called protection of telomeres 1 (POT1) (Baumann *et al*., 2001) and clinical studies of patients suffering from Severe Aplastic Anemia (SAA) presented evidence of telomere shortening and reduced expression of POT1 (Wang *et al*., 2014). It was later suggested that POT1 may function as part of a multi-protein complex with another telomer binding protein called telomere repeat-binding factor 2 (TRF2) (Yang *et al*., 2005).

Both POT1 and TRF2, together with TRF1, TIN2, RAP1 and TPP1, are collectively called the shelterin complex. TRF1, TRF2, and POT1 binds to the TTAGGG repeat sequence and subsequently act to recruit the remaining three proteins TIN2, TPP1, and RAP1 which function to directly protect the telomeres (reviewed by de Lange, 2005). It was recently demonstrated that the covalent binding of a small ubiquitin-like modifier (SUMO) to the TPP1 homolog TPZ1 in *S. pombe*, leads to the negative regulation of telomere lengths (Miyagawa *et al*., 2014). The first discovery of the components of the shelterin complex initially began with the isolation of TRF1 which had a high affinity for TTAGGG repeats in HeLa cells and was initially termed the TTAGGG repeat factor (TRF) (Zhong *et al*., 1992).

Also, the shelterin complex mediated T-loop formation protects the telomeres from Nonhomologous end-joining (NHEJ) via the covalent fusion of two telomeres or homologous recombination between the two telomeres, resulting in inversions and translocations which will have ramifications on the integrity of telomere lengths (reviewed by de Lange, 2005).

1.11 The role of telomeres in meiosis:

There are different hypotheses about the mechanism by which homologous chromosomes are able to identify each other and pair up in a highly regulated and controlled manner. It is suggested that homologue pairing is facilitated by the formation of a classical bouquet structure at the leptotene/zygotene interval, by the pairing of the homologous telomeres at the inner surface of the nuclear membrane (Dernburg *et al*., 1995; Scherthan, 2001). Recent investigations have put forward evidence that the pairing of the telomeres is a dynamic process which brings the chromosomes into close proximity, allowing a dynamic 'telomere swapping' process to occur until all homologues are correctly paired (Cowan *et al*., 2001).

This classical bouquet structure is present in cereals such as wheat (Martinez-Perez *et al*., 1999), maize (Carlton and Cande, 2002b), rye (Cowan and Cande, 2002), rice (Che *et al*., 2011) triticale (Corredor and Naranjo, 2007) and chromosomes of oat origin in an oat-maize addition line (Bass *et al*., 2000). Later studies demonstrated that the bouquet forms as early as late G2 stage in barley (Higgins *et al*., 2012). It must be noted that this bouquet arrangement has not been observed in *Arabidopsis* but instead, a 'transient bouquet' arrangement has been identified in which the telomeres are associated with the nucleolus, facilitating the pairing of the homologues at meiotic interphase (Armstrong *et al*., 2001).

Various investigations have used drugs that inhibit the progression of meiosis, in an attempt to elucidate the mechanisms that control the movements of telomeres in bouquet formation. For example, the treatment of rye at meiotic prophase I with colchicine, led to the inhibition of *'bouquet'* formation (Cowan and Cande, 2002). It was observed that the telomeres in the untreated cells, co-localised within a finite region of the inner surface of the nuclear envelope however, telomeres in colchicine-treated cells, remained dispersed within the nucleus. A further confirmatory test was undertaken, in which colchicine was added to *S. cereale* cells after the formation of the *'bouquet'*, but telomere movement was unaffected (Cowan and

Cande, 2002). This observation puts forward evidence in support of the importance of telomere pairing in '*bouquet*' formation. The treatment of wheat-rye additions at meiotic prophase I with colchicine, also led to an inhibition of the formation of the *'bouquet'*, which resulted in an inhibition of synapsis of the homologous chromosomes (Corredor *et al*., 2007). In addition, investigations were also conducted using a colchicine derivative, colcemid which was shown to inhibit the movement of chromosomes in rat spermatocytes at zygotene (Salonen *et al*., 1982). These observations support the theory that the '*bouquet*' might play a role in bringing homologous chromosomes into close proximity of one another to facilitate subsequent pairing by positioning the homologues within a finite region of the inner nuclear membrane (Sherthan, 2001).

An attempt to disrupt the formation of this *'bouquet'* using colchicine, could lead to incomplete synapsis, as a past study in wild garlic showed that with the effect of colchicine, an isochromosome synapsed normally. However the remaining chromosomes were left unsynapsed (Loidl, 1989).

Furthermore, the microtubule destabilising role of colchicine in bouquet inhibition has been questioned. For example, only the related chemicals, colchicine and podophyllotoxin inhibit bouquet formation. However, other microtubule destabilising agents such as APM and vinblastine did not inhibit bouquet formation (Cowan and Cande, 2002). It was initially found that colchicine and podophyllotoxin associated with different regions of β-tubulin to that by APM and vinblastine (Wilson and Jordan, 1994). This result puts forward the possibility that colchicine may not be targeting the cytoplasmic microtubules when it is inhibiting telomere association, but may be targeting other proteins that are related to tubulin (Stephens, 1986) and even though further tubulins have recently been discovered (δ-, ε-, ζ and η tubulins), the sensitivity of these tubulins to chemicals and their meiotic functions are yet to be studied (Dutcher, 2001).

Further evidence came into light when it was found that 100 µM colchicine inhibited bouquet formation. However, no disruption of the cytoplasmic microtubules was observed (Cowan and Cande, 2002). This result also suggested that a non-microtubule protein may be involved in mediating telomere movements.

Further theories regarding the mechanism by which 'telomere migration' at the inner nuclear periphery occurs using the microtubule associated model, have been put forward. One possible mechanism involves the tethering of chromosomal telomeres to the inner surface of the nuclear envelope via an intermediary association with the nuclear trans-membrane proteins, SUN/KASH, in *Caenorhabditis elegans* (Penkner *et al*., 2007) which in turn, is associated with the cytoplasmic protein dynein. This would permit the contraction and expansion of cytoplasmic microtubules which are in turn associated with dynein, to move the chromosomes and promote the pairing of homologues.

Even though such movements of telomeres are thought to help bring homologous chromosomes together, another emerging theory suggests that distal regions of chromosomes undergo rapid motion at prophase, to disrupt non-homologous associations until homologous association has been achieved. A *pam1* mutation in maize leads to the disruption of chromosome movements, resulting in the failure of bouquet formation and hence, results in subsequent interlocking of chromatin (reviewed by Koszul and Kleckner, 2009).

1.12 The role of histone modifications in meiosis

Histone acetylation and deacetylation both, form a dynamic process which is implemented in the epigenetic control of gene expression, which is under the control of histone acetyltransferases (HATs) and the antagonistic effect of histone deactylases (HDACs), respectively (Servet *et al*., 2010).

The covalent modification of histones which also includes methylation and phosphorylation, has been confirmed to take place on the N-terminal tail of the polypeptide chain causing a re-

organisation of the compaction state and hence, a subsequent alteration of the surrounding chromatin to which the core histone is tethered to, based on a study of a wide range of histone modifications in *S. cerevisiae* (Millar and Grunstein, 2006). Moreover, a more in depth study of histone acetylation confirmed that this process occurs on highly conserved lysine residues by acetyl-CoA acting as an acetyl group donor. The high electron density of the acetyl chain helps to neutralise the positively charged N-terminal histone tails which, subsequently have a weakened attraction for the negatively phosphate back-bone of the surrounding chromatin (Berger, 2007). This leads to the 'loosening' of the surrounding chromatin structure, allowing for the entry of various transcription factors and subsequent epigenetic activation of gene expression. Studies on *Arabidopsis* showed that specific lysine residues (K9, K14, K18, K23, and K27) are the sites of acetylation in histone H3 (Zhang *et al*., 2007), and this is also true for specific lysine residues (K5, K8, K12, K16, and K20) on histone H4 (Earley *et al*., 2007) (**Figure 1.10**).

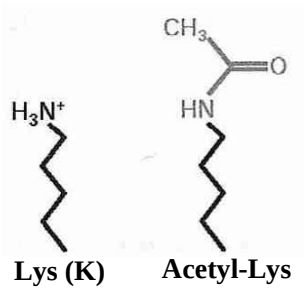
The *Arabidopsis* genome encodes 12 *HAT* and 18 *HDAC* genes (Pandey *et al*., 2002), with the HAT group further sub-divided into four groups (GNAT, MYST, p300/CBP, and TAF1). Extensive research has been undertaken on the HAT activity of GCN5 in yeast and knockdown assays have reported an up and down-regulation of various genes (Grant *et al*., 1997) which functions as an ADA or SAGA multi-protein complex as studies have shown that GCN5 cannot function alone but instead acts as the catalytic subunit of the multi-protein complex (Grant *et al*., 1997).

The manipulation of histone modification has been found to influence meiotic recombination in numerous species. In *Arabidopsis*, histone hyperacetylation led to an increase in the frequency of interstitial crossovers and chromosomal mis-segregation (Perrella *et al*., 2010). The investigation involved the analysis of the role of MEIOTIC CONTROL OF CROSSOVERS1 (MCC1), a GCN5-related histone N-acetyltransferase, which is involved in

the acetylation of histones. The over-expression of this gene by enhancer activation tagging, led to histone hyperacetylation (H3K9K14Ac). *Arabibidopsis* was also treated with trichostatin A (TSA), a histone de-acetylase inhibitor, which led to a phenocopy of the effect that was observed in the *mcc1* mutant (Perrella *et al*., 2010). Therefore, this investigation stresses the importance of histone de-acetylation as a crucial regulating factor required for the correct segregation of chromosomes post-meiosis. Similarly, H4K16 acteylation in barley (**Figure 1.10**) has been shown to be a marker for downstream meiotic recombination events at early prophase I (Higgins *et al*., 2012). The affect of histone hyperacetylation was also confirmed in investigations which studied chromosome segregation in porcine oocytes. Treatment with TSA yielded anaphase and telophase I bridges, which would lead to subsequent unbalanced chromosome segregation (Wang *et al*., 2006). Histone hyperacetylation was confirmed by using antibodies raised against the acetylated form of histones H3 and H4.

Prior to the investigations on the overexpression of AtMCC1 (Perrella *et al*., 2010), other GCN-5-related histone N-acetyltransferase genes such as the GNAT family have been studied, such as the *AtHAG4*/*HAM1* and *AtHAG5*/*HAM2* mutant lines that were semi-sterile as evidenced by reduced seed production in the siliques (Bertrand *et al*., 2003).

The vast majority of histone acetyl transferases (HATs) have a bromodomain (Zeng and Zhuo, 2002) which is a highly conserved acetyl-lysine binding motif found in a broad selection of proteins that are associated with chromatin. The bromodomain was initially discovered in the *Drosophila melanogaster* protein BRAHMA, which is an activator of a group of homeotic genes (Tamkun *et l*., 1992) that represents a highly conserved family of proteins that exist in association with chromatin proteins and in the vast majority of HATs.



(*Arabidopsis* H3: K9, K14, K18, K23, and K27)

(*Arabidopsis* H4: K5, K8, K12, K16, and K20)

(barley H4: K16)

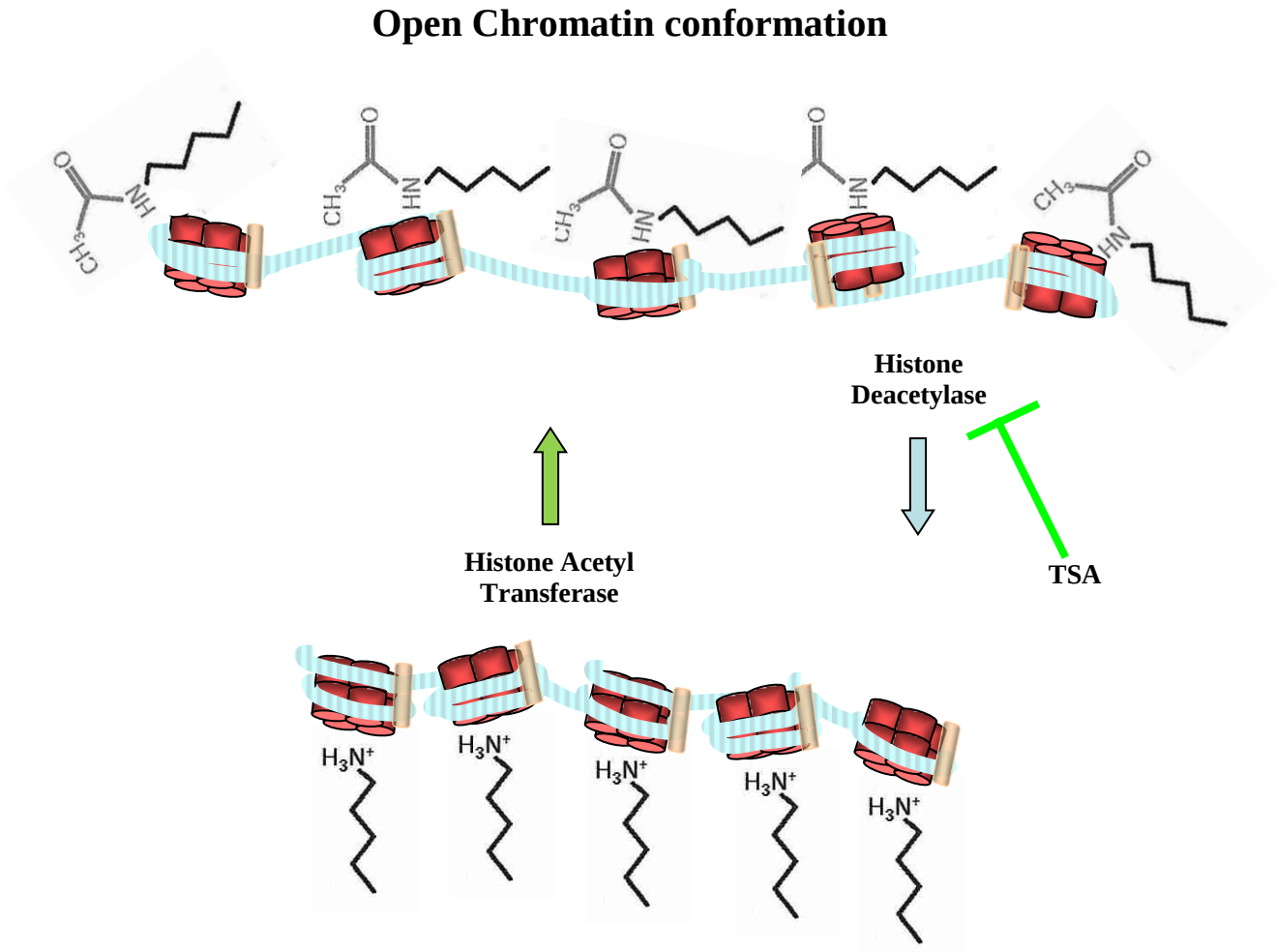


Figure 1.10: The epigenetic modification of chromatin by the acetylation of specific histone lysine residues residues in *Arabidopsis* (Earley *et al*., 2007; Perrella *et al*., 2010; Zhang *et al*., 2007) and barley (higgins *et al*., 2012), resulting in an open chromatin conformation (Earley *et al*., 2007; Zhang *et al*., 2007).

1.13 Crossover homeostasis

1.13.1 The control of crossover formation

The vast majority of organisms exhibit between one to three crossovers per bivalent and it is believed that there is a chromosome-wide control of crossover formation (Jones, 1984). For example, *Caenorhabditis elegans* exhibit a mean number of one crossover per bivalent and an investigation was carried out in which chromosomes three, five and six were fused together (Hillers and Villeneuve, 2003). The single fusion still exhibited an average of one crossover, putting forward the notion that a chromosome-wide mechanism co-ordinates crossover formation. However, it must be noted that at least one crossover must occur between every homologue to ensure that they segregate correctly at metaphase I. This is called the obligate crossover (Jones, 1984).

One possible mechanism is crossover interference, where the frequency of double recombinants is lower than the expected frequency based on the recombination frequencies of individual intervals when in the presence of adjacent crossovers. It is thought that the SC may be involved in interference by mediating the transmission of some type of signal that leads to a regular spacing of the crossovers and that the proteins that constitute the transverse filaments of the SC, might play an important role. In an investigation in yeast mutants lacking the SC proteins ZIP1, ZIP2, ZIP3, MER3, and MSH5, it was found that DSB formation was not affected. However, the formation of SEI's, DHJ's and crossover products were affected, and as these events occur before the formation of the SC, this observation suggests that crossover interference may be independent of the SC (Boerner *et al*., 2004).

Another possible mechanism is called the counting model, in which crossovers are 'aided' in being regularly spaced by being separated by a fixed number of non-

crossovers (Stahl *et al*., 2004). The location of crossovers can be mathematically predicted via the analysis of fungal tetrads and has been successful in the interpretation of data for *Drosophila*. In *Arabidopsis*, the model is successful if the crossovers are combined with the presence of random crossovers, which are known to lack interference (Stahl *et al*., 2004). But further work needs to be carried out to understand the molecular mechanisms that may underlie this process. The analysis of marker recombination patterns in a cross between wild Emmer wheat and a closely related domesticated cultivar, demonstrated negative interference (clustering together of recombination events) around the mid-chromosome arm and distal regions, with the greatest degree of negative interference adjacent to the centromeric regions (Peng *et al*., 2000). A similar pattern of negative interference was observed in barley (Søgaard, 1977; Esch and Weber, 2002). Interestingly, the study with wild Emmer wheat showed that the genome has alternating regions of strong negative and positive interference (a reduced frequency of double crossovers in adjacent regions of the chromosome arms) (Peng *et al*., 2000) in such a way that higher rates of recombination were skewed to gene-rich regions. Therefore, the interplay of positive and negative interference may reduce the occurance of recombination in neighbouring gene-poor regions and would be assumed to potentially increase the efficiency of breeding programs when elite lines are crossed with wild relatives with regard to the cereals (Peng *et al*., 2000).

It has been further noted that DSBs form preferentially at specific regions of DNA called “hotspots”. A hotspot is a small region of DNA, roughly 50-500 base pairs (bp) in length in yeast and recent investigations with this species have shown that DSB formation is suppressed by roughly 2-fold in the centromeric regions, in comparison to the genome average (Buhler *et al*., 2007). One study in particular, used a phase 2

HapMap method, where the single nucleotide polymorphisms (SNPs), of each individual have been identified (Myers *et al*., 2008). The analysis of many related sequences showed that in 40% of crossovers, a 13-mer sequence motif (CCNCCNTNNCCNC) may be the so-called "hotspot". In mammals, meiotic hotspot regions are roughly between 1 to 2 kb and their positions are governed mainly by the PRDM9 zinc finger protein. This protein trimethylates H3K4 within hotspot regions hence, marking these regions for downstream DSB formation and subsequent meiotic recombination events (Baker *et al*., 2014). This integrates well with the effect of epigenetic histone modifications on the meiotic pathway which was mentioned earlier in **Section 1.12** and discussed later in **Chapter 4**: **Sections 4.1** and **4.3**.

1.13.2 The effect of chromatin structure on crossover formation

Further proposals regarding the control of crossover formation, have led to the stress mechanism, in which the chromatin loops that are linked to the axial element of the SC, induce stress along the length of the chromosome when they contract or expand. This stress can be implicated in setting up interference. An analogous model of a metal beam coated with a brittle film has been used to explain this possible mechanism (Kleckner *et al*., 2004). If the brittle film has a crack, any flaws that are adjacent to the crack will be under the influence of reduced stress, whereas flaws further away will not. By applying this model, the expansion of chromatin will be greatly resisted by the axial elements, leading to a 'collapse' of the axial element at a DSB site. The reduced stress in both directions adjacent to the DSB would block the formation of DSB's and hence, further crossovers in nearby regions except at larger distances away from the DSB, where the stress is large enough to initiate further DSB formation (Kleckner *et al*., 2004). Later observations in *Sordaria macrospore*

modified this model as it was found that the sites of SC nucleation are evenly spaced to ensure that complete SC formation occurs along the complete length of the chromatin therefore, ensuring complete synapsis (hence, an even distribution of interference) and it is at these sites where crossovers occur (Zhang *et al*., 2014).

1.14 The resolution of double Holliday junctions

After the crossing over event has occurred, the DHJ is resolved by a resolvase protein to separate the recombinant homologous chromatids. Confirmatory investigations in *S. cerevisiae*, has led to the discovery of protein Mus81-Eme1 as a possible resolvase (Gaiilard *et al*., 2003). However, more recent investigations in *S. cerevisiae* elucidated another resolvase, YEN1 by the screening of a TAP fusion library for Holliday junction resolution activity (West *et al*., 2008). The same investigation also elucidated a human ortholog, GEN1. This human Holliday junction resolvase was identified by using nuclei that were obtained from HeLa cells, which were subsequently screened for Holliday resolution activity (West *et al*., 2008). Finally, the study revealed that GEN1 and YEN1 belong to the Rad2/XPG family of nucleases that harbor a characteristic triad of structural motifs which include the N-terminal (N), internal (I) XPG nuclease domain and a helix-hairpin-helix motif. The investigation also showed that GEN1 and YEN1, cleaved the Holliday junction via a symmetric cutting mechanism, in the same manner as that shown by the *E. coli* resolvase, RuvC (West *et al*., 2008).

In the non-crossover pathway, the elongation of the 3’ end of the invading strand causes its length to surpass the location of the first DSB, causing a disruption of the D-loop. This will be followed by the 3’ end annealing with its original partner strand. This process is mediated by the RecQ family of helicases SGS1 and BLM in yeast and

humans, respectively, that are thought to cause unwinding of ssDNA causing it to dissociate from its homologue (Fasching *et al*., 2015). A study on the possible function of the helicase SGS1, involved the generation of *sgs1* mutant *S. cerevisae* lines, which showed an increased crossover frequency and a reduction in the viability of spores (Roeder, 2003).

In *S. cerevisae,* a return to growth (RTG) method was used to investigate the proteins involved in non-crossover events (Lichten, 2011). This methodology involved the exposure of meiotic cells to a nutritional shift, inducing a return to mitotic cell division where joint molecules (JMs) are resolved as non COs (NCOs). The investigation involved the generation of an *sgs1-DC795* mutant, which lacked the helicase and Holliday junction-binding domains. The study led to find that the resolution of JMs produced both COs and NCOs (Lichten, 2011). The above evidence supports the theory that SGS1 is a "*rescue*" helicase that produces 100% NCOs.

Recently, it has been found that the yeast TOP3 and human TOPOIIIa are homologs and belong to the type IA group of DNA topoisomerases (**Figure 1.11**) and function along with the OB-fold protein RMI, as an SGS1-TOP3-RMI1 complex and BLM-TOPOIIIa-RMI1-RMI2 complex in yeast and humans, respectively (Fasching *et al*., 2015), where RMI enhances the decatanation activity of TOP3 (Bocquet *et al*., 2014). The study by Fasching *et al*., 2015, also demonstrated that mutant lines of TOP3 exhibited increased recombination.

A complete summary of the events of the early crossover decsion model as described from sections **1.7.1** to **1.14** has been depicted in **Figure 1.11**.

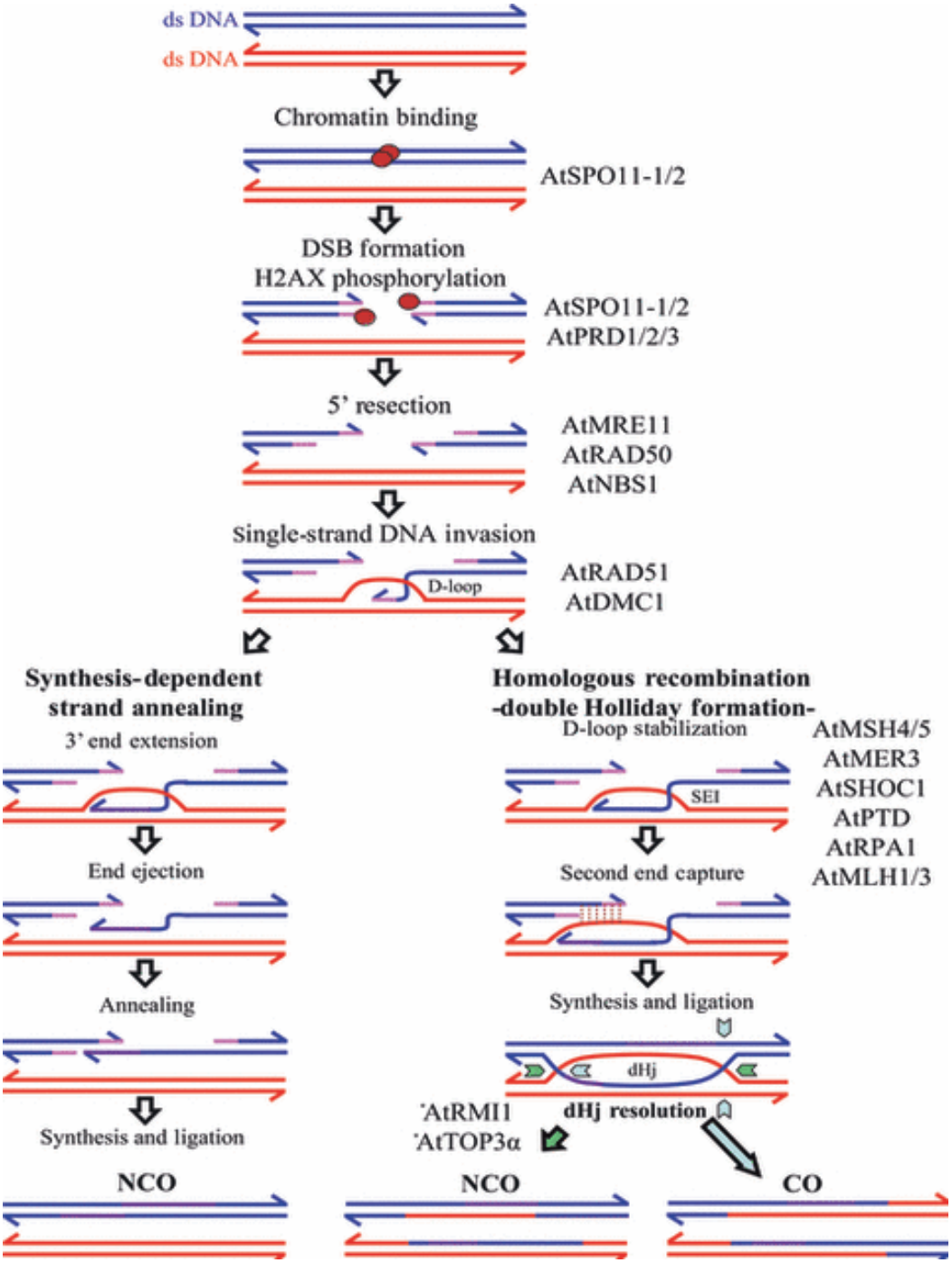


Figure 1.11: The early crossover decision model (taken from Osman *et al*., 2011)

1.15 Cytology of barley

Barley (*H. vulgare* L.) is a member of the tribe Triticeae, which includes rye and wheat and hence, serves as a major cereal that is consumed by a growing world population (reviewed by Higgins *et al*., 2014). Despite the commercial importance of the cereals, the ease of the management of *Arabidopsis* (its higher turnover and smaller genome size in comparison to that for the cereals), has resulted in the preferential development of transformation methods for it, helping to generate a large library of mutants as well as its complete genomic sequence, therefore, establishing it as the model plant species for the study of meiosis. Unfortunately, this has meant that there has been less opportunity to study meiosis in cereals compared to that for *Arabidopsis* (Reviewed by Jenkins *et al*., 2008). In latter years, the development of NGS has allowed for the study of comparative genomics between the cereals (Mayer *et al*., 2011; Mayer *et al*., 2012: refer to **Section *1.17.2***), and between *Arabidopsis* and the cereals with regard to the highly conserved genes that are involved in controlling the meiotic pathway (Reviewed by Jenkins *et al*., 2008). The amalgamation of the improved genetic studies in cereals with the application of cytological studies that have been modified from initial cytological studies in *Arabidopsis* (reviewed by Higgins *et al*., 2014), has made way for detailed studies of the meiotic pathway in Barley (Higgins *et al*., 2012; Barakate *et al*., 2014) and wheat (Colas *et al*., 2008) in recent years.

Subsequently, the cytological analysis of barley has revealed that chiasma formation is predominantly distal (Higgins *et al*., 2012). This pattern of chiasma localisation has also been confirmed by the predominantly distal localisation of HvMLH3 (Phillips *et al*., 2013). To ascertain the possible cause of this phenomenon, including the fact that a large proportion of the antibodies that have been raised against meiotic proteins in

Arabidopsis, were also able to hybridise with the corresponding proteins in barley (reviewed by Higgins *et al*., 2014) (with the exception of ZYP1), has allowed for initial immunolocalisation studies in the barley cultivar Morex, which demonstrated that ASY1 appears as discrete foci on the chromatin loops at G2. At leptotene, there is an appearance of short length linear ASY1 signals along the chromosome axis within sub-telomeric regions, marking the initiation of ASY1 polymerisation until at mid-zygotene, complete polymerisation of ASY1 occurs. At this stage, short stretches of ZIP1 within the sub-telomeric regions as well. The signals begin to linearise and the polymerization of ZIP1 progresses to the centromeric regions until a continuous linear signal is observed at the onset of pachytene (Higgins *et al*., 2012). The same was true for recombination proteins with RAD51 and DMC1 foci appearing along matured chromatin axes at late G2/early leptotene which later appear in interstitial regions when complete ASY1 polymerisation is observed. This suggested that mature chromatin axis formation occurs in the distal regions before the interstitial regions (polarised) and similar studies have shown this to be the case in wheat (Colas *et al*., 2008). This highly polarised nature of chromatin axis formation and synapsis as was demonstrated by the behaviour of ASY1 and recombination proteins, respectively, is reflected in the polarised nature of DNA replication at meiotic S-phase in that distal chromatin is replicated before proximal and interstitial regions, allowing for recombination events to occur in distal regions first. The overall duration of the meiotic pathway is 43 h. As a consequence of the early replication of euchromatin, chiasma formation in barley is predominantly distal (Higgins *et al*., 2012).

1.16 An introduction to the study of desynapsis in plants

The term desynaptic mutant refers to a mutant in which normal pairing occurs between homologous chromosomes at early prophase. However, the chromosomes become unpaired at latter stages of meiosis yielding incomplete pairing of chromosomes at metaphase I (Li *et al*., 1945). This phenomenon has been known to occur largely within plant species which has been proven *via* various cytological studies which reported the presence of univalents, rod bivalents and micronuclei (Katayama, 1964). The rod bivalent forms when one of the chromosome arms fails to pair with its homologous arm, leading to the formation of a rod structure at *metaphase I*. This phenomenon was initially discovered in *Matthiola* (Lesley and Frost, 1927). In contrast, "asynapsis" is used when there is a lack of chromosome synapsis during the early stages of meiosis (Randolph, 1928).

The naturally occurring genes responsible for desynapsis, were also found to be present in subsequent generations of parents that had been subjected to irradiation or chemicals. For example, in *Hordeum* subjected to X-rays (Burnham, 1946), or colchicine treated *Avena* (Dyck and Rajhathy, 1965).

As much as we know, desynapsis is usually under the influence of a recessive gene but, it can also be under the control of a dominant gene. This was shown to be true in the case of *Crepis capillaris* (Hollingshead, 1930). In some cases, desynapsis has been shown to be under the influence of two complementary recessive genes as shown by studies in *Picea* (Andersson, 1947).

Generally, the measure of desynapsis (the frequency of univalents and rod bivalents) at metaphase I has been used to classify desynaptic mutants however, it must be noted that the extent of desynapsis can vary from one nuclei to another. The study of one desynaptic mutant in *Avena strigosa* (bristle oat, $2n = 14$) showed that the number of

univalents ranged from 0 to 14 per nuclei (Dyck and Rajhathy, 1965). Earlier investigations into 14 desynaptic mutants in maize (*2n* = 20), yielded similar results in which a range of differing univalent frequencies from 0 to 20 were observed (Miller, 1963). It is believed that the varying degree of desynapsis at metaphase I amongst the desynaptic mutants is due to they're sensitivity to environmental conditions (Gottschalk and Villalobos-Pietrini, 1965). It is thought that the genes which control early recombination events are succeptible to fluctuations in environmental conditions (Darlington, 1958) such as temperature variations. Increased desynapsis was observed in *Triticum* at low temperatures (Li *et al*., 1945), whereas high temperatures caused an increase in desynapsis in *Oryza* (Wang *et al*., 1965). Furthermore, the effect of both temperature changes and treatments with chemicals, was observed in rye grass (Ahloowalia, 1969). It was found that there was a subsequent increase in the degree of desynapsis at high temperarure growth conditions. But, a treatment with barbiturates (phenobarbital and barbital) led to an increase in bivalent frequency at the same temperature. It was hypothesised that barbiturates are not involved in synapsis but aid in keeping already paired chromosomes together by affecting the re-modeling of chromatin structure by hydrogen bonding as higher temperatures are known to break hydrogen bonds in nucleic acids (Marmur and Doty, 1959). This observation also suggests that the desynaptic mutant may be a thermosensitive compound that is involved in chromosome coiling (Ahloowalia, 1968).

Despite the variability of the desynaptic phenotype (Gottschalk and Villalobos-Pietrini, 1965), a system to classify the degree of desynapsis has established three groups of classification (Prakken, 1943) for plant populations that are grown in tightly controlled environmental conditions. A weak desynaptic mutant harbours a few univalents, a medium strong mutant has many univalents, and a complete mutant will

exhibit exclusively univalents, with a rare occurrence of bivalents. As a general rule, there is a correlation between univalent frequency and the degree of sterility, which was found to be the case with *Avena* (Thomas and Rajhathy, 1966). As the degree of synapsis is sensitive to environmental conditions, then it follows that the fertility of the plant is subsequently be affected.

1.16.1 The study of barley desynaptic mutants

Initially semi-sterile Betzes cultivar stems were harvested in commercial fields growing barley in the late 1960s (Hockett and Eslick, 1969), then cytologically and genetically analysed (chromosome mis-segregation and desynapsis, respectively) to confirm the cause of semi-sterility. The cytological analysis confirmed the desynaptic nature of each mutant line because it was found that the homologous chromosomes paired up at early prophase but, desynapsed from diplotene, onwards.

A total of ten desynaptic mutant lines were chosen and designated as *des* c, d, e, f, g, h, I, j, k and l (Ramage and Hernandez-Soriano, 1971 and 1972). As part of an MSc study at The University of Arizona, each of the ten Betzes mutants were crossed with wild-type Betzes and the ovule fertility of the F2 generation was analysed to devise a segregation map. The results of the segregation study gave evidence in support of a single recessive gene responsible for the cause of desynapsis in every single Betzes mutant line (Soriano, 1973).

Subsequently, allele tests were carried out on the F1 generation of crosses between the desynaptic lines. The results showed that *des d* and *des h*, are allelic to one another, *des c* was not allelic to any of the other lines and renamed *des3*. In addition, it was found that *des* d and h, were allelic to one another and both were renamed *des4* and finally, *des e*, *f* and g, were discovered to be allelic to one another and renamed

collectively as *des5*. The line *des i*, was not allelic to any of other the lines and designated the symbol *des6* and, *des j* was not allelic to the previously reassigned mutant lines and renamed *des7*. Finally, *des k* and *des l*, were found to be allelic to one another and collectively regrouped as *des8* (Soriano, 1973).

Finally, cytological analysis of *metaphase I* spreads was carried out on each reassigned mutant line. Firstly, *des3*, exhibited very weak desynapsis as it harboured a high number of ring bivalents, *des1* and *4* exhibited weak synapsis due to the presence of rod bivalents. The lines *des6, 7* and *8* had a mixture of ring, rod and univalents and were classed as medium desynaptic mutants. Medium-strong desynapsis as depicted by the presence of mostly univalents and a few road bivalents, was exhibited by *des5* (Soriano, 1973). In addition, all mutant lines studied at *anaphase I*, displayed bridges and chromosome mis-segregation in tetrad analysis, except *des3*.

The above mentioned mutants (Ramage and Hernandez-Soriano, 1971 and 1972) have been backcrossed and introgressed into a common Bowman background (Franckowiak *et al*., 1985), to generate a library of mutants for studying meiosis (Druka *et al*., 2011) (see **Chapter 5**).

1.17 Crop breeding

1.17.1 The genomic organisation of the cereals

The *Gramineae* genome (rice: 415 megabases (Mb), maize: 2,500 Mb and barley: 5,300 Mb) is large in comparison to the small size observed for that of *Arabidopsis* (120 Mb) **(**Barakat *et al*., 1998). Despite such a large difference presented in genome size, it has been postulated that the abundance of genes is similar and that the organisation of the genome plays a significant role in differring the distribution of gene clusters between the plant families (Barakat *et al*., 1998). To corroborate this, it

was found that only 10-20 % of the maize genome was comprised of genes within a narrow GC range and interspersed across the genome by a large abundance of repeat sequences (Carels *et al*., 1995). A similar scenario was seen to be the case for the barley genome (Kunzel *et al*., 2000). Repeat sequences have also been observed in the maize genome and by comparing the degree of divergence between a range of linked markers in maize and sorghum, it has been determined that the initiation of the introduction of repeat sequences began roughly six million years ago and that mutations occur at a greater frequency in these non-coding repeat regions in contrast to that for the coding regions (SanMiguel *et al*., 1998). A higher rate of mutation has also been observed in the non-coding regions of sequenced BAC libraries using the barley cultivar Morex as a template (as per conversation with Dr Ramsay, L.). Large scale repeat sequence replication leading to a complete halt in the increase in genome size also seems to be quenched by the eventual repositioning of the region into heterochromatin once it reaches a certain 'threshold length', hence making it inaccesable to key replication factors (Sandhu and Gill, 2002).

Previous to this, reannealing kinetics had already revealed that 62 +/-2.9% of the genome of higher order plants consists of non-transcribing repeat (NTR) sequences, which was the main factor that governs the size the of the various plant genomes (Flavell *et al*., 1974) and later studies revealed a higher gene density closer to the telomeres (Flavell *et al*., 1993). Moreover, a detailed sequence analysis of the NTR sequence regions adjacent to key markers in maize has revealed that the size of such regions surrounding all key makers is very similar, strongly suggesting that repeat sequence insertion was the sole cause of increased genome size after the divergence of the maize genome from roughly 1,200 Mb to around 2,400 Mb, and may well apply to the other cereals (SanMiguel *et al*., 1998). It is now widely accepted that

retrotransposons are the most abundant type of NTR which invaded the host genome of higher order plants and underwent subsequent replication. This region of chromatin underwent a conformation change, repositioning it into heterochromatin (Sandhu and Gill, 2002), which is depicted as C-bands when cytologically studied (Curtis and Lukaszewski, 1991). High resolution physical/gene mapping in conjunction with whole genome shotgun sequencing, further confirmed the high abundance of repeat sequences in the barley genome (Kunzel *et al*., 2000) existing in the form of mobile elements and various repeats making up roughly 84% of the genomic content (Mayer *et al*., 2012), 76% of which was comprised of retrotransposons. As observed in maize (SanMiguel *et al*., 1998) there was a low abundance of retrotransposons within the barley gene-rich regions and in addition to this, a greatly reduced repetitive DNA content in roughly 10% of every arm wthin the subtelomeric regions (Mayer *et al*., 2012).

A high abundance of NTR containing heterochromatin has also been located adjacent to the centromeres (Copenhaver and Preuss, 1999) rendering this region transcriptionally silent especially in the case of polyploidy bread wheat which harbours three copies of the same gene. But, two of the copies are compartmentalised into the centromeric heterochromatin and rendered as transcriptionally silent pseudogenes (Wendel, 2000; Sandhu *et al*., 2001). Polyploidisation is brought about by a high copy number of repeat sequences undergoing rounds of replication (Li *et al*., 2004). It has been postulated that genes which undergo compartmentalisation into heterochromatin are epigenetically "masked" from the transcriptional machinery by the global chromatin structure (Sandhu and Gill, 2002) and that the modification of chromatin associated proteins may play a role in activating transcriptionally silent regions. The inhibition of histone de-acetylation in *S. pombe* was shown to activate

transcription of a centromeric gene cluster (*mat*) and surprisingly led to recombination of this once recombination redundant region (Grewal *et al*., 1998). Another reason for the diploid behaviour of polyploids, namely hexaploid wheat (bread wheat) such that chromosomes can distinguish a homologous chromosome from a homeologous chromosome, is due to diploidisation being controlled by the Pairing homoeologous 1 (*Ph1*) loci that contains an array of *CDC* (Cyclin dependant Kinase) related genes (Martin *et al*., 2014) on chromosome 5B that are thought to control chromosome pairing by the Cdk mediated phosphorylation status of key downstream proteins (Griffiths *et al*., 2006).

1.17.2 The synteny of the grasses and cereals

In the Latter half of the 20th Century, restriction fragment length polymorphism (RFLP) mapping of the wheat homeologous group 7 chromosomes in hexaploid wheat (the three genomes originating from *Triticum urartu, Aegilops squarrosa* and the donor of the B genome which was unknown at the time) displayed a highly degree of similarity (Chao *et al*., 1989). Later, the application of RFLP based comparative mapping studies showed that the gene order (synteny) between wheat and rice was conserved (Kurata *et al*., 1994) and extending the same research showed that the other major grasses such as maize, sorghum, sugar cane, foxtail millet, and the other members of the Triticeae of which wheat belongs to (barley and rye), also exhibited this synteny (Moore *et al*., 1995).

In subsequent years, markers based on simple sequence repeats (SSRs), were developed for barley with the use of sequences that were already available in public databases (Becker and Heun, 1995). SSR based mapping was used to generate information that was collated from a cross between the barley cultivars Lina and

Hordeum spontaneum Canada Park, which generated an F_1 progeny that was analysed, which showed that there was a significant clustering of markers in the centromeric regions amongst the mapping population, which was put down to unequal distribution of recombination (Ramsay *et al*., 2000). The resulting genetic map was very large with a genetic length of 1173 cM and effectively replaced the use of RFLPs to map genes and to undertake linkage studies amongst all *Hordeum* taxa (Ramsay *et al*., 2000).

More detailed information was obtained from barley chromosome 1H, where the sequences of over 5,000 genes were obtained (Mayer *et al*., 2009) and then aligned with similar information from the rice (*Oryza sativa*) genome to generate a map showing the syntenic order of the genes including the synteny between the two grass species.

Later, next generation sequencing (NGS) was applied to the whole of the barley genome by using full-length cDNA (fl-cDNA). The rapid nature of this technique allowed a consensus genome of all of the Triticeae taxa to be devised (Mayer *et al*., 2011). In this investigation, whole barley chromosomes were extracted by flow cytometry, the DNA was amplified and the products were finally shotgun sequenced. This was followed by an observation of synteny with other grass species which aided the gene order of roughly 86% of the known barley genes on specific chromosome arms, to be established (Mayer *et al*., 2011). Furthermore, bioinformatics programs were devised which acted as a genome zippers that aligned the genes of *O. sorghum* (*Sorghum bicolour*) and *Brachypodium distachyon*, to form a synteny map (**Figure 1.12**), allowing 21,766 genes to be placed in a linear order (Mayer *et al*., 2011). In addition, it was observed that the barley genome was similar in structure of that of

hexaploid wheat (*Triticum aestivum*) with a third of the total number of genes being concentrated in the centromeric regions (roughly 10 cM apart; Mayer *et al*., 2011).

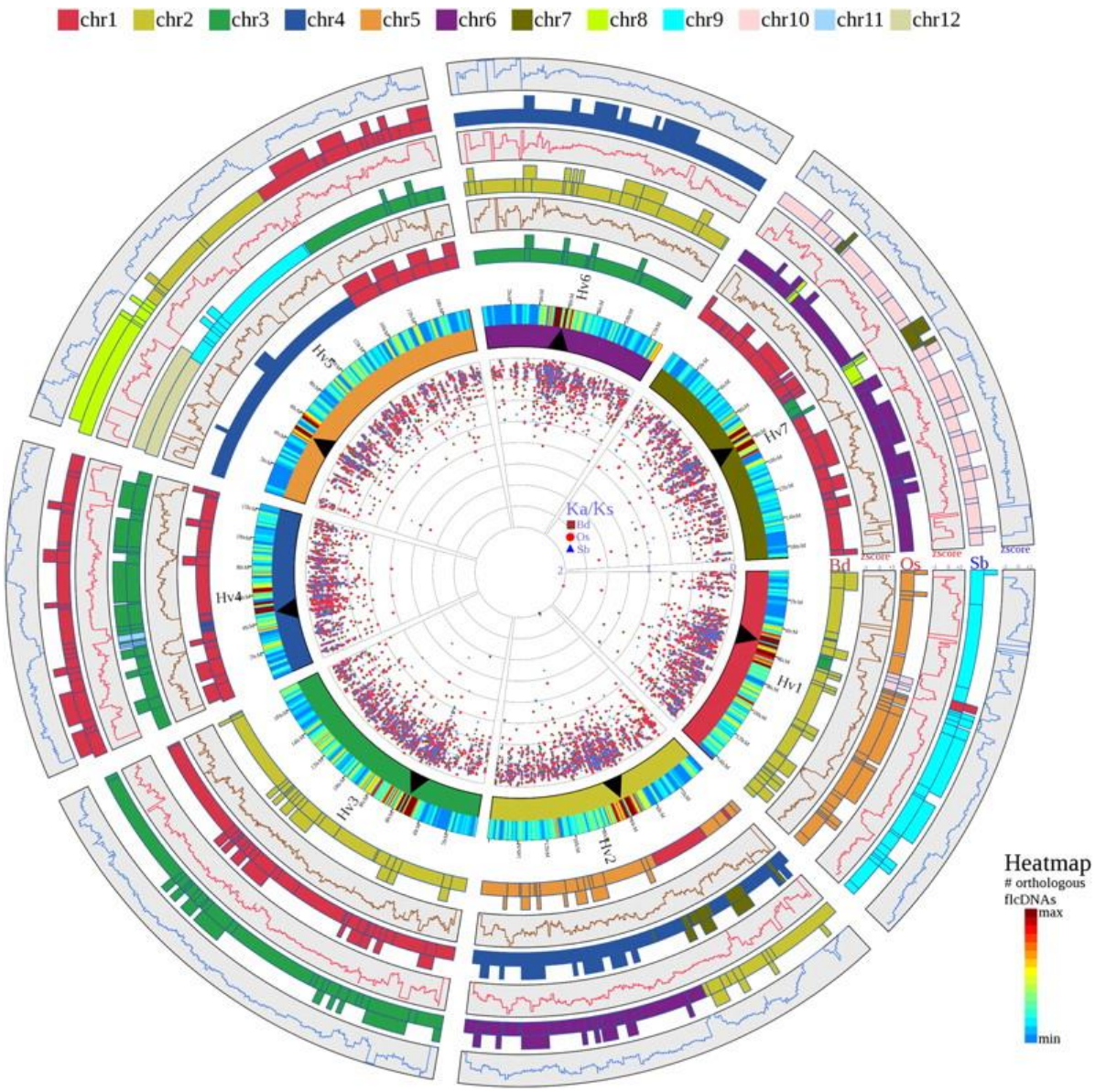


Figure 1.12: A synteny map of the four grass genomes centred on barley. The barley chromosomes are represented by the inner-most circle with heat maps for each chromosome showing the fl-cDNA hybridisation loci. Radiating in an outward direction, the blocks represent synteny with the Brachypodium (Bd), rice (Os) and sorghum (Sb) genomes, respectively (Mayer *et al*., 2011).

The tribe Triticeae generally refers to the subfamily of grasses that comprises the genera barley, wheat and rye (usually domesticated) with a high degree of syntenous genes among the tribe. To confirm this, the linkage maps for chromosome 1 in rice, hulled wheat and Einkorn wheat were aligned with that for barley and rye. The comparative study generated a homeologous group 1 consensus map which revealed a highly conserved linkage between the genes with clusters of highly conserved gene arrangement amongst the tribe (Van Deynze *et al*., 1995). The evidence certainly points to a common ancestor and as a result, comparison of the genomes of the Poaceae family such as wheat and maize using Southern blot analysis was simplistic, in that DNA probes derived from a wheat genome template could be used to probe corresponding genes in maize and vice versa (Devos *et al*., 1994). Furthermore, there was a high degree of alignment of the genetic map for maize chromosome 9 with the group 7 wheat chromosome and a closer comparison of the gene order within the gene clusters revealed inversions, strongly suggesting towards a divergence of maize chromosome 9 from wheat group 7 chromosomes from a common ancestral chromosome (Devos *et al*., 1994). It is widely accepted that *Aegilops tauschii* is the evolutionary predecessor of wheat with an estimated genome size of 4.98 Gb (Rees and Walters, 1965) and similarly to the other grasses, it too consists of predominantly (roughly 90 %) repeat sequence DNA (Li *et al*., 2004). Comparison of a gene map of *A. tauschii* to that for rice revealed that the reduction of the chromosome number from 12 to 7 within *A. tauschii* and other triticea was caused by whole chromosomal insertion into the centromeric areas of a different chromosome (Luo *et al*., 2009) and whole genome shotgun sequencing to construct SNP marker based sequence revealing a high degree of sequence conservation in within the insertion regions speculating that

the rate of sequence evolution was greater in non-insertional regions at the onset of *triticea* divergence (Luo *et al*., 2013).

1.17.3 The relevance of the knowledge of genomic organisation and synteny amongst the cereals

The relevance of the detailed knowledge of the genomic organisation and synteny amongst the grasses has become apparent after recent contradictions. Studies with *zyp1* RNAi *Arabidopsis* lines exhibited a reduction in chiasma frequency (Higgins *et al*., 2005) but the ZEP1 knockdown lines in rice led to an increase in chiasma frequency (Wang *et al*., 2010). It was assumed that because barley is a member of the Poaceae as is rice, the down-regulation of HvZYP1 in barley may also lead to an increase in chiasma frequency (Barakate *et al*., 2014). Despite a high degree of synteny between rice and barley (**Section *1.17.2***: Mayer *et al*., 2009) and genome sizes (rice: 415 Mb and barley: 5,300 Mb) larger than that for *Arabidopsis* (120 Mb) (**Section *1.17.1***: Barakat *et al*., 1998), the knockdown of HvZYP1 in barley led to a drastic reduction in chiasma frequency as was observed in *Arabidopsis* (Higgins *et al*., 2005). The disparity may be due to the presence of an alternative recombination pathway in rice (Barakate *et al*., 2014) or maybe, due to variations in the control of CO formation as suggested by the differences exhibited between *C. elegans* and yeast (Libuda *et al*., 2013).

Also, the synteny between rice and barley (refer to **Section *1.17.2***) will be used as a framework to help delineate and attempt to map a candidate mutant gene in a barley desynaptic mutant in this PhD study (refer to **Chapter 5**: **Section *5.2.4***).

1.17.4 Crossover distribution in cereals

The cytological analysis of wheat chromosomes at *metaphase I* during meiosis, revealed that chiasma formation in chromosomes with short arms, occurred predominantly within distal regions of the chromosome arms and whilst the same was true for chromosomes with long arms, interstitial chiasmata were occasionally observed. This in turn, led to disparities between the physical and genetic distances between the genes (Lukaszewski and Curtis, 1993). This was particularly the case for chromosomes with shorter arms due to the fact that recombination scarcely occurred within proximal regions, meaning that the genetic maps were derived almost purely from distal regions of the chromosomes leading to 70-75% of the proximal regions of short armed chromosomes being absent from the genetic maps (Lukaszewski and Curtis, 1993). A similar recombination pattern was observed in barley with predominantly distal recombination events (Pedersen *at al*., 1995), complicating marker based mapping. A more detailed study of the recombination patterns in wheat revealed that recombination events were completely absent in regions immediately adjacent to the centromeres and that there was an exponential increase in the number of recombination events for a given unit length when the distance from the centromeres was increased (Lukaszewski and Curtis, 1993). A later study with barley utilised integrated translocation breakpoints into an already established genetic map to reveal recombination 'hot-spots' amongst each of the seven barley chromosomes however, they were as previously shown (Pedersen *at al*., 1995), confined to finite regions of the chromosome arms (Kunzel *et al*., 2000). Data revealed high levels of interstitial recombination in the short and long arm of chromosome 1, including 3 recombination hot-spots in distal regions: chromosome 2 was shown to harbour 5 regions of high recombination rates which covered roughly 24% of the chromosomal

length: 3 hot-spot regions were identified for chromosome 3: chromosome 4 displayed high levels of distal and interstitial recombination: 5 hot-spots were identified for chromosome five, one of which shows high levels of proximal recombination in the short arm: recombination events were confined to a third of the length of both the short and long arms of chromosome 6 within the dital regions and a substantial region of the long and short arms of chromosome 7 shows an absence of proximal recombination. It was also found that, similar to what was previously observed in wheat (Lukaszewski and Curtis, 1993), that high levels of recombination were very tightly restricted to 9% of the length of the chromosome length in the distal region. In each case the regions of high recombination were also sub-divided into sub-regions in which the levels of recombination varied from one sub-region to the next (Kunzel *et al*., 2000). later cytological investigations confirmed the distribution of recombination events in relation to the chiasma distribution (Higgins *et al*., 2012). It was demonstrated that distal chiasma formation was observed to occur at a 25-fold greater frequency than for interstitial regions as was already suggested by Pedersen *at al*. (1995), with considerable levels of interstitial chiasma formation being confined to predominantly chromosomes 1, 3 and 4 (Higgins *et al*., 2012), in agreement with the previous mapping studies (Kunzel *et al*., 2000).

The tendency for the occurrence of distal crossovers in wheat may be explained by the fact that synapsis was observed to be initiated at the telomeres as they were seen to pair up at early prophase I which then, clustered to form a bouquet structure at zygotene (Holm, 1986). It was also observed that synapsis subsequently spread progressively from the telomeric regions towards the interstitial regions of chromatin (Holm, 1986) and due to the observance of strong positive interference, there is subsequently a preference for the formation of distal chiasmata (Lukaszewski and

Curtis, 1993). Later it was demonstrated that chromatin remodeling is initiated in the subtelomeric regions of the bouquet at zygotene, which gradually progresses along the whole length of chromatin by diplotene (Colas *et al*., 2008), permitting subsequent synapsis in the same spatiotemporal fashion that was previously observed (Holm, 1986). Later, the analysis of various meiotic proteins in the barley cultivar Morex, showed that the axis-associated protein ASY1 initially undergoes linearisation along the telomeric regions at leptotene which advances towards the interstitial regions by zygotene which is characterised by the classical bouquet structure (Higgins *et al*., 2012), suggesting that mature chromatin axis formation in barley also follows the same pattern of establishment as in wheat (Colas *et al*., 2008), which begins at the telomeric regions and then progresses along the whole length of the chromatin. It was also noted that upon the establishment of the bouquet and mature chromatin axis formation in agreement with what was previously observed in wheat (Colas *et al*., 2008; Holm, 1986), the initiation of synapsis occurred within the telomeric regions as denoted by the beginning of ZYP1 polymerisation along the chromatin axis, which subsequently spread towards interstitial regions by the onset of pachytene (Higgins *et al*., 2012), and that the distal initiation of synapsis was related to the spatial progression of meiotic S-phase. A dual BrdU/EdU time course study showed that DNA replication completed in the distal regions before the interstitial regions by the replication fork, 'allowing' for subsequent meiotic events to occur in the former regions first (Higgins *et al*., 2012). This was also demonstrated to the case in wheat where heterochromatin replicates last (Greer *et al*., 2012), which may explain why chromatin remodeling within these regions, lags behind that in euchromatin in both wheat and barley (Colas *et al*., 2008; Higgins *et al*., 2012). Furthermore, in *Xenopus* embryos, it has been demonstrated that Cdk2 is involved in regulating the initiation of

replication origins and that the inhibiton of Cdk by the chemical Nu6102 (competes for ATP binding sites), led to a reduction in the number of observed replication origins (Krasinska *et a*l., 2008). It has already been demonstrated that the *Ph1* locus in wheat suppresses *Cdk* activity (Greer *et al*., 2012) and in addition to this, it was shown to inhibit premature replication of heterochromatic regions in comparison to *Ph1* deletion lines in which this inhibition was alleviated (Greer *et al*., 2012).

A detailed study of CO distribution in wheat chromosome 3B displayed the same recombination patterns as previously observed (Lukaszewski and Curtis, 1993). However, the genetic map indicated a greatly reduced CO frequency at the telomeric region of the short arm (Saintenac *et al*., 2009) probably due to high levels of heterochromatin in the telomeric region of the short arm of wheat chromosome 3B playing a role in inhibiting CO formation (Gaut *et al*., 2007). A consensus map was constructed depicting gene/recombination distribution for wheat homoeologous group 1 chromosomes and it showed that a typical chromosome harbours eight gene-rich regions, one of which occupies the telomeric region of which contains 1-10% of the total number of chromosomal genes. However, using deletion-line derived physical maps, it was found that recombination frequency was very poor (1-10% of the total number of recombination events on the chromosome) within this region (Van Deynze *et al*., 1995).

1.17.5 Recombination hot spots in cereals

Deletion mapping studies demonstrated that even though gene rich regions are hot-spots for recombination events in this species as well as barley (Sandhu and Gill, 2002), over 30% of the genes in wheat also occupy recombination cold-spots (Erayman *et al*., 2004), confirming a previous observation, making marker based

mapping problematic (Lukaszewski and Curtis, 1993). The same study revealed that upon comparison of the physical and genetic maps, there was greatly reduced recombination in proximal regions as well as virtual absence of recombination in regions adjacent to the centromeres. Even though recombination occurred at a much greater frequency within the distal regions, there was a high degree of variation in recombination rates between the gene rich regions (Erayman *et al*., 2004). In addition, mapping studies in *Ae. tauschii* showed high levels of distal recombination and an almost recombination redundant proximal region as expected (Luo *et al*., 2013). Previously, a physical map/genetic map comparison for the distal region of chromosome 3DS also suggested that the recombination rate was 24.3 fold higher in distal regions compared to that for proximal regions (Fleury *et al*., 2010), which is similar to the cytological scoring of chiasma distribution in barley (25 fold) (Higgins *et al*., 2012).

Interestingly in wheat, it was later found that regions harbouring high recombination frequencies contained genes which are known to take part in vital process such as cell-cell signalling and disease resistance. The recombination of such genes which can undergo vital mutational alterations leading to evolutionary shifts in function (Luo *et al*., 2013) is a key driving force under selection pressure and potentially advantagous to crop breeders. The same recombination pattern was true for barley in which key genes are located within the distal regions of the barley chromosomes (Mayer *et al*., 2012), for which recombination is preferentially skewed towards (Pedersen *et al*., 1995). The encoded proteins within this region includes (1,3)-β-glucan synthase which is involved in the biosynthetic pathway of various polysaccharides, inhibitors of the proteolytic pathway, various transmembrane transporter proteins and most notably, a sequence encoding the NB-ARC domain

(Mayer *et al*., 2012). This nucleotide-binding domain is a common hallmark of plant disease resistance (R) proteins that recognise short chain polypeptides produced by pathogens, inducing downstream resistance pathways (van Ooijen *et al*., 2008). The same recombination pattern was true for genes encoding R proteins in wheat (Luo *et al*., 2013). Also, there was an exaggerated representation of genes that encode cell-cell receptor proteins in the wheat genetic maps (Luo *et al*., 2013), in agreement with the previous mapping study in barley which demonstrated that the distal region of the short arm of chromsome 1 harboured the *MLA* locus (Mayer *et al*., 2012) that encodes a coiled-coil motif, nucleotide-binding domain, and various other proteins (29 confirmed MLA cDNA's) involved in the cell-cell signalling process that together confer resistance to Blumeria *graminis f. sp. hordei* (powdery mildew) (Seeholzer *et al*., 2010). The study also suggested intra-locus recombination and recent gene conversions which have contributed to evolutionary shifts in the functional specificity of resistance. Similarly, the resistance to *Peronospora parasitica* (*RPP8*) locus in *Arabidopsis* which encodes a leucine zipper motif of a subset of R proteins that confer resistance to downy mildew, also displays inta-locus recombination (McDowell *et al*., 1998).

The induction of a shift in the distribution of recombination to proximal regions would not only reduce the disparities between the physical and genetic distances between the genes in the case of wheat (Lukaszewski and Curtis, 1993) and barley (Pedersen *at al*., 1995), it would also enable genes within this recombination redundant region to recombine hence, 'unlocking' a potential source of variation which at the moment, is not accessible for current breeding programs. For example, the gene *FYM11* has been mapped to the proximal region of the long arm of barley chromosome 4 (Lüpken *et al*., 2013), which confers resistance to barley yellow

mosaic virus. The virus usually targets winter barley which is grown in the temperate climate of Europe as well as the East Asian peninsula (Lüpken *et al*., 2013). To date, the existence of seven *RYM11* alleles has been confirmed which would potentially be useful in future breeding programs (Yang *et al*., 2014).

1.17.6 Linkage drag

Another problematic issue for plant breeders is the phenomenon called linkage drag. This effect is observed in a step-wise process called introgression when firstly, a cultivar with a desired phenotype/allele is used to pollenate another cultivar/related crop lacking the desired trait (Brown *et al*., 1989), yielding heterozygotes. This is followed by many generations of back-crossing of the crop with the donor allele into the recipient to produce an increasingly large population of heterozygotes, which are eventually crossed amongst them selves to generate progeny, some of which will be homozygous for the allele (Wall *et al*., 2005). However, during meiosis, genes recombine as 'blocks' (a fragment of the donor genome carrying the desired gene) which means that the introgression of a target/desired gene will also be accompanied by other genes. For example, if the desired gene locus is very close to that for a gene that is unwanted or detrimental to the breeders goals, it is very likely that introgression of the desired gene during recombination would 'drag' along the unwanted gene. Traditionally to overcome this issue, the progeny are allowed to undergo meiosis in the hope that recombination may occur between the wanted and the unwanted gene to 'break' this drag until the desired phenotype is obtained in a large population of the subsequent generation. This method proves time consuming based on the reliance of a recombination event that may be highly unlikely to occur, followed by many rounds of backcrossing to establish a fixation of the desired trait. A

possible example would be the barley *RYD3* gene, which is implicated in defence against Barley yellow dwarf virus and cereal yellow dwarf virus. However, as the gene was initially mapped to the centromeric region of chromosome 6HS (Lüpken *et al*., 2014) for which recombination is virtually absent (Pedersen *at al*., 1995)**,** this will not only complicate marker assisted mapping of the gene but also mean that selective breeding for this gene will no doubt lead to linkage drag of unwanted genes (Lüpken *et al*., 2014). Another possible way of breaking linkage drag could be to induce a 'directed' shift in the distribution of recombination events such that the likelihood of recombination occurring between the desired and undesired gene is increased hence, potentially reducing the time required to bring a commercially viable line into market after initiating introgression from a non-commercial line.

1.17.7 The general issues facing modern crop breeding programs and food security

The general issue with regard to modern crop breeding programs is that breeders are apprehensive to introduce alien germplasm from non-elite, wild relatives into already established elite lines that have undergone many generations of rigorous breeding (Kannenberg and Falk, 1995). However, the increasing demand for food due to the worlds growing population, together with climate change introducing adverse weather conditions which is likely to lead to increased biotic/abiotic stress, means that a greater emphasis needs to be placed on the introgression of genetic variation from alien germplasm. Such attempts will help to further crop improvement with regard to increasing seed number and increasing/broadening of resistance/adaptation (Muñoz-Amatriaín *et al*., 2014).

The very stringent quality control requirements that are expected in modern times along with increased economic competition, means that crop characteristics/qualities

must be strictly kept within a very narrow range which further adds to the apprehensiveness of breeders to increase genetic variation. Such is the case for economically viable cereals such as wheat and barley (Kannenberg and Falk, 1995), that a limited number of progenitor lines now act as the wild relative pool for six-rowed barley, and as little as seven cultivars providing 67% of the genetic pool for two-rowed barley, 32% of this which is of Betzes origin (Kannenberg and Falk, 1995). In addition, it was found that out of roughly 300 races of North American corn, only a single race (Corn Belt Dent) provides the commercially viable germplasm (Goodman, 1985). Worryingly, a study revealed that roughly a quarter of the germplasm pool for Northern and Southern American soybean, originated from five and four progenitor cultivars respectively, and furthermore, the gradual loss of the ancestral populations (due to alterations in land usage for development/urbanisation or catastrophic environmental changes) is leading to a loss of available genetic variation in a phenomenon called 'genetic erosion'. Extrapolations have predicted that by the latter half of the 21st century, approximately half of the available genetic variation may disappear (Gizfice *et al*., 1993).

Another phenomenon contributing to genetic erosion is the founder effect, caused when a very small number of desirable individuals are removed from a large population of plants during the domestication process which are then given priority by breeders over the founding population in agriculture. This leads to subsequent extinction of the individuals from the founder population, reducing the germplasm pool and of course, a genetic bottleneck due to the narrow range adaptation of the newly domesticated crop. Such is the case for *Cicer arietinum L*. (chickpea) and in conjunction with a very low population and poor global distribution of the wild ancestor *C. reticulatum Ladiz,* it has been suggested that a concerted effort be placed

on emphasising increasing the agriculture of wild *Cicer* relatives to replenish the germplasm pool. Additionally, it has been suggested that some of the original traits from the wild *Cicer* progenitors be re-introgressed into domesticated *C. arietinum L* (Abbo *et al*., 2003).

Despite the general reluctance of crop breeders to introduce alien germplasm from non-elite, wild relatives into elite/domesticated crops (Kannenberg and Falk, 1995), the strength of persuasion is continuously gaining weight due to improving knowledge of genetics and improved methods of whole genome sequencing. Over 2,000 barley germline accessions from various global landraces were genotyped, mapping nearly 6,000 SNPs, to generate a high density consensus map for barley (Muñoz- Amatriaín *et al*., 2014). The study also emphasised allelic variations that govern quantitative traits such as spike structure and hull cover providing barley breeders with a wealth of genotyped germplasm libraries which can be referenced and used to introgress the genomic regions of high interest from wild relatives into elite lines in a more 'directed' (Muñoz- Amatriaín *et al*., 2014) or 'data-driven' manner in contrast to previous breeding programs of the past where the outcome had a greater degree of uncertainty, potentially reducing unwanted linkage drag despite the fact that in an 'ideal world' in a breeding context, the purest form of novel selection would be to have as little linkage drag as possible (Young and Tanksley, 1989).

Additionally, a breeding initiative for barley referred to as The Recurrent Introgressive Population Enrichment (RIPE) program which trials male sterile elite lines, are crossed with various wild relatives to generate a large library of offspring from which lines with a commercially viable introgressed trait, can be 'considered' and brought into market (Kannenberg and Falk, 1995). A similar initiative for corn which is referred to as The Hierarchical Open-ended Population Enrichment (HOPE)

program, for which a ranking system is placed where crosses with desirable phenotypes are given a higher ranking and subsequently selected more often for breeding whereas lower ranked offspring are not commercially selected however, are maintained as a source of germplasm variation (Kannenberg and Falk, 1995).

The above mentioned improvements with genotyping (Muñoz- Amatriaín *et al*., 2014) and directed breeding programs (Kannenberg and Falk, 1995) also offer much in the way of persuading breeders to utilise gene banks which contain a broad range of barley (Brown, 1992), wheat, grain, rice, sorghum, maize and soybean accessions (Chang, 1992), and will make way for improved utilisation of gene bank allocated spaces by facilitating the identification and removal of redundant accessions (Muñoz-Amatriaín *et al*., 2014).

1.18 The aims of the project

In cereals such as barley and wheat, meiotic crossovers are skewed towards distal regions. This means that a significant proportion of the genome rarely undergoes recombination, which greatly limits the amount of genetic variation available for crop breeding programs. Thus the aim of this project is to alter the frequency and distribution of crossovers using barley as a model species. If the distribution of crossovers can be directed towards proximal regions, it will allow for the increased recombination of centromeric genes, providing a greatly increased chance of yielding barley strains with novel gene combinations that could confer a selective advantage allowing for a greater crop yield and an increased chance of survival in harsher conditions. Additionally, subtle shifts in crossover distribution may help to disrupt linkage drag and potentially improve the efficiency of crop breeding strategies. This project will attempt to address this issue by:

1) Translating previous karyotyping studies carried out in barley mitotic cells (Leitch and Heslop-Harrison, 1993) to barley meiocytes and reiterating cytological studies (Higgins *et al*., 2012) carried out in barley (the scoring of chiasmata in FISH labeled chromosomes in **Chapter 4** and the meiotic time course in **Chapter 3**), in order to develop the cytological tools for monitoring the affect of specific treatments on the frequency and distribution of meiotic crossovers in barley.

2) Using a method previously devised by Corredor and Naranjo (2007) to administer the microtubule destabilising agent colchicine directly into the transpiration stream, which is known to disrupt the telomere bouquet in a related cereal (a wheat-rye addition) (Corredor and Naranjo, 2007), in order to ascertain the feasibility of using chemicals to affect the meiotic pathway in barley (**Chapter 3**).

3) Proceed to use a chemical that is known to alter the epigenetic modification of chromatin, in order to alter the frequency and distribution of meiotic crossovers, whilst ensuring that fertile seeds can be extracted post-treatment. The effects of the treatment on the meiotic pathway will be determined by cytology and the genetic screening of a treated marker population (**Chapter 4**).

4) Studying a desynaptic barley mutant using cytology to confirm the desynaptic nature of the line and forward genetics to attempt to identify and map the gene that is responsible for the mutant phenotype, as a means of contributing to our current understanding of the control of meiosis in barley (**Chapter 5**).

CHAPTER 2

MATERIALS AND METHODS

Materials and methods:

2.1 The generation/source of the seeds that were used in the project

The *des8* v Morex cross to generate the seeds that would be used to fine map the *des8* gene in the *des8* mutant line (**Chapter 5**), was carried out by myself at Limagrain Uk (LIM) in Rothwell, Lincolnshire (**Figure 2.1(a)**). Firstly, *des8* ears were staged accordingly to ensure that self-pollination had not occurred. As a general rule, the stems were prior to undergoing self-pollination if the awn was just beginning to appear at the top of the stem and were deemed as suitable for crossing. Stems that had awns protruding at a length of 1cm and over, were deemed as already having undergone self-fertilisation and were not used. Suitably staged *des8* spikelets were cut at the top to expose the ovules and then emasculated by removing three pollen anthers from each spikelet using forceps (**Figure 2.1(b)**) and then enclosed in a polythene envelope. The base of each polythene envelope was sealed around the base of the ear using gardeners cable ties (**Figure 2.1(c)**) and the top of the envelope was cut (**Figure 2.1(d)**). A Morex ear at pre-fertlisation stage was cut from its stem and its spikelets were cut at the top to expose the pollen anthers, which was used to pollinate the emasculated *des8* ear. This was carried out positioning the Morex ear in the envelope and twisting/turning the Morex ear to disperse the pollen around the vicinity of the emasaculated *des8* ear (**Figure 2.2(a)**). Finally, the polythene envelope containing the pollinated *des8* ear was sealed to prevent unwanted cross-fertilisation by folding down the top of the envelope and stapling it down (**Figure 2.2(b)**).

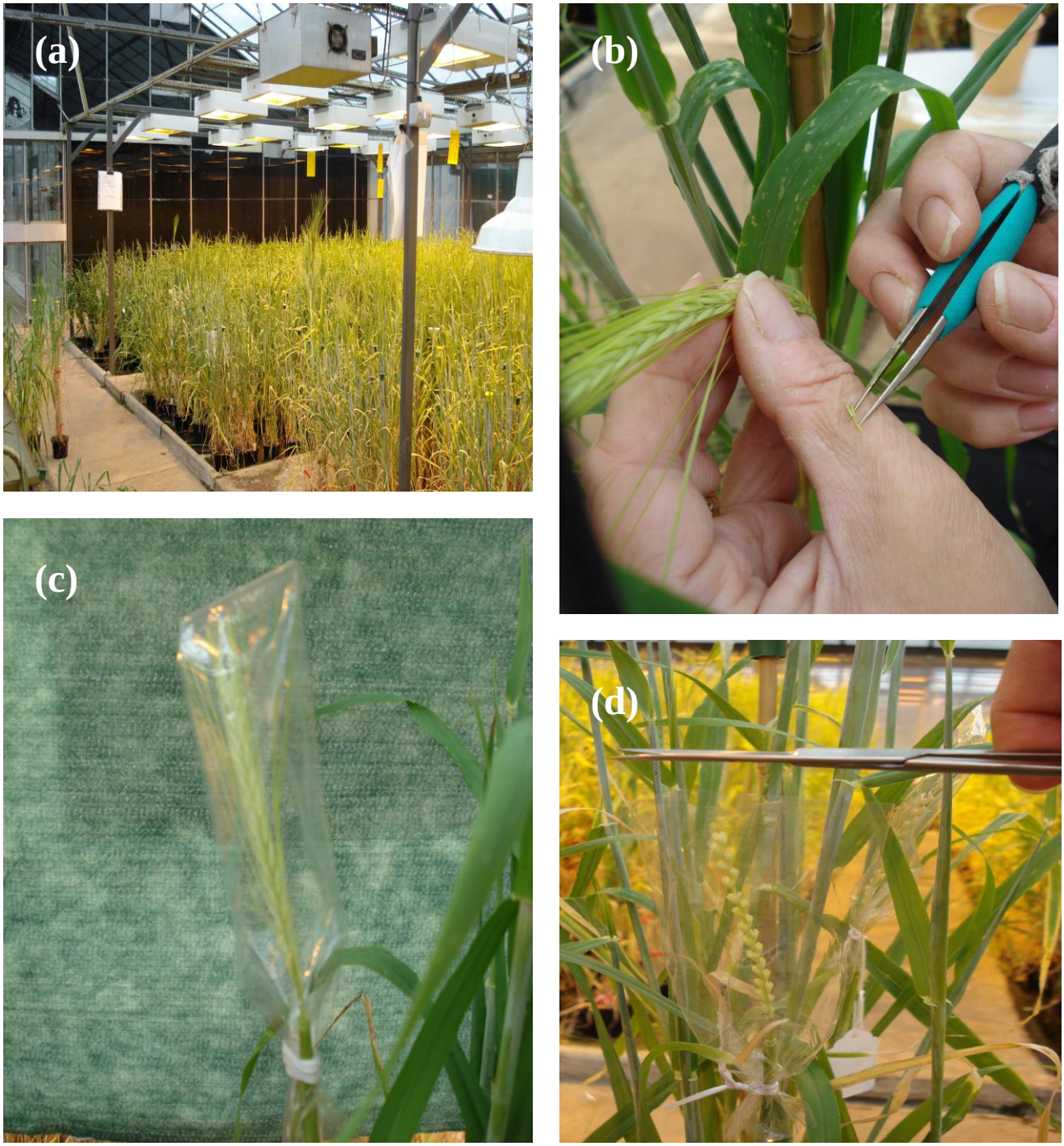


Figure 2.1: The *des8* v Morex cross. The cross was carried out by myself in glass-house facilities based at Limagrain Uk (LIM) in Rothwell, Lincolnshire (a). The *des8* spikelets were cut at the top to expose the ovules which were emasculated by removing three pollen anthers (b) and the ears enclosed in a polythene envelope (c). The base of each polythene envelope was sealed around the base of the ear using gardeners cable ties (c) and the top of the envelope was cut open (d).

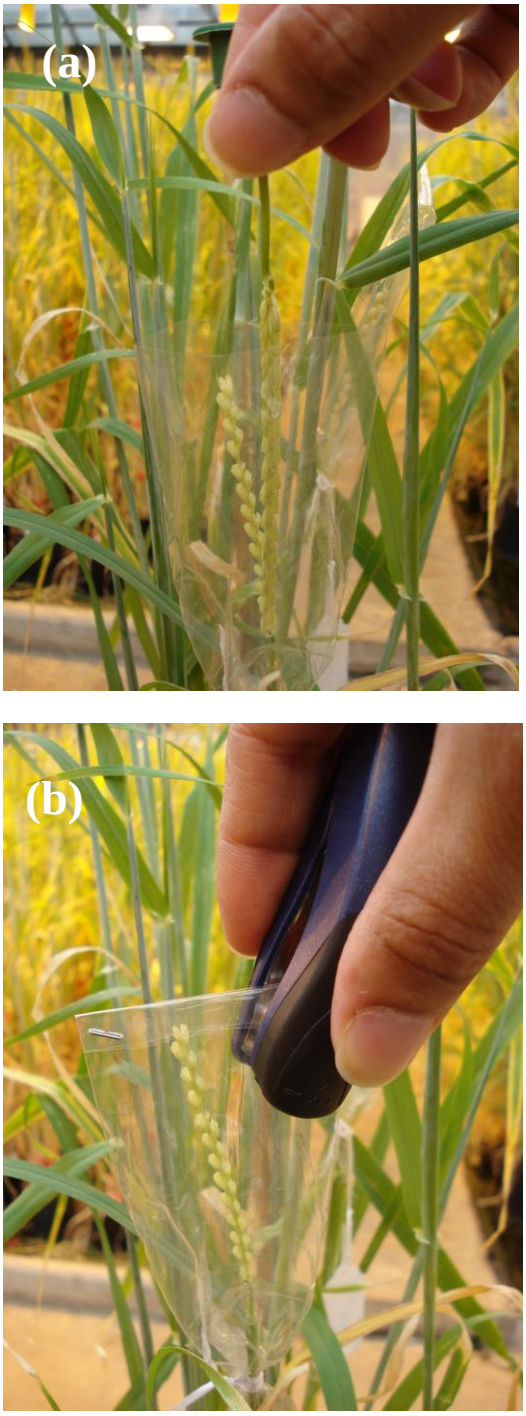


Figure 2.2: The pollination of *des8* by Morex. A Morex ear at pre-fertlisation stage with its pollen anthers exposed, was used to pollinate the emasculated *des8* ear by positioning the Morex ear in the envelope and twisting/turning the Morex ear to disperse the pollen around the vicinity of the emasaculated *des8* ear (a). Then, the polythene envelope was sealed by folding down the top of the envelope and stapling it down (b).

The F1 plants of the Morex v Barke cross (seeds of the crosses provided by senior barley breeder Mark Glew: LIM) used in the study to decipher the effects of TSA treatment by the genetic screening analysis, were grown at JHI and the TSA injections were carried out by myself at the institute. The *des8* mutant and Bowman seeds were provided by Dr Isabelle Colas (JHI), and I carried out cytological studies on both of these lines at the University of Birmingham (UoB). The Morex seeds were provided by Dr James Higgins (UoB). **Table 2.1** shows the source of each type of seed, including the study that each type of seed was used for and the location(s) of each study.

Table 2.1: The type of seed/plant, including the source/provider (a naturally occurring cultivar or cross), and the type of study that they were used in. The table also lists the institutional location(s) in which the studies were carried out and the compartments in which the plants were grown in at the given institute.

Seed/plant	Source/provider	Type of study/investigation	Location(s) of study.
Morex seeds	Provided by Dr James Higgins (UoB) (naturally occuring cultivar).	The affect of colchine on telomere bouquet formation (cytology: **Chapter 3**). The affect of TSA on chiasma frequency and distribution (cytology: **Chapter 4**).	UoB (glasshouse)
Morex v Barke plants.	Seeds of cross provided by Mark Glew (LIM) and plants grown by Dr Luke Ramsay (JHI).	The affect of TSA on marker recombination frequency and distribution (genetic screening: **Chapter 4**).	JHI/UoB (glasshouse)
***Des8* and Bowman seeds.**	Provided by Dr Isabelle Colas (JHI) (*des8* NIL: Franckowiak *et al*., 1985).	A study of the meiotic pathway in *des8* and the Bowman control (cytology: **Chapter 5**).	UoB (glasshouse)
***des8* v Morex seeds.**	Crosses carried out by myself at LIM (**Figures 2.1** and **2.2**).	Fine mapping the *des8* gene in the *des8* mutant line (SNP based marker sequencing: **Chapter 5**).	JHI (polytunnel and glasshouse)

2.2 Growth of plant material.

In all of the locations (JHI, UoB and LIM) except the polytunnels, the barley plants (**Table 2.1**) were grown in a soil-based media, compromised of compost in a glass house which provided supplementary light (a 16 h light, 8hr dark cycle). The average temperature of the glass house was maintained at 18.5 °C. The seeds were sown at a depth of 1.5 cm below the surface of the soil and were left to germinate and grow over a period of approximately five weeks, until they reached a length of between 31 and 36cm.

2.3 Dissection of spikes.

At a stem height within the range of 31-36cm, the base of the spikes were located just above the highest node within the stem, and were dissected using fine scissors at the base of the node and immediately preserved in fixative (3 parts absolute ethanol to 1 part acetic acid) and left to fix overnight at room temperature. The fixative was replenished the following morning.

2.4 Preparation of the slides.

Individual fixed spikes within the range of 1.0-2.3 cm, were placed into a black watch-glass containing fixative and anthers between 0.4 and 1.0 mm were separated from the spike using a forcep and fine needle. Then the anthers were put through two washes with 10 mM citrate buffer (445 µl sodium citrate and 555 µl citric acid, diluted1:10 with sterilised deionised water at pH 5.4). The anthers were then digested in an enzyme solution (0.3% cellulase (0.100g, Sigma C0615) and 0.3 % (w/v) pectolyase (0.100g, Sigma P5936), made up to 10ml with citrate buffer) at 37°C. Anthers up to a length of 0.6 mm, required a digestion period of 30 min, 0.7-0.9 mm

required a digestion period of 60 min and anthers 1 mm and over, required a digestion period of 75 min. Once the anthers were digested, the enzyme solution was replaced with chilled citrate buffer to quench the reaction. Individual anthers, in the order of increasing length were transferred in a small volume of citrate buffer to a microscope slide, using a Pasteur pipette. The anthers were macerated using a fine needle and a diamond pen was used to etch a circle around the sample, on the slide. This was followed by the addition of 5 µl 60% acetic acid, twice and then placed onto a heated block which was pre-set at 45 °C for 30 sec. The material was fixed to the slide by applying 100 µl of fresh fixative (3 parts ethanol: 1 part acetic acid) as a circle around the sample and drained off the slide. The slide was then dried using a commercial hair dryer by applying hot air to the under-surface of the slide.

2.5 Synthesis of probes for fluorescence in situ hybridisation.

2.5.1 Synthesis of telomere probes.

The telomere probes were generated by a polymerase chain reaction (PCR) from primers. The primers were stored as a working solution at a concentration of 5 µM. The oligo Tel_1 had the nucleotide sequence 5' –TTT AGG GTT TAG GGT TTA GGG TTT AGG GTT TAG GG -3', and the oligo Tel_2 had the nucleotide sequence 5' –CCC TAA ACC CTA AAC CCT AAA CCC TAA ACC CTA AA -3'. A PCR reaction mix with a final volume of 100 µl, was made up to generate a primary telomere probe as shown in **Table 2.2**. The 10x PCR buffer (without $MgCl_2$: Roche 11699105001) contained 100 mM Tris-HCL and 500 mM KCl and has been adjusted to pH 8.3. The reaction mix (**Table 2.2**) was then subjected to a temperature cycle as shown in **Table 2.3**, to generate the primary telomere probe. At the completion of this PCR step, 5 µl of the product was run on 1% agarose gel, to ensure that the PCR was

successful. Subsequently, 3 µl of this primary product was added to 23.5 µl SDW and subjected to a 1 cycle PCR at 95 °C for 5 min. The product of this step was added to 23.5 µl of the PCR mixed shown in **Table 2.4**, to generate the DIG-labelled secondary telomere probe by the PCR step shown in **Table 2.5**, where dTTP was replaced by DIG-16-dUTP.

Table 2.2: Reaction mix to generate primary telomere probe

Reagent	**Volume used (µl)**	**Final concentration**
10x buffer	10	50 mM
50 mM $MgCl_2$	4	2 mM
10 mM dATP	2	0.2 mM
10 mM dGTP	2	0.2 mM
10 mM dCTP	2	0.2 mM
10 mM dTTP	2	0.2 mM
Tel_1	6	0.3 µM
Tel_2	6	0.3 µM
5 units/µl Taq polymerase	1	2.5 u/µl
SDW	65	-

Table 2.3: Primary telomere temperature cycle.

Temperature (°C)	Duration (min)	Cycles.
94	1	8
55	0.5	
72	1	
94	1	24
60	0.5	
72	90	
72	5	1

Table 2.4: Reaction mix to generate secondary telomere probe.

Reagent	Volume used (µl)
10x buffer	5
50 mM Mg Cl_2	2
10 mM dATP	1
10 mM dGTP	1
10 mM dCTP	1
10 mM DIG-16-dUTP	1
Tel_1	3
Tel_2	3
5units/µl Taq polymerase	0.5
SDW	6

Table 2.5: Secondary telomere temperature cycle.

Temperature (°C)	Duration (min)	Cycles.
95	1	25
60	0.5	
72	1	
72	2	1

2.5.2 Synthesis of centromere probes.

The centromere probes were generated by PCR from the oligo primers $(GAA)_8$ and $(TTC)_8$, which were stored as stocks of 27.1 pmol/µl and 68.1 pmol/µl, respectively. A primary reaction mix with a total volume of 24.5 µl was made up as shown in **Table 2.6**. This reaction mix was then subjected to a temperature cycle as shown in **Table 2.7**, to generate the primary centromere probe. At completion of this PCR step, 5 µl of this primary product was added to 9.5 µl SDW and subjected to a 1 cycle PCR at 95 °C for 5 min. Finally, the product of this step was added to 35.5 µl of the PCR mix shown in **Table 2.8**, to generate the BIO-labelled secondary centromere probe by the PCR step shown in **Table 2.9**.

Table 2.6: Reaction mix to generate primary centromere probe

Reagent	Volume used (µl)
RED Taq	12.5
OLIGO “GAA”	8.5
OLIGO “TTC”	3.5

Table 2.7: Primary centromere temperature cycle.

Temperature (°C)	Duration (min)	Cycles.
94	1	8
55	0.5	
72	1	
94	1	24
60	0.5	
72	90	
72	5	1

Table 2.8: Reaction mix to generate secondary centromere probe

Reagent	Volume used (µl)
10x buffer	10
50 mM Mg Cl_2	4
10 mM dATP	2
10 mM dGTP	2
10 mM dCTP	2
1 mM BIO-16-dUTP	2
OLIGO GAA	24
OLIGO TTC	24
5units/µl Taq polymerase	1
SDW	0

Table 2.9: Secondary centromere temperature cycle.

Temperature (°C)	Duration (min)	Cycles.
95	1	25
60	0.5	
72	1	
72	2	1

2.6 Preliminary time course study

The BrdU (10 mM: Roche 11 296 736 001) time course study was carried out on the cultivar Morex according to Higgins *et al*. (2012). All chemicals were directly injected into the transpiration stream of the barley stems harbouring the spike (Corredor and Naranjo, 2007) using a hypodermic needle (Becton Dickinson ND400) attached to a 1 ml syringe. As a general rule, each plant was injected with ~300 µl of chemical(s) but was usually treated with a sufficiently large enough volume until the chemical(s) would overflow out of the top of the stem (via an incision made prior to the administration of the chemical). This ensured that the spike (and hence, the anthers) was immersed with the chemical, allowing for its uptake by the anthers via diffusion. The injected BrdU was incorporated into DNA during pre-meiotic S-phase (Armstrong *et al*., 2003; Higgins *et al*., 2012).

2.7 Visualisation of telomeres and BrdU label:

Once the slides were prepared as explained in section 2.3, they were placed into a coplin jar and washed in 2×SSC (10ml 20x SSC with 90 ml SDW) for 10 min. This was followed by a 45 s digestion step in pepsin (0.01g pepsin (Sigma P-7000) with 500 µl 5M hydrochloric acid and 100 ml SDW) at room temperature. The slides were then rinsed with two 2×SSC (a 20x SSC stock was made up of 3M NaCl and 300 mM trisodium citrate, made to pH 7 using hydrochloric acid), followed by a 10 min treatment with 4% paraformaldehyde. This was followed by two steps with SDW to rinse the slides. The slides were put through an ethanol (Fisher E/0650DF/17) series beginning with 70% (42 ml ethanol with 18 ml SDW), 85% (51 ml ethanol with 9 ml SDW) and 100% ethanol, respectively, at room temperature. Each step of the alcohol series was 2 min in duration. 20 µl (14 µl Master Mix with 4 µl telomere-DIG probe

and 2 µl SDW) of the FISH probe mixture was pipetted onto each slide and then a cover slip (VWR 631-0124) was placed over the probe mixture (The Master Mix solution consisted of 5 ml deionised formamide, 1 ml 20x SSC, 1g >500, 000 MW dextran sulphate (Sigma D6001-10G), made up to 7 ml with SDW). The edges of the cover slip were treated with a vulcanising rubber solution and then the slides were placed onto a hot block pre-set at 75 °C for 4 min, to induce breaks in the chromatin allowing the entry of the probes. Finally, the slides were placed into a damp box to maintain humid conditions and left to incubate at 37 °C overnight or for a maximum of 72 h. Following the incubation, the cover slips were removed using fine forceps and the slides were treated three times in 50% formamide-2×SSC at 40 °C for 5 min. This was followed by a 5 min treatment with 2×SSC and then a 5 min treatment with 4×SSC+0.05% Tween 20 (Sigma P1379-500ML), respectively at 40 °C. Finally, the slides were treated with 4×SSC+0.05% Tween 20 at room temperature for 5 min, and then a solution of anti-digoxigenin antibodies tagged with rhodamine (2.5 µl anti-DIG rhodamine (Roche 11207750910) in 97.5 µl DIG block), was added to the slides (100 µl probe solution per slide). The slides were covered with parafilm (parafilm.com PM-996) and incubated in humid conditions at 37 °C for 30 min. The slides were then treated in 4×SSC+0.05% Tween for 5 min, followed by two 5 min washes in phosphate buffered solution (PBS, 1 tablet (Oxoid BR0014G) per 100ml SDW at pH 7). An anti-BrdU primary antibody (Roche 11 296 736 001) was added to each slide slides (50µl per slide: 1:10 dilution of primary antibody in incubation buffer), each slide was covered with parafilm and incubated in humid conditions at 37 °C for 30 min. Then the slides were treated with three 5 min PBS washes, followed by the application of an anti-BrdU-Fluorescein secondary antibody (anti-rabbit-Ig-Fluorescein: Roche 11 296 736 001) to each slide (50 µl per slide: 1:10 dilution of

secondary antibody in PBS). The slides were then incubated in humid conditions at 37 °C for 30 min. Finally, the slides were treated with three 5 min PBS washes and 4',6-diamidino-2-phenylindole (DAPI; 1 µg/ml, Sigma D9542-1MG) solution in vectashield anti-fade medium (Vector H-1000), was added to each slide (2 x 7 µl per slide) and covered with cover slips.

2.8 Visualisation of centromeres and telomeres.

Once the slides were prepared as explained in **Section 2.4** and pre-treated up to and including the ethanol series step (**Section 2.7**), each slide was treated with 20 µl of the probe mix (14 µl Master Mix with 3 µl telomere-DIG probe and 1 µl centromere-BIO probe) (as per the hydridisation protocol in **Section 2.7**).

The centromere probe was detected by a solution of Streptavidin-FITC (1 µl AV-FITC in 199 µl milk block: the tube containing milk block was spun down at 13,500 rpm and the top layer was extracted as used as the medium for Streptavidin-FITC) was added to each slide (100 µl per slide) (the milk block solution was made up of 5 % (w/v) milk powder in 1x PBS), and subjected to the detection protocol described in **Section 2.7**. This was followed by the detection of the telomeres with a solution of anti-digoxingenin antibodies tagged with rhodamine (2.5 µl anti-DIG rhodamine (Roche 11207750910) in 97.5 µl DIG block: Roche 1175041) (100 µl probe solution per slide).

2.9 Time course investigation with colchicine/TSA.

Each stem at meiosis (a stem height between 31 and 36 cm) was injected with ~300 µl of 10 mM BrdU (Roche 11 296 736 001) directly into the region of the transpiration stream harbouring the spike, based on a previous methodology used to introduce

chemicals to the meiocytes in wheat-rye additions (Corredor and Naranjo, 2007). This initiated a 2 hour BrdU pulse, to allow for the uptake of BrdU into replicating DNA at meiotic S-phase. At the end of this 2 h pulse, the BrdU was washed out of the control stem with SDW, which marked the beginning of the time course (0 h). At the same time point (0 h), ~300 µl of working concentrations of colchicine (Sigma C-9754) or TSA (Sigma T8552) were injected into the test stems. The time course was allowed to continue and spikes were extracted at the required time points and fixed (3 part ethanol: 1 part acetic acid) overnight at room temperature (**Section 2.3**), and used for Fluorescence *in situ* Hybridisation (FISH).

Colchicine was purchased as a powder and was dissolved as a stock solution in SDW at a concentration of 10 mM at -20 °C. This stock solution was dissolved in SDW to obtain the various working concentrations of colchicine and the control was pure SDW (**Table 2.10**). TSA was also purchased as a powder and was dissolved as a stock solution in DMSO at a concentration of 10 mg/ml and stored at -20 °C. This stock solution was dissolved in SDW to obtain the various working concentrations of TSA. A single concentration of the DMSO control was used in the complete investigation (which corresponded to 1000 ng/ml TSA: the highest concentration of TSA in the study) (**Table 2.11**).

Table 2.10: The required volumes of reagents to generate the working concentrations of colchicine and the control solution.

Conc. of colchicine required.	Volume of reagents used in test.	Volume of reagents used in control.
100 µM	20 µl stock in 2 ml SDW	SDW only
5 mM	1 ml stock and 1 ml SDW	SDW only

Table 2.11: The required volumes of reagents to generate the working concentrations of TSA and the control solution.

Conc. of TSA required (µg/ml).	Volume of reagents used in test.	Volume of reagents used in control.
10	4 µl stock in 8 ml SDW, then diluted 100 fold.	4 µl DMSO in 8 ml SDW
100	4 µl stock in 8 ml SDW, then diluted 10 fold.	4 µl DMSO in 8 ml SDW
500	4 µl stock in 8 ml SDW then diluted 2 fold.	4 µl DMSO in 8 ml SDW
1000	4 µl stock in 8 ml SDW	4 µl DMSO in 8 ml SDW

2.10 The identification of the individual barley chromosomes in the BrdU/TSA time course investigation.

All of the barley chromosomes were identified at metaphase I by the presence of the 45S and 5S rDNA repeat sequences in chapter 4 and 5 (Leitch and Heslop-Harrison,

1993; Higgins *et al*., 2012). The 45S and 5S probes were generated and provided by Dr James Higgins: The 45S rDNA probe was generated from the template clone pTa71 (from *Triticum aestivum*) comprising a 9 kb EcoRI restriction fragment harbouring the 18S-25S rRNA genes (including the spacer regions) (Higgins, 2013). This probe was nick-translated with digoxin using the DIG nick mix (Roche 11745816910). The 5S rDNA probe was generated from the plasmid pCT4.2 (*Arabidopsis*) template which harbours a 500 bp insert encoding the 5S rDNA gene cloned into pBlu (Higgins, 2013). This probe was nick-translated with biotin using the BIO nick mix (Roche 11745824910). As per the recommendation of the nick mix manufacturers (Roche), approximately 1µg of the probe is required for efficient nick translation. The 45S and 5S probe stock solutions were analysed using a UV/Vis spectrophotometer (Jenway 6305) at a wavelength setting of 260 nm to estimate the concentration of each stock (in a quartz cuvette), and it was calculated that 3 µl of the 45S and 5S stocks contained ~1 µg of probe. Therefore, in the nick translation step, 3 µl of probe was mixed with 13 µl SDW and 4 µl DIG/BIO nick mix and subjected to a single nick-translation step at 15°C for 90 min. 1 µl of 0.5M EDTA was then added to each mix which was then subjected to 60 °C for 10 min. The nick translated rDNA probes were then allowed to cool down to room temperature and were stored at -20 °C.

The metaphase I slides were prepared as explained in **Section 2.4**, and were subjected to the same pre-treatment as described in **Section 2.7** (up to and including ethanol series). Each slide was treated with 20 µl of the rDNA FISH probe mix (14 µl Master Mix with 3 µl 45S-DIG probe and 3 µl 5S-BIO probe) as per the hydrisation protocol described in **Section 2.7**. Then the 45S probe was detected with 50/50 solution of anti-digoxingenin-rhodamine and anti-digoxingenin-FITC antibodies (2.5 µl anti-DIG

rhodamine and 2.5 µl anti-DIG FITC (Roche 11207741910) in 5 µl DIG block) (100 µl probe solution per slide). The 5S probe was detected with a solution of Streptavidine-CY3 (1µl CY3 (Life Technologies 434315) in 199 µl milk block).

The slides were subjected to 2x5 min washes in PBS before being subjected to the BrdU detection protocol outlined in **Section 2.7**. Due to the requirement of a BrdU time course as part of the investigation, it meant that 4 distinct colours had to be used in this case (identification of 45S, 5S, the BrdU label and the DAPI counterstain). The 50/50 mixture of anti-DIG rhodamine and anti-DIG FITC enabled 45S to be identified as orange, CY3 enabled 5S to be identified as red, DAPI counterstain in blue and the BrdU label as green.

2.11 The identification of the individual barley chromosomes in the *des8* mutant line analysis.

The metaphase I slides were prepared as explained in **Section 2.4** and subjected to the same treatment as described in **Section 2.10**, except that 45S was detected by using FITC only (anti-DIG FITC), and no BrdU time course was conducted in this investigation. This allowed 45S to be identified as green, 5S as red and DAPI counterstain as blue.

2.12 Immunolocalisation.

The following immunolocalisation technique was carried out according to Higgins (2013). Spikes were extracted and placed onto damp filter paper in a petri dish to prevent the inflorescences from drying out. Before the dissection, the dissecting microscope graticule was calibrated such that 10 bars were equal to 1mm (using a ruler placed on the objective). Anthers of a required length were removed from the

spike with a fine needle and watchmakers forceps and transferred to 2 µl extraction buffer (2:1 citrate buffer: SDW) on a cavity slide then, the anthers were transversely cut with a razor blade and a thick mounted needle was used to squeeze out the meiocytes. 6µl SDW and 6µl EM digestion mix (0.1g (0.4 %) cytohelicase (Sigma C8274), 0.375g (1.5%) sucrose and 0.25g (1%) polyvinylpyrollidone (MW 40,000: Sigma PVP40-100G) in 25 ml SDW) were added. The slides were incubated at 37°C in a closed damp box for 2 mins. Whilst the meiocytes were incubating, 10µl of 1.5% Lipsol (Appleton Woods LP40023) was pipetted onto a microscope slide and at the end of the incubation period, 10 µl of the digested meiocytes were transferred to the drop of Lipsol using a yellow tip with the end cut off. The mix was spread using a fine needle and 20 µl of 4% paraformaldehyde was added to the cells and mixed using a pipette tip and the slide was left to dry in a fume hood for approximately 3 hours. Once dried, 50 µl of EM block (1% Bovine Serum Albumen (BSA: Sigma A9647) in 1% PBS, and 0.1 % Triton X-100: Sigma T-6878) containing the primary antibody at the specified concentration was added to the slide (see **Table 2.12**). The slides were covered with parafilm and incubated overnight at 4°C or for 30min at 37°C in a sealed damp box. The slides were washed 2 x 5min in washing solution (1 x PBS with 0.1% Triton X-100) followed by the addition of EM block containing the secondary antibody at the required concentration (see **Table 2.12**) and an overnight incubation at 4 °C or for 30 min at 37 °C in a sealed damp box. Slides were washed 2 x 5min in washing solution and the mounting medium DAPI in Vectashield was added.

2.13 Immunolocalisation using fixed anthers (the microwave technique)

The microscope slides which were prepared using spikes which had been fixed in chilled fixative (3 parts ethanol: 1 part acetic acid) as outlined in **Section 2.3**, had to

be subjected to pre-treatment before immunolocalisation studies. The slides were placed into an open lunch box and immersed in SDW and left at room temperature for 2 min. The SDW was then poured off and replaced with antigen unmasking solution (Vector H-3300) (1.5 ml antigen unmasking solution in 160 ml SDW) and the lunch box was sealed with a lid before being placed in a microwave for 5 min (300-400 Watts: medium setting). After this time period the lunch box was checked to ensure that the antigen unmasking solution was still immersing the slides and was topped up if necesarry. The microwave treatment was repeated for another 5 min at the same setting.

At the end of the treatment the antigen unmasking solution was poured off (protective gloves were used as the solution was hot) and replaced with SDW at room temperature to wash the slides. Then the SDW was replaced with PBS and left for 5 min at room tempearure. Following this, the PBS was poured off and the slides were washed 2 x 5min in washing solution (1 x PBS with 0.1% Triton X-100) at room temperature. The slides were then removed, 50 µl of EM block was added to the slide and the slides were covered with parafilm before being transferred to a sealed damp box. The slides were left in the sealed damp box for 40min at room temperature. Finally, the parafilm was removed and EM block containing the primary antibody at the required concentration (see **Table 2.12**) was added to the slides and the protocol as per the remainder of **Section 2.12**, was followed.

Table 2.12: Antibodies with required working dilutions for immunolocalisation.

Antibody	Primary/secondary	Dilution
ZYP1 (Anti-rabbit)	Primary	1:500
ASY1 (Anti-rat)	Primary	1:200
Anti-H3K56Ac (rabbit)	Primary	1:500
Anti-rabbit FITC (Sigma F0382-5ML).	Secondary	1:50
Anti-rat Texas Red (Sigma SAB3700588-2MG).	Secondary	1:200
Anti-rabbit CY3 (Sigma C2306-1ML).	Secondary	1:200

2.14 Fine mapping of the *des8* allele

2.14.1 Growth of the barley des8 plants

The fine mapping study of the *des8* gene was carried out by myself during a placement at The James Hutton institute (JHI: see **Chapter 5**). F2 seeds of a *des8* x Morex cross, were used in this study. 1000 plants were grown in a soil-based media, compromised of compost in a polytunnel (**Section 2.1**) The average temperature of the glass house was maintained at 18.5 °C. The seeds were sown at a depth of 1.5 cm below the surface of the soil and were left to germinate and grow over a period of approximately two weeks, until they reached a length of between 10 and 15 cm.

2.14.2 The disruption of barley leaf material

The young leaf tips of each barley shoot were cut and placed in 96 deep well plates. An extraction buffer master mix which was comprised of 440 µl RNase A (100mg/ml, Qiagen 19101), 440 µl DX enzyme (Qiagen 950120) and 45320 µl DXT (tissue digest buffer: Qiagen 950183) was made up and 420 µl of this mix was added to each well of the 96 well plate (all reagents were from the QIAxtractor® kit: Qiagen 950107). The plate was sealed with two foil lids and sonicated at a frequency of 20 oscillations (hertz) for 1 min to disrupt the leaf material. The plant material was then pulse centrifuged at 3,000 revolutions per minute (RPM) and incubated for 45-60 min, at 65 °C. Finally, the plate was centrifuged for 10 minutes at 5,000 RPM and 220 µl of lysate from each well was pipetted into a QIAxtractor® lysate plate (Qiagen 990600).

2.14.3 The extraction of DNA from disrupted barley leaf material

The DNA was purified using a QIAxtractor instrument (Qiagen: no longer in production)/QIAxtract® protocol. Two racks of filter tips (Qiagen 990610) and a purple elution plate (Qiagen 990602) were placed on the instrument. A rubber gasket (Qiagen 990608) was placed upside down on the lab bench, and a plastic vacuum manifold from the instrument was placed on the gasket and pressed firmly and evenly onto the gasket. The manifold was then placed on the instrument followed by the placement of a carry arm onto the vacuum manifold. Finally, a filter block and capture plate (Qiagen 950911) were positioned according to the QIAxtract® protocol. The buffer reservoirs (volumes specified on screen) were filled and place on the instrument (to make up DXB, 4g (whole bottle) of binding additive (DX: Qiagen 950140) was added to a bottle of DXB (Qiagen 950133). The remainder was stored at 4 °C in the dark). The lysate plate containing the lysate (**Section *2.14.2***) was

positioned on the instrument and a tip bin (with the red lid removed: Qiagen 990550) was attached to the chute of the instrument and the instrument lid was closed. The extraction protocol was run for 90 min. The eluted DNA was pipetted back into the capture plate and spun at 5000 RPM for 2 minutes to increase the yield by roughly 25%.

2.14.4 Designing primers for the KASPar assay of the markers 11_20628, 11_10515, 11_20659 and 11_10747

Using the synteny of barley with the rice genome as a framework, markers within the 10cM region harbouring the *des8* gene, were chosen from the corresponding syntenous region in rice (using the rice genome browser: http://rice.plantbiology.msu.edu/cgi-bin/gbrowse/rice/) to delineate the mutant gene. Assuming that complete synteny between rice and barley holds true, a rice gene within the syntenous region was entered into the EnseblPlants database (http://plants.ensembl.org/index.html) to find the corresponding/homologous gene in barley (11_20628, 11_10515, 11_20659 and 11_10747). A SNP between the Morex and Bowman allele for each marker was chosen from the already established SNP consensus maps and that derived from the Morex x Barke map (Comadran *et al*., 2012) (**Appendix**; 11_20628: **Table A175** on **page 530**, 11_10515: **Table A176** on **page 532**, 11_20659: **Table A173** on **page 526** and 11_10747: **Table A174** on **page 528**), ~20 base pair sequences, one proximal and the other distal to the target SNP, were submitted to KBiosciences® (http://www.kbioscience.co.uk), for which KASP primers were designed (See **Appendix**, **Table A177**: **page 571**). The sequences of the KASP primers designed by KBiosciences® are unknown.

2.14.5 KASPar assay PCR of extracted DNA

The extracted DNA was run on a 1% agarose gel to ensure that there was a sufficient quantity of DNA for the PCR reaction (20-40 ng). 2 µl of each DNA sample was then transferred to each well of a 96 well optical plate. This was then followed by the addition of 2 µl of 2x KASPar v4.0® Reagent and KASP primers to each well (See **Appendix**, **Table A177**: **page 571**). The KASPar v4.0® Reagent and KASP primers were collectively termed the KASP mastermix.

The PCR reaction was carried using a StepOnePlus® PCR machine using a program called KASPar 55 plus 6 cycles as illustrated below:

20 ^{O}C for 2 minutes (Pre PCR read)

94 ^{O}C for 15 minutes

94 ^{O}C for 20 seconds

62 ^{O}C (decreasing by 0.7^{O}C per cycle) for 1 minute (10 cycles)

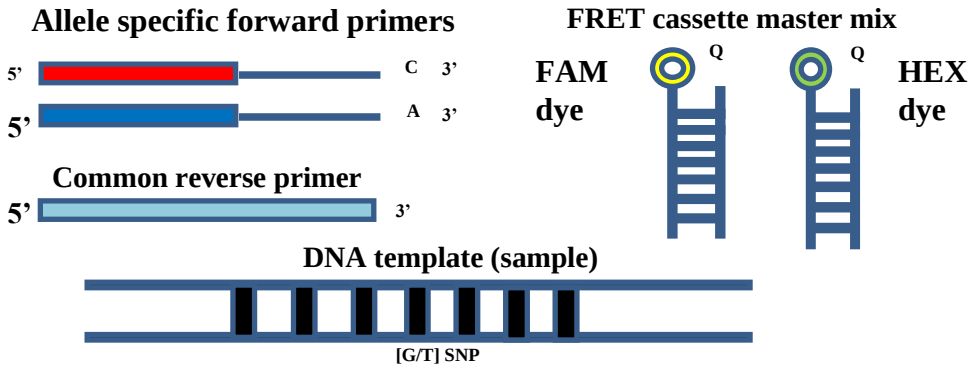
94 ^{O}C for 20 seconds

55 ^{O}C for 1 minute (32 cycles)

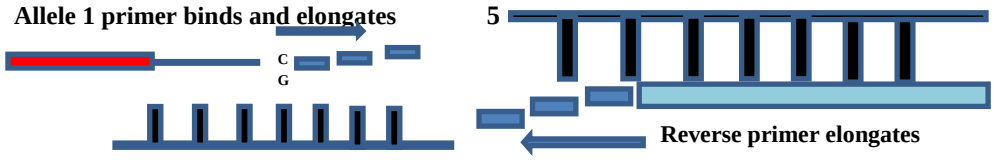
20 ^{O}C for 2 minutes (Post-PCR read)

The KASP mastermix consisted of the FRET cassette reporting system (FAM and HEX labeled 5' tail sequence secondary oligos that are hybridised to a complimentary oligo with corresponding quenchers), Hot-start Taq polymerase, dNTPs and $MgCl_2$ buffer. The three designed primers are the two distinct allele-specific forward primers, each complimentary to the chosen SNP and one common reverse primer (**Figure 2.3(a)**). The initial PCR cycles involved the denaturation of the DNA template and quenched FRET cassette, followed by the hybridisation of the forward primer to one

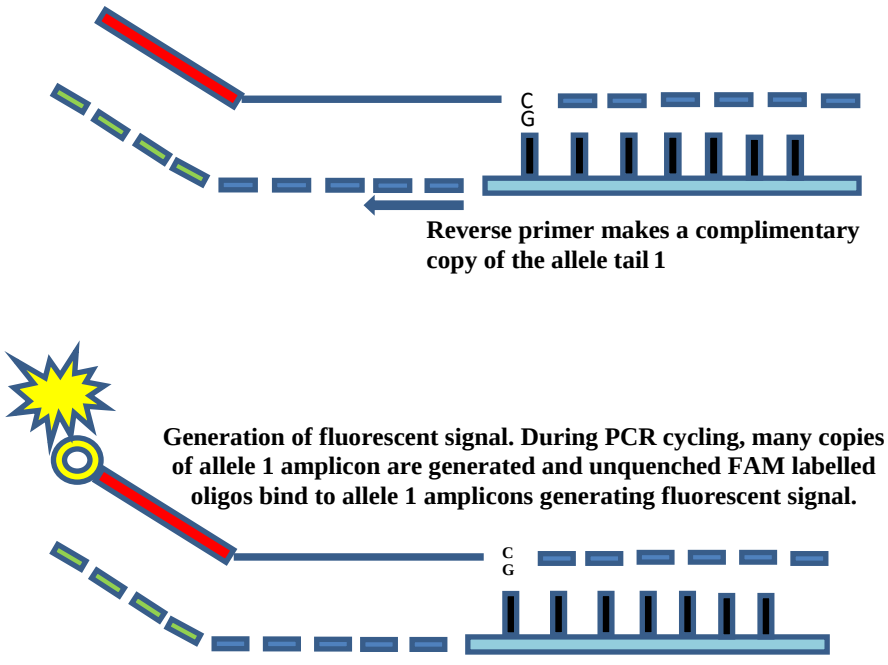
strand of the DNA template and subsequent complimentary base pairing elongation. This step was repeated for the complimentary strand of the denatured DNA template by the common reverse primer (**Figure 2.3(b)**). The second round of the PCR process included the forward primer mediated generation of an allele specific tail end sequnce, followed by the generation of a complimentary copy of the tail by the reverse primer. During the PCR cycling steps, many copies of the amplicon were generated and then unquenched FAM or HEX labeled oligos (depending on the SNP) bind to the tail end of the amplicon, to generate the fluorescent signal (**Figure 2.3(c)**) (adapted from Smith and Maughan, 2015). The fluorescent reading generated by the PCR reaction led to a cluster analysis via the identification of the chosen SNP by the StepOnePlus® software, which was exported and used in the determination of the allelic discrimination.



(a) The KASPar PCR reaction mixture



(b) Denaturation of template and FRET cassette, and annealing (round 1 of PCR)



(c) Compliment of allele specific tail sequence generated (round 2 of PCR)

Figure 2.3: A summary of the mechanism of the KASPar® assay. Adapted from Smith and Maughan, 2015.

2.14.6 Designing primers for the sequencing of the markers MLOC10987, MLOC53985 and MLOC4841

The barley markers MLOC10987, MLOC53985 and MLOC4841, were also chosen based on the synteny of the *des8* region with rice, as outlined in **Section *2.14.4***. By taking into account that the *des8* line was crossed with Morex for this investigation, the full genomic (introns and exons) sequence of the Morex genes MLOC10987 (contig 1560156: **page 543**), MLOC53985 (contig 38798: **page 562**) and MLOC4841 (contig 135563: **page 552**) were run against the corresponding Bowman gene using the JHI in-house software (Barley cultivar contig library: http://bioinf.hutton.ac.uk/iselect/app/), to identify any contigs with SNP(s). A ~100bp sequence around the region of the chosen SNP(s) was used to design the forward and reverse primers using the online Primer3 software (http://bioinfo.ut.ee/primer3-0.4.0/). The G-clamp was set at 2 and the primer sequences calculated by primer3 were also provided with an expected product size. The expected product size data (**Appendix**, **Table A177**: **page 571**) enabled the primers to be tested once they were obtained (the required primer sequences were submitted to Sigma for primer synthesis) via the PCR amplification of the genomic DNA templates isolated from the barley cultivars Morex, Bowman, Barke and Golden Promise. The PCR products were then run on 1% agarose gel (along side an appropriate DNA ladder).

2.14.7 PCR amplification of genomic DNA and sequencing of markers using Big Dye version 3.1

The genotyping (SNP determination) of the markers MLOC10987, MLOC53985 and MLOC4841 was carried out by Big Dye version 3.1 sequencing of the *des8* genomic DNA (**Chapter 5**: **Section *5.2.4***). The already extracted genomic DNA (as outlined in

Section *2.14.3*) was amplified using the Hot Start PCR method using the reaction mix shown in **Table 2.13**, which was subjected to the temperature cycle as shown in **Table 2.14**. The amplified DNA was then subjected to an ExoSap PCR procedure (reaction mix shown in **Table 2.15**) which is an enzyme catalysed cleanup of the PCR product which destroys any unincorporated dNTPs and primers, according to the temperature cycle shown in **Table 2.16**. Finally, the PCR product/ExoSap mixture was subjected to the Big Dye sequencing PCR procedure (reaction mix shown in **Table 2.17**: total volume of 10 µl), according to the temperature cycle shown in **Table 2.18**.

Table 2.13: The reaction mix required for the Hot Start PCR cycle.

Reagent	**Volume used (µl)**
10x Hot Start Taq Buffer (Qiagen 203203).	1
dNTP mix (roche 200uM: 11 581 295 001).	1
Foward primer (1µM)	1
Reverse primer (1µM)	1
Hot Start Taq polymerase (5U/ul: (Qiagen 203203).	0.1
DNA (10-50ng)	1
SDW	4.9

Table 2.14: The Hot Start temperature cycle.

Temperature (°C)	Duration (min)	Cycles.
95	15	Hold
94	3	1
66	1.5	
72	1	
94	0.5	5 (decreasing by 1°C per cycle).
65	1.5	
72	0.5	
94	0.5	24
60	1.5	
72	0.5	
72	5	Hold
8	Forever	Hold

Table 2.15: The reaction mix required for the ExoSap PCR procedure.

Reagent	Volume used (µl)
PCR product	**5**
ExoSap	2

Table 2.16: The ExoSap temperature cycle.

Temperature (°C)	Duration (min)	Cycles.
37	0.25	1
80	0.25	1

Table 2.17: The reaction mix required for the Big Dye version 3.1 sequencing cycle.

Reagent	Volume used (µl)
PCR/ExoSap mixture	3
10µM primer (life Technologies 4337455).	1
Big Dye dilution buffer (life Technologies 4337455).	1.5
Big Dye v3.1 (life Technologies 4337455).	1
SDW	3.5

Table 2.18: The Big Dye version 3.1 temperature cycle.

Temperature (°C)	Duration	Cycles.
96	10 sec	30
50	5 sec	
60	4 min	

2.14.8 The precipitation of DNA from the sequencing reaction mixture

To 10 µl of the reaction mixture (per well) in the 96-well PCR plate from **Table 2.17**, 2.5 µl 125mM EDTA (ph8.0) was added, and was subjected to a pulse centrifugation at 13,000 RPM and vortexed. Then, 30 µl of 95% ethanol was added before being vortexed and pulse centrifuged at 13,000 RPM. The mixture was left at room temperature for 15 min and was centrifuged at 3,000 RPM for 30 min at 4°C, then inverted before being centrifuged again at 100g for 10 sec on tissues. The remaining pellet was washed with 150 µl of 70% ethanol, briefly vortexed and centrifuged at 3,000 RPM for 10 min at 4 °C. Following this, each tube was inverted on a tissue to expel most of the liquid, centrifuged whilst inverted at 100g for 10 sec on tissues and washed again with 150 µl of 70% ethanol. The mixture was vortexed again, centrifuged at 3,000 RPM for 10 min at 4 °C and inverted on a tissue to expel most of the liquid. The remaining liquid was expelled by centrifuging upside down at 100g for 10-20 sec and the remaining pellet was allowed to bench dry at room temperature (the EDTA and ethanol must be added separately to the reaction mixture because adding both at the same time or making a mastermix causes EDTA to precipitate out, leading to salt deposits in the wells. 96-well PCR plate containing the purified product, was submitted to the genomics department (JHI) to generate sequence reads which were analysed to determine the genotype based on the SNP(s).

2.15 The genetic screening of the TSA treated marker population

The F1 generation of a Morex v Barke cross, was pulse treated with 100 ng/ml TSA for 2 hr at meiosis, before being washed out with SDW by myself during a placement at The James Hutton Institute. The treated stems were allowed to produce seeds, which were extracted by Malcolm Macaulay (JHI), sown and left to germinate to generate the F2 population. The shoots were left to grow over a period of approximately two weeks, until they reached a length of between 10 and 15 cm.

The young leaf tips of each barley shoot were cut and genetically screened using SNP based marker sequencing by Malcolm Macaulay (JHI) using the BeadXpress® Platform. The SNP chosen for each marker for a specific chromosome was identified by the BeadXpress® software and determined if the marker was of Morex or Barke origin. This was repeated for the remainder of the chosen markers on the same chromosome for each individual. This data was exported by Malcolm Macaulay (JHI) and used to generate a genetic map showing all of the alleles in the order of the genetic sequence of the markers along the chromosome (**Appendix**: **Tables A5-A172** (**page 355** to **523**)).

The screening data was interpreted by myself at The University of Birmingham (UoB), to determine the mean marker recombination frequencies for the control and treated populations, to ascertain the effect of the TSA treatment on the marker recombination frequency and distribution. The exported data was formatted such that an individual that was homozygous for the Morex allele was denoted as **A** (turquoise box), one that was homozygous for the Barke allele was denoted as **B** (Orange box) and a heterozygote was denoted as **H** (lilac box) (**Appendix: Tables A5-A172**). A single recombination event was determined as the switch from homozygous B to homozygous A, homozygous A to homozygous B, homozygous B to Heterozygous H,

homozygous A to Heterozygous H, Heterozygous H to homozygous B and Heterozygous H to homozygous A (**Appendix: Tables A5-A172**). The order of the markers (from left to right: **Appendix: Tables A5-A172**) reflect the order of the makers from the distal end of the short arm towards the distal end of the long arm on each chromosome. Excerpts from **Tables A167** and **A170** are shown as an example (**Figure 2.4**). For screened genomic DNA (long arm of chromosome 7H) that was extracted from an F2 shoot derived from a seed produced by an F1 plant (**MxB F1_1_TSA_1_seed_12**: **Figure 2.4**) that was treated with TSA, there is a change in genotype from heterozygous to Morex allele and then a change from Morex allele to Heterozygous. This indicates two recombination events in the excerpt (each recombination event is depicted by a black arrow: **Figure 2.4**). The number of recombination events were determined in separate tables of the same format allowing the genotype data (**Appendix: Table A167)** to be superimposed (as shown in **Figure 2.4**) with the recombination data (a single recombination event was denoted as the number **1**: **Appendix: Figures A170**). Markers that were nearest to the centromere were in a yellow shaded cell. The total number of recombination events per chromosome for a single individual was then determined using the recombination data (summing up the recombination events in the short and long arm) (**Appendix: Figures A5-A172),** collated and then the screen was repeated for the remainder of the individuals from each population to determine the mean number of marker recombination events for each chromosome (n=90 individuals) (**Appendix: Figures A5-A172**).

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99
Morex SNP	G	G	c	a	T	g
Barke SNP	c	a	a	g	a	c
MxB_F1_1_TSA_ear_1_seed_1	H	H	H	H	H	A
MxB_F1_1_TSA_ear_1_seed_10	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_11	H	H	H	H	H	B
MxB_F1_1_TSA_ear_1_seed_12	H	H	H	H	A	H
MxB_F1_1_TSA_ear_1_seed_13	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_3	H	H	H	H	A	A

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99
Morex SNP	G	G	c	a	T	g
Barke SNP	c	a	a	g	a	c
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_10	1	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_12	0	0	0	0	1	1
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_2	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	1	0

Figure 2.4: The determination of SNP marker recombination frequency using exported genotyping data generated via the BeadXpress® Platform. Excerpts from the Appendix (Tables A167 and A170) are shown for screened genomic DNA (long arm of chromosome 7H) that was extracted from an F2 shoot derived from a seed produced by an F1 plant (MxB F1_1_TSA_1_seed_12) which was treated with TSA. There is a change in genotype from heterozygous to Morex allele and then a change from Morex allele to Heterozygous (top table). This is indicated as two recombination events in the superimposed table showing each recombination event as (1) (bottom table). The point of each recombination event is depicted by a black arrow.

2.16 Image capture and processing

All of the microscope slides were viewed with a Nikon T600 fluorescence microscope. Smart capture 2.0 software was used to capture and process the images. The photographs of the barley ears were taken with an Olympus OM-D E-M5 camera fitted with a 60 mm F2.8 macro lens, and were processed using a technique called "High Dynamic Range" to correct for the contrast between the subject and the background.

2.17 Statistical analysis and representation of numerical data

All statistical analysis (p values) used to compare the mean telomere counts (**Chapter 3**), including the mean chiasmata frequencies at metaphase I in the TSA experiment (**Chapter 4**) and the analysis of the *des8* mutant (**Chapter 5**), was carried out via single factor ANOVA on Microsoft Excel® (Windows®). Statistical analysis for the genetic screening of the marker population treated with TSA (**Chapter 4**) was carried by single factor ANOVA and chi-square tests. All data are represented as the mean +/- standard deviation (SD).

CHAPTER 3

INVESTIGATING THE ROLE OF TELOMERES IN THE PAIRING OF HOMOLOGOUS CHROMOSOMES.

3.1 INTRODUCTION:

The primary role of telomeres is protecting the ends of the chromosomes (Shakirov *et al*., 2004). Much thought has also been placed on the role of telomeres as means of allowing the large scale movement of homologous chromosomes at early meiosis. This pairing of the chromosomes allows for subsequent downstream meiotic events such as synapsis and recombination to occur. It is thought that in Eukaryotes a universal structure called the bouquet, plays a central role in facilitating the initial pairing of homologous chromosomes at the telomeric ends (Scherthan, 2001), prior to global chromatin reorganisation at the onset of synapsis during the first meiotic division (Schwarzacher, 2003).

The bouquet was initially discovered in the late 1800's by light microscopy but its role in the meiotic pathway was unclear before the rapid advancements in chromosomal studies (reviewed by Scherthan, 2001). The meiotic bouquet, whereby the telomeres are clustered on the nuclear envelope and the chromatin radiates out as in a bouquet of flowers. It has been suggested that the bouquet is a highly conserved structure and hence, has a conserved role in meiosis due to its prevalence in a wide range of species (Bass, 2003). For example, in other Eukaryotes such as fission yeast, it was found that the telomeres clustered to form an elongated chromatin structure that strongly resembles the bouquet (Chikashige *et al*., 1994). The same was so for budding yeast (Trelles-Sticken *et al*., 2003). The *Poaceae* family such as barley (Higgins *et al*., 2012), oat-maize addition lines (Bass *et al*., 2000) and wheat (Richards *et al*., 2012) display a classical bouquet structure, which is characterised by the tight clustering of the telomeres within in small region on the inner face of the nuclear envelope (reviewed by Bass, 2003). The same structure has been found in the animal group of Eukaryotes such as *Chlorthippus parallelus* (grasshopper)

(Darlington, 1937), Salamander (Kezer *et al*., 1989), mice (Scherthan, 2000) and humans spermatocytes (Rasmussen and Holm, 1978). The bouquet is not so well displayed in *Arabidopsis* (see **General introduction**, **page 46**). The sequence of events leading up to bouquet formation is common amongst most species in that the clustering of telomeres is initiated at leptotene, completes at zygotene and remains until pachytene (Bass, 2003).

This chapter will attempt to confirm the importance of the bouquet and hence clarify whether or not the structure is indispensable with regard for promoting telomere pairing by the treatment of barley with colchicine.

Preliminary results

3.2 A detailed preliminary time course study:

3.2.1 The administration of chemicals into the transpiration stream

A preliminary time course study with the cultivar Morex was undertaken in order to estimate the duration of meiosis as well as the time of the onset of the individual stages of this pathway, allowing for the successful targeting of specific stages by various chemicals. Although the meiotic time course for Morex was already established by Higgins *et al*. (2012), the time course was repeated to gain an understanding of the methodology used to establish a time course and to account for any variations that may have arisen due to changes in growth conditions. Also, the time course in this study included more time points than the previous study (Higgins *et al*., 2012) to increase the accuracy of the time course. Each time point was analysed in triplicate (three plants ranging from 31 to 36 cm in height) so that a range of anthers at various meiotic stages could be spread onto a single microscope slide (the total number of meiotic nuclei at each time point (per microscope slide) are shown in

Table 3.1 (a total of 1,316 meiotic nuclei were analysed in the whole time course study: **Table 3.1**). Approximately 300 µl BrdU was injected directly into the region of each stem containing the spike allowing for its uptake at meiotic S-phase.

The study showed that at time -2 hr, there is no uptake of BrdU, but it is taken up by the anther meiocytes at the end of the 2 hr pulse at G2 (0 hr: **Table 3.1 and Figure 3.1(a)**). The time of the first appearance of the BrdU labelling at a specific meiotic stage was taken as the time point of the onset of that specific stage. Even though the BrdU was washed out of the stems at the end of the 2 hr pulse, nuclei at meiotic interphase were still appearing labelled with BrdU as it would still be present in the anthers and spikes. However, this investigation did not provide data on the duration of the persistence of BrdU in the spikes.

3.2.2 The duration of G2 and leptotene:

The duration of each stage was determined by deciphering the time point of the first appearance of BrdU at that stage and then the end point of that stage was determined as the time point at which BrdU first appeared at the next meiotic stage. In this case, the duration of G2 was the time taken for the cells to progress from the end of S-phase to the beginning of leptotene because BrdU could only be taken up by DNA synthesis. After the first appearance of BrdU at meiotic G2 at time 0 hr (**Table 3.1; Figure 3.1(a)**), the first appearance of BrdU at leptotene was at +17 hr (**Figure 3.1(d)**), giving a 17 hr duration for meiotic G2 (**Table 3.1**). The meiotic nuclei are much larger than somatic nuclei, but there seemed to be two sub-groups of nuclei at this stage. One sub-group of nuclei were smaller and did not harbour a prominent nucleolus and corresponded to G1, whereas nuclei at G2 were slightly larger and

contained a much more prominent nucleolus. G1 and G2 were both characterised with uncondensed chromatin.

The first appearance of BrdU labelled leptotene nuclei were at +17 hr, as was mentioned above and its duration was 4 hrs (**Table 3.1**). Leptotene was identified by slight condensation of chromatin (**Figure 3.1(e)**).

3.2.3 The onset and duration of zygotene:

Zygotene (**Figure 3.2(a)**) and subsequent stages were much easier to identify as the stages are completely distinct whereas it is difficult to differentiate between meiotic interphase and leptotene (due to low levels of chromatin condensation). The first appearance of the BrdU label at zygotene was at +24 hr (**Table 3.1**) and its first appearance at pachytene was at +32 hr (**Table 3.1; Figure 3.2(d)**), placing the duration of zygotene at 8 hrs.

3.2.4 The onset of pachytene and metaphase I:

The first appearance of the BrdU label at pachytene was at +32 hr (**Table 3.1**) and its first appearance at metaphase I was at +40 hr (**Table 3.1; Figure 3.3(a)**), placing the duration of pachytene/diplotene/diakinesis at 8 hrs.

3.2.5 The duration of metaphase I, the onset of tetrads and the overall duration of the meiotic pathway:

The first appearance of the BrdU label at tetrad stage was at +43 hr (**Table 3.1; Figure 3.3(d)**), placing the duration of metaphase I at 3 hrs. In addition, the first appearance of BrdU at tetrad stage in the time course (+43 hr) established the duration of meiosis from G2 to tetrad, at 43 hrs.

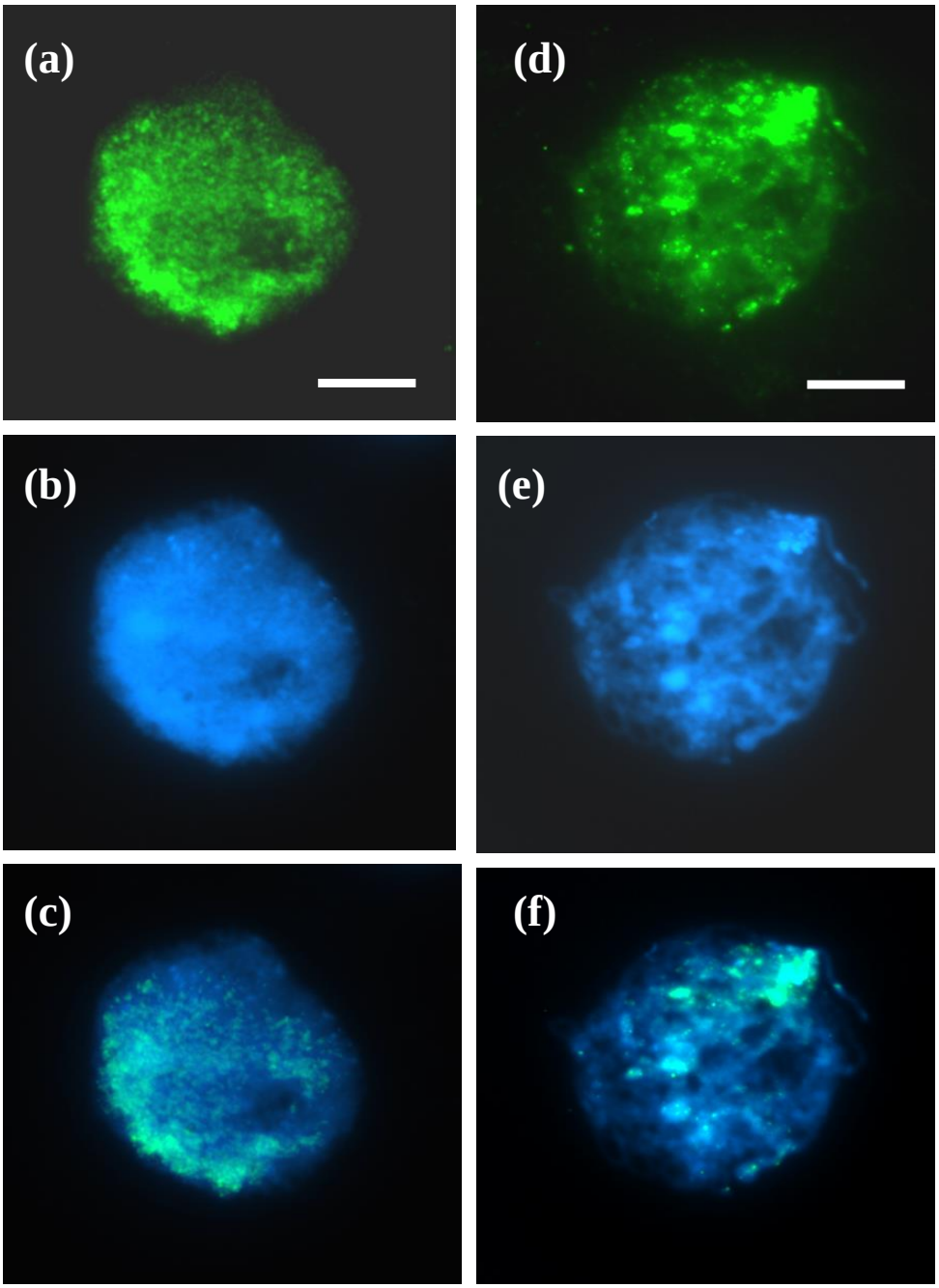


Figure 3.1: The first appearance of BrdU (detected with anti-mouse Ig flourescein) (FITC: green) labelled DNA at G2 (0 hr: (a), (b), (c)) and leptotene (+17 hr: (d), (e), (f)). DAPI counterstain in blue. Bar = 10 µm

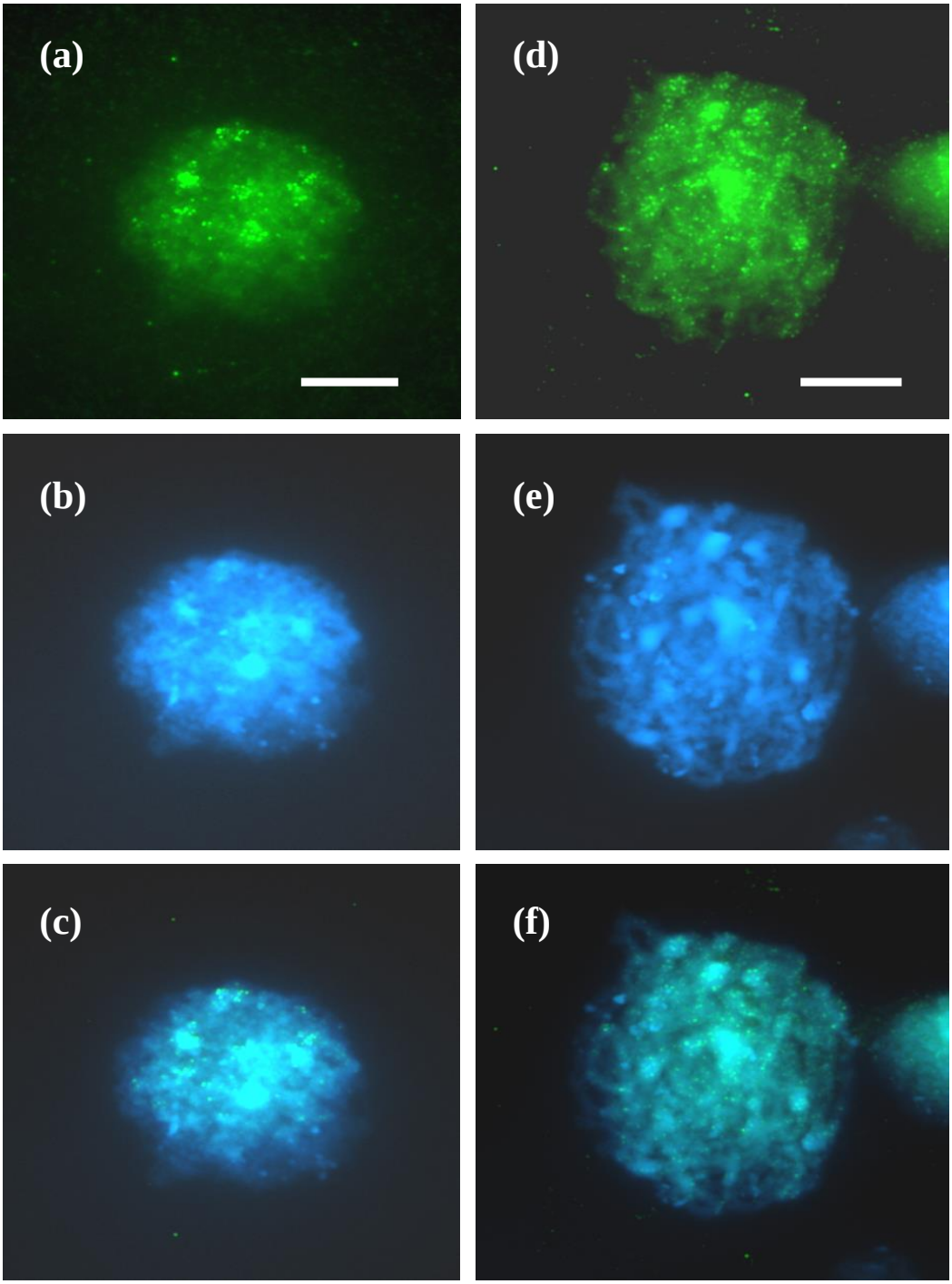


Figure 3.2: The first appearance of BrdU (detected with anti-mouse Ig flourescein) (FITC: green) labelled DNA at zygotene (+24 hr: (a), (b), (c)) and pachytene (+32 hr: (d), (e), (f)). DAPI counterstain in blue. Bar = 10 µm

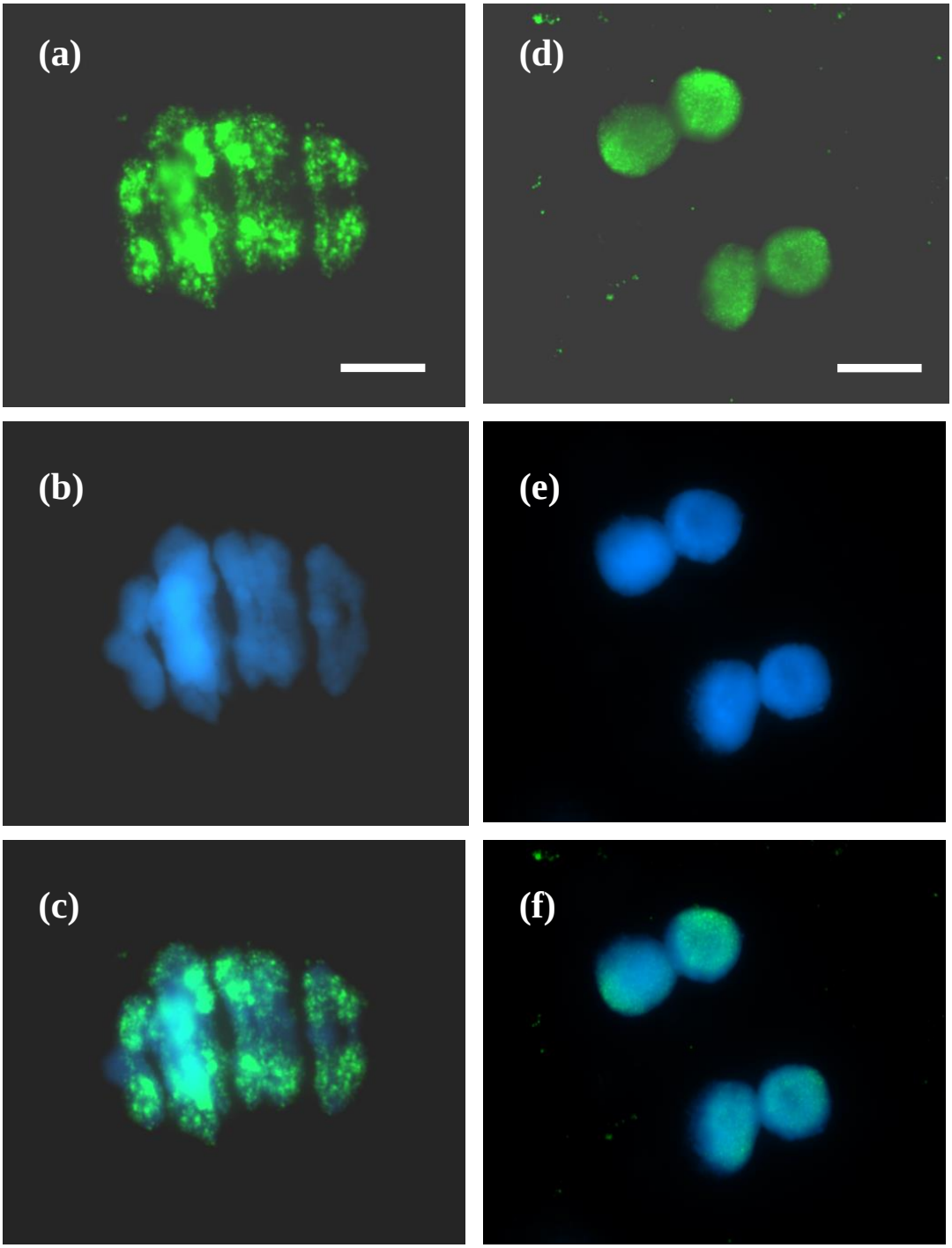


Figure 3.3: The first appearance of BrdU (detected with anti-mouse Ig flourescein) (FITC: green) labelled DNA at metaphase I (+40 hr: (a), (b), (c)) and tetrad stage (+43 hr: (d), (e), (f)). DAPI counterstain in blue. Bar = 10 µm

Table 3.1: The BrdU time course. The number of nuclei at a specific meiotic stage labelled with BrdU against the total number of nuclei at the same stage. The percentage of nuclei that are labelled are shown in parenthesis, with yellow boxes highlighting the first appearance of BrdU at the specific meiotic stage.

Meiotic stage / Time of fixation (h)	Interphase	Leptotene	Zygotene	Pachytene	Diplotene	Diakinesis	MI	Tetrad	Total no. of nuclei at time point.
0	13/28(46.4)	0/6(0)	0/0(0)	0/23(0)	0	0	0	0	57
10	28/45(62.2)	0/5(0)	0/4(0)	0/35(0)	0/7(0)	0	0	0	96
16	19/35(54.3)	0/11(0)	0/7(0)	0/20(0)	0	0	0	0	73
17	14/26(53.8)	3/14(21.4)	0/6(0)	0/38(0)	0/2(0)	0/2(0)	0/4(0)	0/1(0)	93
20	64/122(52.5)	5/10(50)	0	0/33(0)	0	0	0	0	165
23	6/32(18.8)	2/11(18.2)	0/11(0)	0/22(0)	0	0/6(0)	0/8(0)	0/3(0)	93
24	26/46(56.5)	9/18(50)	2/18(11.1)	0/41(0)	0/6(0)	0	0	0/1(0)	130
25	11/23(47.8)	3/6(50)	3/10(30)	0/24(0)	0	0	0	0/3(0)	66
26	45/75(60)	10/19(52.6)	6/14(42.9)	0/4(0)	0	0	0	0	112
31	5/14(35.7)	1/3(30)	2/4(50)	0/22(0)	0/2(0)	0/1(0)	0/7(0)	0/3(0)	56
32	6/16(37.5)	1/3(30)	1/4(25)	3/41(7.3)	0/5(0)	0/3(0)	0/6(0)	0/1(0)	79
33	17/34(50)	3/5(60)	1/2(50)	16/23(69.6)	0	0	0	0	64
39	5/20(25)	2/11(18.2)	2/4(50)	3/17(17.6)	0/3(0)	0/4(0)	0/9(0)	0/11(0)	79
40	3/14(21.4)	2/8(25)	2/3(66.7)	0/8(0)	0/2(0)	0/2(0)	2/15(13.3)	0/3(0)	55
42	2/16(12.5)	1/7(14.3)	0/2(0)	3/8(37.5)	0/2(0)	0/3(0)	0/11(0)	0/8(0)	57
43	3/9(33.3)	1/3(33.3)	1/2(50)	3/10(30)	0/3(0)	0/2(0)	0/3(0)	2/9(22.2)	41
Total number of meiotic nuclei in the complete time course study									1316

3.2.6 The establishment of a meiotic time course

The establishment of the meiotic time course and hence, the knowledge of the onset of specific meiotic stages would be implicated in later chapters where meiocytes at specific meiotic stages are isolated for cytological studies (the affect of chemical intervention on telomere bouquet formation in this chapter and chiasmata frequency and distribution in **Chapter 4**).

Past investigations have proved to be more difficult as tritiated thymidine was commonly used to label replicating DNA, but this method has proved to be a rather cumbersome and lengthy process. However, this method was successfully used to determine the duration of meiosis in wheat (~24 h), rye (~51 hr) and Triticale (~21 h) (Bennett *et al*., 1971).

Due to the complex nature of meiosis with its various checkpoints, it takes a longer duration for this process to complete in comparison to mitosis. One study using the seedling cells of *Arabidopsis* placed the duration of mitosis at 22 °C at 8.5 h (Van't Hof *et al*., 1978), whereas the meiotic pathway has been established with a longer duration of 33 h at 18.5 °C (Armstrong *et al*., 2003). Regardless of the complex nature of meiosis, many male animals to not have certain meiotic checkpoint but the meiotic process has been shown to have a significantly longer duration than that of plants. The duration of the meiotic pathway in *Drosophila melanogaster* was placed at 4 days (Chandley and Bateman, 1962) and 24.3 days in *Homo sapiens* (Heller and Clermont, 1963).

The establishment of the meiotic time course is also a crucial tool which is used to decipher the timing of important molecular events that compromise important functions. The meiotic time course for *Arabidopsis* (Armstrong *et al*., 2003) has allowed for further investigations into the role of AtMSH4 as a protein that is

involved in early recombination events (Higgins *et al*., 2004). The establishment of the meiotic time course in barley has acted as a guide to help elucidate the function of HvZYP1 (Barakate *et al*., 2014).

3.3 Results

3.3.1 Using the effect of colchicine to investigate the role of telomere pairing in the homology search

Various past studies have utilised chemical intervention to better understand the meiotic pathway, with the microtubule destabilising chemical colchicine being used to investigate the functional importance of the bouquet. In barley, the number of telomere signals clustered to form a bouquet at zygotene in nuclei treated with 100 µM, were greater than that in the control nuclei. In addition, the telomeres showed a more "*scattered*" arrangement in the treated nuclei (**Figure 3.5**) in comparison to the control nuclei (**Figure 3.4**), in which the telomeres were tightly associated showing that some telomeres did fail to congregate resulting in a partial disruption of the telomere cluster. In both Figures, the telomeres are shown as red (Cy3) and the centromeres are shown as green (FITC).

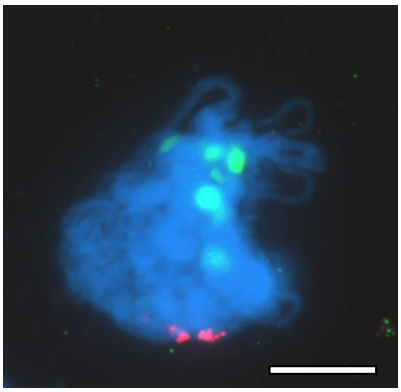


Figure 3.4: The classical bouquet conformation at zygotene in the cultivar Morex (untreated control). The telomeres were tagged with the telomere-DIG probe and detected with anti-DIG rhodamine (red). The centromeres were tagged with the centromere-BIO probe and detected with Streptavidin-FITC (green), with DAPI counterstain (blue). Bar = 10 µm

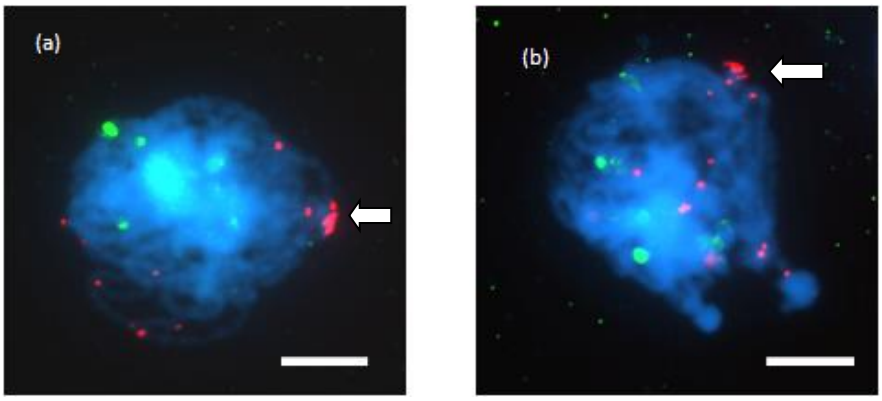


Figure 3.5: The partially disrupted telomere bouquet at zygotene in the cultivar Morex, (a) and (b), showing the displaced telomeres, resulting in a partially disrupted bouquet after a treatment with 100 µM colchicine. The arrows represent the region where most of the telomeres have successfully clustered, forming a partial bouquet. Telomeres were tagged with the telomere-DIG probe and detected with anti-DIG rhodamine (red). The centromeres were tagged with the centromere-BIO probe and detected with Streptavidin-FITC (green), with DAPI counterstain (blue). Bar = 10 µm

3.3.2 The colchicine time course: Identification that the same stage is being observed in the control and test

Both the control stems and test stems were subjected to a 2 hr BrdU pulse, allowing this investigation to be undertaken as a time course. Both the control and test spikes were fixed at time +25 hrs and any BrdU label that was observed, would indicate that the nuclei are at zygotene stage. This was very important in the context of this investigation because an assurance had to be made that the nuclei being observed in the control sample were at the same stage as that in the test sample. In addition, the very nature of this investigation was to investigate the effect of colchicine on telomere pairing and hence, bouquet formation. However, once correctly paired, the telomere pairs begin to separate at late zygotene (Bass, 2003) and this observation may be confused as an "*effect*" by colchicine. By sampling at +25 hrs, it was ensured that only nuclei at early zygotene would be labelled and therefore any observable effect on telomere pairing at this time point would be attributable to the effect of colchicine and not the natural separation of the already paired telomeres, which is observed at late zygotene in all Eukaryotes (Bass, 2003).

Interestingly, it was observed that colchicine did disrupt the clustering of the telomeres in bouquet formation, however it did not disrupt the pairing of the homologous telomeres (**Figure 3.7**). The controls are depicted in **Figure 3.6** showing the tight clustering of the telomeres. In both the control and treated Figures (**3.6** and **3.7**), BrdU was visualised by the FITC filter (green) and the telomeres were visualised by the Cy3 filter (red).

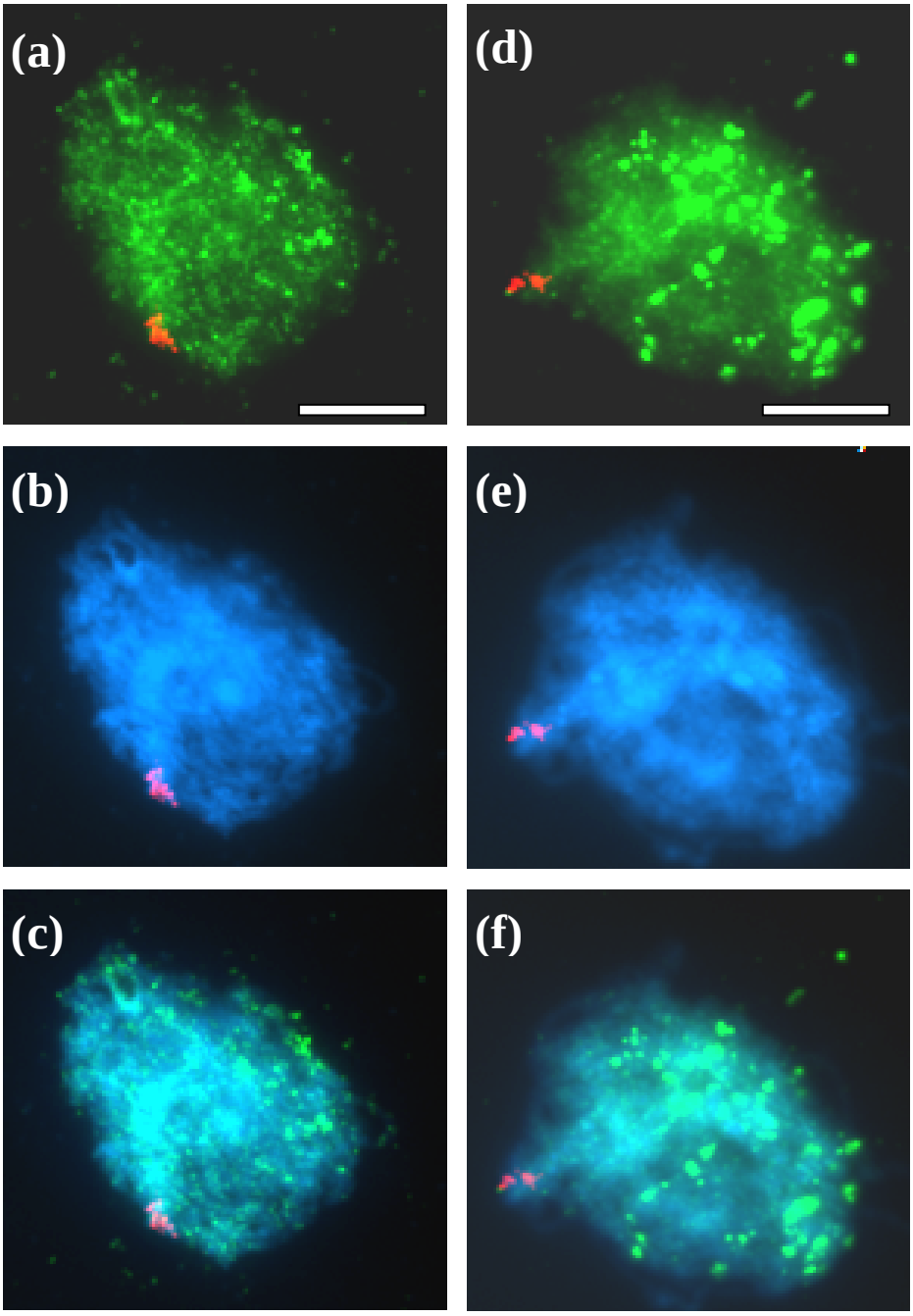


Figure 3.6: FISH detection of the telomere bouquet structure, in two untreated (control) samples (merged: (c) and (f)) showing the clustering of approximately 14 telomeres ((b) and (e)) (tagged with the telomere-DIG probe and detected with anti-DIG rhodamine: red) at zygotene stage in conjunction with a BrdU time course study (+25 hr) ((a) and (d)). BrdU was detected with anti-mouse Ig flourescein (green) and chromatin detected with DAPI counterstain (blue). Bar = 10 µm.

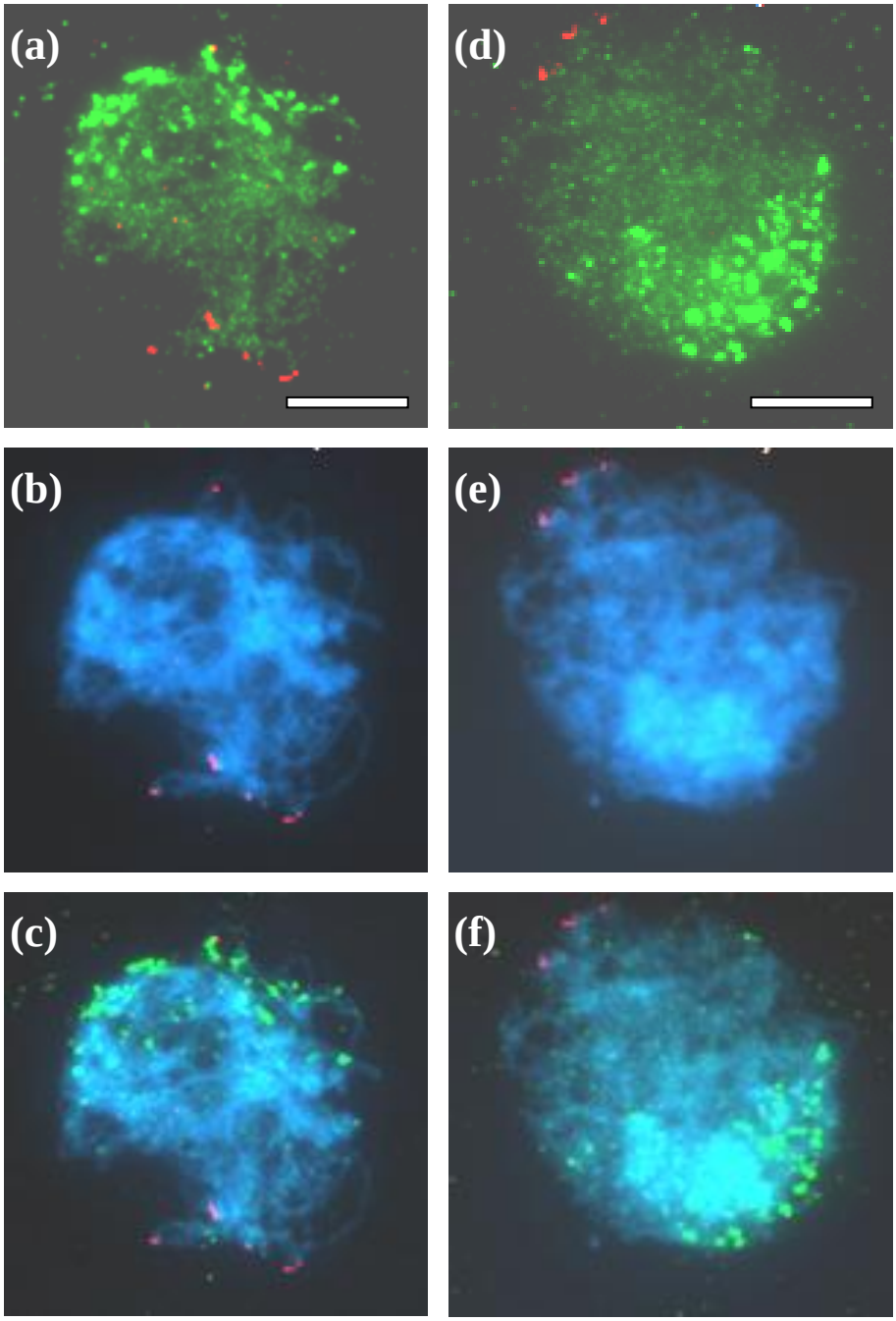


Figure 3.7: FISH detection of the partially disrupted telomere bouquet structure, in two treated (100 µM colchicine) samples (merged: (c) and (f)) showing the clustering of a mean (n=30) of approximately 7 telomeres ((b) and (e)) (tagged with the telomere-DIG probe and detected with anti-DIG rhodamine: red) at zygotene stage in conjunction with a BrdU time course study (+25 hr) ((a) and (d)). BrdU was detected with anti-mouse Ig flourescein (green) and chromatin detected with DAPI counterstain (blue). Bar = 10 µm.

3.3.3 Colchicine disrupts bouquet formation but not the pairing of telomeres at low concentrations (100 **µM***)*

The number of telomere foci, were counted in both the colchicine treated and untreated meiotic nuclei. A further analysis of the total number of telomere foci signals per nuclei revealed that there was no significant difference between the control and test samples. By taking into account the diploid number of barley (2n= 14), we will find 28 telomere foci however, the pairing of homologous telomeres before the first meiotic division leads to the merging of the two homologous telomeres signals to form a single foci, giving a total of 14 foci per meiotic nuclei. The mean total number of telomere foci per cell in the untreated and treated samples, were 14.1 +/- 1.63 SD per cell and 13.93 +/- 1.86 SD per cell, respectively (**Figure 3.9**). Statistical analysis showed no significant difference between the two samples (n= 30, ANOVA p = 0.71). A further analysis of the same nuclei concentrated on counting the number of telomere foci that were clustered together to form the bouquet structure at zygotene. The mean number of telomeres clustered in a bouquet in the control and test samples were 11.63 +/- 2.36 SD per cell and 6.6 +/- 3.19 SD per cell, respectively (**Figure 3.8**). In the test nuclei, telomeres which were not clustered in the partially disrupted bouquet remained dispersed throughout the nuclear periphery. Statistical analysis showed a significant difference between the two samples (n= 30, ANOVA p = 3.54E-09). This result suggests that bouquet formation is sensitive to 100 µM colchicine, whereas telomere pairing is not. Based on this observation, I propose that the pairing of the homologous telomeres and the clustering together of the paired telomeres to form a bouquet, may be controlled to two distinct mechanisms. In wheat-rye additions after the administration of 100µM colchicine, the rye chromosomes could be followed

with GISH and it was shown that the homologous telomeres paired up even though bouquet formation was disrupted (Corredor *et al*., 2007).

An earlier study study in barley showed that bouquet formation occurs as early as late G2 (Higgins *et al*., 2012). This suggests that the telomeres are already paired up at the point of or before the administration of colchicine.

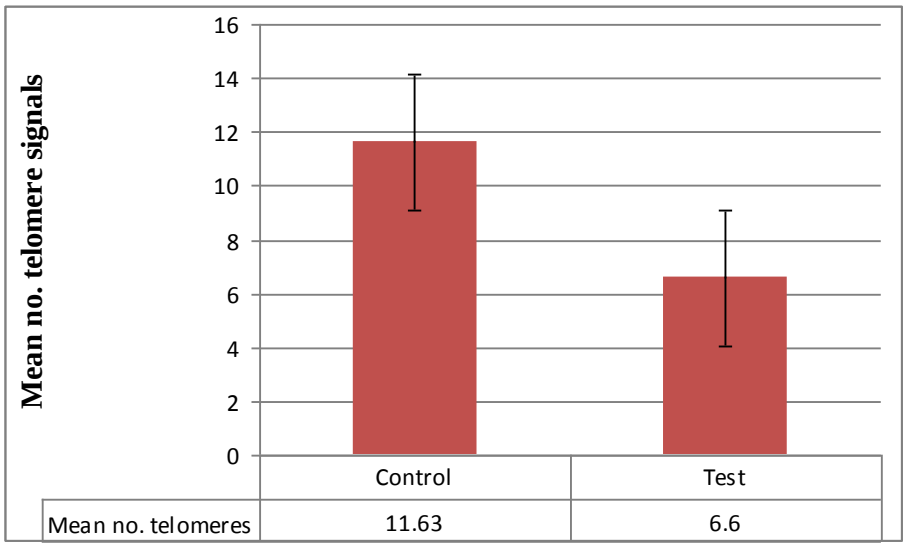


Figure 3.8: A graph showing a significant difference in the mean number of telomere foci clustered together in a bouquet structure at zygotene stage during the time course study (+25 hr), between the untreated control (left) and population treated (right) with 100 µM colchicine (n=30). Standard error bars shown.

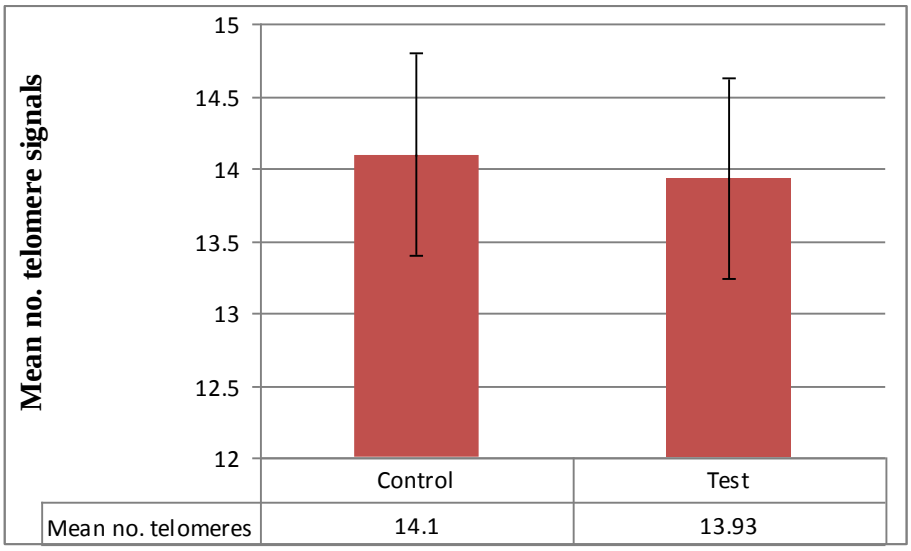


Figure 3.9: A graph showing no significant difference in the mean total number of telomere foci per meiotic nuclei at zygotene stage during the time course study (+25 hr), between the untreated control (left) and population treated (right) with 100 µM colchicine (n=30). Standard error bars shown.

3.3.4 Colchicine disrupts the movement and the pairing of telomeres at high concentrations (5 mM)

Barley meiocytes were also treated with a 50-fold higher concentration of colchicine (5 mM). The mean total number of telomeres per nuclei was determined in both the treated and control samples. It was found that there were a significantly greater mean number of telomere signals in the treated nuclei (19.36 +/- 2.81 SD per cell) compared to that for the control (14.08 +/- 1.47 SD per cell), indicating that there was a disruption in telomere pairing (n= 25, ANOVA p= 7.25E-11) (**Figures 3.10** and **3.12**).

In addition, the mean number of telomeres clustered into a bouquet was determined in both the treated and control samples. It was found that there were a significantly greater mean number of telomere signals clustered to form a bouquet in the control nuclei (11.56 +/- 2.47 SD per cell) compared to that for the test sample (2.04 +/- 2.03 SD per cell), indicating that there was also a disruption in bouquet formation (n= 25, ANOVA p= 1.27E-19) (**Figures 3.10** and **3.11**).

The differing effects of 100 µM and 5 mM colchicine could be due to the fact that telomere pairing is mediated by a different set of tubulin complexes to that which mediate bouquet formation, which differ in sensitivity to different concentrations of colchicine. It has already been noted that there may be other tubulin complexes (δ-, ε-, ζ and η tubulins) that may differ in sensitivity to certain chemical treatments (Dutcher, 2001).

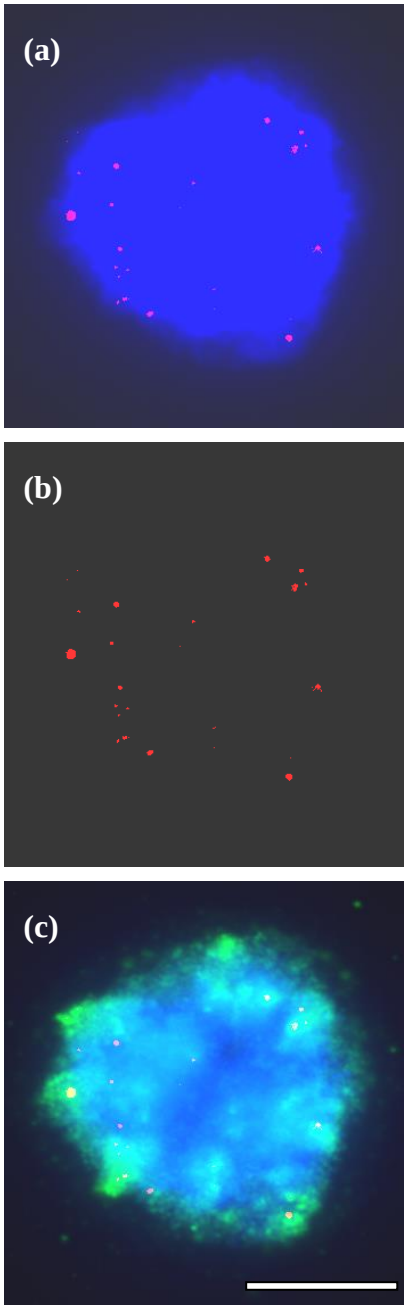


Figure 3.10: FISH detection of the completely disrupted telomere bouquet structure, in a sample treated with 5 mM Colchicine (a), also showing the disruption of telomere pairing (approximately 20 telomere signals: n=25) (tagged with the telomere-DIG probe and detected with anti-DIG rhodamine: red (b)) at zygotene stage in conjunction with a BrdU time course study (+25 hr) (merge: (c)). BrdU was detected with anti-mouse Ig flourescein (green) and chromatin detected with DAPI counterstain (blue). Bar = 10 µm

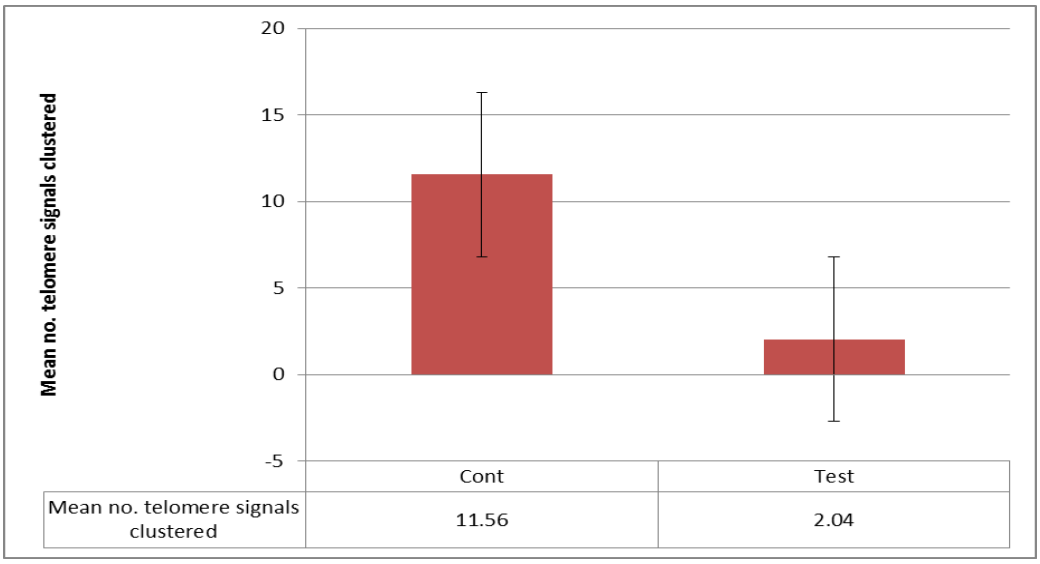


Figure 3.11: A graph showing a significant difference in the mean number of telomere foci clustered together in a bouquet structure at zygotene stage during the time course study (+25 hr), between the untreated control (left) and population treated (right) with 5 mM colchicine (n=25). Standard error bars shown.

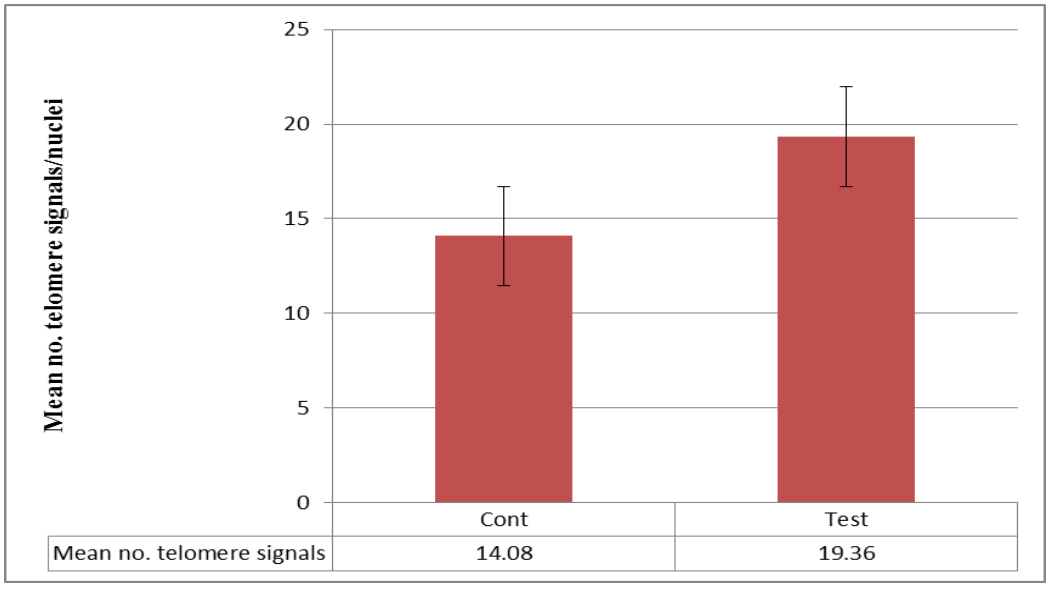


Figure 3.12: A graph showing a significant difference in the mean total number of telomere foci per meiotic nuclei at zygotene stage during the time course study (+25 hr), between the untreated control (left) and population treated (right) with 5 mM colchicine (n=25). Standard error bars shown.

3.3.5 The colchicine-sensitive period in barley

The disruption of the bouquet via the administration of colchicine at the onset of G2, has confirmed that this stage is the colchicine sensitive period in barley. Based on a previous investigation in untreated meiotic nuclei from the same cultivar, it was found that telomere bouquet formation is completed by late G2 (Higgins *et al*., 2012). Therefore, the administration of colchicine at the onset of early G2 just before bouquet formation seems a logical '*window*' in which to disrupt bouquet formation, as was successfully demonstrated in this investigation.

In plant species, the colchicine-sensitive period does vary from one genera to another (Loidl, 1990). The colchicine-sensitive period in wheat has been placed at G1 and the administration of colchicine led to the reduction in chiasma frequency (Dover and Riley, 1973, 1977). In rye it was placed at Leptotene where the treatment with colchicine at this stage, led to the disruption of bouquet formation (Cowan and Cande, 2002). Wheat-rye additions were treated with colchicine at various developmental stages from meiotic interphase to pachytene. The colchicine-sensitive stages ranged from G1 right up to Leptotene and subsequent treatment at any of these stages also led to a disrupted bouquet (Corredor and Naranjo, 2007).

3.4 Discussion

The existence of a classical bouquet structure has been confirmed in a sub-set of grasses, namely rye (Cowan and Cande, 2002) and the related group of cereals such as wheat (Richards *et al*., 2012) and barley (Higgins *et al*., 2012). It is postulated that this structure brings homologous telomeres into close proximity allowing them to carry out a search in which they eventually identify one another and pair up (Cowan *et al*., 2001). Bearing in mind that only a transient bouquet structure has been

observed in *Arabidopsis* (Armstrong *et al*., 2003), the investigation allowed for the direct study of telomere movements by developing a probe complementary to that for the telomere repeat sequence in *Arabidopsis*. The same probe has been used to confirm the existence of a classical bouquet in barley (Higgins *et al*., 2012). Using the same analytical approach as described by Armstrong *et al*., 2003, the effects of the colchicine treatment on telomere behaviour was possible.

The treatment of barley with 100 µM colchicine did lead to a disruption in the migration of some telomeres causing a partial disruption of the bouquet structure. However, it must be pointed out that telomere pairing was not disrupted. In contrast, treatment with 5 mM colchicine not only caused a disruption in bouquet formation but also caused a disruption of telomere pairing. This observation may suggest that telomere pairing and bouquet formation are two distinct processes that are controlled by two distinct mechanisms that differ in colchicine sensitivity (bouquet formation is affected by 100 µM colchicine but telomere pairing is affected by 5 mM colchicine). Even though colchicine is a well known mictrotubule destabilising agent, the investigation suggests that the mechanism controlling the movement of unpaired telomeres to search for a homologous partner and the clustering of the already paired homologous chromosomes, may be under the influence of different types of tubulin complexes which differ in colchicine sensitivity. This possibility has been confirmed in the past where treatments with a range of chemicals have led to a failure in the disruption of the bouquet in some cases despite the fact that they all cause the depolymerisation of microtubules (Cowan and Cande, 2002).

Furthermore, by reassessing the results we find that at a low concentration of colchicine we disrupt bouquet formation but not telomere paring however, at a high concentration we disrupt bouquet formation and telomere pairing. This may suggest

that bouquet formation occurs independantly of telomere pairing. Upon further thought, the data also suggests that disruption of the bouquet will not lead to a disruption in telomere pairing but, a disruption in telomere pairing will lead to a disruption in bouquet formation. This observation points to the possibility that bouquet structure is a chromatin conformation that occurs as a result of telomere pairing. This possibility is supported by studies in budding yeast which investigated the role of the SUN protein MPS3 including NDJ1 and CSM4, which collectively are involved in tethering the telomeres to the cytoskeletal scaffolding. The interpretation of data from *wild-type* and mutant lines of the above mentioned proteins revealed that bouquet formation only occurred in *wild-type* strains and despite the absence of the bouquet in the mutant lines, telomere pairing was not disrupted (Lee *et al*., 2012). The same investigation studied the role of telomere mediated chromosome movements called rapid prophase movements (RPMs) in which the telomeres move randomly leading to contact between non-homologous telomeres as well as homologous telomeres. A collision trap assay revealed a relationship between the spatial migration of telomeres and the rate at which they pair up, supporting the theory that RPMs alone may account for homologous telomere pairing (Lee *et al*., 2012). Furthermore, studies in wild-type *Sordaria* have shown that the telomeres pair up before bouquet formation (Storlazzi *et al*., 2003). Similarly, analysis of mouse oocytes revealed that the initial stages of synapsis between homologous chromosomes occurs in the absence of the bouquet suggesting the possibility of another "force" being accountable for the initiation of chromosome pairing (Tankimanova *et al*., 2004). A further focus on female meiosis in cattle ovaries extracted from fetuses showed a similar pattern (Pfeifer *et al*., 2003).

Contrary to the proposed RPM model put forward by Lee *et al*. (2012), it must be taken into consideration that RPM is dependant on MPS3, NDJ1 and CSM4 and the study of yeast mutant lines of these proteins showed that telomere movements were impeded as well as being more randomly distributed in the nucleus as opposed to being attached to the inner face of the nucleus hence, failing to form a bouquet (Conrad *et al*., 2008). It has previously been demonstrated that telomeres fail to attach to the inner surface of the NE when the Ndj1 binding domain of Mps3 is removed, suggesting that both proteins function as interacting partners in promoting the attachment of telomeres to the NE (Conrad *et al*., 2007). However, the investigation into telomeres movements by Lee *et al*., (2012) demonstrated that the telomeres did pair up in the absence of the bouquet despite displaying mildly impeded movement. This suggests that a combination of non-bouquet mediated RPMs and random Brownian motion of the telomeres is accountable for homologous telomere pairing independent of bouquet formation, given the fact that an absence of the bouquet only led to a delay in the progression of meiosis (Lee *et al*., 2012). Similarly, a delay in chromosome pairing was observed in *csm4* lines that exhibited abnormal bouquet conformations (Conrad *et al*., 2008).

Further studies in which colchicine was used to disrupt bouquet formation in wheat-rye additions, analysis of the cytoskeleton revealed that the chemical treatment had no effect on the integrity of the microtubules despite disrupting bouquet formation, further suggesting the possible role of bouquet-independent RPMs mediating telomere pairing as proposed by Lee *et al*., (2012). Even though SUN/KASH proteins have yet to be characterised in wheat (Richards *et al*., 2012) a mathematical model was used to create a simulation of telomere clustering based on data previously collected regarding telomere kinetics when attached to the NE, assuming each nucleus to be a

perfect sphere (Richards *et al*., 2012). The data revealed that diffusion alone can lead to bouquet formation however, not within the time-frame that is observed in *wild-type* wheat. A trial using a drift model instead, provided a much better fit to the expected values. The proposed theory suggests that pure drift (directed motion) of telomeres brings them within close distance, followed by less significant diffusion in the homology search. A drift model would suggest the need for a role for the cytoskeleton and a SUN/KASH domain (Richards *et al*., 2012) but the study only makes reference to the clustering of the telomeres to form a bouquet instead of telomere pairing. A recent study in maize showed that SUN arranges itself in a half-belt structure along the NE and that the telomeres of the bouquet conformation are located within this structure (Murphy *et al*., 2014). In addition, mutational analysis of this protein revealed an irregular structure of the "SUN-belt", suggesting that SUN is involved in mediating telomere movements during meiosis, but the study didn't demonstrate any evidence of the failure of telomere pairing (Murphy *et al*., 2014). Similarly, even though SUN1 and SUN2 mutants in *Arabidopsis* exhibited incomplete synapsis and reduced chiasma frequency, there was also no reference to any failure of telomere pairing (Varas *et al*., 2015). Reiterating this, studies in *S. pombe* also make reference to the KASH homologue Kms1 in mediating the clustering of telomeres and that telomere pairing in *Arabidopsis* occurs before telomere clustering (the transient bouquet) (reviewed by Roberts *et al*., 2013). Further, a new model suggests that the movement of the chromosome arms is influenced by the premeiotic conformation of the chromosomes (Naranjo, 2014). It was argued that impeded telomere migration occurred more often with chromosomes with short arms with the exception of the short arm of chromosome 1R, which localizes to the bouquet cluster before the short arms chromosomes 5R and 6R. Coincidently, chromosome 1R harbours the NOR and

it has been postulated that the migration of the short arm towards the telomere cluster is aided by nucleolar fusion at early zygotene (Naranjo, 2014).

Bearing in mind that telomeres can pair up in the absence of a bouquet (Lee *et al*., 2012: Corredor and Naranjo, 2007), mathematical models (Richards *et al*., 2012) and recent studies in maize (Murphy *et al*., 2014) have stressed the importance of cytoskeletal mediated telomeres movements via a SUN/KASH domain, but only in the context of bouquet formation (telomere clustering instead of telomere pairing). It has been demonstrated that the bouquet may play a role in the recombination process or act as a scaffold which helps to facilitate the formation of correct recombination intermediates (Storlazzi *et al*., 2010). Null mutant analysis has revealed that Mer3, Mlh1 and Msh4 are vital for a normal bouquet conformation (Storlazzi *et al*., 2010) and it has even been found that RPMs occurs at the same time as early recombination events with the observance of SPO11, REC8 and DMC1 along the chromosome axis (Conrad *et al*., 2008) and mutant lines of the above proteins lead to changes in RPM. Based on this, it has been suggested that such alterations in RPMs are in place to cause a disruption in unstable recombination intermediates. The analysis of associated homologues in *spo11* lines revealed that the intermediate is short-lived possibly due to RPMs forcing the unstable association part (Conrad *et al*., 2008). Analysis of the bouquet in *Tetrahymena* has revealed that the conformation is important for mediating recombination between homologues recombination hotspots by correctly aligning the homologous chromatid regions (Loidl *et al*., 2012). Interestingly, even though the disruption of the bouquet with colchicine in a wheat-rye addition didn't impede telomere pairing, there was an impairment of synapsis (Corredor and Naranjo, 2007; reviewed by Naranjo, 2012), possibly suggesting that there was a failure of sub-telomeric homologous re-association after the RPM mediated disruption of unstable

recombination intermediates (Conrad *et al*., 2008), maybe due to the absence of the bouquet structure. Hence, this observation in the wheat-rye addition (Corredor and Naranjo, 2007) may also support the theory that the bouquet has a role in facilitating the formation of correct recombination intermediates (Storlazzi *et al*., 2010). This possibility was also supported by the analysis of the SUN1 and SUN2 mutants in *Arabidopsis* which exhibited incomplete synapsis (Varas *et al*., 2015).

Additionally, studies have shown that centromere pairing occurs upstream of bouquet formation in budding yeast (Trelles-Sticken *et a*l., 2003) and wheat lines with a deleted *Ph1* locus was shown to exhibit failure of centromere mediated homologue pairing (Aragón-Alcaide *et al*., 1997), it was found that at premiotic interphase, there is considerable association of non-homologues, before telomere pairing. A repeat of the same study in a *Ph1* mutant line revealed that non-homologous centromere association was not alleviated (Martínez-Pérez *et al*., 1999), showing that the locus ensures centromere mediated correct association of homologues (Martinez-Perez *et al*., 2001), hence suggestive of a central role for the Ph1 locus in initiating homologous pairing (Richards *et al*., 2012).

3.5 A proposed model to explain homologous chromosome pairing and telomere clustering

To account for the various effects brought into consideration which show that telomeres can pair up in the absence of a bouquet in this study using barley, in rye (Corredor and Naranjo, 2007) and budding yeast (Lee *et al*., 2012), the presence of an intact cytoskeleton despite a disruption in bouquet formation in wheat-rye additions (Cowan and Cande, 2002) showing evidence against the role of or possibly even an existence of SUN-like transmembrane proteins in cereals (Richards *et al*., 2012), we

also need to take into consideration the initiation of homologous pairing at the centromeres (Aragón-Alcaide *et al*., 1997) as well as the contributing effects of RPMs and directed movements of telomeres (Richards *et al*., 2012).

To neatly marry up the above mentioned scenarios, this study proposes a "directed-diffusion-RPM model". With this model, the centromeres are dragged together to form a cluster, possibly aided by the microtubules to carry out a homology search at premeiotic interphase (Aragón-Alcaide *et al*., 1997). At this stage, the telomeres also attach to the inner face of the NE (**Figure 3.13 (b)**). The directed force that may account for telomere pairing as observed in wheat-rye additions (Richards *et al*., 2012) may be due to the initial clustering of the centromeres, bringing the chromosomes into close proximity allowing for homologous telomeres to pair up by diffusion (**Figure 3.13 (c)**). This can sufficiently account for telomere pairing in the absence of the bouquet as shown in barley, rye (Corredor and Naranjo, 2007) and account for a mechanism other than the role of cytoskeletal microtubules (Cowan and Cande, 2002). Finally, the cluster of paired centromeres breaks down, followed by the clustering of the already paired telomeres to form a bouquet (Aragón-Alcaide *et al*., 1997), with NOR bearing shorts arms clustering (**Figure 3.13 (d)**) before non-NOR bearing short arms (**Figure 3.13 (e)**) (NOR bearing sub-telomeric pairing aided by nucleolar fusion: Naranjo, 2014). Once in the bouquet arrangement with tightly clustered telomeres, RPMs are in place to break down unstable recombination intermediates (Conrad *et al*., 2008). The tight association of telomeres in the bouquet conformation subsequently allows RPMS or diffusion to cause homologous re-association after the breakdown of the unstable intermediates, until stable recombination intermediates are formed, allowing downstream meiotic events to occur.

Indeed we do have a bouquet "involved" in the meiotic recombination process however, the proposed model suggests that the bouquet is not a specialised chromosomal structure as previously thought (Scherthan, 2001) but a chromosomal conformation that "occurs" as a result of centromere pairing and downstream telomere pairing. Further, the bouquet may be a relic of a once vital conformation that was required to help initiate homologous recombination before the evolution of the various recombination proteins, such that the absence of the bouquet in current studies only leads to a delay in meiosis (Lee *et al*., 2012: Conrad *et al*., 2008).

Bearing in mind the proposed model, this study has demonstrated that telomere pairing is one part of a vital process for homologous chromosome association during meiosis.

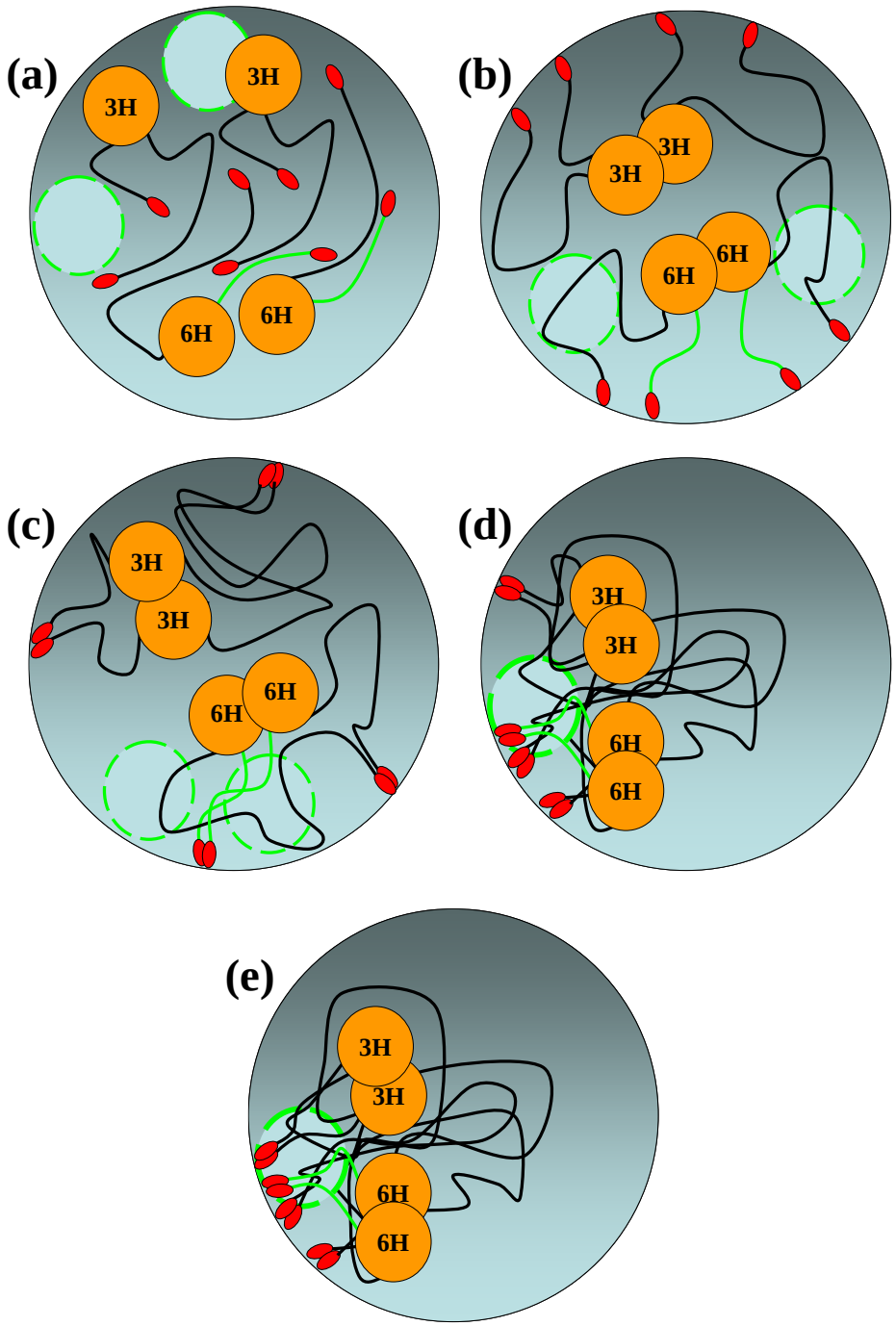


Figure 3.13: A proposed model of homologous chromosome pairing and telomere clustering. The centromeres (orange) cluster and pair at premeiotic interphase (Aragón-Alcaide *et al.*, 1997). The telomeres (red) also attach to the inner face of the NE (b). The clustering of the centromeres brings the telomeres into close proximity (b) allowing for telomere pairing (Richards *et al.*, 2012) (c). Then the paired telomeres of the NOR (green line) short arms (aided by nucleolar fusion (green circle): Naranjo, 2014) and long arms (long black line) cluster into a bouquet before the non-NOR short arms (short black line) (d). The non-NOR short arms cluster last (e).

CHAPTER 4

THE EPIGENETIC EFFECT OF HISTONE HYPERACETYLATION ON MEIOTIC RECOMBINATION FREQUENCY AND DISTRIBUTION

4.1 INTRODUCTION

The epigenetic influences of DNA methylation and histone modifications have been documented in the control of meiotic crossover frequency and distribution (refer to **Introduction**: **Section 1.12** and **Section *1.17.4***). One such factor is the histone methylation status in budding yeast and its influence on the distribution of DSB formation. It has been demonstrated that there is a high abundance of histone H3 lysine 4 trimethylation sites in close proximity to the regions of DSB formation at premeiotic interphase (Borde *et al*., 2009). A deletion of the gene encoding the H3K4 methyltransferase protein SET1, led to a significant reduction in DSB formation in the corresponding regions in comparison to the *wild-type*. However, other regions which exhibit low levels of trimethylation in the *wild-type* were not affected in the test sample (Borde *et al*., 2009). The influence of H3K4 trimethylation on DSB formation has also been observed in mice (Buard *et al*., 2009).

The epigenetic effect of the alteration of CG rich DNA methylation status on meiotic chiasma frequency in *Arabidopsis* has been studied in depth (Yelina *et al*., 2012). The study of *methyltransferase 1* (*met1*) mutants showed that subsequent histone hypomethylation leads to an increase in the proportion of proximal COs around the centromeric regions compared to that for the *wild-type*. This was also accompanied by a reduction in COs in the pericentromeric regions and an increase in distal regions. However, there was no effect on the mean overall chiasma frequency (Yelina *et al*., 2012). The centromeric regions in *Arabidopsis* have a high abundace of repeat sequences (Copenhaver *et al*., 1999) and are these regions of the genome that exhibit the highest abundance of DNA methylation (Yelina *et al*., 2012). Coincidently, it is these highly methylated centromeric regions that lack CO formation (Yelina *et al*., 2012) in contrast to the distal gene rich regions of the genome for which CO

occurrence is preferentially skewed with occasional preicentromeric CO forming in the long arms of the chromosomes due to reduced interference based on the interpretation of high density gene maps (Drouaud *et al*., 2007). The same is also true for barley in that CO distribution is skewed towards the distal regions of the chromosomes (Pedersen *et al*., 1995) that harbour genes which are crucial for the maintenance of key metabolic and developmental pathways (Mayer *et al*., 2012). An in-depth analysis of the effect of hypomethylation on chromosome 3 in *Arabidopsis* showed that there was a significant shift in CO distribution to pericentromeric regions probably due to the fact that the region has a low nucleosome density making the region epigenetically more accessible (Yelina *et al*., 2012). The same effect was observed by Mirouze *et al*., 2012, and alterations in methylation status caused a direct effect on recombination distribution in *cis* rather than *trans* (altering the transcriptional status of key meiotic genes) by way of transcriptomic analysis. The study also revealed that the methylation status can vary within a species potentially influencing shifts in recombination distribution that are crucial for driving evolutionary changes in plants (Mirouze *et al*., 2012).

Another form of epigenetic modification is the acetylation status of chromatin associated histones. The study of yeast strains harbouring a mutated gene which encodes a histone deacetylase protein (Sir2p) showed a significant increase in the abundance of DSBs in sub-telomeric regions as well as an increase/decrease in the recombination frequencies of key markers within other regions adjacent to the sub-telomeric regions, indicating a shift in recombination distribution (Mieczkowski *et al*., 2007). Sir2 belongs to a family of proteins called Sirtuins which are involved in deactylation pathways in an NAD+ dependant manner (Sauve *et al*., 2006). They carry out this function by the hyrdolysis of the covalent bond between the acetyl

group and the associated histone to form an acetyl-Sir2p-NAD+ intermediate which subsequently disassociates to form a 2'-O-acetyl-ADP-ribose product (Sauve *et al*., 2006). They have been observed to associate with the telomeric regions of chromatin in yeast (Lieb *et al*., 2001) and normally mediate histone deacetylation within these regions to transcriptionally silence genes that are transcribed when yeast are moved to growth mediums lacking glucose, to activate the gluconeogenesis pathway (Robyr *et al*., 2002). Coincidently, the meiotic recombination frequency in yeast is greatly reduced in sub-telomeric regions (Su *et al*., 2000). The deletion of a yeast gene encoding the deacetylase protein RPD3 has also led to the increased recombination of a key markers within an already recombination hot-spot region (Merker *et al*., 2008).

The effect of histone hyperacetylation on meiotic chiasma frequency and distribution has also been studied in the plant *Arabidopsis* by way of the analysis of lines overexpressing a histone acetyltransferase gene called MEIOTIC CONTROL OF CROSSOVERS1 (MCC1) (Perrella *et al*., 2010). There was an increase in the proportion of proximal crossovers accompanied by a reduction proportion of distal crossovers on the same arm of chromosome 4, compared to the control lines, indicating a shift in chiasma distribution for this chromosome (distal to proximal direction). This effect was phenocopied by the histone deactylase inhibitor trichostatin A (Perrella *et al*., 2010).

It was demonstrated in yeast that histone trimethylation and acetylation may work antogonistically in euchromatin. In yeast, histone methyltransferases (SET1) mediate H3-K4 methylation to antagonise conformational changes brought about about by SIR proteins to reposition genes into euchromatic regions which would lead epigentic transcriptional silencing (Venkatasubrahmanyam *et al*., 2007). Secondly, H3K4 trimethylation may cause the “initial” small-scale conformational changes which

allows for the NURF complex (chromatin remodelling complex) to gain access to the chromatin framework. NURF then, induces the large scale changes in chromatin conformation changes necessary that enable the proteins involved in the epigenetic modification of histones (Li *et al*., 2006), to regulate downstream transcription. With regards to meiosis, it is postulated that either NURF complex recruitment (Li *et al*., 2006) or the antagonistic affects of histone acetylation/methylation to alter the global chromatin structure (Venkatasubrahmanyam *et al*., 2007), or a combination of both the effects of the NURF complex and histone modification proteins, may be responsible for epigenetically altering the the global chromatin structure, hence allowing access to the proteins involved in DSB formation and hence, subsequent downstream events of the meiotic pathway (Borde *et al*., 2009).

This chapter will focus on chemical intervention to induce histone hyperacetylation in barley by using the histone deacetylase inhibitor trichostatin A, in an attempt to alter meiotic crossover frequency and distribution, as it has been successfully used in the plant *Arabidopsis* (Perrella *et al*., 2010).

4.2 Results

4.2.1 Evidence demonstrating the uptake of TSA by the meiocytes via the transpiration stream

To investigate whether TSA was taken up successfully by the meiocytes via the transpiration stream and caused hyperacetylation of chromatin, an immunolocalisation technique was carried out using an antibody raised against the acetylated form of histone H3 (anti-H3K56ac).

Fixed anthers were studied at pachytene stage using the microwave technique (see **Materials and methods**: **Section 2.13**) and it was found that there was an enrichment

of acetylation (red foci) for meiocytes treated with 1,000ng/ml TSA, compared to that for the control (**Figure 4.1**), suggesting that hyperacetylation of histone H3 has occurred.

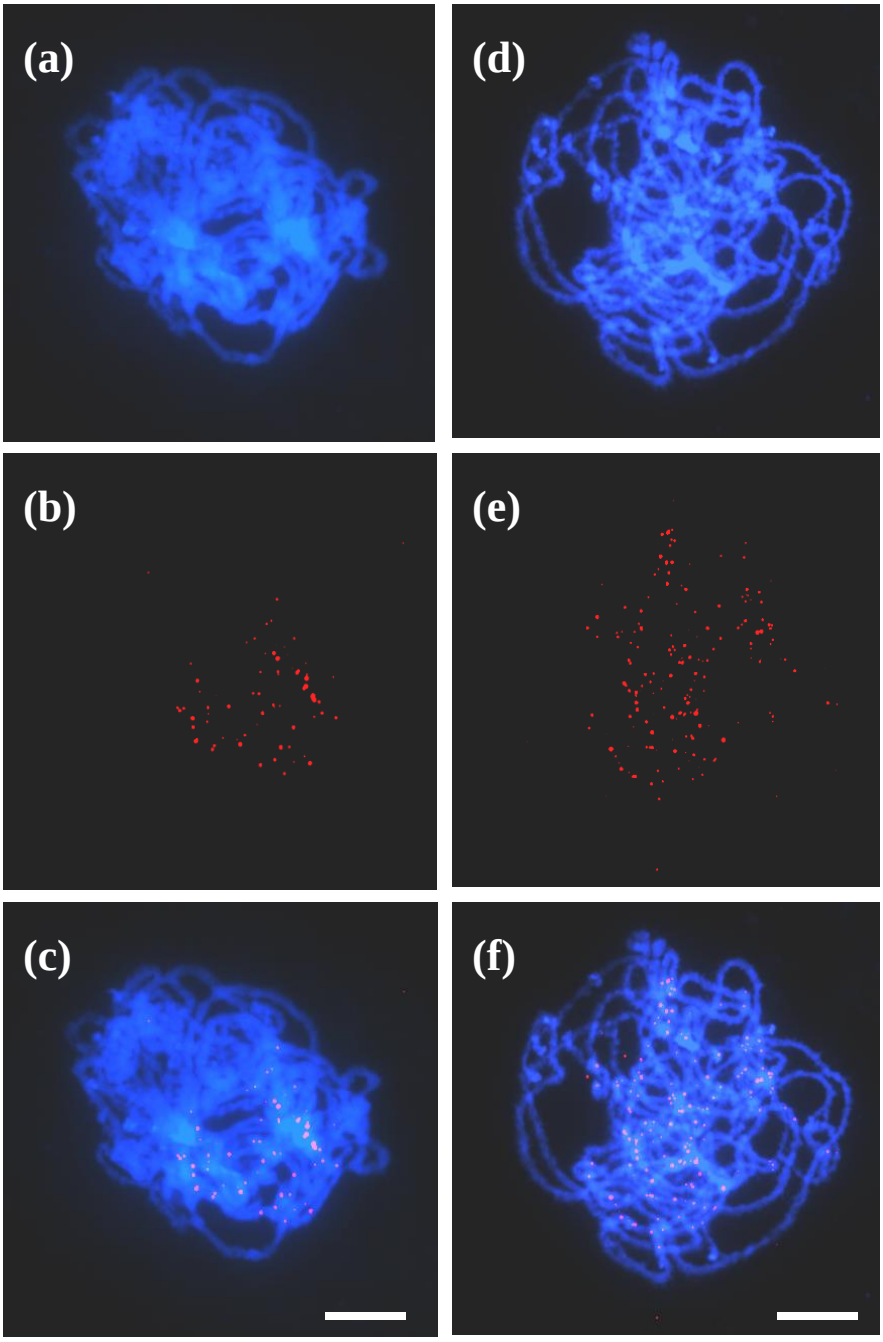


Figure 4.1: The detection of H3K56ac foci (red) (control: (b) and treated: (e)) at pachytene stage by immunolocalisation (tagged with anti-H3K56Ac (primary antibody: rabbit) and detected with anti-rabbit CY3: secondary antibody) using the microwave technique (explained in section 2.13). The analysis demonstrates an enrichment of H3K56 acetylation in the sample treated with 1,000ng/ml TSA (merge; (f)) compared to that for the control (merge: (c)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

Cytology reveals that treatment with TSA reduces chiasma frequency

The physical mapping studies of rDNA sites on monotelotrisomic mitotic barley chromosomes using FISH, have shown that 5S rDNA repeats are located on the long arms of chromosome 2H and 3H, and the short arm of 7H. The study didn't detect 5S rDNA on telotrisomic 4H, even though measurements suggest that it physically maps to the long arm of 4H and is therefore, depicted as a dotted red signal on the ideogram (**Figure 4.2**) (Leitch and Heslop-Harrison, 1993). Similarly, 45S rDNA has been physically mapped to the short arms of 5H and 6H (Pickering *et al*., 2004). The 5S signal is strongest on chromosome 2H, intermediate strength on 3H and 7H, and weakest on 4H (Leitch and Heslop-Harrison, 1993). Further, silver nitrate staining has shown that 6H has a larger NOR than 5H (von Bothmer *et al*., 2003). The ideogram of the barley chromosomes (**Figure 4.2**) depicts the physical locations and approximate relative sizes of 5S rDNA (adapted from Leitch and Heslop-Harrison, 1993) and 45S rDNA repeats (adapted from Pickering *et al*., 2004 and von Bothmer *et al*., 2003).

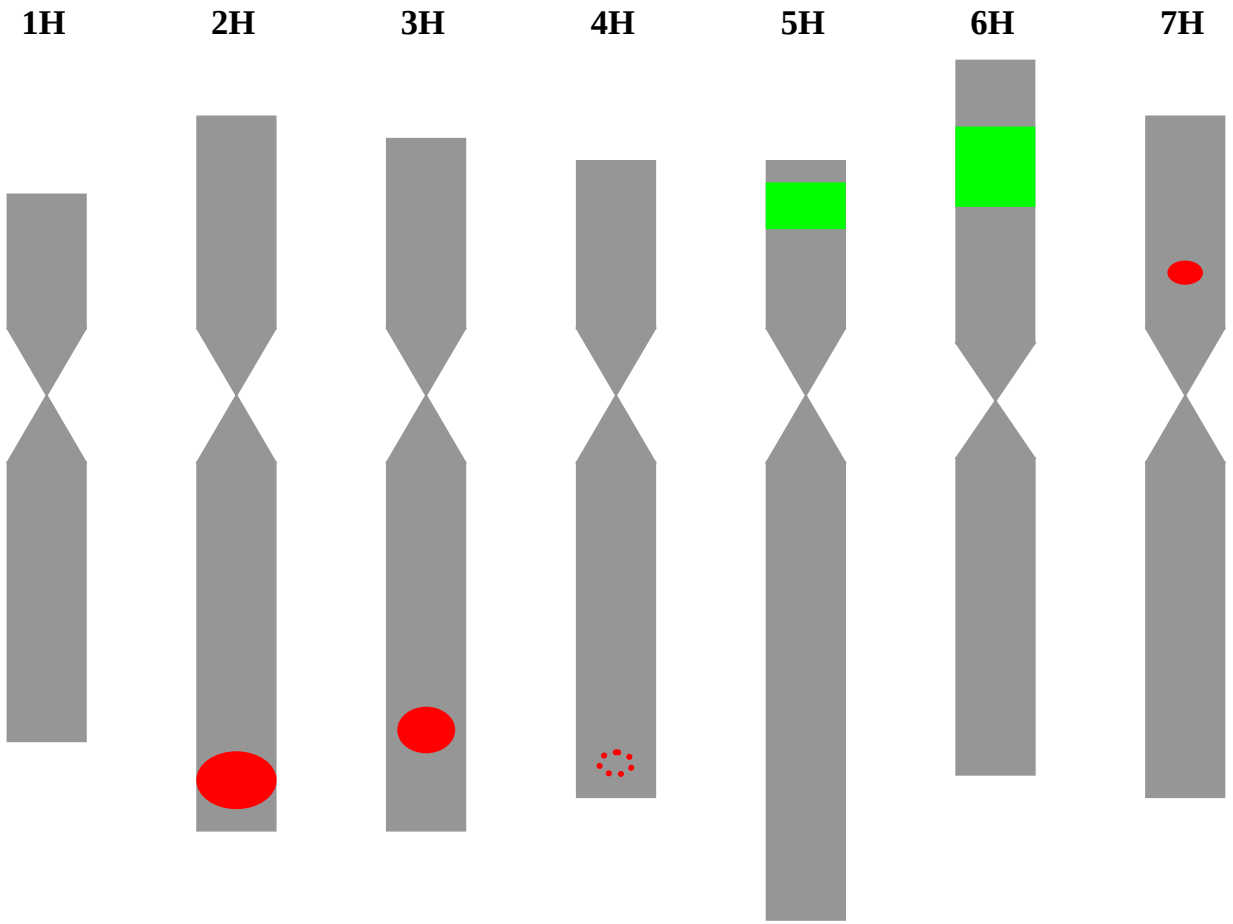


Figure 4.2: An ideogram depicting the FISH detection of the physical locations of the rDNA repeats in barley. In this study 45S rDNA was detected on chromosomes 5H and 6H with anti-DIG (FITC: (green: chapter 5); anti-DIG FITC/rhodamine: (orange: chapter 4)) and 5S was detected on chromosomes 2H, 3H and 7H with BIO-5S (red: chapters 4 and 5). The relative sizes of the rDNA repeats are shown in approximation (Pickering *et al.*, 2004; von Bothmer *et al.*, 2003). Adapted from Leitch and Heslop-Harrison, (1993).

In this PhD project, the individual meiotic chromosomes at metaphase I were identified using 5S (red) and 45S rDNA (green/orange) probes (**Figure 4.3**) by FISH (Leitch and Heslop-Harrison, 1993; Pickering *et al*., 2004). The relative strengths of the 5S signals were in agreement with the karyotyping studies (including the absence of the 5S signal on 4H), conducted by Leitch and Heslop-Harrison, 1993. The same was true for the relative sizes of the 45S rDNA signal on 5H and 6H (Pickering *et al*., 2004; von Bothmer *et al*., 2003). Chromosomes 1H and 4H can be distinguished from one another due to the fact that 4H is slightly physically larger than 1H (Leitch and Heslop-Harrison, 1993). But the distinction between 1H and 4H was complicated in this investigation due to the fact that at metaphase I, the chromosomes undergo expansion/contraction cycles when they align onto the metaphase plate (Kleckner *et al*., 2004) and this may vary from one chromosome to another. Additionally, a definite distinction between 1H and 4H depends on the chromosomes being very well spread onto the microscope slide (**Figure 4.3**) which was not possible in every single attempt. Further complications regarding this distinction arose due to TSA causing expansion of the chromatin structure (Toth *et al*., 2004; Shogren-Knaak *et al*., 2006) and the fact that the chromosome arms of rod bivalents and univalents tend to overlap each other at metaphase I (treatment with TSA and desynapsis in **Chapter 5**). To overcome this issue, the sum of the chiasmata for what I thought was chromosome 1H (labeled as 1H/4H) plus that for what I thought was 4H (labeled as 4H/1H) (1H+4H: this chapter and **Chapter 5**) was implemented in both the test and control (n = 100 for chromosome 1H+4H and n = 50 for the remaining chromosomes for statistical analysis). Also, as the 5S repeat sequence on chromosome 7H is much shorter than that for chromosome 2H, the 5S probe signal was difficult to locate against the blue DAPI exposure. Therefore, to identify chromosome 7H in each case, the DAPI

exposure was set to grey to discern the 5S signal (arrows: **Figure 4.4**). **Figure 4.3** identifies the FISH labeled barley meiotic chromosomes at metaphase I, reiterating the same study that was previously carried out by Higgins *et al*. (2012).

Chiasmata that are in subtelomeric regions as demonstrated by chromosomes 2H, 4H and 7H (**Figure 4.3**), were designated as distally occurring. The white arrow identifies an interstitial chiasma on chromosome 3H which was classified as such if it occurred one third to half the length of the chromosome arm towards the centromere (**Figure 4.3**). The classification of the positions of the chiasmata was also carried out as per the investigation by Higgins *et al*. (2012) for consistency. Coincidentally, the interstitial chiasma on chromosome 3H occurred at the same position as the physical location of the 5S rDNA repeat (**Figure 4.3**) whereas the distal chiasma was distal to the 5S rDNA. Therefore, the positions of the chiasmata were also deciphered based on their positions relative to the rDNA sites which is similar to the method that was used demonstrate the positions of chiasmata based on their distal or proximal location relative to the physical location of rDNA sites in FISH labeled meiotic rye chromosomes at metaphase I (Schwarzacher, 1996).

Thirdly, the shapes of the bivalents also helped in determining the positions of the chiasmata and vice versa, in the FISH labelled metaphase barley chromosomes. Moreover, the distinct shapes of bivalents also aid in identifying the individual chromosomes in plants (reviewed by Schwarzacher, 2003) and this methodology was also applied in this project to identify each barley chromosome. The cartoon of the barley chromosomes at metaphase I (**Figure 4.5**) demonstrates that a single chiasma at both subtelomeric (distal) regions (yellow) leads to the formation of the classical ring bivalent. A chromosome with three chiasmata, where two chiasmata on the same arm are distally located, will result in the formation of a buckle shaped ring bivalent

(**Figure 4.5**). This buckle shape is demonstrated by chromosome 7H (**Figure 4.3**). If one of the two chiasmata on the same arm occupies an interstitial position (red), the bivalent takes on a key shape (**Figure 4.5**) as demonstrated by chromosome 3H (**Figure 4.3**). A bivalent assumes a classical rod bivalent shape when it harbours a single distal obligate chiasma but a rod bivalent taking on a bulged shape, does so because of the presence two distal chiasma on the same arm (**Figure 4.6**).

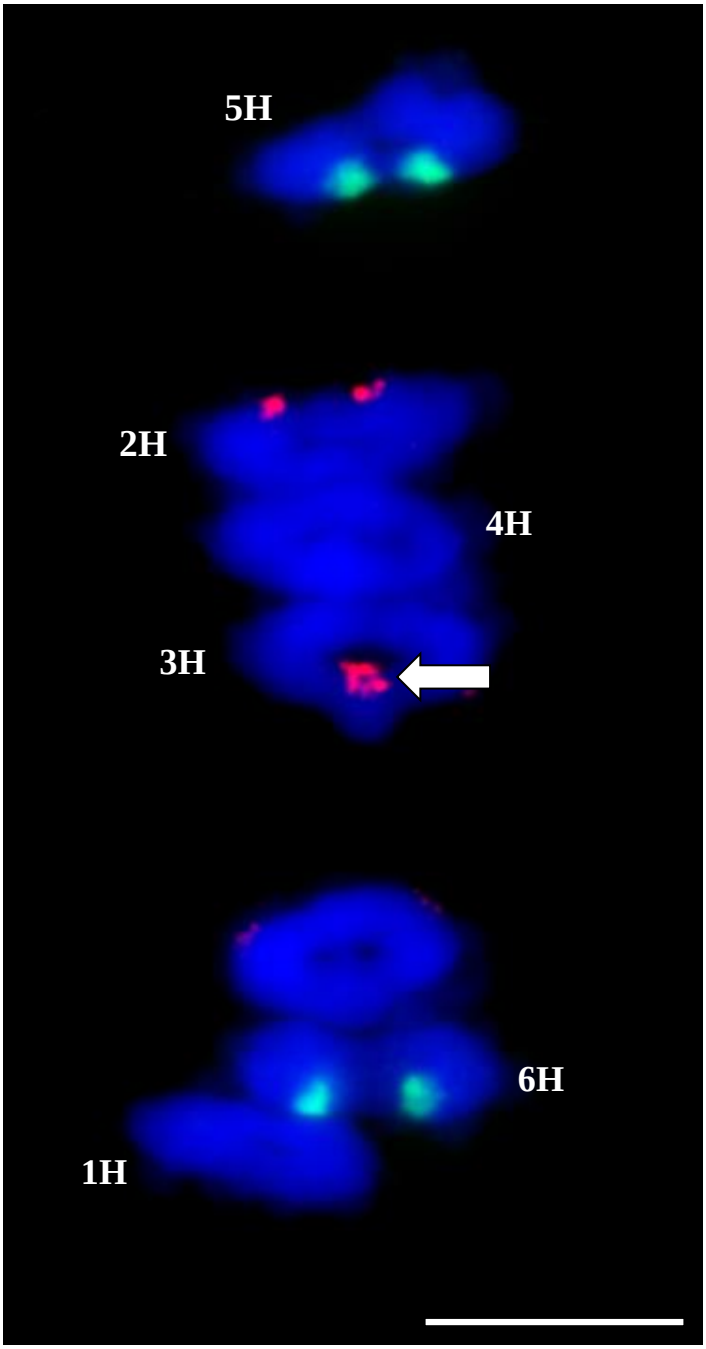


Figure 4.3: The FISH detection of the physical locations of the rDNA repeats on the meiotic chromosome spreads at metaphase I (barley cultivar Morex). 45S rDNA was tagged with the 45S rDNA-DIG probe on chromosomes 5H and 6H, and detected with anti-DIG-FITC (green). 5S was tagged with the 5S rDNA-BIO probe on chromosomes 2H and 3H, and detected with streptavidine-CY3 (red). The arrow points to an interstitial chiasma. Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

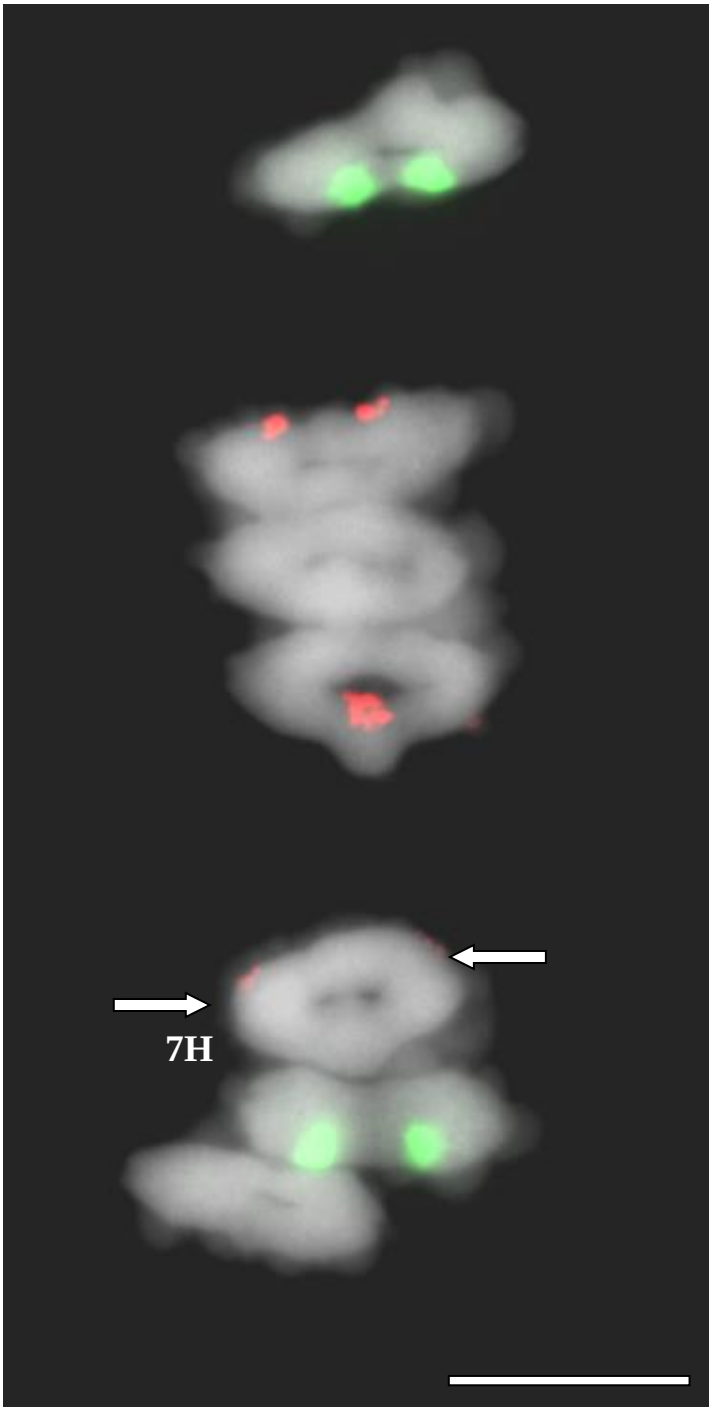


Figure 4.4: The FISH detection of the physical locations of the 5S rDNA (tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3: red) repeats on chromosome 7H in meiotic chromosome spreads at metaphase I (barley cultivar Morex). This figure is an alteration of the DAPI exposure in Figure 4.3 from blue to grey, allowing the 5S rDNA (arrows) on chromosome 7H to be discerned. Bar = 10 µm

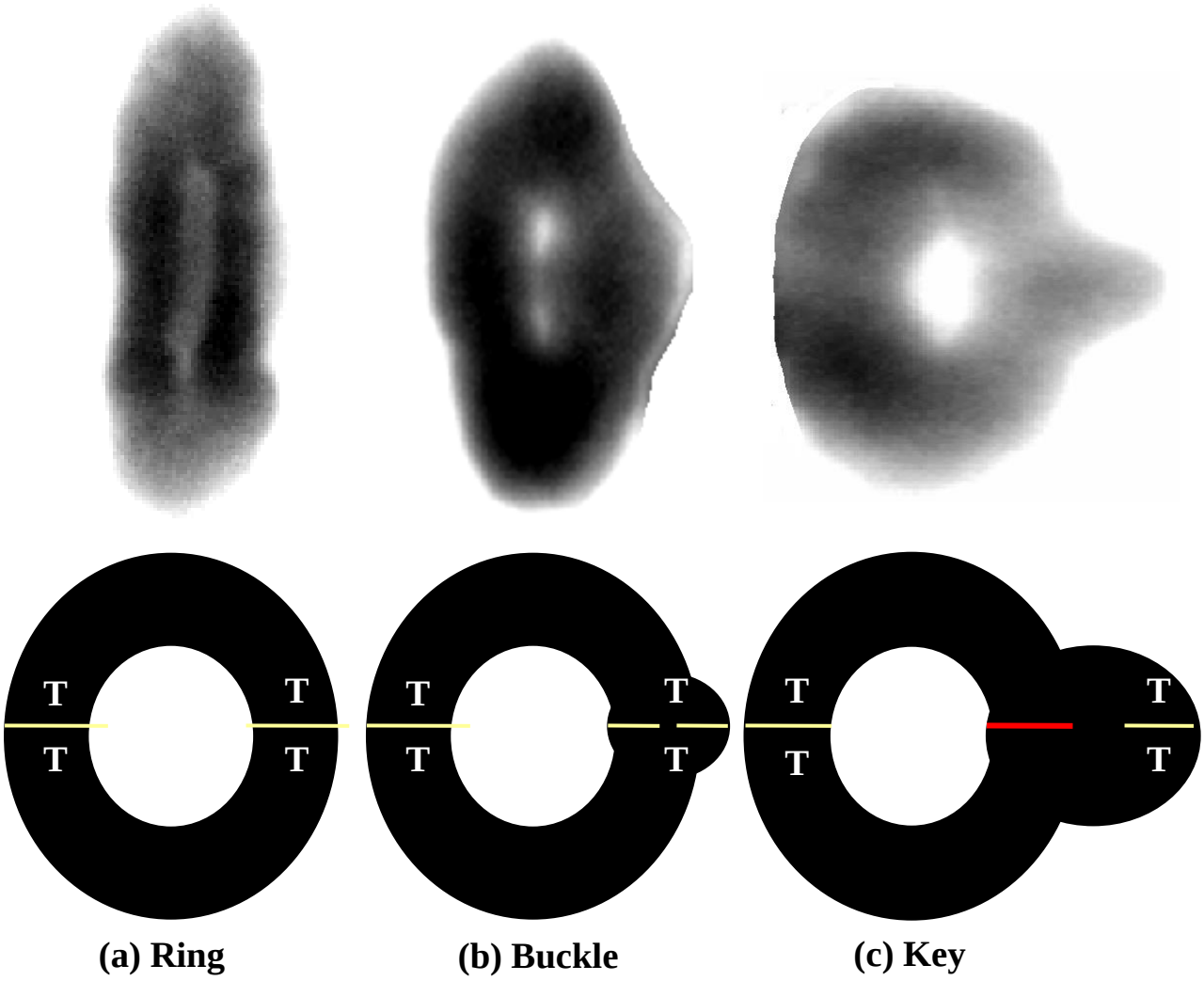


Figure 4.5: A cartoon depicting the shapes of the closed bivalents at metaphase I during meiosis in barley, including cytological images of actual barley chromosomes above each cartoon. The classic closed ring (a) shape has single distal chiasmata (yellow) on each end of each chromosome arm. A closed bivalent with two distal chiasmata on one arm causes the chromosomal region to take on a buckle shape (b), and a closed bivalent in which one arm has a distal (yellow) and interstitial (red) chiasmata, will take on a key shaped conformation (c). The subtelomeric region of each chromosome is depicted as (T).

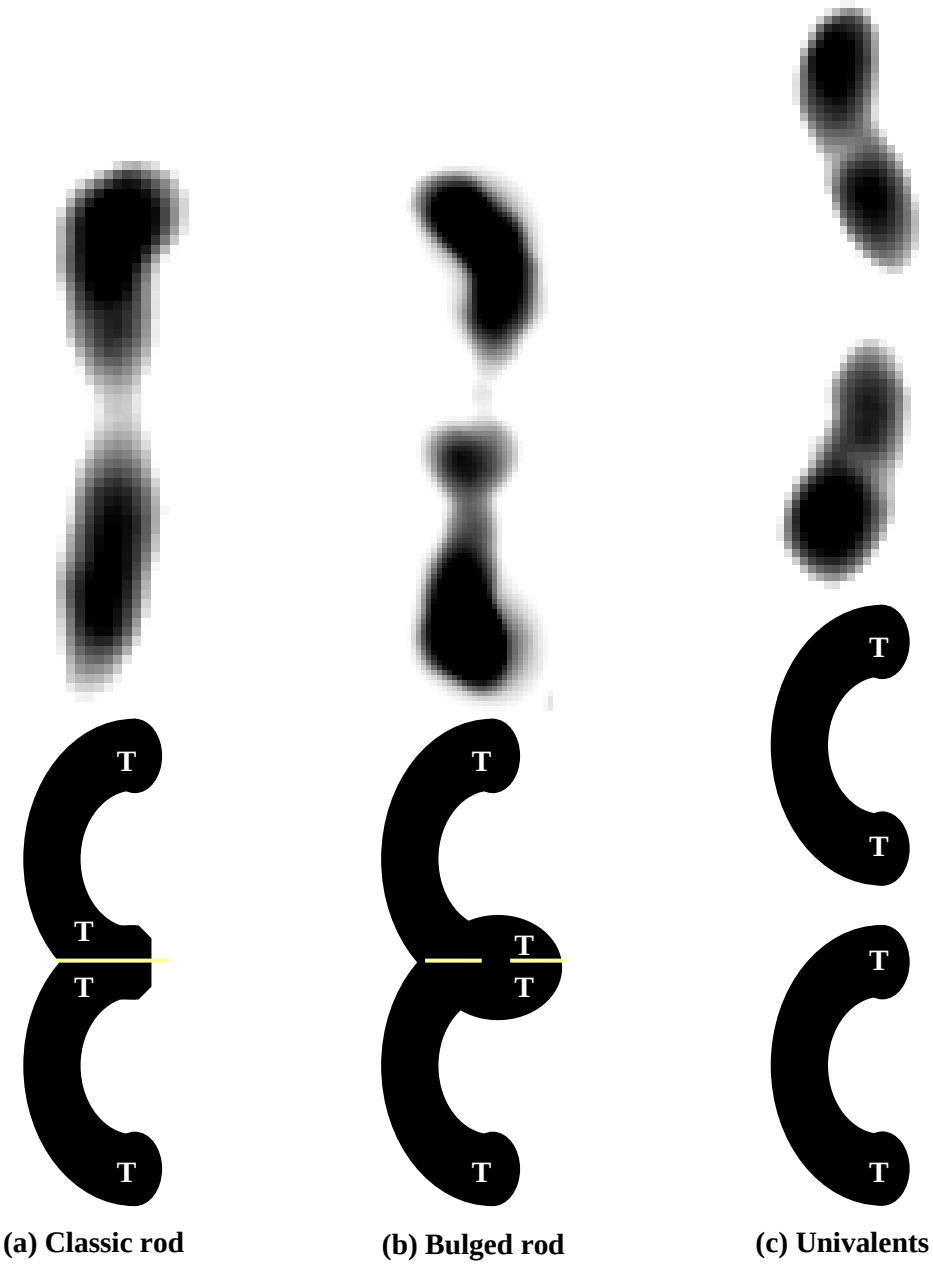


Figure 4.6: A cartoon depicting the shapes of the open bivalents at metaphase I during meiosis in barley, including cytological images of actual barley chromosomes above each cartoon. A classic rod bivalent (a) has one distal chiasmata on one end the chromosome arm whereas a bulged rod bivalent (b) will have two distal chiasmata on one end the chromosome arm. The univalent has no chiasmata (c). The subtelomeric region of each chromosome is depicted as (T).

4.2.3 TSA reduces chiasma frequency in a concentration dependent manner (cytological analysis)

To decipher whether TSA would affect meiotic recombination, fluorescence *in situ* hybridisation (FISH) was carried out utilising probes complementary to the DNA sequences encoding ribosomal RNA (45S-DIG and 5S-BIO) in barley, in conjunction with a BrdU time course (stems treated with 500 ng/ml TSA, were not subjected in conjunction with a BrdU time course). The stems were subjected to a 2hr BrdU allowing for its uptake during meiotic S-phase, which was washed out by either sterilised deionised water (SDW) containing the appropriate volume of DMSO, as a control (see **Materials and Methods: Section 2.9**, **Table 2.11**), to account for any affects that may occur to the meiotic pathway as a result of DMSO alone. TSA was initially dissolved in DMSO and stored as a stock solution at a concentration of 10mg/ml). The required concentrations of TSA for the stems which were subjected to the treatment, were obtained by diluting the appropriate volume of the TSA stock solution in the correct volume of SDW (see **Materials and Methods: Section 2.9**, **Table 2.11**). The individual test samples were treated with TSA (10, 100, 500 and 1,000ng/ml, respectively). The spikes were isolated and fixed at +48 h to isolate BrdU labeled chromosomes at metaphase I. The fixation of the spikes at +48 h instead of +40 h, took into account any delay that TSA might have caused to the progression of meiosis (see **Chapter 3**: **Section *3.2.4***).The anthers were isolated and tapped out on microscopic slides as described in section **2.4**. BrdU was detected using an anti-BrdU antibody, followed by a secondary antibody covalently conjugated to the fluorophore, fluorescein isothiocyanate. The 45S probe was detected using a 1:1 mixture of anti-DIG-rhodamine: anti-DIG-FITC and the 5S probe was detected by Cy3 (see **Materials and Methods**: **Section 2.10**). The preliminary time course study (**Chapter 3: Table 3.1**) and the treatment of anthers with TSA in conjunction with the time course study

demonstrated that roughly 30-50% of the meiotic nuclei in each anther (that are at the same stage) do not incorporate BrdU (also the same proportion for cells that were treated with TSA treatment and exhibited an affect on chiasmata frequency). Two control FISH labeled metaphase spreads without incorporated BrdU are shown as an example (**Figure 4.7)** despite the fact that they were on the same microscope slide (from the same anther) as the metaphase spreads that did incorporate BrdU in **Figure 4.8**. Data from the BrdU time course study in *Arabidopsis* also demonstrated that a similar proportion of the meiotic nuclei at the same stage did not incorporate BrdU at pre-meiotic S-phase (Armstrong *et al*., 2003).

Figure 4.9 illustrates that recombination appears to be not affected by treatment with 10ng/ml TSA when compared to a BrdU labelled Metaphase I, from an untreated control (**Figure 4.8)**. Statistical analysis (n = 50: ANOVA p = 0.22) showed no significant difference in the mean chiasma frequency per nuclei between the test and control (14.30 +/- 1.18 SD and 14.64 +/- 1.57 SD, respectively). Upon analysing the individual chromosomes, it was observed that there was a slight but significant decrease in CO frequency for chromosome 1H+4H (ANOVA p = 0.0041) and a slight but significant increase in CO frequency for chromosome 6H (ANOVA p = 0.042) (**Table 4.1**). **Figure 4.10** reveals the significant emergence of rod-shaped bivalents by treatment with 100ng/ml TSA for chromosomes 1H+4H (10), 2H (10), 5H (27) and 6H (2) (**Table 4.2**). There was a significantly lower mean overall CO frequency per cell in the test (13.48 +/- 1.30 SD) compared to the control (ANOVA p = 0.00012) indicating that this concentration is the threshold at which a significant reduction in mean overall CO frequency occurs (**Table 4.2**). **Figure 4.11** shows that 500ng/ml TSA is the threshold at which univalent formation occurs, with a significant reduction in chiasma frequency for chromosomes 1H+4H (21 rod bivalents and 6 univalents), 2H (5 rod-bivalents) and 5H (16 rod-bivalents and 6 univalents) (**Table 4.3**). The mean overall

chiasma frequency per nuclei was 12.84 +/- 2.61 SD in the test sample. Treatment with 1,000ng/ml TSA caused a further decrease in chiasma frequency for chromosomes 1H+4H (38 rod-bivalents and 30 univalents), 2H (28 rod-bivalents), 3H (15 rod-bivalents), 5H (25 rod-bivalents and 34 univalents), 6H (21 rod-bivalents and 16 univalents) and 7H (14 rod-bivalents and 16 univalents) (**Figure 4.12** and **Table 4.4**). The mean overall chiasma frequency per nuclei in the test sample was 9.2 +/- 2.19 SD.

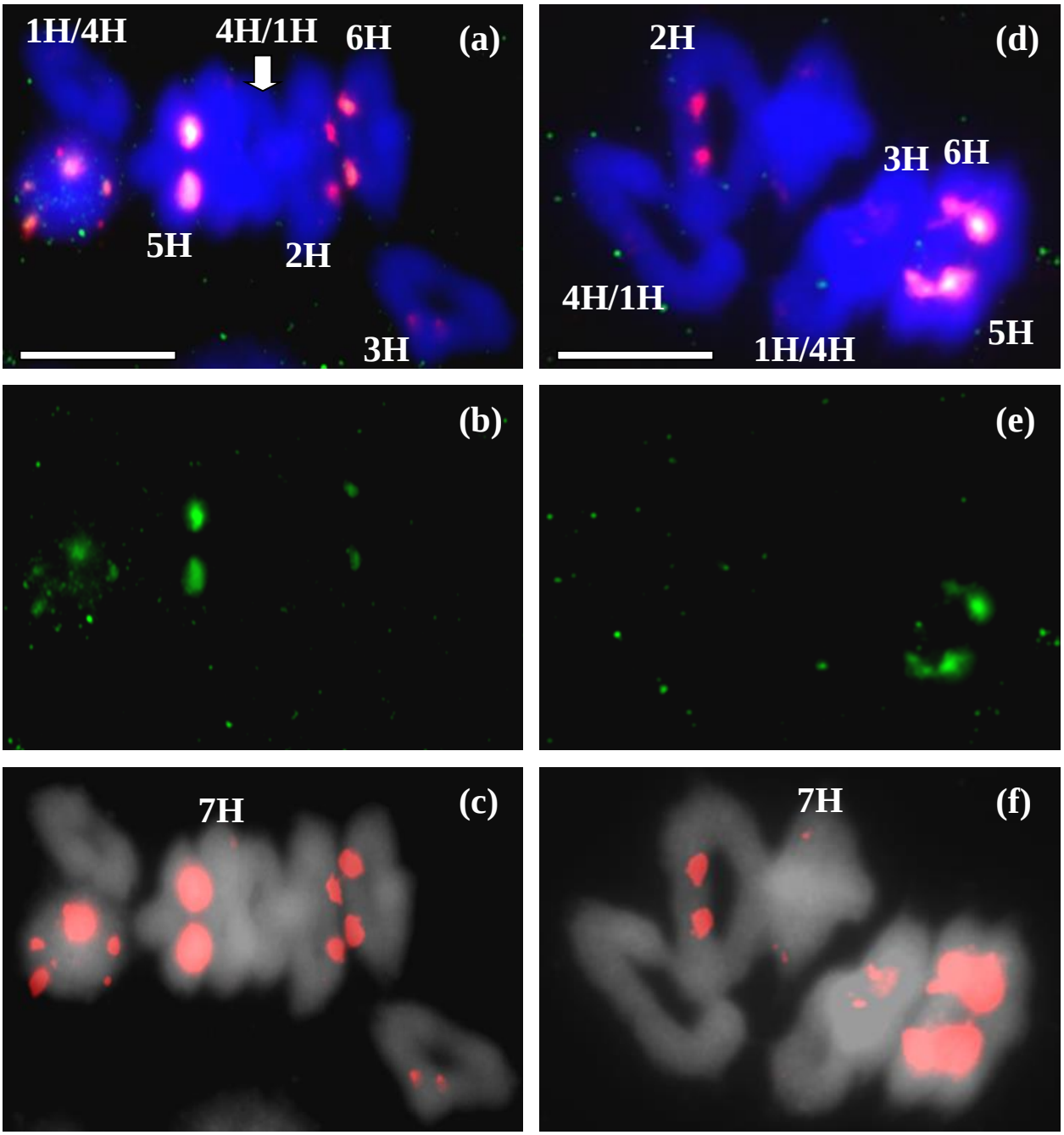


Figure 4.7: Two metaphase I spreads ((a) and (d)) from Morex treated with the DMSO control (unincorporated BrdU) in conjunction with a BrdU time course ((b) and (e): anti-mouse Ig flourescein/green) and FISH labelled 45S (tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC: anti-DIG rhodamine (orange)) and 5S (tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3: red) rDNA repeats. (a) Has three ring bivalents (2H, 4H/1H, and 7H), two key shaped bivalent (3H and 5H), and two buckle ring bivalents (1H/4H and 6H). (d) Has four ring bivalents (1H/4H, 2H, 4H/1H and 6H) and two key shaped-bivalents (3H and 7H). DAPI counterstain in blue ((a) and (d)) and grey ((c) and (f)). Bar = 10 µm

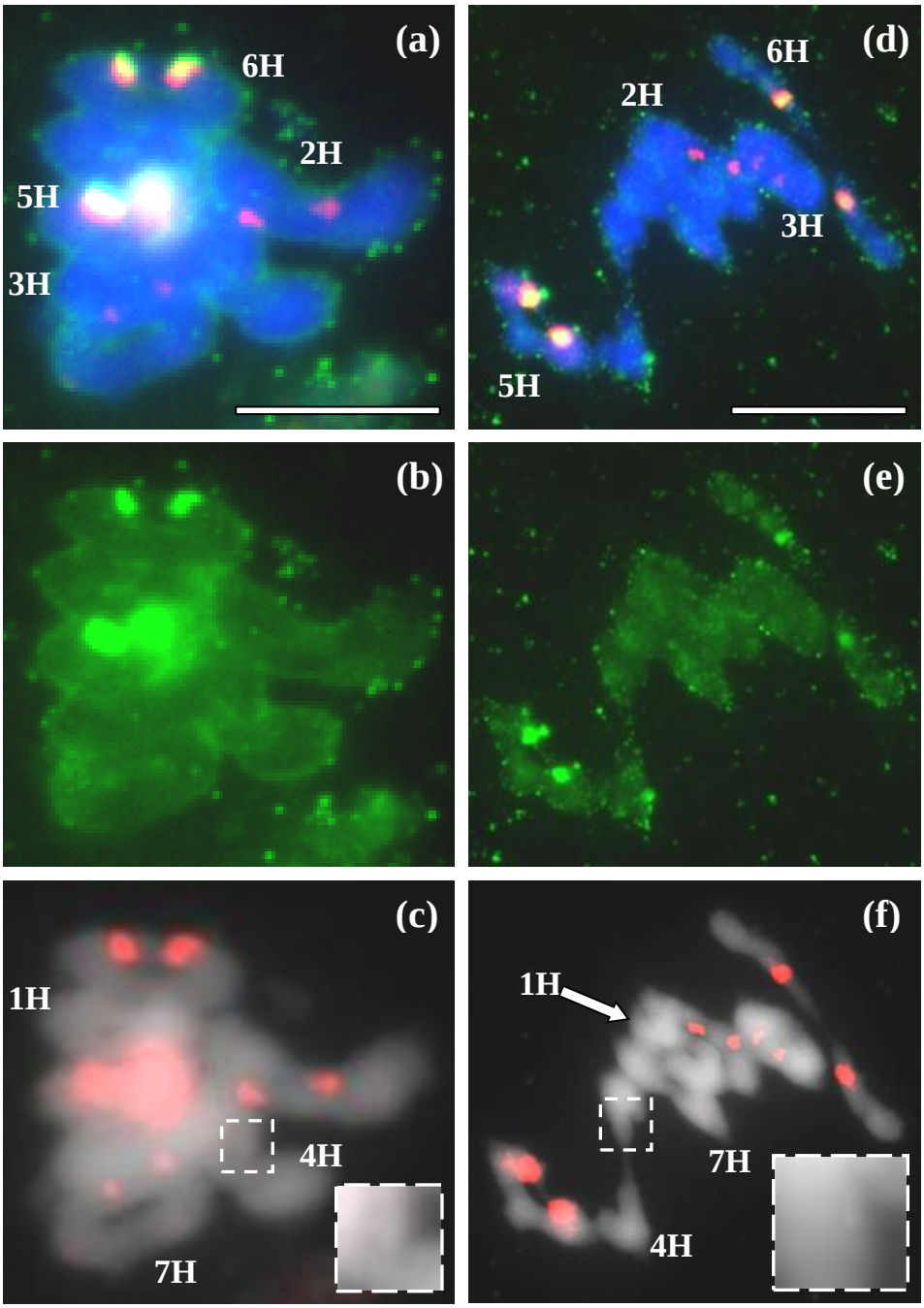


Figure 4.8: Two metaphase I spreads ((a) and (d)) from Morex treated with the DMSO control (incorporated BrdU) in conjunction with a BrdU time course ((b) and (e): anti-mouse Ig flourescein/green) and FISH labelled 45S (tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC: anti-DIG rhodamine (orange)) and 5S (tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3: red) rDNA repeats. (a) Has five ring bivalents (1H, 2H, 3H, 4H (5S on 4H shown in inset (c)) and 6H), one key shaped bivalent (5H), and one buckle ring bivalent (7H). (d) Has four ring bivalents (1H, 2H, 3H and 7H (5S on 7H shown in inset (f)), one key shaped-bivalent (5H) and one rod bivalent (6H). DAPI counterstain in blue ((a) and (d)) and grey ((c) and (f)). Bar = 10 µm

Table 4.1: The effect of 10 ng/ml TSA on mean CO frequency. Treatment caused a significant increase in the mean CO frequency for chromosome 6H and a decrease for chromosome 1H+4H (n=100 for 1H+4H and n= 50 for remainder of chromosomes).

Chromosome	Mean CO frequency in Control.	Mean CO frequency in sample treated with 10 ng/ml TSA.	ANOVA (p < 0.05 = Sig. diff. in CO freq).
1H+4H	2.16 +/- 0.53 SD	1.97 +/- 0.39 SD	0.00409
2H	2.08 +/- 0.34 SD	2.04 +/- 0.20 SD	0.474352
3H	2.44 +/- 0.50 SD	2.4 +/- 0.49 SD	0.688943
5H	2.1 +/- 0.71 SD	2.02 +/- 0.77 SD	0.58941
6H	1.76 +/- 0.48 SD	1.92 +/- 0.27 SD	0.042186
7H	1.94 +/- 0.31 SD	1.98 +/- 0.25 SD	0.480059

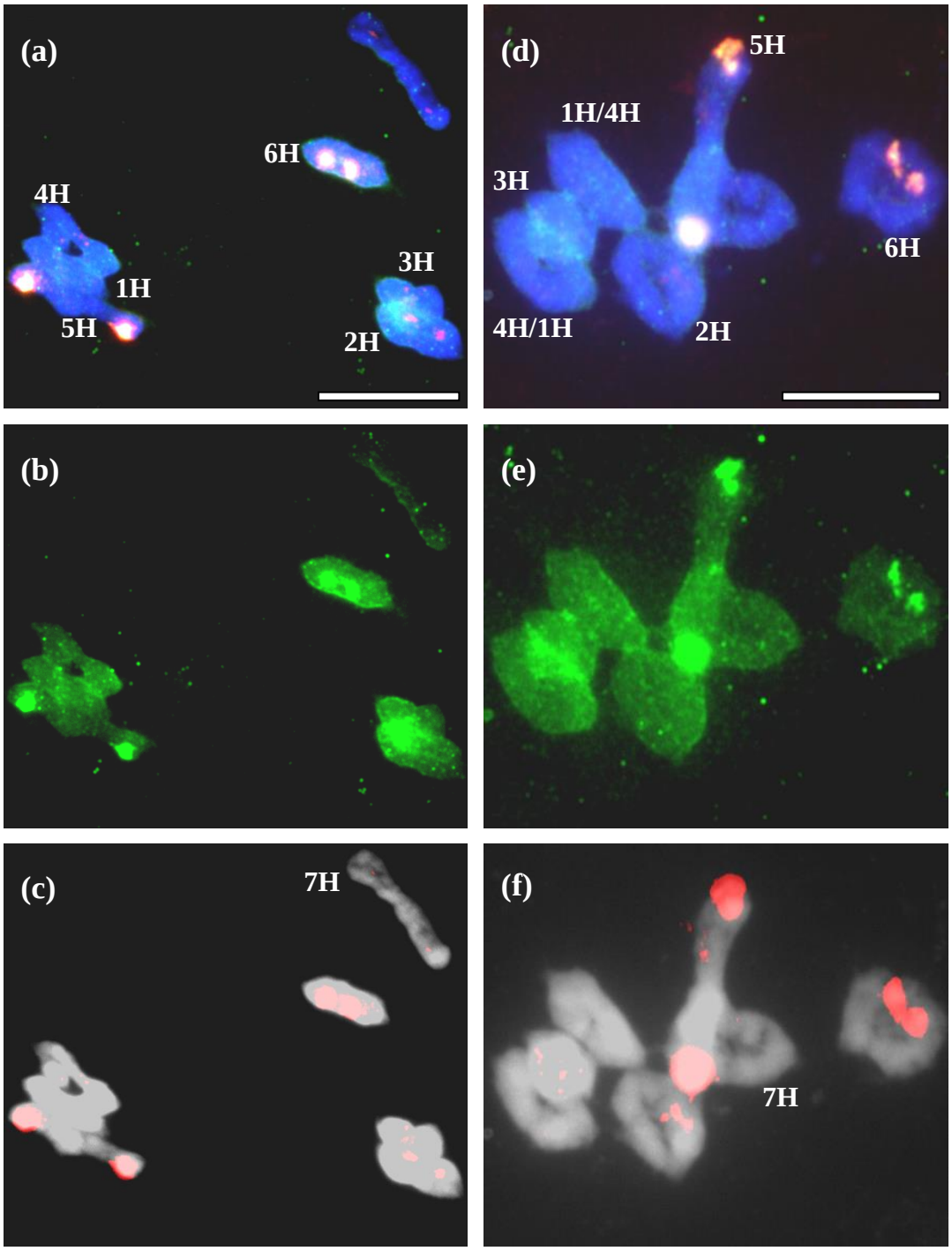


Figure 4.9: Two metaphase I spreads ((a) and (d)) from Morex treated with 10 ng/ml TSA in conjunction with a BrdU time course ((b) and (e): anti-mouse Ig flourescein/green) and FISH labelled 45S (tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC: anti-DIG rhodamine (orange)) and 5S (tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3: red) rDNA repeats. (a) Has four ring bivalents (1H, 2H, 4H and 6H), one key shaped bivalent (3H), one bulged rod-bivalent (5H) and one classic rod-bivalent (7H). (d) Has four ring bivalents (1H, 2H, 4H and 7H), one buckle shaped bivalent (6H) and one bulged rod-bivalent (5H). DAPI counterstain in blue ((a) and (d)) and grey ((c) and (f)). Bar = 10 µm

Table 4.2: The effect of 100 ng/ml TSA on mean CO frequency. Treatment caused a significant decrease in the mean CO frequency for chromosomes 1H+4H, 2H, 5H and 6H (n=100 for 1H+4H and n= 50 for remainder of chromosomes).

Chromosome	Mean CO frequency in Control.	Mean CO freq. in sample treated with 100 ng/ml TSA.	ANOVA (p < 0.05 = Sig. diff. in CO freq).
1H+4H	2.16 +/- 0.53 SD	1.94 +/- 0.37 SD	0.000773
2H	2.08 +/- 0.34 SD	1.76 +/- 0.43 SD	8.01E-05
3H	2.44 +/- 0.50 SD	2.3 +/- 0.46 SD	0.150079
5H	2.1 +/- 0.71 SD	1.7 +/- 0.76 SD	0.007733
6H	1.76 +/- 0.48 SD	1.96 +/- 0.20 SD	0.007272
7H	1.94 +/- 0.31 SD	1.88 +/- 0.33 SD	0.352349

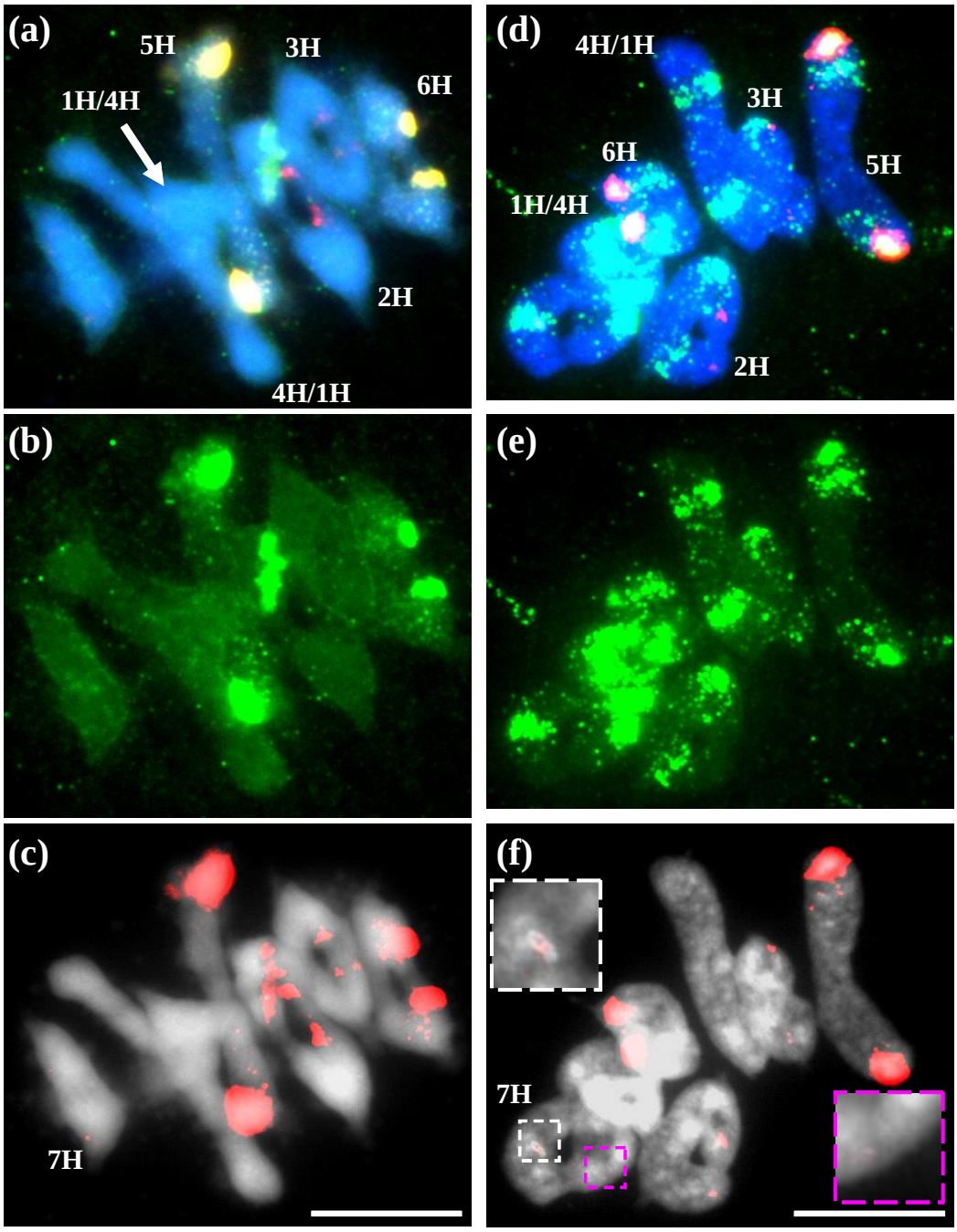


Figure 4.10: Two metaphase I spreads ((a) and (d)) from Morex treated with 100 ng/ml TSA in conjunction with a BrdU time course ((b) and (e): anti-mouse Ig flourescein/green) and FISH labelled 45S (tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC: anti-DIG rhodamine (orange)) and 5S (tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3: red) rDNA repeats. (a) Has four bivalents (2H, 3H, 6H and 7H), one key shaped bivalent (1H/4H), and two classic rod-bivalents (4H/1H and 5H). (d) Has four ring bivalents (1H/4H, 2H, 3H and 6H), one buckle shaped bivalent (7H (5S on 7H shown in insets (f))) and two classic rod-bivalents (4H/1H and 5H). DAPI counterstain in blue ((a) and (d)) and grey ((c) and (f)). Bar = 10 µm

Table 4.3: The effect of 500 ng/ml TSA on mean CO frequency. Treatment caused a significant decrease in the mean CO frequency for chromosomes 1H+4H, 2H, 3H and 5H (n=100 for 1H+4H and n= 50 for remainder of chromosomes).

Chromosome	Mean CO frequency in Control.	Mean CO freq. in sample treated with 500 ng/ml TSA.	ANOVA (p < 0.05 = Sig. diff. in CO freq).
1H+4H	2.16 +/- 0.53 SD	1.75 +/- 0.59 SD	5.62E-07
2H	2.08 +/- 0.34 SD	1.9 +/- 0.30 SD	0.006291
3H	2.44 +/- 0.50 SD	2.18 +/- 0.56 SD	0.016262
5H	2.1 +/- 0.71 SD	1.66 +/- 0.69 SD	0.002147
6H	1.76 +/- 0.48 SD	1.74 +/- 0.56 SD	0.848577
7H	1.94 +/- 0.31 SD	1.86 +/- 0.45 SD	0.306521

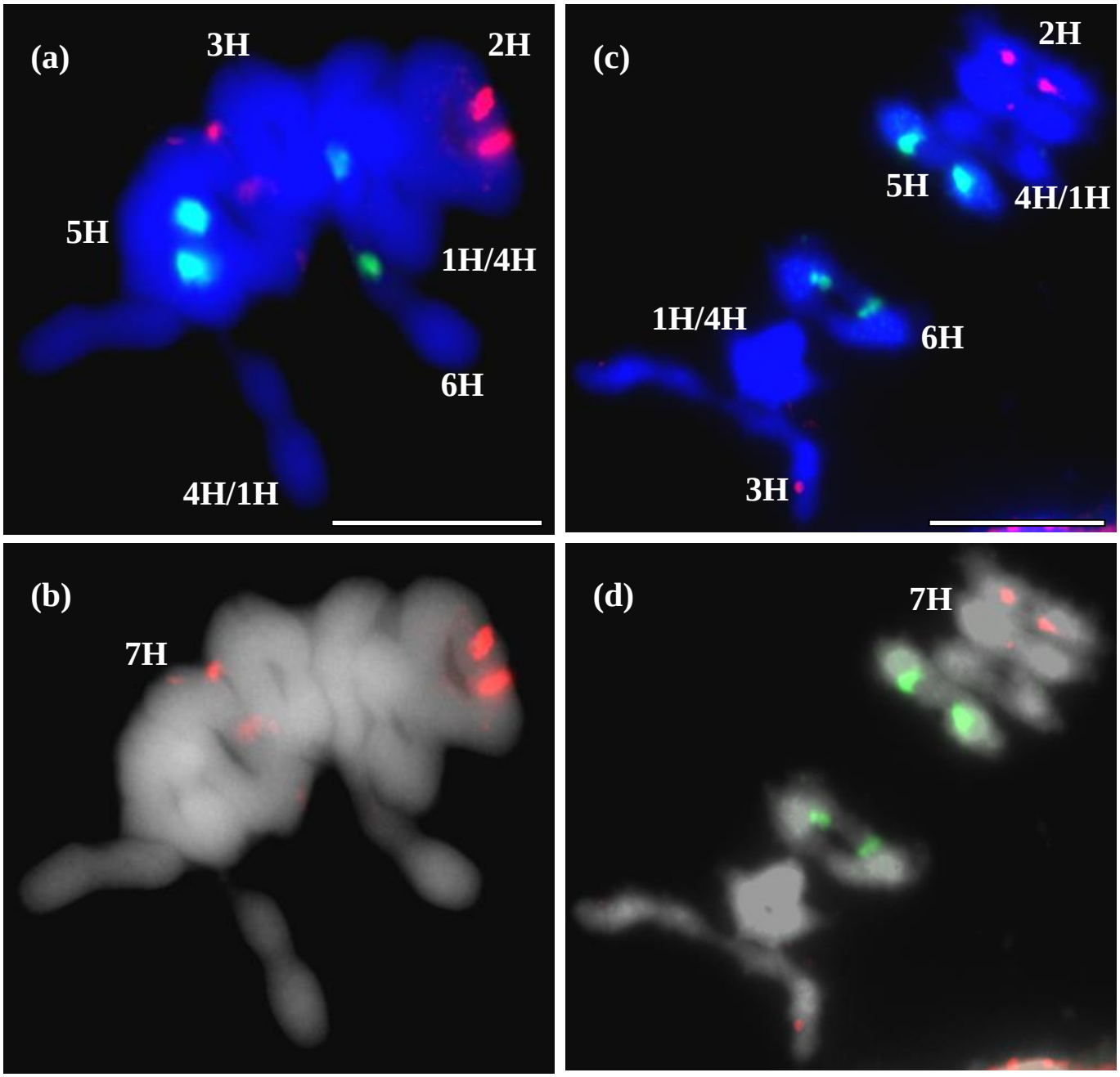


Figure 4.11: Two metaphase I spreads ((a) and (c)) from Morex treated with 500 ng/ml TSA (not in conjunction with a BrdU time course) with FISH labelled 45S (tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC: green) and 5S (tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3: red) rDNA repeats. (a) Has four bivalents (2H, 3H, 7H and 1H/4H), one buckle-shaped bivalent (5H), one rod-bivalent (6H) and two univalents (4H/1H). (c) Has four ring bivalents (2H, 4H/1H, 3H, 6H and 7H), one bulged rod-bivalent (5H) one rod-bivalent (3H) and one key shaped ring bivalent (1H/4H). DAPI counterstain in blue ((a) and (c)) and grey ((b) and (d)). Bar = 10 µm

Table 4.4: The effect of 1000 ng/ml TSA on mean CO frequency. Treatment caused a significant decrease in the mean CO frequency for chromosomes 1H+4H, 2H, 3H, 5H, 6H and 7H (n=100 for 1H+4H and n= 50 for remainder of chromosomes).

Chromosome	Mean CO frequency in Control.	Mean CO freq. in sample treated with 1000 ng/ml TSA.	ANOVA (p < 0.05 = Sig. diff. in CO freq).
1H+4H	2.16 +/- 0.53 SD	1.31 +/- 0.75 SD	2.78E-17
2H	2.08 +/- 0.34 SD	1.36 +/- 0.53 SD	1.32E-12
3H	2.44 +/- 0.50 SD	1.78 +/- 0.71 SD	5.12E-07
5H	2.1 +/- 0.71 SD	0.84 +/- 0.74 SD	7.42E-14
6H	1.76 +/- 0.48 SD	1.26 +/- 0.72 SD	9.08E-05
7H	1.94 +/- 0.31 SD	1.34 +/- 0.75 SD	8.96E-07

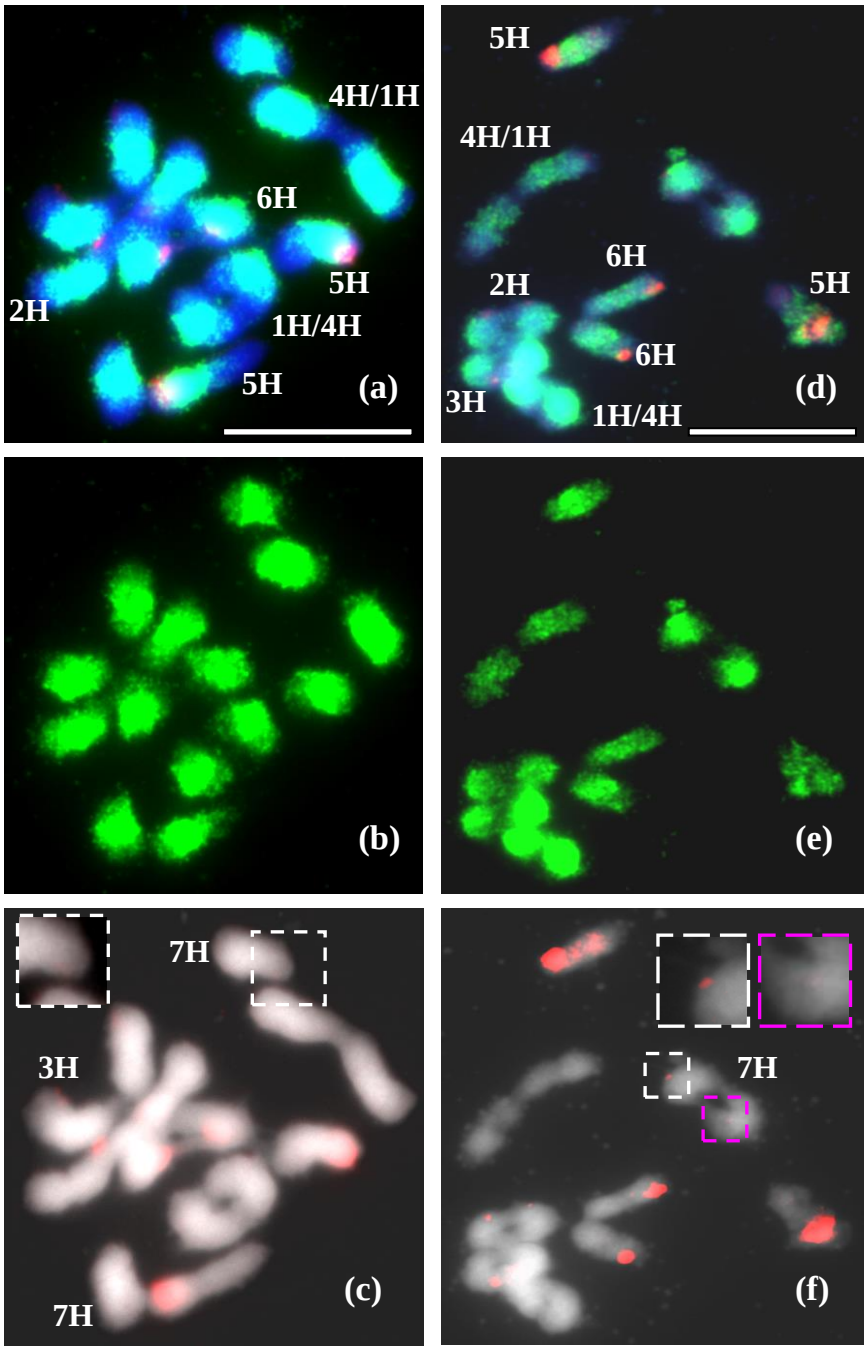


Figure 4.12: Two metaphase I spreads ((a) and (d)) from Morex treated with 1000 ng/ml TSA in conjunction with a BrdU time course ((b) and (e): anti-mouse Ig flourescein/green) and FISH labelled 45S (tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC: anti-DIG rhodamine (orange)) and 5S ((tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3: red) rDNA repeats. (a) Has two ring bivalents (1H/4H and 6H), three rod bivalents (2H, 3H and 4H/1H), and four univalents (5H and 7H). (d) Has four ring bivalents (1H/4H, 2H, 3H and 7H), one classic rod-bivalent (4H/1H) and four univalents (5H and 6H). 5S on 7H shown in insets ((c) and (f)). DAPI counterstain in blue ((a) and (d)) and grey ((c) and (f)). Bar = 10 µm

4.2.4 Treatment with high concentrations of TSA causes anaphase I bridges

The cytological analysis of Morex treated with 1000 ng/ml TSA also revealed the presence of anaphase I bridges (**Figure 4.13(a) and (b)**). This may be due to TSA induced hyperacetylation causing the chromatin to be less compacted (Toth *et al*., 2004; Shogren-Knaak *et al*., 2006), such that the synchronicity between chromatin contraction and expansion which occurs at metaphase I/anaphase I (Kleckner et al., 2004) is disrupted in some chromosomes more so than others, leading to a loss of the synchronicity of the separation of the bivalents (possibly a delay in homologue separation). Secondly, the disruption of the balance between chromatin contraction and expansion may be affecting the association of the bivalents with the meiotic spindle.

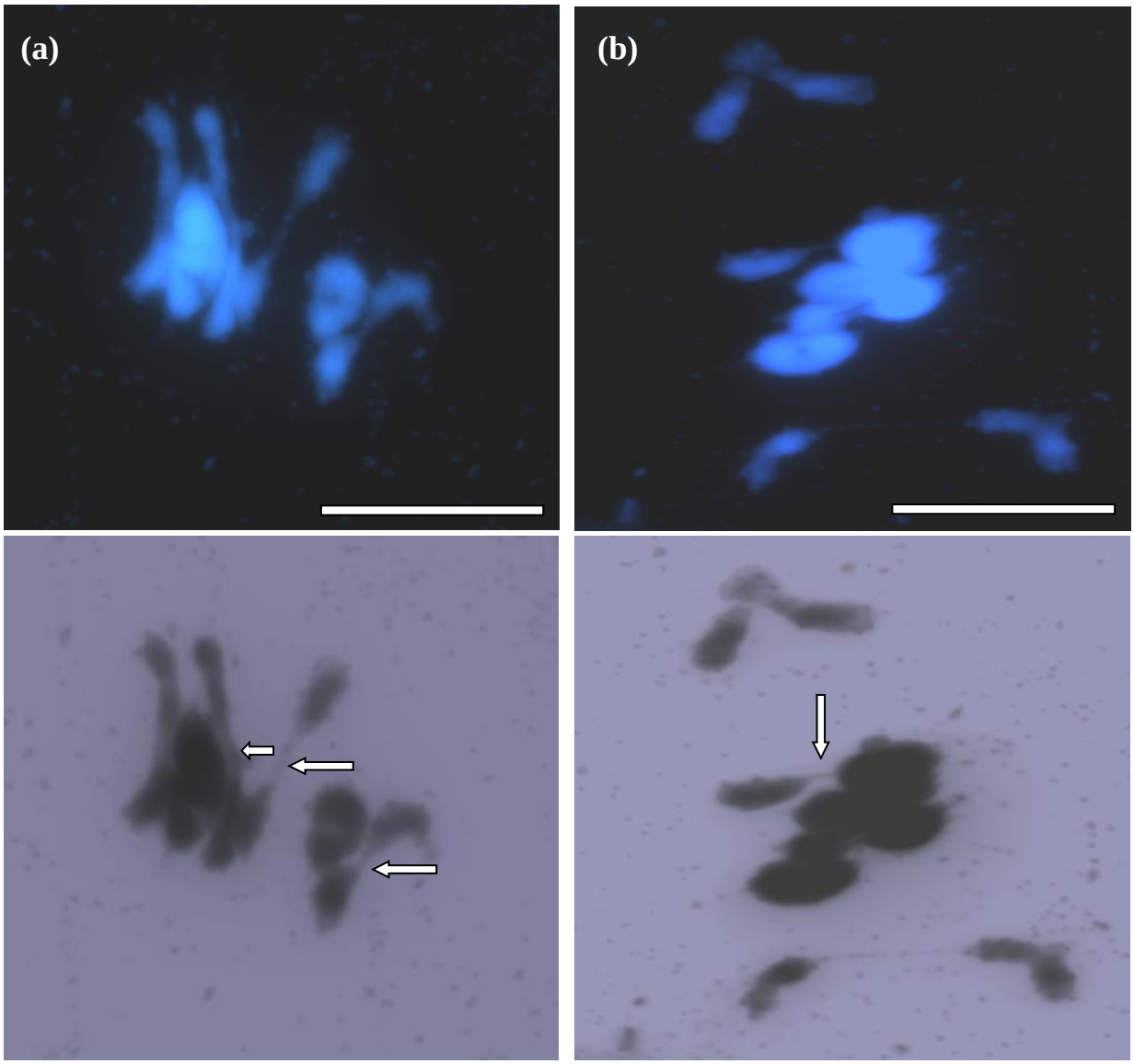


Figure 4.13: Treatment with 1000ng/ml TSA leads to anaphase I bridges ((a) and (b)) which are identified by white arrows. DAPI counterstain was originally shown in blue but the exposure was changed to dark grey to allow the thin anaphase bridges to be discerned. Bar = 10 µm

4.2.5 The genetic screening of the marker population treated with TSA

The analysis of a genetic screening of the marker population (Morex v Barke) treated with 100 ng/ml TSA showed no evidence for a reduced chiasma frequency (n=90 plants, **table 4.5**), indicating the absence of rod-bivalents that were expected as per the cytological analysis (see **Section 4.2.2**). The raw data of the BeadXpress® analysis showing the determination of the mean overall SNP marker recombination frequency per chromosome in the control and treated population is shown in the appendix (**Tables A5** to **A172**: **page 355** to **523**). All of the genetic maps for the test showed no absence of SNP markers at the ends of the maps when compared to the control indicating no absence in recombination of markers in those regions. ANOVA analysis of the mean number of recombination events for each of the seven chromosomes revealed no significant difference between the control and treated population (**Table 4.5**). This is in contrast to cytological analysis which revealed a significant reduction in chiasma frequency for chromosomes 1H+4H, 2H, 5H and 6H as depicted in the form of rod-bivalents (see **Section 4.2.2**). Instead, subtle variations in the recombination frequencies of clusters of markers was observed with some regions exhibiting reduced and neighbouring regions exhibiting increased levels of recombination, suggesting slight shifts in the distribution of recombination events.

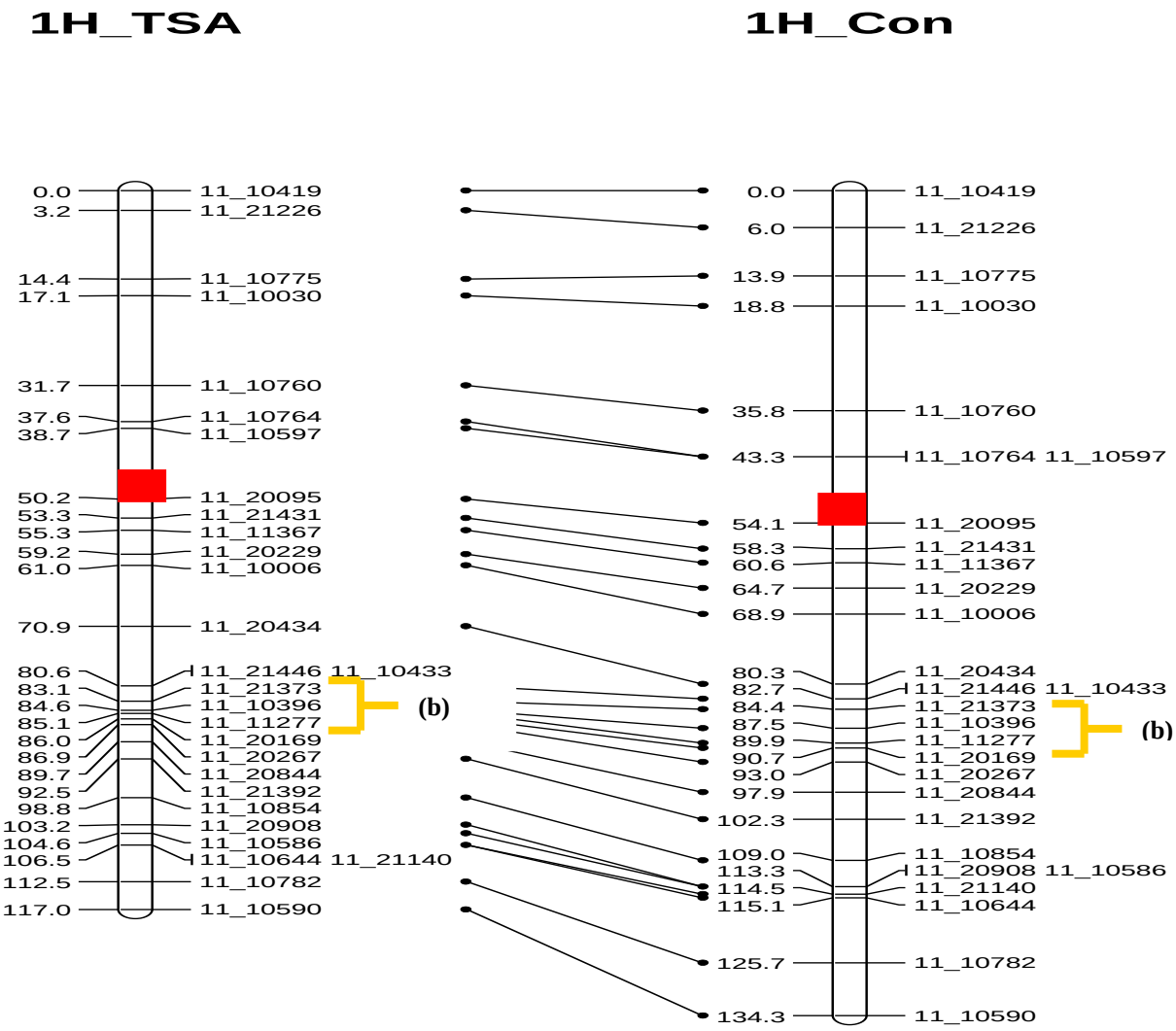
The genetic map of the long arm of chromosome 1H (**Figure 4.14(a)**) indicated a slight shift in recombination in a proximal direction within the region containing the markers 11_21373, 11_10396 and 11_11277 (proximal to distal order). This was depicted by an increased recombination frequency of marker 11_21373 and a subsequent reduction in the recombination frequency of markers 11_10396 and 11_11277 (**Figure 4.14(b)**). The genetic map of the long arm of chromosome 3H indicated a slight shift in the distribution recombination in a proximal direction within the region containing the markers 11_10728, 11_11191 and 11_10335 (proximal to distal order) (**Figure 4.16(a)**). This was depicted by an increased recombination frequency of markers 11_10728 and 11_11191 and a subsequent

reduction in the recombination frequency of marker 11_10335 (**Figure 4.16(b)**). Chi-squared statistical data (5.83) showed that this shift was significant for this interval (below the critical value of 5.9 for d.f.=2). This may correspond to the interstitial crossover that is cytologically observed at a high frequency (see **Section *4.2.1***). Next along the long arm we observe a shift in recombination distribution towards a distal direction for the two markers 11_20628 and 11_10515 as shown by a decrease in the recombination frequency of 11_20628 and the appearance of two recombination events for 11_10515 in the treated population in comparison to no recombination for this marker in the control (**Figure 4.16(d)**). Further along the long arm, treatment leads to a decrease in the recombination frequency of the two neighbouring markers 11_20612 and 11_20527 (**Figure 4.16(c)**). No obvious changes in recombination frequencies for gene clusters were observed for chromosomes 4H and 5H (**Figures 4.17** and **4.18**).

There is an increase in the recombination frequencies of the two neighbouring markers 11_10994 and 11_10939 on the short arm of chromosome 6H after treatment (**Figure 4.19(b)**). Further along the same arm in the centromeric direction, treatment leads causes a decrease in the recombination frequencies for the neighbouring markers 11_10462 and 11_10817 (**Figure 4.19(c)**). Treatment led to a complete loss of recombination for 11_10817. No observable changes in recombination frequencies for gene clusters were observed for chromosome 7H (**Figure 4.20**).

Table 4.5: The mean SNP marker recombination frequency for each chromosome in the Morex x Barker line in the treated population and the untreated control. The data suggests that the treatment with 100 ng/ml TSA had no significant effect on the overall mean marker recombination frequency for each of the seven barley chromosomes in the population (n=90). Raw data and determination of the mean SNP marker recombination frequencies is shown in the Appendix (Tables A5-A172: page 355 to 523).

Chromosome	Mean SNP marker recombination freq. in Control.	Mean SNP marker recombination freq. in sample treated with TSA.	ANOVA (p < 0.05 = Sig. diff. in CO freq).
1H	2.49 +/- 1.17 SD	2.21 +/- 1.05 SD	0.096576
2H	2.77 +/- 1.43 SD	2.82 +/- 1.20 SD	0.778402
3H	2.77 +/- 1.14 SD	2.73 +/- 1.41 SD	0.862002
4H	1.81 +/- 0.98 SD	1.62 +/- 1.10 SD	0.225198
5H	3.58 +/- 1.48 SD	3.51 +/- 1.38 SD	0.754994
6H	2.49 +/- 1.17 SD	2.22 +/- 1.06 SD	0.111008
7H	2.61 +/- 1.42 SD	2.57 +/- 1.46 SD	0.836297



(b)

Marker	11_21373	11_10396	11_11277
Map position	1H|95.42	1H|96.92	1H|97.68
Mean recomb, freq./cell (control)	3.333333	5.555556	4.444444
Mean recomb, freq./cell (test)	5	3	1

Figure 4.14: Genetic maps (a) for chromosome 1H corresponding to the Morex x Barke lines treated with 100 ng/ml TSA (1H_TSA) and the untreated control (1H_Con). (b) shows a mild shift in the distribution of recombination in the interval. The red block denotes the centromeres.

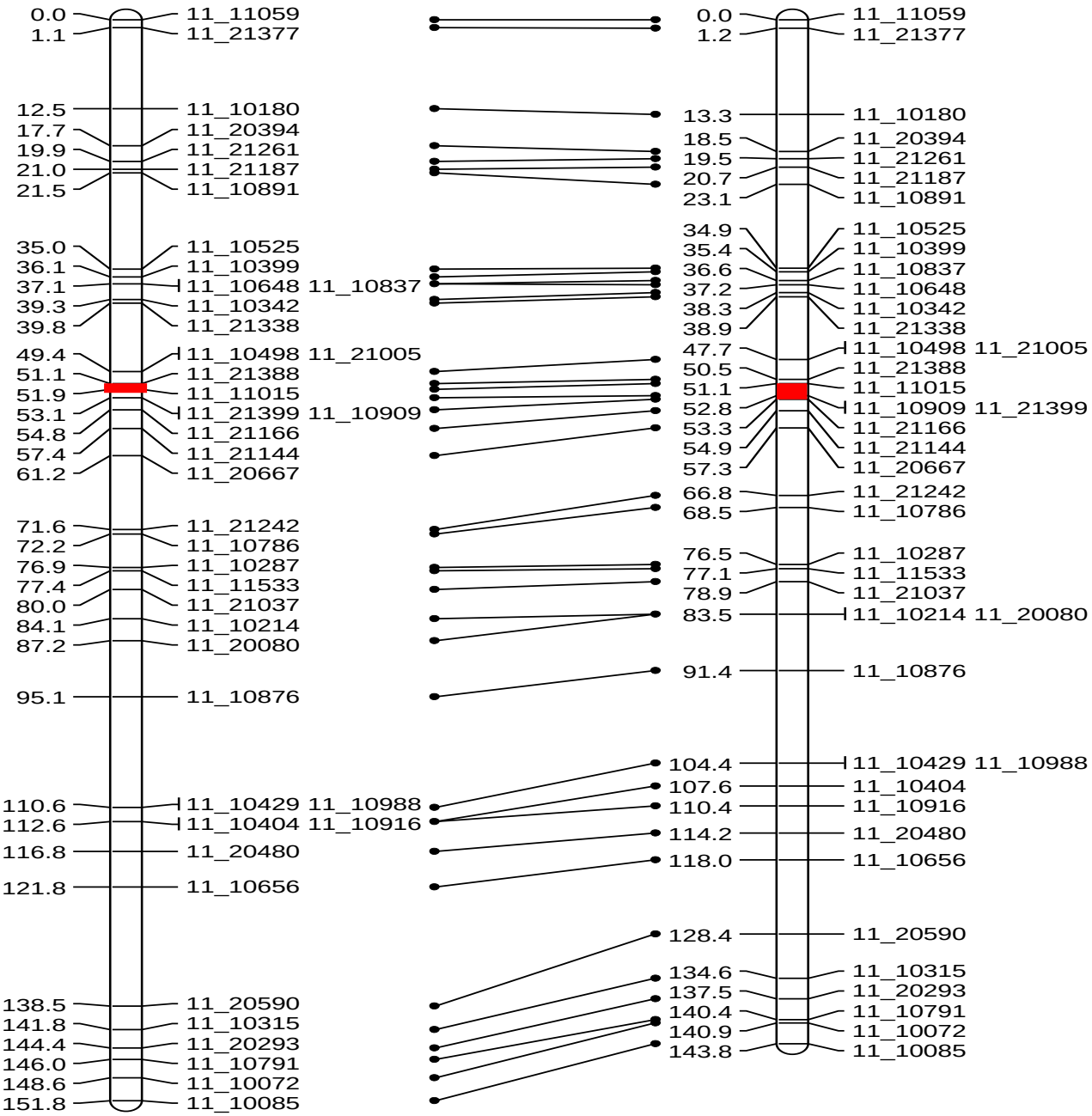
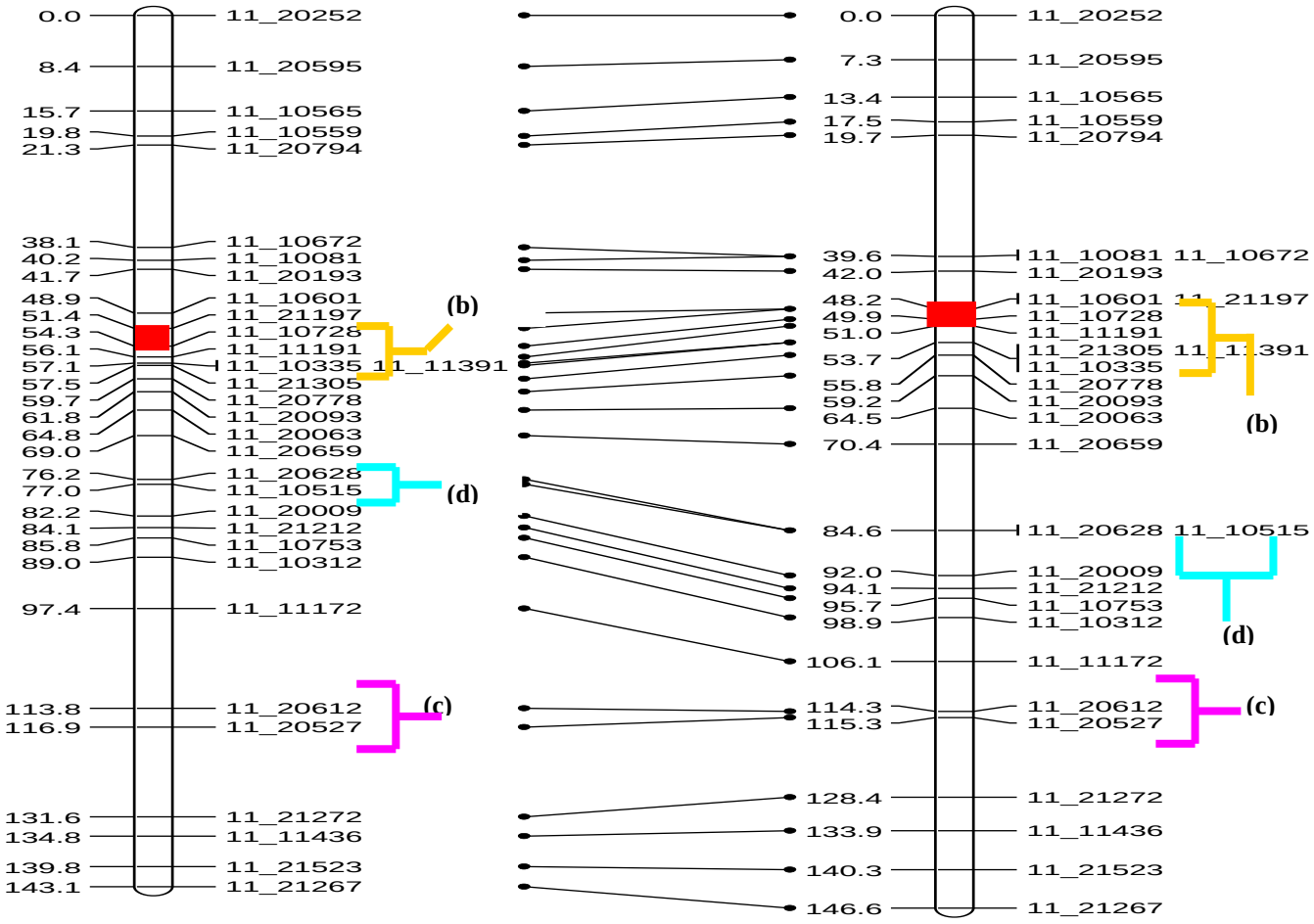


Figure 4.15: Genetic maps for chromosome 2H corresponding to the Morex x Barke lines treated with 100 ng/ml TSA (2H_TSA) and the untreated control (2H_Con). The red block denotes the centromere located between markers 11_11015 and 11_10909.

(a) 3H_TSA 3H_Con



Marker	11_10728	11_11191	11_10335
Map position	3H|62.99	3H|64.19	3H|65.52
Recomb, freq./cell (control)	3.333333	2.222222	5.555556
Recomb, freq./cell (test)	6	4	2

(b)

Marker	11_20628	11_10515
Map position	3H|98.49	3H|99.89
Recomb, freq./cell (control)	24.44444	0
Recomb, freq./cell (test)	14	2

(d)

(c)

Marker	11_20612	11_20527
Map position	3H|131.59	3H|134.31
Recomb, freq./cell (control)	29	6
Recomb, freq./cell (test)	15.55556	2.222222

Figure 4.16: Genetic maps (a) for chromosome 3H corresponding to the Morex x Barke lines treated with 100 ng/ml TSA (3H_TSA) and the untreated control (3H_Con) and (b) showing a significant shift in recombination frequency of markers. Centromere between markers 11_21197 and 11_10728 (red block).

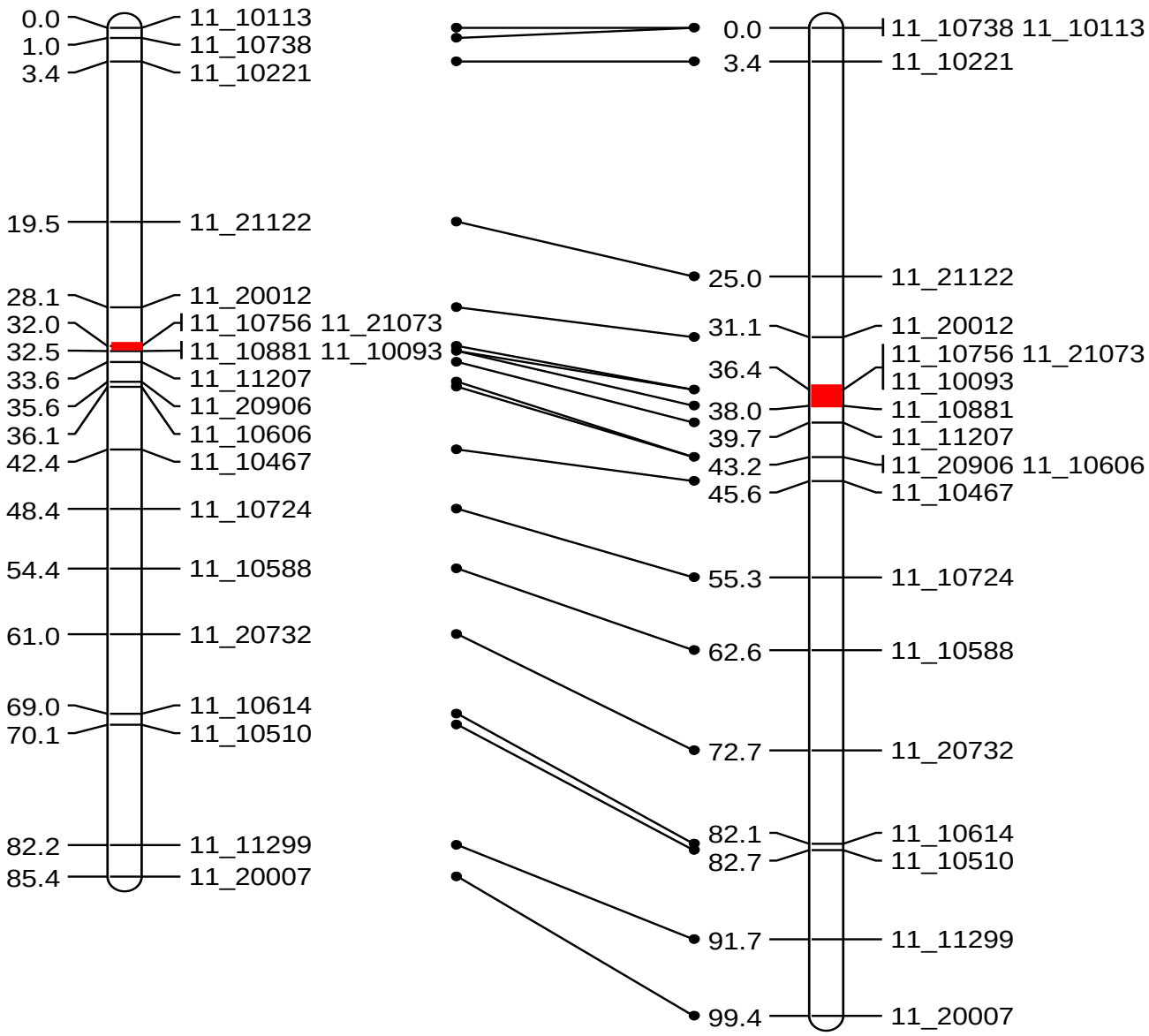


Figure 4.17: Genetic maps for chromosome 4H corresponding to the Morex x Barke lines treated with 100 ng/ml TSA (4H_TSA) and the untreated control (4H_Con). The red block denotes the centromere located between markers 11_10093 and 11_10881.

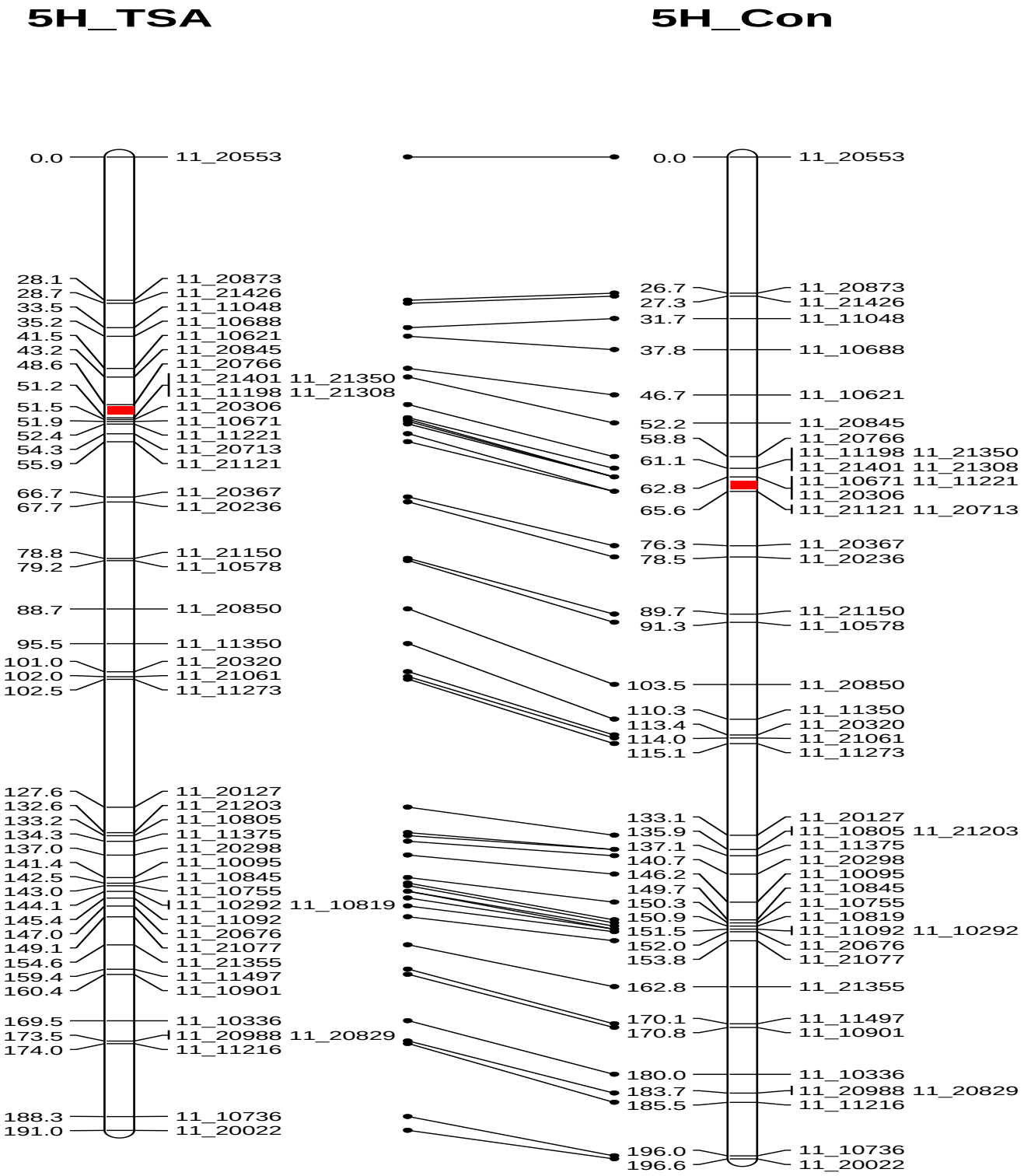
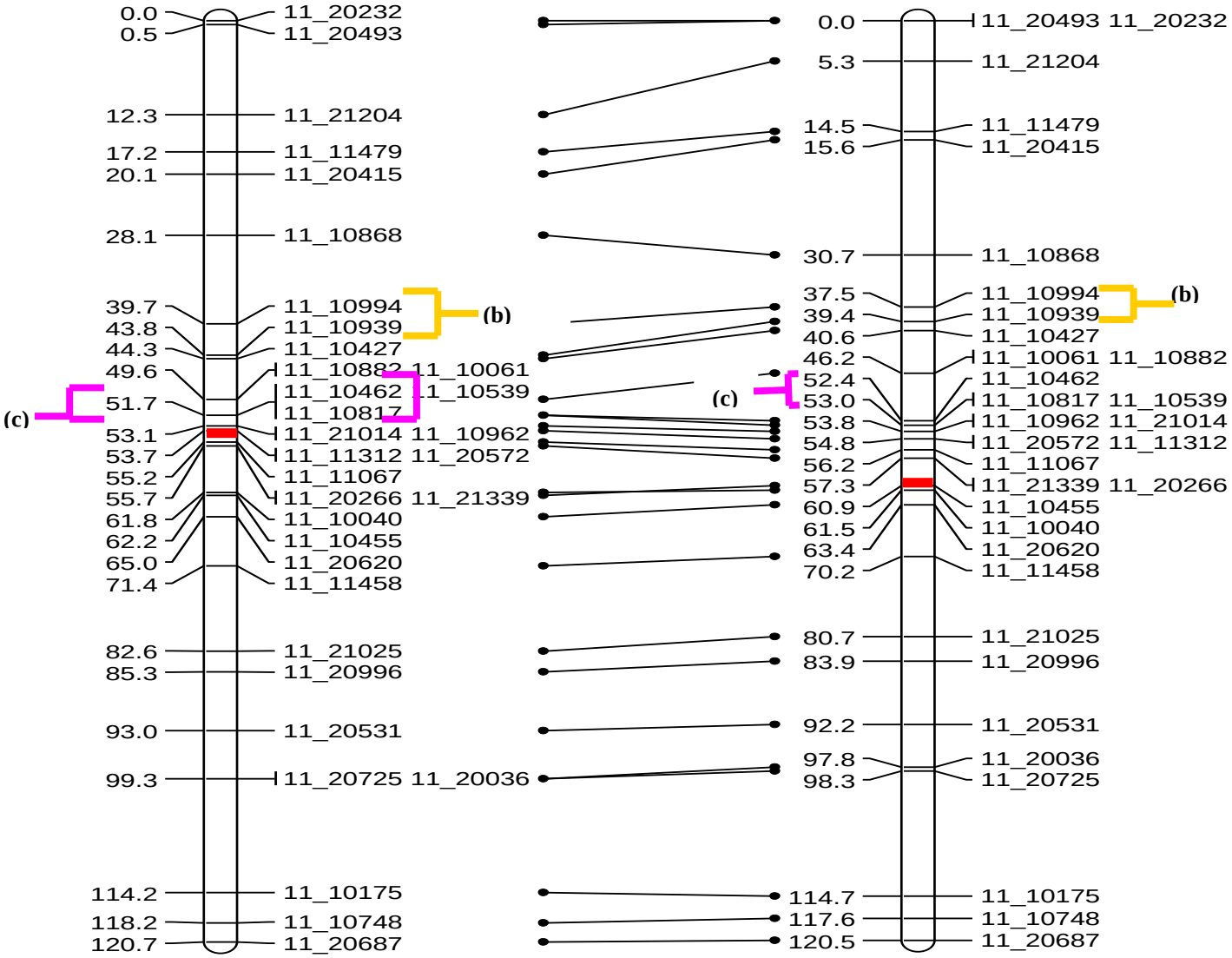


Figure 4.18: Genetic maps for chromosome 4H corresponding to the Morex x Barke lines treated with 100 ng/ml TSA (4H_TSA) and the untreated control (4H_Con). The red block denotes the centromere located between markers 11_21350 and 11_20306.

(a)



(b)

Marker	11_10994	11_10939
Map position	6H|31.73	6H|33.74
Recomb, freq./cell (control)	12.22222	3.333333
Recomb, freq./cell (test)	21	8

(c)

Marker	11_10462	11_10817
Map position	6H|44.77	6H|45.44
Recomb, freq./cell (control)	12.22222	1.111111
Recomb, freq./cell (test)	4	0

Figure 4.19: Genetic maps (a) for chromosome 6H corresponding to the Morex x Barke lines treated with 100 ng/ml TSA (6H_TSA) and the untreated control (6H_Con) and (b) showing a mild shift in recombination frequency of markers. Centromere between markers 11_11312 and 11_20572 (red block).

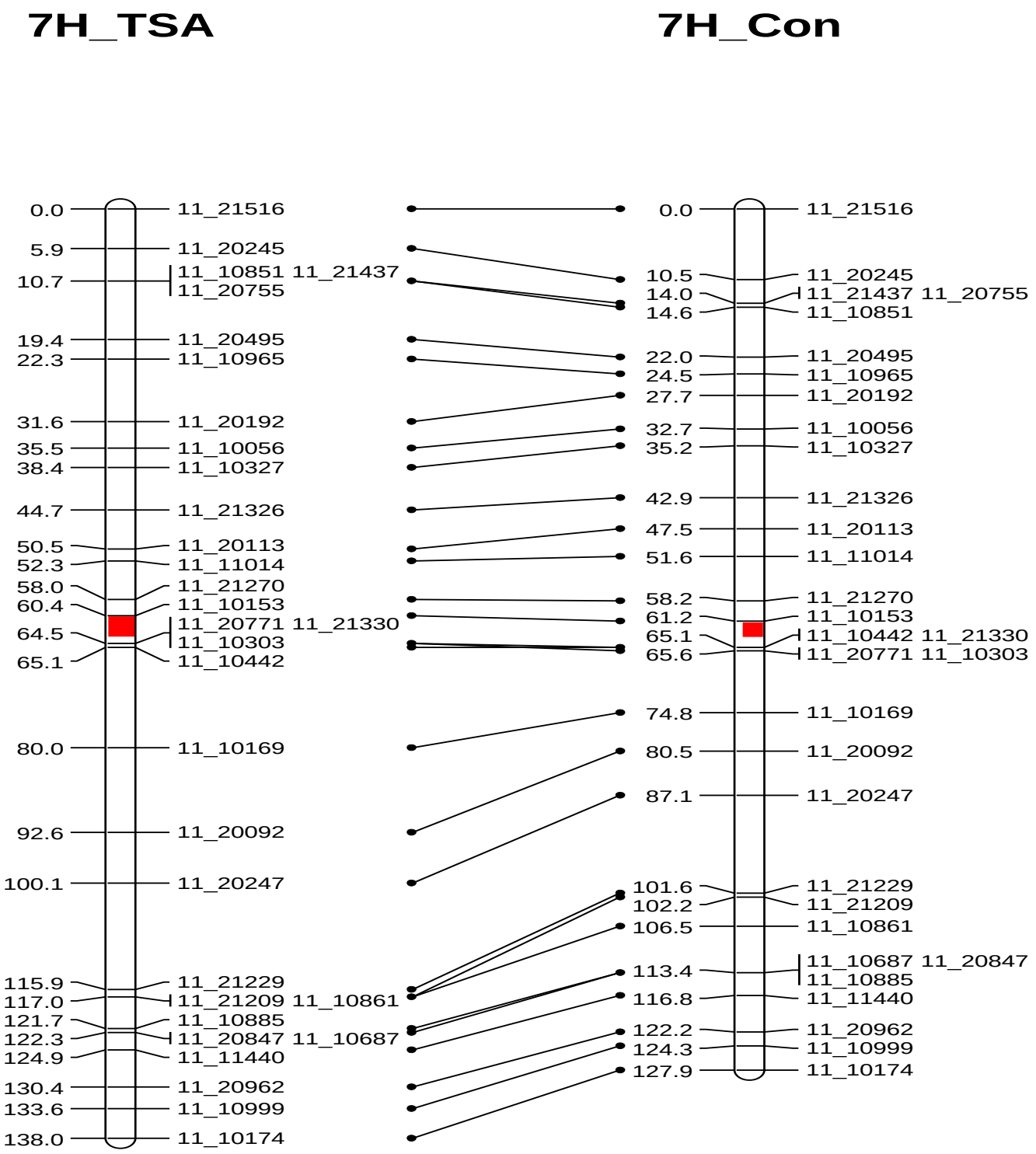


Figure 4.20: Genetic maps for chromosome 7H corresponding to the Morex x Barke lines treated with 100 ng/ml TSA (7H_TSA) and the untreated control (7H_Con). The red block denotes the centromere located between markers 11_10153 and 11_10442.

4.2.6 The effect of TSA treatment on ASY1/ZYP1 loading and polymerisation

The analysis of pollen mother cells in the control and the test sample treated with 1,000ng/ml TSA showed that ASY1 in both samples, appeared as distinct foci at meiotic G2 along the chromatin structure (**Figure 4.21**). The ASY1 signal became progressively linear from leptotene (**Figure 4.22**) onwards until at zygotene, the signal spanned the full length of the chromatin axis, which was also accompanied by the appearance of short stretches of ZYP1 in the control (**Figure 4.23(b)**). In contrast, the treated nuclei did display short stretches of ZYP1 (**Figure 4.23(e)**) but, the ASY1 signal was more diffuse (**Figure 4.23(d)**), showing that significant regions of chromatin seem to be indicative of G2 and leptotene (**Figure 4.26(b)**). At the onset of pachytene the treated sample was indistinguishable for the control at which it exhibited a slightly depleted ASY1 signal and complete linearization of ZYP1 (**Figure 4.24**). The ZYP1 signals and ASY1 signals became progressively intermittent at the onset of diplotene (**Figure 4.25**), showing that pachytene and diplotene in the test sample is indistinguishable from the control.

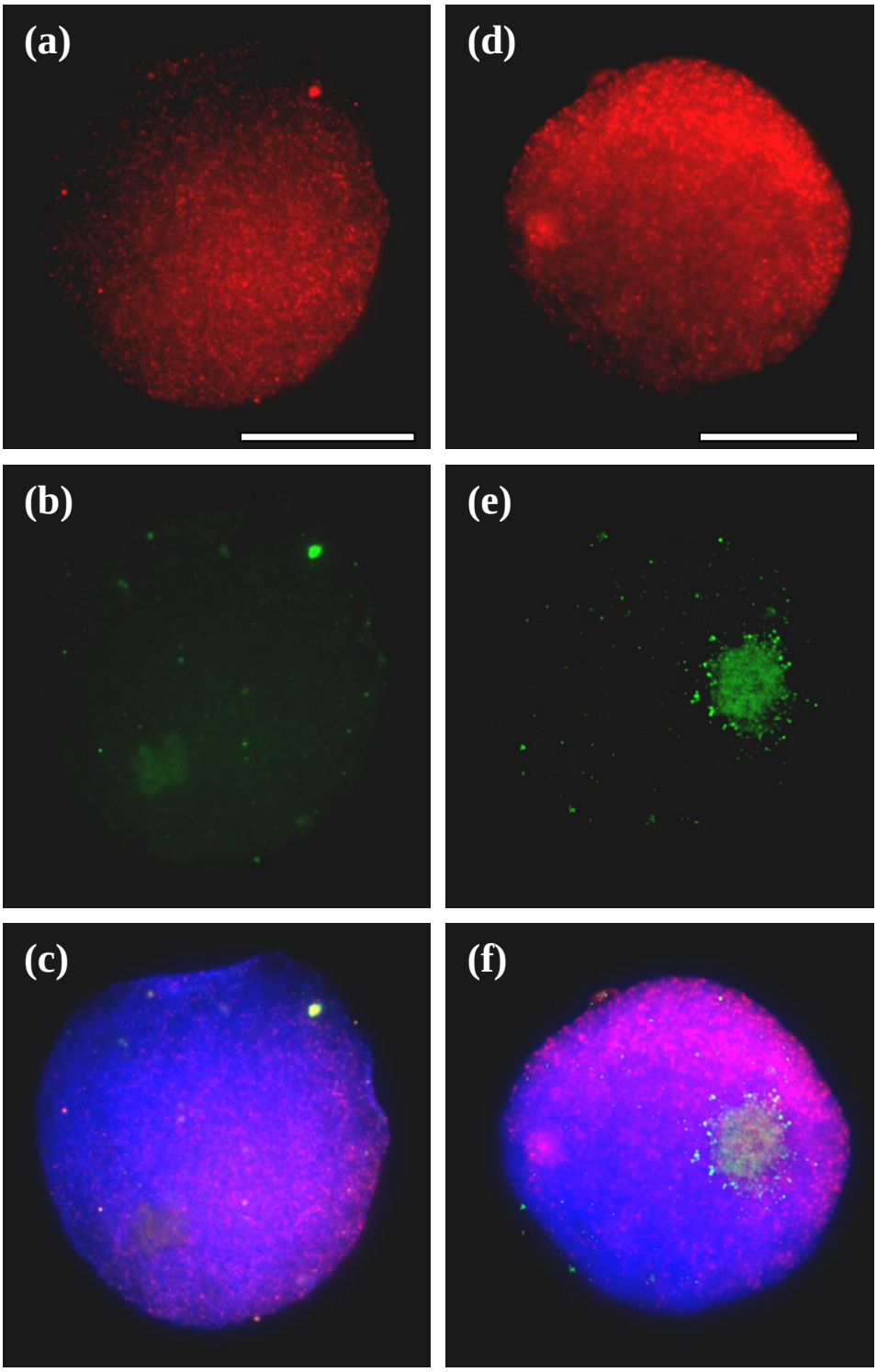


Figure 4.21: The loading of ASY1 at G2 stage in the Morex control ((a), (b), and (c)) and population treated with 1000 ng/ml TSA ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

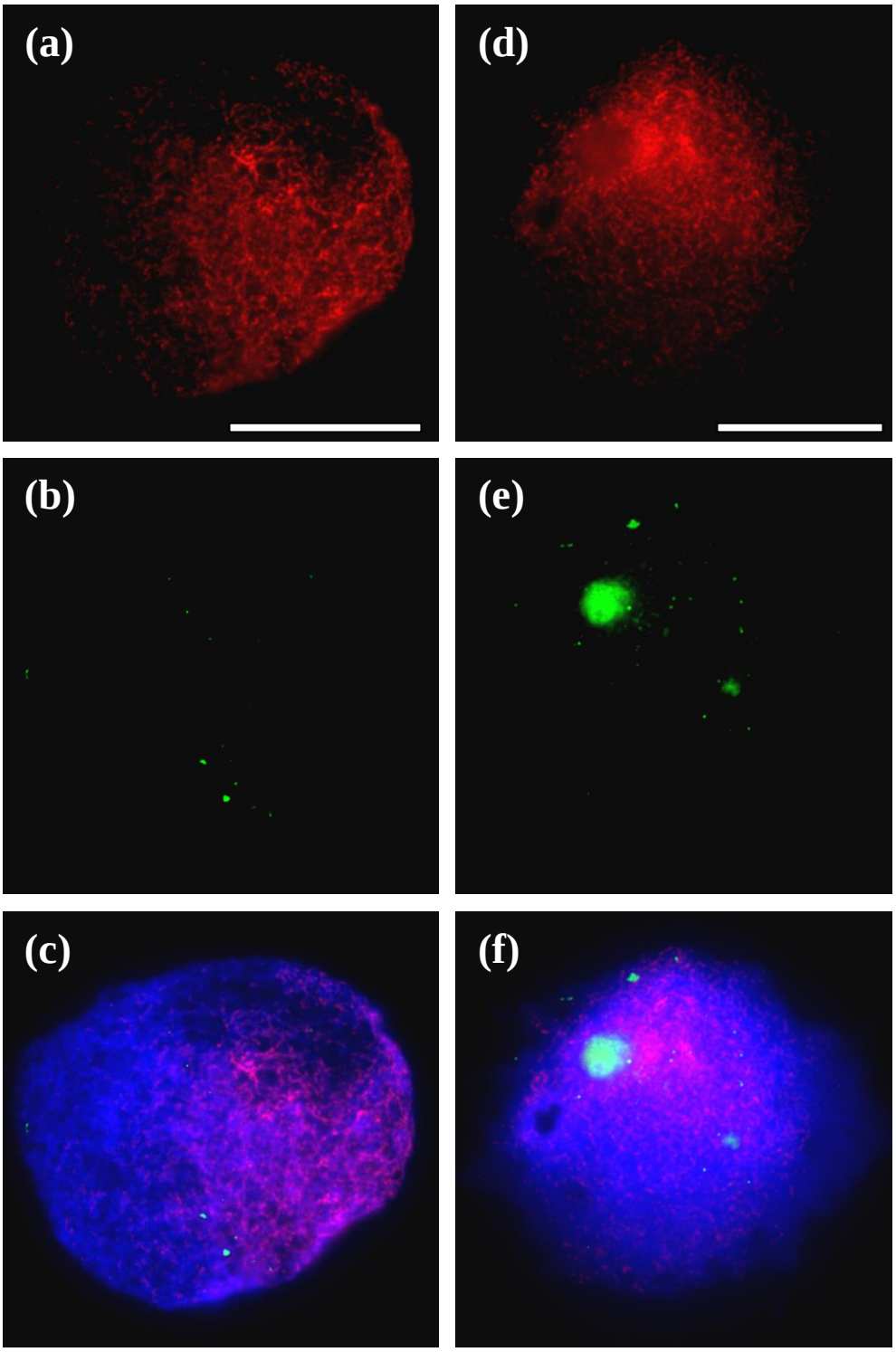


Figure 4.22: The initiation of ASY1 linearisation at leptotene stage in the Morex control ((a), (b), and (c)) and population treated with 1000 ng/ml TSA ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

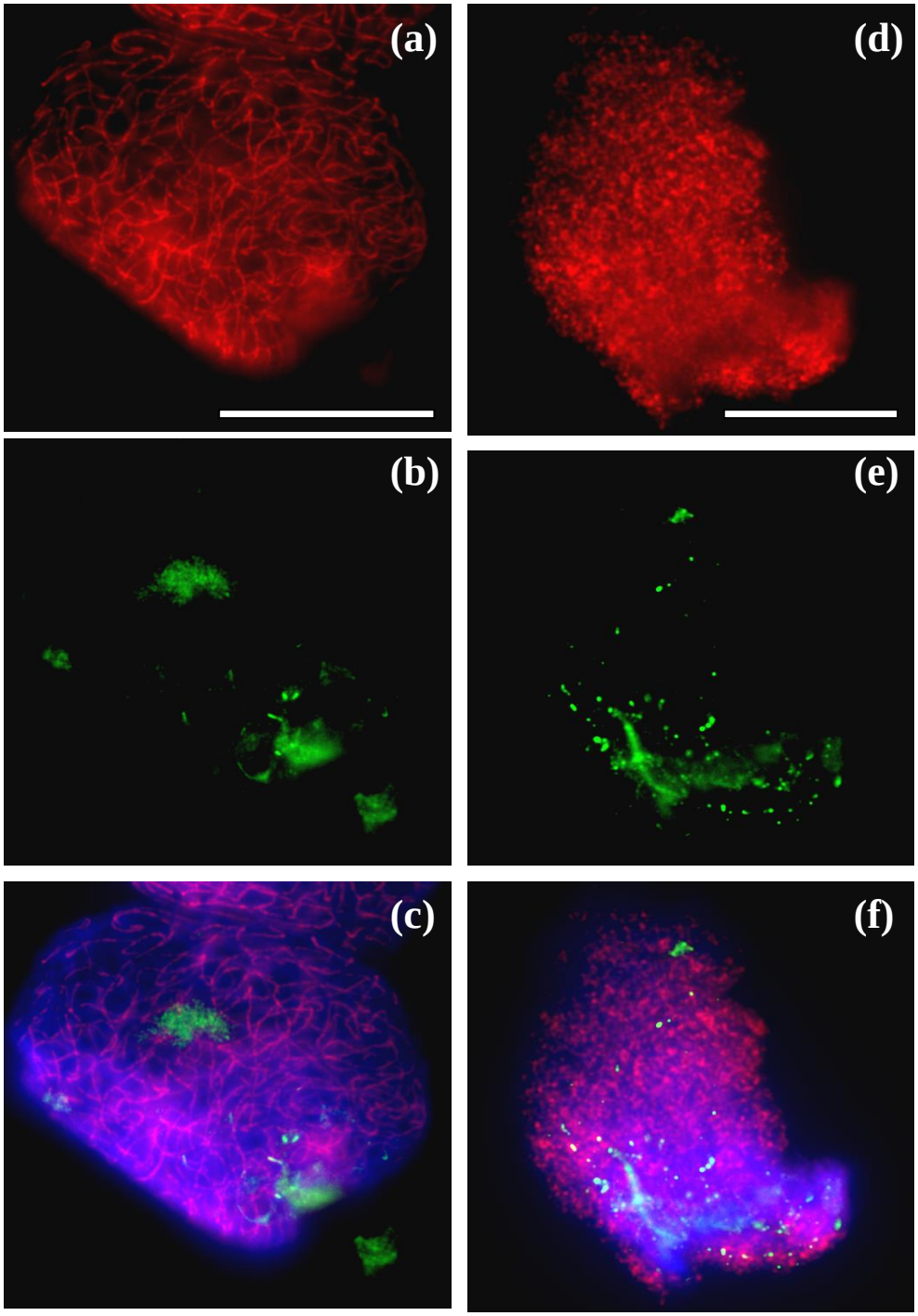


Figure 4.23: The complete linearisation of ASY1 at zygotene stage in the Morex control ((a), (b), and (c)) in contrast to regions of perturbed ASY1 linearisation in the population treated with 1000 ng/ml TSA ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm. Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

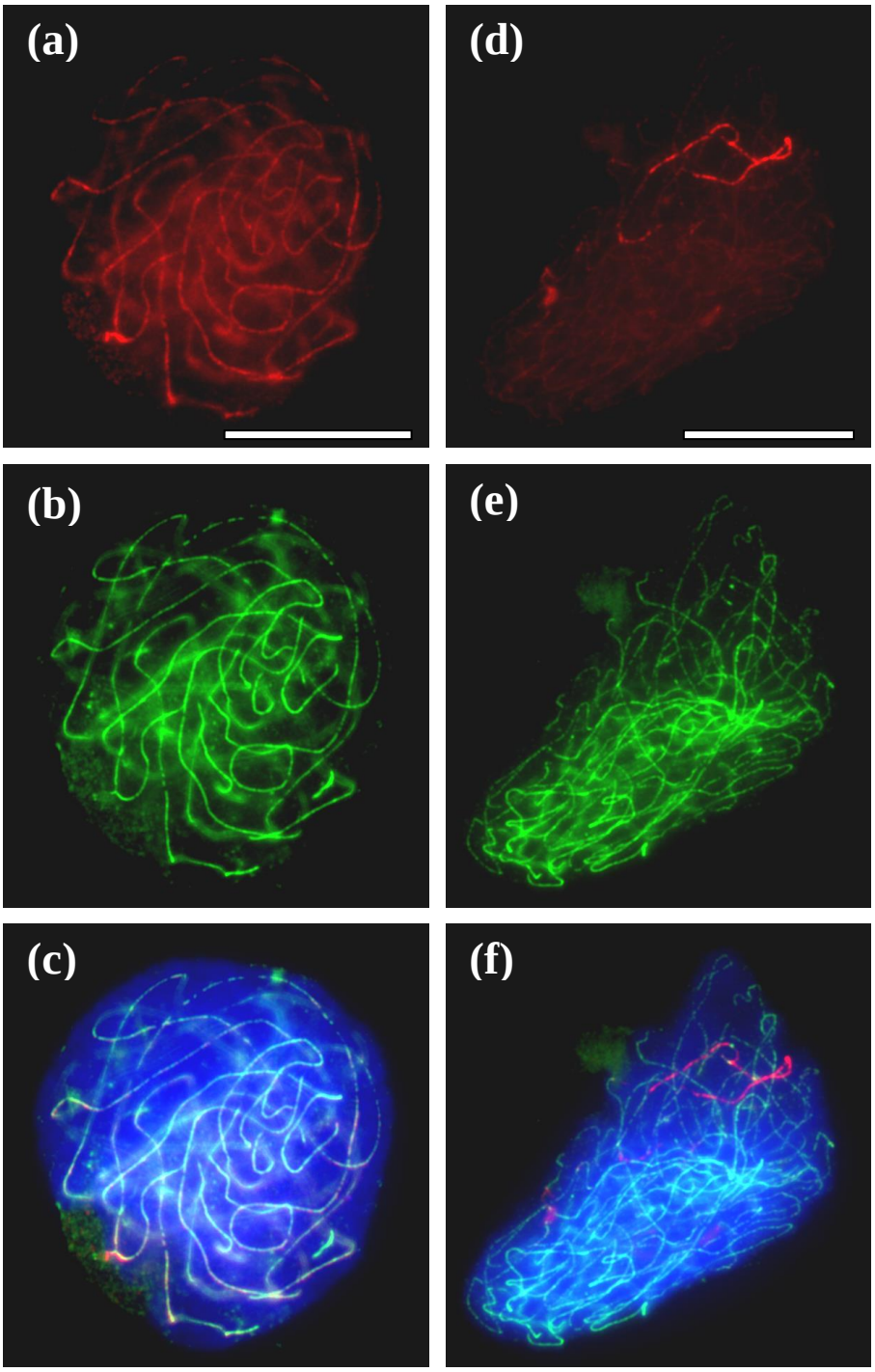


Figure 4.24: The complete linearisation of ZYP1 at pachytene stage, indicating complete synapsis in both the Morex control ((a), (b), and (c)) and the population treated with 1000 ng/ml TSA ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm. Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

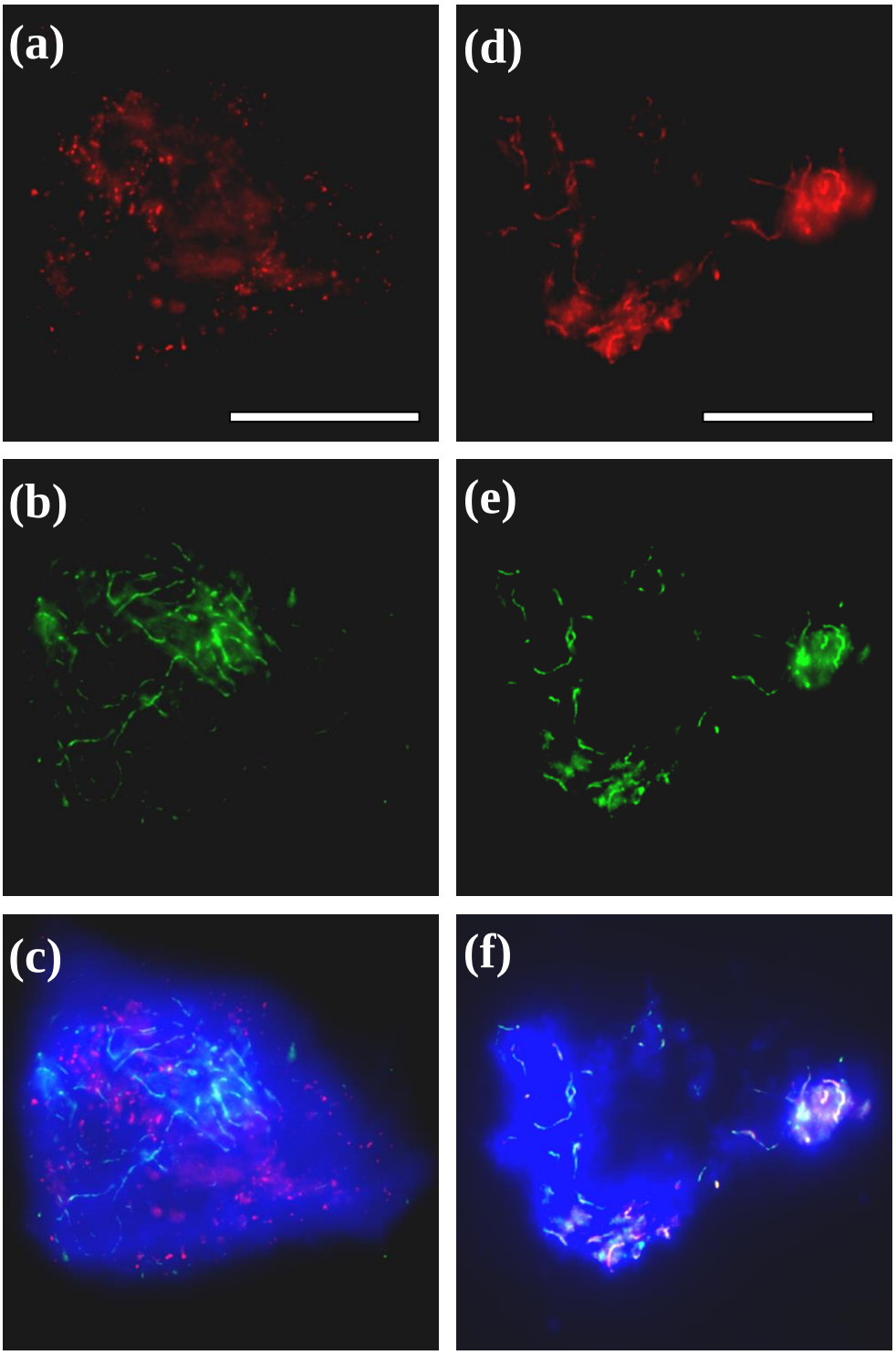


Figure 4.25: The depletion of ASY1 and ZYP1 at diplotene stage in the Morex control ((a), (b), and (c)) and population treated with 1000 ng/ml TSA ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

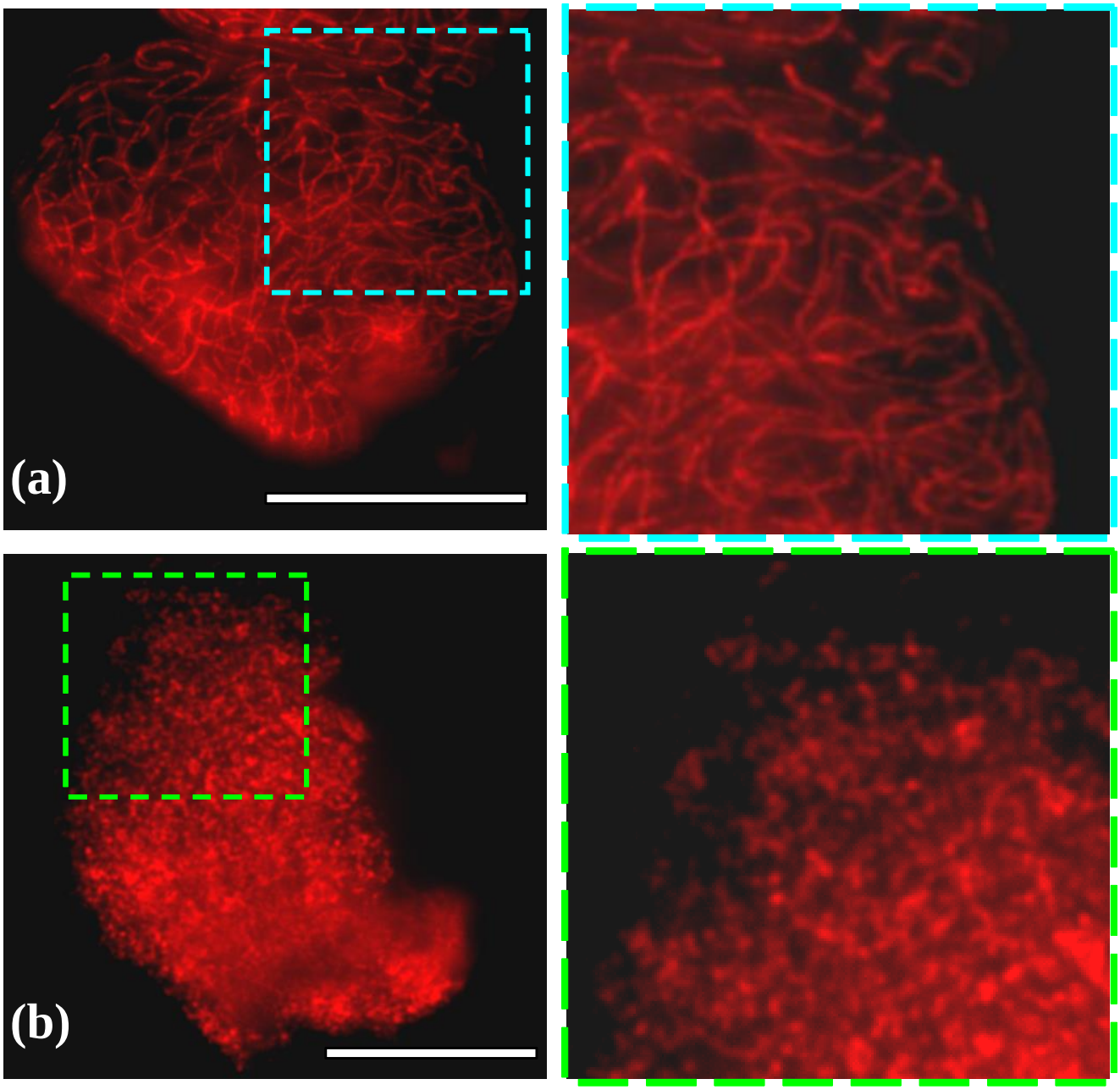


Figure 4.26: An enlarged view of Figure 4.23 with the FITC (ZYP1: green) exposure deactivated, allowing for the ASY1 (red) signal to be studied. The complete linearisation of ASY1 at zygotene stage in the Morex control (a) demonstrates that mature chromation axis formation has occurred (blue inset and expanded view). Regions of non-linearised ASY1 at zygotene stage in the population treated with 1000 ng/ml TSA (b) demonstrates perturbed chromatin axis formation (green inset and expanded view). Immunolocalisation was used to detect ASY1 (anti-rat: red) and ZYP1 (anti-rabbit: green). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

4.2.7 The effect of TSA treatment on the duration of meiosis

Barley stems were subjected to a 2 h pulse treatment with 1,000 ng/ml TSA which then, was followed by the injection of BrdU. The 2 h pulse treatment ensured that TSA was taken up by the meiocytes before the commencement of the time course study, allowing the effects of TSA on the progression of meiosis to be monitored. The anthers in the control and test sample were fixed at various time points. A preliminary analysis showed that in both the test and control, anthers at a length of 0.4 mm corresponded to G2/leptotene stage. Anthers between a length of 0.9 to 1.0 mm in the control and anthers at a length of 0.9 mm in the test sample corresponded to metaphase I. Finally, anthers ranging from 1.2 to 1.3 mm in the control and anthers at a length of 1.2 mm in the test population corresponded to tetrad stage. As both the control and test anthers corresponded to the same stage at a particular length, it was suspected that the treatment had no effect on the progression of meiosis. To ensure that the 2 h TSA pulse did exert an effect on meiosis, one stem was fixed 45h post TSA pulse treatment, and DAPI stained spreads confirmed the high abundance of univalents.

To further confirm that the treatment had no effect on the time course, the same slides were subjected to BrdU detection and it was found that G2 stages were labeled with BrdU at +18 h in both the test and control (**Table 4.6**). G2 stage was identified by the presence of discrete ASY1 foci (red) (**Figure 4.27**). Leptotene stages were labeled at +20 h (**Table 4.6**; **Figure 4.27**) and tetrad stages were labeled at +45 h (**Table 4.6**; **Figure 4.27**), in both the test and control. This analysis confirmed that the treatment with 1000 ng/ml TSA had no effect on the progression of meiosis.

Table 4.6: The first appearance of BrdU at a specific meiotic stage during the time course study in the untreated control (control) and sample treated with 1000 ng/ml TSA (test). In both the control and test sample, the first appearance of BrdU at G2 stage was at +18 hr. This was also the case for leptotene stage at +20 hr. The first appearance of BrdU at tetrad stage in the control and test sample was +45 hr, demonstrating that the treatment with 1000 ng/ml TSA had no effect on the duration of the meiotic pathway in the cultivar Morex.

Meiotic stage	First appearance of BrdU labeled meiotic stage					
	+18hr		+20hr		+45hr	
	Control	Test	Control	Test	Control	Test
G2	✓	✓	✓	✓	✓	✓
Leptotene			✓	✓	✓	✓
Tetrad					✓	✓

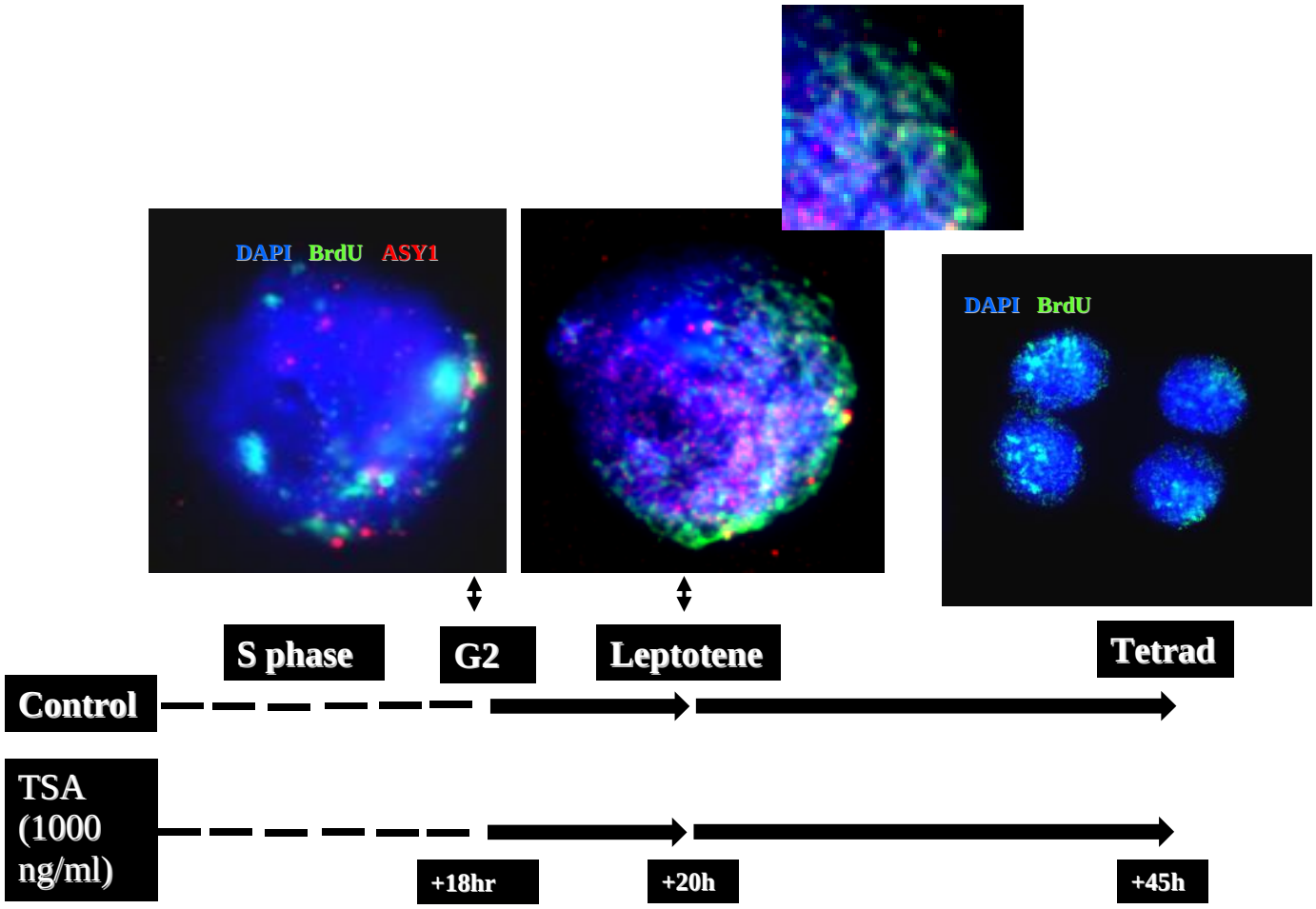


Figure 4.27: A dual BrdU time course/ASY1 immunolocalisation study using the microwave technique, showing no differeance in the duration of the meiotic pathway between the control and sample treated with 1000 ng/ml TSA. G2 was identified by the appearance of discrete ASY1 (anti-rat) foci (Cy3: red) and the entry into leptotene stage was depicted by the appearance short linear ASY1 signals (expanded view). The first appearance of BrdU at tetrad stage in both the control and test sample was at +45 hr of the time course. BrdU was detected with anti-mouse Ig flourescein (FITC: green). Chromatin was detected with DAPI counterstain (blue).

4.2.8 The effect of TSA on fertility and growth

In addition to affecting recombination using TSA, it was vitally important to yield fertile seeds from the treatment. Barley stems were injected with 100 and 1,000ng/ml TSA and left to grow and develop. 10ng/ml TSA was not used as the previous investigation showed that this concentration had no effect on recombination. After 1 week, the stems exhibited retarded growth and died by the fourth week.

The treatment was modified such that the stems were treated with pulses of 100 and 1,000ng/ml TSA for 5h, 10h, 20h and 40h, each, before being washed out with 4x10ml SDW. All plants pulse treated with 1,000ng/ml TSA died. However, stems pulse treated with 100ng/ml TSA for up to 20h did survive. The plants were less fertile and had shorter ears than the control plants (**Figure 4.28**). Stems treated with 100ng/ml TSA produced a significantly lower mean number of seeds per ear (12.8) compared to that for the control (37) (ANOVA p= 5.9E-25, n=40) (**Figure 4.29**). The analysis of the length of the same ears showed that the treated ears had a significantly shorter mean length (5.1cm) compared to the control ears (6.7cm) (ANOVA p=1.6E-11, n=40) (**Figure 4.30**).

Figure 4.28: A harvested ear from a Morex plant that was treated with 100 ng/ml TSA (right) at meiosis alongside an ear from an untreated control plant (left), showing reduced fertility as well as perturbed growth and development. Bar = 1 cm

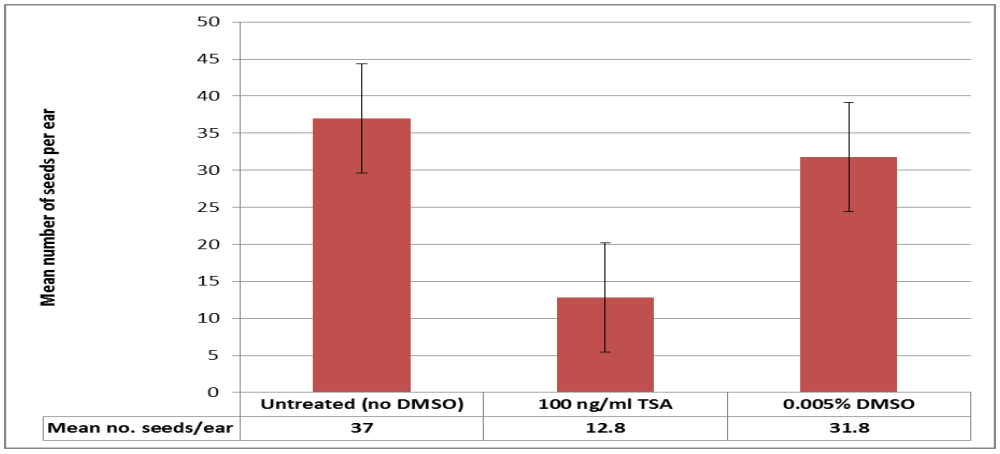


Figure 4.29: A graph depicting the mean number of seeds per ear for the untreated control, 100 ng/ml TSA treated population and the control (0.005% DMSO) (n=40 plants).

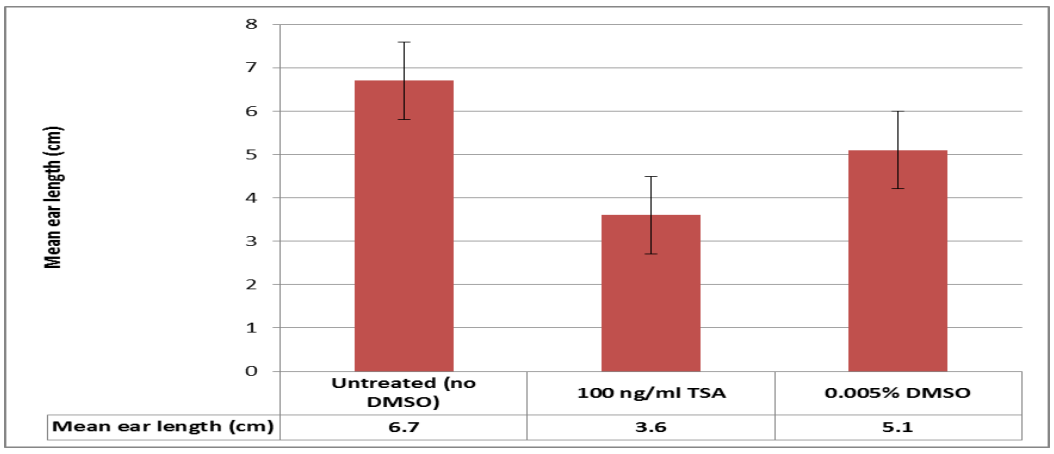


Figure 4.30: A graph depicting the mean ear length for the untreated control, 100 ng/ml TSA treated population and the control (0.005% DMSO) (n=40 plants).

4.3 Discussion

The cytological analysis of the effects of TSA revealed that treatment with this chemical causes a reduction, as well as a shift in the distribution of meiotic chiasma frequency at metaphase I. This is consistent with the effect observed in *Arabidopsis* using the same treatment (Perrella *et al*., 2010). Bearing in mind that no significant effect on the mean CO frequency per nuclei was observed with all concentrations of TSA (10, 100 and 1,000 ng/ml) in *Arabidopsis* (Perrella *et al*., 2010), a significant effect was observed at concentrations above 10 ng/ml in barley. There was a slight but significant reduction in CO frequency for chromosome 1H+4H and a slight increase in CO frequency for chromosome 6H. Interestingly, **Figures 4.9(a)** and **(c)** (post-treatment with 10 ng/ml TSA) appear to show the successful detection of the 5S rDNA repeat on chromosome 4H unlike the untreated control (Leitch and Heslop-Harrison, 1993). This is probably due to TSA induced hyperacetylation promoting a more open chromatin structure (Toth *et al*., 2004; Shogren-Knaak *et al*., 2006), allowing for the access of the probe to the region of chromatin harbouring the 5S rDNA repeat. This may be important in this case as the 5S repeat on 4H is very small (Leitch and Heslop-Harrison, 1993). But, with the varying degree of chromatin contraction/expansion cycles that occur at metaphase I/anaphase I (probably to ensure correct chromosome segregation: Kleckner *et al*., 2004) along with the complicated issue of varying degrees of TSA induced chromatin expansion (Toth *et al*., 2004; Shogren-Knaak *et al*., 2006), the successful detection of 5S rDNA on chromosome 4H was still a very rare occurance post-TSA treatment in this PhD study. Additionally, the 5S signal on 4H was identified in some control samples (**Figure 4.8**) but again, the rarity of this occurance as mentioned earlier, may also be due to a dependance on the chromosome spreading technique (the orientation of 4H on the slide such that the 5S rDNA repeat is facing the front and hence, in the field of view) and the varying degree of the chromosome

contraction/expansion cycles (Kleckner *et al*., 2004). The fact that the 5S signal on 4H was occasionally detected in the control may be due to cultivar specific differences between the study by Leitch and Heslop-Harrison (1993) (Betzes, Sultan and monotelotrisomic lines of 1HS, 2HL, 3HL and 4HL) and this study (Morex). The second reason for this disparity may be due to the fact that the study by Leitch and Heslop-Harrison (1993) analysed mitotic chromosomes (extracted from the root tips) whereas this study examined meiotic chromosomes (extracted from the anthers), such that there may be slight difference between the relative sizes/physical locations of the 5S repeats and slight differences in the global chromatin structure that harbours the 5S repeats, between mitotic and meiotic chromosomes.

The second disparity between the effect of TSA in *Arabidopsis* and barley noticed upon cytological analysis was that there was no increase in the proportion of proximal chiasma in barley but this affect was was observed in *Arabidopsis* (Perrella *et al*., 2010). There was a decrease in the mean overall chiasma frequency and surprisingly a reduction in the proportion of interstitial COs for chromosome 3H at the highest dose of TSA. This is in contrast to *Arabidopsis* for which there was no alteration in the mean overall chiasma frequency as well as an increase in the proportion of proximal COs for chromosome number 4 (Perrella *et al*., 2010). This could be explained by the fact that barley chromosomes have a much higher abundance of repeat sequences than *Arabidopsis* (Barakat *et al*., 1998; refer to **Inroduction**, **section *1.17.1***) which account for up to 84% of the total genomic content (Mayer *et al*., 2012) such that, barley chromosomes may be more sensitive to the treatment. Studies in maize have demonstrated that histone hyperacetylation occurs in the repeat as well the non-repeat sequences when the the histone deacetylase gene Rpd3-type hda 101, was down-regulated (Rossi *et al*., 2007). The threshold concentration seems to have the greatest effect on chromosome 5H as it exhibited the greatest decrease in chiasma frequency of

all the chromosomes, most notably in the short arm. This chromosome occasionally lost of one of the two chiasma in the distal region of the long arm and exhibited the greatest number of univalents at 1,000 ng/ml TSA. This chromosome seems to be the most succeptible of all the chromosomes to the treatment and this may be explained by the fact that the short arm harbours the NOR (Higgins *et al*., 2012). A mutational analysis of the histone deacetylase *HDA6* in *Arabidopsis* confirmed a significant and preferential increase in histone H4 hyperacetyaltion in the NOR region leading to decondensation of the rDNA repeats within this region (Probst *et al*., 2004). Despite the fact that chromosome 6H also contains an NOR (Higgins *et al*., 2012), it didn't experience the same degree in loss of chiasmata as chromosomes 1H/4H and 2H (not habouring NORs). However it did exhibit rod-bivalents at the threshold concentration. Upon cytological analysis of the barley chromosomes, it is observed that chromosomes 2H and 5H are physically larger than chromosome 6H suggesting that larger chromosomes are more susseptable to the effects of hyperacetylation. Further, we notice that at the threshold concentration, all of the chromosomes containing 45S rDNA repeats (most notably in the subtelomeric regions of the short arms) exhibited a significant reduction in chiasma frequency (chromosomes 5H and 6H). In contrast, the only chromosomes containing 5S rDNA repeats which did experience a significant reduction in chiasma frequency were chromosomes 2H and 4H despite the fact that chromosomes 3H and 7H also contain 5S rDNA repeat sequences (Stephens *et al*., 2004). This observation puts forward the possibility that chromosome arms containing 45S rDNA sequences are more sensitive to the effects of hyperacetylation than that whose arms contain 5S rDNA repeats. It has already been demonstrated that the mutation of a key histone deacetylase in *Arabidopsis* (Probst *et al*., 2004) only leads to decondensation of rDNA repeats which comprise the NOR (45S). Hence, there may be a greater degree of decondensation of regions of the genome that harbour 45S repeats

compared to regions containing 5S repeats, which may account for the difference in sensitivities between chromosomes. Chromosome 3H, as well as being smaller than chromosome 2H and of a similar size to chromosomes 1H and 4H, does harbour a much more prominent 5S signal (the signal in chromosome 4H is very weak: Leitch and Heslop-Harrison (1993)). Coincidently chromosome 3H is the most resistant to the treatment such that at the highest concentration of TSA (1,000 ng/ml), it only exhibits rod-bivalent formation by losing 1 CO on the short arm and the insterstitial CO on the long arm leaving a single obligate CO in the distal end of the long arm bearing the 5S rDNA repeat. At 10 mg/ml TSA, the significant decrease in the mean CO frequency for chromosome 1H+4H was due to the fact that in the control, 23 nuclei exhibited 2 chiasmata on the same arm but only 6 nuclei in the test sample displayed this. The slight increase in CO frequency for chromosome 6H at this concentration could be due to the fact that although it harbours an NOR, its relatively small size compared to other the chromosomes may lead to an antagonistic effect between both opposing factors such that there is a slight but overall decondensation of the global chromatin structure allowing access to key meiotic factors. Despite this significant effect, there was no significant increase in the proportion of proximal to distal COs or *vise versa* but rather an increase in the CO frequency at the distal end of the short arm, where CO assurance is not well maintained even in the wild-type. This may mean that the observance of the increased number of COs in the short arm may be mistaken for the distal ends of both short arms overlapping in resonse to a slight confomational change in the global chromatin structure induced by hyperacetyaltion. This discussion suggests that a combination of three effects 1) the presence of an NOR 2) the type of rDNA repeat and 3) the size of the chromosome, may be important factors that determine the sensitivity of a chromosome to the effects of hyperacetylation during meiosis. As a result, this discussion proposes the “Region type/size model”, in which some factors may enhance

or antagonise the effects of the other factors depending on the content of the chromosomal regions and the size of the chromosomes. This proposed model seems to be in agreement with the effects observed in the *Arabidopsis* MCC1 overexpression line (Perrella *et al*., 2010). In *Arabidopsis* Chromosomes 2 and 4 are NOR and hence, 45S rDNA sequence harbouring chromosomes (Lam *et al*., 2005) however, only chromosome 2 exhibits univalent formation (up to 8%) whereas chromosome 4 remains as a ring bivalent probably due to the fact that it also harbours 5S rDNA sequences. Chromosome 5 only contains the 5S rDNA sequence and is unaffected by the effects of hyperacetylation. Further, one of the two smallest chromosomes (chromosome 3) didn't exhibit a reduction in chiasma frequency (Perrella *et al*., 2010). The possible role played by the differing sizes of the chromosomes in response to histone hyperacetylation was also suggested by Perrella *et al*., 2010. The data presented by the effects of histone hyperacetylation during meiosis in *Arabidopsis* seem to be in agreement with the proposed "Region type/size model" such that the increase in the proportion of proximal chiasma in chromosome 4 may be due to the interplay of the antagonistic effects of 45S and 5S on the same chromosome and the absence of this effect in barley could may well be due to the fact that non of its chromosomes contain both types of sequences, but only one or the other. Further, the subtle shift in the distribution of the interstitial CO in chromosome 3 as suggested by the genetic screening data for barley as well as the cytologically observed but not significant increase in the proportion of proximal COs in *Arabidopsis* chromosome 3 (Perrella *et al*., 2010) may be due in part to their relatively small size in comparison to the remaining chromosomes of their respective genomes and in particular, the interplay of chromosome size and the presence of a prominent 5S rDNA sequence in barley chromosome 3H.

The choice for treating the marker population (for genetic screening) with a TSA concentration of 100 ng/ml was due to the fact that 10 ng/ml TSA caused no significant effect on mean chiasma frequency when cytologically oberved. Despite the fact that 1,000 ng/ml TSA greatly reduced chiasma frequency and shifted the chiasma distribution of the obligate chiasmata in the rod-bivalents from a distal to a sub-telomeric position upon cytological analysis, the high toxicity of this high dose led to premature plant death and hence, no F2 seed production. The treatment with 100 ng/ml led to a significant increase in the incidences of rod-bivalents for chromosomes 1H+4H, 2H, 5H and 6H without completely impacting fertility, as mentioned earlier.

The differences between the effects oberserved by the genetic screening and cytological analysis at a TSA concentration of 100 ng/ml may be due to the fact that only the anthers (sites of male meiosis) were studied for cytological analysis whereas genetic screening picks up the effects of the treatment on both male and female meiosis. As is the case for *Arabidopsis*, the sites for male meiosis are preferentially studied as they produce more meiocytes in addition to the ease at which meiocytes can be extracted (Armstrong and Jones, 2001). The study of female meiosis in *Arabidopsis* concluded that meiosis takes place place in the embryo sack mother cells (EMCs) in gynoecia that are bigger than the buds (sites of male meiosis), suggesting that meiosis proceeds further along the developmental stage of the EMCs (Armstrong and Jones, 2001) and may well mean that female meiosis is lagging being male meiosis. Female meiosis has not been cytologically studied in barley as of yet hence, there is no knowledge as to wheather female meiosis is lagging or preceding male meiosis. This information may be vital with regard to the timing of TSA administration in that the TSA sensitive period in is not coinciding with the time point of exposure to chemical treatment.

Further, the lack of significant changes in the mean marker recombination frequencies in the genetic screen may be due to the possibility that the chromosomes in the anthers

respond differently to equivalent chromosomes in the gynoecia, such that the decrease in chiasma frequency in a chromosome in the anthers may be offset by an increase in chiasma frequency in the same arm of the equivalent chromosome in the gynoecia. Similarly, a shift in recombination distribution in one direction within a certain region of markers in a chromosome in the anthers, may be offset by an almost equal but opposite shift in the direction of recombination distribution within the same region of markers on the equivalent chromosome in the gynoecia. It has already been demonstrated by the analysis of genetic linkage maps that the recombination frequency in female meiosis is greater than that in males in humans (Donis-Keller *et al*., 1987) and domesticated dog (Neff *et al*., 1999). The same is true for pig families however, the genetic linkage map for chromosome 1 in the female showed that the overall total genetic length of the chromosome was not greater than that for the male due to the centromeric regions exhibiting lower rates of recombination (Mikawa *et al*., 1999). Even though the overall recombination frequency in human females is greater than that for males (Donis-Keller *et al*., 1987), the recombination frequency in the telomeric regions in the male are greater than that for the female (Matise *et al*., 2003). Conversely, in sheep the recombination frequency during male meiosis is greater than that for female meiosis (Crawford *et al*., 1995). This possibility may account for the reason why only subtle/negligible shifts rather than significant shifts in recombination frequency and distribution were observed during the screening of the barley F2 population however, the subtle/negligible changes from one region to the next and so forth on the same chromosome may be plant specific as exhibited by study of male and female recombination during meiosis in *Arabidopsis* (Vizir and Korol, 1990). The investigation showed that some parts of the *Arabidopsis* genome show no sex differences as well as well as a strong difference in the majority of the genome (particularly chromosomes 1 and 4). The changes in the recombination frequencies of

regions neighbouring the gene which encodes a nitrate reductase protein (ch1-2) were studied in response to stimulants such as nitrate ions and repressors such as ammonium ions and it was demonstrated that there was a sex difference where specific chromosomal regions exhibited reduced recombination frequency in one sex but the opposite effect in the other sex. This suggests that male and female meiosis can respond differently to the same chemical stimulus (Vizir and Korol, 1990). Even though linkage maps have shown that there are minor differences in the recombination frequencies between male and female meiosis in a mapping population generated for Oregon Wolfe Barley (Devaux *et al*., 1995), the sex differences governing the direction of the alteration of recombination in response to chemical stimuli (Vizir and Korol, 1990) may be a stronger factor in this investigation. In addition, no studies as of yet have been carried out to decipher whether there are differences in meiotic recombination frequencies in male meiosis between Morex and Barke, as well as the influence of sex differences.

Bearing in mind the influence of sex differences in patterns of recombination, in contrast to the cytological analysis which used Morex, the screening investigation used a marker line which was a cross between two different barley cultivars (Morex x Barke) and hence, a cultivar specific variation may exist with regards to the differing sex specific recombination patterns. Studies with various *Brassica* cultivars revealed that there was no significant difference in the patterns of recombination between male and female meiosis in *Brassica napus* (Kelly *et al*., 1997). *Brassica nigra* exhibited greater rates of recombination in the telomeric regions in male meiosis and greater rates of recombination in centromeric regions in female meiosis (Lagercrantz and Lydiate, 1995). Female meiosis exhibited an overall higher recombination frequency than that for male meiosis in *Brassica oleracea* (Kearsey *et al*., 1996). Sex differences as well as cultivar influenced sex differences must be brought into consideration when carrying

out genetic screens and breeding initiatives when attempting to cross plant relatives (Lagercrantz and Lydiate, 1995).

One way to acertain the effects of TSA treatment on female meiosis in barley would be to cytologically analyse the gynoecia. Secondly, to genetically screen the effects that the treatment would exert on male and female meiosis individually, the anthers can be removed from the F1 treated plant before the release of pollen and subsequently used to pollinate a monomorphic line such as Morex, to screen for the effects of the treatment on male meiosis in the F2 population. Next, other F1 treated plants can be emasculated and pollinated with anthers from a monomorphic line such as Morex, allowing for the effects of the treatment on female meiosis to be determined in the screening of the F2 progeny. Both backcrosses would have been carried out if there was more time in the investigation.

Aside from cultivar influenced sex differences playing a role in differences in meiotic recombination patterns, the differences in such patterns between the various cultivars in male meiosis alone, must be strongly considered. For example, recombination patterns in the buds (sites of male meiosis) of eight *Arabidopsis* accessions were studied and it was found that there were variations in the mean overall chiasma frequencies amongst the cultivars, from 7.9 for Cape Verde Islands (CVI) to 9.36 in Santa Marı´a de Feira (Fei-0) (Sanchez-Moran *et al*., 2002). A similar study on male meiosis in various two-rowed North European barley cultivars demonstrated variations in the recombination frequencies between the cultivars (Sall, 1990). Another study into the barley cultivars Alva, Gull and Weihenstephaner Melthauresistente I showed significant differences in chiasma frequency between the cultivars however, no significant differences in the distribution of chiasma (Nilsson and Pelger, 1991).

Another possibility explaining the subtle effects observed in the genetic screening assay may be due to the fact that meiocytes which did experience a significant alteration in

recombination patterns in response to the treatment by TSA, did not progress to the seed stage. For example, even though the chromosomes may have segregated correctly at anaphase I and II (as suggested by the presence of an obligate chiasma at a concentration of 100 ng/ml TSA), the highly toxic nature of TSA may have led to the abortion of mitotic pollen development. This would have led to subsequent failure of self-fertilisation and therefore, failure of seed development. Also, as TSA has been shown to inhibit the mitotic deveopment of the ear leading to perturbed ear length (**Figure 4.28** And **Figure 4.30**), this may reduce the total number of seeds that the ear can contain because shorter ears are able to harbour fewer seeds compared to longer ears. Therefore, fewer seeds were available to extract and grow out the F2 population for screening, which may harbour chromosomes that underwent a significant alteration in recombination patterns. Lastly, the timing of TSA administration could be of importance as some meiocytes may have progressed passed the TSA sensitive stage at the time of administration.

4.3.1 A possible mechanism explaining the action of TSA

Previously, an *in-vitro* analysis of a hyperacetylated form of histone H4 at lysine residues was chemically induced and incorporated into nucleosomes. It was found that the global chromatin structure was greatly affected due to the inhibition of the formation of the highly ordered chromatin fiber (Shogren-Knaak *et al*., 2006), yielding a less condensed chromatin structure.

Previous to this, it was observed that over 80% of histone H4 exists in an acetylated form, specifically at lysine 16 in budding yeast, which corresponded to chromatin existing in a decondensed state (Lizuka and Smith, 2003). *In-vitro* studies were also carried out on the chromatin structure of HeLa cells and it was found that the treatment of the cell lines with TSA, induced the decondensation of dense regions of chromatin

(Toth *et al*., 2004). Microscopy studies showed that TSA treatment increased chromatin length from 200 nm, to over 1 µm which is in agreement with a more open of chromatin structure. Furthermore, flow cytometry analysis revealed that treatment with TSA also caused cell cycle arrest at S phase, which led to the subsequent induction of apoptosis. Even though a more open chromatin structure was cytologically observed in treated barley nuclei at pachytene, it wasn't statistically verified. This is consistent with the observed decondensation of *Arabidopsis* chromatin in lines which haboured a defective histone deacetylase (Probst *et al*., 2004).

Based on the above information, the surprising finding that histone hyperacetylation had no effect on the meiotic time course (see **Section *4.2.6***) suggests that there was no effect on the duration of S-phase and subsequent stages. In addition, the normal behaviour of ZYP1 (**Figure 4.24(e)**) demonstrating complete synapsis of chromatin at pachytene is supportive of the data presented by the time course investigation. This is consistent with data presented by Perrella *et al*., (2010) which suggested that histone hyperacetylation in *Arabidopsis* has no effect on ZYP1 behaviour and no effect on the progression of meiosis from G2 to the end of prophase I. The phenotypic effects of histone hyperacetylation in both *Arabidopsis* (Perrella *et al*., 2010) and barley become apparent at metaphase I.

In contrast, the effect of hyperacetylation on the polymerization of ASY1 in barley became apparent by mid-zygotene such that some regions on the same nuclei had discrete foci which would be indicative of G2, other regions had short stretches indicative of leptotene and the central region of chromatin was more representative of zygotene (**Figure 4.26(b)**). This suggests that treatment has led to failure of chromosome axis formation as demonstrated by the perturbed localisation of ASY1 on the chromatin axis, as it was still localized on the chromatin loops. The same pattern of ASY1 loading and polymerisation was observed in MCC1 overexpression *Arabidopsis*

lines (Perrella *et al*., 2010). This may be related to the effect of elevated temperature on chiasma distribution in barley, as it was found that at ambient temperatures, most chiasmata are confined to distal regions of chromatin during meiosis due to the fact that DNA replication is completed in heterochromatic regions before euchromatic regions hence, allowing for subsequent recombination events to initiate in the former regions before entry into meiosis (Higgins *et al*., 2012). However, it was found that when barley was grown at moderately higher temperatures, replication was more synchrononous in both regions, leading to a significant increase in the formation interstitial chiasma. It was proposed that a higher temperature promotes a more open chromatin structure in centromeric regions, allowing for the access of replication factors to the former regions as well as telomeric regions, allowing DNA replication in both regions to be more synchronized (Higgins *et al*., 2012). This may permit the observed loading of ASY1 at G2 to be less polarized hence, allowing downstream meiotic events in centromeric regions to be more synchronous with that for telomeric regions (Higgins *et al*., 2012). Therefore, the disruption of the synchronicity of ASY1 polymerisation as observed in barley (**Figure 4.26(b)**), may be leading to failure of downstream DMC1 mediated meiotic events, especially within regions of chromatin exhibiting failure of ASY1 polymerisation. The study of an *Arabidopsis asy1* mutant showed that DMC1 localises normally along the chromatin axes. However, it immediately delocalises in contrast to the control in which it persists for roughly 12h. Analysis of metaphase I spreads revealed a significant reduction in chiasma frequency in the *asy1* mutant (Sanchez-Moran *et al*., 2007).

Indeed, observations have suggested that the loss of histone deacetylase activity in yeast leads to increased DSB formation in the corresponding regions of chromatin (Mieczkowski *et al*., 2007) and increased recombination frequencies within recombinagenic hot-spots (Merker *et al*., 2008). Conversely, hypoacetylation of rDNA

encoding regions of the yeast genome are correlated with poor recombination (Millar and Grunstein, 2006). The confirmation of a similar effect was demonstrated in *Arabidopsis* in that there was an alteration in the distribution of meiotic COs (Perrella *et al*., 2010). Further, hyperacetylation in *Arabidopsis* enhances histone H3 trimethylation (Probst *et al*., 2004) in contrast to yeast which demonstrates that the two processes are antagonistic (Venkatasubrahmanyam *et al*., 2007). TSA induced hyperacetylation in *Neurospora crassa* also leads to a negative regulation of DNA methylation (Selker, 1998). The above mentioned information suggests that the acetyaltion/methylation status of different histones varies amongst species with regard to the epigenetic control of transcription and meiosis. For example, in barley H3K9me3, H3K27me3, H3K4me3 and H4K16ac are markers of meiotic prophase I (Higgins *et al*., 2012) and mark euchromatic (higly transcribed) regions in *Arabidopsis* (Naumann *et al*., 2005). The heterochromatic regions in *Arabidopsis* are marked by H3K9me2, H3K27me2, and H4K20me1. Conversely in barley, the same marks are present throughout the genome however, with less abundance in the distal regions which is in agreement with the higly repetitive nature of the interstitial heterochromatic regions (Kunzel *et al*., 2000). Additionally, the analysis of mitotic cells in maize lines in which the gene encoding the histone deacetylase gene Rpd3-type hda 101 was down-regulated, demonstrated an increase in H3K4me2 but a decrease in H3K9me2 (Rossi et al., 2007). As little is understood about how histone modifications may affect meiosis and TAR, including the fact that using chemical means to induce histone hyperacetylation in barley suggests that both histones H3 and H4 may be hyperacetylated, a broad perspective must be taken into consideration when discussing the possible mechanisms that are altering the recombination patterns in this study. For example, histone hyperacetylation may be decondensing the NOR regions (Preuss and Pikaard, 2007) but instead inhibiting histone trimethylation (Sarg *et al*., 2004) and

therefore, leading to inhibition of downstream transcription associated recombination (TAR) in the NOR regions (Cesarini *et al*., 2012) which may be the reason why NOR bearing chromosomes are more sensitive to the treatment. Another possibility could be that histone hyperacetylation may be leading to the inhibition (Sarg *et al*., 2004) of H3K9, H3K27 and H3K4 trimethylation (Higgins *et al*., 2012) such that downstream meiotic events are inhibited.

Thirdly, *Arabidopsis* chromosomes have been shown to exhibit interference sensitive and insensitive CO formation however, in NOR bearing chromosomes interference insensitive CO occurred less commonly than non-NOR bearing chromosomes (Lam *et al*., 2005). This may explain the lack of CO assurance on the short arm of *Arabidopsis* chromosomes 2 such that histone hyperacetylation induced chromatin decondensation may be exacerbating the issue of poor CO assurance with the NOR bearing chromosome 5H in barley. Despite the observance of poor CO assurance in chromosome arms bearing NORs, very little is known as to why this is the case and further analysis to ascertain this relationship needs to be conducted (Lam *et al*., 2005).

Fourthly and most likely, the highly repetative nature of the barley genome could mean that the histone hyperacetylation induced decondensation of chromatin may be increasing the distance between adjacent ASY1 subunits along the chromatin axes, preventing ASY1 from polymerising and mediating the function of downstrean strand invasion by DMC1 (Sanchez-Moran *et al*., 2007). In conclusion, the epigenetic alteration of the global structure of the chromatin axes may be leading to perturbed ASY1 localisation.

4.3.2 Explaining the effect of TSA on fertility and growth

The reduced fertility could be explained due to the fact that TSA causes chromosome mis-segregation leading of abortion of gametes as previously demonstrated by the treatment of *Arabidopsis* (Perrella *et al*., 2010). However, we were unable to extract meiocytes at anaphase I or II in this investigation. The hindrance of spike development and subsequent reduced length of the mature ears (**Figure 4.28**), could be the effect of hyperacetylation on mitotic chromatin, leading to subsequent inhibition of downstream mitotic events involved in plant growth and development. Previous studies showed that apoptosis was caused by TSA and sodium butyrate (another histone de-acetylase inhibitor) induced histone hyperacetylation in rat thymocytes (Lee *et al*., 1996). Furthermore, prolonged incubation of HeLa cells with 50 and 100 ng/ml TSA also induced cell cycle arrest and subsequent apoptosis due to the saturation of a single HDAC (Toth *et al*., 2004). This is in agreement with the pulse treatment of barley stems with 100 ng/ml TSA, as the subsequent removal of TSA with SDW after exposing meiocytes for a total 20 hours (see **Section *4.2.7***), allows for an observed effect on recombination during meiosis, but its removal prevents excessive further cell cycle arrest in mitotic tissue, which would lead to subsequent apoptosis and death of vegetative tissue (Toth *et al*., 2004).

Despite the fact that meiocytes treated with 1,000ng/ml TSA progressed to metaphase I, the high degree of univalent formation suggests that highly unbalanced chromosome segregation may have led to the failure of tetrad formation, which might explain why it was not possible to find meiocytes at tetrad stage. The surprising finding that 100 ng/ml significantly impacted fertility (**Figure 4.29**) despite the fact that the treatment only induced rod-bivalent formation (see **Section *4.2.2***) hence, insuring correct segregation of the chromosomes at prophase I by way of the obligate CO (Jones 1984; Jones and Franklin 2006), may be due to the effect of the treatment on mitotic development. As

previously mentioned, treated meiocytes may have progressed to tetrad stage however, impeded mitotic development of the floral tissue may have led to aborted seed development and subsequent apoptosis (Lee *et al*., 1996). The possible impeded mitotic development of the ears resulting in shorter ear lengths in comparison to the control may have been a limiting factor governing the total number of seeds that the ear can contain, further reducing the yield in seed number.

CHAPTER 5

ANALYSIS OF THE MEIOTIC PATHWAY IN THE BARLEY DESYNAPTIC MUTANT *des8*

5.1 Introduction

The phenomenon of desynapsis in which homologous chromosomes synapse normally during early prophase I during meiosis right up to pachytene and then become unpaired at diplotene (Li *et al*., 1945; Bione *et al*., 2002), resulting in a loss of chiasmata at diakinesis, has been widely reported in the study of a wide variety of plants (Katayama, 1964) such as soybean (Bione *et al*., 2002), maize (Murphy and Bass, 2012) and barley (Franckowiak *et al*., 1985; Druka *et al*., 2011). For example, a cytological screen of 55 accessions of the forage grass *Brachiaria humidicola* of Brazil showed that one is desynaptic (Calisto *et al*., 2008) as demonstrated by desynapsis after diakinesis and chromosome mis-segregation in the gametes. A maize *desynaptic* (*dy*) mutant was also cytologically characterised where complete synapsis was observed at pachytene but exhibited univalents at late prophase I (Maguire *et al*.,1991; Maguire *et al*., 1993). In wild-type maize, the telomeres become attached to the inner surface of the N.E at the unset of early prophase I to form at bouquet by zygotene and remained attached through pachytene but become unattached when the chromatin begins to condense at the onset of diplotene. However, in the mutant the telomeres separated from the N.E at the inset of pachytene (Bass *et al*., 2003). A later investigation using a homozygous mutant to verify this effect revealed that between 60/-70% of telomeres are clustered into a bouquet compared to just over 90% in wild-type, in addition there was a persistence of polymerised ASY1 at pachytene in the mutant whereas in the wild-type, the signal become weaker and increasingly intermittent (Murphy and Bass, 2012). It was postulated that the trans-nuclear membrane proteins SUN or KASH could be the candidate genes and using forward genetics, the *dy* mutant was initially mapped to a 9 cM region on the long arm of chromosome 3 and fine mapping showed that this region harbours the ZmSUN3 gene. A screening of the splice variants revealed one of the mRNAs encodes a truncated form of ZmSUN3p (Murphy and Bass, 2012).

There are 14 non-allelic barley desynaptic (*des*) near isogenic lines (NILs) that have been generated via an initiative in the 1980s to backcross and introgress known morphological mutant (Ramage and Hernandez-Soriano, 1971 and 1972) loci into a common Bowman background (Franckowiak *et al*., 1985). This library of mutants provides a framework for investigating key alleles involved in the meiotic pathway using forward genetics, where genetic screens are carried out in an attempt to identify the allele responsible for the phenotype (Druka *et al*., 2011). This chapter will use the same approach (including cytology) in an attempt to map and subsequently identify the mutant gene responsible for the desynaptic phenotype that was initially observed in *des8* (Hernandez-Soriano, 1973).

5.2 Results

5.2.1 Preliminary staging of anthers

Bowman and BW248 (*des8.l* x Bowman Bc_4F_3) (denoted subsequently as *des8*) ears were harvested and preliminary staging analysis revealed that Bowman ears had over 15 seeds and *des8* ears had no more than 5 seeds per ear, suggesting greatly reduced fertility in the mutant (**Figure 5.1**).

A study of the progression of meiosis along the length of the spikes for both Bowman and *des8* was conducted (both spikes were 1.8cm in length). The most abundant meiotic stage in an anther from each corresponding spikelet along the length of both spikes was determined. Bowman demonstrated a sequential progression of meiosis from interphase to anaphase I in anthers ranging from 0.4 to 1.1mm however, *des8* showed a delay in meiosis as anthers between the length of 0.8 and 1.0mm, remained at pachytene demonstrating a possible delay at this stage, followed by a subsequent commencement of the remaining stages of meiosis thereafter, in a longer spike. In addition, when metaphase I stage was analysed to score the mean chiasma frequency, it was noticed

that this stage was present in Bowman at an anther length of 1.0mm, whereas in *des8* the anther length required to isolate this stage was 1.2mm. Nearly all meiotic stages (interphase to anaphase I) were present along the length of the Bowman spike however, the latest stage of meiotic pathway that could be isolated from the *des8* spike, was pachytene. *des8* spikes at a length of 2.0cm, were required to isolate anthers at metaphase I stage. This suggests that the there may be a delay in the progression of the meiotic pathway in the mutant relative to the wild-type.

Figure 5.1: The comparison of fertility between Bowman (left) and *des8* (right) ears. Bowman had over fifteen seeds per ear and *des8* had no more than five seeds per ear. Bar = 1 cm

5.2.2 Analysis of recombination

In order to further study the reduced chiasma frequency in the meiotic atlas, FISH analysis was carried out on metaphase I spreads, utilising probes complimentary to the DNA sequences encoding ribosomal RNA (45S-DIG and 5S-BIO) in barley. The 45S probe was detected using anti-DIG-FITC (green) and the 5S probe was detected by Cy3 (red) (see **Materials and Methods**: **Section 2.11**). Analysis of the mean chiasma frequency for the individual chromosomes was undertaken and statistical analysis using ANOVA, showed a significantly lower chiasma frequency in comparison to the Bowman control (**Table 5.1**). The mean overall chiasma frequency per nuclei for Bowman was 14.84 +/-1.75 SD and that for *des8* was 7.66 +/-2.04 SD. Chromosome 6H exhibited the greatest number of univalents (64) (an NOR bearing chromosome). Despite the fact that chromosome 5H also harbours an NOR, it exhibited fewer univalents (24) than chromosome 1H+4H (6+54), however it did exhibit the most number of rod-bivalents (35) with 26 representing classic rod-bivalent conformations and 9 representing "bulge" rod-bivalents (**Table 5.2**). The "bulge" rod-bivalent conformation occurs as a result of the absence of the single chiasma on the short arm leaving two distal chiasmata on the long arm, that are seen as a bulge on the distal end of the long arm (**Figure 5.2(c)**). The classic rod-bivalent conformation occurs due to the absence of the chiasma from the short arm and the innermost chiasma on the distal arm of the long arm, leaving a single chiasma per bivalent (on the distal end of the long arm) (explained earlier in **Chapter 4**: **Section 4.2.1**). Even though chromosome 5H has naturally occurring bulged rod-bivalents in the wild-type (41), the mutant had a significantly greater number of classical rod-bivalents (26) compared to the wild-type (3) (ANOVA p= 4.13E-12). The same was true for chromosome 6H which exhibited 18 rod-bivalents in contrast to the wild-type which exhibited 2 (ANOVA p= 5.96E-34) (**Tables 5.1** and **5.2**). Univalents were also

observed for chromosomes 1H/4H (6), 3H (10) and 7H (16) (**Table 5.2**). Chromosome 2H showed no evidence of univalent formation and seemed to be the least affected chromosome with fewer rod-bivalents (27) than chromosomes 1H/4H (31) and 7H (29). Even though it exhibited a greater number of rod-bivalents than chromosomes 3H (21), 4H/1H (6) and 6H (18), these chromosomes exhibited univalents unlike chromosome 2H (**Table 5.2**). Also, some of the desynapsed chromosomes (mainly the univalents) were overlapping each other and the other bivalents, complicating the scoring of the chiasmata frequency as well as the identification of the chromosomes (**Figure 5.4(d)**: the 1H/4H univalent is overlapping the 6H bivalent and could only be discerned when the DAPI exposure was inverted to grey/white).

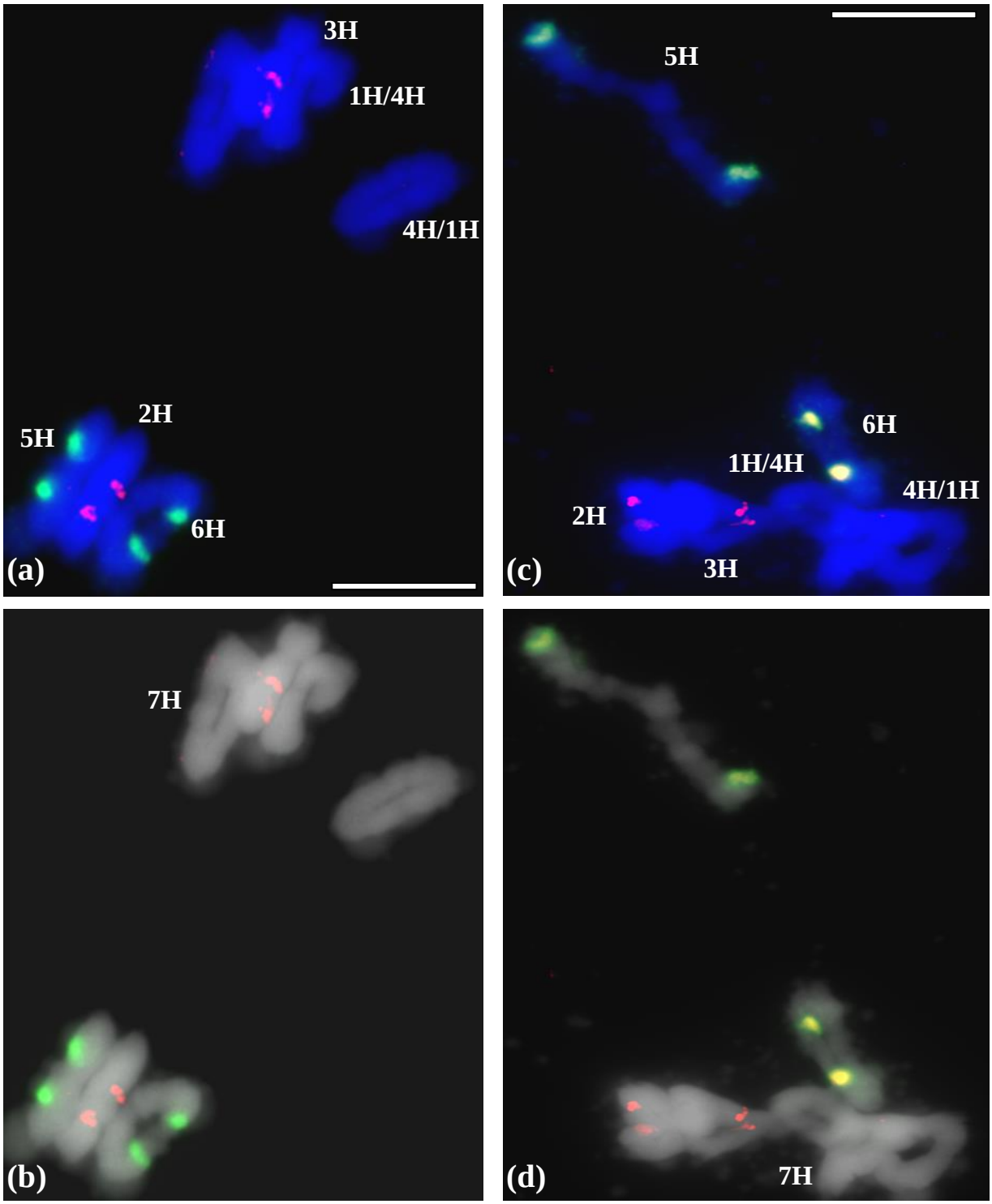


Figure 5.2: FISH detection of rDNA in two DAPI counterstained (blue) metaphase I spreads in Bowman ((a) and (c)). 45S on chromosomes 5H and 6H was tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC (green). 5S was tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3 (red) on chromosomes 2H and 3H, with grey DAPI exposure to discern 5S on chromosome 7H ((b) and (d)). Metaphase spread (a) has 7 closed bivalents and (c) has 6 closed bivalents and one bulged rod-bivalent (5H). Bar = 10 µm

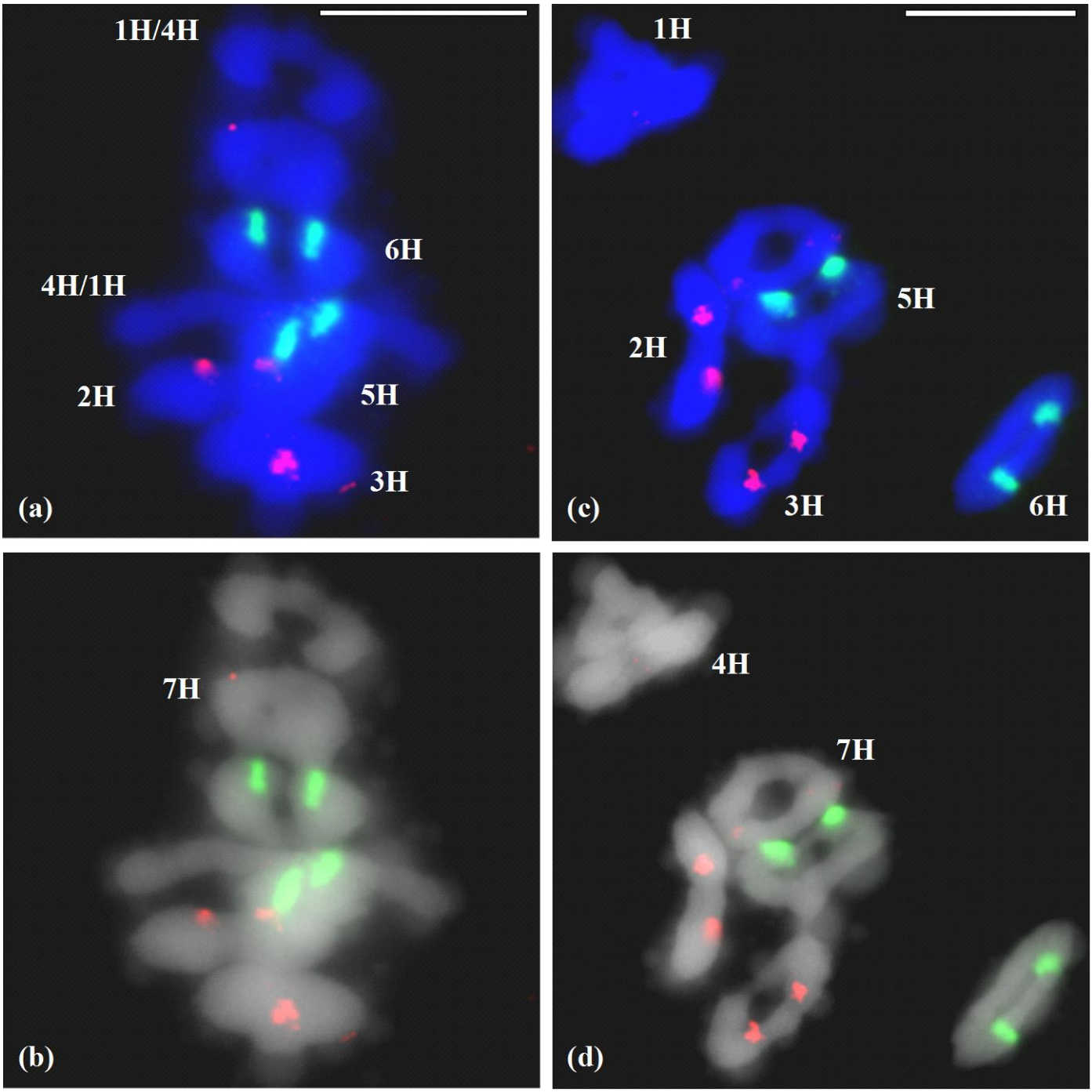


Figure 5.3: FISH detection of rDNA in two DAPI counterstained (blue) metaphase I spreads in Bowman ((a) and (c)). 45S on chromosomes 5H and 6H was tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC (green). 5S was tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3 (red) on chromosomes 2H and 3H, with grey DAPI exposure to discern 5S on chromosomes 4H (d) and 7H ((b) and (d)). Metaphase spread (a) has 5 ring bivalents, one rod-bivalent (4H/1H) and one key-shaped bivalent (3H). Metaphase spread (c) has 5 ring bivalents, one bulged rod-bivalent (5H) and one key-shaped bivalent (1H). Bar = 10 µm

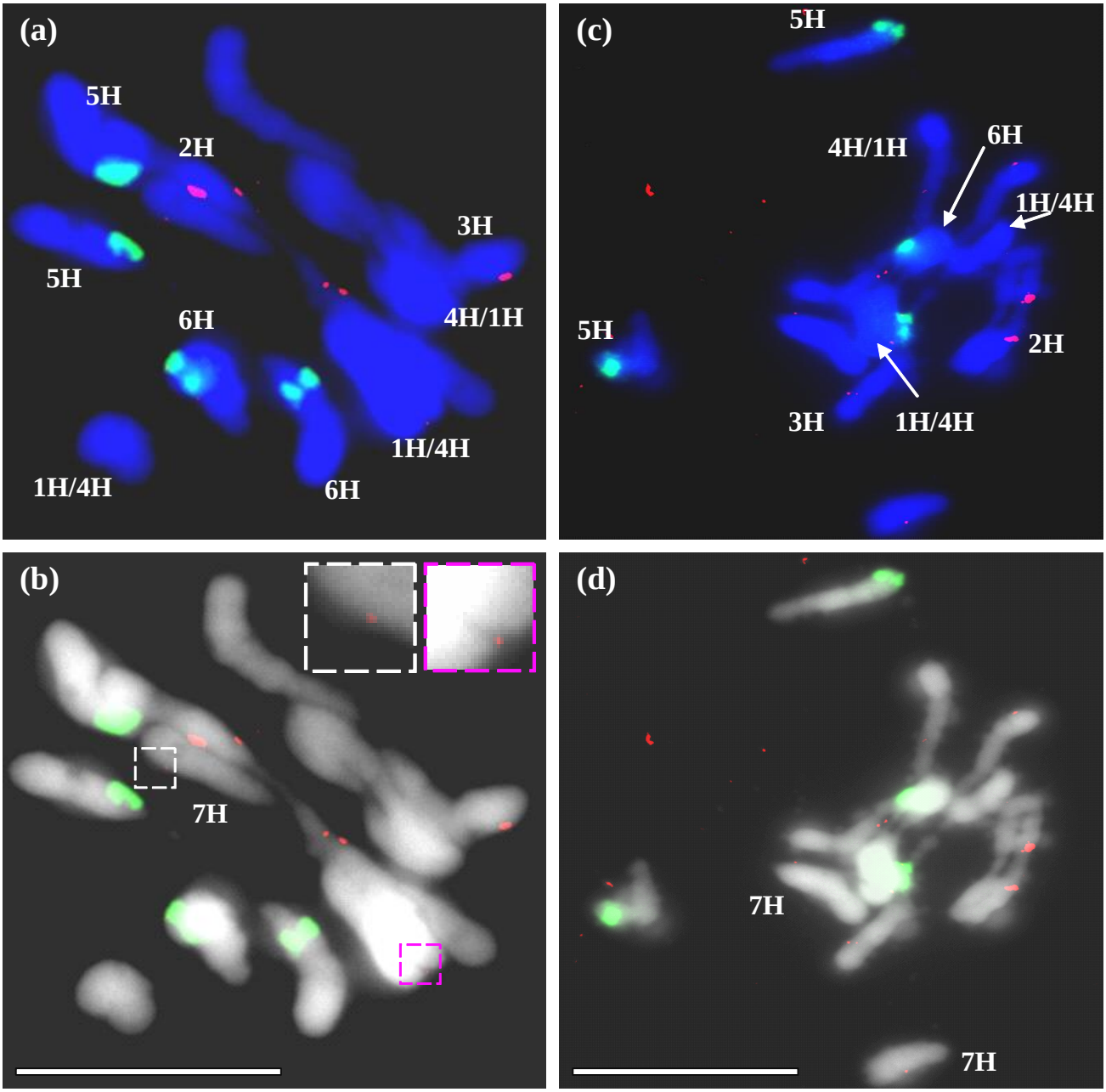


Figure 5.4: FISH detection of rDNA in two DAPI counterstained (blue) metaphase I spreads in *des8* ((a) and (c)). 45S on chromosomes 5H and 6H was tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC (green). 5S was tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3 (red) on chromosomes 2H and 3H, with grey DAPI exposure to discern 5S on chromosome 7H ((b) and (d); also enhanced by the insets (b)). Metaphase spread (a) has one ring bivalent (4H/1H), two rod-bivalents (2H and 3H) and three univalents (1H/4H, 5H and 6H). Metaphase spread (c) has two ring bivalents (2H and 6H), two rod-bivalents (3H and 7H) and three univalents (1H/4H, 4H/1H and 5H). Bar = 10 µm

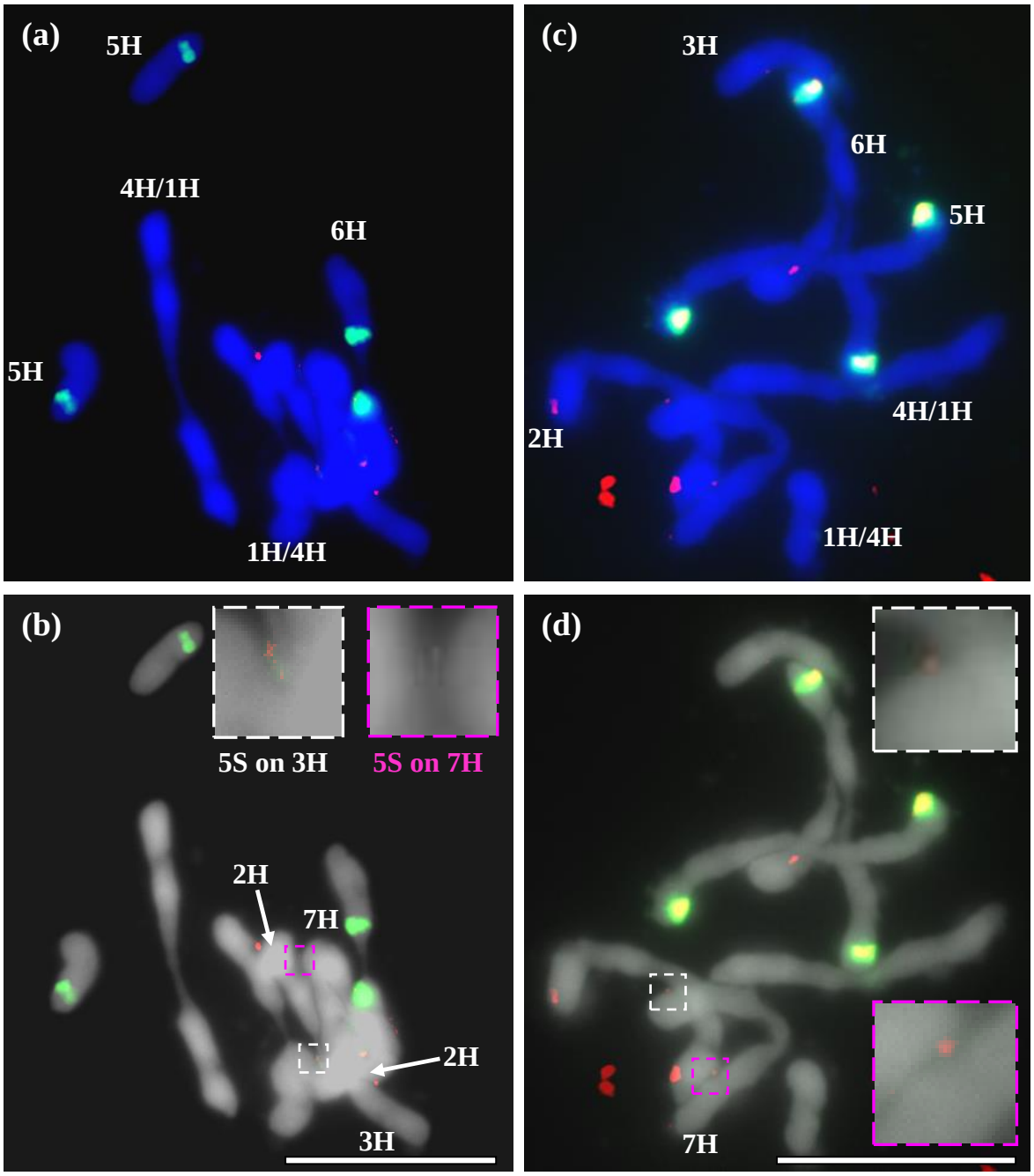


Figure 5.5: FISH detection of rDNA in two DAPI counterstained (blue) metaphase I spreads in *des8* ((a) and (c)). 45S on chromosomes 5H and 6H was tagged with the 45S rDNA-DIG probe and detected with anti-DIG-FITC (green). 5S was tagged with the 5S rDNA-BIO probe and detected with streptavidine-CY3 (red) on chromosomes 2H and 3H (enhanced by the inset as 5S on 3H is partially hidden behind chromosomes 2H and 7H (b)), with grey DAPI exposure to discern 5S on chromosome 7H ((b) and (d); also enhanced by the insets ((b) and (d))). Metaphase spread (a) has three ring bivalents (1H, 3H and 7H), three rod-bivalents (2H, 4H and 6H) and one univalent (5H). Metaphase spread (c) has six rod-bivalents (2H, 3H, 4H/1H, 5H, 6H and 7H) and one univalent (1H/4H). Bar = 10 µm

Table 5.1: The mean CO frequency in the *des8* mutant and wild-type Bowman. The mutant had a significantly lower mean CO frequency than the wild-type for all seven chromosomes (n=100 for 1H+4H; n=50 for the remaining chromosomes).

Chromosome	Mean CO frequency in *des8*.	Mean CO frequency in Bowman.	ANOVA (p < 0.05 = Sig. diff. in CO freq).
1H+4H	1.07 +/- 0.87 SD	2.11 +/- 0.55 SD	1.05E-19
2H	1.5 +/- 0.54 SD	2.08 +/- 0.34	5.59E-09
3H	1.46 +/- 0.86 SD	2.52 +/- 0.54	5.89E-11
5H	1.06 +/- 0.82 SD	2.12 +/- 0.48 SD	4.13E-12
6H	0.36 +/- 0.48 SD	1.92 +/- 0.34 SD	5.96E-34
7H	1.14 +/- 0.73 SD	2.08 +/- 0.34 SD	6.92E-13

Table 5.2: The abundance of the types of the bivalents found in Bowman and *des8* (n=50).

	Bowman							***des8***					
Chromosome	**Ring**	**Key**	**Buckle**	**Rod**	**Bulge rod**	**Univalent**		**Ring**	**Key**	**Buckle**	**Rod**	**Bulge rod**	**Univalent**
1H/4H	34	1	6	7	0	2		16	0	0	31	0	6
2H	44	0	5	1	0	0		23	0	1	27	0	0
3H	22	27	0	1	0	0		17	7	0	21	0	10
4H/1H	37	11	1	1	0	0		12	4	0	6	1	54
5H	0	0	9	3	38	0		0	0	3	26	9	24
6H	47	0	0	2	0	2		0	0	0	18	0	64
7H	44	2	3	1	0	0		11	0	2	29	0	16

5.2.3 Analysis of the behaviour of ASY1 and ZYP1

The analysis of pollen mother cells in the Bowman control and *des8* showed that ASY1 in both samples, appeared as distinct foci at meiotic G2 along the chromatin structure (**Figure 5.6**). The ASY1 signal became progressively linear from leptotene (**Figure 5.7**) onwards in a polarised manner through early zygotene (**Figure 5.8**) until at mid-zygotene, the signal spanned the full length of the chromatin axis, which was observed in *des8* (**Figure 5.11**). Early zygotene was also accompanied by the appearance of short stretches of ZYP1 in the control wild-type and mutant (**Figure 5.8**). At the onset of pachytene the mutant was indistinguishable from the wild-type at which it exhibited slightly depleted ASY1 along the chromatin axes and complete linearisation of ZYP1 (**Figure 5.9**). The ZYP1 signals and ASY1 signals became progressively intermittent at the onset of diplotene (**Figure 5.10**), indicating no difference in the behaviour of both proteins in the mutant and wild-type in the meiotic pathway.

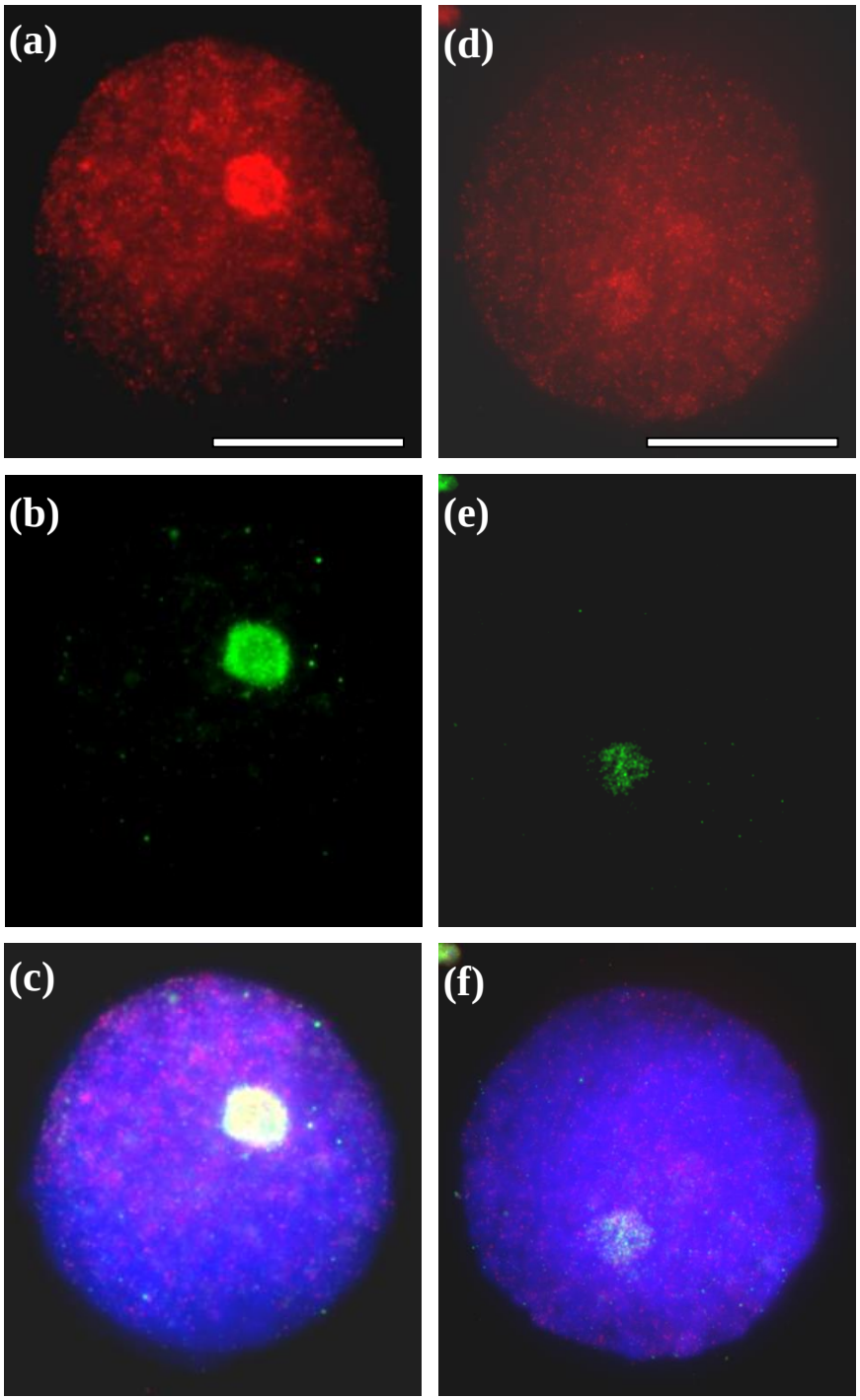


Figure 5.6: The loading of ASY1 at G2 stage in Bowman ((a), (b), and (c)) and *des8* ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

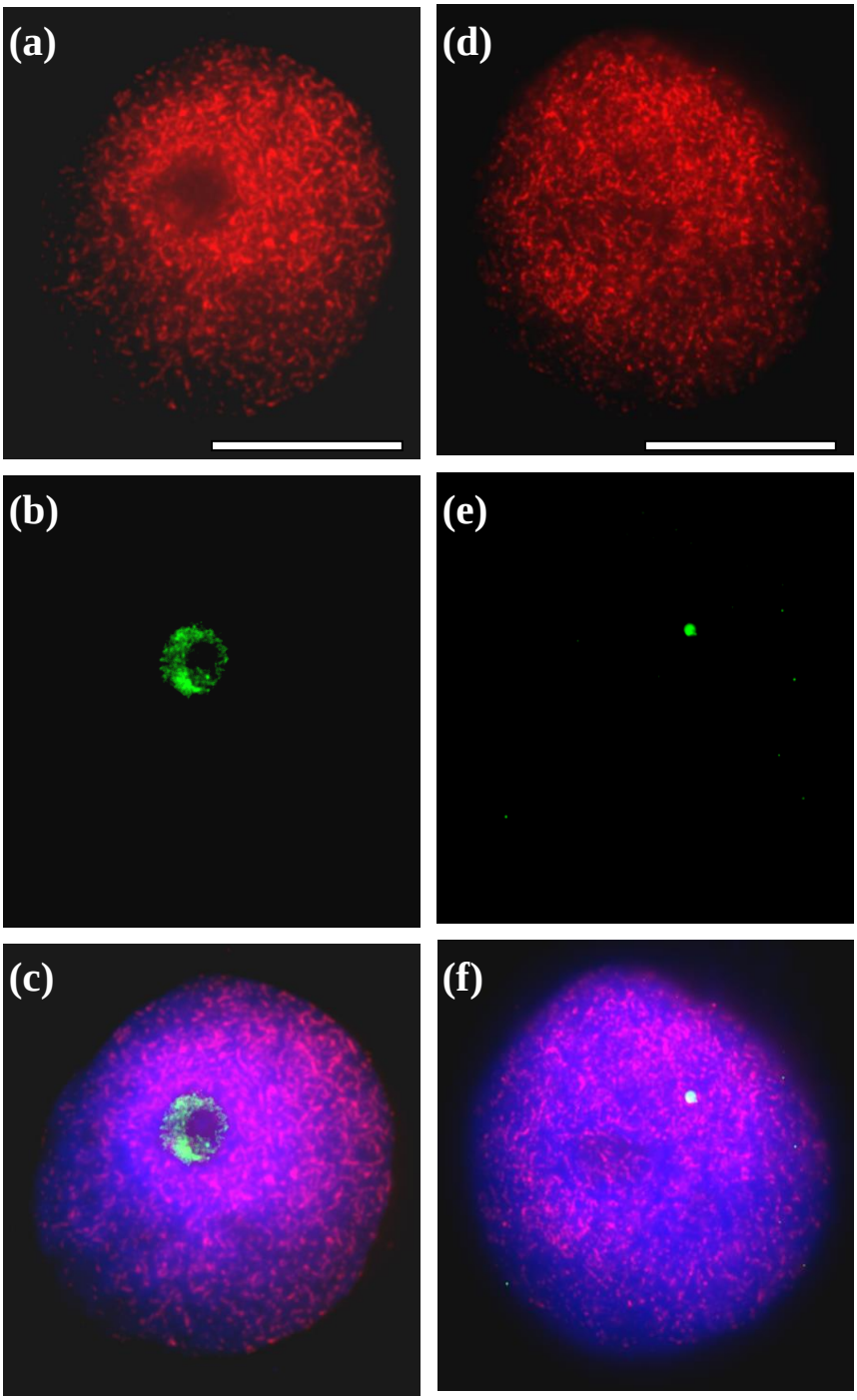


Figure 5.7: The initiation of ASY1 linearisation at leptotene stage in Bowman ((a), (b), and (c)) and *des8* ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

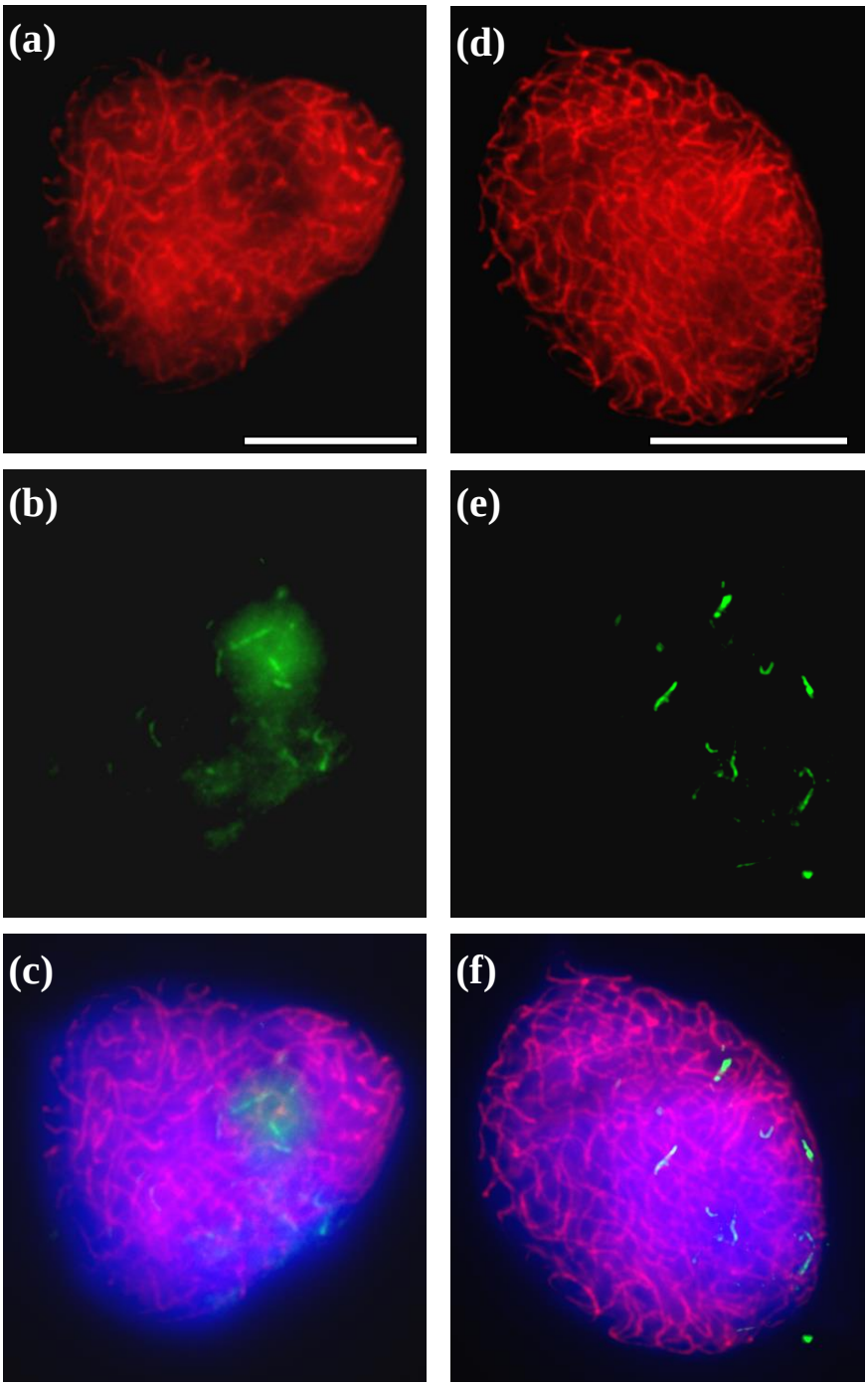


Figure 5.8: Further linearisation of ASY1 at early zygotene stage with short stretches of ZYP1 in Bowman ((a), (b), and (c)) and *des8* ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

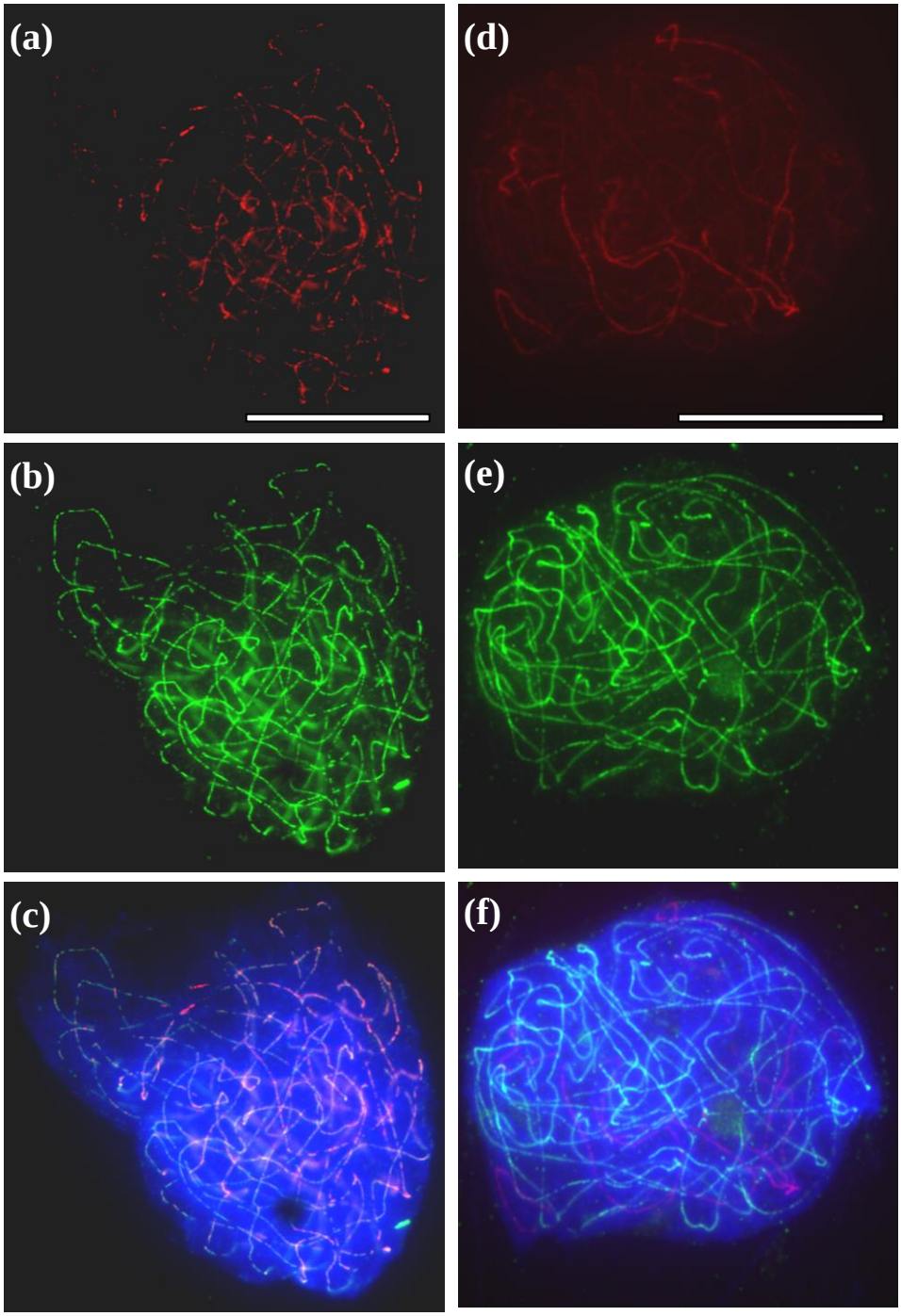


Figure 5.9: The complete linearisation of ZYP1 at pachytene stage, indicating complete synapsis in both Bowman ((a), (b), and (c)) and *des8* ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

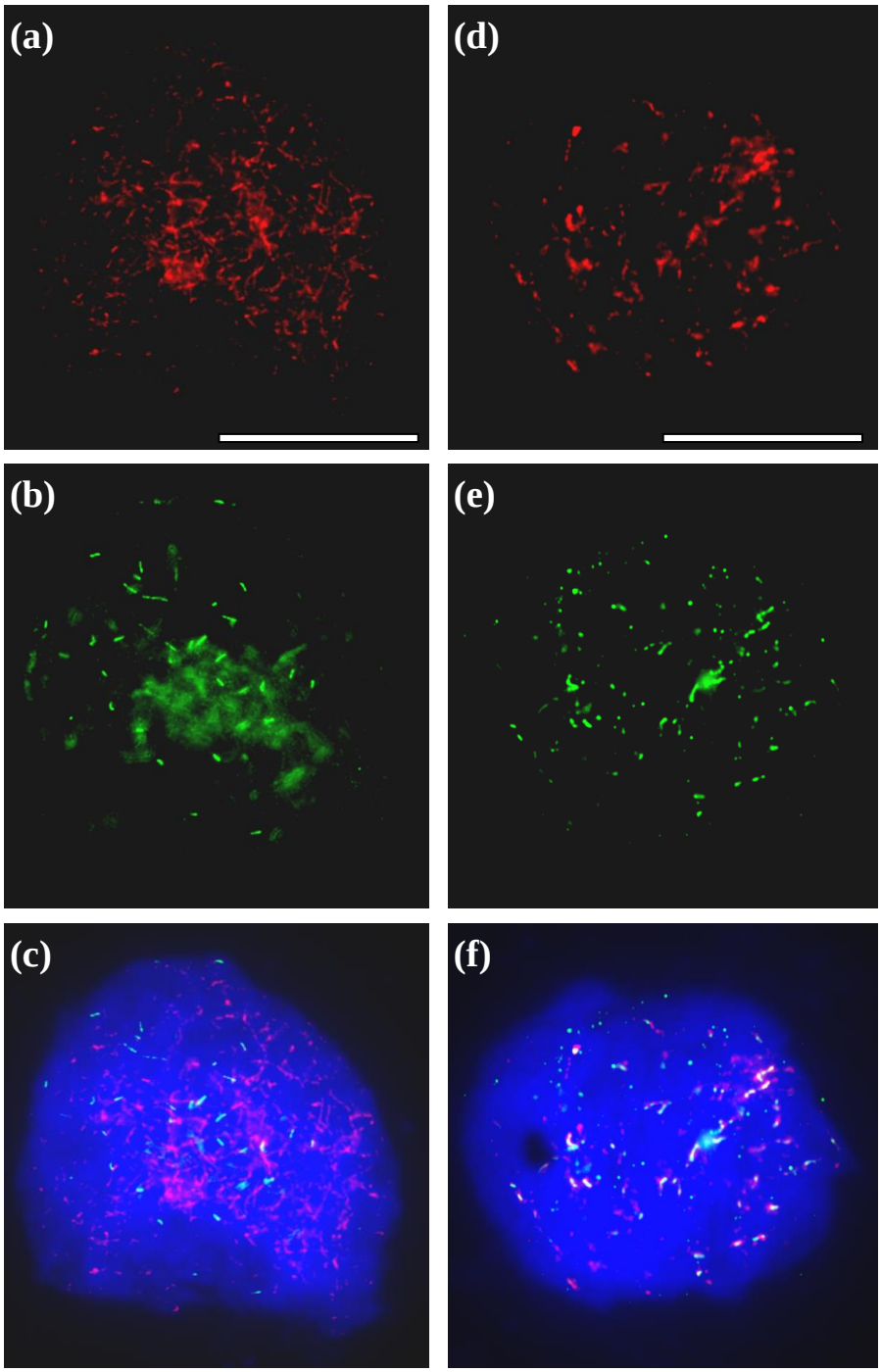


Figure 5.10: The depletion of ASY1 and ZYP1 at diplotene stage in Bowman ((a), (b), and (c)) and *des8* ((d), (e) and (f)). Immunolocalisation was used to detect ASY1 (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: red (Cy3)) and ZYP1 (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC: green) with merged ((c) and (f)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

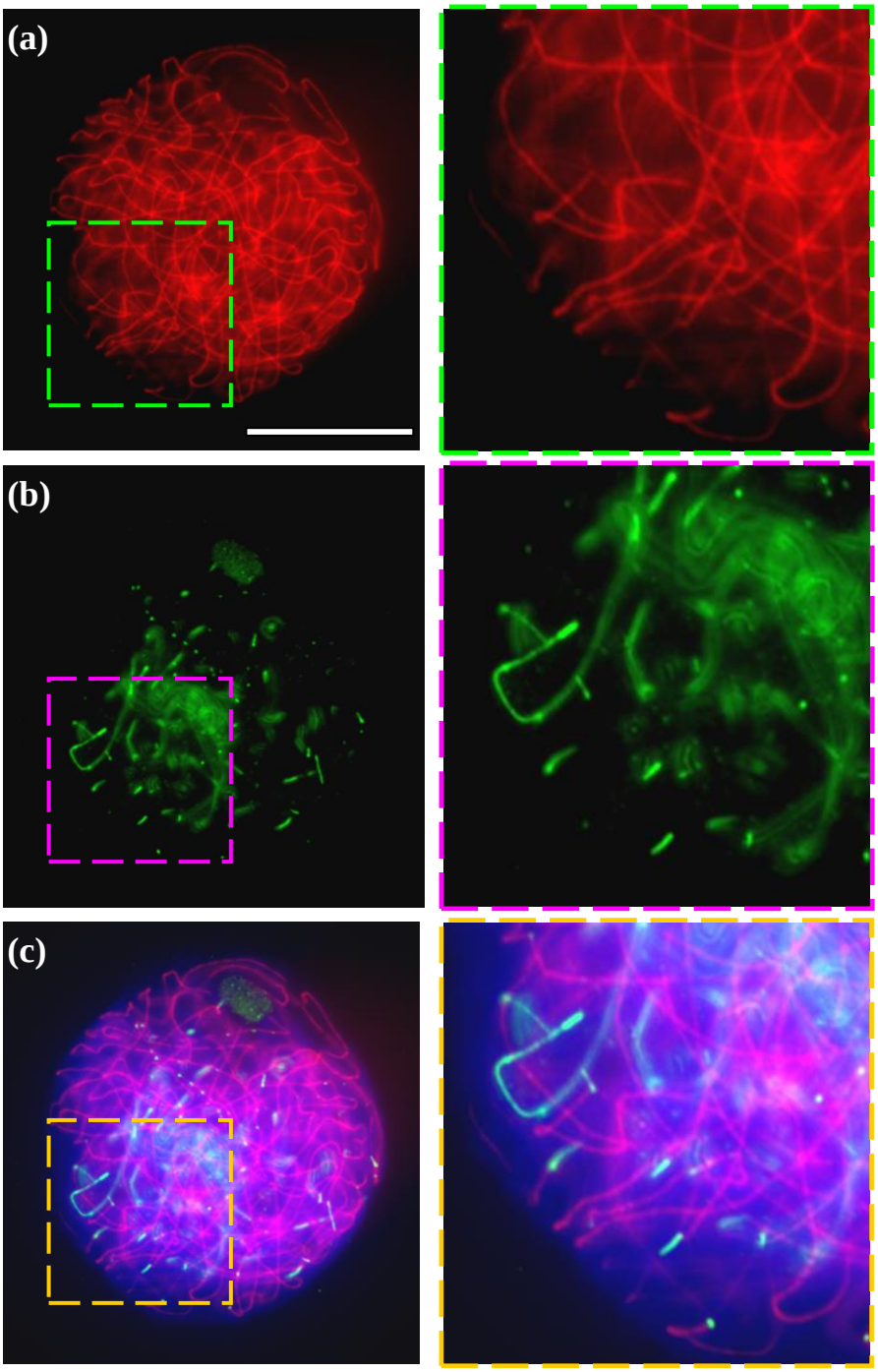


Figure 5.11: Zygotene stage in *des8*, showing the complete linearisation of ASY1 (shown in red (a)) (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: (Cy3)), with short stretches of ZYP1 (green (b)) and merged (c) (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC), indicating normal behaviour of ASY1 and no delay in the onset of synapsis. Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

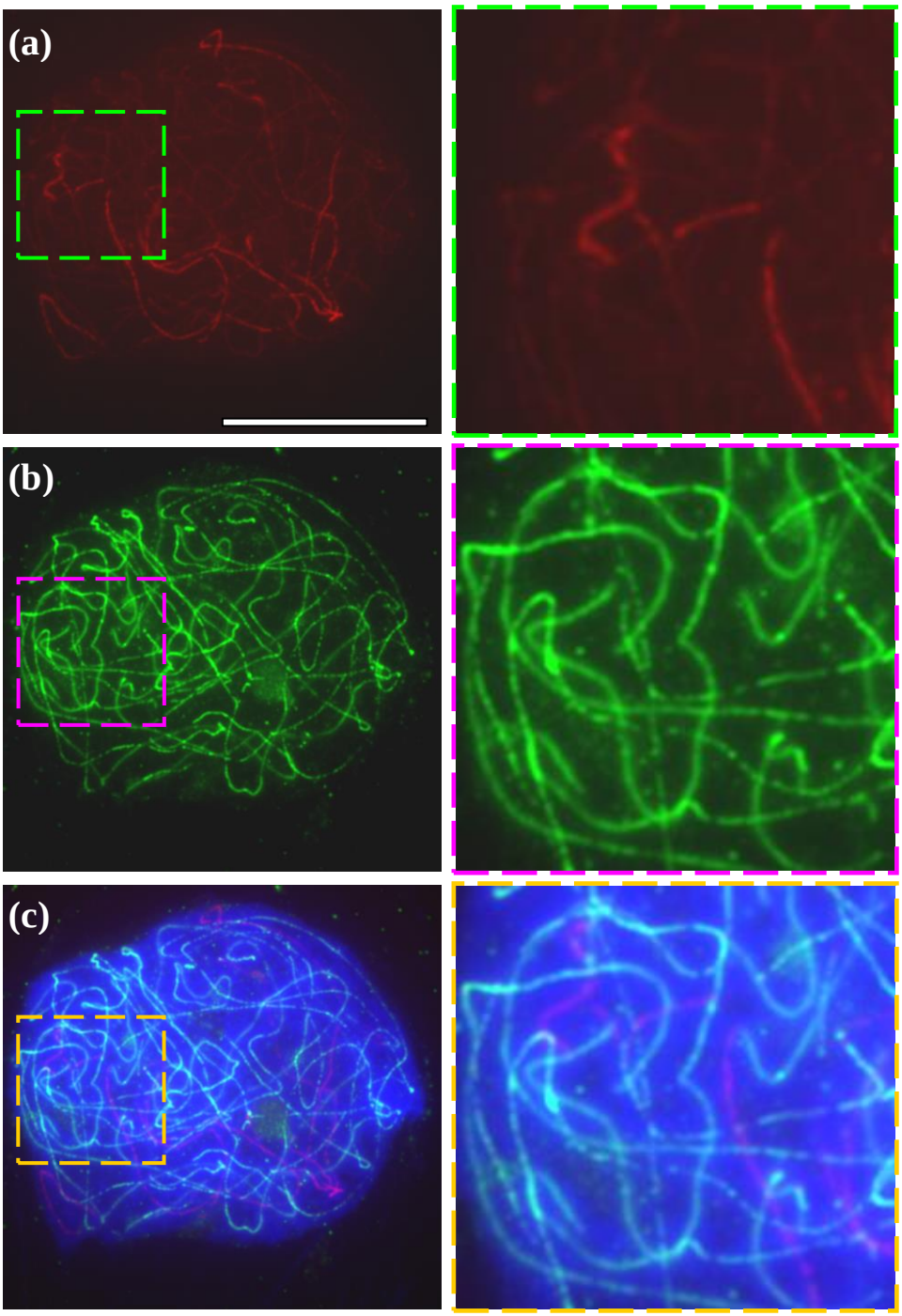


Figure 5.12: Pachytene stage in *des8*, showing the complete linearisation of ZYP1 (green (b)) and merged (c) (tagged with ZYP1 primary antibody (anti-rabbit) and detected with anti-rabbit (secondary antibody) FITC), indicating complete synapsis with normal depletion of ASY1 (red (a)) (tagged with ASY1 primary antibody (anti-rat) and detected with anti-rat (secondary antibody) Texas red: (Cy3)). Chromatin was detected with DAPI counterstain (blue). Bar = 10 µm

5.2.4 Fine mapping of the des8 allele

The initial mapping of *des8.l* was carried out using a population of 96 F_2 plants derived from a cross between BW248 (*des8.l* x Bowman Bc_4F_3) x cltv Barke (crosses provided by senior barley breeder Mark Glew: LIM). Using the BeadXpress® Illumina SNP genotyping platform with an in-house 384 SNP Oligo Pool Assay (OPA) the *des8* mutation was delineated to a 10 cM region of the long arm of chromosome 3H (which shares a high degree of synteny with rice chromosome 1: Mayer *et al*., 2011; refer to **Introduction**, **section *1.17.2***). This synteny is also demonstrated by the strudel software in **Figures 5.13** and **5.14** (https://ics.hutton.ac.uk/strudel/download-strudel/). The initial BeadXpress® mapping was carried out by Malcolm Macaulay: JHI).

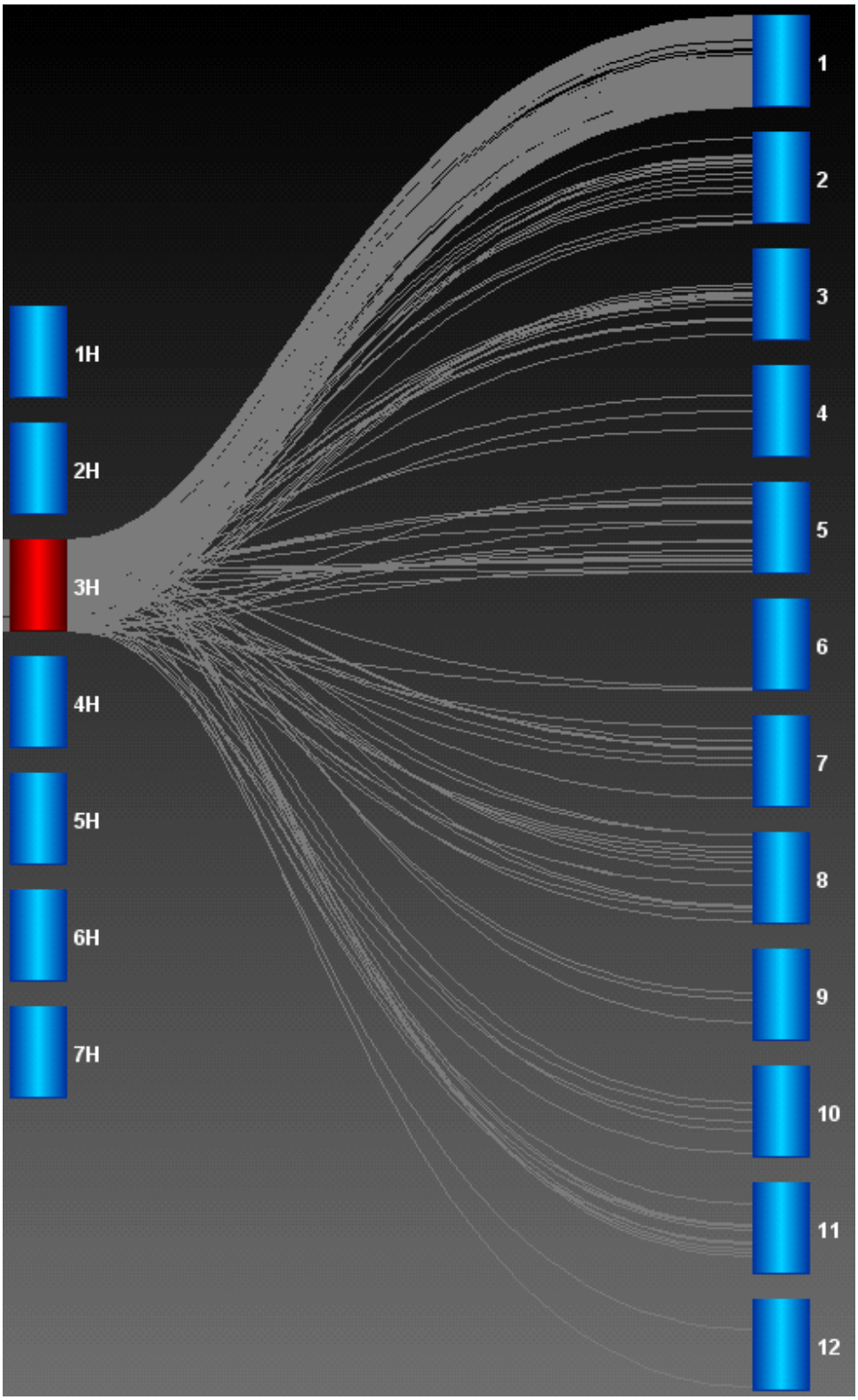


Figure 5.13: Barley chromosome 3H shares a high degree of synteny with rice chromosome 1 (Mayer *et al.*, 2011). Image is courtesy of Strudel® (https://ics.hutton.ac.uk/strudel/download-strudel/).

Using this information the mutation was fine mapped in a larger F_2 population derived from the cross between BW248 (*des8.l* x Bowman Bc_4F_3) x cltv Morex (crosses carried out by myself (LIM); see **Materials and Methods**: **Table 2.1**, including **Figures 2.1** and **2.2**), using KASPar® SNP assays (fine mapping with KASPar® SNP assays was carried out by myself: JHI). The mechanism of the KASPar® assay is explained earlier (**Materials and methods**: **Section 2.14.4** and **Figure 2.3**). The F_2 population derived from the cross with Morex was used for the fine mapping as it is a wider cross (between a two-rowed and six-rowed cultivar) that improved the polymorphism(s) available for mapping as shown by the genome sequence of the parental lines (Mayer *et al*., 2012). This population was grown up in a polytunnel in 2013 (see **Materials and Methods**: **Table 2.1**) and the phenotype of the plants scored as being either fertile or semi-sterile, which defined the allelic state of the *des8* locus.

The SNPs shown to be flanking *des8* in the initial mapping (11_20659 and 11_10515) were used in KASPar assays to screen the larger F2 population derived from the *des8* x Morex cross (480 plants). These SNPs were also polymorphic in this cross and in a population of 480 individuals 78 showed recombination between the SNP markers (recombination frequency of 0.082), of which 48 were informative (involving a recombinant between a SNP homozygous for the BW248 and another heterozygous, Table A5) that gave information about the position of the recombination event relative to the allelic state of the *des8* locus (see **Appendix**: **Table A178** (**page 601**) **and Figures A9-A18** (**page 576** to **585**)). The SNPs were derived from genetic sequences which were the barley homologues of the rice genes LOC_Os01g60230 and LOC_Os01g64170, respectively (**Table 5.3**). Close inspection of the genetic map derived from standard poulations (e.g. Morex x Barke, Comadran *et al*., 2012) indicated that there was a break in the synteny between the two species with the

colinearity running from LOC_Os01g60230 - LOC_Os01g60940 and then LOC_Os01g65670 - LOC_Os01g64170. This equates to the interval containing ~220 rice gene models indicating that the region is fairly recombinogenic.

Using information available from the SNP consensus maps and that derived from the Morex x Barke map (Comadran *et al*., 2012) further markers distal and proximal however, closer to the des8 region compared to the previous two markers were selected and checked for polymorphisms. The SNP markers 11_20628 and 11_10747 which were homologous to the rice genes LOC_Os01g64770 and LOC_Os01g60440, respectively (**Table 5.3**), were used for subsequent KASPar assays using the informative F_2 individuals (**Appendix**: **Table A179** on **page 606**). These two SNP loci mapped to either side of the *des8* locus but the interval remained large particularly between 11_10747 and *des8* (**Table 5.3** and **Figure 5.14**; Strudel: https://ics.hutton.ac.uk/strudel/download-strudel/).

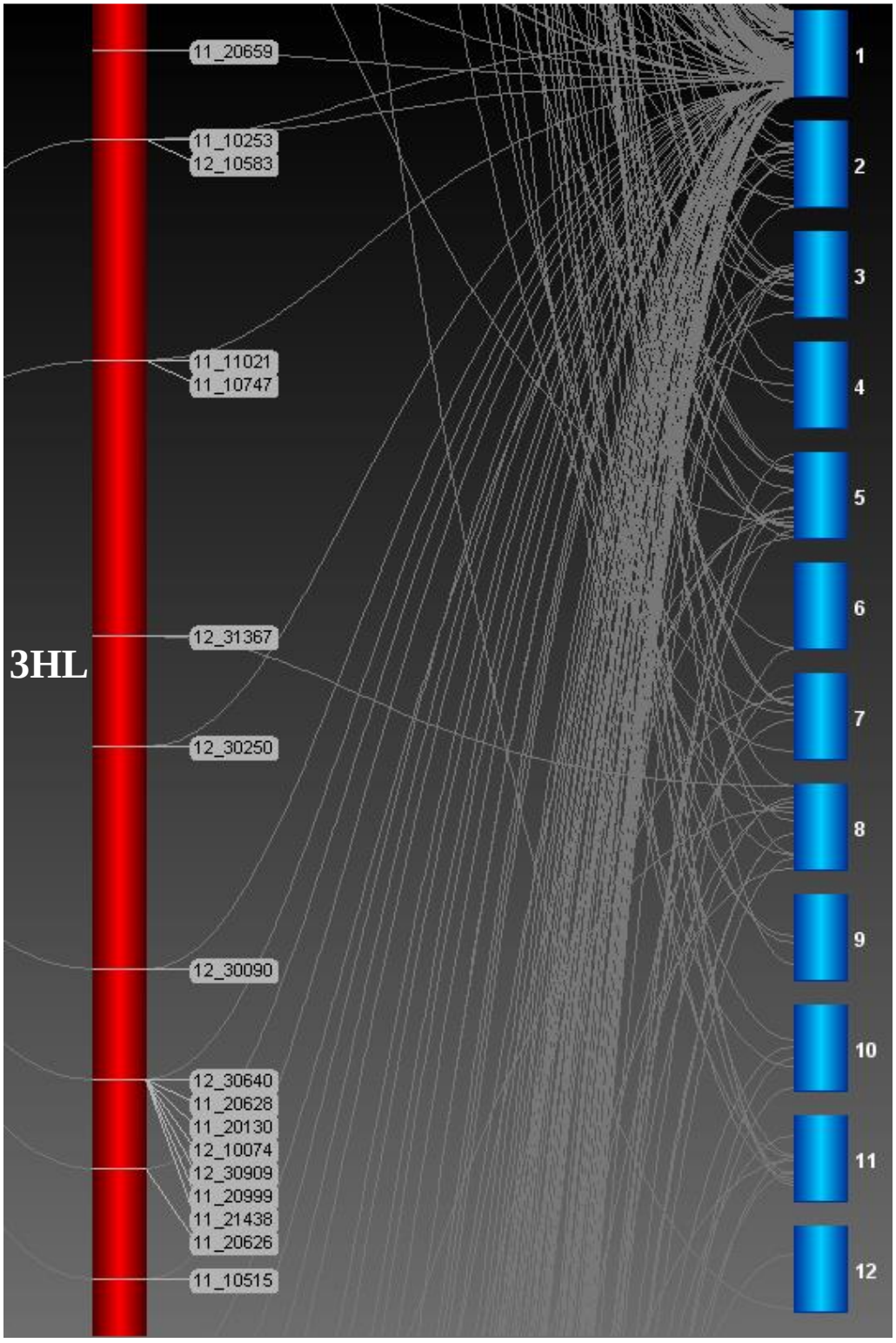


Figure 5.14: The 10 cM region of 3HL harbouring *des8*, flanked by the markers 11_20659 and 11_10515. The markers 11_20628 and 11_10747 are closer to *des8* but the interval remained large between 11_10747 and *des8*. Image is courtesy of Strudel® (https://ics.hutton.ac.uk/strudel/download-strudel/).

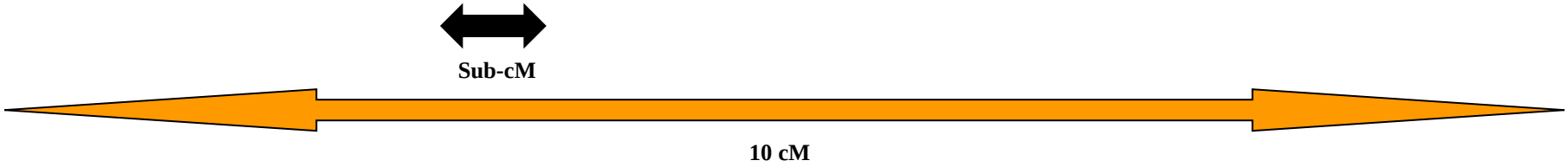
Therefore, using the known barley: rice synteny in this region, rice gene sequences were used to find barley homologues, that were derived from the whole shot gun sequencing of the barley genome (Mayer *et al*., 2012). Three barley genes selected were MLOC10987, MLOC53985 and MLOC4841 which were homologous to the rice genes LOC_Os01g65050, LOC_Os01g65320 and LOC_Os01g60900, respectively (**Table 5.3**). The sequence of the whole shotgun contigs containing these genes were analysed to look for SNP(s) between Morex and Bowman and then primers were designed using Primer3 (see **Materials and Methods**: **Section *2.14.5***, including **Appendix**: **Table A177** on **page 571**) to sequence the regions of the contigs harbouring the SNP(s). Initial sequencing using both forward and reverse primers for the markers (MLOC10987, MLOC53985 and MLOC4841), was carried out as a test. Primers that successfully yielded a PCR product (MLOC10987R02, MLOC53985R01 and MLOC4841R01) were used to sequence the contig that they corresponded to and genotyped using the Big Dye version 3.1 sequencing platform (see **Materials and Methods**: **Section *2.14.5***, including **Appendix**: **Table 177**) for specific SNP(s) for informative individuals. The results for MLOC4841 and MLOC10987 mapped well and related to the phenotype along with the previous markers that were used in the KASPar assays (**Table 5.3** and **Appendix**: **Table A179** on **page 606**). However, the segregation shown by MLOC53985 meant that that this SNP did not map to this region (**Table 5.3**).

The SNP markers MLOC_10987 and 11_20628 flanked *des8* and delineated the mutation to a sub-centimorgan interval (**Table 5.3** and **Figure 5.15**). As MLOC_10987 and 11_20628 were derived from genes homologous to rice genes LOC_Os01g65050 (**Figure 5.16**) and LOC_Os01g64770 (**Figure 5.19**) respectively, which would indicate that the delineated region contains roughly 28 genes, if the

synteny between barley and rice is complete (according to the rice genome browser: **Figures 5.16** to **5.19**: reading from right to left from **Figure 5.16** to **5.19**).

Table 5.3: A summary of the relationship between the genotype (SNP data) and phenotype for each marker that was used to progressively delineate *des8*. Pilot SNP based KASPar assays were conducted to determine the informative individuals using the markers 11_10515 and 11_20659 flanking the 10 cM region (Comadran *et al*., 2012). This was followed by further delineation by KASPar assays using only the informative indivuals for markers 11_20628 and 11_10747. Finally Big Dye v3.1 sequencing of SNP(s) for MLOC10987, MLOC4841 and MLOC53985 in *des8* were compared to the previously sequenced contig library (Mayer *et al*., 2012) to help delineate *des8* to a sub-cM interval between 11_20628 and MLOC10987.

Rice marker	LOC_Os 01g64170	LOC_Os01g64770	*Des8*	LOC_Os01g65050	LOC_Os01g60900	LOC_Os01g65320	LOC_Os01g60440	LOC_Os01g60230
Homologous barley marker used for KASPar assay/single primer (reverse or forward) based Big Dye v3.1 sequencing).	11_10515	11_20628	*Des8*	MLOC10987R02	MLOC4841R01	MLOC53985R01	11_10747	11_20659
Number of phenotypes matching the genotype.	22	22		27	18	13	7	7
Number of non-matches between the phenotype and genotype.	7	2		1	9	2	14	22
Number of undetermined genotypes.	0	5		1	2	14	8	0
Number of undetermined phenotypes.	4	4		4	4	4	4	4



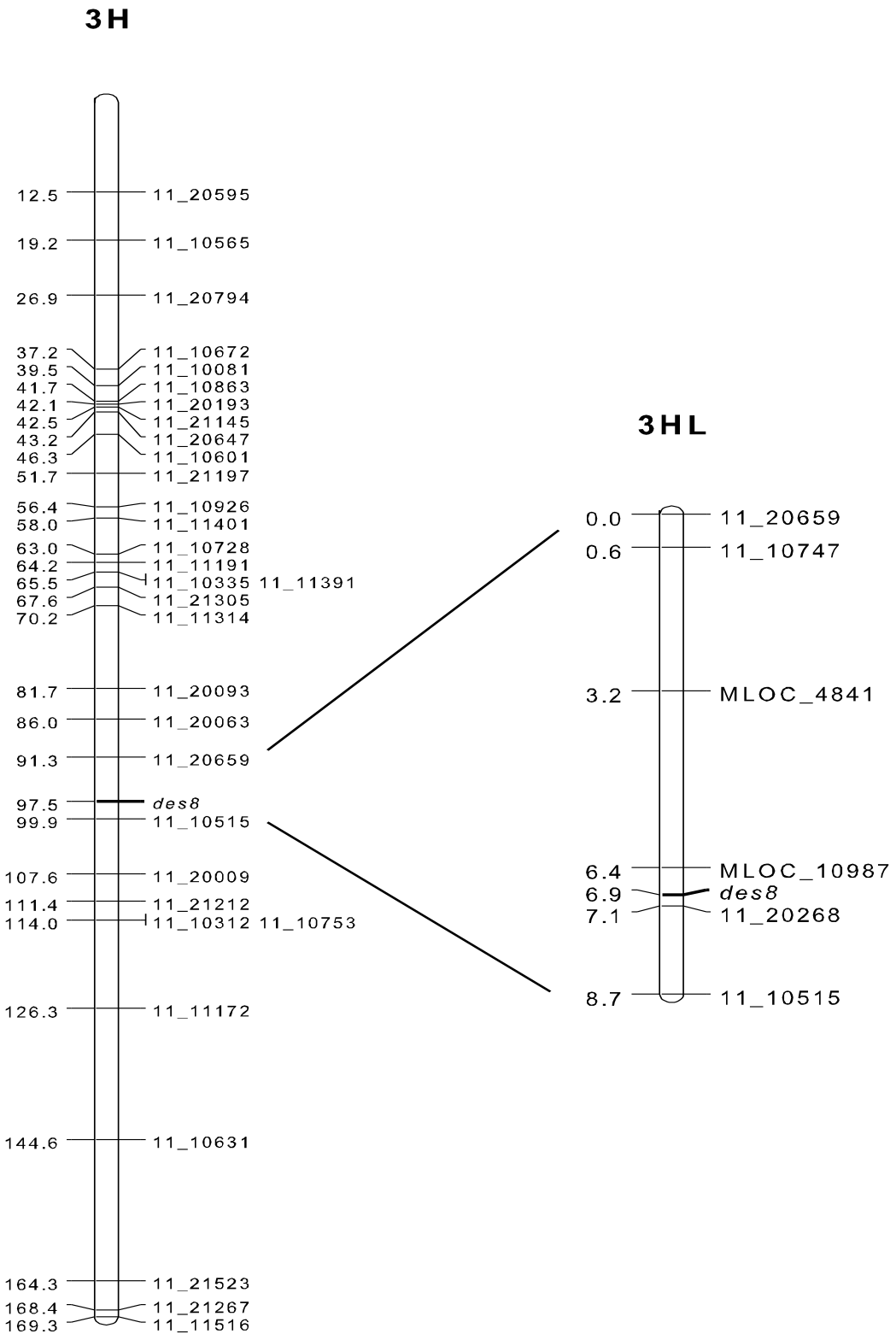


Figure 5.15: The current genetic map postulating the approximate locus of the *des8* gene on the long arm of chromosome 3H.

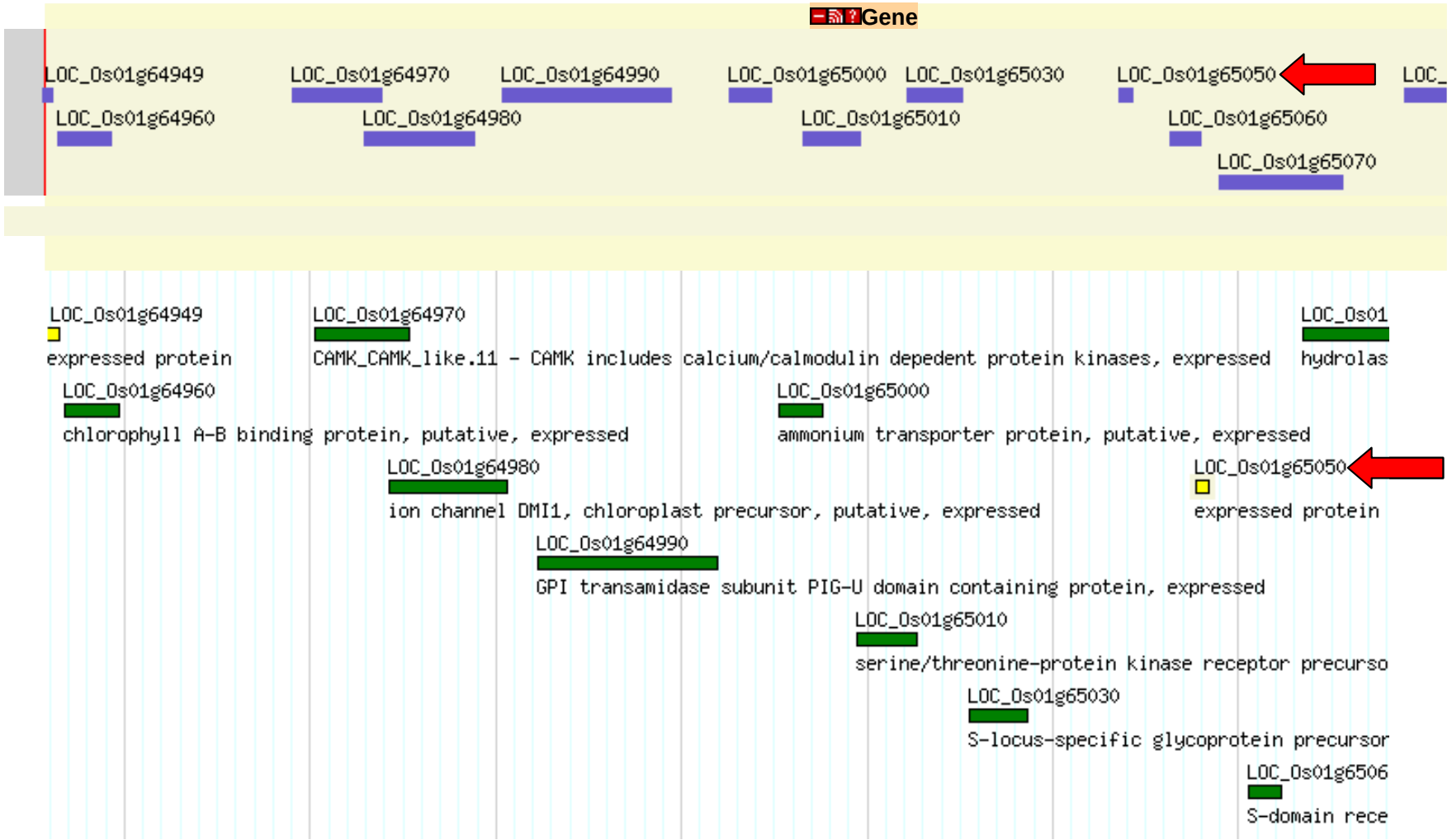


Figure 5.16: An excerpt of a portion of the syntenous region of rice chromosome 1 corresponding to the sub-cM interval harbouring *des8* (read from right to left), from the flanking marker LOC_Os01g65050 (red arrow) to LOC_Os01g64960. MLOC_10987 is homologous to LOC_Os01g65050. Courtesy of Rice Genome Browser.

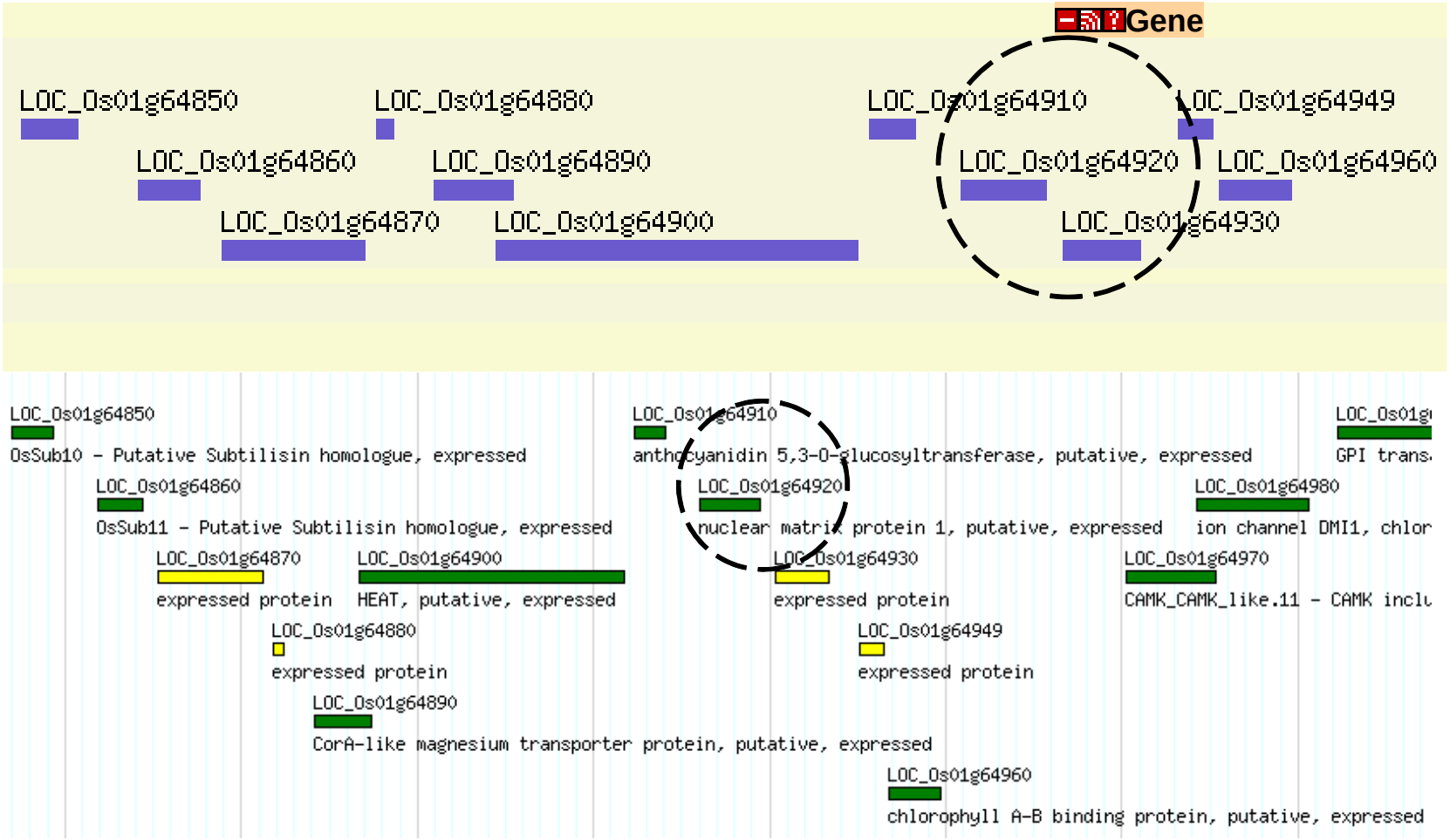


Figure 5.17: A second excerpt showing another portion of the syntenous region of rice chromosome 1 corresponding to the sub-cM interval harbouring *des8* (read from right to left), from the marker LOC_Os01g64960 (overlapping with that for Figure 5.16) to LOC_Os01g64850. A possible candidate gene is LOC_Os01g64920 which encodes a nuclear matrix protein (highlighted with a circle). Courtesy of Rice Genome Browser.

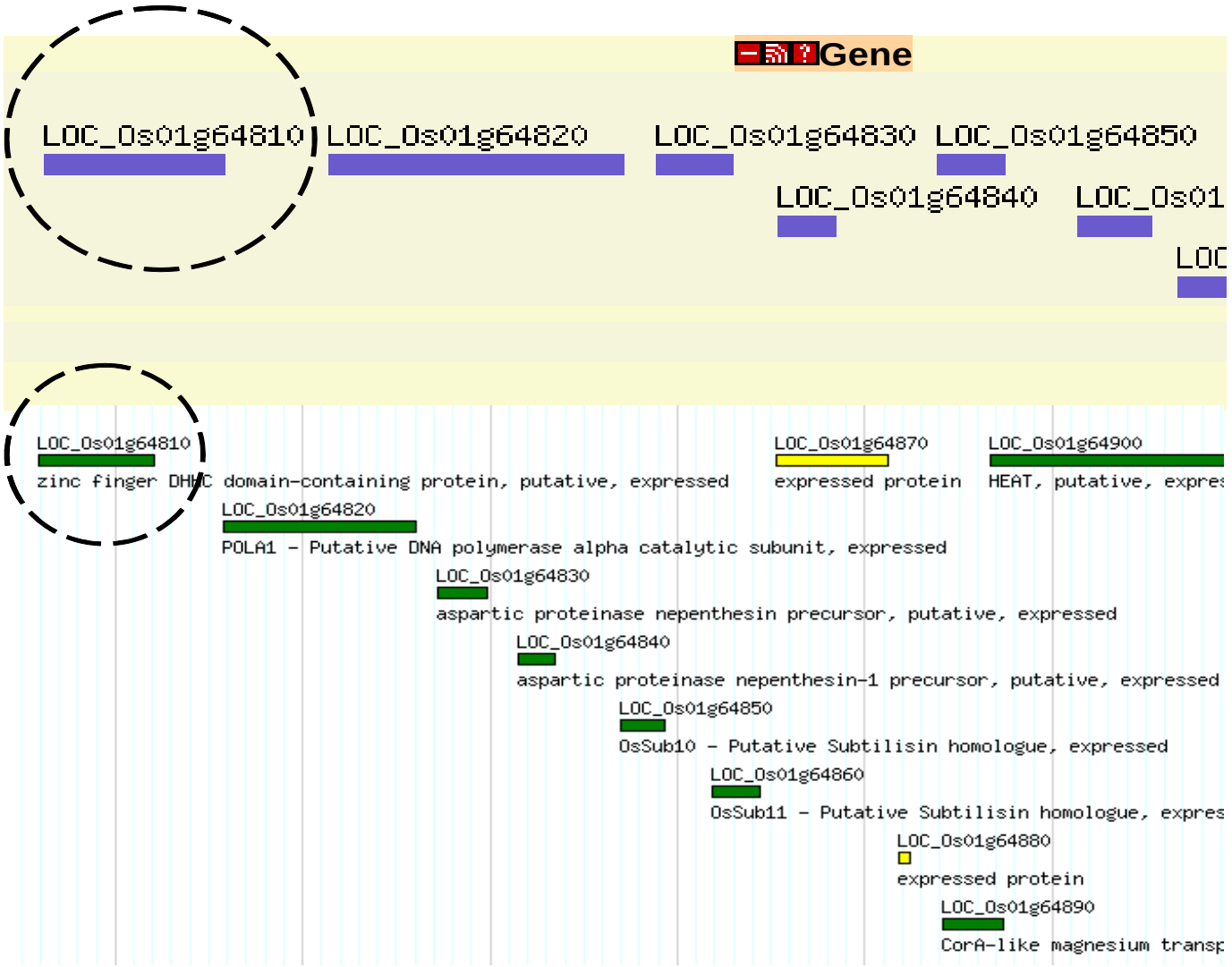


Figure 5.18: A third excerpt showing the third portion of the syntenous region of rice chromosome 1 corresponding to the sub-cM interval harbouring *des8* (read from right to left), from the marker LOC_Os01g64850 (overlapping with that for Figure 5.17) to the candidate gene LOC_Os01g64810, which encodes a zinc finger domain (highlighted with a circle). Courtesy of Rice Genome Browser.

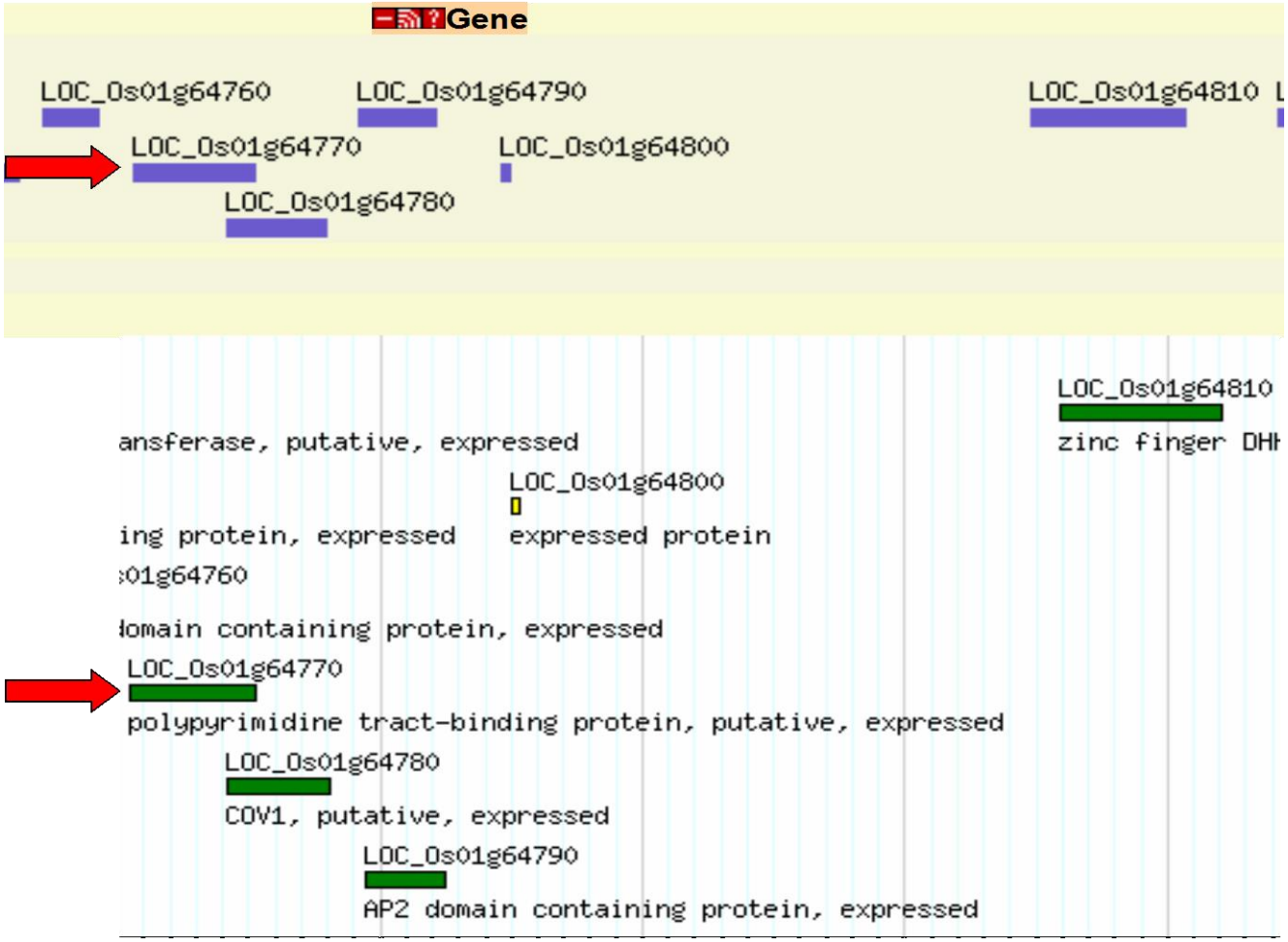


Figure 5.19: A fourth excerpt showing the last portion of the syntenous region of rice chromosome 1 corresponding to the sub-cM interval harbouring *des8* (read from right to left), from the marker LOC_Os01g64810 (overlapping with Figure 5.18) to LOC_Os01g64770 (the marker flanking the other end of the region syntenous to the sub-cM *des8* region: red arrow). Courtesy of Rice Genome Browser.

5.3 Discussion

5.3.1 Cytology

The preliminary analysis of DAPI stained nuclei at early stages up to pachytene had already suggested that normal progression of meiotic events and complete synapsis may be occurring in the mutant. The analysis of dual ASY1/ZYP1 immuno-labelled nuclei from G2 to diplotene (**Figures 5.6** to **5.10**), demonstrated that the mutant and wild-type were indistinguishable from each other with regard to the behavior of both proteins. The complete polymerisation of ZYP1 at pachytene stage in the mutant (**Figure 5.12**), served as a confirmation of complete synapsis and therefore, the desynaptic nature of *des8* with regard to significant desynapsis observed at metaphase I therefore (see **Section 5.2.2**), being in agreement with the classical definition of a desynaptic mutant (Li *et al*., 1945).

As the preliminary staging and FISH analysis of metaphase I spreads demonstrated that *des8* had a mixture of ring bivalents, rod bivalents and univalents (**Table 5.2**), it came under the category of a medium desynaptic mutant, in agreement with the system of the classification of the degrees of desynapsis (Prakken, 1943) and as previously confirmed for this line (Hernamndez-Soriano, 1973). In an analysis of 50 nuclei at metaphase I stage, chromosome 6H exhibited the greatest number of univalents (64) (**Table 5.2**) which is indicative of the fact that it is an NOR bearing chromosome. The location of the NOR or the short arm is indicative of the lack of CO assurance in this arm where rod-bivalents are concerned and may be exacerbated in the desynaptic background. The incidence of rod-bivalent formation in barley chromosomes carrying a NOR was initially postulated by Stoinova, (1994). A later study confirmed that this was indeed the case for chromosome 5H when compared to other non-NOR bearing chromosomes of the genome (Pickering *et al*., 2005). Despite

the fact that the study showed that this was also the case for the short arm of chromosome 6H, it was suggested that the failure of CO formation was probably due to an introgressed region of the *H. bulbosum* genome which harbours the pSc119.2 marker. The marker was used to help distinguish chromosomes 5H and 6H as both had 45S rDNA. However, it was suspected that the introgressed region may have hindered recombination due to the fact that it was a terminal and large introgressed region (Pickering *et al*., 2004). The incidence of rod-bivalent formation in NOR chromosomes has also been reported in *Hordeum marinum* (sea barley) (Linde-Laursen and Von Bothmer, 2012). Even though chromosome 5H exhibited fewer univalents (24) than chromosome 4H (54), it did exhibit the greatest number of rod-bivalents (35) (**Table 5.2**) which is in agreement with Pickering *et al*. (2005). A lower than expected abundance of univalents may be due to the fact that in the *wild-type* background, chromosome 5H has 2 to 3 CO per bivalent with 1 CO on the NOR bearing short arm and up to 2 COs in the distal region of the long arm. In contrast, 1 to 2 COs are observed in chromosome 6 in the *wild-type* (Higgins *et al*., 2012). However, the loss of the CO only in the NOR arm in the rod-bivalents is consistent with the observance of poor CO assurance in NOR bearing arms in *Arabidopsis* chromosomes (Lam *et al*., 2005) and in agreement with data presented by Pickering *et al*., 2005 showing that rod-bivalent formation only occurs due to a failure in CO formation in the short arm in barley. Based on this, it could be argued that 5H yields fewer univalents than 6H as it can have as much as 2 COs on the long arm, increasing the likelihood of an obligate CO being present. This was the case as there were two types of rod bivalent present: the bulged (8) and classic (26) rod-bivalents (**Table 5.2**) hence, a greater number of COs in a wild-type background would render a desynaptic

phenotype as being less "apparent" in the equivalent chromosome in the mutant, by way of greater CO assurance in the long arm.

That NOR bearing arms seem to be most effected by the *des8* mutation, the cause of the lack of CO assurance in the wild-type (Pickering *et al*., 2005) alone must be brought into consideration, in order to attempt to ascertain the possible genetic cause of CO failure in the mutant. It was noticed that in *Hordeum marinum spp. gussoneanum*, Giemsa staining of the meiotic chromosomes generated C-banding of the rDNA regions that resembles the banding pattern of heterochromatin (Linde-Laursen *et al*., 1992), and recombination occurs poorly in heterochromatin (Linde-Laursen and Von Bothmer, 2012). In conclusion, the fact that NOR bearing arms show the lowest CO frequency in the mutant may just be due to the fact that because they resemble heterochromatin (Linde-Laursen *et al*., 1992) and therefore sites of poor recombination (Linde-Laursen and Von Bothmer, 2012), the effect of desynapsis may simply be exacerbated in chromosomes bearing the NOR.

In *des8*, the observance of complete synapsis at pachytene (**Figure 5.12**) followed by a greater degree of asynapsis in NOR bearing arms in comparison to non-NOR bearing chromosomes suggests that the candidate mutant allele may encode a cohesion-like protein that ensures the cohesion of bivalents into late prophase I and that the over-expression of the successfully identified allele in the wild-type background may serve as a possible route to ensuring CO assurance in the NOR bearing short arms of the barley genome. This could be useful to resolve the issue of linkage disequilibrium in barley 5HS (Pickering *et al*., 2005), aiding barley breeders to potentially require smaller populations of plants than currently required, to generate novel gene combinations.

In addition, the residual COs in the mutant are strongly distal. Bowman lines had a 3.7 fold greater number of interstitial COs (41) than the mutant (11) though, Bowman lines had a 1.8 fold greater number of distal COs (678) than the mutant (370). However, the relative lack of interstitial COs may relate to the spatiotemporal progression of synapsis such that COs are preferentially skewed towards distal regions (Higgins *et al*., 2012). In addition, the chiasma counts are considerably higher than that for a barley ZYP1 RNAi knockdown line (Barakate *et al*., 2014) such that there are no random residual COs. This suggests that the class I pathway is still acting and that *des8* is not a ZMM mutant. If we speculate that the *des8* allele may encode a cohesion-like protein, the clustering of telomeres to form a bouquet at early *prophase I* in barley (Higgins *et al*., 2012) may help to stabilise homologous recombination in distal regions (Barakate *et al*., 2014). It has even been suggested that rapid prophase movements (RPMs) of telomeres occurs at the same time as early recombination events to disrupt unstable recombination intermediates, allowing recommencement of interhomologue recombination between the tightly clusters telomeres until a stable recombination intermediate is formed (Conrad *et al*., 2008). The possible role that the bouquet may have as a scaffold, to help to facilitate the formation of correct recombination intermediates was also postulated by Storlazzi *et al*., 2010 (discussed earlier in **Chapter 3**: **Section 3.4**). Hence, the formation of stable recombination intermediates may be less dependent on cohesins in distal regions.

5.3.2 Genetic mapping of the des8 allele

A collection of *des8* mutant lines were crossed with Morex to generate a large segregating population that would be used for the genetic mapping of the *des8* mutant gene. The ratio of wild-type: mutant phenotype in the F_2 population was roughly 3:1,

confirming the recessive nature of the mutant allele, which was already established in a previous study (Hernandez-Soriano, 1973).

The initial mapping of *des8* was achieved using the GoldenGate® genotyping assay, which mapped the allele to within a 10 cM region of the long arm of chromosome 3H. Later, KASPar® assays were designed for the flanking markers (11_20659 and 11_10515) and run on the larger F2 population (**Table 5.3**). Even though it was already known from the initial mapping data that *des8* would fall between these two markers, the assay was carried out as an exercise to generate data for individuals that would be informative (**Appendix**, **Table A178**: **page 601**). The remainder of the assays used only these informative individuals from the above assay with further markers distal and proximal however, closer to the *des8* region compared to the previous to markers (11_20659 and 11_10515) to progressively delineate the *des8* gene (**Table 5.3**; **Appendix**: **Table A179** on **page 606**).

The SNP mapping allowed the delineation of the genomic region containing *des8* to a sub-centimorgan interval between MLOC_10987 and 11_20628 (**Table 5.3** and **Figure 5.15**). As these markers were derived from genes homologous to rice genes LOC_Os01g65050 and LOC_Os01g64770 respectively, this indicates that the delineated region contains roughly 28 genes if the synteny between barley and rice holds (**Figures 5.16** to **5.19**). This high cM: gene content ratio reflects the recombinogenic nature of this region of chromosome 3H.

The syntenic region of rice between LOC_Os01g65050 and LOC_Os01g64770 contains 23 genes. Close examination of this region using the rice genome browser indicated possible candidates that include LOC_Os01g64770 which encodes a polypyrimidine tract-binding domain (**Figure 5.19**), LOC_Os01g64810 which encodes a zinc-finger domain (**Figure 5.18**) and LOC_Os01g64920 which encodes a

nuclear matrix protein (**Figure 5.17**). But, the tissue/organs in which these proteins are expressed in rice, has not yet been determined according to the EnsemblPlants database. Further screening analysis of the sub-centimorgan interval between MLOC_10987 and 11_20628 will be required to identify the candidate gene.

CHAPTER 6

GENERAL DISCUSSION

Introduction

The generation of novel gene combinations during meiosis is essential to the survival of species under altering selection pressures. Such is the case with a growing world population and climate change, that a concerted effort is placed on human intervention to aid the generation of such novel gene combinations in cereals despite the fact that recombination during meiosis is strongly localised to distal ends of the chromosomes. As a result, this has presented crop breeders with limited genetic variation to tackle the growing issue of food security as vast regions of the genomes in cereals will be recombination redundant. The aim of this project was to address this issue by modifying the mechanisms that control the recombination process. This investigation describes the methods that were used to investigate the mechanisms controlling meiotic recombination and the approaches used to modify these mechanisms in order to alter patterns of recombination.

The role of the telomeres in homologous chromosome pairing in barley

There is an ongoing debate regarding the mechanism by which homologous chromosomes are able to identify each other and pair up in a tightly controlled manner. It has been suggested that the dynamic motion of telomeres brings the chromosomes into close proximity forming a bouquet (Scherthan, 2001), facilitating correct homologue pairing (Cowan *et al*., 2001). The treatment of barley with 5 mM colchicine via the transpiration stream, led to the failure of pairing of homologous telomeric regions as demonstrated by the presence of unpaired telomeres at zygotene, as well as a disrupted bouquet (**Chapter 3**: **Section 3.3.4**). Treatment with 100 µM colchicine did disrupt the bouquet but, telomere pairing was unperturbed (**Chapter 3**: **Section 3.3.3**). The same effect was also observed in a wheat-rye addition lines

(Corredor and Naranjo, 2007). Even though this data puts into question the importance of the bouquet it does nevertheless demonstrate that the bouquet is a conformation that occurs as a consequence of telomere pairing. The clustering of telomeres into a bouquet at early prophase I was previously demonstrated in barley (Higgins *et al*., 2012) and it has been speculated that it may help to stabilise homologous recombination in distal regions (Barakate *et al*., 2014). This possibility was also postulated by Storlazzi *et al*. (2010) and that RPMs of telomeres as observed in yeast during early recombination events may be in place to disrupt unstable recombination intermediates, allowing recommencement of interhomologue recombination between the tightly clusters telomeres (via the bouquet) until a stable recombination intermediate is formed (Conrad *et al*., 2008). Later, it was demonstrated that telomeres pair up independently of the bouquet by dynamic telomeric movements alone (Lee *at al*., 2012).

Aside from the debate regarding the importance of the bouquet, the importance of tubulin or "tubilin-like" mediated telomere movements in barley (using colchicine) have been shown to be vital in the telomere pairing process. Even though the treatment of *Allium fistulosum* L. with colchicine led to failure of homologue pairing and subsequent univalent formation at metaphase I, the study didn't identify the cause of this failure (Jenkins and Okumus, 1992). Confirmation of the role played by subtelomeric regions in homologue pairing during meiosis was provided in an investigation in *Hordeum chilense*, for which the subtelomeric region on one end of each chromosome was absent (del Carmen *et al*., 2014). It was found that homologous arms lacking the subtelomeric region failed to pair up but homologue pairing was eventually achieved by late pachytene in the other arm for which the subtelomeric region was intact, as evidenced by the formation of the obligate CO and subsequently

rod-bivalents. In addition, MLH1 foci were only observed in chromosome arms for which the subtelomeric region was intact (del Carmen *et al*., 2014). But this study only made reference to the failure of the pairing of subtelomeric regions and not the centromeric regions of the chromosomes. Additionally, telomerase deficient-mice exhibited irregular telomere lengths which subsequently led to compromised homologous pairing and recombination as evidenced by reduced MLH1 foci (Liu *et al*., 2004). Similarly, in *Arabidopsis*, a T-DNA *tert* mutant exhibited failure of homologous pairing as demonstrated by univalents as a consequence of telomere shortening (Puizina and Samanic, 2013). Even so, both studies (Liu *et al*., 2004; Puizina and Samanic, 2013) didn't analyse centromere pairing and that the failure of homologous pairing may have been the result of the failure of the re-association of subtelomeric homologous chromosome regions after the breakdown of unstable recombination intermediates as a result of defective bouquet formation (Barakate *et al*., 2014; Lee *at al*., 2012; Storlazzi *et al*., 2010).

The failure of telomere pairing in barley by chemical intervention, as well as the use of various mutants that perturb telomere integrity in other plants (Puizina and Samanic, 2013) and mammals (Liu *et al*., 2004), has revealed the role of the sub-telomeric regions of the chromosomes in homologue pairing process during meiosis. But further, investigations must be carried out in which both the effects of telomere and centromere pairing/dynamics on the overall homologue pairing process are studied. Such an investigation will provide a more concise model as the model of chromosome pairing that was proposed by this study (**Section 3.5**) is only speculative as centromere pairing was not investigated. Nevertheless, the treatment of barley with colchicine has demonstrated the feasibility of using chemicals to alter meiotic progression in order to affect chromosome pairing.

Altering the epigenetic modification of chromatin influences meiotic recombination

The alteration of the global chromatin structure by the epigenetic modifications of CG islands and histones have previously been implemented in the alteration of meiotic crossover frequency and distribution in other species. This effect was successfully demonstrated by histone hyperacetylation in *Arabidopsis* (Perrella *et al*., 2010) and yeast (Mieczkowski *et al*., 2007), including CG island hypomethylation in *Arabidopsis* (Yelina *et al*., 2012).

TSA induced hyperacetylation of histone H4 in mouse oocytes led to the induction of chromosomal decondensation which was demonstrated by a greater occupation of the total nuclear volume, and subsequent disturbance of global chromatin remodelling (Yang *et al*., 2012). Interestingly, the study also showed that the nucleolus is surrounded by heterochromatin in control oocytes but this configuration was absent in the TSA treated population, as well as chromosome mis-segregation at Anaphase I (Yang *et al*., 2012). Giemsa staining of meiotic chromosomes in *Hordeum marinum spp. gussoneanum*, resulted in a C-banding pattern of the rDNA regions, which is similar to the banding pattern of heterochromatin (Linde-Laursen *et al*., 1992). As recombination occurs poorly in heterochromatin (Linde-Laursen and Von Bothmer, 2012), the high succeptability of NOR regions to treatment in barley may be as a result of their early detachment from the nucleolus, assuming that these regions are preferentially decondensed due to the inhibition of histone H4 deactylation as was previously demonstrated in *Arabidopsis* (Probst *et al*., 2004).

In barley it has been documented that chromatin undergoes cycles of expansion and contraction during the meiotic pathway and the expansion cycles are associated with the loading of ASY1 at early G2 and RAD51 at early leptotene in distal regions of

chromatin (Higgins *et al*., 2012). Based on this it could be suggested that the contraction cycles especially during entry into mid G2, may be associated with axis formation and that histone hyperacetylation induced chromatin decondensation as demonstrated by Yang *et al*. (2012), may be preventing chromatin contraction and subsequently, axis formation as evidenced by regions of perturbed ASY1 polymerisation (see **Chapter 4**; **Section *4.2.5***: **Figure 4.26(b)**).

Using forward genetics to understand the mechanisms controlling recombination in barley

Forward genetics has been a traditional methodology used to attempt to ascertain a genotype that is responsible for the phenotype in model plants that have been put through many generations of breeding to generate NILs (Druka *et al*., 2011). This approach is usually initiated with naturally occurring or even chemically induced mutants as is the case for ethylmethanesulfonate (EMS) treated barley populations (Caldwell *et al*., 2004). Seeds from EMS treated barley that displayed a phenotype of interest such as abnormal ear structure and stature, were used to generate a library for forward genetics to screen for suspected mutations in the genes of interest (Caldwell *et al*., 2004).

Whilst the approach can be labour intensive using traditional map-based cloning with regard to the high number of F_2 individual that are required (usually over 1,000) when progressing to the stages of fine-mapping (Jander *et al*., 2002), the development of high throughput next-generation sequencing (NGS) has accelerated the progress of forward genetics (Krothapalli *et al*., 2013). It has also enabled mutant genes generated by EMS induction in *Arabidopsis* to be successfully cloned given its relatively small genome size, by whole-genome shotgun sequencing (Lindner *et al*., 2012). In recent

years, the ullimina® sequencing platform has been used to successfully identify mutant genes in other model organisms such as *C. elegans* (Sarin *et al*., 2008), including EMS induced mutant genes in *Drosophila* (Blumenstiel *et al*., 2009) and yeast (Irvine *et al*., 2009). NGS has subsequently been used to sequence larger and more complex genomes such as maize to identify regions of mutator transposon insertion regions using the Illumina platform® generating high-density sequence reads (Williams-Carrier *et al*., 2010). Another method called MutMap, in which a mutant line is crossed with the wild-type and subsequently selfed, such that the F_2 generation is within a narrow phenotypic range, has been effective in rice to map agronomically important mutant genes responsible for dwarfism, whilst reducing the number of F_2 individuals required (Abe *et al*., 2012).

The Illumina platform® was also utilised to initially map the *des8* mutation to within a 10 cM region on the long arm of 3H, followed by KASPar® assays to attempt to fine map the gene (see **Chapter 5**: **Section *5.2.4***). The sequencing data does not point to a gene which encodes a class I recombination protein within the region harbouring the gene, which is in agreement with the chiasma scoring data which does not fit a random Poisson distribution. Nevertheless, complete synapsis as demonstrated by ZYP1 analysis has confirmed the desynaptic nature of this line (**Figure 5.12**).

Future objectives

The study into the control of chromosome pairing has revealed that a tubulin or "tubulin-like" mediated mechanism controlling telomere movements is vital for the pairing of sub-telomeric regions in barley. Even though the bouquet has been traditionally postulated to facilitate homologous pairing (Bass *et al*., 2000), we must bear in mind that it has been demonstrated that telomeres can pair up in the absence of

a bouquet conformation in barley, wheat-rye additions (Corredor and Naranjo, 2007) and yeast (Lee *at al*., 2012). Therefore, further analysis must be undertaken to decipher the specific mechanisms involved in telomere movements with regard to pairing and clustering to form a bouquet, as it has been suggested that both processes may be two distinct processes as supported by studies in barley and wheat-rye additions (Corredor and Naranjo, 2007), such that colchicine may be targeting different groups of characterised or maybe even other tubulin complexes that are yet to be discovered. Maybe live-cell tubulin labelling could be used to track the involvement of the cytoskeleton during both telomere pairing and bouquet formation and to visualise if the integrity of the cytoskeleton has been compromised following chemical treatment. Finally, the direction of research will be along a clearer path once we know whether or not genes encoding SUN-like proteins can be characterised in barley or even wheat, for which it still has not been (Richards *et al*., 2012).

By taking the genetic screening results of TSA treatment at "face value", the subtle shifts in recombination distribution within specific neighbouring gene clusters (**Figure 4.16(b)**) suggests that even though histone hyperacetylation may not be suitable to cause strong shifts in recombination distribution from distal to proximal positions to help eliminate the disparities between the physical and genetic maps for barley (Kunzel *et al*., 2000) and other cereals such as wheat (Lukaszewski and Curtis, 1993), it may be a feasible method to break the linkage drag of an unwanted gene with a desirable gene in breeding programs (Brown *et al*., 1989). Bearing in mind that the shifts in recombination distribution were on a small scale (by one marker in a given direction), this may be advantageous in that the application of chemicals can be used to cause a subtle directional shift in recombination to break the linkage drag of an unsuitable marker that may be immediately adjacent to the desired marker.

Once genes encoding the various proteins involved in the epigenetic modification of chromatin or the meiotic recombination pathway have been fully characterised, it may be possible to replace chemical treatments with the administration RNAi oligonucleotides directly into the transpiration stream. For example, rather than using okadaic to up-regulate Cdk2-type activity in wheat (Greer *et al*., 2012), it may be possible to phenocopy this effect by utilising RNAi oligonucleotides to down-regulate the *ph1* locus and potentially induce homeologous recombination. Lately, a *ph1b* mutant wheat line was crossed with *Hordeum vulgare* and *Hordeum chilense* and genomic *in situ* hybridisation (GISH) demonstrated that recombination occurred between the barley chromosome 4H and a wheat chromosome (Rey *et al*., 2015). Another example may be to directly administer RNAi oligonucleotides to down-regulate specific genes encoding histone deacetylases. Chemical treatments are potentially advantageous compared to the use of mutants in that the investigations are not going to be hampered by temperature sensitive mutants and that the effect of the chemical treatment will be immediately exerted (Spring, 2005). This also means that an effect can be exerted on meiotic recombination patterns only in the parent population to generate novel gene combinations which can then potentially be maintained in subsequent generations. The disadvantage with chemical treatments has been demonstrated in this investigation in that there are a wide range of non-specific effects that are deleterious to the growth as well as meiotic development of the plant, resulting in hampered fertility. The use of directly administered RNAi oligonucleotides into the transpiration stream could potentially be a way forward as they will only affect a single target gene hence, reducing non-specific effects and will be degraded such that it will only affect recombination in the parent. Infact, the very rapid degradagation and instability of RNAi is problematic in that its potential

effectiveness may be nullified (reviewed by Lee *et al*., 2013). The development of RNAi(s) which can spontaneously change their conformation to form stable hairpin structures and are able to coalesce, forming microspheres, have been developed (Lee *et al*., 2012). After they are taken up by the target cell, the cellular RNAse(s) breakdown this hairpin structure to yield functional (linear) RNAi(s). Such an approach holds great potential as a means of effectively delivering RNAi to cells to treat cancer patients (reviewed by Lee *et al*., 2013). Other studies have explored the potential use of RNAi delivery methods such as lipid nanoparticles and cyclodextrin polymer conjugates (Reviewed by Kanasty *et al*., 2013). Such means of RNAi delivery to the target cells may hold the promise of an effective means of manipulating meiotic recombination patterns in cereals by using the established approach of injecting chemicals directly into the transpiration stream (Corredor and Naranjo, 2007).

Ongoing debates still question the feasibility of inducing large scale shifts of recombination events to interstitial regions as it is argued that certain combinations of genes within heterochromatic regions, have been evolutionarily conserved and that the induction of recombination of genes to disrupt such clusters may have deleterious consequences in subsequent generations. However, it can be argued that we don't know what the potential results may be and that the effects may even produce novel gene combinations that may well confer a selective advantage to crops. Failing this, the successful shifting of recombination to interstitial regions as demonstrated in barley at elevated temperatures (Higgins *et al*., 2012), will allow breeders to reduce the disparities between the physical and genetic maps for barley (Pedersen *at al*., 1995) and wheat (Lukaszewski and Curtis, 1993). This in turn will help to generate genetic maps with a greater resolution than what is available today and potentially aid

the assessment of the viability of inserting a gene by CRISPR technology (reviewed by Puchta and Fauser, 2013) into certain genomic regions harbouring gene clusters encoding specific molecular pathways.

NGS has greatly improved the efficiency of forward genetics and has been pivotal to initiate studies to fine map key mutations to help us improve our understanding of meiosis in barley. Nevertheless, the process is still time consuming however, a method similar to the one in which a mutant line is crossed with the wild-type and subsequently selfed, permitting the F_2 generation to be within a narrow phenotypic range yielding a high number of infomative individuals (Abe *et al*., 2012), was used to map a mutant gene responsible for the nodded dwarf phenotype in barley (Mascher *et al*., 2014). This involved mapping-by-sequencing in which bulk genomic regions of the mutant line were sequenced and compared to existing gene maps to identify the deletion of a candidate gene which encodes a cytochrome P450 in only one sequencing experiment (Mascher *et al*., 2014). Such an approach could be used in future mapping studies involving the *des* barley mutants.

Closing remarks

The growing concern about food security amongst world leaders has prompted much in the way of biotechnological research into crops and has been pivotal in initiating efforts to apply the knowledge gained regarding meiosis in *Arabidopsis*, to commercially viable crops. Current studies have revealed the complexity of the meiotic pathway with regard to the mechanisms involved in homologous chromosome pairing and the ways in which downstream recombination events are tightly controlled such that their modification can potentially be useful to alter recombination patterns. Even though much effort is beginning to be placed into various issues to

tackle food security using biotechnological means, the National Aeronautics and Space Administration (NASA) is also using satellite technology to inform world leaders about climate change and how it can affect regional and global food security (Parry *et al*., 2005). In simple words, we cannot make significant progress in tackling food security by treating the space program, GM/CRISPR technology and meiosis research as competing interests. Instead, world leaders must find a way to marry up all of these interests as a combined effort by improved collaborations between representatives within these fields, to ensure food security for future generations of humanity.

REFERENCES

Abe, A., Kosugi, S., Yoshida, K., Natsume, S., Takagi, H., Kanzaki, H., Matsumura, H., Yoshida, K., Mitsuoka, C., Tamiru, M., Innan, H., Cano, L., Kamoun, S. and Terauchi, R. (2012). Genome sequencing reveals agronomically important loci in rice using MutMap. *Nat Biotechnol*, **30**: 174-178.

Abbo, S., Berger, J. and Turner, N,C. (2003). Evolution of cultivated chickpea: four bottlenecks limit diversity and constraint adaptation. *Funct Plant Biol*, **30**: 1081-1087.

Ahloowalia, B.S. (1969). Effect of temperature and barbiturates on a desynaptic mutant of ryegrass. *Mutat. Res*, **7**: 205-213.

Al-Kaff, N., Knight, E., Bertin, I., Foote, T., Hart, N., Griffiths, S. and Moore, G. (2008). Detailed dissection of the chromosomal region containing the *Ph1* locus in wheat Triticum aestivum: With deletion mutants and expression profiling. *Ann Bot*, **101:** 863-872.

Alani, E., Padmore, R., and Kleckner, N. (1990). Analysis of wild-type and *rad50* mutants of yeast suggests an intimate relationship between meiotic chromosome synapsis and recombination. *Cell*, **61:** 419-436.

An, X.J., Deng, Z.Y. and Wang, T. (2011). OsSpo11-4, a rice homologue of the archaeal TopVIA protein, mediates double-strand DNA cleavage and interacts with OsTopVIB. *PLoS One*, **6**(5):e20327. doi: 10.1371/journal.pone.0020327.

Anderson, L.K. and Stack, S.M. (2005). Recombination nodules in plants. *Cytogenetics and Genome Research*, **109**: 198-204.

Andersson, E. (1947). A case of asyndesis in Picea abies. *Hereditas*, **33**: 301-347.

Aragón-Alcaide, L., Reader, S., Beven, A., Shaw, P., Miller, T. and Moore, G. (1997). Association of homologous chromosomes during floral development. *Curr Biol*, **7**, 905-908.

Argueso, J.L., Wanat, J., Gemici, Z., and Alani, E. (2004). Competing crossover pathways act during meiosis in Saccharomyces cerevisiae**.** *Genetics*, **168**: 1805-1816.

Armstrong, S.J., Franklin, F.C. and Jones, G.H. (2001). Nucleolus-associated telomere clustering and pairing precede meiotic chromosome synapsis in Arabidopsis thaliana. *J Cell Sci*, **114**(23): 4207-17.

Armstrong, and Jones, G.H. (2001). Female meiosis in wild-type Arabidopsis thaliana and in two meiotic mutants. *Sexual Plant Reproduction*, **13:** 177-183.

Armstrong, S.J. Caryl, A.P., Jones, G.H. and Franklin, F.C.H. (2002). Asy1, a protein required for meiotic chromosome synapsis, localizes to axis-associated chromatin in Arabidopsis and Brassica, *Journal Of Cell Science*, **115**: 3645-3655.

Armstrong, S.J., Franklin, F.C.H. and Jones, G.H. (2003), A meiotic time-course for Arabidopsis thaliana. *Sex. Plant Reprod*, 16: 141-149.

Baker, C.L., Kajita, S., Walker, M., Saxl, R.L., Raghupathy, N., Choi, K., Petkov, P.M., and Paigen, K. (2014). PRDM9 Drives Evolutionary Erosion of Hotspots in *Mus musculus* through Haplotype-Specific Initiation of Meiotic Recombination. *PLoS Genet*, **11**(1): e1004916.

Barakat, A., Matassi, G. and Bernardi, G. (1998). Distribution of genes in the genome of Arabidopsis thaliana and its implications for the genome organization of plants. *Proc Natl Acad Sci USA*, **95**: 10044-10049.

Barakate, A., Higgins, J.D., Vivera, S., Stephens, J., Perry, R.M., Ramsay, L., Colas, I., Oakey, H., Waugh, R., Franklin, F.C,, Armstrong, S.J. and Halpin, C. (2014). The synaptonemal complex protein ZYP1 is required for imposition of meiotic crossovers in barley. *Plant Cell*, **26**(2): 729-40.

Bass, H.W., Riera-Lizarazu, O., Ananiev, E.V., Bordoli, S.J., Rines, H.W., Phillips, R.L., Sedat, J.W., Agard D.A. and Cande, W.Z. (2000). Evidence for the coincident initiation of homolog pairing and synapsis during the telomere-clustering (bouquet) stage of meiotic prophase. *J Cell Sci*, **113**(6): 1033-42.

Bass, H.W. (2003). Telomere dynamics unique to meiotic prophase: formation and significance of the bouquet. *Cell Mol Life Sci*, **60**: 2319-2324.

Bass, H.W., Bordoli, S.J. and Foss, E.M. (2003). The desynaptic (dy) and desynaptic1 (dsy1) mutations in maize (Zea mays L) cause distinct telomere misplacement phenotypes during meiotic prophase. *J Exp Bot*, **54**: 39-46.

Bastin-Shanower, S.A., Frickem W,M,, Mullen, J.R. and Brill, S.J. (2003). The mechanism of Mus81-Mms4 cleavage site selection distinguishes it from the homologous endonuclease Rad1-Rad10. *Molecular and Cellular Biology*, **23**: 3487-3496.

Becker, J. and Heun, M. (1995). Barley microsatellites: allele variation and mapping. *Plant Mol Biol*, **27**(4):835-845.

Benn, H. (2009). House of Commons Environment, Food and Rural Affairs Committee Securing Food Supplies up to 2050: The Challenges Faced by the UK. Q254. Fourth Report of Session 2008e09, vol. II.

Bennett, M.D., Chapman. V. and Riley, R. (1971). The duration of meiosis in pollen mother cells of wheat, rye and Triticale. *Proc R Soc London Ser B*, **178**: 259-275.

Bennett, M.D. and Smith, J.B. (1976). Nuclear DNA amounts in angiosperms. *Philos Trans R Soc Lond B Biol Sci*, **274**(933): 227-274.

Bertrand, C., Bergounioux, C., Domenichini, S., Delarue, M. and Zhou, D.X. (2003). Arabidopsis histone acetyltransferase AtGCN5 regulates the floral meristem activity through the WUSCHEL/AGAMOUS pathway. *J Biol Chem*, **278**: 28246-28251.

Bione, N.C., Pagliarini, M.S. and De, Almeida, L.A. (2002). A new and distinctive male-sterile, female-fertile desynaptic mutant in soybean (Glycine max). *Hereditas*, **136**(2): 97-103.

Bishop, D.K., Park, D., Xu, L.Z. and Kleckner, N. (1992). DMC1-a meiosis-specific yeast homolog of *Escherichia coli* recA required for recombination, synaptonemal complex-formation, and cell-cycle progression. *Cell*, **69**: 439-456.

Blackburn, E.H. (1992). Telomerases. *Annu Rev Biochem*, **61**: 113-129.

Blumenstiel, J.P., Noll, A.C., Griffiths, J.A., Perera, A.G., Walton, K.N., Gilliland, W,D., Hawley, R.S. and Staehling-Hampton, K. (2009). Identification of EMS-induced mutations in Drosophila melanogaster by whole-genome sequencing. *Genetics*, **182**: 25-32.

Bleuyard, J.Y., Gallego, M.E. and White, C.I. (2004). Meiotic defects in the Arabidopsis rad50 mutant point to conservation of the Mrx complex function in early stages of meiotic recombination. *Chromosoma*, **113**: 197-203.

Bleuyard, J.Y., Gallego, M.E., Savigny, F. and White, C.I. (2005). Differing requirements for the *Arabidopsis* Rad51 paralogs in meiosis and DNA repair. *Plant Journal*, **41**: 533-545.

Borde, V., Robine, N., Lin, W., Bonfils, S., Geli, V. and Nicolas, A. (2009). Histone H3 lysine 4 trimethylation marks meiotic recombination initiation sites. *EMBO Journal*, **28**: 99-111.

Boerner, G.V., Kleckner, N., Hunter, N. (2004). Crossover/noncrossover differentiation, synaptonemal complex formation, and regulatory surveillance at the leptotene/zygotene transition of meiosis, *Cell*, **117**: 29-4.

Borner, G.V., Barot, A. and Kleckner, N. (2008). Yeast Pch2 promotes domainal axis organization, timely recombination progression, and arrest of defective recombinosomes during meiosis. *Proc Natl Acad Sci USA*, **105**: 3327-3332.

Britten, R.J. (1986). Rates of DNA sequence evolution differ between taxonomic groups. *Science*, **231**: 1393-1398.

Brown, A.H.D., Lawrence, G.J., Jenkin, M., Douglass, J. and Gregory, E. (1989). Linkage Drag in Backcross Breeding in Barley. *Journal of Heredity*, **80**: 234-239.

Brown, A.H.D. (1992). Genetic variation and resources in cultivated barley and world Hordeum. *Barley Genet*, **6**: 669-682.

Buard, J., Barthes, P., Grey, C. and de Massy, B. (2009). Distinct histone modifications define initiation and repair of meiotic recombination in the mouse. *EMBO Journal*, **28**: 2616-2624.

Buhler, C., Borde, V., Lichten, M. (2007). Mapping meiotic single-strand DNA reveals a new landscape of DNA double-strand breaks in Saccharomyces cerevisiae. *PLoS biology*. **59**(12): e324.

Burnham, C. R. (1946). A gene for "long"chromosomes in barley. *Genet*, **31**: 212-213.

Calisto, V., Fuzinatto, V.A., Message, H.J., Mendes-Bonato, A.B., Boldrini, K.R., Pagliarini, M.S. and do Valle, C.B. (2008). Desynapsis and precocious cytokinesis in *Brachiaria humidicola* (Poaceae) compromise meiotic division. *J Genet*, **87**: 27-31.

Cameron, D. (2008). David Cameron's Speech at NFU Centenary Conference, February 2008 Available at. http://www.fwi.co.uk/blogs/farming-news-blog/2008/02/david-camerons-speech-at-nfu-c.html.

Cao, L., Alani, E. and Kleckner, N. (1990). A pathway for generation and processing of double-strand breaks during meiotic recombination in S. cerevisiae. *Cell*, **61:** 1089-1101.

Carels, N., Barakat, A. and Bernardi, G. (1995). The gene distribution of the maize genome. *Proc Natl Acad Sci USA*, **92**: 11057-11060.

Carney, J.P., Maser, R.S., Olivares, H., Davis, E.M., Le Beau, M., Yates, J.R. III, Hays, L., Morgan, W.F. and Petrini, J.H. (1998). The hMre11/hRad50 protein complex and Nijmegen breakage syndrome: linkage of double-strand break repair to the cellular DNA damage response. *Cell*, **93:** 477-486.

Carpenter, A.T.C. (1975). Electron microscopy of meiosis in Drosophila melanogaster females. II. The recombination nodule–a recombination-associated structure at pachytene? *Proc Natl Acad Sci USA*, **72**: 3186-3189.

Cassman, K. G. (1999). Ecological intensification of cereal production systems: Yield potential, soil quality, and precision agriculture. *Proc Natl Acad Sci USA*, **96**: 5952.

Ceccarelli, S., Grando, S., Bailey, E., Amri, A., El-Felah, M., Nassif, F., Rezgui, S. and Yahyaoui, A. (2001). Farmer participation in barley breeding in Syria, Morocco and Tunisia, *Euphytica*, **122:** 521-536.

Calderón Mdel, C., Rey, M.D., Cabrera, A. and Prieto P. (2014). The subtelomeric region is important for chromosome recognition and pairing during meiosis. *Sci Rep*, **4**: 6488. Epub. doi: 10.1038/srep06488.

Caldwell DG, McCallum N, Shaw P, Muehlbauer GJ, Marshall DF, Waugh R. (2004). A structured mutant population for forward and reverse genetics in Barley (Hordeum vulgare L.). *Plant J*, **40**: 143-150.

Carlton, P.M. and Cande, W.Z. (2002b). Telomeres act autonomously in maize to organize the meiotic bouquet from a semipolarized chromosome orientation. *J Cell Biol*, **157**(2): 231-242.

Caryl, A.P., Armstrong, S.J., Jones, G.H. and Franklin, F.C. (2000). A homologue of the yeast HOP1 gene is inactivated in the Arabidopsis meiotic mutant asy1, *Chromosoma*, **109**(1-2): 62-71.

Cesarini, E., D'Alfonso, A. and Camilloni, G. (2012). H4K16 acetylation affects recombination and ncRNA transcription at rDNA in Saccharomyces cerevisiae. *Mol Biol Cell*, **23**(14): 2770-2781.

Chandley, A.C. and Bateman, A.J. (1962). Timing of spermatogenesis in Drosophila melanogaster using tritiated thymidine. *Nature*, **193**: 299-300.

Chang, T.T. (1992). Availability of plant germplasm for use in crop improvement. Pages 17-35 in H. T. Stalker and J. P. Murphy, eds. *Plant breeding in the 1990s*. CAB, International, Wallingford, UK.

Chao, S., Sharp, P.J., Worland, A.J., Warham, E.J., Koebner, R.M.D. and Gale, M.D. (1989). RFLP-based genetic maps of the wheat homoeologous group 7 chromosomes. *Theor Appl Gen*, **78**: 495-504.

Che, L., Tang, D., Wang, K., Wang, M., Zhu, K., Yu, H., Gu, M. and Cheng, Z. (2011). OsAM1 is required for leptotene-zygotene transition in rice. *Cell Res*, **21**(4): 654-65.

Chelysheva, L., Gendrot, G., Vezon, D., Doutriaux, M.P., Mercier, R. and Grelon, M. (2007). Zip4/Spo22 is required for class I CO formation but not for synapsis completion in Arabidopsis thaliana. *PLoS Genetics*, **3**: 802-813.

Chen, C.B., Zhang, W., Timofejeva, L., Gerardin, Y. and Ma, H. (2005). The Arabidopsis ROCK-n-ROLLERS gene encodes a homolog of the yeast Atp-dependent DNA helicase Mer3 and is required for normal meiotic crossover formation. *Plant Journal*, **43**: 321-334.

Chicheportiche, A., Bernardino-Sgherri, J., de Massy, B. and Dutrillaux, B. (2007). Characterization of Spo11-dependent and independent phospho-H2AX foci during meiotic prophase I in the male mouse. *J Cell Sci*, **120**: 1733-1742.

Chikashige, Y., Ding, D.Q,, Funabiki, H., Haraguchi, T., Mashiko, S., Yanagida, M. and Hiraoka, Y. (1994) Telomere-led premeiotic chromosome movement in fission yeast. *Science*, **264:** 270-273.

Chong, L., Chong, L., van Steensel, B., Broccoli, D., Erdjument-Bromage, H., Hanish, J., Tempst, P., and de Lange, T. (1995). A human telomeric protein. *Science*, **270**: 1663-1667.

Colas, I., Shaw, P., Prieto, P., Wanous, M., Spielmeyer, W., Mago, R., and Moore, G. (2008). Effective chromosome pairing requires chromatin remodeling at the onset of meiosis. *Proc Natl Acad Sci USA*, **105**: 6075-6080.

Cole, F., Keeney, S. and Jasin, M. (2010). Evolutionary conservation of meiotic DSB proteins: more than just Spo11. *Genes & Development*, **24**: 1201-1207.

Collins, K. (1999). Ciliate telomerase biochemistry. *Annu Rev Biochem*, **68:** 187-218.

Comadran, J., Kilian, B., Russell, J.R., Ramsay, L., Stein, N., Ganal, M., Shaw, P., Bayer, M., Thomas, W.T.B., Marshall, D.F., Hedley, P.E., Tondelli, A., Pecchioni, N., Francia, E., Korzun, V., Walther, A. and Waugh, R. (2012). Natural variation in a homolog of *Antirrhinum CENTRORADIALIS* contributed to spring growth habit and environmental adaptation in cultivated barley. *Nature Genetics*, 44: 1388-1392.

Conrad, M.N., Lee, C.Y., Wilkerson, J.L. and Dresser, M.E. (2007). MPS3 mediates meiotic bouquet formation in Saccharomyces cerevisiae. *Proc Natl Acad Sci USA*, **104**: 8863-8868.

Conrad, M.N., Lee, C.Y., Chao, G., Shinohara, M., Kosaka, H., Shinohara, A., Conchello, J.A. and Dresser, M.E. (2008). Rapid telomere movement in meiotic prophase is promoted by NDJ1, MPS3 and CSM4 and is modulated by recombination. *Cell*, **133**: 1175-1187.

Copenhaver, G.P., Nickel, K., Kuromori, T., Benito, M.I., Kaul, S., Lin, X., Bevan, M., Murphy, G., Harris, B., Parnell, L.D., McCombie, W.R., Martienssen, R.A., Marra, M. and Preuss, D. (1999). Genetic definition and sequence analysis of Arabidopsis centromeres. *Science*, **286**: 2468-2474.

Copenhaver, G.P. and Preuss, D. (1999). Centromeres in the genomic era: unraveling paradoxes. *Curr Opin Plant Biol*, **2**: 104-108.

Corredor, E., and Naranjo, T. (2007). Effect of colchicine and telocentric chromosome conformation on centromere and telomere dynamics at meiotic prophase I in wheat-rye additions. *Chromosome Res*, **15:** 231-245.

Couteau F, Belzile F, Horlow C, Grandjean O, Vezon D, Doutriaux MP. (1999). Random chromosome segregation without meiotic arrest in both male and female meiocytes of a dmc1 mutant of Arabidopsis. *Plant Cell*, **11**: 1623-1634.

Cowan CR., P.M. Carlton and W.Z. Cande. (2001). The polar arrangement of telomeres in interphase and meiosis. Rabl organization and the bouquet. *Plant Physiol*, **125**(2): 532-8.

Cowan, C.R. and Cande, W.Z. (2002). Meiotic telomere clustering is inhibited by colchicine but does not require cytoplasmic microtubules. *J Cell Sci*, **115**: 3747-756.

Cowan, C.R., Carlton, P.M. and Cande, W.Z. (2002). Reorganization and polarization of the meiotic bouquet-stage cell can be uncoupled from telomere clustering. *J Cell Sci*, **115**: 3757-66.

Crawford, A.M., Dodds, K.G., Ede, A.J., Pierson, C.A., Montgomery, G.W., Garmonsway, H.G., Beattie, A.E., Davies, K., Maddox, J.F., Kappes, S.W., Stone, R.T., Nguyen, T.C., Penty, J.M., Lord, E.A., Broom, J.E., Buitkamp, J., Schwaiger, W., Epplen, J.T., Matthew, P., Matthews, M.E., Hulme, D.J., Beh, K.J., McGraw, R.A. and Beattie, C.W. (1995). An autosomal genetic linkage map of the sheep genome. *Genetics*, **140**: 703-724.

Curtis, C.A. and Lukaszewski, A.J. (1991). Genetic linkage between C-bands and storage protein genes in chromosome 1B of tetraploid wheat. *Theor Appl Genet*, **81**: 245-252.

Daoudal-Cotterell, S., Gallego, M.E. and White, C.I. (2002). The plant Rad50–Mre11 protein complex. *Febs Letters*, **516**: 164-166.

Darlington C.D. (1937). Meiosis in diploids and polypoids. In: *Recent Advances in Cytology*, pp. 85–134. Darlington C. D. (ed.), Churchill, London.

Darlington, C.D. (1958). The evolutionof genetic systems. *2nd edition*, Basic books: New York.

Dayani, Y., Simchen, G. and Lichten, M. (2011). Meiotic Recombination Intermediates Are Resolved with Minimal Crossover Formation during Return-to-Growth, an Analogue of the Mitotic Cell Cycle. *PLoS Genet.* **7**: e1002083.

de Lange, T. (2005). Shelterin: the protein complex that shapes and safeguards human telomeres. *Genes Dev*, **19**: 2100-2110.

de los Santos, T., Hunter, N., Lee, C., Larkin, B., Loidl, J., and Hollingsworth, N.M. (2003). The Mus81/Mms4 endonuclease acts independently of double-Holliday junction resolution to promote a distinct subset of crossovers during meiosis in budding yeast. *Genetics*, **164:** 81-94.

de Jager, M., van Noort, J., van Gent, D.C., Dekker, C., Kanaar, R. and Wyman, C. (2001). Human Rad50/Mre11 is a flexible complex that can tether DNA ends. *Mol Cell*, **8:** 1129-1135.

Dernberg, A.F. (1995). Cytology of telomeres. *Cold harbour spring laboratory press*, 295-337.

Desai-Mehta, A., Cerosaletti, K.M. and Concannon, P. (2001). Distinct functional domains of nibrin mediate Mre11 binding, focus formation, and nuclear localization, *Mol. Cell Biol*., **21:** 2184-2191.

Devaux, P., Kilian, A. and Kleinhofs, A. (1995). Comparative mapping of the barley genome with male and female recombination-derived, doubled haploid populations. *Mol Gen Genet*, **249**: 600-608.

Devos, K.M., Chao, S., Li, Q.Y., Simonetti, M.C. and Gale, M.D. (1994) Relationship between chromosome 9 of maize and wheat homeologous group 7 chromosomes. *Genetics*, **138**: 1287-1292.

Dion, E., Li, L.L., Jean, M. and Beizile, F. (2007). An Arabidopsis mlh1 mutant exhibits reproductive defects and reveals a dual role for this gene in mitotic recombination. *Plant Journal*, **51**: 431-440.

Dong, H. and Roeder, G.S. (2000). Organization of the yeast Zip1 protein within the central region of the synaptonemal complex. *J Cell Biol*, **148**: 417-426.

Donis-Keller, H., Green, P., Helms, C., Cartinhour, S., Weiffenbach, B., Stephens, K., Keith, T.P., Bowden, D.W., Smith, D.R., Lander, E.S., Botstein, D., Akots, G., Rediker, K.S., Gravius, T., Brown, V.A., Rising, M.B., Parker, C., Powers, J.A., Watt, D.E., Kauffman, E.R., Bricker, A., Phipps, P., Muller-Kahle, H., Fulton, T.R., Ng, S., Schumm, J.W., Braman, J.C., Knowlton, R.G., Barker, D.F., Crooks, S.M., Lincoln, S.E., Daly, M.J. and Abrahamson, J. (1987). A genetic linkage map of the human genome. *Cell*, **51**: 319-337.

Drouaud, J., Mercier, R., Chelysheva, L., Bérard, A., Falque, M., Martin, O., Zanni, V., Brunel, D. and Mézard, C. (2007). Sex-specific crossover distributions and variations in interference level along Arabidopsis thaliana chromosome 4. *PLoS Genet,* **3**:e106. doi: 10.1371/journal.pgen.0030106.

Dutcher, S.K. (2001). The tubulin fraternity: alpha to eta. *Curr Opin Cell Biol*, **13**: 49-54.

Dover, G.A. and Riley, F.R.S. (1973). The effect of spindle inhibitors applied before meiosis on meiotic chromosome pairing. *J Cell Sci*, **12**: 143-161.

Dover, G.A. and Riley, F.R.S. (1977). Inferences from genetical evidence on the course of meiotic chromosome pairing in plants. *Phil Trans R Soc Lond B*, **277**: 313-326.

Druka, A., Franckowiak, J., Lundqvist, U., Bonar, N., Alexander, J., Houston, K., Radovic, S., Shahinnia, F., Vendramin, V., Morgante, M., Stein, N. and Waugh, R. (2011). Genetic Dissection of Barley Morphology and Development. *Plant Physiol*, **155**(2): 617-627.

Dubcovsky, J., Luo, M.C., Zhong, G.Y., Bransteitter, R., Desai, A., Kilian, A., Kleinhofs, A. and Dvorák, J. (1996). Genetic map of diploid wheat, Triticum monococcum L., and its comparison with maps of Hordeum vulgare L. *Genetics*, **143**(2): 983-999.

Dyck, P. L. and Rajhathy, T. (1965). A desynaptic mutant in Avena strigosa. *Can J Genet Cytol*, **7**: 418-421.

Edelmann, W., Cohen, P.E., Kane, M., Lau, K., Morrow, B., Bennett, S., Umar, A., Kunkel, T., Cattoretti, G., Chaganti, R., Pollard, J.W., Kolodner, R.D. and Kucherlapati, R. (1996). Meiotic pachytene arrest in MLH1-deficient mice. *Cell*, **85**: 1125-1134.

Erayman, M., Sandhu, D., Sidhu, D., Dilbirligi, M., Baenziger, P.S. and Gill, K.S. (2004). Demarcating the gene-rich regions of the wheat genome. *Nucleic Acids Res*, **32**: 3546-3565.

Erickson DL, Smith BD, Clarke AC, Sandweiss DH, Tuross N (2005). An Asian origin for a 10,000-year-old domesticated plant in the Americas. *Proc Natl Acad Sci USA*, **102**(51): 18315-20.

Esch, E. and Weber, E. (2002). Investigation of crossover interference in barley (Hordeum vulgare L.) using the coefficient of coincidence. *Theor Appl Genet*, **104**(5): 786-796.

Fajkus, J., Kovarik, A., Kralovics, R., and Bezdek, M. (1995). Organization of telomeric and subtelomeric chromatin in the higher plant Nicotiana tabacum. *Mol Gen Genet*, **247:** 633-638.

FAO (2009). How to Feed the World in 2050, Paper Prepared for the High Level Expert Forum. Rome 12e19 October 2009. Available at. http://www.fao.org/ fileadmin/templates/wsfs/docs/expert_paper/How_to_Feed_the_World_in_ 2050.pdf.

Fasching, C.L., Cejka, P., Kowalczykowski, S.C. and Heyer, W.D. (2015). Top3-rmi1 dissolve rad51-mediated d loops by a topoisomerase-based mechanism. Mol Cell, **57**(4): 595-606.

Fawcett, D.W. (1956). The fine structure of chromosomes in the meiotic prophase of vertebrate spermatocytes. *J Cell Biol*, **2**: 403-406.

Ferdous, M., Higgins, J.D., Osman, K., Lambing, C., Roitinger, E., Mechtler, K., Armstrong, S.J., Perry, R., Pradillo, M., Cuñado, N. and Franklin, F.C. (2012). Inter-homolog crossing-over and synapsis in Arabidopsis meiosis are dependent on the chromosome axis protein AtASY3. *PLoS Genet*, **8**(2): e1002507

Flavell, R. B., Bennett, M. D., Smith, J. B. and Smith, D. B. (1974). Genome size and the proportion of repeated nucleotide sequence DNA in plants. *Biochem Gene*, **12**: 257-269.

Flavell, R. B., Gale, M. D., O'Dell, M., Murphy, G. and Moore, G. (1993). Molecular organisation of genes and repeats in the large cereal genomes and implications for the isolation of genes by chromosome walking. *Chromosomes Today*, **11**: 199-213.

Fleury, D., Luo, M.C., Dvorak, J., Ramsay, L., Gill, B.S., Anderson, O.D., You, F.M,, Schoaei, Z., Deal, K.R. and Langridge, P. (2010). Physical mapping of a large plant genome using global high-information-content-fingerprinting: the distal region of the wheat ancestor Aegilops tauschii chromosome 3DS. *BMC Genomics*, **11**: 382. doi: 10.1186/1471-2164-11-382.

Franklin, F.C.H, Higgins, J.D., Sanchez-Moran, E., Armstrong, S.J., Osman, K.E., Jackson, N and Jones, G.H. (2006). Control of meiotic recombination in Arabidopsis: role of the MutL and MutS homologues. *Biochemical Society Transactions*, **34**: 542-544.

Fitzgerald, M.S., Riha, K., Gao, F., Ren, S., McKnight, T.D., and Shippen, D.E. (1999). Disruption of the telomerase catalytic subunit gene from Arabidopsis inactivates telomerase and leads to a slow loss of telomeric DNA. *Proc Natl Acad Sci USA,* **96:** 14813-14818.

Forstemann, K. and Lingner, J. (2001). Molecular basis for telomere repeat divergence in budding yeast. *Mol Cell Biol*, **21**: 7277-7286.

Franckowiak, J.D., Foster, A.E., Pederson, V.D. and Pyler, R.E. (1985). Registration of 'Bowman' barley. *Crop Sci*, **25**: 883.

Fuchs, J., Brandes, A. and Schubert, I. (1995). Telomere sequence localization and karyotype evolution in higher plants. *Plant Syst Evol*, **196:** 227-241.

Gaillard, P.H., Noguchi, E., Shanahan, P. and Russell, P. (2003). The endogenous Mus81-Eme1 complex resolves Holliday junctions by a nick and counter-nick mechanism. *Mol Cell*, **12**:747-759.

Gaut, B. S., S. I. Wright, C. Rizzon, J. Dvorak and Anderson, L. K. (2007). Recombination: an underappreciated factor in the evolution of plant genomes. *Nat Rev Genet*, **8**: 77-84.

Gerton, J.L. and Hawley, R.S. (2005). Homologous chromosome interactions in meiosis: diversity amidst conservation. *Nat Rev Genet*, **6**(6): 477-87.

Ghabrial, A. and Schupbach, T. (1999). Activation of a meiotic checkpoint regulates translation of Gurken during Drosophila oogenesis. *Nat Cell Biol*, **1**: 354-357.

Godfray, H., Beddington, J.R., Crute, I.R., Haddad, L., Lawrence., Muir., Pretty, J., Robinson, S., Thomas, S., Toulmin, C. (2010). Food security: the challenge of feeding 9 billion people. *Science*, **327**(5967): 812-818.

Golubovskaya, I.N., Wang, C.J., Timofejeva, L. and Cande, W.Z. (2011). Maize meiotic mutants with improper or non-homologous synapsis due to problems in pairing or synaptonemal complex formation. *J Exp Bot*, **62**(5): 1533-44.

Goodman, M.M. (1985). Exotic maize germplasm: status, prospects, and remedies. *Iowa State J Res*, **59**(4): 497-527.

Gottschalk, W., and R. Villalobos-Pietrini (1965).The influenceof mutant geneson chiasmata formation in Pisum sativum. *Cytologia*, **30**: 88-97.

Grandin, N., Damon, C. and Charbonneau, M. (2001). Cdc13 prevents telomere uncapping and Rad50-dependent homologous recombination. *EMBO J*, 20**:** 6127-6139.

Grant, P.A., Duggan, L., Côté, J., Roberts, S.M., Brownell, J.E., Candau, R., Ohba, R., Owen-Hughes, T., Allis, C.D., Winston, F., Berger, S.L. and Workman, J.L. (1997). Yeast Gcn5 functions in two multisubunit complexes to acetylate nucleosomal histones: characterization of an Ada complex and the SAGA (Spt/Ada) complex. *Genes Dev*, **11**: 1640-1650.

Greer, E., Martin, A.C., Pendle, A., Colas, I., Jones, A.M., Moore, G. and Shaw, P. (2012). The Ph1 Locus Suppresses Cdk2-Type Activity during Premeiosis & Meiosis in Wheat. *The Plant Cell*, **24**(1): 152-162.

Greider, C.W., and Blackburn, E.H. (1985). Identification of a specific telomere terminal transferase activity in Tetrahymena extracts. *Cell*, **43:** 405-413.

Greider, C.W., and Blackburn, E.H. (1987). The telomere terminal transferase of Tetrahymena is a ribonucleoprotein enzyme with two kinds of primer specificity. Cell, **51:** 887-898.

Greider, C.W., and Blackburn, E.H. (1989). A telomeric sequence in the RNA of Tetrahymena telomerase required for telomere repeat synthesis. *Nature*, **337:** 331-337.

Grelon, M., Vezon, D., Gendrot, G. and Pelletier, G. (2001). AtSPO11-1 is necessary for efficient meiotic recombination in plants. *EMBO Journal*, **20**: 589-600.

Grewal, S.I., Bonaduce. M.J. and Klar, A.J. (1998). Histone deacetylase homologs regulate epigenetic inheritance of transcriptional silencing and chromosome segregation in fission yeast. *Genetics*, **150**: 563-576.

Griffith, J.D., Comeau, L., Rosenfield, S., Stansel, R.M., Bianchi, A., Moss, H. and de Lange, T. (1999). Mammalian telomeres end in a large duplex loop. *Cell*, **97**: 503-514.

Griffiths, S., Sharp, R., Foote, T.N., Bertin, I., Wanous, M., Reader, S., Colas, I. and Moore, G. (2006). Molecular characterization of Ph1 as a major chromosome pairing locus in polyploid wheat. *Nature*, **439:** 749-752.

Hartung, F. and Puchta, H. (2000). Molecular characterisation of two paralogous Spo11 homologues in *Arabidopsis thaliana*. *Nucleic Acids Research*, **28**: 1548-1554.

Hartung, F. and Puchta, H. (2001). Molecular characterization of homologues of both subunits A (SPO11) and B of the archaebacterial topoisomerase 6 in plants. *Gene*, **271**(1): 81-6.

Hartung, F., Angelis, K.J., Meister, A., Schubert, I., Melzer, M., and Puchta, H. (2002). An archaebacterial topoisomerase homolog not present in other eukaryotes is indispensable for cell proliferation of plants. *Curr Biol*, **12:** 1787-1791.

Hartung F, Wurz-Wildersinn R, Fuchs J, Schubert I, Suer S, Puchta H. (2007). The catalytically active tyrosine residues of both SPO11-1 and SPO11-2 are required for meiotic double-strand break induction in Arabidopsis. *Plant Cell*, **19**: 3090-3099.

Haruta N, Kurokawa Y, Murayama Y, Akamatsu Y, Unzai S, Tsutsui Y, Iwasaki H. (2006). The Swi5–Sfr1 complex stimulates Rhp51/Rad51- and Dmc1-mediated DNA strand exchange in vitro. *Nature Structural & Molecular Biology*, **13**: 823-830.

Heller, C.G. and Clermont, Y. (1963). Spermatogenesis in man: an estimate of its duration. *Science*, **140**: 184-186.

Heller-Uszynska, K., Schnippenkoetter, W., and Kilian, A. (2002). Cloning and characterization of rice (Oryza sativa L) telomerase reverse transcriptase, which reveals complex splicing patterns. *Plant J*, **31:** 75-86.

Hernandez-Soriano, M. (1973). Desynaptic mutants in Betzes barley. *MSc thesis*. The University Of Arizona.

Higgins, J.D., Sanchez-Moranm E., Armstrongm S.J., Jones, G.H. and Franklin, F.C.H. (2005). The Arabidopsis synaptonemal complex protein ZYP1 is required for chromosome synapsis and normal fidelity of crossing over. *Genes dev*, **19**: 2488-2500.

Higgins, J.D., Vignard, J., Mercier, R., Pugh, A.G., Franklin, F.C. and Jones, G.H. (2008). AtMSH5 partners AtMSH4 in the class I meiotic crossover pathway in Arabidopsis thaliana, but is not required for synapsis. *Plant J*, **55**(1): 28-39.

Higgins, J.D., Perry, R.M., Barakate, A., Ramsay, L., Waugh, R., Halpin, C., Armstrong, S.J. and Franklin, F.C.H. (2012). Spatiotemporal asymmetry of the meiotic program underlies the predominantly distal distribution of meiotic crossovers in barley. *The Plant Cell*, **24**: 4096-4109.

Higgins, J.D. (2013). Analyzing meiosis in barley. *Methods Mol Biol*, **990**: 135-44.

Hillers, K.J. and Villeneuve, A.M. (2003). Chromosome-Wide Control of Meiotic Crossing over in C. elegans. *Current biology*, **13**: 1641-1647.

Hillers, K.J. (2004). Crossover interference. *Curr Biol*, **14:** 1036-1037.

Hillman, G., Hedges, R., Moore, A., Colledge, S. and Pettitt, P. (2001). New evidence of late glacial cereal cultivation at Abu Hureyra on the Euphrates. *Holocene*, **11**(4): 383-393.

Hiraoka, Y., Henderson, E. and Blackburn, E.H. (1998). Not so peculiar: fission yeast telomere repeats. *Trends Biochem Sci*, **23**: 126.

Hockett, L.E.A. and Eslick, R.F. (1969). Spontaneous frequencies of genetic and other sterilities in barley, Hordeum vulgare L. *Crop Sci*, **9**: 23-24.

Hollingshead, L. (1930). Cytological study of haploid Crepis capillaris plants. *Univ Calif Pub Agr Sci*, **6**: 107-134.

Hollingsworth, N.M., Goetsch, L. and Byers, B. (1990). The *HOP1* gene encodes a meiosis-specific component of yeast chromosomes. *Cell*, **61**: 73-84.

Hollingsworth, N.M., Ponte, L. and Halsey, C. (1995). MSH5, a novel MutS homolog, facilitates meiotic reciprocal recombination between homologs in Saccharomyces cerevisiae but not mismatch repair. *Genes Dev*, **9:** 1728-1739.

Hollingsworth, N. M. and Ponte, L. (1997). Genetic interactions between HOP1, RED1 and MEK1 suggest that MEK1 regulates assembly of axial element components during meiosis in the yeast, *Saccharomyces cerevisiae*. *Genetics*, **147**: 33-42.

Holm, P.B. (1986). Chromosome pairing and chiasma formation in allohexaploid wheat, Triticum aestivum, analyzed by spreading of meiotic nuclei. *Carlsberg Res Commun*, **51**: 239-294.

Hopfner, K.P., Karcher, A., Craig, L., Woo, T.T., Carney, J.P. and Tainer, J.A. (2001). Structural biochemistry and interaction architecture of the DNA double-strand break repair Mre11 nuclease and Rad50-ATPase. *Cell*, **105**: 473-485.

Horvath, M. P., Schweiker, V. L., Bevilacqua, J. M., Ruggles, J. A. and Schultz, S. C. (1998). Crystal structure of the Oxytricha nova telomere end binding protein complexed with single strand DNA. *Cell*, **95**(7): 963-74.

Hoshikawa, Y., Kwon, H. J., Yoshida, M., Horinouchi, S. and Beppu, T. (1994). Trichostatin A induces morphological changes and gelsolin expression by inhibiting histone deacetylase in human carcinoma cell lines. *Exp Cell Res*, **214**: 189-197.

Houghtaling, B.R., Cuttonaro, L., Chang, W., and Smith, S. (2004). A dynamic molecular link between the telomere length regulator TRF1 and the chromosome end protector TRF2. *Curr Biol*, **14**: 1621-1631.

Hunter, N. and Borts, R.H. (1997). Mlh1 is unique among mismatch repair proteins in its ability to promote crossing-over during meiosis. *Genes Dev*, **11**: 1573-1582.

Hunter, N. and Kleckner, N. (2001). The single-end invasion: a symmetric intermediate at the double-strand break to double-Holliday junction transition of meiotic recombination. *Cell*, **106**: 59-70.

Inokoshi, J., Katagiri, M., Arima, S., Tanaka, H., Hayashi, M., Kim, Y. B., Furumai, R., Yoshida, M., Horinouchi, S. and Omura, S. (1999). Neuronal differentiation of neuro 2a cells by inhibitors of cell cycle progression, trichostatin A and butyrolactone I. *Biochem Biophys Res Commun*, **256**: 372-376.

Ip, S.C., Rass, U., Blanco, M.G., Flynn, H.R., Skehel, J.M. and West, S.C. (2008). Identification of Holliday junction resolvases from humans and yeast. *Nature*, **456**: 357-361.

Irvine, D.V., Goto, D.B., Vaughn, M.W., Nakaseko, Y., McCombie, W.R., Yanagida, M. and Martienssen, R. (2009). Mapping epigenetic mutations in fission yeast using whole-genome next-generation sequencing. *Genome Res*, **19**: 1077-1083.

Ishibashi, T., Kimura, S. and Sakaguchi, K. (2006). A higher plant has three different types of Rpa heterotrimeric complex. *Journal of Biochemistry*, **139**: 99-104.

Jackson, N., Sanchez-Moran, E., Buckling, E., Armstrong, S.J., Jones, G.H. and Franklin, F.C.H. (2006). Reduced meiotic crossovers and delayed prophase I progression in AtMLH3-deficient Arabidopsis. *EMBO Journal*, **25**: 1315-1323.

Jain, M., Tyagi, A.K. and Khurana, J.P. (2006). Overexpression of putative topoisomerase 6 genes from rice confers stress tolerance in transgenic *Arabidopsis* plants. *Febs Journal*, **273**: 5245-5260.

Jander, G., Norris, S.R., Rounsley, S.D., Bush, D.F., Levin, I.M. and Last, R.L. (2002). Arabidopsis map-based cloning in the post-genome era. *Plant Physiol*, **129**: 440-450.

Jenkins, G. and Okumus, A. (1992). Indiscriminate synapsis in achiasmate Allium fistulosum L. (Liliaceae). *Journal of Cell Science*, **103**: 415-422.

Jolivet, S., Vezon, D., Froger, N. and Mercier, R. (2006). Non conservation of the meiotic function of the Ski8/Rec103 homolog in Arabidopsis. *Genes to Cells*, **11**: 615-622.

Jones, G.H. (1984). The control of chiasma distribution. *Symp Soc Exp Biol*, **38**: 293-320.

Jones, G.H. and Franklin, F.C.H. (2006). Meiotic crossing-over: Obligation and interference. *Cell*, **126:** 246-248.

Kanasty, R., Dorkin, J.R., Vegas, A. and Anderson, D. (2013). Delivery materials for siRNA therapeutics. *Nat Mater*, **12**(11): 967-77.

Kannenberg, L.W. and Falk, D.E. (1995). Models for activation of plant genetic resources for crop breeding programs. *Canadian Journal of Plant Science*, **75**(1): 45-53.

Kanoh, J. and Ishikawa, F. (2003). Composition and conservation of the telomeric complex. *Cell Mol Life Sci*, **60**: 2295-2302.

Katayama T. (1964). Further review on the heritable asynapsis in plants. *La Kromosomo*, **57**(59): 1934-1942.

Kearsey, M.J., Ramsay, L.D., Jennings, D.E., Lydiate, D.J., Bohuon, E.J. and Marshall, D.F. (1996). Higher recombination frequencies in female compared to male meisoses in Brassica oleracea. *Theor Appl Genet*, **92**: 363-367.

Keeney, S. (2001). mechanism and control of meiotic recombination initiation. *Current topics in developmental biology*, **52**: 1-53.

Kelly, A.L., Sharpe, A.G., Nixon, J.H., Evans, E.J. and Lydiate, D.J. (1997). Indistinguishable patterns of recombination resulting from mate and female meioses in Brassica napus (oilseed rape). *Genome*, **40**: 49-56.

Kezer, J., Sessions, S.K. and Leon, P. (1989). The meiotic structure and behavior of the strongly heteromorphic X/Y sex chromosomes of neotropical plethodontid salamanders of the genus Oedipina. *Chromosoma*, **98:** 433-442.

Khoo, K.H., Able, A.J. and Able, J.A. (2012). The isolation and characterisation of the wheat molecular ZIPper I homologue, TaZYP1. *BMC Res Notes*, **5**:106. doi: 10.1186/1756-0500-5-106.

Kleckner, N., Zickler, D., Jones, G. H., Dekker, J., Padmore, R., Henle, J., Hutchinson, J. (2004). A mechanical basis for chromosome function. *Proc Natl Acad Sci USA*, **101**: 12592-12597.

Klimyuk, V.I. and Jones, J.D.G. (1997). *AtDMC1*, the Arabidopsis homologue of the yeast *Dmc1* gene: characterization, transposon-induced allelic variation and meiosis-associated expression. *Plant Journal*, **11**: 1-14.

Klutstein, M., Shaked, H., Sherman, A., Avivi-Ragolsky, N., Shema, E., Zenvirth, D., Levy, A.A. and Simchen, G. (2008). Functional conservation of the yeast and *Arabidopsis* Rad54-like genes. *Genetics*, **178**: 2389-2397.

Kniewel, R. and **Keeney**, S. (2009). Histone methylation sets the stage for meiotic DNA breaks. *EMBO J*, **28**(2): 81-83.

Komatsuda, T., Pourkheirandish, M., He, C., Azhaguvel, P., Kanamori, H., Perovic, D., Stein, N., Graner, A., Wicker, T., Tagiri, A., Lundqvist, U.,

Fujimura, T., Matsuoka, M., Matsumoto, T. and Yano, M. (2006). Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. *Proceedings of the National Academy of Sciences of the United States of America*, **104**(4): 1424-1429.

Koonin, E.V. (2006). The origin of introns and their role in eukaryogenesis: a compromise solution to the introns-early versus introns-late debate? *Biol Direct*, **1**(22): doi: 10.1186/1745-6150-1-22.

Krasinska, L., Besnard, E., Cot, E., Dohet, C., Méchali, M., Lemaitre, J.M. and Fisher, D. (2008). Cdk1 and Cdk2 activity levels determine the efficiency of replication origin firing in Xenopus. *EMBO J*, **27**: 758-769.

Krothapalli, K., Buescher, E.M., Li, X., Brown, E., Chapple, C., Dilkes, B.P. and Tuinstra, M.R. (2013). Forward Genetics by Genome Sequencing Reveals That Rapid Cyanide Release Deters Insect Herbivory of Sorghum bicolour. *Genetics*, **195**: 309-318.

Kumar, R., Bourbon, H.M. and de Massy, B. (2010). Functional conservation of Mei4 for meiotic DNA double-strand break formation from yeasts to mice. *Genes & Development*, **24**: 1266-1280.

Kunzel, G., Korzum, L. and Meister, A. (2000) Cytologically integrated physical restriction fragement length polymorphism maps for the barley genome based on translocation breakpoints. *Genetics*, **154**: 397-412.

Koszul, R. and Kleckner, N. (2009). Dynamic chromosome movements during meiosis: a way to eliminate unwanted connections? *Trends Cell Biol*, **19**: 716-724.

Kurata, N., Moore, G., Nagamura, Y., Foote, T., Yano, M., Minobe, Y. and Gale, M. (1994) Conservation of genome structure between rice and wheat. *Nature Biotech*, **12**: 276-278.

Lagercrantz, U. and Lydiate, D.J. (1995). Rflp mapping in Brassica nigra indicates differing recombination rates in male and female meioses. *Genome*, **38**: 255-264.

Lam, I. and Keeney, S. (2014). Mechanism and regulation of meiotic recombination initiation. *Cold Spring Harb Perspect Biol*, **7**(1): a016634. doi: 10.1101/cshperspect.a016634.

Lam, S.Y., Horn, S.R., Radford, S.J., Housworth, E.A., Stahl, F.W. and Copenhaver, G.P. (2005) Crossover interference on nucleolus organizing region-bearing chromosomes in Arabidopsis. *Genetics*, **170**: 807-812.

Libuda, D.E., Uzawa, S., Meyer, B.J. and Villeneuve, A.M. (2013). Meiotic chromosome structures constrain and respond to designation of crossover sites. *Nature*, **502**(7473): 703-6.

Lieb, J.D., Liu, X., Botstein, D. and Brown, P.O. (2001). Promoter-specific binding of Rap1 revealed by genome-wide maps of protein-DNA association. *Nat Genet*, **28**: 327-334.

Lee, E., Furukubo, T., Miyabe, T., Yamauchi, A. and Kariya, K. (1996). Involvement of histone hyperacetylation in triggering DNA fragmentation of rat thymocytes undergoing apoptosis. *FEBS Lett*, **395**: 183-187.

Lee, C.Y., Conrad, M.N. and Dresser, M.E. (2012). Meiotic chromosome pairing is promoted by telomere-led chromosome movements independent of bouquet formation. *PLoS Genet*, 8: e1002730.

Lee, J.B., Hong, J., Bonner, D.K., Poon, Z. and Hammond, P.T. (2012). Self-assembled RNA interference microsponges for efficient siRNA delivery. *Nat Mater*, **11**(4): 316-22.

Lee, J.M., Yoon, T.J. and Cho, Y.S. (2013). Recent developments in nanoparticle-based siRNA delivery for cancer therapy. *Biomed Res Int*, **2013**(782041). doi: 10.1155/2013/782041.

Lesley, M. and Frost, H.B. (1927). Mendelian inheritance of chromosome shape in Matthiola. *Genet*, **12**: 449-460.

Li, H., Ilin, S., Wang, W., Duncan, E.M., Wysocka, J., Allis, C.D. and Patel, D.J. (2006). Molecular basis for site - specific read - out of histone H3K4me3 by the BPTF PHD finger of NURF. *Nature*, **442**: 91-95.

Li, L., Dion, E., Richard, G., Domingue, O., Jean, M. and Belzile, F.J. (2009). The Arabidopsis DNA mismatch repair gene *PMS1* restricts somatic recombination between homeologous sequences. *Plant Molecular Biology*, **69**: 675-684.

Li, H.W., Pao, W.K. and Li, C.H. (1945). Desynapsis in common wheat. *Amer J Bot*, **32**: 92-101.

Li, W., Zhang, P., Fellers, J.P., Friebe, B. and Gill, B.S. (2004) Sequence composition, organization, and evolution of the core Triticeae genome. *Plant J*, **40**(4): 500-511.

Li, X.C. and Schimenti, J.C. (2007). Mouse pachytene checkpoint 2 (trip13) is required for completing meiotic recombination but not synapsis. *PLoS genetics*, **3**: 1365-1376.

Linde-Laursen, I., Ibsen, E., Von Bothmer, R. and Giese, H. (1992). Physical localization of active and inactive rRNA gene loci in Hordeum marinum ssp. gussoneanum (4x) by in situ hybridization. *Genome*, **35**: 1032-1036.

Linde-Laursen, I. and Von Bothmer, R. (2012). Connection between rod bivalents and incomplete meiotic association at NORs in Hordeum marinum Huds. *Hereditas*, **149**: 139-145.

Lindner, H., Raissig, M.T., Sailer, C., Shimosato-Asano, H., Bruggmann, R. and Grossniklaus, U. (2012). SNP-Ratio Mapping (SRM): Identifying Lethal Alleles and Mutations in Complex Genetic Backgrounds by Next-Generation Sequencing. *Genetics*, **191**(4): 1381-1386.

Lingner, J., Hughes, T.R., Shevchenko, A., Mann, M., Lundblad, V., and Cech, T.R. (1997). Reverse transcriptase motifs in the catalytic subunit of telomerase. *Science*, **276:** 561-567.

Lipkin, S.M., Wang, V., Jacoby, R., Banerjee-Basu, S., Baxevanis, A.D., Lynch, H.T., Elliott, R.M. and Collins, F.S. (2000). MLH3: a DNA mismatch repair gene associated with mammalian microsatellite instability. *Nat Genet*, **24**, 27-35.

Liu, D., O'Connor, M.S., Qin, J., and Songyang, Z. (2004). Telosome, a mammalian telomere-associated complex formed by multiple telomeric proteins. *J Biol Chem*, **279**: 51338-51342.

Iizuka, M. and Smith, M.M. (2003). Functional consequences of histone modifications. *Curr Opin Genet Dev*, **13**: 154-160.

Lukaszewski, A.J and Curtis, C.A. (1993). Physical distribution of recombination in B-genome chromosomes of tetraploid wheat. *Theor Appl Genet*, **86**: 121-127.

Loidl, J. (1989). Colchicine action at meiotic prophase revealed by SC- spreading. *Genetica*, **78**: 195 -203.

Loidl, J. (1990). The initiation of meiotic chromosome pairing: the cytological view. *Genome*, **33**: 759-778.

Loidl, J., Lukaszewicz, A., Howard-Till, R.A. and Koestler, T. (2012). The Tetrahymena meiotic chromosome bouquet is organized by centromeres and promotes interhomolog recombination. *J Cell Sci*, **125**: 5873-5880.

Luo, M.C., Deal, K.R., Akhunov, E.D., Akhunova, A.R., Anderson, O.D., Anderson, J.A., Blake, N., Clegg, M.T., Coleman-Derr, D., Conley, E.J., Crossman, C.C., Dubcovsky, J., Gill, B.S., Gu, Y.Q., Hadam, J., Heo, H.Y., Huo, N., Lazo, G., Ma, Y., Matthews, D.E., McGuire, P.E., Morrell, P.L., Qualset, C.O., Renfro, J., Tabanao, D., Talbert, L.E., Tian, C., Toleno, D.M., Warburton, M.L., You, F.M., Zhang, W. and Dvorak, J. (2009). Genome comparisons reveal a dominant mechanism of chromosome number reduction in grasses and accelerated genome evolution in Triticeae. *Proc Natl Acad Sci USA*, **106**(37): 15780-15785.

Luo, M.C., Gu, Y.Q., You, F.M., Deal, K.R., Ma, Y., Hu, Y., Huo, N., Wang, Y., Wang, J., Chen, S., Jorgensen, C.M,, Zhang, Y., McGuire, P.E., Pasternak, S., Stein, J.C., Ware, D., Kramer, M., McCombie, W.R., Kianian, S.F., Martis, M.M., Mayer, K.F., Sehgal, S.K., Li, W., Gill, B.S., Bevan, M.W., Simková, H., Dolezel, J., Weining, S., Lazo, G.R, Anderson, O.D. and Dvorak, J. (2013). A 4-gigabase physical map unlocks the structure and evolution of the complex genome of Aegilops tauschii, the wheat D-genome progenitor. *Proc Natl Acad Sci*, **119:** 7940-45.

Luo, Q., Li, Y., Shen, Y. and Cheng, Z. (2014). Ten years of gene discovery for meiotic event control in rice. *J Genet Genomics*, **41**(3): 125-37.

Lüpken, T., Stein, N., Perovic, D., Habekuss, A., Krämer, I., Hähnel, U., Steuernagel, B., Scholz, U., Zhou, R., Ariyadasa, R., Taudien, S., Platzer, M., Martis, M., Mayer, K., Friedt, W. and Ordon, F. (2013). Genomics-based high-resolution mapping of the BaMMV/BaYMV resistance gene rym11 in barley (Hordeum vulgare L.). *Theor Appl Genet*, **126**(5): 1201-12.

Lüpken, T., Stein, N., Perovic, D., Habekuss, A., Serfling, A., Krämer, I., Hähnel, U., Steuernagel, B., Scholz, U., Ariyadasa, R., Martis, M., Mayer, K., Niks, R.E., Collins, N.C., Friedt, W. and Ordon, F. (2014). High-resolution mapping of the barley Ryd3 locus controlling tolerance to BYDV, **33**(2): 477-488.

MacQueen, A.J. and Roeder, G.S. (2009). Fpr3 and Zip3 ensure that initiation of meiotic recombination precedes chromosome synapsis in budding yeast. *Current Biology*, **19**: 1519-1526.

Maguire, M.P., Paredes, A.M. and Riess, R.W. (1991). The desynaptic mutant of maize as a combined defect of synaptonemal complex and chiasma maintenance. *Genome*, **34**: 879-887.

Maguire, M.P., Riess, R.W. and Paredes, A.M. (1993). Evidence from a maize desynaptic mutant points to a probable role of synaptonemal complex central region components in provision for subsequent chiasma maintenance. *Genome*, **36**: 797-807.

Maleki, S., Neale, M.J., Arora, C., Henderson, K.A., and Keeney, S. (2007). Interactions between Mei4, Rec114, and other proteins required for meiotic DNA double-strand break formation in Saccharomyces cerevisiae. *Chromosoma*, **116:** 471-486.

Maplecroft. (2012). Food Security Index and interactive global map. https://maplecroft.com/about/news/Food_Security_Pressrelease.pdf.

Marmur, J. and Doty, P. (1959). Heterogeneity in deoxyribonucleic acids. I. Dependence on composition of the configurational stability of deoxyribonucleic acids. *Nature*, **183**(4673): 1427-1429.

Marti, T.M., Kunz, C. and Fleck, O. (2002). DNA mismatch repair and mutation avoidance pathways. *J Cell Physiol*, **191**: 28-41.

Martin, A., Shaw, P., Phillips, D., Reader, S. and Moore, G. (2014). Licensing MLH1 sites for crossover during meiosis. *Nat Commun*, **5**(4580): doi: 10.1038/ncomms5580.

Martínez-Pérez, E., Shaw, P., Reader, S., Aragón-Alcaide, L., Miller, T. and Moore, G. (1999). Homologous chromosome pairing in wheat. *J Cell Sci*, **112** (11): 1761-9.

Martinez-Perez, E., Shaw, P. and Moore, G. (2001). The Ph1 locus is needed to ensure specific somatic and meiotic centromere association. *Nature*, **411**(6834): 204-7.

Mascher, M., Jost, M., Kuon, J.E., Himmelbach, A., Aßfalg, A., Beier, S, Scholz, U., Graner, A. and Stein, N. (2014). Mapping-by-sequencing accelerates forward genetics in barley. *Genome Biol*, **15**: R78. doi: 10.1186/gb-2014-15-6-r78.

Matise, T.C., Sachidanandam, R., Clark, A.G., Kruglyak, L., Wijsman, E., Kakol, J., Buyske, S., Chui, B., Cohen, P., de Toma, C., Ehm, M., Glanowski, S., He, C., Heil, J., Markianos, K., McMullen, I., Pericak-Vance, M.A., Silbergleit, A., Stein, L., Wagner, M., Wilson, A.F., Winick, J.D., Winn-Deen, E.S., Yamashiro, C.T., Cann, H.M., Lai, E. and Holden, A.L. (2003). A 3.9-centimorgan-resolution human single-nucleotide polymorphism linkage map and screening set. *Am J Hum Genet*, **73**: 271-284.

Mayer, K.F., Taudien, S., Martis, M., Simková, H., Suchánková, P., Gundlach, H., Wicker, T., Petzold, A., Felder, M., Steuernagel, B., Scholz, U., Graner, A., Platzer, M., Dolezel, J. and Stein, N. (2009). Gene content and virtual gene order of barley chromosome 1H. *Plant Physiol*, **151***:* 496-505.

Mayer, K.F., Waugh, R., Brown, J.W., Schulman, A., Langridge, P., Platzer, M., Fincher, G.B., Muehlbauer, G.J., Sato, K., Close, T.J., Wise, R.P. and Stein, N. (2012). A physical, genetic and functional sequence assembly of the barley genome. *Nature*, **491**: 711-716.

McCormick-Graham, M., Haynes, W.J. and Romero, D.P. (1997). Variable telomeric repeat synthesis in Paramecium tetraurelia is consistent with misincorporation by telomerase. *EMBO J*, **16:** 3233-3242.

McDowell, J. M., Dhandaydham, M., Long, T. A., Aarts, M. G. M., Goff, S., Holub, E. B., and Dangl, J. L. (1998). Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis. *Plant Cell*, **10**: 1861-1874.

McEachern, M.J., Krauskopf, A., and Blackburn, E.H. (2000). Telomeres and their control. *Annu Rev Genet*, **34**: 331-358.

Mehta, A. and Haber, J.E. (2014). Sources of DNA double-strand breaks and models for recombinational DNA repair. *Cold Spring Harb Perspect Biol*, doi: 10.1101/cshperspect. a016428.

Melamed-Bessudo, C., Yehuda, E., Stuitje, A.R. and Levy, A.A. (2005) A new seed-based assay for meiotic recombination in Arabidopsis. *Plant Journal*, **43**: 458-466.

Merker, J.D., Dominska, M., Greenwell, P.W., Rinella, E., Bouck, D.C., Shibata, Y., Strahl, B.D., Mieczkowski, P. and Petes, T.D. (2008). The histone methylase Set2p and the histone deacetylase Rpd3p repress meiotic recombination at the HIS4 meiotic recombination hotspot in Saccharomyces cerevisiae. *DNA Repair (Amst)*, **7**: 1298-1308.

Meuwissen, R.L.J., Meerts, I., Hoovers, J.M.N., Leschot, N.J., and Heyting, C. (1997). Human synaptonemal complex protein 1 (SCP1): Isolation and characterization of the cDNA and chromosomal localization of the gene. *Genomics*, **39**: 377-384.

Meyne, J., Ratliff, R.L. and Moyzis, R.K. (1989) Conservation of the human telomere sequence (TTAGGG)n among vertebrates. *Proc Nat Acad Sci USA*, **86**: 7049-7053.

Meyerowitz, E. (1987). Arabidopsis thaliana. *Annu Rev Genet*, **21**: 93-111.

Mieczkowski, P.A., Dominska, M., Buck, M.J., Lieb, J.D. and Petes, T.D. (2007). Loss of a histone deacetylase dramatically alters the genomic distribution of Spo11p-catalyzed DNA breaks in Saccharomyces cerevisiae. *Proc Natl Acad Sci USA*, **104**: 3955-3960.

Mikawa, S., Akita, T., Hisamatsu, N., Inage, Y., Ito, Y., Kobayashi, E., Kusumoto, H., Matsumoto, T., Mikami, H., Minezawa, M., Miyake, M., Shimanuki, S., Sugiyama, C., Uchida, Y., Wada, Y., Yanai, S. and Yasue, H. (1999). A linkage map of 243 DNA markers in an intercross of Gottingen miniature and Meishan pigs. *Anim Genet*, **30**: 407-417.

Millar, C.B. and Grunstein, M. (2006). Genome-wide patterns of histone modifications in yeast. *Nat Rev Mol Cell Biol*, **7**: 657-666.

Miller, O.L (1963). Cytological studies in asynaptic maize. *Genet*, **48**: 1445-1466.

Mimitou, E.P. and Symington, LS. (2009). DNA end resection: many nucleases make light work. *DNA Repair: Checkpoint Response to DNA Damage*, **8**: 983-995.

Mirouze, M., Lieberman-Lazarovich, M., Aversano, R., Bucher, E., Nicolet, J., Reinders, J. and Paszkowski, J. (2012). Loss of DNA methylation affects the recombination landscape in Arabidopsis. *Proc Natl Acad Sci USA*, **109**(15): 5880-5.

Miyagawa, K., Low, R.S., Santosa, V., Tsuji, H., Moser, B.A., Fujisawa, S., Harland, J.L., Raguimova, O.N., Go, A., Ueno, M., Matsuyama, A., Yoshida, M., Nakamura, T.M. and Tanaka, K. (2014). SUMOylation regulates telomere length by targeting the shelterin subunit Tpz1(Tpp1) to modulate shelterin-Stn1 interaction in fission yeast. *Proc Natl Acad Sci USA*, **111**(16): 5950-5.

Moore, G., Devos, K., Wang, Z. and Gale, M. (1995). Cereal genome evolution: Grasses, line up and form a circle. *Curr. Biol*, **5**: 737-739.

Moses, M.J. (1956). Chromosomal structures in crayfish spermatocytes. *J Cell Biol*, **2**: 215-218.

Muñoz-Amatriaín, M., Cuesta-Marcos, A., Endelman, J.B., Comadran, J., Bonman, J.M., Bockelman, H.E., Chao, S., Russell, J., Waugh, R., Hayes, P.M. and Muehlbauer, G.J. (2014). The USDA barley core collection: genetic diversity, population structure, and potential for genome-wide association studies. *PloS One*, **9**(4). e94688. doi: 10.1371/journal.pone.0094688.

Murphy, S.P. and Bass, H.W. (2012). The maize (Zea mays) desynaptic (dy) mutation defines a pathway for meiotic chromosome segregation, linking nuclear morphology, telomere distribution and synapsis. *J Cell Sci*, **125**: 3681-3690.

Murphy, S.P., Gumber, H.K., Mao, Y. and Bass, H.W. (2014). A dynamic meiotic SUN belt includes the zygotene-stage telomere bouquet and is disrupted in chromosome segregation mutants of maize (**Zea mays** L.). *Front Plant Sci*, **5**: 314. doi: 10.3389/fpls.2014.00314.

Myers, S., Freeman, C., Auton, A., Donnelly, P. and McVean, G. (2008). A common sequence motif associated with recombination hot spots and genome instability in humans. *Nat Genet*, **40**(9): 1124-9.

K. Nairz and F. Klein. (1997). mre11S-a yeast mutation that blocks double-strand-break processing and permits nonhomologous synapsis in meiosis, *Genes Dev*, **11**: 2272-2290.

Nakagawa, T., Flores-Rozas, H. and Kolodner, R.D. (2001). The Mer3 helicase involved in meiotic crossing over is stimulated by single-stranded DNA-binding proteins and unwinds DNA in the 3' to 5' direction. *Journal of Biological Chemistry*, **276**: 31487-31493.

Naranjo, T. (2012). Finding the correct partner: the meiotic courtship. *Scientifica* (Cairo), **509073**: doi: 10.6064/2012/509073. Epub.

Naranjo, T. (2014). Dynamics of Rye Telomeres in a Wheat Background during Early Meiosis. *Cytogenet Genome Res*, **143**: 60-68.

Naumann, K., Fischer, A., Hofmann, I., Krauss, V., Phalke, S., Irmler, K., Hause, G., Aurich, A.C., Dorn, R., Jenuwein, T. and Reuter, G. (2005). Pivotal role of AtSUVH2 in heterochromatic histone methylation and gene silencing in Arabidopsis. *EMBO J*, **24**: 1418-1429.

Neale, M.J. and keeney, S. (2006). clarifying the mechanisms of dna strand exchange in meiotic recombination. *Nature*, **442**, 153-158.

Neff, M.W., Broman, K.W., Mellersh, C.S., Ray, K., Acland, G.M., Aguirre, G.D., Ziegle, J.S., Ostrander, E.A. and Rine, J. (1999). A second-generation genetic linkage map of the domestic dog, Canis familiaris. *Genetics*, **151**: 803-820.

Nilsson, N.O., and Pelger, S. (1991). The relationship between natural variation in chiasma frequencies and recombination frequencies in barley. *Hereditas*, **115:** 121-126.

Nonomura, K.I., Nakano, M., Murata, K., Miyoshi, K., Eiguchi, M., Miyao, A., Hirochika, H. and Kurata, N. (2004). An insertional mutation in the rice PAIR2 gene, the ortholog of Arabidopsis ASY1, results in a defect in homologous chromosome pairing during meiosis. *Molecular Genetics and Genomics*, **271**: 121-129.

Oh, S.D., Lao, J.P., Taylor, A.F., Smith, G.R. and Hunter, N. (2008). RecQ helicase, Sgs1, and Xpf family endonuclease, Mus81-Mms4, resolve aberrant joint molecules during meiotic recombination. *Molecular Cell*, **31**: 324-336.

Osakabe, K., Yoshioka, T., Ichikawa, H. and Toki, S. (2002). Molecular cloning and characterization of RAD51-like genes from Arabidopsis thaliana. *Plant Molecular Biology*, **50**: 71-81.

Osman, K., Higgins, J.D., Sanchez-Moran, E., Armstrong, S.J. and Franklin, F.C. (2011). Pathways to meiotic recombination in Arabidopsis thaliana. *New Phytol*, **190**: 523-544.

Page, S.L. and Hawley, R.S. (2001). c(3)G encodes a Drosophila synaptonemal complex protein. *Genes & Dev*, **15:** 3130-3143.

Pandey, R., Muller, A., Napoli, C.A., Selinger, D.A., Pikaard, C.S., Richards, E.J., Bender, J., Mount, D.W. and Jorgensen, R.A. (2002). Analysis of histone acetyltransferase and histone deacetylase families of Arabidopsis thaliana suggests functional diversification of chromatin modification among multicellular eukaryotes. *Nucleic Acids Res*, **30**: 5036-5055.

Parry, M., Rosenzweig, C. and Livermore, M. (2005). Climate change, global food supply and risk of hunger. *Philos Trans R Soc Lond B Biol Sci*, **360**(1463): 2125-2138.

Paszkowski, J., Baur, M., Bogucki, A. and Potrykus, I. (1988). Gene targeting in plants. *EMBO J*, **7**: 4021-4026.

Pedersen, C., Giese, H. and Linde-Lauresen, I. (1995). Towards an integration of the physical and the genetic chromosome maps of barley by in situ hybridisation. *Hereditas*, **123**: 77-88.

Peng, J., Korol, A.B., Fahima, T., Röder, M.S., Ronin, Y.I., Li, Y.C. and Nevo, E. (2000). Molecular genetic maps in wild emmer wheat, Triticum dicoccoides: genome-wide coverage, massive negative interference, and putative quasi-linkage. *Genome Res*, **10**(10): 1509-31.

Penkner, A., Tang, L., Novatchkova, M., Ladurner, M., Fridkin, A., Gruenbaum, Y., Schweizer, D., Loidl, J. and Jantsch, V. (2007). The nuclear envelope protein Matefin/SUN-1 is required for homologous pairing in C. elegans meiosis. *Dev Cell*, **12**: 873-885.

Pennock, E., Buckley, K. and Lundblad, V. (2001). Cdc13 delivers separate complexes to the telomere for end protection and replication. *Cell*, **104:** 387-396.

Perrella, G., Consiglio, M.F., Aiese-Cigliano, R., Cremona, G., Sanchez-Moran, E., Barra, L., Errico, A., Bressan, R.A., Franklin, F.C. and Conicella, C. (2010), Histone hyperacetylation affects meiotic recombination and chromosome segregation in Arabidopsis. *Plant J*, **62**: 796-806.

Pfeifer, C., Scherthan, H. and Thomsen, P.D. (2003). Sex-specific telomere redistribution and synapsis initiation in cattle oogenesis. *Dev Biol*, **255**: 206-215.

Phillips, D., Wnetrzak, J., Nibau, C., Barakate, A., Ramsay, L., Wright, F., Higgins, J.D., Perry, R.M. and Jenkins, G. (2013). Quantitative high resolution mapping of HvMLH3 foci in barley pachytene nuclei reveals a strong distal bias and weak interference. *J Exp Bot*, **64**(8): 2139-2154.

Pickering, R., Johnston, P.A. and Ruge, B. (2004): Importance of the secondary genepool in barley genetics and breeding I. Cytogenetics and molecular analysis. *Czech J Genet Plant Breed*, **40**: 73-78.

Pickering, R., Klatte, S. and Butler, R.C. (2005). Reduced chromosome association between the short arms of 5H homologues in Hordeum vulgare L. at metaphase I. *Plant Breeding*, **124**: 416-418.

Pickersgill, B. (2007). Domestication of Plants in the Americas: Insights from Mendelian and Molecular Genetics. *Annals of Botany*, **100**(5): 925-940.

Prakken, R. (1943). Studies of synapsis in rye. *Hereditas*, **29**: 475-495.

Preuss, S. and Pikaard, C.S. (2007). rRNA gene silencing and nucleolar dominance: Insights into a chromosome-scale epigenetic on/off switch. *Biochim Biophys Acta*, **1769**: 383-392.

Probst, A.V., Fagard, M., Proux, F., Mourrain, P., Boutet, S., Earley, K., Lawrence, R.J., Pikaard, C.S., Murfet,t J., Furner, I., Vaucheret, H., Mittelsten Scheid, O. (2004). Arabidopsis histone deacetylase HDA6 is required for maintenance of transcriptional gene silencing and determines nuclear organization of rDNA repeats. *Plant Cell*, **16**: 1021-1034.

Puchta, H. and Fauser, F. (2013). Gene targeting in plants: 25 years later. *Int J Dev Biol*. **57**(6-8): 629-37.

Puizina, J., Siroky, J., Mokros, P., Schweizer, D. and Riha, K. (2004). MRE11 deficiency in Arabidopsis is associated with chromosomal instability in somatic cells and SPO11-dependent genome fragmentation during meiosis. *Plant Cell*, **16**: 1968-1978.

Puizina, J. and Šamanić, I. (2013). Reduced Fertility and Meiotic Abnormalities in Late Generations of Telomerase-Deficient Arabidopsis Thaliana. *Acta Biologica Cracoviensia s Botanica*, **55**(1): 7-15.

Ramage, R.T., and Hernandez-Soriano, J.M. (1971). Desynaptic genesin Betzes barley. *Barley Genet Newsletter*, **1**: 38.

Ramage, R.T. and Hernandez-Soriano, J.M. (1972). Desynaptic genesin Betzes barley. *Barley Genet Newsletter*, **2**: 65-68.

Ramsay, L., Macaulay M., degli Ivanissevich, S., MacLean, K., Cardle, L., Fuller, J., Edwards, K.J., Tuvesson, S., Morgante, M., Massari, A., Maestri, E., Marmiroli, N., Sjakste, T., Ganal, M., Powell, W. and Waugh, R. (2000). A simple sequence repeat-based linkage map of barley. *Genetics*, **156**: 1997-2005.

Randolph, L.F. (1928). Chromosome numbers in *Zea mays* L. *Cornell Univ Agr Exp Sta Mem*, **117**: 1-44.

Rasmussen S.W. and Holm P.B. (1978). Human Meiosis II. Chromosome pairing and recombination nodules in human spermatocytes. *Carlsberg Res Comm*, **43:** 275-327.

Recht, J., Tsubota, T., Tanny, J.C., Diaz, R.L., Berger, J.M., Zhang, X., Garcia, B.A., Shabanowitz, J., Burlingame, A.L., Hunt, D.F., Kaufman, P.D. and Allis, C.D. (2006). Histone chaperone Asf1 is required for histone H3 lysine 56 acetylation, a modification associated with S phase in mitosis and meiosis. *Proc Natl Acad Sci USA*, **103**(18): 6988-93.

Rees, H. and Walters, M.R. (1965) Nuclear DNA and evolution of wheat. *Heredity*, **20**(1): 73-82.

Rey, M.D., Calderón, M.C. and Prieto, P. (2015). The use of the ph1b mutant to induce recombination between the chromosomes of wheat and barley. *Front Plant Sci*, **6**:160. doi: 10.3389/fpls.2015.00160.

Richards, E.J. and Ausubel, F.M. (1988). Isolation of a higher eukaryotic telomere from Arabidopsis thaliana. *Cell*, **53**: 127-136.

Richards, D.M., Greer, E., Martin, A.C., Moore, G., Shaw, P.J. and Howard, M. (2012). Quantitative dynamics of telomere bouquet formation. *PLoS Comput Biol*, **8**(12): e1002812.

Roberts N. Y., Osman K., Chris F., Franklin H., Pradillo M., Varas J., Santos, J.L. and Armstrong, S.J. (2013). Telomeres in plant meiosis: their structure, dynamics and function. *Annual Plant Reviews*, **46**: 191-228.

Robyr, D., Suka, Y., Xenarios, I., Kurdistani, S.K., Wang, A., Suka, N. and Grunstein, M. (2002). Microarray deacetylation maps determine genome-wide functions for yeast histone deacetylases. *Cell*, **109**: 437-446.

Rockmill, B., Fung, J.C., Branda, S.S. and Roeder, G.S. (2003) The Sgs1 helicase regulates chromosome synapsis and meiotic crossing over. *Curr Biol*, **13**: 1954-1962.

Roeder, G.S. (1997). Meiotic chromosomes: it takes two to tango. *Genes Dev*, **11**(20): 2600-21.

Ross, K. J., Fransz, P. and Jones, G.H. (1996). A light microscopic atlas of meiosis in *Arabidopsis thaliana*, *Chromosome Research*, **4**: 507-515.

Ross, K.J., Fransz, P., Armstrong, S.J., Vizir, I., Mulligan, B., Franklin, F.C. and Jones, G.H. (1997). Cytological characterization of four meiotic mutants of *Arabidopsis* isolated from T-DNA-transformed lines. *Chromosome Res*, **5**: 551-559.

Rossi, V., Locatelli, S., Varotto, S., Donn, G., Pirona, R., Henderson, D.A., Hartings, H. and Motto, M. (2007). Maize histone deacetylase hda101 is involved in plant development, gene transcription, and sequence-specific modulation of histone modification of genes and repeats. *Plant Cell*, **19**(4): 1145-62.

Ross-Macdonald, P. and Roeder, G.S. (1994). Mutation of a meiosis-specific MutS homolog decreases crossing over but not mismatch correction. *Cell*, **79**(6): 1069-80.

Royal Society of London. (2009). Reaping the Benefits: Science and the Sustainable Intensification of Global Agriculture (Royal Society, London). ISBN: 978-0-85403-784-1.

Saintenac, C., Falque, M., Martin, O.C., Paux, E., Feuillet, C. and Sourdille, P. (2009). Detailed recombination studies along chromosome 3B provide new insights on crossover distribution in wheat (Triticum aestivum L.). *Genetics*, **181**: 393-403.

Sall, T. (1990). Genetic control of recombination in barley. II. Variation in linkage between marker genes. *Hereditas*, **112:** 171-178.

Salonen, K., Paranko, J. and Parvinen, M. (1982). A colcemid-sensitive mechanism invovled in regulation of chromosome movements during meiotic prophase. *Chromosoma*, **85**: 611-618.

San Filippo, J., Sung, P. and Klein, H. (2008). Mechanism of eukaryotic homologous recombination. *Annual Review of Biochemistry*, **77**: 229-257.

San-Segundo, P.A. and Roeder, G.S. (1999). Pch2 links chromatin silencing to meiotic checkpoint control. *Cell*, **97**: 313-324.

Sanchez-Moran, E., Armstrong, S.J., Santos, J.L., Franklin, F.C.H. and Jones G.H. (2002). Variation in chiasma frequency among eight accessions of Arabidopsis thaliana. *Genetics*, **162**(3): 1415-1422.

Sanchez-Moran, E., Santos, J.L., Jones, G.H. and Franklin, F.C.H. (2007). ASY1 mediates AtDMC1 dependent interhomolog recombination during meiosis in Arabidopsis. *Genes Dev*, **21**(17): 2220-33.

Sandhu, D., Champoux, J.A., Bondareva, S.N. and Gill, K.S. (2001) Identification and physical localization of useful genes and markers to a major gene-rich region on wheat group 1S chromosomes. *Genetics*, **157**: 1735-1747.

Sandhu, D. and Gill, K.S. (2002). Gene-containing regions of wheat and the other grass genomes. *Plant Physiol*, **128**: 803-811.

SanMiguel, P., Gaut, B.S., Tikhonov, A., Nakajima, Y. and Bennetzen, J.L. (1998) The paleontology of intergene retrotransposons of maize. *Nat Genet*, **20**: 43-45.

Sarg, B., Helliger, W., Talasz, H., Koutzamani, E. and Lindner, H.H. (2004). Histone H4 Hyperacetylation Precludes Histone H4 Lysine 20 Trimethylation. *J Biol Chem*, **279**(51): 53458-53464.

Sarin, S., Prabhu, S., O'Meara, M.M., Pe'er, I. and Hobert, O. (2008). Caenorhabditis elegans mutant allele identification by whole-genome sequencing. *Nat Methods*, **5**: 865-867.

Sauve, A.A., Wolberger, C., Schramm, V.L. and Boeke, J.D. (2006). The biochemistry of sirtuins. *Annu Rev Biochem*, 75: 435-465.

Scherthan, H., Jerratsch, M., Li, B., Smith, S., Hultén, M., Lock, T. and de Lange, T. (2000). Mammalian meiotic telomeres: protein composition and redistribution in relation to nuclear pores. *Mol Biol Cell*, **11**: 4189-4203.

Scherthan, H. (2001). A bouqet makes ends meet. *Nature Rev Mol Cell Biol*, **2**:621-627.

Schwarzacher, T. (1996). The physical organization of Triticeae chromosomes. *Symp Soc Exp Biol*, **50**: 71-5.

Schwarzacher, T. (2003). Meiosis, recombination and chromosomes: a review of gene isolation and fluorescent in situ hybridization data in plants. *Journal of Experimental Botany*, **54**(380): 11-23.

Schwarzacher, T. (2003b). DNA, chromosomes, and in situ hybridization. *Genome*, **46**(6): 953-62.

Seeholzer, S., Tsuchimatsu, T., Jordan, T., Bieri, S., Pajonk, S., Yang, W., Jahoor, A., Shimizu, K.K., Keller, B. and Schulze-Lefert, P. (2010). Diversity at the Mla powdery mildew resistance locus from cultivated barley reveals sites of positive selection. *Mol. Plant Microbe Interact*, **23**, 497-509.

Selker, E.U. (1998). Trichostatin A causes selective loss of DNA methylation in Neurospora. *Proc Natl Acad Sci USA*, **95:** 9430-9435.

Servet, C., Silva, N.C. and Zhuo, D.X. (2010). Histone Acetyltransferase AtGCN5/HAG1 Is a Versatile Regulator of Developmental and Inducible Gene Expression in Arabidopsis. *Mol. Plant*, **3**(4): 670-677.

Shahinnia, F., Druka, A., Franckowiak, J., Morgante, M., Waugh, R. and Stein, N. (2012). High resolution mapping of Dense spike-ar (dsp.ar) to the genetic centromere of barley chromosome 7H. *Theor Appl Genet*, **124**(2): 373-84.

Shakirov, E.V. and Shippen, D.E. (2004) Length regulation and dynamics of individual telomere tracts in wild-type Arabidopsis. *Plant Cell*, **16**: 1959-1967.

Sharp, P.A. (1985) On the origin of RNA splicing and introns. *Cell*, **42**: 397-400.

Shaked, H., Avivi-Ragolsky, N. and Levy, A.A. (2006). Involvement of the Arabidopsis SWI2/SNF2 chromatin remodeling gene family in DNA damage response and recombination. *Genetics*, **173**: 985-994.

Shampay, J., Szostak, J.W., and Blackburn, E.H. (1984). DNA sequences of telomeres maintained in yeast. *Nature*, **310:** 154-157.

Shinohara, M., Sakai, K., Shinohara, A. and Bishop, D.K. (2003). Crossover interference in *Saccharomyces cerevisiae* requires a Tid1/Rdh54- and Dmc1-dependent pathway. *Genetics*, **163**: 1273-1286.

Shogren-Knaak, M., Ishii, H., Sun, J.-M., Pazin, M. J., Davie, J. R. and Peterson, C.L. (2006). Histone H4-K16 acetylation controls chromatin structure and protein interactions. *Science*, **311**: 844-847.

Shultz, R.W., Tatineni, V.M., Hanley-Bowdoin, L. and Thompson, W.F. (2007). Genome-wide analysis of the core DNA replication machinery in the higher plants Arabidopsis and rice. *Plant Physiology*, **144**: 1697-1714.

Smith, A.V. and Roeder, G.S. (1997). The yeast Red1 protein localizes to the cores of meiotic chromosomes. *J Cell Biol*, **136**: 957-967.

Smith, S.M. and Maughan, P.J. (2015). SNP genotyping using KASPar assays. *Methods Mol Biol*, **1245**: 243-56.

Snowden, T., Acharya, S., Butz, C., Berardini, M. and Fishel, R. (2004) hMSH4-hMSH5 recognizes Holliday junctions and forms a meiosis-specific sliding clamp that embraces homologous chromosomes. *Mol Cell*, **15**, 437-451.

Søgaard, B. (1977). The localization of eceriferum loci in barley. V. Three point tests of genes on chromosome 1 and 3 in barley. *Carlsberg Res Commun*, **42**: 67-75.

Spring, D.R. (2005). Chemical genetics to chemical genomics: small molecules offer big insights. *Chem Soc Rev*, **34**: 472-482.

Stacey, N.J., Kuromori, T., Azumi, Y., Roberts, G., Breuer, C., Wada, T., Maxwell, A., Roberts, K., Sugimoto-Shirasu, K. (2006). Arabidopsis SPO11-2 functions with SPO11-1 in meiotic recombination. *Plant Journal*, **48**: 206-216.

Stahl, F.W., Foss, H.M., Young, L.S., Borts, R.H., Abdulla, M.F.F. and Copenhaver, G.P. (2004). Does crossover interference count in *Saccharomyces cerevisiae*? *Genetics*, **168**: 35-48.

Stephens, J.L., Brown, S.E, Lapitan, N.L. and Knudson, D.L. (2004). Physical mapping of barley genes using an ultrasensitive fluorescence in situ hybridization technique. *Genome*, **47**(1): 179-89.

Stoinova, J. (1994). Characteristics of meiosis in some winter barley varieties. *Cytologia*, **59**: 423-426.

Storlazzi, A., Tessé, S., Gargano, S., James, F., Kleckner, N. and Zickler, D. (2003). Meiotic double strand breaks at the interface of chromosome movement, chromosome remodeling, and reductional division. *Genes Dev*, **17**: 2675-2687.

Storlazzi, A., Gargano, S., Ruprich-Robert, G., Falque, M., David, M., Kleckner, N. and Zickler, D. (2010). Recombination Proteins Mediate Meiotic Spatial Chromosome Organization and Pairing. *Cell*, **141**(1): 94-106.

Su, Y., Barton, A.B. and Kaback, D.B. (2000). Decreased meiotic reciprocal recombination in subtelomeric regions in Saccharomyces cerevisiae. *Chromosoma*, **109**: 467-475.

Sugiyama, T., Zaitseva, E.M. and Kowalczykowski, S.C. (1997). A single-stranded DNA-binding protein is needed for efficient presynaptic complex formation by the Saccharomyces cerevisiae Rad51 protein. *Journal of Biological Chemistry*, **272**: 7940-7945.

Sung P. (1997). Function of yeast Rad52 protein as a mediator between replication protein a and the rad51 recombinase. *Journal of Biological Chemistry*, **272**: 28194-28197.

Sýkorová, E., Lim, K.Y., Kunická, Z., Chase, M.W., Bennett, M.D., Fajkus, J. and Leitch, A.R. (2003). Telomere variability in the monocotyledonous plant order Asparagales. *Proc Biol Sci*, **270**(1527): 1893-904.

Sym, M., Engebrecht, J., and Roeder, G.S. (1993). Zip1 is a synaptonemal complex protein required for meiotic chromosome synapsis. *Cell*, **72:** 365-378.

Sym, M. and Roeder, G.S. (1995). Zip1-induced changes in synaptonemal complex structure and polycomplex assembly. *J Cell Biol*, **128**(4):455-66.

Symington, L.S. (2002). Role of Rad52 epistasis group genes in homologous recombination and double-strand break repair. *Microbiology and Molecular Biology Reviews*, **66**: 630-670.

Tamkun, J.W., Deuring, R., Scott, M.P., Kissinger, M., Pattatucci, A.M., Kaufman, T.C., Kennison, J.A. (1992). *Brahma*-a regulator of Drosophila homeotic genes structurally related to the yeast transcriptional activatorSNF2/SWI2. *Cell*, **68:** 561-572.

Tankimanova, M., Hulten, M.A. and Tease, C. (2004). The initiation of homologous chromosome synapsis in mouse fetal oocytes is not directly driven by centromere and telomere clustering in the bouquet. *Cytogenet Genome Res*, **105**: 172-181.

Terasawa, M., Ogawa, H., Tsukamoto, Y., Shinohara, M., Shirahige, K., Kleckner. N. and Ogawa, T. (2007). Meiotic recombination-related DNA synthesis and its implications for cross-over and non-cross-over recombinant formation. *Proceedings of the National Academy of Sciences USA*, **104**: 5965-5970.

Thomas, H. and Rajhathy, T. (1966). A gene for desynapsisans aneuploidy in tetraploid avena. *Can J Genet Cytol*, **8**: 506-515.

Toth, K. F., Knoch, T. A., Wachsmuth, M., Frank-Stohr, M., Stohr, M., Bacher, C. P., Muller, G., and Rippe, K. (2004). Trichostatin A-induced histone acetylation causes decondensation of interphase chromatin. *J Cell Sci*, **117:** 4277-4287.

Trelles-Sticken, E., Loidl, J. and Scherthan, H. (2003). Increased ploidy and KAR3 and SIR3 disruption alter the dynamics of meiotic chromosomes and telomeres. *J Cell Sci*, **116:** 2431-2442.

Tung, K.S. and Roeder, G.S. (1998). Meiotic chromosome morphology and behavior in zip1 mutants of Saccharomyces cerevisiae. *Genetics*, **149**: 817-832.

Tsubouchi, H. and Ogawa, H. (1998). A novel mre11 mutation impairs processing of double-strand breaks of DNA during both mitosis and meiosis, *Mol Cell Biol*, **18:** 260-268.

Tsubouchi, T, Zhao. H.Y. and Roeder, G.S. (2006). The meiosis-specific Zip4 protein regulates crossover distribution by promoting synaptonemal complex formation together with Zip2. *Developmental Cell*, **10**: 809-819.

Van Deynze, A.E., Dubcovsky, J., Gill, K.S., Nelson, J.C., Sorrells, M.E., Dvorak, J., Gill, B.S., Lagudah, E.S., McCouch, S.R. and Appels, R. (1995) Molecular-genetic maps for group 1 chromosomes of Triticeae species and their relation to chromosomes in rice and oat. *Genome*, **38**: 45-59.

van Ooijen, G., Mayr, G., Kasiem, M.M., Albrecht, M., Cornelissen, B.J. and Takken, F.L. (2008). Structure-function analysis of the NB-ARC domain of plant disease resistance proteins. *J Exp Bot*, **59**: 1383-1397.

Van't Hof, J., Kuniyuki, A. and Bjerknes, C.A. (1978). The size and number of replicon families of chromosomal DNA of *Arabidopsis thaliana*. *Chromosoma*, **68**: 269-285.

Varas, J., Graumann, K., Osman, K., Pradillo, M., Evans, D.E., Santos, J.L. and Armstrong, S.J. (2015). Absence of SUN1 and SUN2 proteins in Arabidopsis thaliana leads to a delay in meiotic progression and defects in synapsis and recombination. *Plant J*, **81**(2): 329-346.

Venkatasubrahmanyam, S., Hwang, W.W., Meneghini, M.D., Tong, A.H. and Madhani, H.D. (2007). Genome-wide, as opposed to local, antisilencing is mediated redundantly by the euchromatic factors Set1 and H2A.Z. *Proc Natl Acad Sci USA*, **104**: 16609-16614.

Villasante, A., Abad, J.P. and Méndez-Lago, M. (2007). Centromeres were derived from telomeres during the evolution of the eukaryotic chromosome. *Proc Natl Acad Sci USA*, **104**: 10542-10547.

Vizir, I.Y. and Korol, A.B. (1990) Sex Difference in recombination frequency in Arabidopsis. *Heredity*, **65**: 379-383.

Wall, E., Visscher, P.M., Hospital, F. and Woolliams, J.A. (2005) Genomic contributions in livestock gene introgression programmes. *Genet Sel Evol*, **37**(3): 291-313.

Wang, S., P. Yeh, S. S. Y. Lee, and H. W. Li (1965). Effect of low temperature on desynapsis in rice. *Botan Bull Acad Sinica*, **6**: 197-207.

Wang, T.F., Kleckner, N. and Hunter, N. (1999). Functional specificity of MutL homologs in yeast: evidence for three Mlh1-based heterocomplexes with distinct roles during meiosis in recombination and mismatch correction. *Proc Natl Acad Sci USA*, **96**: 13914-13919.

Wang, Q., Yin, S., Ai, J.S., Liang, C.G., Hou, Y., Chen, D.Y., Schatten, H. and Sun, Q,Y. (2006). Histone deacetylation is required for orderly meiosis. *Cell Cycle*, **7**: 766-774.

Wang, M., Wang, K.J., Tang, D., Wei, C.X., Li, M., Shen, Y., Chi, Z.C., Gu, M.H. and Cheng, Z.K. (2010). The central element protein ZEP1 of the synaptonemal complex regulates the number of crossovers during meiosis in rice. *Plant Cell*, **22**: 417-430.

Wang, T., Mei, S.C., Fu, R., Wang, H.Q. and Shao, Z,H. (2014). Expression of Shelterin Component POT1 Is Associated with Decreased Telomere Length and Immunity Condition in Humans with Severe Aplastic Anemia. *J Immunol Res*, **2014**(439530): doi: 10.1155/2014/439530.

Watson, M. (1952). Spermatogenesis in the Adult Albino Rat as Revealed by Tissue Sections in the Electron Microscope, Report U.R.-185, Univ. *Rochester Atomic Energy Proj*.

Wendel, J.F. (2000) Genome evolution in polyploids. *Plant Mol Biol*, **42**: 225-249.

Williams-Carrier, R., Stiffler, N., Belcher, S., Kroeger, T., Stern, D.B., Monde, R.A., Coalter, R. and Barkan, A. (2010). Use of Illumina sequencing to identify transposon insertions underlying mutant phenotypes in high-copy Mutator lines of maize. *Plant J*, **63**: 167-177.

Wilson, L. and Jordan, M.A. (1994). Pharmacological probes of microtubule function. In Microtubules. Vol. 13 (eds J. S. Hyams and C. W. Lloyd), pp. 59-83. New York: Wiley-Liss, Inc.

Xu, L., Petreaca, R.C., Gasparyan, H.J., Vu, S. and Nugent, C.I. (2009) TEN1 is essential for CDC13-mediated telomere capping. Genetics, **183**(3): 793-810.

Yamashita, Y., Shimada, M., Harimoto, N., Rikimaru, T., Shirabe, K., Tanaka, S. and Sugimachi, K. (2003). Histone deacetylase inhibitor trichostatin A induces cell-cycle arrest/apoptosis and hepatocyte differentiation in human hepatoma cells. *Int J Cancer*, **103**: 572-576.

Yang, F., Baumann, C., Viveiros, M.M. and De La Fuente, R. (2012). Histone hyperacetylation during meiosis interferes with large-scale chromatin remodeling, axial chromatid condensation and sister chromatid separation in the mammalian oocyte. *Int J Dev Biol*, **56**: 889-899.

Yang, P., Habekuß, A., Ordon, F. and Stein, N. (2014) Analysis of bymovirus resistance genes on proximal barley chromosome 4HL provides the basis for precision breeding for BaMMV/BaYMV resistance. *Theor Appl Genet*, **127**(7): 1625-34.

Yang, Q., Zheng, Y.L. and Harris, C.C. (2005). POT1 and TRF2 Cooperate To Maintain Telomeric Integrity. *Mol Cell Biol*, **25**(3): 1070-1080.

Yanowitz, J. (2010). Meiosis: making a break for it. *Curr Opin Cell Biol*, **22**(6): 744-51.

Ye, X., Al-Babili, S., Klöti, A., Zhang, J., Lucca, P., Beyer, P. and Potrykus, I. (2000). Engineering the provitamin A (beta-carotene) biosynthetic pathway into (carotenoid-free) rice endosperm. *Science*, **287**(5451): 303-5.

Yelina, N.E., Choi, K., Chelysheva, L., Macaulay, M., de Snoo, B., Wijnker, E., Miller, N., Drouaud, J., Grelon, M., Copenhaver, G.P., Mezard, C., Kelly, K.A. and Henderson, I.R. (2012). Epigenetic Remodeling of Meiotic Crossover Frequency in Arabidopsis thaliana DNA Methyltransferase Mutants. *PLoS Genet*, **8**(8): e1002844. doi: 10.1371/journal.pgen.1002844.

Yoshida, M. and Beppu, T. (1988). Reversible arrest of proliferation of rat 3Y1 fibroblasts in both the G1 and G2 phases by trichostatin A. *Exp Cell Res*, **177**: 122-131.

Young, N.D. and Tanksley, S.D. (1989). RFLP analysis of the size of chromosomal segments retained around the *Tm-2* locus of tomato during backcross breeding. *Theor Appl Gene*, **77**: 353-359.

Zalevsky, J., MacQueen, A.J., Duffy, J.B., Kemphues, K.J. and Villeneuve, A.M. (1999). Crossing over during Caenorhabditis elegans meiosis requires a conserved MutS-based pathway that is partially dispensable in budding yeast. *Genetics*, **153**: 1271-1283.

Zeng, L. and Zhou, M.M. (2002). Bromodomain: an acetyl-lysine binding domain. *FEBS Lett*, **513**: 124-128.

Zhang, K., Sridhar, V.V., Zhu, J., Kapoor, A. and Zhu, J.K. (2007). Distinctive core histone post-translational modification patterns in Arabidopsis thaliana. *PloS One*, **2**(11): e1210.

Zhang, L., Espagne, E., de Muyt, A., Zickler, D. and Kleckner, N.E. (2014). Interference-mediated synaptonemal complex formation with embedded crossover designation. *Proc Natl Acad Sci U S A*, **111**(47): E5059-68.

Zhong, Z., Zhong, Z., Shiue, L., Kaplan, S., and de Lange, T. (1992). A mammalian factor that binds telomeric TTAGGG repeats in vitro. *Mol Cell Biol*, **12**: 4834-4843.

Zohary, D. and Hopf, M. (2000). Domestication of Plants in the Old World: The Origin and Spread of Cultivated Plants in West Asia, Europe, and the Nile Valley (3rd ed.). *Oxford University Press*. pp. 59-69. ISBN 0198503571.

APPENDIX

Table of Contents

Raw data for chapter 3: The determination of the mean number of telomere signals clustered into a bouquet and the mean number of telomere signals per cell in the untreated control and population treated with 100 µM/5mM colchicine.

Table A1: Raw data for ANOVA analysis for telomers clustered into a bouquet (100 µM colchicine). N=30, P-value= 3.54E-09, F crit= 4.006873, F= 48.31779.

	No. Telomere signals clustered/nuclei	No. Telomere signals clustered/nuclei
	Control	**100 µM colchicine**
	11	5
	14	5
	14	2
	12	5
	13	3
	11	2
	14	8
	14	5
	11	12
	11	3
	10	2
	14	8
	11	7
	14	6
	9	6
	9	5
	11	8
	6	12
	12	4
	8	6
	7	9
	14	5
	15	11
	10	11
	14	4
	10	9
	11	8
	14	14
	14	8
	11	5
Mean	**11.63**	**6.6**
Variance	**5.55**	**10.18**
Standard deviation.	**2.36**	**3.19**

Table A2: Raw data for ANOVA analysis for telomere count per cell (100 µM colchicine). N=30, P-value= 0.71276, F crit= 4.006873, F= 0.13687.

	No. Telomere signals/nuclei	No. Telomere signals/nuclei
	Control	**100 µM colchicine**
	13	14
	16	15
	15	16
	14	12
	14	13
	14	14
	13	11
	14	15
	15	13
	14	18
	11	14
	15	14
	14	13
	15	15
	13	16
	17	14
	14	14
	14	16
	17	14
	14	13
	18	14
	14	13
	12	12
	14	9
	11	14
	15	14
	14	11
	14	17
	11	14
	14	16
Mean	**14.1**	**13.93**
Variance	**2.65**	**3.44**
Standard deviation.	**1.63**	**1.86**

Table A3: Raw data for ANOVA analysis for telomers clustered into a bouquet (5 mM colchicine). N=25, P-value= 1.27E-19, F crit= 4.042652, F= 221.8433.

	No. Telomere signals clustered/nuclei	No. Telomere signals clustered/nuclei
	Control	**5 mM colchicine**
	11	2
	14	0
	14	2
	12	4
	13	0
	11	2
	14	2
	14	2
	11	0
	11	2
	10	0
	14	2
	11	4
	14	2
	9	0
	9	6
	11	5
	6	7
	12	0
	8	0
	7	0
	14	3
	15	2
	10	0
	14	4
Mean	**11.56**	**2.04**
Variance	**6.09**	**4.12**
Standard deviation.	**2.47**	**2.03**

Table A4: Raw data for ANOVA analysis for telomere count per cell (5 mM colchicine). N=25, P-value= 7.25E-11, F crit= 4.042652, F= 69.23444.

	No. Telomere signals/nuclei	No. Telomere signals/nuclei
	Control	**5 mM colchicine**
	13	18
	16	24
	15	16
	14	20
	14	22
	14	22
	13	18
	15	16
	14	18
	11	20
	15	20
	14	16
	15	26
	13	20
	17	20
	14	18
	14	20
	17	24
	14	18
	14	16
	12	20
	14	20
	11	18
	15	20
	14	14
Mean	**14.08**	**19.36**
Variance	**2.16**	**7.91**
Standard deviation.	**1.47**	**2.81**

Raw data for chapter 4: The determination of the mean chiasma frequency per cell in the untreated control and population treated with 10, 100, 500 and 1000 ng/ml TSA.

	Chr 1H	Chr 1H
	Control	10 ng/ml TSA
Mean CO freq.	2.12	1.9
Variance	0.27	0.255

P-value=0.03445 (F crit=3.938111, F=4.59969)

	Chr 2H	Chr 2H
	Control	10 ng/ml TSA
Mean CO freq.	2.08	2.04
Variance	0.12	0.04

P-value=0.474352 (F crit=3.938111, F=0.515789)

	Chr 3H	Chr 3H
	Control	10 ng/ml TSA
Mean CO freq.	2.44	2.4
Variance	0.25	0.25

P-value=0.688943 (F crit=3.938111, F=0.161184)

	Chr 4H	Chr 4H
	Control	10 ng/ml TSA
Mean CO freq.	2.2	2.04
Variance	0.29	0.04

P-value=0.049955 (F crit=3.938111, F=3.939698)

	Chr 5H	Chr 5H
	Control	10 ng/ml TSA
Mean CO freq.	2.1	2.02
Variance	0.5	0.59

P-value=0.58941 (F crit=3.938111, F=0.293194)

	Chr 6H	Chr 6H
	Control	10 ng/ml TSA
Mean CO freq.	1.76	1.92
Variance	0.23	0.08

P-value=0.042186 (F crit=3.938111, F=4.237838)

	Chr 7H	Chr 7H
	Control	10 ng/ml TSA
Mean CO freq.	1.94	1.98
Variance	0.1	0.06

P-value=0.480059 (F crit= 3.938111, F=0.502564)

Figure A1: Summary of ANOVA analysis for meiocytes treated with 10 ng/ml TSA (n=50).

	Chr 1H	Chr 1H
	Control	100 ng/ml TSA
Mean CO freq.	2.12	1.88
Variance	0.27	0.23

P-value=0.018423 (F crit=3.938111, F=5.745928)

	Chr 2H	Chr 2H
	Control	100 ng/ml TSA
Mean CO freq.	2.08	1.76
Variance	0.12	0.19

P-value=8.01E-05 (F crit=3.938111, F=16.95135)

	Chr 3H	Chr 3H
	Control	100 ng/ml TSA
Mean CO freq.	2.44	2.3
Variance	0.25	0.21

P-value=0.150079 (F crit=3.938111, F=2.104294)

	Chr 4H	Chr 4H
	Control	100 ng/ml TSA
Mean CO freq.	2.2	2
Variance	0.29	0.04

P-value=0.015046 (F crit=3.938111, F=6.125)

	Chr 5H	Chr 5H
	Control	100 ng/ml TSA
Mean CO freq.	2.1	1.7
Variance	0.5	0.58

P-value=0.007733 (F crit=3.938111, F=7.396226)

	Chr 6H	Chr 6H
	Control	100 ng/ml TSA
Mean CO freq.	1.76	1.96
Variance	0.23	0.04

P-value=0.007272 (F crit=3.938111, F=7.515337)

	Chr 7H	Chr 7H
	Control	100 ng/ml TSA
Mean CO freq.	1.94	1.88
Variance	0.1	0.11

P-value=0.352349 (F crit=3.938111, F=0.873267)

Figure A2: Summary of ANOVA analysis for meiocytes treated with 100 ng/ml TSA (n=50).

	Chr 1H	Chr 1H
	Control	500 ng/ml TSA
Mean CO freq.	2.12	1.62
Variance	0.27	0.28

P-value=6.75E-06 (F crit=3.938111, F=22.63489)

	Chr 2H	Chr 2H
	Control	500 ng/ml TSA
Mean CO freq.	2.08	1.9
Variance	0.12	0.09

P-value=0.006291 (F crit=3.938111, F=7.797642)

	Chr 3H	Chr 3H
	Control	500 ng/ml TSA
Mean CO freq.	2.44	2.18
Variance	0.25	0.31

P-value=0.016262 (F crit=3.938111, F=5.979061)

	Chr 4H	Chr 4H
	Control	500 ng/ml TSA
Mean CO freq.	2.2	1.88
Variance	0.29	0.39

P-value=0.007186 (F crit=3.938111, F=7.538462)

	Chr 5H	Chr 5H
	Control	500 ng/ml TSA
Mean CO freq.	2.1	1.66
Variance	0.5	0.47

P-value=0.002147 (F crit=3.938111, F=9.939648)

	Chr 6H	Chr 6H
	Control	500 ng/ml TSA
Mean CO freq.	1.76	1.74
Variance	0.23	0.32

P-value=0.848577 (F crit=3.938111, F=0.036649)

	Chr 7H	Chr 7H
	Control	500 ng/ml TSA
Mean CO freq.	1.94	1.86
Variance	0.1	0.2

P-value=0.306521 (F crit=3.938111, F=1.056604)

Figure A3: Summary of ANOVA analysis for meiocytes treated with 500 ng/ml TSA (n=50).

	Chr 1H	Chr 1H
	Control	1000 ng/ml TSA
Mean CO freq.	2.12	1.16
Variance	0.27	0.42

P-value=1.22E-12 (F crit=3.938111, F=66.40941)

	Chr 2H	Chr 2H
	Control	1000 ng/ml TSA
Mean CO freq.	2.08	1.36
Variance	0.12	0.28

P-value=1.32E-12 (F crit=3.938111, F=66.15

	Chr 3H	Chr 3H
	Control	1000 ng/ml TSA
Mean CO freq.	2.44	1.78
Variance	0.25	0.5

P-value=5.12E-07 (F crit=3.938111, F=28.92195)

	Chr 4H	Chr 4H
	Control	1000 ng/ml TSA
Mean CO freq.	2.22	1.46
Variance	0.26	0.66

P-value=1.89E-07 (F crit=3.938111, F=31.44711)

	Chr 5H	Chr 5H
	Control	1000 ng/ml TSA
Mean CO freq.	2.1	0.84
Variance	0.5	0.54

P-value=7.42E-14 (F crit=3.938111, F=75.93948)

	Chr 6H	Chr 6H
	Control	1000 ng/ml TSA
Mean CO freq.	1.76	1.26
Variance	0.23	0.52

P-value=9.08E-05 (F crit=3.938111, F=16.6712)

	Chr 7H	Chr 7H
	Control	1000 ng/ml TSA
Mean CO freq.	0.94	1.34
Variance	0.1	0.56

P-value=8.96E-07 (F crit=3.938111, F=27.52809)

Figure A4: Summary of ANOVA analysis for meiocytes treated with 1000 ng/ml TSA (n=50)

Raw data for chapter 5: The determination of the mean chiasma frequency per cell in the Bowman control and the *des8* population.

	Chr 1H	Chr 1H
	Bowman	*des8*
Mean CO freq.	2	1.26
Variance	0.37	0.32

P-value= 7.85E-09 (F crit= 3.938111, F= 39.90541)

	Chr 2H	Chr 2H
	Bowman	*des8*
Mean CO freq.	2.08	1.5
Variance	0.12	0.3

P-value= 5.59E-09 (F crit= 3.938111, F= 40.84143)

	Chr 3H	Chr 3H
	Bowman	*des8*
Mean CO freq.	2.52	1.46
Variance	0.3	0.74

P-value= 5.89E-11 (F crit= 3.938111, F= 54.08291)

	Chr 4H	Chr 4H
	Bowman	*des8*
Mean CO freq.	2.22	0.88
Variance	0.22	1.13

P-value= 1.08E-12 (F crit= 3.938111, F= 66.79654)

	Chr 5H	Chr 5H
	Bowman	*des8*
Mean CO freq.	2.12	1.06
Variance	0.23	0.67

P-value= 4.13E-12 (F crit= 3.938111, F= 62.42222)

	Chr 6H	Chr 6H
	Bowman	*des8*
Mean CO freq.	1.92	0.36
Variance	0.12	0.24

P-value= 5.96E-34 (F crit= 3.938111, F= 346.6465)

	Chr 7H	Chr 7H
	Bowman	*des8*
Mean CO freq.	2.08	1.14
Variance	0.12	0.53

P-value= 6.92E-13 (F crit= 3.938111, F= 68.29085)

Figure A5: Summary of ANOVA analysis for *des8* and Bowman (n=50).

BeadXpress® genotyping data and calculations of the mean marker recombination frequencies for F2 individuals derived from the untreated (control) F1 population.

Table A5: The genotype for untreated individuals 1-30, for markers on the short arm of 1H. Marker 11_10597 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52
Morex SNP	A	A	A	G	A	A	G
Barke SNP	g	g	g	a	g	g	a
MxB_F1_1_cont_ear1_seed_1	B	B	B	H	A	A	A
MxB_F1_1_cont_ear1_seed_10	H	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_11	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_12	H	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_13	H	A	A	A	A	H	H
MxB_F1_1_cont_ear1_seed_14	A	A	A	A	A	H	H
MxB_F1_1_cont_ear1_seed_15	A	H	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_16	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_18	H	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_19	B	B	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_3	H	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_4	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_5	B	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_6	A	A	A	A	H	H	H
MxB_F1_1_cont_ear1_seed_7	H	H	H	H	A	A	A
MxB_F1_1_cont_ear1_seed_8	B	B	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_9	H	H	H	H	A	H	H
MxB_F1_1_untrt_ear1_seed_1	A	A	A	A	A	H	H
MxB_F1_1_untrt_ear1_seed_10	B	B	H	H	A	A	A
MxB_F1_1_untrt_ear1_seed_11	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear1_seed_2	A	A	A	A	H	H	H
MxB_F1_1_untrt_ear1_seed_3	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_4	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_5	H	H	H	H	B	B	B
MxB_F1_1_untrt_ear1_seed_6	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_7	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_8	A	A	A	A	H	H	H
MxB_F1_1_untrt_ear1_seed_9	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_1	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_10	H	H	H	H	H	H	H

Table A6: The genotype for untreated individuals 31-60, for markers on the short arm of 1H. Marker 11_10597 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52
Morex SNP	A	A	A	G	A	A	G
Barke SNP	g	g	g	a	g	g	a
MxB_F1_1_untrt_ear2_seed_2	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_3	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_4	H	H	H	H	H	A	A
MxB_F1_1_untrt_ear2_seed_5	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_6	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_7	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_8	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_9	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_1	B	B	B	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear3_seed_3	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear3_seed_4	H	H	H	H	A	H	H
MxB_F1_1_untrt_ear3_seed_5	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_6	A	A	A	A	H	H	H
MxB_F1_1_untrt_ear3_seed_7	B	B	B	B	H	H	H
MxB_F1_1_untrt_ear3_seed_8	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	A	A	A
MxB_F1_2_cont_ear1_seed_1	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_10	B	B	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_11	H	H	H	A	A	A	A
MxB_F1_2_cont_ear1_seed_12	B	B	B	B	H	H	H
MxB_F1_2_cont_ear1_seed_2	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_3	H	H	H	H	A	A	A
MxB_F1_2_cont_ear1_seed_6	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_7	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_8	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_1	B	B	B	B	B	H	H
MxB_F1_2_untrt_ear1_seed_10	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_11	B	B	B	B	B	B	B

Table A7: The genotype for untreated individuals 61-90, for markers on the short arm of 1H. Marker 11_10597 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52
Morex SNP	A	A	A	G	A	A	G
Barke SNP	g	g	g	a	g	g	a
MxB_F1_2_untrt_ear1_seed_3	H	A	A	A	A	H	H
MxB_F1_2_untrt_ear1_seed_4	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_5	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_6	A	A	A	A	A	H	H
MxB_F1_2_untrt_ear1_seed_7	H	H	H	A	A	A	A
MxB_F1_2_untrt_ear1_seed_8	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	B	B	H	H	A	A	A
MxB_F1_2_untrt_ear2_seed_1	H	H	H	B	B	H	H
MxB_F1_2_untrt_ear2_seed_10	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear2_seed_2	A	A	A	A	A	H	H
MxB_F1_2_untrt_ear2_seed_3	B	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_4	B	B	B	B	A	A	A
MxB_F1_2_untrt_ear2_seed_5	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_7	A	A	A	H	H	H	H
MxB_F1_2_untrt_ear2_seed_8	B	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_9	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear3_seed_1	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_10	A	A	A	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_12	B	B	B	B	H	H	H
MxB_F1_2_untrt_ear3_seed_2	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_4	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear3_seed_5	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_6	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_7	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_9	A	A	A	A	A	A	A

Table A8: The recombination data for markers on the short arm of 1H for untreated individuals 1-30. Superimposed with Table A5

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597	Total recomb. Events per arm
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52	
Morex SNP	A	A	A	G	A	A	G	
Barke SNP	G	G	G	A	G	G	A	
MxB_F1_1_cont_ear1_seed_1		0	0	1	1	0	0	2
MxB_F1_1_cont_ear1_seed_10		0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_11		0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_12		0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_13		1	0	0	0	1	0	2
MxB_F1_1_cont_ear1_seed_14		0	0	0	0	1	0	1
MxB_F1_1_cont_ear1_seed_15		1	1	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_16		0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_18		0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_19		0	1	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_3		0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_4		0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_5		1	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_6		0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_7		0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_8		0	1	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_9		0	0	0	1	1	0	2
MxB_F1_1_untrt_ear1_seed_1		0	0	0	0	1	0	1
MxB_F1_1_untrt_ear1_seed_10		0	1	0	1	0	0	2
MxB_F1_1_untrt_ear1_seed_11		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear1_seed_2		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear1_seed_3		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_4		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_5		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear1_seed_6		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_7		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_8		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear1_seed_9		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_1		0	1	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_10		0	0	0	0	0	0	0

Table A9: The recombination data for markers on the short arm of 1H for untreated individuals 31-60. Superimposed with Table A6

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597	Total recomb. Events per arm
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52	
Morex SNP	A	A	A	G	A	A	G	
Barke SNP	G	G	G	A	G	G	A	
MxB_F1_1_untrt_ear2_seed_11		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear2_seed_2		0	1	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_3		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_4		0	0	0	0	1	0	1
MxB_F1_1_untrt_ear2_seed_5		0	1	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_7		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_8		0	1	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_9		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_1		0	0	1	0	0	0	1
MxB_F1_1_untrt_ear3_seed_2		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear3_seed_3		0	0	1	0	0	0	1
MxB_F1_1_untrt_ear3_seed_4		0	0	0	1	1	0	2
MxB_F1_1_untrt_ear3_seed_5		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_6		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear3_seed_7		0	0	0	1	0	0	1
MxB_F1_1_untrt_ear3_seed_8		0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_9		0	0	0	1	0	0	1
MxB_F1_2_cont_ear1_seed_1		0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_10		0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_11		0	0	1	0	0	0	1
MxB_F1_2_cont_ear1_seed_12		0	0	0	1	0	0	1
MxB_F1_2_cont_ear1_seed_2		0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_3		0	0	0	1	0	0	1
MxB_F1_2_cont_ear1_seed_6		0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_7		0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_8		0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_1		0	0	0	0	1	0	1
MxB_F1_2_untrt_ear1_seed_10		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_11		0	0	0	0	0	0	0

Table A10: The recombination data for markers on the short arm of 1H for untreated individuals 61-90. Superimposed with Table A7

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597	Total recomb. Events per arm
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52	
Morex SNP	A	A	A	G	A	A	G	
Barke SNP	G	G	G	A	G	G	A	
MxB_F1_2_untrt_ear1_seed_2		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_3		1	0	0	0	1	0	2
MxB_F1_2_untrt_ear1_seed_4		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_5		0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_6		0	0	0	0	1	0	1
MxB_F1_2_untrt_ear1_seed_7		0	0	1	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8		1	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_9		0	1	0	1	0	0	2
MxB_F1_2_untrt_ear2_seed_1		0	0	1	0	1	0	2
MxB_F1_2_untrt_ear2_seed_10		0	0	0	0	1	0	1
MxB_F1_2_untrt_ear2_seed_2		0	0	0	0	1	0	1
MxB_F1_2_untrt_ear2_seed_3		1	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_4		0	0	0	2	0	0	2
MxB_F1_2_untrt_ear2_seed_5		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_6		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_7		0	0	1	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8		1	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_9		0	0	0	1	0	0	1
MxB_F1_2_untrt_ear3_seed_1		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_10		0	0	1	0	0	0	1
MxB_F1_2_untrt_ear3_seed_11		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_12		0	0	0	1	0	0	1
MxB_F1_2_untrt_ear3_seed_2		1	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_3		1	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_4		0	0	0	0	1	0	1
MxB_F1_2_untrt_ear3_seed_5		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_6		1	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_7		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_8		0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_9		0	0	0	0	0	0	0
						Total recomb. Events in population		70

Table A11: The genotype for untreated individuals 1-30, for markers on the long arm of 1H. Marker 11_20095 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g
MxB_F1_1_cont_ear1_seed_1	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	A
MxB_F1_1_cont_ear1_seed_11	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_13	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H
MxB_F1_1_cont_ear1_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_15	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_16	H	H	H	H	H	H	h	H	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_cont_ear1_seed_18	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	B
MxB_F1_1_cont_ear1_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_4	H	B	B	B	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_5	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_cont_ear1_seed_6	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_untrt_ear1_seed_1	B	B	B	H	H	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_11	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	B
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear1_seed_4	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_6	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_7	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_8	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_untrt_ear1_seed_9	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A12: The genotype for untreated individuals 31-60, for markers on the long arm of 1H. Marker 11_20095 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a
MxB_F1_1_untrt_ear2_seed_2	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_4	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_untrt_ear2_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_6	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_7	A	A	A	A	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_untrt_ear2_seed_9	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H
MxB_F1_1_untrt_ear3_seed_1	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_3	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_4	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_untrt_ear3_seed_5	H	H	H	H	H	H	H	H	H	H	H	B	H	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_9	a	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_cont_ear1_seed_1	H	H	H	H	H	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_10	H	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_cont_ear1_seed_11	A	A	A	A	A	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_12	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_3	H	H	H	H	H	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_6	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_8	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H
MxB_F1_2_untrt_ear1_seed_1	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear1_seed_11	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H

Table A13: The genotype for untreated individuals 61-90, for markers on the long arm of 1H. Marker 11_20095 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a
MxB_F1_2_untrt_ear1_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_4	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_6	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_7	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_10	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_untrt_ear2_seed_2	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_3	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_4	A	A	A	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_untrt_ear2_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_untrt_ear2_seed_7	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_8	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_untrt_ear3_seed_11	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_12	H	H	H	H	H	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_untrt_ear3_seed_2	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_4	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear3_seed_7	B	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_9	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B

Table A14: The recombination data for markers on the long arm of 1H for untreated individuals 1-30. Superimposed with Table A11

Marker	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854
Position on chromosome	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80
Morex SNP	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C
Barke SNP	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a
MxB_F1_1_cont_ear1_seed_1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_11	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MxB_F1_1_cont_ear1_seed_13	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_16	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
MxB_F1_1_cont_ear1_seed_19	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_4	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
MxB_F1_1_untrt_ear1_seed_11	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_4	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
MxB_F1_1_untrt_ear1_seed_6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_8	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_9	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table A15: The recombination data for markers on the long arm of 1H for untreated individuals 31-60. Superimposed with Table A12

Marker	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854
Position on chromosome	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80
Morex SNP	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C
Barke SNP	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a
MxB_F1_1_untrt_ear2_seed_11	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MxB_F1_1_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_7	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MxB_F1_1_untrt_ear2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_1_untrt_ear3_seed_1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear3_seed_5	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
MxB_F1_1_untrt_ear3_seed_6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
MxB_F1_2_cont_ear1_seed_1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_10	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MxB_F1_2_cont_ear1_seed_11	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_12	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_3	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_7	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_8	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
MxB_F1_2_untrt_ear1_seed_1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MxB_F1_2_untrt_ear1_seed_11	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

Table A16: The recombination data for markers on the long arm of 1H for untreated individuals 61-90. Superimposed with Table A13 Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782	11_10590	Total recomb. Events per arm
Position on chromosome	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89	1H|138.31	
Morex SNP	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A	A	
Barke SNP	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g	g	
MxB_F1_2_untrt_ear1_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_6	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_9	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_10	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear2_seed_3	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_4	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_8	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_untrt_ear2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_untrt_ear3_seed_10	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear3_seed_11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_12	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	3
MxB_F1_2_untrt_ear3_seed_2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear3_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_untrt_ear3_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_untrt_ear3_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear3_seed_7	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear3_seed_8	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear3_seed_9	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
																					Total recomb. Events in population	136

Mean marker recomb. Freq./cell = 70(1HS)+136(1HL)/90 individuals = 2.29/cell

Table A17: The genotype for untreated individuals 1-30, for markers on the short arm of 2H. Marker 11_11015 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a
MxB_F1_1_cont_ear1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_11	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_12	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_13	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_14	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_15	H	H	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_16	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_18	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_3	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_5	A	A	A	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_6	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_7	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_cont_ear1_seed_9	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_10	A	A	A	A	A	A	A	A	A	H	H	H	H	B	B	B	B
MxB_F1_1_untrt_ear1_seed_11	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_3	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_4	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_6	H	H	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_7	H	H	H	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_8	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H

Table A18: The genotype for untreated individuals 31-60, for markers on the short arm of 2H. Marker 11_11015 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a
MxB_F1_1_untrt_ear2_seed_11	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_2	A	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_4	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_5	A	A	A	A	A	A	A	A	A	A	A	A	A	B	B	B	B
MxB_F1_1_untrt_ear2_seed_6	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear2_seed_7	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_3	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_untrt_ear3_seed_4	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear3_seed_5	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_untrt_ear3_seed_9	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_11	H	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_12	A	A	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_cont_ear1_seed_2	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_cont_ear1_seed_3	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_cont_ear1_seed_6	B	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_8	A	A	A	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear1_seed_1	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_10	H	H	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_11	B	B	B	H	H	H	H	H	H	H	H	B	B	B	B	B	B

Table A19: The genotype for untreated individuals 61-90, for markers on the short arm of 2H. Marker 11_11015 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a
MxB_F1_2_untrt_ear1_seed_2	B	B	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_untrt_ear1_seed_3	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_4	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_5	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_untrt_ear1_seed_7	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_8	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_10	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_5	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_7	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_8	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_9	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_10	A	A	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear3_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_2	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_3	B	B	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_untrt_ear3_seed_4	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_5	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_7	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A20: The recombination data for markers on the short arm of 2H for untreated individuals 1-30. Superimposed with Table A17

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015	Tot. rec. events/arm
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67	
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G	
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a	
MxB_F1_1_cont_ear1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_10		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_11		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_13		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_14		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_15		0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_18		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_cont_ear1_seed_19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_5		0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_cont_ear1_seed_9		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_10		0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear1_seed_5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_6		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_7		0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_8		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_1		0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear2_seed_10		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Table A21: The recombination data for markers on the short arm of 2H for untreated individuals 31-60. Superimposed with Table A18

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015	Tot. rec. events/arm
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67	
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G	
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a	
MxB_F1_1_untrt_ear2_seed_11		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear2_seed_7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_untrt_ear3_seed_4		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear3_seed_5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_untrt_ear3_seed_9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_11		1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_12		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_cont_ear1_seed_2		0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_cont_ear1_seed_3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_cont_ear1_seed_6		0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_8		0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear1_seed_1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_10		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_11		0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2

Table A22: The recombination data for markers on the short arm of 2H for untreated individuals 61-90. Superimposed with Table A19

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015	Tot. rec. events/arm
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67	
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G	
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a	
MxB_F1_2_untrt_ear1_seed_2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_untrt_ear1_seed_3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_untrt_ear1_seed_7		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_10		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_untrt_ear2_seed_4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_5		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_9		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_10		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_3		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_7		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_8		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
																	Total recomb. Events in population	87

Table A23: The genotype for untreated individuals 1-30, for markers on the long arm of 2H. Marker 11_10909 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g
MxB_F1_1_cont_ear1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_11	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_12	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_13	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_14	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_15	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_16	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_cont_ear1_seed_18	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	A
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_cont_ear1_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_1	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_11	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	B	B	B
MxB_F1_1_untrt_ear1_seed_3	A	A	A	A	A	H	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_1_untrt_ear1_seed_4	H	H	H	H	H	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_6	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_8	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	H	H
MxB_F1_1_untrt_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear2_seed_10	H	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A24: The genotype for untreated individuals 31-60, for markers on the long arm of 2H. Marker 11_10909 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g
MxB_F1_1_untrt_ear2_seed_11	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_2	B	B	B	H	H	H	H	H	H	H	B	B	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	H	h	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_4	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_5	B	B	B	B	B	A	A	A	A	A	A	A	A	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_6	H	H	H	H	A	A	A	A	A	A	H	H	H	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_7	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_9	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B	H
MxB_F1_1_untrt_ear3_seed_1	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_5	H	H	H	A	A	H	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	B	B	B	B	B	B	B	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	H	h	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_1	A	A	A	A	A	A	A	H	H	H	B	B	B	B	B	B	B	B	B	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_11	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_6	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_8	B	B	B	B	B	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B

Table A25: The genotype for untreated individuals 61-90, for markers on the long arm of 2H. Marker 11_10909 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g
MxB_F1_2_untrt_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_4	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	A
MxB_F1_2_untrt_ear1_seed_5	A	A	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_6	A	A	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_8	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear1_seed_9	A	A	A	A	A	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_untrt_ear2_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_4	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_7	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_8	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_9	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_1	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear3_seed_10	B	B	B	B	B	B	B	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_2	A	A	A	A	A	H	H	H	H	H	H	H	H	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_4	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_5	H	H	H	H	A	H	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_6	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H
MxB_F1_2_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B

Table A26: The recombination data for markers on the long arm of 2H for untreated individuals 1-30. Superimposed with Table A23

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085	Total recomb. Events per arm
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72	
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A	
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g	
MxB_F1_1_cont_ear1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_11	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_12	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_15	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_cont_ear1_seed_18	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	3
MxB_F1_1_cont_ear1_seed_19	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	3
MxB_F1_1_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_cont_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	3
MxB_F1_1_untrt_ear1_seed_3	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4
MxB_F1_1_untrt_ear1_seed_4	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_8	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	4
MxB_F1_1_untrt_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	3
MxB_F1_1_untrt_ear2_seed_10	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2

Table A27: The recombination data for markers on the long arm of 2H for untreated individuals 31-60. Superimposed with Table A24

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015	Tot. rec. events/arm
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67	
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G	
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a	
MxB_F1_1_untrt_ear2_seed_11		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear2_seed_7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_untrt_ear3_seed_4		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear3_seed_5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_untrt_ear3_seed_9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_11		1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_12		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_cont_ear1_seed_2		0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_cont_ear1_seed_3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_cont_ear1_seed_6		0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_8		0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear1_seed_1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_10		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_11		0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2

Table A28: The recombination data for markers on the long arm of 2H for untreated individuals 61-90. Superimposed with Table A25 Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085	Total recomb. Events per arm
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72	
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A	
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g	
MxB_F1_2_untrt_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	3
MxB_F1_2_untrt_ear1_seed_5	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	3
MxB_F1_2_untrt_ear1_seed_6	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear1_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_10	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_4	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear2_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_10	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear3_seed_11	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear3_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_5	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	4
MxB_F1_2_untrt_ear3_seed_6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
																							Total recomb. Events.			162

Mean marker recomb. Freq./cell = 87(2HS)+162(2HL)/90 individuals = 2.77/cell

Table A29: The genotype for untreated individuals 1-30, for markers on the short arm of 3H. Marker 11_21197 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73
Morex SNP	G	C	G	G	A	G	A	G	C	G
Barke SNP	a	a	a	a	g	a	g	a	a	a
MxB_F1_1_cont_ear1_seed_1	B	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	A	A	H	H	H	H	H	H	B	B
MxB_F1_1_cont_ear1_seed_11	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_12	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_13	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_14	B	H	H	H	H	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_15	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_16	H	H	H	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_18	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_3	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_4	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_5	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_6	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_cont_ear1_seed_7	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_8	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_9	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_1	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_10	A	A	A	A	A	H	H	B	B	B
MxB_F1_1_untrt_ear1_seed_11	B	B	B	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_2	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_3	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_4	A	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_6	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_7	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_8	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear1_seed_9	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_10	B	B	B	B	B	B	B	B	B	B

Table A30: The genotype for untreated individuals 31-60, for markers on the short arm of 3H. Marker 11_21197 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73
Morex SNP	G	C	G	G	A	G	A	G	C	G
Barke SNP	a	a	a	a	g	a	g	a	a	a
MxB_F1_1_untrt_ear2_seed_11	A	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_2	H	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_4	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_5	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_untrt_ear2_seed_6	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_7	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_8	A	H	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_9	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_1	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_untrt_ear3_seed_3	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_4	H	H	H	A	A	H	H	H	B	B
MxB_F1_1_untrt_ear3_seed_5	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_8	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_9	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_1	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_cont_ear1_seed_10	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_11	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_12	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_2	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_3	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_6	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_7	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_cont_ear1_seed_8	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_untrt_ear1_seed_1	H	H	H	A	A	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_10	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_11	B	B	B	B	B	B	B	B	B	B

Table A31: The genotype for untreated individuals 61-90, for markers on the short arm of 3H. Marker 11_21197 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73
Morex SNP	G	C	G	G	A	G	A	G	C	G
Barke SNP	a	a	a	a	g	a	g	a	a	a
MxB_F1_2_untrt_ear1_seed_2	A	A	H	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear1_seed_3	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_untrt_ear1_seed_4	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_5	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_6	B	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_7	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_8	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_9	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_1	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_10	A	A	A	A	A	H	H	H	B	B
MxB_F1_2_untrt_ear2_seed_2	H	H	H	H	H	A	A	A	H	H
MxB_F1_2_untrt_ear2_seed_3	A	A	A	A	A	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_4	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_5	B	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_7	A	A	A	A	A	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_8	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_9	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_1	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_10	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_12	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_4	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_5	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_9	A	A	A	A	A	B	B	B	B	B

Table A32: The recombination data for markers on the short arm of 3H for untreated individuals 1-30. Superimposed with Table A29

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197	Total recomb. Events per arm
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73	
Morex SNP	G	C	G	G	A	G	A	G	C	G	
Barke SNP	a	a	a	a	g	a	g	a	a	a	
MxB_F1_1_cont_ear1_seed_1		1	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_10		0	1	0	0	0	0	0	1	0	2
MxB_F1_1_cont_ear1_seed_11		0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_12		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_13		0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_14		1	0	0	0	1	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_15		0	0	1	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_16		0	0	1	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_18		0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_19		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_3		1	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_4		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_5		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_6		0	0	0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_7		0	0	1	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_8		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_9		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_1		0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_10		0	0	0	0	1	0	1	0	0	2
MxB_F1_1_untrt_ear1_seed_11		0	0	1	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_2		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_3		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_4		1	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_5		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_6		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_7		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_8		0	0	0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear1_seed_9		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_10		0	0	0	0	0	0	0	0	0	0

Table A33: The recombination data for markers on the short arm of 3H for untreated individuals 31-60. Superimposed with Table A30

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197	Total recomb. Events per arm
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73	
Morex SNP	G	C	G	G	A	G	A	G	C	G	
Barke SNP	a	a	a	a	g	a	g	a	a	a	
MxB_F1_1_untrt_ear2_seed_11		1	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2		1	0	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_3		0	0	0	1	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_4		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_5		0	0	0	0	0	0	0	1	0	1
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_7		1	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_8		1	0	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_9		0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_1		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_2		0	0	0	0	0	0	0	1	0	1
MxB_F1_1_untrt_ear3_seed_3		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_4		0	0	1	0	1	0	0	1	0	3
MxB_F1_1_untrt_ear3_seed_5		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_6		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_7		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_8		0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_9		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_1		0	0	0	0	0	0	0	1	0	1
MxB_F1_2_cont_ear1_seed_10		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_11		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_12		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_2		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_3		0	1	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_6		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_7		0	0	0	0	0	0	0	1	0	1
MxB_F1_2_cont_ear1_seed_8		0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear1_seed_1		0	0	1	0	1	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_10		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_11		0	0	0	0	0	0	0	0	0	0

Table A34: The recombination data for markers on the short arm of 3H for untreated individuals 61-90. Superimposed with Table A31

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197	Total recomb. Events per arm
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73	
Morex SNP	G	C	G	G	A	G	A	G	C	G	
Barke SNP	a	a	a	a	g	a	g	a	a	a	
MxB_F1_2_untrt_ear1_seed_2		0	1	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear1_seed_3		0	0	0	0	0	0	0	1	0	1
MxB_F1_2_untrt_ear1_seed_4		0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_5		0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_6		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_7		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_9		0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_1		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_10		0	0	0	0	1	0	0	1	0	2
MxB_F1_2_untrt_ear2_seed_2		0	0	0	0	1	0	0	1	0	2
MxB_F1_2_untrt_ear2_seed_3		0	0	0	0	2	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_4		0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_5		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_6		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_7		0	0	0	0	2	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_8		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_9		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_10		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_11		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_12		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_2		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_3		0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_4		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_5		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_6		0	0	0	0	0	0	0	1	0	1
MxB_F1_2_untrt_ear3_seed_7		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_8		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_9		0	0	0	0	2	0	0	0	0	2
							Total recomb. Events in population				78

Table A35: The genotype for untreated individuals 1-30, for markers on the long arm of 3H. Marker 11_10728 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a
MxB_F1_1_cont_ear1_seed_1	H	H	H	H	H	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_11	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_12	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_cont_ear1_seed_13	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H
MxB_F1_1_cont_ear1_seed_14	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_cont_ear1_seed_15	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_cont_ear1_seed_16	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_18	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_cont_ear1_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_4	A	A	A	A	A	A	H	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_1_cont_ear1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_cont_ear1_seed_6	A	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_cont_ear1_seed_8	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_cont_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_untrt_ear1_seed_1	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_untrt_ear1_seed_10	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_11	A	A	A	A	A	A	A	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_untrt_ear1_seed_2	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_1_untrt_ear1_seed_3	A	A	A	A	A	A	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_4	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_5	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_untrt_ear1_seed_6	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_7	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_8	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B	H	H	H	H	H	B	B
MxB_F1_1_untrt_ear1_seed_9	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	H	H	H	H	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_10	B	B	B	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A	A	A	A

Table A36: The genotype for untreated individuals 31-60, for markers on the long arm of 3H. Marker 11_10728 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a
MxB_F1_1_untrt_ear2_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	H	H	H	H	H	B	B
MxB_F1_1_untrt_ear2_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_4	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_untrt_ear2_seed_5	B	B	B	B	B	B	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_1_untrt_ear2_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_8	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	A	A	A	A	H	H
MxB_F1_1_untrt_ear2_seed_9	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H	H	A	A	H	H
MxB_F1_1_untrt_ear3_seed_1	H	H	H	H	H	B	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H
MxB_F1_1_untrt_ear3_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	B	B	B	B
MxB_F1_1_untrt_ear3_seed_3	H	H	H	H	H	H	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_4	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear3_seed_7	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	H	H	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_untrt_ear3_seed_9	B	H	H	H	H	H	H	H	H	H	H	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_10	A	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	A
MxB_F1_2_cont_ear1_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	H	H	A	A	A
MxB_F1_2_cont_ear1_seed_12	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	B	H
MxB_F1_2_cont_ear1_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B
MxB_F1_2_cont_ear1_seed_3	A	A	A	A	A	A	A	H	H	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_2_cont_ear1_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	A	A	A	H	H	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_8	B	B	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_1	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_10	h	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_11	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	A	A	A

Table A37: The genotype for untreated individuals 61-90, for markers on the long arm of 3H. Marker 11_10728 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a
MxB_F1_2_untrt_ear1_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	A
MxB_F1_2_untrt_ear1_seed_3	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear1_seed_4	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H
MxB_F1_2_untrt_ear1_seed_5	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	H	B	B	B
MxB_F1_2_untrt_ear1_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_10	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_2	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_5	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	H	H	H	B	B
MxB_F1_2_untrt_ear2_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_9	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_1	H	H	H	H	H	H	H	H	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear3_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear3_seed_12	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_untrt_ear3_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H
MxB_F1_2_untrt_ear3_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_untrt_ear3_seed_6	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H	H	H	A	A	A	A
MxB_F1_2_untrt_ear3_seed_9	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A38: The recombination data for markers on the long arm of 3H for untreated individuals 1-30. Superimposed with Table A35

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	11_10753	11_10312	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267	Total recomb. Events per arm
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40	
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G	
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a	
MxB_F1_1_cont_ear1_seed_1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_12	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_cont_ear1_seed_13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	3
MxB_F1_1_cont_ear1_seed_14	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_cont_ear1_seed_15	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_cont_ear1_seed_16	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_19	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	3
MxB_F1_1_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_4	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	3
MxB_F1_1_cont_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_cont_ear1_seed_8	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_cont_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_11	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	3
MxB_F1_1_untrt_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_untrt_ear1_seed_3	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_4	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3
MxB_F1_1_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	1	0	4
MxB_F1_1_untrt_ear1_seed_9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2

Table A39: The recombination data for markers on the long arm of 3H for untreated individuals 31-60. Superimposed with Table A36

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	11_10753	11_10312	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267	Total recomb. Events per arm
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40	
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G	
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a	
MxB_F1_1_untrt_ear2_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	3
MxB_F1_1_untrt_ear2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	2
MxB_F1_1_untrt_ear2_seed_3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_untrt_ear2_seed_5	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear2_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	3
MxB_F1_1_untrt_ear2_seed_9	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	4
MxB_F1_1_untrt_ear3_seed_1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	4
MxB_F1_1_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2
MxB_F1_1_untrt_ear3_seed_3	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_8	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_1_untrt_ear3_seed_9	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_cont_ear1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_10	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	4
MxB_F1_2_cont_ear1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	3
MxB_F1_2_cont_ear1_seed_12	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	3
MxB_F1_2_cont_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	2
MxB_F1_2_cont_ear1_seed_3	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	3
MxB_F1_2_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	3
MxB_F1_2_cont_ear1_seed_8	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	2

Table A40: The recombination data for markers on the long arm of 3H for untreated individuals 31-60. Superimposed with Table A37 Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	11_10753	11_10312	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267	Total recomb. Events per arm
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40	
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G	
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a	
MxB_F1_2_untrt_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	2
MxB_F1_2_untrt_ear1_seed_3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_untrt_ear1_seed_4	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0	0	3
MxB_F1_2_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_untrt_ear1_seed_9	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_10	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear2_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	3
MxB_F1_2_untrt_ear2_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_9	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	2
MxB_F1_2_untrt_ear3_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_untrt_ear3_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear3_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_untrt_ear3_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	3
MxB_F1_2_untrt_ear3_seed_9	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
																						Total recomb. Events in population	171

Mean marker recomb. Freq./cell = 78(3HS)+171(3HL)/90 individuals = 2.77/cell

Table A41: The genotype for untreated individuals 1-30, for markers on the short arm of 4H. Marker 11_10093 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50
Morex SNP	A	G	G	G	A	G	A	A
Barke SNP	g	a	c	a	g	a	c	g
MxB_F1_1_cont_ear1_seed_1	B	B	B	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	B	B	B	B	B	H	H	H
MxB_F1_1_cont_ear1_seed_11	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_12	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_13	H	H	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_14	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_15	H	H	H	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_16	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_18	H	H	H	H	B	H	H	H
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_3	H	H	H	H	B	B	B	B
MxB_F1_1_cont_ear1_seed_4	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_5	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_6	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_7	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_8	B	B	B	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_9	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_1	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	A	A	A	H	H	B	B	B
MxB_F1_1_untrt_ear1_seed_11	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_3	H	H	H	B	B	H	H	H
MxB_F1_1_untrt_ear1_seed_4	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear1_seed_6	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_7	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_8	H	H	H	A	H	H	H	H
MxB_F1_1_untrt_ear1_seed_9	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_1	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_10	A	A	A	A	A	A	A	A

Table A42: The genotype for untreated individuals 31-60, for markers on the short arm of 4H. Marker 11_10093 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50
Morex SNP	A	G	G	G	A	G	A	A
Barke SNP	g	a	c	a	g	a	c	g
MxB_F1_1_untrt_ear2_seed_11	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear2_seed_2	B	B	B	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear2_seed_4	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_5	H	H	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_6	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_7	B	B	B	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_8	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_9	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_1	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_2	B	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_3	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_4	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_5	B	B	B	B	H	H	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	A	A	A	A
MxB_F1_1_untrt_ear3_seed_8	H	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_9	H	h	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_1	H	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_10	A	A	H	H	B	B	B	B
MxB_F1_2_cont_ear1_seed_11	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_12	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_2	H	H	H	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_3	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_6	A	A	A	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	H	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_8	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_1	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_10	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_11	A	A	A	A	A	A	A	A

Table A43: The genotype for untreated individuals 61-90, for markers on the short arm of 4H. Marker 11_10093 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50
Morex SNP	A	G	G	G	A	G	A	A
Barke SNP	g	a	c	a	g	a	c	g
MxB_F1_2_untrt_ear1_seed_2	H	H	H	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_3	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_4	H	H	H	H	H	B	B	B
MxB_F1_2_untrt_ear1_seed_5	B	B	B	B	A	A	A	A
MxB_F1_2_untrt_ear1_seed_6	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_7	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_8	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_1	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_10	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_2	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_3	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_5	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_6	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_7	A	A	H	H	B	B	B	B
MxB_F1_2_untrt_ear2_seed_8	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_9	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_1	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_10	A	A	A	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	A	A	H	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_12	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_2	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_3	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_4	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_5	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_6	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_7	B	B	B	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_8	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_9	H	H	H	H	H	A	A	A

Table A44: The recombination data for markers on the short arm of 4H for untreated individuals 1-30. Superimposed with Table A41

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093	Total recomb. Events per arm
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50	
Morex SNP	A	G	G	G	A	G	A	A	
Barke SNP	g	a	c	a	g	a	c	g	
MxB_F1_1_cont_ear1_seed_1		0	0	1	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_10		0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_11		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_12		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_13		0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_14		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_15		0	0	1	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_16		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_18		0	0	0	1	1	0	0	2
MxB_F1_1_cont_ear1_seed_19		0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_3		0	0	0	1	0	0	0	1
MxB_F1_1_cont_ear1_seed_4		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_5		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_6		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_7		0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_8		0	0	1	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_9		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_1		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_10		0	0	1	0	1	0	0	2
MxB_F1_1_untrt_ear1_seed_11		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_2		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_3		0	0	1	0	1	0	0	2
MxB_F1_1_untrt_ear1_seed_4		0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear1_seed_5		0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear1_seed_6		0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_7		0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_8		0	0	1	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_9		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_1		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_10		0	0	0	0	0	0	0	0

Table A45: The recombination data for markers on the short arm of 4H for untreated individuals 31-60. Superimposed with Table A42

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093	Total recomb. Events per arm
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50	
Morex SNP	A	G	G	G	A	G	A	A	
Barke SNP	g	a	c	a	g	a	c	g	
MxB_F1_1_untrt_ear2_seed_11		0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear2_seed_2		0	0	2	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_3		0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear2_seed_4		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_5		0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_7		0	0	2	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_8		0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_9		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_1		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_2		0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_3		0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_4		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_5		0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear3_seed_6		0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_7		0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear3_seed_8		0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_9		0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_1		0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_10		0	1	0	1	0	0	0	2
MxB_F1_2_cont_ear1_seed_11		0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_12		0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_2		0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_3		0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_6		0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_7		0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_8		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_1		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_10		0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_11		0	0	0	0	0	0	0	0

Table A46: The recombination data for markers on the short arm of 4H for untreated individuals 61-90. Superimposed with Table A43

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093	Total recomb. Events per arm
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50	
Morex SNP	A	G	G	G	A	G	A	A	
Barke SNP	g	a	c	a	g	a	c	g	
MxB_F1_2_untrt_ear1_seed_2		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_3		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_4		0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear1_seed_5		0	0	0	2	0	0	0	2
MxB_F1_2_untrt_ear1_seed_6		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_7		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_9		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_1		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_10		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_2		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_3		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_4		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_5		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_6		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_7		0	1	0	1	0	0	0	2
MxB_F1_2_untrt_ear2_seed_8		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_9		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_1		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_10		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_11		0	1	1	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_12		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_2		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_3		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_4		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_5		0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_6		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_7		0	0	2	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_8		0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_9		0	0	0	0	1	0	0	1
					Total recomb. Events in population				58

Table A47: The genotype for untreated individuals 1-30, for markers on the long arm of 4H. Marker 11_10881 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a
MxB_F1_1_cont_ear1_seed_1	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_1_cont_ear1_seed_11	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_cont_ear1_seed_12	H	H	H	H	H	B	B	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_13	B	B	B	B	B	B	B	B	H	H	A	A
MxB_F1_1_cont_ear1_seed_14	H	H	H	H	H	H	H	H	B	B	B	H
MxB_F1_1_cont_ear1_seed_15	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_16	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_18	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_cont_ear1_seed_19	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_3	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_4	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_6	H	H	H	H	A	A	A	A	A	A	H	H
MxB_F1_1_cont_ear1_seed_7	A	A	A	A	A	A	A	H	B	B	B	H
MxB_F1_1_cont_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_9	H	H	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_1	H	H	H	H	H	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	B	B	B	B	B	B	B	H	H	H	A	A
MxB_F1_1_untrt_ear1_seed_11	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_untrt_ear1_seed_3	H	H	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_untrt_ear1_seed_4	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	H	H	H	H	H	H	H	B	H	H	H	H
MxB_F1_1_untrt_ear1_seed_6	H	H	H	H	H	H	B	B	B	B	B	H
MxB_F1_1_untrt_ear1_seed_7	H	H	H	H	H	H	B	B	H	H	H	H
MxB_F1_1_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_untrt_ear1_seed_9	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_1	A	A	A	A	A	H	H	H	B	B	H	H
MxB_F1_1_untrt_ear2_seed_10	A	A	A	A	A	A	A	A	H	H	B	B

Table A48: The genotype for untreated individuals 31-60, for markers on the long arm of 4H. Marker 11_10881 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a
MxB_F1_1_untrt_ear2_seed_11	A	A	A	A	A	A	A	H	H	H	B	B
MxB_F1_1_untrt_ear2_seed_2	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_3	A	A	A	A	A	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_4	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_untrt_ear2_seed_5	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_7	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_9	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_1	B	B	B	B	B	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_3	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_4	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_5	H	H	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_7	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_8	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_1	A	A	A	A	A	A	A	H	H	H	H	B
MxB_F1_2_cont_ear1_seed_10	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_11	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_12	B	B	B	B	B	H	H	A	A	A	H	H
MxB_F1_2_cont_ear1_seed_2	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_3	B	B	B	B	B	B	B	B	B	B	H	A
MxB_F1_2_cont_ear1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_cont_ear1_seed_8	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_untrt_ear1_seed_1	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_10	B	B	B	B	B	B	B	H	H	H	A	A
MxB_F1_2_untrt_ear1_seed_11	A	A	A	A	A	H	H	H	H	H	H	H

Table A49: The genotype for untreated individuals 61-90, for markers on the long arm of 4H. Marker 11_10881 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a
MxB_F1_2_untrt_ear1_seed_2	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_3	B	B	B	B	B	B	B	B	B	B	A	A
MxB_F1_2_untrt_ear1_seed_4	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_5	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear1_seed_6	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_8	H	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	H	H	H	H	H	H	H	H	B	B	B	H
MxB_F1_2_untrt_ear2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_10	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_2	B	B	B	B	B	H	H	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_3	H	H	H	H	H	H	H	H	A	A	A	H
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	H	A	A	A	H
MxB_F1_2_untrt_ear2_seed_5	B	B	B	B	B	B	H	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_6	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_7	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_8	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_9	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_1	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_10	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_12	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_4	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_untrt_ear3_seed_5	H	H	H	H	H	H	B	B	B	B	H	H
MxB_F1_2_untrt_ear3_seed_6	H	H	A	A	A	A	H	H	H	H	A	A
MxB_F1_2_untrt_ear3_seed_7	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_8	A	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear3_seed_9	H	H	H	H	H	H	H	H	H	H	H	H

Table A50: The recombination data for markers on the long arm of 4H for untreated individuals 1-30. Superimposed with Table A47

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007	Total recomb. Events per arm
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09	
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G	
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a	
MxB_F1_1_cont_ear1_seed_1	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_1_cont_ear1_seed_11	1	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_cont_ear1_seed_12	0	0	0	0	0	1	0	1	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_13	0	0	0	0	0	0	0	0	1	0	1	0	2
MxB_F1_1_cont_ear1_seed_14	0	0	0	0	0	0	0	0	1	0	0	1	2
MxB_F1_1_cont_ear1_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_18	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_cont_ear1_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_4	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_6	0	0	0	0	1	0	0	0	0	0	1	0	2
MxB_F1_1_cont_ear1_seed_7	0	0	0	0	0	0	0	1	1	0	0	1	3
MxB_F1_1_cont_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_9	0	0	1	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_1	0	0	0	0	0	1	0	0	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_10	0	0	0	0	0	0	0	1	0	0	1	0	2
MxB_F1_1_untrt_ear1_seed_11	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_1_untrt_ear1_seed_3	0	0	1	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_untrt_ear1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_5	0	0	0	0	0	0	0	1	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_6	0	0	0	0	0	0	1	0	0	0	0	1	2
MxB_F1_1_untrt_ear1_seed_7	0	0	0	0	0	0	1	0	1	0	0	0	2
MxB_F1_1_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_1_untrt_ear1_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1	0	0	0	0	0	1	0	0	1	0	1	0	3
MxB_F1_1_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	1	0	1	0	2

Table A51: The recombination data for markers on the long arm of 4H for untreated individuals 31-60. Superimposed with Table A48

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007	Total recomb. Events per arm
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09	
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G	
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a	
MxB_F1_1_untrt_ear2_seed_11	0	0	0	0	0	0	0	1	0	0	1	0	2
MxB_F1_1_untrt_ear2_seed_2	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_3	0	0	0	0	0	2	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_4	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear2_seed_5	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_1	0	0	0	0	0	2	0	1	0	0	0	0	3
MxB_F1_1_untrt_ear3_seed_2	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_3	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_4	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_5	0	0	1	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_untrt_ear3_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_8	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_9	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_1	0	0	0	0	0	0	0	1	0	0	0	1	2
MxB_F1_2_cont_ear1_seed_10	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_11	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_12	0	0	0	0	0	1	0	1	0	0	1	0	3
MxB_F1_2_cont_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	1	1	2
MxB_F1_2_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_7	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_cont_ear1_seed_8	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_untrt_ear1_seed_1	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_10	0	0	0	0	0	0	0	1	0	0	1	0	2
MxB_F1_2_untrt_ear1_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	1

Table A52: The recombination data for markers on the long arm of 4H for untreated individuals 61-90. Superimposed with Table A49 Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007	Total recomb. Events per arm
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09	
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G	
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a	
MxB_F1_2_untrt_ear1_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	2	0	2
MxB_F1_2_untrt_ear1_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear1_seed_6	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_8	0	1	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_9	0	0	0	0	0	0	0	0	1	0	0	1	2
MxB_F1_2_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_2	0	0	0	0	0	1	0	1	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	1	0	0	1	2
MxB_F1_2_untrt_ear2_seed_4	0	0	0	0	0	0	0	0	1	0	0	1	2
MxB_F1_2_untrt_ear2_seed_5	0	0	0	0	0	0	1	1	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_7	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_9	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_12	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_2	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_3	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_4	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_untrt_ear3_seed_5	0	0	0	0	0	0	1	0	0	0	1	0	2
MxB_F1_2_untrt_ear3_seed_6	0	0	1	0	0	0	1	0	0	0	1	0	3
MxB_F1_2_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_8	0	1	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear3_seed_9	1	0	0	0	0	0	0	0	0	0	0	0	1
									Total recomb. Events in population				105

Mean marker recomb. Freq./cell = 58(4HS)+105(4HL)/90 individuals = 1.81/cell

Table A53: The genotype for untreated individuals 1-30, for markers on the short arm of 5H. Marker 11_21350 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a
MxB_F1_1_cont_ear1_seed_1	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_11	H	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_12	B	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_13	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_14	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_15	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_16	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_18	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_19	H	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_3	H	H	H	B	B	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_4	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_5	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_6	H	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_7	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_9	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_1	H	H	H	B	B	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_11	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_3	B	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_4	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	H	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_6	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_7	H	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_8	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_9	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_10	H	B	B	B	B	B	H	H	H	H	H	H

Table A54: The genotype for untreated individuals 31-60, for markers on the short arm of 5H. Marker 11_21350 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a
MxB_F1_1_untrt_ear2_seed_11	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_2	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_3	H	H	H	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_4	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_5	A	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_6	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_7	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_9	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_1	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_3	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_4	A	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_5	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_untrt_ear3_seed_6	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	H	H	H	H	H	H	h	H
MxB_F1_2_cont_ear1_seed_1	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_10	B	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_11	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_12	H	H	H	H	A	A	A	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_2	B	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_3	B	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_6	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_8	B	B	B	B	H	H	H	H	A	A	A	A
MxB_F1_2_untrt_ear1_seed_1	H	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_10	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_11	A	A	A	H	H	H	H	H	H	H	H	H

Table A55: The genotype for untreated individuals 61-90, for markers on the short arm of 5H. Marker 11_21350 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a
MxB_F1_2_untrt_ear1_seed_2	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_3	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_4	B	B	B	B	H	H	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_5	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_6	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_untrt_ear1_seed_7	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_8	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_9	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_1	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_10	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_2	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_3	B	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_5	A	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_6	A	A	A	H	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_7	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear2_seed_9	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_1	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_10	H	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	A	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_12	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_2	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_4	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_5	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_6	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_7	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_9	H	H	H	H	H	H	A	A	A	A	A	A

Table A56: The recombination data for markers on the short arm of 5H for untreated individuals 1-30. Superimposed with Table A53

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350	Total recomb. Events per arm
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00	
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G	
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a	
MxB_F1_1_cont_ear1_seed_1		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_10		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_11		1	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_12		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_13		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_14		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_15		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_16		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_18		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_19		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_3		0	0	1	0	1	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_4		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_5		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_6		1	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_7		0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_9		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_1		0	0	1	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_10		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_11		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_2		0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_3		1	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_4		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_5		1	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_6		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_7		1	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_9		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_10		1	0	0	0	0	1	0	0	0	0	0	2

Table A57: The recombination data for markers on the short arm of 5H for untreated individuals 31-60. Superimposed with Table A54

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350	Total recomb. Events per arm
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00	
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G	
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a	
MxB_F1_1_untrt_ear2_seed_11		0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_3		0	0	1	0	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_4		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_5		1	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_7		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_8		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_9		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_1		0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_2		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_3		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_4		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_5		0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear3_seed_6		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_7		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_8		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_9		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_1		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_10		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_11		0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_12		0	0	0	1	0	0	1	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_2		1	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_3		1	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_6		0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_7		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_8		0	0	0	1	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear1_seed_1		1	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_10		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_11		0	0	1	0	0	0	0	0	0	0	0	1

Table A58: The recombination data for markers on the short arm of 5H for untreated individuals 61-90. Superimposed with Table A55

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350	Total recomb. Events per arm
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00	
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G	
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a	
MxB_F1_2_untrt_ear1_seed_2		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_3		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_4		0	0	0	1	0	1	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_5		0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_6		0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_untrt_ear1_seed_7		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_9		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_1		0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_10		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_2		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_3		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_4		0	0	0	0	1	1	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_5		1	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_6		0	0	1	0	0	1	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_7		0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8		0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_untrt_ear2_seed_9		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_10		1	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_11		1	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_12		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_2		0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_3		0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_4		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_5		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_6		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_7		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_8		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_9		0	0	0	0	0	1	0	0	0	0	0	1
									Total recomb. Events in population				97

Table A59: The genotype for untreated individuals 1-30, for markers on the long arm of 5H. Marker 11_20306 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a
MxB_F1.1_cont_ear1_seed.1	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1.1_cont_ear1_seed.10	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1.1_cont_ear1_seed.11	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1.1_cont_ear1_seed.12	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1.1_cont_ear1_seed.13	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	B	B
MxB_F1.1_cont_ear1_seed.14	A	A	A	H	H	H	H	H	H	B	B	B	B	B	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1.1_cont_ear1_seed.15	A	A	A	A	A	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1.1_cont_ear1_seed.16	B	B	B	B	B	B	B	B	B	B	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1.1_cont_ear1_seed.18	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1.1_cont_ear1_seed.19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1.1_cont_ear1_seed.3	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1.1_cont_ear1_seed.4	B	B	B	B	B	B	B	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1.1_cont_ear1_seed.5	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1.1_cont_ear1_seed.6	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1.1_cont_ear1_seed.7	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1.1_cont_ear1_seed.8	H	H	H	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1.1_cont_ear1_seed.9	B	B	B	B	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1.1_untrt_ear1_seed.1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1.1_untrt_ear1_seed.10	H	H	H	H	H	H	H	H	H	H	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1.1_untrt_ear1_seed.11	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1.1_untrt_ear1_seed.2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1.1_untrt_ear1_seed.3	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1.1_untrt_ear1_seed.4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1.1_untrt_ear1_seed.5	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	B	B	B	B	B	B
MxB_F1.1_untrt_ear1_seed.6	H	H	H	H	H	H	H	H	A	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1.1_untrt_ear1_seed.7	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1.1_untrt_ear1_seed.8	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1.1_untrt_ear1_seed.9	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1.1_untrt_ear2_seed.1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1.1_untrt_ear2_seed.10	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	B	B

Table A60: The genotype for untreated individuals 31-60, for markers on the long arm of 5H. Marker 11_20306 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|84.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a
MxB_F1_1_untrt_ear2_seed_11	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_2	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_4	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_6	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_7	H	H	H	H	H	H	H	H	H	B	B	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	H	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_9	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_4	B	B	B	B	B	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_5	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_6	B	B	B	B	B	B	B	H	H	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_untrt_ear3_seed_8	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	H	B	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B	B
MxB_F1_2_cont_ear1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_10	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_11	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_cont_ear1_seed_12	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_2	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	B	B
MxB_F1_2_cont_ear1_seed_3	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_8	A	A	A	A	A	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_1	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B

Table A61: The genotype for untreated individuals 61-90, for markers on the long arm of 5H. Marker 11_20306 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022
Position on chromosome	5H|50.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a
MxB_F1_2_untrt_ear1_seed_2	A	A	A	A	A	B	B	B	B	B	B	H	H	H	H	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_untrt_ear1_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_4	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_5	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_6	A	A	A	A	A	A	A	H	H	B	H	H	H	H	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_7	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_8	B	B	B	B	B	B	B	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_9	B	B	B	B	B	B	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_1	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear2_seed_10	B	B	B	B	B	B	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear2_seed_3	A	A	A	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_5	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_6	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H
MxB_F1_2_untrt_ear2_seed_7	A	A	A	A	A	A	A	A	A	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_2_untrt_ear2_seed_9	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_1	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_10	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_11	B	B	B	B	B	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_12	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	H	H
MxB_F1_2_untrt_ear3_seed_3	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_untrt_ear3_seed_4	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_5	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_untrt_ear3_seed_6	A	A	A	A	A	A	A	B	B	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_9	A	A	A	H	H	H	H	H	H	A	A	A	A	A	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B

Table A62: The recombination data for markers on the long arm of 5H for untreated individuals 1-30. Superimposed with Table A59

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022	Total recomb. Events per arm
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43	
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G	
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a	
MxB_F1.1_cont_ear1_seed_1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1.1_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1.1_cont_ear1_seed_11	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1.1_cont_ear1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1.1_cont_ear1_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	3
MxB_F1.1_cont_ear1_seed_14	0	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
MxB_F1.1_cont_ear1_seed_15	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.1_cont_ear1_seed_16	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	4
MxB_F1.1_cont_ear1_seed_18	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1.1_cont_ear1_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1.1_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.1_cont_ear1_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.1_cont_ear1_seed_5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3
MxB_F1.1_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1.1_cont_ear1_seed_7	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	3
MxB_F1.1_cont_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	4
MxB_F1.1_cont_ear1_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1.1_untrt_ear1_seed_1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	3
MxB_F1.1_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.1_untrt_ear1_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1.1_untrt_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	3
MxB_F1.1_untrt_ear1_seed_3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1.1_untrt_ear1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1.1_untrt_ear1_seed_5	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	3
MxB_F1.1_untrt_ear1_seed_6	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4
MxB_F1.1_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1.1_untrt_ear1_seed_8	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.1_untrt_ear1_seed_9	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1.1_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	3
MxB_F1.1_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	3

Table A63: The recombination data for markers on the long arm of 5H for untreated individuals 31-60. Superimposed with Table A60

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022	Total recomb. Events per arm
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43	
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G	
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a	
MxB_F1_1_untrt_ear2_seed_11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3
MxB_F1_1_untrt_ear2_seed_6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_7	0	0	0	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	5
MxB_F1_1_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	3
MxB_F1_1_untrt_ear2_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_4	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_untrt_ear3_seed_5	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	4
MxB_F1_1_untrt_ear3_seed_6	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	5
MxB_F1_1_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_1_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_9	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	5
MxB_F1_2_cont_ear1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_cont_ear1_seed_12	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_cont_ear1_seed_2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	4
MxB_F1_2_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_8	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	4
MxB_F1_2_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	3
MxB_F1_2_untrt_ear1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Table A64: The recombination data for markers on the long arm of 5H for untreated individuals 61-90. Superimposed with Table A61 Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022	Total recomb. Events per arm
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43	
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G	
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a	
MxB_F1_2_untrt_ear1_seed_2	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	6
MxB_F1_2_untrt_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_5	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear1_seed_6	0	0	0	0	0	0	0	1	0	1	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
MxB_F1_2_untrt_ear1_seed_7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_8	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	4
MxB_F1_2_untrt_ear1_seed_9	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	4
MxB_F1_2_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_untrt_ear2_seed_10	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear2_seed_3	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_untrt_ear2_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	3
MxB_F1_2_untrt_ear2_seed_7	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear2_seed_9	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_10	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	5
MxB_F1_2_untrt_ear3_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_12	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	4
MxB_F1_2_untrt_ear3_seed_3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4
MxB_F1_2_untrt_ear3_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_untrt_ear3_seed_6	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	5
MxB_F1_2_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_9	0	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
																																				Total recomb. Events in population		225

Mean marker recomb. Freq./cell = 97(5HS)+225(5HL)/90 individuals = 3.58/cell

Table A65: The genotype for untreated individuals 1-30, for markers on the short arm of 6H. Marker 11_11312 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a
MxB_F1_1_cont_ear1_seed_1	H	H	H	H	H	H	H	H	h	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_10	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_11	B	B	B	B	B	B	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_12	A	A	A	A	A	A	A	A	a	A	A	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_13	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_14	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_15	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_16	B	B	B	B	B	B	B	B	b	B	B	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_18	H	H	H	H	H	H	H	H	b	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_19	A	A	A	H	H	H	H	H	h	H	H	B	B	B	B	B	H
MxB_F1_1_cont_ear1_seed_3	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_4	H	H	H	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_5	A	A	A	A	A	A	A	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_6	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_7	H	H	H	H	H	H	H	H	h	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_8	H	H	H	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_9	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_1	B	B	B	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	A	A	A	A	A	H	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_11	A	A	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_3	B	B	B	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_4	B	B	B	B	B	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	H	H	H	B	B	B	B	B	b	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_6	H	H	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_7	A	A	A	A	H	H	H	H	h	H	H	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_9	B	B	B	B	B	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	H	H	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_10	B	B	B	H	H	H	H	H	h	H	H	H	H	H	H	H	H

Table A66: The genotype for untreated individuals 31-60, for markers on the short arm of 6H. Marker 11_11312 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a
MxB_F1_1_untrt_ear2_seed_11	B	B	B	B	B	B	B	B	b	B	B	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_2	A	A	A	A	A	H	H	H	h	H	H	H	H	H	B	B	B
MxB_F1_1_untrt_ear2_seed_3	B	B	B	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_4	H	H	H	H	H	B	B	B	b	B	B	B	B	B	B	B	H
MxB_F1_1_untrt_ear2_seed_5	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_6	H	H	H	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_7	A	A	A	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_8	H	H	H	H	H	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_9	B	B	B	B	B	H	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_1	H	H	H	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_2	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_3	H	H	H	H	H	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_4	B	B	B	B	B	B	B	B	b	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_5	H	H	H	H	H	H	H	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	A	A	A	A	a	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	B	B	B	B	B	B	B	B	b	B	B	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	H	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_1	H	H	H	H	H	H	H	H	h	H	H	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_10	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_11	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_12	H	H	A	A	A	A	A	A	a	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_2	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_3	H	H	A	A	A	A	A	A	a	A	A	A	A	A	H	H	H
MxB_F1_2_cont_ear1_seed_6	A	A	A	A	A	H	H	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_7	A	A	A	A	A	A	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_8	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_1	B	B	B	H	H	H	H	H	h	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_10	H	H	B	B	B	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_11	H	H	H	H	H	H	H	H	h	H	H	A	A	A	A	A	A

Table A67: The genotype for untreated individuals 61-90, for markers on the short arm of 6H. Marker 11_11312 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a
MxB_F1_2_untrt_ear1_seed_2	H	H	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_3	H	H	H	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_4	H	H	H	H	H	H	H	H	b	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_5	B	B	B	B	B	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_6	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_7	B	B	B	B	B	B	B	B	b	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	A	A	A	A	A	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_1	A	A	A	A	A	A	A	A	a	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_10	B	B	B	B	B	B	B	B	b	B	B	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_2	H	H	A	A	A	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_3	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_4	B	B	B	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_5	H	H	H	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_7	H	H	H	A	A	A	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	h	H	H	h	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_9	H	H	H	H	H	H	B	B	b	B	B	B	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_1	A	A	A	H	H	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_10	A	A	A	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	B	B	B	B	B	B	B	B	b	B	B	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_12	H	H	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_3	B	B	B	B	B	B	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_4	B	B	B	B	B	B	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_5	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_6	H	H	A	A	A	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_7	A	A	A	A	A	A	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_9	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H

Table A68: The recombination data for markers on the short arm of 6H for untreated individuals 1-30. Superimposed with Table A65

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	11_10427	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312	Total recomb. Events per arm
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	6H|34.40	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00	
Morex SNP	A	C	G	a	g	A	G	G	a	G	G	G	C	A	A	A	G	
Barke SNP	g	a	a	c	a	g	a	c	g	a	c	a	a	c	g	g	a	
MxB_F1_1_cont_ear1_seed_1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_11		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_12		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_13		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_16		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_18		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_19		0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1	3
MxB_F1_1_cont_ear1_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_7		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_8		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_10		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_11		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_5		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_7		0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_10		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Table A69: The recombination data for markers on the short arm of 6H for untreated individuals 31-60. Superimposed with Table A66

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	11_10427	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312	Total recomb. Events per arm
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	6H|34.40	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00	
Morex SNP	A	C	G	a	g	A	G	G	a	G	G	G	C	A	A	A	G	
Barke SNP	g	a	a	c	a	g	a	c	g	a	c	a	a	c	g	g	a	
MxB_F1_1_untrt_ear2_seed_11		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2		0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_1_untrt_ear2_seed_3		0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_untrt_ear2_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_7		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_8		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_9		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_6		0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_8		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_12		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_3		0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_cont_ear1_seed_6		0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_7		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_1		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_10		0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_11		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1

Table A70: The recombination data for markers on the short arm of 6H for untreated individuals 61-90. Superimposed with Table A67

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	11_10427	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312	Total recomb. Events per arm
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	6H|34.40	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00	
Morex SNP	A	C	G	a	g	A	G	G	a	G	G	G	C	A	A	A	G	
Barke SNP	g	a	a	c	a	g	a	c	g	a	c	a	a	c	g	g	a	
MxB_F1_2_untrt_ear1_seed_2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_5		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_7		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_10		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_2		0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_7		0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_9		0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_1		0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_10		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_11		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_12		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_6		0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_7		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_8		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
																		90

Table A71: The genotype for untreated individuals 1-30, for markers on the long arm of 6H. Marker 11_20572 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a
MxB_F1_1_cont_ear1_seed_1	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	A
MxB_F1_1_cont_ear1_seed_11	H	H	H	H	H	H	A	A	A	A	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_12	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_13	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_14	A	A	A	A	A	A	A	A	A	A	H	H	H	B	B	B
MxB_F1_1_cont_ear1_seed_15	A	A	A	A	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_16	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_18	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H
MxB_F1_1_cont_ear1_seed_3	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_4	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_5	H	H	H	H	H	H	H	H	H	H	H	B	B	H	H	H
MxB_F1_1_cont_ear1_seed_6	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	B
MxB_F1_1_cont_ear1_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_8	A	A	A	A	A	A	A	A	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_1	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_1_untrt_ear1_seed_10	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_11	H	H	H	H	H	H	H	B	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear1_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_3	A	H	H	H	H	H	H	H	H	H	A	A	A	H	H	H
MxB_F1_1_untrt_ear1_seed_4	H	H	H	H	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear1_seed_6	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	H
MxB_F1_1_untrt_ear1_seed_7	B	B	B	B	B	B	B	B	B	B	H	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_untrt_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_1	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_10	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A

Table A72: The genotype for untreated individuals 31-60, for markers on the long arm of 6H. Marker 11_20572 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a
MxB_F1_1_untrt_ear2_seed_11	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_2	B	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_3	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_4	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_1_untrt_ear2_seed_6	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_7	H	H	H	H	H	H	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_8	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_9	A	A	A	A	A	A	A	A	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_1	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_1_untrt_ear3_seed_3	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_4	H	H	H	H	H	H	H	H	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_5	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H
MxB_F1_1_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B
MxB_F1_1_untrt_ear3_seed_9	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_1	B	B	B	B	B	B	B	B	B	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_10	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_12	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_cont_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_3	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_cont_ear1_seed_8	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_1	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_11	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A

Table A73: The genotype for untreated individuals 61-90, for markers on the long arm of 6H. Marker 11_20572 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a
MxB_F1_2_untrt_ear1_seed_2	A	A	A	A	A	A	A	H	H	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_4	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_5	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_6	A	A	A	A	A	A	A	A	A	A	H	H	H	B	B	B
MxB_F1_2_untrt_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_untrt_ear2_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_untrt_ear2_seed_10	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H
MxB_F1_2_untrt_ear2_seed_2	H	H	H	H	H	H	H	H	H	H	H	B	B	H	H	H
MxB_F1_2_untrt_ear2_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_untrt_ear2_seed_5	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear2_seed_6	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_7	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear2_seed_8	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_untrt_ear3_seed_1	B	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_untrt_ear3_seed_10	H	H	H	H	H	H	H	H	H	H	A	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_3	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_4	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H
MxB_F1_2_untrt_ear3_seed_5	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_6	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_untrt_ear3_seed_8	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_9	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H

Table A74: The recombination data for markers on the long arm of 6H for untreated individuals 1-30. Superimposed with Table A71

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687	Total recomb. Events per arm
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85	
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G	
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a	
MxB_F1_1_cont_ear1_seed_1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	2
MxB_F1_1_cont_ear1_seed_11	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0	0	3
MxB_F1_1_cont_ear1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_13	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_14	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	2
MxB_F1_1_cont_ear1_seed_15	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_18	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
MxB_F1_1_cont_ear1_seed_19	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
MxB_F1_1_cont_ear1_seed_3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2
MxB_F1_1_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
MxB_F1_1_cont_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_8	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_1_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_11	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	3
MxB_F1_1_untrt_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_3	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	3
MxB_F1_1_untrt_ear1_seed_4	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear1_seed_6	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	3
MxB_F1_1_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1

Table A75: The recombination data for markers on the long arm of 6H for untreated individuals 31-60. Superimposed with Table A72

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687	Total recomb. Events per arm
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85	
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G	
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a	
MxB_F1_1_untrt_ear2_seed_11	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_7	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_8	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_9	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear3_seed_3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_4	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_untrt_ear3_seed_6	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
MxB_F1_1_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	2
MxB_F1_1_untrt_ear3_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_10	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_cont_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_cont_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_cont_ear1_seed_8	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table A76: The recombination data for markers on the long arm of 6H for untreated individuals 61-90. Superimposed with Table A73 Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687	Total recomb. Events per arm
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85	
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G	
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a	
MxB_F1_2_untrt_ear1_seed_2	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_4	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	2
MxB_F1_2_untrt_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear2_seed_2	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2
MxB_F1_2_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear2_seed_6	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_7	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
MxB_F1_2_untrt_ear2_seed_8	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear3_seed_1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear3_seed_10	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2
MxB_F1_2_untrt_ear3_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear3_seed_5	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_6	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_9	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
																	109

Mean marker recomb. Freq./cell = 90(6HS)+109(6HL)/90 individuals = 2.21/cell

Table A77: The genotype for untreated individuals 1-30, for markers on the short arm of 7H. Marker 11_10153 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a
MxB_F1_1_cont_ear1_seed_1	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_11	H	H	H	H	H	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_cont_ear1_seed_12	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_cont_ear1_seed_13	H	H	A	H	H	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_cont_ear1_seed_14	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_15	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_16	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_19	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_cont_ear1_seed_3	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_4	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_5	B	B	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_cont_ear1_seed_6	H	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_cont_ear1_seed_7	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_8	A	A	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_9	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_untrt_ear1_seed_1	H	H	H	H	H	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_11	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_3	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_4	B	H	B	B	B	B	B	B	B	B	B	B	H	A	A
MxB_F1_1_untrt_ear1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_6	H	B	B	B	B	B	H	H	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_8	H	H	H	H	H	B	B	H	H	H	A	A	A	A	A
MxB_F1_1_untrt_ear1_seed_9	B	B	B	B	B	B	B	B	B	B	B	B	B	H	B
MxB_F1_1_untrt_ear2_seed_1	B	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_untrt_ear2_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H

Table A78: The genotype for untreated individuals 31-60, for markers on the short arm of 7H. Marker 11_10153 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a
MxB_F1_1_untrt_ear2_seed_11	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_untrt_ear2_seed_2	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	H	H	H	B	B	B	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_4	H	H	H	H	H	A	H	H	H	H	H	H	H	H	B
MxB_F1_1_untrt_ear2_seed_5	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_1_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_1	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_untrt_ear3_seed_2	H	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_untrt_ear3_seed_4	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_5	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_6	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_7	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_8	B	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_10	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_11	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_cont_ear1_seed_12	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	H	A	A
MxB_F1_2_cont_ear1_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H
MxB_F1_2_cont_ear1_seed_6	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_7	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_8	B	B	B	B	B	H	H	H	H	H	H	A	A	A	H
MxB_F1_2_untrt_ear1_seed_1	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_10	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_11	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A

Table A79: The genotype for untreated individuals 61-90, for markers on the short arm of 7H. Marker 11_10153 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a
MxB_F1_2_untrt_ear1_seed_2	H	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_3	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_4	B	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear1_seed_5	A	A	A	A	A	A	A	A	A	A	H	B	B	B	B
MxB_F1_2_untrt_ear1_seed_6	A	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_2_untrt_ear1_seed_8	B	B	B	B	B	H	H	H	B	B	B	B	B	B	H
MxB_F1_2_untrt_ear1_seed_9	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_1	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_10	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear2_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_5	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_6	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_7	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_8	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_9	B	B	B	B	B	B	B	B	B	B	B	B	H	A	A
MxB_F1_2_untrt_ear3_seed_1	B	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_untrt_ear3_seed_10	B	B	B	B	B	B	B	B	H	H	H	A	A	A	A
MxB_F1_2_untrt_ear3_seed_11	B	B	B	B	B	H	H	H	H	H	A	A	A	H	H
MxB_F1_2_untrt_ear3_seed_12	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H
MxB_F1_2_untrt_ear3_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_4	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_5	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_7	H	H	H	H	H	A	A	A	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear3_seed_8	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear3_seed_9	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H

Table A80: The recombination data for markers on the short arm of 7H for untreated individuals 1-30. Superimposed with Table A77

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153	Total recomb. Events per arm
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75	
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G	
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a	
MxB_F1_1_cont_ear1_seed_1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_11		0	0	0	0	1	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_cont_ear1_seed_12		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_cont_ear1_seed_13		0	1	1	0	1	0	0	0	0	0	0	0	1	0	4
MxB_F1_1_cont_ear1_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_16		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_19		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_cont_ear1_seed_3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_5		0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_cont_ear1_seed_6		1	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_cont_ear1_seed_7		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_8		0	1	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_9		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear1_seed_1		0	0	0	0	1	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_10		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_11		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_4		1	1	0	0	0	0	0	0	0	0	0	1	1	0	4
MxB_F1_1_untrt_ear1_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_6		1	0	0	0	0	1	0	0	0	1	0	0	0	0	3
MxB_F1_1_untrt_ear1_seed_7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_8		0	0	0	0	1	0	1	0	0	1	0	0	0	0	3
MxB_F1_1_untrt_ear1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	1	1	2
MxB_F1_1_untrt_ear2_seed_1		2	0	0	0	0	0	0	0	0	0	0	0	0	1	3
MxB_F1_1_untrt_ear2_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1

Table A81: The recombination data for markers on the short arm of 7H for untreated individuals 31-60. Superimposed with Table A78

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153	Total recomb. Events per arm
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75	
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G	
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a	
MxB_F1_1_untrt_ear2_seed_11		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_3		0	0	0	0	0	0	1	0	0	1	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_4		0	0	0	0	1	1	0	0	0	0	0	0	0	1	3
MxB_F1_1_untrt_ear2_seed_5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_7		0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_untrt_ear2_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear3_seed_2		1	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_untrt_ear3_seed_4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_5		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_8		2	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_10		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_12		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_2		0	0	0	0	0	0	0	0	0	0	0	1	1	0	2
MxB_F1_2_cont_ear1_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_cont_ear1_seed_6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_8		0	0	0	0	1	0	0	0	0	0	1	0	0	1	3
MxB_F1_2_untrt_ear1_seed_1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_10		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_11		1	0	0	0	0	0	0	0	0	1	0	0	0	0	2

Table A82: The recombination data for markers on the short arm of 7H for untreated individuals 61-90. Superimposed with Table A79

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153	Total recomb. Events per arm
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75	
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G	
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a	
MxB_F1_2_untrt_ear1_seed_2		1	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_4		1	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear1_seed_5		0	0	0	0	0	0	0	0	0	1	1	0	0	0	2
MxB_F1_2_untrt_ear1_seed_6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_7		0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear1_seed_8		0	0	0	0	1	0	0	1	0	0	0	0	0	1	3
MxB_F1_2_untrt_ear1_seed_9		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_10		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_untrt_ear2_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_7		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_9		0	0	0	0	0	0	0	0	0	0	0	1	1	0	2
MxB_F1_2_untrt_ear3_seed_1		1	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear3_seed_10		0	0	0	0	0	0	0	1	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_11		0	0	0	0	1	0	0	0	0	1	0	0	1	0	3
MxB_F1_2_untrt_ear3_seed_12		0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear3_seed_2		0	0	0	0	0	0	0	0	0	1	0	1	0	0	2
MxB_F1_2_untrt_ear3_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear3_seed_7		0	0	0	0	1	0	0	1	0	0	1	0	0	0	3
MxB_F1_2_untrt_ear3_seed_8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_9		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
																114

Table A83: The genotype for untreated individuals 1-30, for markers on the long arm of 7H. Marker 11_10442 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g
MxB_F1_1_cont_ear1_seed_1	B	B	B	B	B	B	B	H	H	A	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_cont_ear1_seed_11	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_12	B	B	B	B	b	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_13	H	H	H	H	H	B	B	B	B	B	B	B	B	A	A	A	A
MxB_F1_1_cont_ear1_seed_14	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_15	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_16	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_18	H	H	H	H	B	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_19	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_cont_ear1_seed_3	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_4	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_cont_ear1_seed_5	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_cont_ear1_seed_8	B	B	B	B	B	H	H	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_cont_ear1_seed_9	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_10	H	H	H	H	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_11	A	A	A	A	A	A	A	H	H	H	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_3	H	H	H	H	H	H	H	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_4	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear1_seed_5	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_6	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_untrt_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	H	H
MxB_F1_1_untrt_ear1_seed_9	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B

Table A84: The genotype for untreated individuals 31-60, for markers on the long arm of 7H. Marker 11_10442 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g
MxB_F1_1_untrt_ear2_seed_11	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_3	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_4	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear2_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear2_seed_6	B	B	B	B	B	H	H	H	H	H	H	H	H	H	B	H	H
MxB_F1_1_untrt_ear2_seed_7	B	B	B	B	B	B	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear2_seed_8	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	H
MxB_F1_1_untrt_ear2_seed_9	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_1	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_3	B	B	B	B	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_4	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_untrt_ear3_seed_5	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_untrt_ear3_seed_6	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_7	B	B	B	B	B	B	B	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_untrt_ear3_seed_8	A	A	A	A	A	A	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_untrt_ear3_seed_9	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H
MxB_F1_2_cont_ear1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_10	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_11	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_cont_ear1_seed_12	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_cont_ear1_seed_2	A	A	A	A	A	A	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_cont_ear1_seed_3	H	H	H	H	H	H	H	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_6	H	H	H	H	B	B	B	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_cont_ear1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_cont_ear1_seed_8	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_10	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear1_seed_11	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	A	A

Table A85: The genotype for untreated individuals 61-90, for markers on the long arm of 7H. Marker 11_10442 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g
MxB_F1_2_untrt_ear1_seed_2	H	H	H	H	H	H	B	B	B	H	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_3	B	B	B	B	H	A	A	A	A	A	H	H	H	H	H	H	B
MxB_F1_2_untrt_ear1_seed_4	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_5	B	B	B	B	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear1_seed_6	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_7	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_untrt_ear1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear1_seed_9	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H
MxB_F1_2_untrt_ear2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_4	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_5	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_6	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear2_seed_7	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear2_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_untrt_ear2_seed_9	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_1	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_10	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_untrt_ear3_seed_12	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_2	H	H	H	H	H	H	H	H	B	B	B	B	B	B	H	H	H
MxB_F1_2_untrt_ear3_seed_3	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_untrt_ear3_seed_4	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_untrt_ear3_seed_5	A	A	A	A	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_untrt_ear3_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_untrt_ear3_seed_7	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_untrt_ear3_seed_8	B	B	B	B	B	B	B	B	B	B	H	H	H	H	A	A	A
MxB_F1_2_untrt_ear3_seed_9	H	H	A	A	A	H	H	H	H	B	B	B	B	B	B	B	B

Table A86: The recombination data for markers on the long arm of 7H for untreated individuals 1-30. Superimposed with Table A83

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174	Total recomb. Events per arm
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56	
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A	
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g	
MxB_F1_1_cont_ear1_seed_1	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	3
MxB_F1_1_cont_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_cont_ear1_seed_11	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_12	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_13	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	3
MxB_F1_1_cont_ear1_seed_14	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_15	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_16	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_18	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_cont_ear1_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_5	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_cont_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_cont_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_cont_ear1_seed_8	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	3
MxB_F1_1_cont_ear1_seed_9	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_10	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_11	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear1_seed_3	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_4	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear1_seed_5	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_untrt_ear1_seed_7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear1_seed_8	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	3
MxB_F1_1_untrt_ear1_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1

Table A87: The recombination data for markers on the long arm of 7H for untreated individuals 31-60. Superimposed with Table A84

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174	Total recomb. Events per arm
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56	
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A	
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g	
MxB_F1_1_untrt_ear2_seed_11	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear2_seed_4	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear2_seed_6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	3
MxB_F1_1_untrt_ear2_seed_7	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear2_seed_8	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	4
MxB_F1_1_untrt_ear2_seed_9	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_3	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_untrt_ear3_seed_5	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_untrt_ear3_seed_7	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	1	4
MxB_F1_1_untrt_ear3_seed_8	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_untrt_ear3_seed_9	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_cont_ear1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_10	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_cont_ear1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_cont_ear1_seed_12	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_cont_ear1_seed_2	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_3	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_cont_ear1_seed_6	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	3
MxB_F1_2_cont_ear1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_cont_ear1_seed_8	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_10	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_11	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	2

Table A88: The recombination data for markers on the long arm of 7H for untreated individuals 61-90. Superimposed with Table A85 Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174	Total recomb. Events per arm
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56	
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A	
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g	
MxB_F1_2_untrt_ear1_seed_2	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	3
MxB_F1_2_untrt_ear1_seed_3	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0	0	1	4
MxB_F1_2_untrt_ear1_seed_4	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_5	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear1_seed_6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear1_seed_7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_untrt_ear1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear1_seed_9	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	2
MxB_F1_2_untrt_ear2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_5	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_6	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_untrt_ear2_seed_7	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_untrt_ear2_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_10	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_untrt_ear3_seed_12	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
MxB_F1_2_untrt_ear3_seed_3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_untrt_ear3_seed_5	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_untrt_ear3_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_untrt_ear3_seed_7	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_untrt_ear3_seed_8	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	2
MxB_F1_2_untrt_ear3_seed_9	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	3
																		121

Mean marker recomb. Freq./cell = 114(7HS)+121(7HL)/90 individuals = 2.61/cell

BeadXpress® genotyping data and calculations of the mean marker recombination frequencies for F2 individuals derived from the F1 population treated with 100 ng/ml TSA.

Table A89: The genotype for treated individuals 1-30, for markers on the short arm of 1H. Marker 11_10597 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52
Morex SNP	A	A	A	G	A	A	G
Barke SNP	g	g	g	a	g	g	a
MxB_F1_1_TSA_ear_1_seed_1	H	H	H	H	B	B	B
MxB_F1_1_TSA_ear_1_seed_10	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_11	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_12	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_14	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_2	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_3	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_4	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_5	B	B	B	B	H	H	H
MxB_F1_1_TSA_ear_1_seed_6	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_7	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_8	H	H	H	H	A	A	A
MxB_F1_1_TSA_ear_1_seed_9	A	A	A	H	B	B	B
MxB_F1_1_TSA_ear_2_seed_1	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_2_seed_10	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_2_seed_11	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_12	H	H	A	A	H	H	H
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_16	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_17	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_18	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_19	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_2	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_20	A	A	A	H	B	B	B
MxB_F1_1_TSA_ear_2_seed_21	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_22	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_23	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_24	H	H	H	H	B	B	B

Table A90: The genotype for treated individuals 31-60, for markers on the short arm of 1H. Marker 11_10597 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52
Morex SNP	A	A	A	G	A	A	G
Barke SNP	g	g	g	a	g	g	a
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_4	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_6	H	H	H	H	B	H	H
MxB_F1_1_TSA_ear_2_seed_7	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_8	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_9	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_1_seed_1	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_11	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_1_seed_12	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_1_seed_13	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_14	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_15	B	B	H	H	A	A	A
MxB_F1_2_TSA_ear_1_seed_17	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_1_seed_18	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_2	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_20	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_21	B	B	B	B	H	H	H
MxB_F1_2_TSA_ear_1_seed_3	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_4	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_5	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_6	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_1_seed_7	B	B	B	B	B	B	H
MxB_F1_2_TSA_ear_1_seed_8	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_1_seed_9	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_12	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_2_seed_13	A	A	A	A	A	A	A

Table A91: The genotype for treated individuals 61-90, for markers on the short arm of 1H. Marker 11_10597 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52
Morex SNP	A	A	A	G	A	A	G
Barke SNP	g	g	g	a	g	g	a
MxB_F1_2_TSA_ear_2_seed_14	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_2_seed_17	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_18	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_19	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_2	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_20	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_2_seed_21	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_2_seed_3	B	B	B	B	H	H	H
MxB_F1_2_TSA_ear_2_seed_4	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_5	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_2_seed_6	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_7	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_8	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_9	H	H	h	H	B	B	B
MxB_F1_2_TSA_ear_3_seed_1	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_10	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_3_seed_11	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_13	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_3_seed_15	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_16	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_3_seed_17	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_18	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_19	B	B	B	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_2	H	H	A	A	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_21	A	A	A	A	A	A	A

Table A92: The recombination data for markers on the short arm of 1H for treated individuals 1-30. Superimposed with Table A89

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597	Total recomb. Events per arm
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52	
Morex SNP	A	A	A	G	A	A	G	
Barke SNP	g	g	g	a	g	g	a	
MxB_F1_1_TSA_ear_1_seed_1		0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_1_seed_10		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_11		0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_12		0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_13		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_14		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_2		0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_3		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_4		0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_5		0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_1_seed_6		0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_7		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_8		0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_1_seed_9		0	0	1	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_1		0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_10		0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_11		0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_12		0	1	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_14		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_15		0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_16		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_17		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_18		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_19		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_2		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_20		0	0	1	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_21		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_22		1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_23		0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24		0	0	0	1	0	0	1

Table A93: The recombination data for markers on the short arm of 1H for treated individuals 31-60. Superimposed with Table A90

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597	Total recomb. Events per arm
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52	
Morex SNP	A	A	A	G	A	A	G	
Barke SNP	g	g	g	a	g	g	a	
MxB_F1_1_TSA_ear_2_seed_25		0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_4		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_6		0	0	0	1	1	0	2
MxB_F1_1_TSA_ear_2_seed_7		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_8		0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_9		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_1		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_10		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_11		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_12		0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_13		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_14		1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_15		0	1	0	1	0	0	2
MxB_F1_2_TSA_ear_1_seed_17		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_18		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_19		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_2		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_20		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_21		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_3		0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_4		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_5		1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_6		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_7		0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_1_seed_8		0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_1_seed_9		1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_1		0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_11		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_12		0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_13		0	0	0	0	0	0	0

Table A94: The recombination data for markers on the short arm of 1H for treated individuals 61-90. Superimposed with Table A91

Marker	11_10419	11_21226	11_10775	11_10030	11_10760	11_10764	11_10597	Total recomb. Events per arm
Position on chromosome	1H|3.75	1H|8.77	1H|17.26	1H|18.05	1H|34.83	1H|40.99	1H|42.52	
Morex SNP	A	A	A	G	A	A	G	
Barke SNP	g	g	g	a	g	g	a	
MxB_F1_2_TSA_ear_2_seed_14		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_15		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_17		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18		1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_19		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_20		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_21		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_22		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_3		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_4		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_5		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_6		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7		1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_8		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_9		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_3_seed_1		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_10		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_3_seed_11		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_12		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_13		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_3_seed_14		0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_3_seed_15		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_16		0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_3_seed_17		0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_18		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_19		0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_2		0	1	0	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_20		0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21		0	0	0	0	0	0	0
								65

Table A95: The genotype for treated individuals 1-30, for markers on the long arm of 1H. Marker 11_20095 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782	11_10590
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89	1H|138.31
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A	A
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g	g
MxB_F1_1_TSA_ear_1_seed_1	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_11	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_1_seed_12	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H
MxB_F1_1_TSA_ear_1_seed_13	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_14	B	B	B	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_TSA_ear_1_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_3	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_1_seed_4	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_1_seed_5	H	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_6	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_8	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_9	B	B	B	B	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_1	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_10	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_11	A	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_12	B	B	B	B	B	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_15	H	H	H	H	H	H	h	H	H	H	H	H	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_TSA_ear_2_seed_16	H	H	H	H	H	H	H	H	H	H	H	H	H	A	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_17	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_18	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_19	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_20	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_22	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_23	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H
MxB_F1_1_TSA_ear_2_seed_24	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A96: The genotype for treated individuals 31-60, for markers on the long arm of 1H. Marker 11_20095 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782	11_10590
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89	1H|138.31
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A	A
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g	g
MxB_F1_1_TSA_ear_2_seed_25	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_4	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_6	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_8	H	H	H	H	B	B	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_11	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_12	B	B	B	B	B	B	H	h	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_13	H	H	H	H	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_15	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_17	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_20	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_21	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_3	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_4	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_1_seed_7	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_9	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_2_seed_11	A	A	A	A	A	A	A	A	A	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_12	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_13	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H

Table A97: The genotype for treated individuals 61-90, for markers on the long arm of 1H. Marker 11_20095 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782	11_10590
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89	1H|138.31
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A	A
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g	g
MxB_F1_2_TSA_ear_2_seed_14	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_15	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_17	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_20	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_2_seed_21	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_3	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_TSA_ear_2_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_5	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_6	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_7	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_9	B	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_10	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_11	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_13	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_3_seed_15	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_16	H	H	H	H	H	H	h	h	H	H	H	H	H	H	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_17	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_18	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_3_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_3_seed_20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_21	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H

Table A98: The recombination data for markers on the long arm of 1H for treated individuals 1-30. Superimposed with Table A95

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782	11_10590	Total recomb. Events per arm
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89	1H|138.31	
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A	A	
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g	g	
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_1_seed_12	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_1_TSA_ear_1_seed_2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_1_seed_4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_1_seed_5	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_9	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_10	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_11	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_12	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_14	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_15	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	3
MxB_F1_1_TSA_ear_2_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_18	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_19	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_20	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_21	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_23	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	3
MxB_F1_1_TSA_ear_2_seed_24	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Table A99: The recombination data for markers on the long arm of 1H for treated individuals 31-60. Superimposed with Table A96

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782	11_10590	Total recomb. Events per arm
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89	1H|138.31	
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A	A	
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g	g	
MxB_F1_1_TSA_ear_2_seed_25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_6	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_8	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	4
MxB_F1_1_TSA_ear_2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_12	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_13	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_1_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_20	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_21	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_7	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_9	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_2_seed_11	1	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_12	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1

Table A100: The recombination data for markers on the long arm of 1H for treated individuals 61-90. Superimposed with Table A97. Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_20095	11_21431	11_11367	11_20229	11_10006	11_20434	11_21446	11_10433	11_21373	11_10396	11_11277	11_20169	11_20267	11_20844	11_21392	11_10854	11_20908	11_10586	11_21140	11_10644	11_10782	11_10590	Total recomb. Events per arm
Position on chromosome	1H|60.77	1H|64.91	1H|66.70	1H|71.43	1H|73.94	1H|88.23	1H|92.04	1H|93.95	1H|95.42	1H|96.92	1H|97.68	1H|99.95	1H|101.45	1H|108.31	1H|114.84	1H|117.80	1H|121.12	1H|121.77	1H|126.01	1H|127.10	1H|131.89	1H|138.31	
Morex SNP	A	A	G	G	G	A	T	G	G	C	A	G	C	T	G	C	A	G	G	A	A	A	
Barke SNP	g	t	c	a	a	t	a	a	a	g	g	c	a	a	a	a	g	a	a	g	g	g	
MxB_F1_2_TSA_ear_2_seed_14	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_17	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_19	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_20	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_2_seed_21	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_22	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_2_seed_4	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_5	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_9	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_12	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_13	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_3_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_17	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_18	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_3_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_3_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
																							135

Mean marker recomb. Freq./cell = 65(1HS)+135(1HL)/90 individuals = 2.22/cell

Table A101: The genotype for treated individuals 1-30, for markers on the short arm of 2H. Marker 11_11015 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a
MxB_F1_1_TSA_ear_1_seed_1	A	A	A	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_11	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_13	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_14	A	A	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_2	B	B	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_4	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_5	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_6	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_7	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_8	B	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_1	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_11	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_12	A	A	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_16	a	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_17	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_19	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_2	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_20	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_21	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_22	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_23	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_24	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A102: The genotype for treated individuals 31-60, for markers on the short arm of 2H. Marker 11_11015 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_4	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_7	A	A	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_1	H	H	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_TSA_ear_1_seed_11	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_12	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_17	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_18	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_20	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_21	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_1_seed_4	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_6	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_7	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_8	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_12	H	H	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_13	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A103: The genotype for treated individuals 61-90, for markers on the short arm of 2H. Marker 11_11015 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a
MxB_F1_2_TSA_ear_2_seed_14	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_15	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_17	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_18	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_19	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_20	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_21	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_22	H	H	B	H	H	H	H	H	H	H	H	h	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_4	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_5	A	A	A	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_6	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_7	H	H	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_8	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_1	B	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_10	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_11	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_12	B	B	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_13	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_15	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_16	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_17	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_3_seed_19	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_21	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B

Table A104: The recombination data for markers on the short arm of 2H for treated individuals 1-30. Superimposed with Table A101

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015	Total recomb. Events per arm
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67	
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G	
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a	
MxB_F1_1_TSA_ear_1_seed_1		0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_11		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_13		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_14		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_4		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_5		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_8		0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_12		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_17		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_19		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_20		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_21		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_22		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_23		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table A105: The recombination data for markers on the short arm of 2H for treated individuals 31-60. Superimposed with Table A102

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015	Total recomb. Events per arm
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67	
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G	
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a	
MxB_F1_1_TSA_ear_2_seed_25		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_7		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_1		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_1_seed_11		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_12		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_13		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_14		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_17		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_18		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_20		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_21		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_6		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_7		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_8		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_11		0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_12		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_13		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Table A106: The recombination data for markers on the short arm of 2H for treated individuals 61-90. Superimposed with Table A103

Marker	11_11059	11_21377	11_10180	11_20394	11_21261	11_21187	11_10891	11_10525	11_10399	11_10837	11_10648	11_10342	11_21338	11_10498	11_21005	11_21388	11_11015	Total recomb. Events per arm
Position on chromosome	2H|7.14	2H|8.57	2H|21.61	2H|27.29	2H|28.44	2H|29.15	2H|31.02	2H|38.03	2H|39.10	2H|40.50	2H|41.66	2H|44.13	2H|44.84	2H|49.07	2H|50.49	2H|54.95	2H|55.67	
Morex SNP	G	G	C	G	A	G	C	A	A	A	C	G	G	G	A	A	G	
Barke SNP	a	a	g	a	g	a	a	c	g	c	a	a	a	a	g	c	a	
MxB_F1_2_TSA_ear_2_seed_14		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_15		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_17		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_19		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_2		0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_20		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_21		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_22		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_5		0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_6		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_8		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_1		1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_10		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_12		0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_13		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_15		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_16		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_17		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_3_seed_19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_20		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_21		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
																		89

Table A107: The genotype for treated individuals 1-30, for markers on the long arm of 2H. Marker 11_10909 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g
MxB_F1_1_TSA_ear_1_seed_1	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_1_TSA_ear_1_seed_11	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_12	B	B	B	B	B	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_14	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_TSA_ear_1_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_3	A	A	A	A	A	a	A	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_5	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_6	B	B	H	H	H	h	H	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_1_TSA_ear_1_seed_8	A	A	A	A	A	B	B	B	B	B	B	B	B	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_1_TSA_ear_2_seed_10	B	B	B	B	B	B	B	B	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_11	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_12	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_15	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_16	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_17	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_18	H	H	H	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_19	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_2	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_20	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	H	H	H	H	H	H	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_22	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_23	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_24	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	H	H	H	H	H	H

Table A108: The genotype for treated individuals 31-60, for markers on the long arm of 2H. Marker 11_10909 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g
MxB_F1_1_TSA_ear_2_seed_25	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_4	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_9	H	H	H	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_1	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_10	H	H	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_11	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_1_seed_12	H	H	H	H	H	h	h	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_1_seed_13	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_14	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	H	A	A	A	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_17	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_2	A	A	A	A	A	A	A	A	A	A	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_20	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_21	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_3	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	A	A	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_4	A	A	A	A	A	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_9	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_12	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_13	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B

Table A109: The genotype for treated individuals 61-90, for markers on the long arm of 2H. Marker 11_10909 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g
MxB_F1_2_TSA_ear_2_seed_14	B	B	B	B	B	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	H	H	H	B	B	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_17	A	A	A	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_2	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_21	A	A	A	A	A	H	H	A	A	A	A	A	A	A	A	A	A	A	A	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_3	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_2_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_5	B	B	B	B	B	B	B	H	H	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_6	B	B	B	B	H	h	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	A	A	A	A	A	h	H	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_10	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_11	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_13	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	b	B	B	H	H
MxB_F1_2_TSA_ear_3_seed_15	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_3_seed_16	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_3_seed_17	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_18	H	H	H	H	H	h	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H
MxB_F1_2_TSA_ear_3_seed_19	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_3_seed_20	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_21	B	B	B	B	B	B	B	B	B	B	B	B	A	A	A	A	A	A	A	H	H	H	H	H	H

Table A110: The recombination data for markers on the long arm of 2H for treated individuals 1-30. Superimposed with Table A107

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085	Total recomb. Events per arm
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72	
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A	
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g	
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_12	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_6	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_1_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_1_TSA_ear_1_seed_8	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	4
MxB_F1_1_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_TSA_ear_2_seed_10	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_11	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_15	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_17	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_18	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_21	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_1_TSA_ear_2_seed_22	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	2

Table A111: The recombination data for markers on the long arm of 2H for treated individuals 31-60. Superimposed with Table A108

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085	Total recomb. Events per arm
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72	
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A	
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g	
MxB_F1_1_TSA_ear_2_seed_25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_4	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_9	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_1_seed_10	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_15	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_1_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_18	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_20	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_21	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_3	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	4
MxB_F1_2_TSA_ear_1_seed_4	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_12	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1

Table A112: The recombination data for markers on the long arm of 2H for treated individuals 61-90. Superimposed with Table A109. Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10909	11_21399	11_21166	11_21144	11_20667	11_21242	11_10786	11_10287	11_11533	11_21037	11_10214	11_20080	11_10876	11_10988	11_10429	11_10404	11_10916	11_20480	11_10656	11_20590	11_10315	11_20293	11_10791	11_10072	11_10085	Total recomb. Events per arm
Position on chromosome	2H|63.53	2H|63.53	2H|66.83	2H|69.25	2H|72.33	2H|82.75	2H|82.75	2H|85.92	2H|87.33	2H|88.74	2H|93.50	2H|95.64	2H|100.37	2H|113.48	2H|115.08	2H|117.20	2H|117.91	2H|126.03	2H|128.26	2H|137.51	2H|141.28	2H|147.94	2H|150.67	2H|151.37	2H|156.72	
Morex SNP	A	A	A	A	A	G	G	A	G	T	A	G	C	C	G	A	C	C	A	G	G	G	C	A	A	
Barke SNP	t	g	c	g	g	a	a	g	a	a	g	a	a	a	a	g	a	g	g	c	c	a	a	c	g	
MxB_F1_2_TSA_ear_2_seed_14	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_15	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_21	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	4
MxB_F1_2_TSA_ear_2_seed_22	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	3
MxB_F1_2_TSA_ear_2_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_5	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_10	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_12	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_13	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_3_seed_15	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3
MxB_F1_2_TSA_ear_3_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_3_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_18	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	3
MxB_F1_2_TSA_ear_3_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_3_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	3
																										166

Mean marker recomb. Freq./cell = 89(2HS)+166(2HL)/90 individuals = 2.83/cell

Table A113: The genotype for treated individuals 1-30, for markers on the short arm of 3H. Marker 11_21197 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73
Morex SNP	G	C	G	G	A	G	A	G	C	G
Barke SNP	a	a	a	a	g	a	g	a	a	a
MxB_F1_1_TSA_ear_1_seed_1	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_10	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_11	B	B	B	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_12	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_13	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_2	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_3	A	H	B	B	B	B	B	B	B	H
MxB_F1_1_TSA_ear_1_seed_4	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_TSA_ear_1_seed_5	H	H	H	H	H	A	H	H	H	B
MxB_F1_1_TSA_ear_1_seed_6	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_7	B	B	B	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_8	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_1	H	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_10	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_11	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_12	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_14	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_16	H	H	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_17	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_18	A	A	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_19	A	A	A	A	A	A	A	H	H	H
MxB_F1_1_TSA_ear_2_seed_2	H	H	H	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_20	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_22	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_23	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_24	B	B	B	B	B	B	B	B	B	B

Table A114: The genotype for treated individuals 31-60, for markers on the short arm of 3H. Marker 11_21197 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73
Morex SNP	G	C	G	G	A	G	A	G	C	G
Barke SNP	a	a	a	a	g	a	g	a	a	a
MxB_F1_1_TSA_ear_2_seed_25	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_4	B	H	H	H	H	H	H	H	H	A
MxB_F1_1_TSA_ear_2_seed_6	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_7	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_TSA_ear_2_seed_9	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_1	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_1_seed_10	H	H	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_1_seed_11	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_12	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_13	B	B	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_17	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_18	H	H	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_1_seed_19	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_2	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_20	H	B	B	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_21	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_1_seed_3	B	B	B	B	B	B	B	B	B	H
MxB_F1_2_TSA_ear_1_seed_4	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_5	H	H	H	B	B	B	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_6	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_7	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_1	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_12	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_13	A	A	A	A	A	A	A	A	A	A

Table A115: The genotype for treated individuals 61-90, for markers on the short arm of 3H. Marker 11_21197 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73
Morex SNP	G	C	G	G	A	G	A	G	C	G
Barke SNP	a	a	a	a	g	a	g	a	a	a
MxB_F1_2_TSA_ear_2_seed_14	H	A	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_15	B	B	B	B	B	H	H	H	A	A
MxB_F1_2_TSA_ear_2_seed_17	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_20	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_21	H	H	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_3	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_4	B	B	B	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_5	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_6	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_7	B	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_3_seed_1	H	H	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_10	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_11	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	H	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_3_seed_13	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_14	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_15	H	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_16	A	A	A	A	A	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_17	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_18	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_19	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_3_seed_21	H	H	H	H	H	B	B	B	B	B

Table A116: The recombination data for markers on the short arm of 3H for treated individuals 1-30. Superimposed with Table A113

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197	Total recomb. Events per arm
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73	
Morex SNP	G	C	G	G	A	G	A	G	C	G	
Barke SNP	a	a	a	a	g	a	g	a	a	a	
MxB_F1_1_TSA_ear_1_seed_1		1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_10		0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_11		0	0	1	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_12		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_13		0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_14		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_2		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_3		1	1	0	0	0	0	0	0	1	3
MxB_F1_1_TSA_ear_1_seed_4		0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_1_seed_5		0	0	0	0	1	1	0	0	1	3
MxB_F1_1_TSA_ear_1_seed_6		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_7		0	0	1	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_8		0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_1		1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_10		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_11		0	0	0	0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_2_seed_12		0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_14		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_15		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_16		0	1	0	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_17		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_18		0	1	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_2_seed_19		0	0	0	0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_2_seed_2		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_20		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_21		0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_22		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_23		0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24		0	0	0	0	0	0	0	0	0	0

Table A117: The recombination data for markers on the short arm of 3H for treated individuals 31-60. Superimposed with Table A114

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197	Total recomb. Events per arm
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73	
Morex SNP	G	C	G	G	A	G	A	G	C	G	
Barke SNP	a	a	a	a	g	a	g	a	a	a	
MxB_F1_1_TSA_ear_2_seed_25		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_4		1	0	0	0	0	0	0	0	1	2
MxB_F1_1_TSA_ear_2_seed_6		0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_7		0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_8		0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_9		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_1		0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_10		0	1	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_1_seed_11		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_12		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_13		0	1	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_14		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_15		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_17		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_18		0	1	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_1_seed_19		0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_2		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_20		1	0	1	0	0	0	0	1	0	3
MxB_F1_2_TSA_ear_1_seed_21		0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_1_seed_3		0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_1_seed_4		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_5		0	0	1	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_6		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_7		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_8		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_1		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_11		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_12		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_13		0	0	0	0	0	0	0	0	0	0

Table A118: The recombination data for markers on the short arm of 3H for treated individuals 61-90. Superimposed with Table A115

Marker	11_20252	11_20595	11_10565	11_10559	11_20794	11_10672	11_10081	11_20193	11_10601	11_21197	Total recomb. Events per arm
Position on chromosome	3H|6.03	3H|12.46	3H|19.15	3H|24.99	3H|26.90	3H|37.17	3H|39.45	3H|42.06	3H|46.31	3H|51.73	
Morex SNP	G	C	G	G	A	G	A	G	C	G	
Barke SNP	a	a	a	a	g	a	g	a	a	a	
MxB_F1_2_TSA_ear_2_seed_14		1	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_15		0	0	0	0	1	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_17		0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_19		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2		0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_20		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_21		0	1	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_22		0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_3		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_4		0	0	1	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_5		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_6		0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_8		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_9		0	0	0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_3_seed_1		0	1	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_10		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_11		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_12		1	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_3_seed_13		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_14		1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_15		1	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_16		0	0	0	0	2	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_17		0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_18		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_19		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_2		0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_20		0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_3_seed_21		0	0	0	0	1	0	0	0	0	1
											88

Table A119: The genotype for treated individuals 1-30, for markers on the long arm of 3H. Marker 11_10728 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a
MxB_F1_1_TSA_ear_1_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_10	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_11	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_14	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_5	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_6	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_7	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	B	B	B	H	H	H
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_10	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_11	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H	H	B	B	B
MxB_F1_1_TSA_ear_2_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	B	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_16	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H
MxB_F1_1_TSA_ear_2_seed_17	H	H	H	H	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_18	B	B	B	B	B	B	B	B	H	H	H	H	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_2_seed_19	H	H	H	H	H	H	H	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_2	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	B
MxB_F1_1_TSA_ear_2_seed_20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_22	A	A	A	A	A	A	A	A	A	H	H	H	H	H	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_23	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_24	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	A	A	A	A

Table A120: The genotype for treated individuals 31-60, for markers on the long arm of 3H. Marker 11_10728 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a
MxB_F1_1_TSA_ear_2_seed_25	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_4	A	A	A	A	A	A	H	H	H	B	B	B	B	B	B	B	H	H	H	H	A	A
MxB_F1_1_TSA_ear_2_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_7	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	H	H	H	H	H	A
MxB_F1_1_TSA_ear_2_seed_8	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_1_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_12	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	B	H
MxB_F1_2_TSA_ear_1_seed_13	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_15	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_17	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_19	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_2	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_20	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_21	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_4	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	H	B	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_7	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	H	H	H
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	H	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_12	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_13	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H

Table A121: The genotype for treated individuals 61-90, for markers on the long arm of 3H. Marker 11_10728 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a
MxB_F1_2_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_2_seed_15	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_17	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_20	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	H	H	H	A	A	A
MxB_F1_2_TSA_ear_2_seed_21	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_4	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_5	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_6	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_7	H	H	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	H	H	H	H	H	H	H	B	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_3_seed_1	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	A	A	A
MxB_F1_2_TSA_ear_3_seed_10	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_11	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	H	H	H	H	A	A	A	H	H	H	H	H	H	H	B	B	H	H
MxB_F1_2_TSA_ear_3_seed_13	A	A	A	A	A	A	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_3_seed_14	B	B	B	B	B	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_15	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_16	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_17	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_18	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_19	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	H	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_3_seed_20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_21	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	B	B	B	B	B

Table A122: The recombination data for markers on the long arm of 3H for treated individuals 1-30. Superimposed with Table A119

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267	Total recomb. Events per arm	
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40		
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G		
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a		
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
MxB_F1_1_TSA_ear_1_seed_10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3	
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
MxB_F1_1_TSA_ear_1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	2	
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	
MxB_F1_1_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	2	
MxB_F1_1_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2	
MxB_F1_1_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	
MxB_F1_1_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	
MxB_F1_1_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	
MxB_F1_1_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	1	0	0	3	
MxB_F1_1_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	
MxB_F1_1_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	2	
MxB_F1_1_TSA_ear_2_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	
MxB_F1_1_TSA_ear_2_seed_11	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	4	
MxB_F1_1_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	
MxB_F1_1_TSA_ear_2_seed_14	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	2	
MxB_F1_1_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	3	
MxB_F1_1_TSA_ear_2_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	2	
MxB_F1_1_TSA_ear_2_seed_17	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	
MxB_F1_1_TSA_ear_2_seed_18	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	3	
MxB_F1_1_TSA_ear_2_seed_19	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	
MxB_F1_1_TSA_ear_2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	2	
MxB_F1_1_TSA_ear_2_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
MxB_F1_1_TSA_ear_2_seed_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
MxB_F1_1_TSA_ear_2_seed_22	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	3	
MxB_F1_1_TSA_ear_2_seed_23	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	3	
MxB_F1_1_TSA_ear_2_seed_24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	2	

Table A123: The recombination data for markers on the long arm of 3H for treated individuals 31-60. Superimposed with Table A120

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267	Total recomb. Events per arm
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40	
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G	
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a	
MxB_F1_1_TSA_ear_2_seed_25	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_4	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	1	0	4
MxB_F1_1_TSA_ear_2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	4
MxB_F1_1_TSA_ear_2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_10	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	3
MxB_F1_2_TSA_ear_1_seed_11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	3
MxB_F1_2_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_19	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	3
MxB_F1_2_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_20	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_2_seed_1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1

Table A124: The recombination data for markers on the long arm of 3H for treated individuals 61-90. Superimposed with Table A121. Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10728	11_11191	11_10335	11_11391	11_21305	11_20778	11_20093	11_20063	11_20659	11_20628	11_10515	11_20009	11_21212	*11_10753*	*11_10312*	11_11172	11_20612	11_20527	11_21272	11_11436	11_21523	11_21267	Total recomb. Events per arm
Position on chromosome	3H|62.99	3H|64.19	3H|65.52	3H|65.52	3H|67.57	3H|76.20	3H|81.66	3H|85.99	3H|91.25	3H|98.49	3H|99.89	3H|107.63	3H|111.42	3H|114.00	3H|114.00	3H|126.27	3H|131.59	3H|134.31	3H|150.37	3H|155.85	3H|164.29	3H|168.40	
Morex SNP	A	C	G	A	A	C	A	A	A	A	A	G	G	G	G	G	C	A	G	C	G	G	
Barke SNP	g	a	a	c	g	g	g	g	g	t	g	c	a	a	a	a	a	c	c	g	a	a	
MxB_F1_2_TSA_ear_2_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_20	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	0	0	1	0	0	4
MxB_F1_2_TSA_ear_2_seed_21	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_22	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_4	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_5	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	1	0	4
MxB_F1_2_TSA_ear_2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_7	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_9	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_TSA_ear_3_seed_1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0	3
MxB_F1_2_TSA_ear_3_seed_10	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_12	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	1	0	4
MxB_F1_2_TSA_ear_3_seed_13	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_TSA_ear_3_seed_14	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_17	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_18	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_19	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_2	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	3
MxB_F1_2_TSA_ear_3_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
																							160

Mean marker recomb. Freq./cell = 88(3HS)+160(3HL)/90 individuals = 2.76/cell

Table A125: The genotype for treated individuals 1-30, for markers on the short arm of 4H. Marker 11_10093 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50
Morex SNP	A	G	G	G	A	G	A	A
Barke SNP	g	a	c	a	g	a	c	g
MxB_F1_1_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_10	H	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_11	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_12	H	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_14	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_3	B	B	B	B	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_4	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_5	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_6	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_8	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_1	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_10	H	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_11	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_12	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	A	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_16	B	B	B	B	B	b	b	B
MxB_F1_1_TSA_ear_2_seed_17	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_18	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_19	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_2	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_20	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_21	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_22	B	B	B	B	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_23	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_24	A	A	A	A	A	A	A	A

Table A126: The genotype for treated individuals 31-60, for markers on the short arm of 4H. Marker 11_10093 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50
Morex SNP	A	G	G	G	A	G	A	A
Barke SNP	g	a	c	a	g	a	c	g
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_4	B	B	B	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_6	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_7	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_8	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_9	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_1	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_1_seed_11	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_12	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_14	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_17	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	A	A	A	H	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_2	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_20	H	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_21	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_3	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_4	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_5	B	B	B	B	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_6	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_9	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_1	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_11	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_12	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_13	A	A	A	A	A	H	H	H

Table A127: The genotype for treated individuals 61-90, for markers on the short arm of 4H. Marker 11_10093 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50
Morex SNP	A	G	G	G	A	G	A	A
Barke SNP	g	a	c	a	g	a	c	g
MxB_F1_2_TSA_ear_2_seed_14	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_17	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_18	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_20	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_21	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_3	H	H	A	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_4	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_2_seed_5	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_6	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_7	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	H	H	A	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_1	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_10	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_11	A	A	A	A	H	B	B	B
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_13	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_15	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_16	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_17	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_18	H	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_3_seed_19	A	A	A	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_2	B	B	H	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_20	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_21	B	B	B	B	B	H	H	H

Table A128: The recombination data for markers on the short arm of 4H for treated individuals 1-30. Superimposed with Table A125

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093	Total recomb. Events per arm
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50	
Morex SNP	A	G	G	G	A	G	A	A	
Barke SNP	g	a	c	a	g	a	c	g	
MxB_F1_1_TSA_ear_1_seed_1		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_10		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_11		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_12		1	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_13		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_14		0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_2		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_3		0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_4		0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_5		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_6		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_7		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_8		0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_9		0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_1		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_10		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_11		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_12		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_14		0	0	1	1	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_15		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_16		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_17		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_18		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_19		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_2		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_20		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_21		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_22		0	0	0	1	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_23		0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24		0	0	0	0	0	0	0	0

Table A129: The recombination data for markers on the short arm of 4H for treated individuals 31-60. Superimposed with Table A126

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093	Total recomb. Events per arm
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50	
Morex SNP	A	G	G	G	A	G	A	A	
Barke SNP	g	a	c	a	g	a	c	g	
MxB_F1_1_TSA_ear_2_seed_25		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_4		0	0	1	1	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_6		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_7		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_8		0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_9		1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_1		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_10		0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_1_seed_11		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_12		0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_13		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_14		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_15		0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_17		0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_18		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_19		0	0	1	1	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_2		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_20		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_21		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_3		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_4		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_5		0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_6		0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_7		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_8		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_9		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_1		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_11		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_12		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_13		0	0	0	0	1	0	0	1

Table A130: The recombination data for markers on the short arm of 4H for treated individuals 61-90. Superimposed with Table A127

Marker	11_10113	11_10738	11_10221	11_21122	11_20012	11_21073	11_10756	11_10093	Total recomb. Events per arm
Position on chromosome	4H|19.52	4H|19.52	4H|21.61	4H|33.38	4H|39.76	4H|48.50	4H|48.50	4H|48.50	
Morex SNP	A	G	G	G	A	G	A	A	
Barke SNP	g	a	c	a	g	a	c	g	
MxB_F1_2_TSA_ear_2_seed_14		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_15		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_17		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_18		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_19		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_20		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_21		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_22		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_3		0	1	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_4		0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_5		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_6		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_7		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_8		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_9		0	1	1	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_1		0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_10		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_11		0	0	0	1	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_12		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_13		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_14		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_15		0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_16		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_17		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_18		0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_3_seed_19		0	0	2	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_2		0	1	1	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_20		0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21		0	0	0	0	1	0	0	1
									55

Table A131: The genotype for treated individuals 1-30, for markers on the long arm of 4H. Marker 11_10881 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a
MxB_F1_1_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_11	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_1_seed_12	H	H	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_TSA_ear_1_seed_2	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_3	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_TSA_ear_1_seed_4	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_5	A	A	H	H	H	H	H	A	A	A	H	H
MxB_F1_1_TSA_ear_1_seed_6	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_9	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_1	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_10	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_11	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_12	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_15	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_TSA_ear_2_seed_16	b	b	b	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_17	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_2_seed_18	A	A	A	A	A	A	A	A	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_19	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_2	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_20	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_22	A	A	A	A	A	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_23	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_24	A	A	A	A	A	H	H	B	B	B	B	B

Table A132: The genotype for treated individuals 31-60, for markers on the long arm of 4H. Marker 11_10881 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_4	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_6	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_7	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_8	B	B	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_9	B	B	B	B	B	B	B	H	H	H	B	B
MxB_F1_2_TSA_ear_1_seed_1	H	H	H	H	H	H	H	A	A	A	A	H
MxB_F1_2_TSA_ear_1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_11	H	H	H	H	H	H	B	B	B	B	B	H
MxB_F1_2_TSA_ear_1_seed_12	B	B	B	B	B	B	H	H	H	H	H	A
MxB_F1_2_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	H	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_15	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_17	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_2	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_20	B	B	B	B	B	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_21	H	H	H	H	H	H	A	A	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_3	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_4	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_1_seed_6	B	B	B	B	B	B	B	B	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_7	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_1	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_12	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_13	H	H	H	H	H	H	H	H	B	B	H	A

Table A133: The genotype for treated individuals 61-90, for markers on the long arm of 4H. Marker 11_10881 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a
MxB_F1_2_TSA_ear_2_seed_14	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_2_seed_17	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_18	B	B	B	B	H	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	A	A	A	A	A	A	H	H	H	B	B	B
MxB_F1_2_TSA_ear_2_seed_20	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_21	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_3	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_4	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_5	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_6	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_7	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_2_seed_8	H	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_1	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_10	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_11	B	B	B	B	B	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_13	H	H	H	H	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_TSA_ear_3_seed_15	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_16	H	H	H	H	H	H	B	B	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_17	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_18	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_19	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_3_seed_2	A	A	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_20	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_21	H	H	H	H	H	A	A	A	A	A	A	A

Table A134: The recombination data for markers on the long arm of 4H for treated individuals 1-30. Superimposed with Table A131

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007	Total recomb. Events per arm
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09	
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G	
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a	
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_1_seed_12	0	0	1	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_1_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_5	0	0	1	0	0	0	0	1	0	0	1	0	3
MxB_F1_1_TSA_ear_1_seed_6	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_10	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_11	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_14	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_18	0	0	0	0	0	0	0	0	2	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_19	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_2	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_20	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_21	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_22	0	0	0	0	0	1	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_23	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_24	0	0	0	0	0	1	0	1	0	0	0	0	2

Table A135: The recombination data for markers on the long arm of 4H for treated individuals 31-60. Superimposed with Table A132

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007	Total recomb. Events per arm
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09	
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G	
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a	
MxB_F1_1_TSA_ear_2_seed_25	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_7	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_8	0	0	1	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_2_seed_9	0	0	0	0	0	0	0	1	0	0	1	0	2
MxB_F1_2_TSA_ear_1_seed_1	0	0	0	0	0	0	0	1	0	0	0	1	2
MxB_F1_2_TSA_ear_1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_11	0	0	0	0	0	0	1	0	0	0	0	1	2
MxB_F1_2_TSA_ear_1_seed_12	0	0	0	0	0	0	1	0	0	0	0	1	2
MxB_F1_2_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_14	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_15	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_20	0	0	0	0	0	1	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_21	0	0	0	0	0	0	1	0	1	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	1	0	1	0	2
MxB_F1_2_TSA_ear_1_seed_7	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	1	0	1	0	2
MxB_F1_2_TSA_ear_1_seed_9	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_11	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_13	0	0	0	0	0	0	0	0	1	0	1	1	3

Table A136: The recombination data for markers on the long arm of 4H for treated individuals 61-90. Superimposed with Table A133. Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10881	11_11207	11_20906	11_10606	11_10467	11_10724	11_10588	11_20732	11_10614	11_10510	11_11299	11_20007	Total recomb. Events per arm
Position on chromosome	4H|54.25	4H|62.83	4H|65.05	4H|67.46	4H|72.08	4H|82.42	4H|89.39	4H|92.38	4H|100.74	4H|102.37	4H|111.68	4H|119.09	
Morex SNP	A	A	A	G	A	C	A	A	G	A	C	G	
Barke SNP	g	g	c	a	g	g	g	g	a	g	g	a	
MxB_F1_2_TSA_ear_2_seed_14	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_18	0	0	0	0	1	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2	0	0	0	0	0	0	1	0	0	1	0	0	2
MxB_F1_2_TSA_ear_2_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_21	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_22	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_4	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_5	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_6	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_8	0	1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_1	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_10	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_11	0	0	0	0	0	2	0	0	1	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_12	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_13	0	0	0	0	1	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_14	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_3_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_16	0	0	0	0	0	0	1	0	1	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_18	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_19	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_3_seed_2	0	0	1	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21	0	0	0	0	0	1	0	0	0	0	0	0	1
													91

Mean marker recomb. Freq./cell = 55(4HS)+91(4HL)/90 individuals = 1.62/cell

Table A137: The genotype for treated individuals 1-30, for markers on the short arm of 5H. Marker 11_21350 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a
MxB_F1_1_TSA_ear_1_seed_1	B	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_11	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_12	A	A	A	A	A	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_13	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_3	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_4	A	A	A	H	H	H	H	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_5	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_6	H	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_8	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_9	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_1	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_10	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_11	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_12	B	B	B	B	B	B	B	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_14	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_16	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_17	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_18	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_19	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_2	B	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_20	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_22	H	H	H	B	B	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_23	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_24	H	H	H	H	H	H	H	H	H	H	H	H

Table A138: The genotype for treated individuals 31-60, for markers on the short arm of 5H. Marker 11_21350 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_4	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_6	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_7	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_8	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_9	A	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_1	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_11	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_12	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_13	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_14	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_17	H	H	H	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_18	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_2	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_20	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_21	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_3	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_4	B	B	B	B	B	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_6	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_7	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_8	H	H	H	H	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_11	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_12	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_13	H	H	H	H	H	H	H	H	H	H	H	H

Table A139: The genotype for treated individuals 61-90, for markers on the short arm of 5H. Marker 11_21350 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a
MxB_F1_2_TSA_ear_2_seed_14	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_17	A	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_18	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_19	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	H	H	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_20	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_21	B	B	B	B	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_3	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_4	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_5	H	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_6	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_7	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_8	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_9	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_1	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_10	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_11	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_12	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_13	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_14	B	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_15	H	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_16	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_17	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_18	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_19	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_2	H	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_21	B	H	H	H	H	H	H	H	H	H	H	H

Table A140: The recombination data for markers on the short arm of 5H for treated individuals 1-30. Superimposed with Table A137

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350	Total recomb. Events per arm
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00	
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G	
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a	
MxB_F1_1_TSA_ear_1_seed_1		2	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_11		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_12		0	0	0	0	1	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_13		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_14		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_2		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_3		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_4		0	0	1	0	0	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_5		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_6		1	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_7		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_8		0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_9		0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_1		0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_10		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_11		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_12		0	0	0	0	0	0	2	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_14		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_15		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_16		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_17		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_18		0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_19		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_2		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_20		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_21		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_22		0	0	1	0	1	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_23		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24		0	0	0	0	0	0	0	0	0	0	0	0

Table A141: The recombination data for markers on the short arm of 5H for treated individuals 31-60. Superimposed with Table A138

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350	Total recomb. Events per arm
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00	
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G	
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a	
MxB_F1_1_TSA_ear_2_seed_25		0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_4		0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_6		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_7		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_8		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_9		2	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_1		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_10		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_11		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_12		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_13		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_14		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_15		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_17		0	0	1	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_18		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_19		0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_2		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_20		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_21		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_3		0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_4		0	0	0	0	1	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_5		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_6		0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_7		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_8		0	0	0	1	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_1		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_11		0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_12		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_13		0	0	0	0	0	0	0	0	0	0	0	0

Table A142: The recombination data for markers on the short arm of 5H for treated individuals 61-90. Superimposed with Table A139

Marker	11_20553	11_20873	11_21426	11_11048	11_10688	11_10621	11_20845	11_20766	11_21401	11_11198	11_21308	11_21350	Total recomb. Events per arm
Position on chromosome	5H|2.81	5H|26.28	5H|27.00	5H|29.90	5H|34.25	5H|37.11	5H|39.97	5H|46.23	5H|48.83	5H|48.83	5H|50.27	5H|51.00	
Morex SNP	A	A	A	A	G	A	G	C	C	G	C	G	
Barke SNP	g	g	g	t	a	g	a	a	a	a	g	a	
MxB_F1_2_TSA_ear_2_seed_14		0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_15		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_17		2	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_18		0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_19		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2		0	0	0	0	1	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_20		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_21		0	0	0	1	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_22		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_3		0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_4		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_5		1	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_6		0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_8		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_9		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_1		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_10		0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_11		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_12		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_13		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_14		1	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_15		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_16		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_17		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_18		1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_19		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_2		1	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_20		0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21		1	0	0	0	0	0	0	0	0	0	0	1
										Total recomb. Events in population			82

Table A143: The genotype for treated individuals 1-30, for markers on the long arm of 5H. Marker 11_20306 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11082	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a
MxB_F1_1_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_10	H	H	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_11	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_12	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	H	H	H	H	H	A	A	A	A	A	A	A	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_3	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_4	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_6	H	H	H	H	H	A	A	H	H	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	H	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_10	B	B	B	H	H	H	H	H	H	A	A	A	A	A	H	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_11	H	H	H	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_12	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	H	H	H	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_15	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_16	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	b	B	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_17	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_18	A	A	A	A	A	A	A	A	A	H	H	B	B	B	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_19	B	B	H	H	H	A	A	A	A	A	A	A	A	A	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_2	A	A	A	A	A	A	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_2_seed_20	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_1_TSA_ear_2_seed_21	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_22	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_23	A	A	A	A	A	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_24	H	H	H	H	H	H	H	H	H	H	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B

Table A144: The genotype for treated individuals 31-60, for markers on the long arm of 5H. Marker 11_20306 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a
MxB_F1_1_TSA_ear_2_seed_25	A	A	A	H	H	H	H	H	H	H	H	H	H	H	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_4	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_6	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_8	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_9	B	B	B	B	B	B	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_1	H	H	H	H	H	H	H	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_12	B	B	B	B	B	B	B	B	B	B	H	H	h	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_14	B	B	B	B	B	B	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	A	A	A	H	H
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_17	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_20	H	H	H	H	H	H	H	H	H	H	H	A	A	A	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_21	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_3	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	B
MxB_F1_2_TSA_ear_1_seed_4	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_7	H	H	H	H	H	H	H	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_1_seed_8	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_2_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_13	H	H	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B

Table A145: The genotype for treated individuals 61-90, for markers on the long arm of 5H. Marker 11_20306 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a
MxB_F1_2_TSA_ear_2_seed_14	A	A	A	A	A	A	A	A	A	A	A	A	A	A	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_17	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_19	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_21	A	A	A	A	A	A	A	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_4	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_6	H	H	H	H	H	H	H	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_8	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_9	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_10	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	B	B
MxB_F1_2_TSA_ear_3_seed_11	A	A	A	A	A	A	A	A	A	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	B	B
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_13	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_15	H	H	H	H	H	A	A	H	H	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_16	B	B	B	B	B	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_17	H	H	H	H	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_3_seed_18	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_3_seed_19	A	A	A	A	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_3_seed_21	H	H	H	H	H	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Table A146: The recombination data for markers on the long arm of 5H for treated individuals 1-30. Superimposed with Table A143

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022	Total recomb. Events per arm
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43	
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G	
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a	
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_10	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	3
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_12	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	4
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_6	0	0	0	0	0	1	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	6
MxB_F1_1_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	3
MxB_F1_1_TSA_ear_1_seed_9	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_10	0	0	0	1	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	5
MxB_F1_1_TSA_ear_2_seed_11	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_2_seed_14	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	3
MxB_F1_1_TSA_ear_2_seed_16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_18	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
MxB_F1_1_TSA_ear_2_seed_19	0	0	1	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
MxB_F1_1_TSA_ear_2_seed_2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	3
MxB_F1_1_TSA_ear_2_seed_20	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	4
MxB_F1_1_TSA_ear_2_seed_21	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_22	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_23	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	4
MxB_F1_1_TSA_ear_2_seed_24	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3

Table A147: The recombination data for markers on the long arm of 5H for treated individuals 31-60. Superimposed with Table A144

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	11_10336	11_20988	11_20829	11_11216	11_10736	11_20022	Total recomb. Events per arm
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43	
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G	
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a	
MxB_F1_1_TSA_ear_2_seed_25	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4
MxB_F1_1_TSA_ear_2_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_8	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_9	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_1_seed_1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	4
MxB_F1_2_TSA_ear_1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_12	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_14	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1	0	5
MxB_F1_2_TSA_ear_1_seed_15	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_TSA_ear_1_seed_17	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_18	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_19	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_20	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_1_seed_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	4
MxB_F1_2_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_7	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_13	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3

Table A148: The recombination data for markers on the long arm of 5H for treated individuals 61-90. Superimposed with Table A145. Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_20306	11_10671	11_11221	11_20713	11_21121	11_20367	11_20236	11_21150	11_10578	11_20850	11_11350	11_20320	11_21061	11_11273	11_20127	11_21203	11_10805	11_11375	11_20298	11_10095	11_10845	11_10755	11_10819	11_10292	11_11092	11_20676	11_21077	11_21355	11_11497	11_10901	*11_10336*	*11_20988*	11_20829	11_11216	11_10736	11_20022	Total recomb. Events per arm
Position on chromosome	5H|58.70	5H|59.40	5H|60.74	5H|65.49	5H|68.35	5H|75.40	5H|80.61	5H|94.43	5H|95.08	5H|102.06	5H|104.50	5H|108.18	5H|110.26	5H|111.68	5H|123.52	5H|129.41	5H|130.13	5H|130.84	5H|132.63	5H|137.16	5H|142.20	5H|142.20	5H|143.92	5H|144.63	5H|145.35	5H|146.00	5H|146.00	5H|153.51	5H|155.13	5H|158.37	5H|161.58	5H|161.58	5H|168.79	5H|171.66	5H|180.71	5H|181.43	
Morex SNP	A	G	C	A	G	C	C	A	A	G	A	A	C	G	A	A	G	A	A	C	A	G	G	G	A	a	A	A	C	A	A	T	C	A	A	G	
Barke SNP	g	a	a	c	a	a	a	c	c	a	g	c	a	a	t	c	a	g	g	a	c	c	a	c	g	c	g	g	a	g	g	a	a	g	g	a	
MxB_F1.2_TSA_ear_2_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.2_TSA_ear_2_seed_15	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	4
MxB_F1.2_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	4
MxB_F1.2_TSA_ear_2_seed_18	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.2_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	3
MxB_F1.2_TSA_ear_2_seed_2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	4
MxB_F1.2_TSA_ear_2_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1.2_TSA_ear_2_seed_21	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1.2_TSA_ear_2_seed_22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1.2_TSA_ear_2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1.2_TSA_ear_2_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	3
MxB_F1.2_TSA_ear_2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1.2_TSA_ear_2_seed_6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	4
MxB_F1.2_TSA_ear_2_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	2
MxB_F1.2_TSA_ear_2_seed_8	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.2_TSA_ear_2_seed_9	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1.2_TSA_ear_3_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1.2_TSA_ear_3_seed_10	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	3
MxB_F1.2_TSA_ear_3_seed_11	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	6
MxB_F1.2_TSA_ear_3_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1.2_TSA_ear_3_seed_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.2_TSA_ear_3_seed_14	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1.2_TSA_ear_3_seed_15	0	0	0	0	0	1	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	5
MxB_F1.2_TSA_ear_3_seed_16	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	4
MxB_F1.2_TSA_ear_3_seed_17	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	4
MxB_F1.2_TSA_ear_3_seed_18	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3
MxB_F1.2_TSA_ear_3_seed_19	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	4
MxB_F1.2_TSA_ear_3_seed_2	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1.2_TSA_ear_3_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1.2_TSA_ear_3_seed_21	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
																																				Total recomb. Events in population	234

Mean marker recomb. Freq./cell = 82(5HS)+234(5HL)/90 individuals = 3.51/cell

Table A149: The genotype for treated individuals 1-30, for markers on the short arm of 6H. Marker 11_11312 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a
MxB_F1_1_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_10	A	A	A	H	H	H	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_11	H	H	H	H	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_12	B	B	B	B	B	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	H	H	H	B	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_14	A	A	A	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	B	B	B	B	B	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_3	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_4	H	H	H	H	H	H	H	H	h	H	H	H	H	H	B	B	B
MxB_F1_1_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_6	H	H	H	H	H	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_7	A	A	A	H	H	H	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_8	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	h	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_1	H	H	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_10	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_11	B	B	H	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_12	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_14	H	H	A	A	A	A	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	H	H	H	H	H	H	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_16	H	H	H	H	H	H	H	H	h	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_17	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_18	H	H	H	A	A	A	A	A	a	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_19	H	H	B	B	B	B	B	B	b	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_2	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_20	B	B	H	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_21	H	H	H	H	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_22	B	B	B	B	B	B	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_23	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_24	A	A	A	A	A	A	H	B	b	B	B	B	B	B	B	B	B

Table A150: The genotype for treated individuals 31-60, for markers on the short arm of 6H. Marker 11_11312 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	A	A	A	A	a	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_4	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_6	H	H	H	H	H	H	B	B	b	B	B	B	B	B	B	B	H
MxB_F1_1_TSA_ear_2_seed_7	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_8	H	H	H	B	B	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_9	H	H	H	H	H	H	H	H	h	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_1	B	B	B	H	H	H	H	H	h	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_10	B	B	B	B	B	B	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_11	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_12	A	A	H	H	H	H	h	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_13	B	B	B	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	H	H	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_17	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_18	B	B	B	B	H	H	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_19	A	A	A	A	A	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_2	A	A	H	H	H	H	H	H	h	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_20	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_21	A	A	H	H	H	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_3	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_4	H	H	B	B	B	B	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_5	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_6	H	H	H	A	A	A	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_8	B	B	B	B	B	B	B	B	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_1	A	A	A	A	A	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_11	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_12	H	H	H	H	H	H	H	H	h	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_13	A	A	A	A	A	A	H	H	h	H	H	H	H	H	H	H	H

Table A151: The genotype for treated individuals 61-90, for markers on the short arm of 6H. Marker 11_11312 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a
MxB_F1_2_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	h	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_15	B	B	H	H	H	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_17	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	A	A	a	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_19	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	H	H	H	B	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_20	H	H	A	A	A	A	H	B	b	B	B	B	B	B	H	H	H
MxB_F1_2_TSA_ear_2_seed_21	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	A	A	A	A	A	H	H	H	h	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_2_seed_3	H	H	H	H	H	H	H	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_4	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_5	A	A	A	A	A	A	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_6	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_7	B	B	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_8	A	A	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	A	A	H	H	H	H	H	H	h	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_1	H	H	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_10	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_11	A	A	A	A	A	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_13	B	B	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	H	H	B	B	B	B	B	B	b	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_15	A	A	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_16	H	H	H	H	H	H	H	H	h	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_17	B	B	B	B	B	A	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_18	H	H	H	H	H	H	H	H	h	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_19	A	A	A	A	A	A	A	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_2	H	H	A	A	A	A	H	H	h	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	B	B	B	B	B	H	A	A	a	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_21	A	A	H	H	H	H	H	H	h	H	H	H	H	H	H	H	H

Table A152: The recombination data for markers on the short arm of 6H for treated individuals 1-30. Superimposed with Table A149

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312	Total recomb. Events per arm
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00	
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G	
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a	
MxB_F1_1_TSA_ear_1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_10		0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_11		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_12		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_13		0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_14		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_1_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_7		0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_11		0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_14		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_15		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_16		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_17		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_18		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_19		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_20		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_21		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_22		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_23		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_24		0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2

Table A153: The recombination data for markers on the short arm of 6H for treated individuals 31-60. Superimposed with Table A150

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312	Total recomb. Events per arm
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00	
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G	
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a	
MxB_F1_1_TSA_ear_2_seed_25		0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_TSA_ear_2_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_8		0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_9		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_1		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_10		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_12		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_13		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_15		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_17		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_18		0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_19		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_2		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_20		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_21		0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_4		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_6		0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_12		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_13		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1

Table A154: The recombination data for markers on the short arm of 6H for treated individuals 61-90. Superimposed with Table A151

Marker	11_20232	11_20493	11_21204	11_11479	11_20415	11_10868	11_10994	11_10939	*11_10427*	11_10061	11_10882	11_10462	11_10817	11_10539	11_10962	11_21014	11_11312	Total recomb. Events per arm
Position on chromosome	6HS|0.00	6H|1.34	6H|6.07	6H|12.54	6H|13.21	6H|24.36	6H|31.73	6H|33.74	*6H|34.40*	6H|42.36	6H|42.36	6H|44.77	6H|45.44	6H|46.11	6H|54.60	6H|54.60	6H|55.00	
Morex SNP	A	C	G	a	g	A	G	G	*a*	G	G	G	C	A	A	A	G	
Barke SNP	g	a	a	c	a	g	a	c	*g*	a	c	a	a	c	g	g	a	
MxB_F1_2_TSA_ear_2_seed_14		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_15		0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_17		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_18		0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2		0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_20		0	1	0	0	0	1	1	0	0	0	0	0	0	1	0	0	4
MxB_F1_2_TSA_ear_2_seed_21		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_22		0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_2_seed_3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_9		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_13		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_14		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_15		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_16		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_17		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_18		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_19		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_2		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_20		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_21		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
														Total recomb. Events in population				90

Table A155: The genotype for treated individuals 1-30, for markers on the long arm of 6H. Marker 11_20572 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a
MxB_F1_1_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_10	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_11	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_12	H	H	H	H	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	H	H	H	H	H	H	H	H	B	B	B	B	B	H	H	B
MxB_F1_1_TSA_ear_1_seed_3	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_4	B	B	B	B	B	B	B	B	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_1_TSA_ear_1_seed_8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_9	A	A	A	A	A	A	A	A	A	A	H	H	H	B	B	B
MxB_F1_1_TSA_ear_2_seed_1	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	b	H	A	A
MxB_F1_1_TSA_ear_2_seed_11	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B	B
MxB_F1_1_TSA_ear_2_seed_12	B	B	B	B	B	B	B	B	B	B	B	H	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_15	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_16	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B	b
MxB_F1_1_TSA_ear_2_seed_17	B	B	B	B	B	B	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_2	H	H	H	H	H	H	H	H	B	B	B	B	B	H	H	H
MxB_F1_1_TSA_ear_2_seed_20	A	A	A	A	H	H	H	B	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_22	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_23	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_24	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B

Table A156: The genotype for treated individuals 31-60, for markers on the long arm of 6H. Marker 11_20572 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_4	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_6	H	H	H	H	H	H	H	H	H	H	H	h	H	A	A	A
MxB_F1_1_TSA_ear_2_seed_7	A	A	A	A	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_TSA_ear_2_seed_8	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_9	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_1_seed_1	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	H	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_11	H	H	H	H	A	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_12	H	H	h	H	H	H	H	H	h	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_13	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_15	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_17	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_18	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_1_seed_2	B	B	B	B	B	B	B	B	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_21	B	B	B	B	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_3	B	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_1_seed_5	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_6	H	H	H	H	H	H	H	H	H	H	H	H	H	A	H	B
MxB_F1_2_TSA_ear_1_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_1_seed_8	H	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_11	B	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_2_seed_12	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_13	H	H	H	H	H	H	H	H	H	H	B	B	B	B	B	B

Table A157: The genotype for treated individuals 61-90, for markers on the long arm of 6H. Marker 11_20572 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a
MxB_F1_2_TSA_ear_2_seed_14	B	B	B	B	B	B	B	B	B	B	B	B	B	A	A	A
MxB_F1_2_TSA_ear_2_seed_15	A	A	A	A	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_2_seed_17	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_19	B	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_20	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H
MxB_F1_2_TSA_ear_2_seed_21	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_22	B	B	B	B	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_3	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_4	B	B	B	B	H	H	H	H	H	A	A	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_2_seed_6	A	A	A	A	A	A	A	A	H	H	H	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_7	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_8	H	H	H	H	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_3_seed_1	A	A	A	A	A	A	A	A	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_3_seed_10	H	H	H	H	H	H	A	A	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_11	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	H	H	H	H	H	H	H	H	H	H	B	B	B	H	H	H
MxB_F1_2_TSA_ear_3_seed_13	H	H	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_15	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_16	A	A	A	A	A	A	H	H	H	H	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_17	A	A	A	A	H	H	H	H	H	B	B	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_18	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_19	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	H	H	H	H	H	H	A	A	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_21	H	H	H	H	A	A	A	A	H	H	A	A	A	A	A	A

Table A158: The recombination data for markers on the long arm of 6H for treated individuals 1-30. Superimposed with Table A155

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687	Total recomb. Events per arm
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85	
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G	
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a	
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_10	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_12	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	1	3
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2
MxB_F1_1_TSA_ear_2_seed_11	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_16	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_17	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_2	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_20	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_21	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_22	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_2_seed_23	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table A159: The recombination data for markers on the long arm of 6H for treated individuals 31-60. Superimposed with Table A156

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687	Total recomb. Events per arm
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85	
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G	
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a	
MxB_F1_1_TSA_ear_2_seed_25	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_2_seed_7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_2_seed_8	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_9	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_1_seed_1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_10	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_11	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	3
MxB_F1_2_TSA_ear_1_seed_12	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_13	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_14	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_15	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_17	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_21	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	3
MxB_F1_2_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_8	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2
MxB_F1_2_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_11	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_2_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_13	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1

Table A160: The recombination data for markers on the long arm of 6H for treated individuals 61-90. Superimposed with Table A157. Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_20572	11_11067	11_21339	11_20266	11_10455	11_10040	11_20620	11_11458	11_21025	11_20996	11_20531	11_20036	11_20725	11_10175	11_10748	11_20687	Total recomb. Events per arm
Position on chromosome	6H|55.65	6H|58.01	6H|58.55	6H|59.56	6H|64.36	6H|65.03	6H|70.04	6H|81.17	6H|89.57	6H|93.12	6H|97.39	6H|105.60	6H|105.60	6H|119.02	6H|123.84	6H|124.85	
Morex SNP	G	A	G	G	A	g	G	G	A	C	G	A	G	A	A	G	
Barke SNP	a	g	c	a	g	a	c	a	g	a	a	g	a	c	g	a	
MxB_F1_2_TSA_ear_2_seed_14	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	2
MxB_F1_2_TSA_ear_2_seed_15	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_2_seed_17	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_20	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_2_seed_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_22	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_4	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_6	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_8	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_2_seed_9	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_10	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_3_seed_12	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_13	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_14	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_15	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_16	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_17	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_19	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_2	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_21	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	3
													Total recomb. Events in population				114

Mean marker recomb. Freq./cell = 90+114/90 individuals = 2.27/cell

Table A161: The genotype for treated individuals 1-30, for markers on the short arm of 7H. Marker 11_10153 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a
MxB_F1_1_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_1_TSA_ear_1_seed_10	H	H	B	B	B	B	B	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_1_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_12	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	H	H	H	H	H	A	H	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_2	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_3	H	H	H	H	H	H	H	H	A	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_4	B	B	B	B	B	H	H	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_5	B	B	H	H	H	H	H	H	A	A	A	A	A	H	B
MxB_F1_1_TSA_ear_1_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_8	A	A	A	A	A	A	A	A	A	A	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_1	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_10	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_12	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_14	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_15	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_1_TSA_ear_2_seed_16	H	H	H	H	H	B	B	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_17	H	H	H	H	H	B	B	B	B	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_19	A	A	A	A	A	H	H	H	H	H	H	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_20	B	H	H	H	H	H	H	H	H	H	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_21	A	A	A	A	A	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_22	B	B	B	B	B	B	B	H	H	H	H	H	H	A	A
MxB_F1_1_TSA_ear_2_seed_23	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_24	H	H	H	H	H	A	A	A	A	A	H	H	H	H	H

Table A162: The genotype for treated individuals 31-60, for markers on the short arm of 7H. Marker 11_10153 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a
MxB_F1_1_TSA_ear_2_seed_25	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_4	H	H	H	H	H	H	B	B	B	B	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_8	B	B	H	H	H	H	H	H	H	A	A	A	A	H	H
MxB_F1_1_TSA_ear_2_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_10	H	H	H	H	H	A	A	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_1_seed_11	H	A	A	A	A	A	A	A	A	H	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_12	B	b	B	B	B	B	B	B	B	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_13	B	H	H	H	H	H	H	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_14	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_1_seed_15	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_17	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	H	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_2	A	A	A	A	A	A	A	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_20	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_21	B	B	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_2_TSA_ear_1_seed_3	A	A	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_4	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_5	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_6	A	A	H	H	H	B	B	B	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_7	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_8	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_9	B	B	B	B	B	B	B	B	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_2_seed_12	A	A	A	A	A	A	A	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_13	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H

Table A163: The genotype for treated individuals 61-90, for markers on the short arm of 7H. Marker 11_10153 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a
MxB_F1_2_TSA_ear_2_seed_14	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	H	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_17	B	B	B	B	B	B	B	B	B	B	B	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_18	H	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_20	B	B	B	B	B	B	B	B	B	B	B	B	B	H	H
MxB_F1_2_TSA_ear_2_seed_21	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_3	B	B	B	B	B	B	B	B	B	B	H	H	H	A	A
MxB_F1_2_TSA_ear_2_seed_4	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_5	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_6	H	H	H	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_7	A	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_8	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_9	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_10	H	H	A	A	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_2_TSA_ear_3_seed_11	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_12	H	B	B	B	B	B	B	B	B	B	H	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_13	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_14	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_15	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_16	H	H	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_17	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_18	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_19	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_2	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	B	B	B	B	B	B	B	B	B	B	H	H	H	H	A
MxB_F1_2_TSA_ear_3_seed_21	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B

Table A164: The recombination data for markers on the short arm of 7H for treated individuals 1-30. Superimposed with Table A161

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153	Total recomb. Events per arm
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75	
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G	
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a	
MxB_F1_1_TSA_ear_1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_1_TSA_ear_1_seed_10		0	1	0	0	0	0	1	0	0	0	0	0	1	0	3
MxB_F1_1_TSA_ear_1_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_12		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_13		0	0	0	0	1	1	1	0	0	0	0	0	0	0	3
MxB_F1_1_TSA_ear_1_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_2		1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_3		0	0	0	0	0	0	0	1	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_4		0	0	0	0	1	0	1	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_5		0	1	0	0	0	0	0	1	0	0	0	0	1	1	4
MxB_F1_1_TSA_ear_1_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_8		0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_10		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_1_TSA_ear_2_seed_12		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_14		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_15		0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_1_TSA_ear_2_seed_16		0	0	0	0	1	0	1	0	0	1	0	0	0	0	3
MxB_F1_1_TSA_ear_2_seed_17		0	0	0	0	1	0	0	0	1	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_19		0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_20		1	0	0	0	0	0	0	0	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_21		0	0	0	0	1	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_22		0	0	0	0	0	0	1	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_2_seed_23		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_24		0	0	0	0	1	0	0	0	0	1	0	0	0	0	2

Table A165: The recombination data for markers on the short arm of 7H for treated individuals 31-60. Superimposed with Table A162

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153	Total recomb. Events per arm
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75	
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G	
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a	
MxB_F1_1_TSA_ear_2_seed_25		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_4		0	0	0	0	0	1	0	0	0	1	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_8		0	1	0	0	0	0	0	0	1	0	0	0	1	0	3
MxB_F1_1_TSA_ear_2_seed_9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_10		0	0	0	0	1	0	1	0	0	0	0	0	0	1	3
MxB_F1_2_TSA_ear_1_seed_11		1	0	0	0	0	0	0	0	1	1	0	0	0	0	3
MxB_F1_2_TSA_ear_1_seed_12		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_13		1	0	0	0	0	0	1	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_15		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_17		0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_19		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_20		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_21		0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_1_seed_3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_6		0	1	0	0	1	0	0	1	0	0	0	0	1	0	4
MxB_F1_2_TSA_ear_1_seed_7		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_9		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_11		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_2_seed_12		0	0	0	0	0	0	1	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_13		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1

Table A166: The recombination data for markers on the short arm of 7H for treated individuals 61-90. Superimposed with Table A163

Marker	11_21516	11_20245	11_10851	11_20755	11_21437	11_20495	11_10965	11_20192	11_10056	11_10327	11_21326	11_20113	11_11014	11_21270	11_10153	Total recomb. Events per arm
Position on chromosome	7HS|0.00	7H|12.42	7H|14.96	7H|15.93	7H|17.20	7H|25.70	7H|29.82	7H|34.82	7H|40.18	7H|42.60	7H|49.68	7H|56.81	7H|60.69	7H|68.46	7H|73.75	
Morex SNP	T	C	G	G	G	C	A	G	G	G	G	C	A	G	G	
Barke SNP	a	g	a	a	a	g	g	a	a	a	a	a	g	a	a	
MxB_F1_2_TSA_ear_2_seed_14		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_15		0	0	0	0	1	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_17		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18		1	0	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_20		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_21		0	0	0	0	2	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_22		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_3		0	0	0	0	0	0	0	0	0	1	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_6		0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_8		0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_10		0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_11		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_12		1	0	0	0	0	0	0	0	0	1	1	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_13		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_16		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_17		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_19		0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_20		0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
MxB_F1_2_TSA_ear_3_seed_21		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
															Total recomb. Events in population	107

Table A167: The genotype for treated individuals 1-30, for markers on the long arm of 7H. Marker 11_10442 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g
MxB_F1_1_TSA_ear_1_seed_1	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_11	H	H	H	H	H	B	B	H	H	H	H	H	H	H	H	A	A
MxB_F1_1_TSA_ear_1_seed_12	H	H	H	H	A	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_13	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_1_seed_14	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_2	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_3	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_4	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_5	B	B	B	B	H	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_1_TSA_ear_1_seed_6	B	B	B	B	H	H	H	H	A	A	A	A	A	A	A	A	H
MxB_F1_1_TSA_ear_1_seed_7	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_8	H	H	H	H	A	A	A	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_1	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_10	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_1_TSA_ear_2_seed_11	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_12	H	H	H	H	H	H	A	A	A	A	A	A	A	A	H	H	H
MxB_F1_1_TSA_ear_2_seed_14	H	H	H	H	B	B	B	H	H	H	H	H	H	H	H	H	A
MxB_F1_1_TSA_ear_2_seed_15	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_16	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_17	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_18	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_19	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_2	A	A	A	A	A	A	A	H	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_20	A	A	A	A	B	B	B	B	B	B	B	B	B	B	H	H	H
MxB_F1_1_TSA_ear_2_seed_21	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_22	A	A	A	A	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_23	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_24	H	H	H	H	B	B	B	B	B	B	H	A	A	A	A	A	A

Table A168: The genotype for treated individuals 31-60, for markers on the long arm of 7H. Marker 11_10442 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g
MxB_F1_1_TSA_ear_2_seed_25	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_1_TSA_ear_2_seed_6	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_1_TSA_ear_2_seed_7	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_1_TSA_ear_2_seed_8	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H
MxB_F1_1_TSA_ear_2_seed_9	A	A	A	A	A	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_1	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_1_seed_10	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_11	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_12	H	H	H	H	h	H	H	H	H	H	H	h	H	H	H	H	h
MxB_F1_2_TSA_ear_1_seed_13	A	A	A	A	A	H	H	H	H	H	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_14	H	H	H	H	A	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_15	A	A	A	A	A	A	H	B	B	B	H	H	H	H	H	H	A
MxB_F1_2_TSA_ear_1_seed_17	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_18	H	H	H	H	b	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_19	B	B	B	B	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_2	B	B	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_20	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_21	H	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_3	H	H	H	H	A	A	A	A	A	A	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_4	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A
MxB_F1_2_TSA_ear_1_seed_6	A	A	A	A	H	B	B	H	H	H	H	H	H	H	H	H	B
MxB_F1_2_TSA_ear_1_seed_7	A	A	A	A	A	A	A	A	A	A	A	A	A	H	H	H	H
MxB_F1_2_TSA_ear_1_seed_8	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_1_seed_9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	B	B
MxB_F1_2_TSA_ear_2_seed_1	H	H	H	H	H	H	H	H	H	H	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_11	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_12	B	B	B	B	H	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_13	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A

Table A169: The genotype for treated individuals 61-90, for markers on the long arm of 7H. Marker 11_10442 is flanking the centromere (orange box). An allele of Barke origin is shown as B (orange), that of Morex origin is shown as A (turquoise) and a heterozygote is shown as H (lilac).

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g
MxB_F1_2_TSA_ear_2_seed_14	B	B	B	B	B	B	H	H	H	H	H	H	H	H	B	B	B
MxB_F1_2_TSA_ear_2_seed_15	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_17	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_18	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_2_seed_20	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_21	A	A	A	A	A	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_22	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	H	H
MxB_F1_2_TSA_ear_2_seed_3	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_4	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_5	B	B	B	B	B	H	H	H	H	H	H	H	H	B	B	B	B
MxB_F1_2_TSA_ear_2_seed_6	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_7	H	H	H	H	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_2_seed_8	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_2_seed_9	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_1	H	H	H	H	B	H	H	H	H	H	H	H	H	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_10	H	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	H
MxB_F1_2_TSA_ear_3_seed_11	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_12	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H
MxB_F1_2_TSA_ear_3_seed_13	H	H	H	H	H	H	H	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_14	B	B	B	B	B	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_15	H	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_16	A	A	A	A	A	A	A	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_17	A	A	A	A	H	H	H	H	H	H	H	H	H	H	A	A	A
MxB_F1_2_TSA_ear_3_seed_18	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
MxB_F1_2_TSA_ear_3_seed_19	H	H	H	H	H	B	B	B	B	B	B	B	B	B	B	B	B
MxB_F1_2_TSA_ear_3_seed_2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
MxB_F1_2_TSA_ear_3_seed_20	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	H	B
MxB_F1_2_TSA_ear_3_seed_21	B	B	B	B	H	H	H	H	H	H	H	H	H	H	A	A	A

Table A170: The recombination data for markers on the long arm of 7H for treated individuals 1-30. Superimposed with Table A167

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174	Total recomb. Events per arm
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56	
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A	
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g	
MxB_F1_1_TSA_ear_1_seed_1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_11	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	3
MxB_F1_1_TSA_ear_1_seed_12	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_13	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_14	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_1_seed_4	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_5	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_1_TSA_ear_1_seed_6	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	3
MxB_F1_1_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_1_seed_8	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	3
MxB_F1_1_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_10	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_1_TSA_ear_2_seed_11	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_12	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_1_TSA_ear_2_seed_14	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	3
MxB_F1_1_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_16	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_17	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_18	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_19	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_2	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_20	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	3
MxB_F1_1_TSA_ear_2_seed_21	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_22	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_1_TSA_ear_2_seed_23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_24	0	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	3

Table A171: The recombination data for markers on the long arm of 7H for treated individuals 31-60. Superimposed with Table A168

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174	Total recomb. Events per arm
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56	
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A	
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g	
MxB_F1_1_TSA_ear_2_seed_25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_1_TSA_ear_2_seed_7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_1_TSA_ear_2_seed_8	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	2
MxB_F1_1_TSA_ear_2_seed_9	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_11	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_1_seed_13	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_14	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_15	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	1	4
MxB_F1_2_TSA_ear_1_seed_17	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_18	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_19	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_21	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_3	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_1_seed_4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_1_seed_6	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	1	4
MxB_F1_2_TSA_ear_1_seed_7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_8	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_1_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
MxB_F1_2_TSA_ear_2_seed_1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_12	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_13	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1

Table A172: The recombination data for markers on the long arm of 7H for treated individuals 61-90. Superimposed with Table A169. Includes the calculation of the mean overall marker recombination frequency for the whole chromosome.

Marker	11_10442	11_21330	11_20771	11_10303	11_10169	11_20092	11_20247	11_21229	11_21209	11_10861	11_10885	11_20847	11_10687	11_11440	11_20962	11_10999	11_10174	Total recomb. Events per arm
Position on chromosome	7H|84.92	7H|86.44	7H|87.21	7H|87.97	7H|104.78	7H|110.99	7H|116.33	7H|128.36	7H|129.91	7H|133.79	7H|139.72	7H|140.21	7H|140.99	7H|144.45	7H|149.80	7H|161.43	7H|166.56	
Morex SNP	G	G	c	a	T	g	c	a	a	c	T	G	C	A	T	G	A	
Barke SNP	c	a	a	g	a	c	g	g	g	a	a	a	a	t	a	a	g	
MxB_F1_2_TSA_ear_2_seed_14	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_2_seed_15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_17	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_18	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
MxB_F1_2_TSA_ear_2_seed_20	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_21	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_22	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
MxB_F1_2_TSA_ear_2_seed_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_2_seed_4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_5	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	2
MxB_F1_2_TSA_ear_2_seed_6	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	3
MxB_F1_2_TSA_ear_2_seed_7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_8	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_2_seed_9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_1	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	3
MxB_F1_2_TSA_ear_3_seed_10	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	2
MxB_F1_2_TSA_ear_3_seed_11	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
MxB_F1_2_TSA_ear_3_seed_13	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_15	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2
MxB_F1_2_TSA_ear_3_seed_16	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_17	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
MxB_F1_2_TSA_ear_3_seed_18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_19	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
MxB_F1_2_TSA_ear_3_seed_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MxB_F1_2_TSA_ear_3_seed_20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2
MxB_F1_2_TSA_ear_3_seed_21	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	2
														Total recomb. Events in population				121

Mean marker recomb. Freq./cell = 107(7HS)+121(7HL)/90 individuals = 2.53/cell

The JHI in-house Morex x Barke consensus maps (Comadran *et al*., 2012) that were used (in conjunction with already established mapping data (Mayer *et al*., 2012), highlighting the chosen SNPs between Morex and Bowman for the markers 11_20659, 11_10747, 11_20628 and 11_10515.

Table A173: The Morex x Barke consensus map highlighting (in yellow) the chosen SNP (A/G) for the KASPar® assay of the marker 11_20659

Current Assigned Position on Morex x Barke Map : 3H 77.3 cM

Class	Value
Marker Name	**11_20659**
Illumina ID	BOPA1_4019-302-0_B_R_1867785277
Old Name	4019-302
iSelect Name	BOPA1_4019-302
Illumina Strand	BOT
SNP	[T/C]
Address A ID	31706491
Allele A Probe Sequence	TACCTCCACAGCAGCTGCCACCATGGCTTCAGTAGCTATTGTACACTTCA
Address B ID	
Allele B Probe Sequence	
Genome Build	0
Ploidy	diploid
Species	Hordeum vulgare
Source	0
Source Version	0
Source Strand	TOP

Class	Value
Source Sequence	GTTCTCCATGGCGGGGTGGATTATTTTCTACTTGACGTTGCTCTTCTAAAT CTGTGCTGAACTGGAACATCCGCAAATAGTAGATACCATGAGAAAACATGG AGAAGATAATAGTGTC[A/G]TGAAGTGTACAATAGCTACTGAAGCCATGG GGCAGCTGCTGTGGAGGTACGAGTTGTATCGGTACAGATAATGGGTTCCTC TACCCATCTTTGTGTACATGCTTCCGTTATGTTAATT
Top Genomic Sequence	GTTCTCCATGGCGGGGTGGATTATTTTCTACTTGACGTTGCTCTTCTAAAT CTGTGCTGAACTGGAACATCCGCAAATAGTAGATACCATGAGAAAACATGG AGAAGATAATAGTGTC[A/G]TGAAGTGTACAATAGCTACTGAAGCCATGG GGCAGCTGCTGTGGAGGTACGAGTTGTATCGGTACAGATAATGGGTTCCTC TACCCATCTTTGTGTACATGCTTCCGTTATGTTAATT
Bead Set ID	448
New H35 Designation From BLAST	2257
Previous H35 Designation	2257
Comparison Previous vs New H35 Designation	same top hit

Table A174: The Morex x Barke consensus map highlighting (in yellow) the chosen SNP (A/G) for the KASPar® assay of the marker 11_10747

1. Background Information

Class	Value
Marker Name	**11_10747**
Illumina ID	BOPA1_5224-1560-0_B_R_1867785449
Old Name	5224-1560
iSelect Name	BOPA1_5224-1560
Illumina Strand	BOT
SNP	[T/C]
Address A ID	69730333
Allele A Probe Sequence	TACACAATTGTGATATTATACAACGGGCAGAGTTCAAGCAATGTTCATGT
Address B ID	
Allele B Probe Sequence	
Genome Build	0
Ploidy	diploid
Species	Hordeum vulgare
Source	0
Source Version	0
Source Strand	TOP

Class	Value
Source Sequence	CAACCGGCATGTAGAGTGCCATGATACAGTTGTTGTACAAGGATGCAACTT TTCTCCTTTTCTTTTGTCCTTGACGTGYCTAGGAGATCCTCTTTGTAAACT GCCCAATCATTTATAC[A/G]ACATGAACATTGCTTGAACTCTGCCCGTTG ATAATATCACAATTGTGTAATATGGTGGTAGCTCAGGAAATTTATGTACAT ACAGGTACAGTGCTTGAACTGTGCCATCAATATATGT
Top Genomic Sequence	CAACCGGCATGTAGAGTGCCATGATACAGTTGTTGTACAAGGATGCAACTT TTCTCCTTTTCTTTTGTCCTTGACGTGYCTAGGAGATCCTCTTTGTAAACT GCCCAATCATTTATAC[A/G]ACATGAACATTGCTTGAACTCTGCCCGTTG ATAATATCACAATTGTGTAATATGGTGGTAGCTCAGGAAATTTATGTACAT ACAGGTACAGTGCTTGAACTGTGCCATCAATATATGT
Bead Set ID	448
New H35 Designation From BLAST	2725
Previous H35 Designation	2725
Comparison Previous vs New H35 Designation	same top hit

Table A175: The Morex x Barke consensus map highlighting (in yellow) the chosen SNP (A/T) for the KASPar® assay of the marker 11_20628

1. Background Information

Current Assigned Position on Morex x Barke Map : 3H 87.4 cM

Class	Value
Marker Name	**11_20628**
Illumina ID	BOPA1_3791-1525-0_B_R_1867120456
Old Name	3791-1525
iSelect Name	BOPA1_3791-1525
Illumina Strand	BOT
SNP	[T/A]
Address A ID	25741447
Allele A Probe Sequence	TTCTTTCTCCCAGATGCAGAACATATAGCAGTTCTTCCTGGAAAAAGTGT
Address B ID	10766444
Allele B Probe Sequence	TTCTTTCTCCCAGATGCAGAACATATAGCAGTTCTTCCTGGAAAAAGTGA
Genome Build	0
Ploidy	diploid
Species	Hordeum vulgare
Source	0
Source Version	0
Source Strand	TOP

Class	Value
Source Sequence	CAAGCTGGCATCATTTTACAACCATCACAGAAGATACAGGCAACAATCCTT GTCATGGTGCAAACAAAGACAGGTACACATAACAAACTTGGAAAGTTTAGA AGAAAGAGGGGTCATC[A/T]CACTTTTTCCAGGAAGAACTGCTATATGTT TGCATCTGGGAGAAAGAAATCCTAATGGTGGATCCCTCGAGCTTGCTCGCA GCTTACAGACCAGAGCTTCGGTCGCCTCTTCCTCGCT
Top Genomic Sequence	CAAGCTGGCATCATTTTACAACCATCACAGAAGATACAGGCAACAATCCTT GTCATGGTGCAAACAAAGACAGGTACACATAACAAACTTGGAAAGTTTAGA AGAAAGAGGGGTCATC[A/T]CACTTTTTCCAGGAAGAACTGCTATATGTT TGCATCTGGGAGAAAGAAATCCTAATGGTGGATCCCTCGAGCTTGCTCGCA GCTTACAGACCAGAGCTTCGGTCGCCTCTTCCTCGCT
Bead Set ID	448
New H35 Designation From BLAST	985
Previous H35 Designation	985
Comparison Previous vs New H35 Designation	same top hit

Table A176: The Morex x Barke consensus map highlighting (in yellow) the chosen SNP (A/G) for the KASPar® assay of the marker 11_10515

1. Background Information

Current Assigned Position on Morex x Barke Map : 3H 88.8 cM

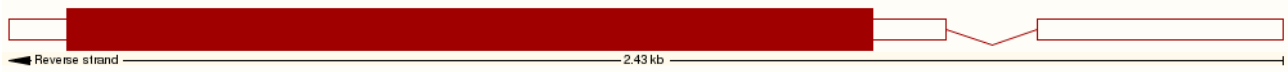
Class	Value
Marker Name	**11_10515**
Illumina ID	BOPA1_3674-1352-0_T_F_1867785236
Old Name	3674-1352
iSelect Name	BOPA1_3674-1352
Illumina Strand	TOP
SNP	[A/G]
Address A ID	66608440
Allele A Probe Sequence	TGTACAACGAATGATGATGATGAATCGCTAGCTTAGTTTAATTTAATTTG
Address B ID	
Allele B Probe Sequence	
Genome Build	0
Ploidy	diploid
Species	Hordeum vulgare
Source	0
Source Version	0
Source Strand	TOP

Class	Value
Source Sequence	GGACGGGCATTTTTTTTTTTTTTTTTTTCCGAATCTCACCCTGCCCCATAA TGATTTACAGGCTTCCGGTGTACAACGAATGATGATGATGAATCGCTAGCT AGTTTAATTTAATTTG[A/G]TTTAGCTCGCCAACAATGCTGACACCATGG CAATACCAGCAGTAGCGYCAAAGAAGATAATCTTCTTCTTACCGAGGCCGC AGTCTTGACGCGGACGAGAACATGGACTGCGACGAGT
Top Genomic Sequence	GGACGGGCATTTTTTTTTTTTTTTTTTTCCGAATCTCACCCTGCCCCATAA TGATTTACAGGCTTCCGGTGTACAACGAATGATGATGATGAATCGCTAGCT AGTTTAATTTAATTTG[A/G]TTTAGCTCGCCAACAATGCTGACACCATGG CAATACCAGCAGTAGCGYCAAAGAAGATAATCTTCTTCTTACCGAGGCCGC AGTCTTGACGCGGACGAGAACATGGACTGCGACGAGT
Bead Set ID	448
New H35 Designation From BLAST	16375
Previous H35 Designation	16375
Comparison Previous vs New H35 Designation	same top hit

Ensembl plant data and the JHI in-house contig library for the barley markers MLOC10987, MLOC4841 and MLOC53985, showing the aligned Morex and Bowman contigs.

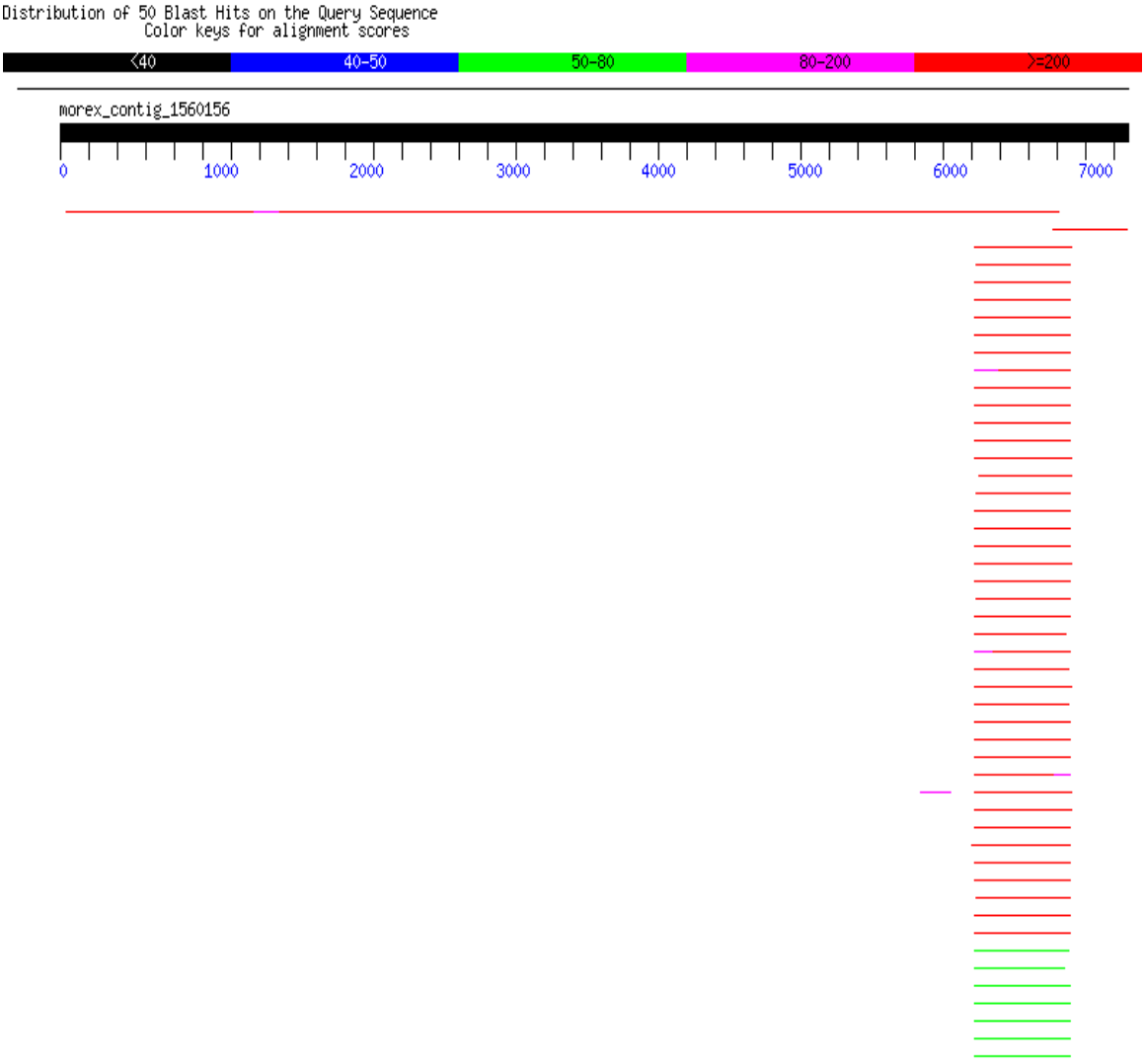
MLOC 10987

Ensebl plant data



Statistics
Exons: 2 **Coding exons:** 1 **Transcript length:** 2,260 bps **Translation length:** 512 residues
Type
Novel protein coding

WGS Morex contig match data



Database: assembly5_WGSBowman34x_renamed_blastable.fasta
2,077,901 sequences; 1,779,486,241 total letters

Query= morex_contig_1560156 CAJW011560156 carma=3HL
Length=7323

Sequences producing significant alignments:	Score (Bits)	E Value
bowman_contig_855417 CAJX010850522 carma=3HL	1.194e+04	0.0
bowman_contig_1368909 CAJX011363749 carma=3HL	848	0.0

> bowman_contig_855417 CAJX010850522 carma=3HL
Length=6813

Score = 1.194e+04 bits (13242), Expect = 0.0
Identities = 6743/6818 (98%), Gaps = 17/6818 (0%)
Strand=Plus/Plus

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Query  41    ccgcccccgttgccgttccccgttcctcctcgtcgcgtccccgcccgcGATTTCGGGCAT  100
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CCGCCCCCGTCGCCGTTCCCCGTTCCTCCTCGTCGCGTCCCCGCCCGCGATTTCGGGCAT  60

Query  101   TGGGGTGTTTTCAGGTACGATCTTGTTTTCGTCCGGTGATTCGTTGAATGAAACCCCACC  160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGGGGTGTTTTCAGGTACGATCTTGTTTTCGTCCGGTGATTCGTTGAATGAAACCCCACC  120

Query  161   TGACTCCCGCAATTTGCGGGTGCGTCGGCTCGCACCAGGCGCACCATCTAGATCTGCCCC  220
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  121   TGACTCCCGCAATTTGCGGGTGCGTCGGCTCGCACCAGGCGCACCATCTAGATCCGCCCC  180

Query  221   TGGTTGGGGCTCTGAAAATTTTGATTGTGAGATTTTCAACCAGTCATGACAGTGGCCTTC  280
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |
Sbjct  181   TGGTTGGGGCTCTGAAAATTTTGATTGTGAGATTTTCAACCAGTCATGACAGCGGCCTCC  240

Query  281   TATATTCGT--------GAGGAACAATGGGGGCATTGCACAGTATCCTGTTTTGAGTTGTT  333
             |||||||||       ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TATATTCGTTCTTCTTGAGGAACAATGGGGGCATTGCACAGTATCCTGTTTTGAGTTGTT  300

Query  334   AAAATTGGGATAGTTTACAAATTGGCGTTGAACTGTTCTGTTCCCCTTCGCTGAAAAACT  393
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  301   AAAATTGGGATAGTTTACAAATTGGCGTTGAACTGTTGTGTTCCCCTTCGCTGAAAAACT  360

Query  394   CAGATAGCACGTAATTTGGTCCGCTGGTGCGAATAGATCCCCAATTCTATGTAGTATATA  453
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CAGATAACACGTAATTTGGTCCGCTGGTGCGAATAGATCCCCAATTCTATGTAGTATATA  420

Query  454   CTGATTAACAACTTCCTATGGCTGAGCGTATGCAACCTGGAACCGCCGCTTATAGTTATG  513
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CTGATTAACAACTTCCTATGGCTGAGCGTATGCAACCTGGAACCGCCGCTTATAGTTATG  480

Query  514   ATGCAAAATTTAGGAAGTAATTGAATTGCCTGACATGCTTTCCCTTTTAGTTACTGAAAC  573
             || ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  481   ATACAAAATTTAGGAAGTAATTGAATTGCCTGACATGCTTTCCTTTTTAGTTACTGAAAC  540

Query  574   AACAATCTTGCTAAAGAAAATGCTTGAGCCGTATTTCATCTGGCTCTGTCTGTTTCATTC  633
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AACAATCTTGCTAAAGAAAATGCTTGAGCCGTATTTCATCTGGCTCTGTCTGTTTCATTC  600


Query  634   CTTGTCTCTGTTTTGTAGTTCAGCTGAACAGTGAGAACAAATCTATTTAAGTCATCAGAT  693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   CTTGTCTCTGTTTTGTAGTTCAGCTGAACAGTGAGAACAAATCTATTTAAGTCATCAGAT  660
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Query  694   GAGAGGGCTTGTTTCAAATCACTCACTGAATTCTAGATAATTTGACAGATTAATGATATA  753
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  661   GAGAGGGCTTGTTTCAAATCACTCACTAAATTCTAGATAATTTGACAGATTAATGATATA  720

Query  754   TGCAACTAAAAAAGGGATACCCCGGCCTTCCTTAACCTCTGAAGAGCTCCAGTACTGGTT  813
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   TGCAACTAAAAAAGGGATACCCCGGCCTTCCTTAACCTCTGAAGAGCTCCAGTACTGGTT  780

Query  814   CTTTGTTTTGCCTACCTTAAGATAATAACACAAGTCTTGAATTCGACAGAATTGTTTACT  873
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   CTTTGTTTTGCCTACCTTAAGATAATAACACAAGTCTTGAATTCGACAGAATTGTTTACT  840

Query  874   TGTACTGAAATATTTTCCTGATAGTTGCTTCTTCTGCTGCAGTAATCACCAATCTCAGCT  933
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   TGTACTGAAATATTTTCCTGATAGTTGCTTCTTCTGCTGCAGTAATCACCAATCTCAGCT  900

Query  934   CTACCATAATCATGAGTCTAGCTTGTCTCGTATGCCATGGGATGAGCAGTCCCTCCCAGT  993
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901   CTACCATAATCATGAGTCTAGCTTGTCTCGTATGCCATGGGATGAGCAGTCCCTCCCAGT  960

Query  994   CTTTCAGAAGCTATTCAGTCTCAAGCTCAGAGGATGAAAACAGGTGTGGAGCTGCTGTTG  1053
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961   CTTTCAGAAGCTATTCAGTCTCAAGCTCAGAGGATGAAAACAGGTGTGGAGCTGCTGTTG  1020

Query  1054  CCTGCCTGTCGCGGAAAATTATGGCCGCAGGACCTGCTAACCGTGTGGGAACATCAAAGG  1113
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  1021  CCTGCCTGTCGCGGAAAATTATGGCCGCGGGACCTGCTAACCGTGTGGGAACATCAAAGG  1080

Query  1114  TGACGCCTGTAATGGCCACTGGACAAGGCATCGAAGGTGCTCCTCGCCTTCAAAGGAGCC  1173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081  TGACGCCTGTAATGGCCACTGGACAAGGCATCGAAGGTGCTCCTCGCCTTCAAAGGAGCC  1140

Query  1174  GTGCTGTTTCAAGGGATCTTGTTAGGGACTGGAACTTCGACGAGATTGTTGTTGGGAACT  1233
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141  GTGCTGTTTCAAGGGATCTTGTTAGGGACTGGAACTTCGACGAGATTGTTGTTGGGAACT  1200

Query  1234  AGAGTAGTAGGGTGCCAGCAGTTATCCCCAGGCTGGACATTGGACTATTATCTGGCAGGA  1293
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201  AGAGTAGTAGGGTGCCAGCAGTTATCCCCAGGCTGGACATTGGACTATTATCTGGCAGGA  1260

Query  1294  GTTGATGTACATTTTCTAGTATACATCTGGATATCTATGTACTCCCTCTGACCAACAATA  1353
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  1261  GTTGATGTACATTTTCTAGTATACATCTGGATATCTATGTACTCCCTCCGACCAACAATA  1320

Query  1354  TAAGACGTTTTTGCAAACAAACATAGCTTACAAAAACGTCTTATATTATGGGACGAAGGG  1413
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321  TAAGACGTTTTTGCAAACAAACATAGCTTACAAAAACGTCTTATATTATGGGACGAAGGG  1380

Query  1414  AGTACTCCCTGTGTACCTAAATAATTGTAGTTGGAGAGAATAATCTAGTTTTCCTCAACT  1473
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1381  AGTACTCCCTGTGTACCAAAATAATTGTAGTTGGAGAGAATAATCTAGTTTTCCTCAACT  1440

Query  1474  ACAATTATTTAGGTACAGAGGGAGTACTATATTAGTACGCGCCCAATGAAAGAGCAAATT  1533
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441  ACAATTATTTAGGTACAGAGGGAGTACTATATTAGTACGCGCCCAATGAAAGAGCAAATT  1500

Query  1534  ATTTAATAGTACTTGTTACCACCTATAGAGACCCCTCCTGGCTTGTTATATAATTTGCCA  1593
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  1501  ATTTAATAGTACTTGTTACCACCTATAGAGACCCCTTCTGGCTTGTTATATAATTTGCCA  1560

Query  1594  ATTTGTGTAGTAAGCATCCATTTTTCTGTTTCTGCGTCTGAATGATAAATCTAATCTAAT  1653
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  1561  ATTTGTGTAGTAAGCATCCATTTTTCTGTTTCTGCGTCTGAATGATAAATCAAATCTAAT  1620

Query  1654  TTTCCTGAGATGTCAATTGATGCTCTATCAAGTCTAGATATTTTCACAGGCTATTGGATG  1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1621  TTTCCTGAGATGTCAATTGATGCTCTATCAAGTCTAGATATTTTCACAGGCTATTGGATG  1680

Query  1714  GTGGCGCATTCTTTTGATGTATTATTGATGTCAAGTGTCCATCCATGAGGGCCATGAGAA  1773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1681  GTGGCGCATTCTTTTGATGTATTATTGATGTCAAGTGTCCATCCATGAGGGCCATGAGAA  1740


Query  1774  ATCCAGCTgtttggtttggttttattttgtatttttgtatttttttttggctgtttgtat  1833
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  1741  ATCCAGCTGTTTGGTTTGGTTTTATTTTGTATTTTTGTATTTTTTTT-GGCTGTTTGTAT  1799
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Query  1834  aatctttgtttgtTCACCTTGACGTGGCTACTTGACCTGCTAAAATACCAGTTGTTTGGC  1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1800  AATCTTTGTTTGTTCACCTTGACGTGGCTACTTGACCTGCTAAAATACCAGTTGTTTGGC  1859

Query  1894  AAACCAATATGTGGTTGGATGGTTTGAGGGATAGTGATATCCCTAGTCCACCAAGGTTTA  1953
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1860  AAACCAATCTGTGGTTGGATGGTTTGAGGGATAGTGATATCCCTAGTCCACCAAGGTTTA  1919

Query  1954  AATCCTGATGTTTTGCATTATTTCTGGATTTATTTTAGGGTTTCCCGTCGACGACGAGGC  2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1920  AATCCTGATGTTTTGCATTATTTCTGGATTTATTTTAGGGTTTCCCGTCGACGACGAGGT  1979

Query  2014  GCCTACGGTGACTTCGTAAAAATGAAGATGATATGCCGGCTTAGTCTCTCGAAGGTGTTC  2073
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  1980  GCCTACGGTGACTTCGTAAAAATCAAGATGATATGCCGGCTTAGTCTCTCGAAGGTGTTC  2039

Query  2074  ATAGGGGTAGGGTGTGCGTTTATAGGTTTGGGTGTATGCGTGTGTATATGAGCGCTTGCG  2133
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2040  ATAAGGGTAGGGTGTGCGTTTATAGGTTTGGGTGTATGCGTGTGTATATGAGCGCTTGCG  2099

Query  2134  TCTGTACTATGTCaaaaaaaT-AGCTGtttggtttgatttggtttttattttgtatttttg  2192
             ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  2100  TCTGTACTATGTCAAAAAAAACAGCTGTTTGGTTTGATTTGGTTTTATTTTGTATTTTTG  2159

Query  2193  TaaaaaaaaTTGGATGTCTGTATGATCTTTGTTTGTTCACCTTGATGTGGCTACTTGACC  2252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2160  TAAAAAAAATTGGATGTCTGTATGATCTTTGTTTGTTCACCTTGATGTGGCTACTTGACC  2219

Query  2253  TGCTAAAATATTCTGCCCGAGGATCAACTGCATGTGCTGATGCAATCCTGAAGTTATTTT  2312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2220  TGCTAAAATATTCTGCCCGAGGATCAACTGCATGTGCTGATGCAATCCTGAAGTTATTTT  2279

Query  2313  CCGTGAAAATGTGACAAAGTTTAACAGATTGCTCCAACTGGAATTAATTTTTTCAGGAGA  2372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2280  CCGTGAAAATGTGACAAAGTTTAACAGATTGCTCCAACTGGAATTAATTTTTTCAGGAGA  2339

Query  2373  TAAATTTCAGAACAGCTGAAGTTCCCAGTAAGGCCTGGTTTGCCGGAATGGATTCCTATT  2432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2340  TAAATTTCAGAACAGCTGAAGTTCCCAGTAAGGCCTGGTTTGCCGGAATGGATTCCTATT  2399

Query  2433  CCTATGTAGGTAGGGATAGGAGTCAATCCTTCACATTTCAGAGAAAAAGAAACATTAACC  2492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2400  CCTATGTAGGTAGGGATAGGAGTCAATCCTTCACATTTCAGAGAAAAAGAAACATTAACC  2459

Query  2493  TCAATGGAAAAAATTCTTATCCTATGCATGTCATCTCACTTCCCATTATTTTCCTATTCC  2552
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Sbjct  2460  TCAATGGAAAAAATTCTTATCCTATGCATGTCATCTCACTTCCCATTATTTTCCTATTCC  2519

Query  2553  TATACTATTCCTATCCTATGAACCAAATGAGGCCTAAGATAAAAAATGATAGGCAAATAT  2612
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Sbjct  2520  TATACTATTCCTATCCTATGAACCAAATGAGGCCTAAGATAAAAAATGATAGGCAAATAT  2579

Query  2613  TTCACTGGAAGAGGTAAAATTTCCTCTGAGAATCAAAAAGGCCCTAGTACGGTAGTACGA  2672
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Sbjct  2580  TTCACTGGAAGAGGTAAAATTTCCTCTGAGAATCAAAAAGGCCCTAGTACGGTAGTACGA  2639

Query  2673  GTACTAGGGATTGAACACAACTATTCTTGACTTCTCTGATATGGTGATTTCTATCTTGGC  2732
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Query  2733  TTTTGCTCAACTGGTATTGCATTCGACGTTTCACTCAACCTGGAAAGATTCCACCCTGCT  2792
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Query  2793  ATGACAAATATTGATTTCACCGAGGCGCCAACGCGGATAAAGAAAATAATATATATTTAA  2852
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Query  2853  CAATTGAGACTTTCAAATCTATATATGTAAGTGCTTGATCATTATTGATGACCACAAACT  2912
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Sbjct  2820  CAATTGAGACTTTCAAATCTATATATGTAAGTGCTTGATCATTATTGATGACCACAAACT  2879


Query  2913  AAAGTACACTTAAGAAAGAGGCATGGACCAAAATGGCTCCCTGAATAGAGGAAGAACCGA  2972
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Sbjct  2880  AAAGTACACTTAAGAAAGAGGCATGGACCAAAATGGCTCCCTGAATAGAGGAAGAACCGA  2939
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Query  2973  GACCGACATACATATAACATTCATACATAACAATTGACACCATCATGGTTGTCTATGACG  3032
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Query  3033  ACGAGCTCCATCAGTTGTCTCCACTAAGCTGCCCAAAACTGCATGACCCGGGTCCCGAAG  3092
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Query  3153  CACCGAAGCATGGGTCGAAGTTCAAGGGCGAGAAATAACCACGTGTGTCATCGGCAACTT  3212
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Sbjct  3120  CACCGAAGCATGGGTCGAAGTTCAAGGGCGAGAAATAACCACGTGTGTCATCGGCAACTT  3179

Query  3213  TCATGTCTAGATTCGGAACACCATCAGACGTGCTGCCTGGGAAGTTATACCCTGTGCTCC  3272
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Sbjct  3240  CTACCATGTCGTCCATCGCCTCACTCCCCTGAGGCTGCTCCGATGCTCCTGTTGCTTTGA  3299

Query  3333  TATCATCCATTGGAAGAGCAGGTGTGTGCCCTTGGAAAAGGGCAACATGCCCGAATAGCT  3392
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Query  3393  TATCCTTTCTTGAGAAGGTCGTTCCACATGAGCAGAGCCACTTGTCACGCCCGCAGTGCT  3452
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Query  3453  TCTCATGAGTCTTCAAGTCCGCAATGACTGAGAACTTCTTGGTGTTGCATCGGCTGCAGG  3512
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Query  3513  TATACCTCTTGTCACAGTGGCTTCTCTTGTAGTGGTTCTTCACACACAAGATTGTCTTGA  3572
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Query  3753  CCTTGCCACATATAACACAGAAATGAGTATGTGGTGCTAAAATCTCCTCCTTCTCCAATT  3812
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Query  3813  GCAAGACCACATAAGAACCAGGGGGGAGATGCTCTGCCTCGCCACCATCATCACTCTCCT  3872
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Query  3993  AGTCAGATGTCTTACTAATGTCAGGAATCATCTCCTCCCTGGTTGCGCTTGGCCGCTGAT  4052
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Query  4053  TCGCAGTCGAGCCGAAGCCCATGGTAGAACCAGGCGTGTTTATTTGCCTGACCGCTGGAT  4112
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Query  4113  TGCTGCTAAGGAGCGGGGTCTTCATGGAAGGAAGCATGGAGCCGGCAGTCGAGATGAGCT  4172
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Query  4173  GAATTATGATGGAAGTCAGATCGGCAGTGACGAGCTGCTGCTTTGCGGCAAGCTCGCAGG  4232
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Query  4233  AAGCACCACCAACCTGGCTCCCTCGGTTACCCATGGACTGCACGATATCTTTCACCTGCT  4292
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Sbjct  4380  CAGGAAGGTAAAAGTTGGAAGATTGAGGGCCAAAGAACGGAGGATAACCAGGGATTGACT  4439

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Query  4533  GGTCTGTGTTCCCTGACGCGTCGCCTGCCATGGACGACGAAGCTTTCATGGAAATTTCTG  4592
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Query  5252  TGTATATTTTTCAATTATGGCACAAACTGTAGGATCCTCGCGTGCATGAGTTGTATGCAA  5311
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Query  5492  GACCGTGAAGTTCTTTCttttttttACTTTCCTCTTTCTTTGGAGGGGGCAGCCGCGCCTG  5551
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Query  6032  ATCCAGTCTTTGTTAGTGTGTGTTCGTGTCTACAGGTTGGATTCTTTCGATTCACGCTTC  6091
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Sbjct  6296  TGAGTGACCCAAGGTTTATAAATCCATGGAAGGTGTAGGATGAAGATGATCTCTCTCAAA  6355
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Query  6390  CAACCCTGCAATCAAGTACGAGCAATCTCTTATGTCCCCAACATAACCAATACAAGGATA  6449
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Query  6749  CCACCTCAAAATTATCCTTTCCAATCAATCTATTGAGCCATCCTTATAAGTGTCACAAAC  6808
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Query  6809  ATCCCTAGAGTTTGTACTAGAATAACACCTATAATACA  6846
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Score = 91.5 bits (100), Expect = 4e-15
Identities = 73/88 (82%), Gaps = 0/88 (0%)
Strand=Plus/Minus

```
Query  1414  AGTACTCCCTGTGTACCTAAATAATTGTAGTTGGAGAGAATAATCTAGTTTTCCTCAACT  1473
             |||||||||| ||||||||||||||||||||  || ||  |  |  || ||  |||||
Sbjct  1468  AGTACTCCCTCTGTACCTAAATAATTGTAGTTGAGGAAAACTAGATTATTCTCTCCAACT  1409

Query  1474  ACAATTATTTAGGTACAGAGGGAGTACT  1501
             |||||||||| |||||| ||||||||||
Sbjct  1408  ACAATTATTTTGGTACACAGGGAGTACT  1381
```

Score = 77.0 bits (84), Expect = 8e-11
Identities = 69/87 (79%), Gaps = 0/87 (0%)
Strand=Plus/Minus

```
Query  1332  GTACTCCCTCTGACCAACAATATAAGACGTTTTTGCAAACAAACATAGCTTACAAAAACG  1391
             |||||||||  | || | |||||||||||||||||| || | |   | | || ||||||||
Sbjct  1385  GTACTCCCTTCGTCCCATAATATAAGACGTTTTTGTAAGCTATGTTTGTTTGCAAAAACG  1326

Query  1392  TCTTATATTATGGGACGAAGGGAGTAC  1418
             ||||||||| | || || |||||||||
Sbjct  1325  TCTTATATTGTTGGTCGGAGGGAGTAC  1299
```

> bowman_contig_1368909 CAJX011363749 carma=3HL
Length=706

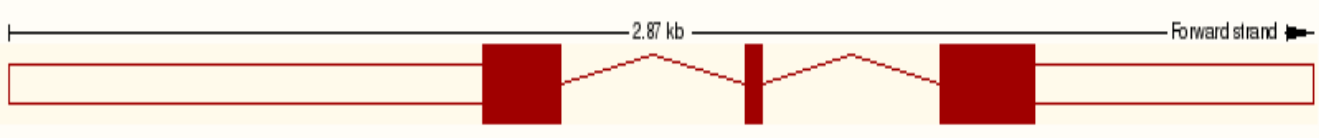
Score = 848 bits (940), Expect = 0.0
Identities = 503/517 (97%), Gaps = 0/517 (0%)
Strand=Plus/Plus

```
Query  6806  AACATCCCTAGAGTTTGTACTAGAATAACACCTATAATACACATCAATCAACTCTAATGT  6865
              ||||  ||||||||||| |||||||||||||||||| ||||||||||||||||||||
Sbjct  1      AACAACCCTAGAGTTTTTACTAGAATAACACCTATGATACACATCAATCAACTCTANNNN  60

Query  6866  nnnnnnnaTACTCCAATGTCACCACAAGTACTCGTTAGTCGATTATTCGACATGCATCGA  6925
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  61     NNNNNNNATACTCCAATGTCACCACAAGTACTCGTTAGTCGATTATTCGACATGCATCAA  120

Query  6926  ACAATTTTGTGCCCCACTTTGCTTAGTTTTGCTTGTTTTTGTCCCACTGGCTTAGCTTTC  6985
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACAATTTTGTGCCCCACTTTTCTTAGTTTTGCTTGTTTTTGTCCCACTGGCTTAGCTTTC  180

Query  6986  CTCGTTTTTGCCCTACTTCGCTCTATCCACTCTTGCAGGCGACCAAACGGGGCATTTCAG  7045
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  181   CTCGTTTTTGCCCTACTTCGCTCTATCCACTCTCGCAGGCGACCAAACGGGGCATTTCAG  240

Query  7046  TCTAGTCAACCTCCTTTGATAGTTACGTCGCCTGACTAGTGGGGTTGGCCCGGGGCACCT  7105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TCTAGTCAACCTCCTTTGATAGTTACGTCGCCTGACTAGTGGGGTTGGCCCGGGGCACCT  300

Query  7106  CATCGCACTTATGAGTGGGGCTTTATCAGGCAAGTGGGCCCACACGGGAATGACTCGTCT  7165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CATCGCACTTATGAGTGGGGCTTTATCAGGCAAGTGGGCCCACACGGGAATGACTCGTCT  360

Query  7166  CTCGTTGGCCCACGGAGGACCGACAACGGCGATGCCGAGGCTACTTTGATCTGTCCACGT  7225
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  361   CTCGTTGGCCCACGGAGGACCGACAGCGGCGATGCCGAGGCTACTTTGATCTGTCCACGT  420

Query  7226  GGGAACGAATCTTCTCCCGCTGGCACACCGGGCAGCGACTGCGGCGACGCTTCTACTTTG  7285
              |||||||| ||||||||| |||||||||||||||||||| ||||||||||||||||||||
Sbjct  421   GGGAACGACTCTTCTCCCCCTGGCACACCGGGCAGCGACAGCGGCGACGCTTCTACTTTG  480

Query  7286  ACCGGTCCCAACGCAGGAACGACTCGTCTCCCGCTGG  7322
              |||||||||||||||||||||||||||||||||||||
Sbjct  481   ACCGGTCCCAACGCAGGAACGACTCGTCTCCCGCTGG  517
```

```
morex_contig_1560156 v bowman_contig_855417

Query  5372  AAGAGTGAATTGCTACCGTCACGTATAATGGTGGGCAACAGCATATGCCTGCCTCGTCAC  5431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5337  AAGAGTGAATTGCTACCGTCACGTATAATGGTGGGCAACAGCATATGCCTGCCTCGTCAC  5396

Query  5432  TCCACATAGTAGATAAAAAGATACATAAATGGTTGTTCGAGCCTAACTACACCCAATACA  5491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5397  TCCACATAGTAGATAAAAAGATACATAAATGGTTGTTCGAGCCTAACTACACCCAATACA  5456

Query  5492  GACCGTGAAGTTCTTTCttttttttACTTTCCTCTTTCTTTGGAGGGGGCAGCCGCGCCTG  5551
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  5457  GACTGTGAAGTTCTTTCTTTTTTTACTTTCCTCTTTCTTTGGAGGGGGCAGCCACGCCTG  5516

Query  5552  CGATTTTCGACCGTTGCTATCATTTTATTTTTGTAATCTTATTTTACTATTGTTAGGTTC  5611
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  5517  CGATTTTCGACCGTTGCTATCATTTTATTTTT-TAATCTTATTTTACTATTGTTAGGTTC  5575

Query  5612  GAAAAGTGTAATAGGAAAGTAAATAAAATTACTCATTGGACTGCATCAGGTACGTAGGCT  5671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5576  GAAAAGTGTAATAGGAAAGTAAATAAAATTACTCATTGGACTGCATCAGGTACGTAGGCT  5635

Query  5672  GCGAGAAGACATGCACAGGATGACCGCTTGTACCGTGCATTCACTGTGCAAGGGTTTTTT  5731
             |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||
Sbjct  5636  GCGAGAAGACATGCACAGGATGACCGCTTGTACCGTGCATCCACTGTGCTAGGGTTTTTT  5695

Query  5732  CTGTCTTCCGTTGGCGTCGCCGTCGGTCTACCCCGTCTTATGTCGTCTTAGGACCATGGA  5791
             ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5696  CTGTCTTCCTTTGACGTCGCCGTCGGTCTACCCCGTCTTATGTCGTCTTAGGACCATGGA  5755

Query  5792  GACGTGATGGATCCCGTCCCTTGACAGCGGAAGGGCTTCATTTTTGATTAttttttttATT  5851
             |||||||||||||||||||||||||| |||||||||||||||| |||||||||||| ||
Sbjct  5756  GACGTGATGGATCCCGTCCCTTGACAACGGAAGGGCTTCATTTTTTATTATTTTTTTGTT  5815

Query  5852  AGGGTTTGTGTCTTGTTCATAGATGCGAGGTTGCGTTGGCTCTCAACAGATGGAGTAATG  5911
             | ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  5816  AAGGTTTGTGTCTTGTTCATAGATGCGAGGTTGCGTTGGCTCTCAATAGATGGAGTAATG  5875

Query  5912  TCCTCCCTGCCTAGCCCCCATTCGATGGTGTTTCTAGCATCGTCGAAGTGAGTGTTAAGG  5971
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  5876  TCCTCCCTGCCTAGCCCCCATTCGATGGTGTTTCTAGCATCGTCGAAGTGGGTGTTAAGG  5935

Query  5972  TTTGTCTTTGCCGGATCTCGCGGAATTCGATCGGCGTTTGTCTTTGATGGATTCACGTGG  6031
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5936  TTTGTCTTTGCCGGATCTCGCGGAATTCGATCGGCGTTTGTCTTTGATGGATTCACGTGG  5995

Query  6032  ATCCAGTCTTTGTTAGTGTGTGTTCGTGTCTACAGGTTGGATTCTTTCGATTCACGCTTC  6091
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5996  ATCCAGTCTTTGTTAGTGTGTGTTCGTGTCTACAGGTTGGATTCTTTCGATTCACGCTTC  6055
```

MLOC_4841

Ensebl plant data



Statistics
Exons: 2 **Coding exons:** 1 **Transcript length:** 1,959 bps **Translation length:** 90 residues
Type
Novel protein coding

WGS Morex contig match data

Database: assembly3_WGSMorex_renamed_blastable.fasta
2,670,738 sequences; 1,868,648,155 total letters

Query= MLOC_4841.1 cds:KNOWN_protein_coding
Length=414

Sequences producing significant alignments:	Score (Bits)	E Value
morex_contig_135563 CAJW010135563 carma=3HL	379	3e-103
morex_contig_45365 CAJW010045365 carma=1H	201	2e-49
morex_contig_45442 CAJW010045442 carma=4HL	107	3e-21

> morex_contig_135563 CAJW010135563 carma=3HL
Length=4401

Score = 379 bits (420), Expect = 3e-103
Identities = 210/210 (100%), Gaps = 0/210 (0%)
Strand=Plus/Plus

```
Query  205   CAGGATCGGTCAAGAGCCAGCGGGAGCGGGAGCCGGCGGCGGCTGACGGTGGAAGGGCCG  264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2694  CAGGATCGGTCAAGAGCCAGCGGGAGCGGGAGCCGGCGGCGGCTGACGGTGGAAGGGCCG  2753

Query  265   GGGTCGTACCCGCCGCGGTGCACGTCCAAGTGCGGCGGCTGCAACCCGTGCTACCCGGTG  324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2754  GGGTCGTACCCGCCGCGGTGCACGTCCAAGTGCGGCGGCTGCAACCCGTGCTACCCGGTG  2813

Query  325   CACGTGGCCGTGCCGCCGGGGGTGCCGGTCACCACGGAGTACTACCCGGAGGCGTGGCGG  384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2814  CACGTGGCCGTGCCGCCGGGGGTGCCGGTCACCACGGAGTACTACCCGGAGGCGTGGCGG  2873

Query  385   TGCAGGTGCGGCAACCGGCTCTACATGCCA  414
             |||||||||||||||||||||||||||||
Sbjct  2874  TGCAGGTGCGGCAACCGGCTCTACATGCCA  2903
```

Score = 306 bits (338), Expect = 5e-81
Identities = 169/169 (100%), Gaps = 0/169 (0%)
Strand=Plus/Plus

```
Query  1     ATGGAGGGCTCCCGGGGGAGGTGGAGGTGGGGTGGCAGGCGCAGATCCGTGCTGATGGTG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1693  ATGGAGGGCTCCCGGGGGAGGTGGAGGTGGGGTGGCAGGCGCAGATCCGTGCTGATGGTG  1752

Query  61    GCGCTGGCCCTGTGCTTCGTCGTGGCCGCCGTCGTCTCCCTGTGCTGCTGCTGCTGCGCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1753  GCGCTGGCCCTGTGCTTCGTCGTGGCCGCCGTCGTCTCCCTGTGCTGCTGCTGCTGCGCC  1812

Query  121   CGGCCCGGGGCTTGCGGTGGCAGGAGTACTGTGGTGGTGCTCCCTTCAG  169
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1813  CGGCCCGGGGCTTGCGGTGGCAGGAGTACTGTGGTGGTGCTCCCTTCAG  1861
```

Score = 77.0 bits (84), Expect = 4e-12
Identities = 47/50 (94%), Gaps = 0/50 (0%)
Strand=Plus/Plus

```
Query  167   CAGATTTTTGGAGACGAGCAGCAGCATCGTTTGTTAATCAGGATCGGTCA  216
             ||||||||||||||||||||||||||||||||||||||||||  || |||
Sbjct  2266  CAGATTTTTGGAGACGAGCAGCAGCATCGTTTGTTAATCAGGTGCGTTCA  2315
```

Database: assembly5_WGSBowman34x_renamed_blastable.fasta
2,077,901 sequences; 1,779,486,241 total letters

Query= MLOC_4841.1 cds:KNOWN_protein_coding
Length=414

Sequences producing significant alignments:	Score (Bits)	E Value
bowman_contig_126920 CAJX010122805 carma=3HL	379	3e-103
bowman_contig_144436 CAJX010140186 carma=1H	185	1e-44
bowman_contig_850896 CAJX010846001 carma=4HL	111	2e-22

> bowman_contig_126920 CAJX010122805 carma=3HL
Length=3975

Score = 379 bits (420), Expect = 3e-103
Identities = 210/210 (100%), Gaps = 0/210 (0%)
Strand=Plus/Plus

```
Query  205   CAGGATCGGTCAAGAGCCAGCGGGAGCGGGAGCCGGCGGCGGCTGACGGTGGAAGGGCCG  264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2774  CAGGATCGGTCAAGAGCCAGCGGGAGCGGGAGCCGGCGGCGGCTGACGGTGGAAGGGCCG  2833

Query  265   GGGTCGTACCCGCCGCGGTGCACGTCCAAGTGCGGCGGCTGCAACCCGTGCTACCCGGTG  324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2834  GGGTCGTACCCGCCGCGGTGCACGTCCAAGTGCGGCGGCTGCAACCCGTGCTACCCGGTG  2893

Query  325   CACGTGGCCGTGCCGCCGGGGGTGCCGGTCACCACGGAGTACTACCCGGAGGCGTGGCGG  384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2894  CACGTGGCCGTGCCGCCGGGGGTGCCGGTCACCACGGAGTACTACCCGGAGGCGTGGCGG  2953

Query  385   TGCAGGTGCGGCAACCGGCTCTACATGCCA  414
             ||||||||||||||||||||||||||||||
Sbjct  2954  TGCAGGTGCGGCAACCGGCTCTACATGCCA  2983
```

Score = 306 bits (338), Expect = 5e-81
Identities = 169/169 (100%), Gaps = 0/169 (0%)
Strand=Plus/Plus

```
Query  1     ATGGAGGGCTCCCGGGGGAGGTGGAGGTGGGGTGGCAGGCGCAGATCCGTGCTGATGGTG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1773  ATGGAGGGCTCCCGGGGGAGGTGGAGGTGGGGTGGCAGGCGCAGATCCGTGCTGATGGTG  1832

Query  61    GCGCTGGCCCTGTGCTTCGTCGTGGCCGCCGTCGTCTCCCTGTGCTGCTGCTGCTGCGCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1833  GCGCTGGCCCTGTGCTTCGTCGTGGCCGCCGTCGTCTCCCTGTGCTGCTGCTGCTGCGCC  1892

Query  121   CGGCCCGGGGCTTGCGGTGGCAGGAGTACTGTGGTGGTGCTCCCTTCAG  169
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1893  CGGCCCGGGGCTTGCGGTGGCAGGAGTACTGTGGTGGTGCTCCCTTCAG  1941
```

Score = 77.0 bits (84), Expect = 4e-12
Identities = 47/50 (94%), Gaps = 0/50 (0%)
Strand=Plus/Plus

```
Query  167   CAGATTTTTGGAGACGAGCAGCAGCATCGTTTGTTAATCAGGATCGGTCA  216
             ||||||||||||||||||||||||||||||||||||||||||  || |||
Sbjct  2346  CAGATTTTTGGAGACGAGCAGCAGCATCGTTTGTTAATCAGGTGCGTT
```

Query= morex_contig_135563 CAJW010135563 carma=3HL Length=4401

> bowman_contig_126920 CAJX010122805 carma=3HL
Length=3975

Score = 7019 bits (7784), Expect = 0.0
Identities = 3894/3895 (99%), Gaps = 0/3895 (0%)
Strand=Plus/Plus

```
Query  1     CCCATGCAACGTTCCCCAACAGATCATGGGTTTCAGTTTCAAGATGACAATGTTGTGCGT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    CCCATGCAACGTTCCCCAACAGATCATGGGTTTCAGTTTCAAGATGACAATGTTGTGCGT  140

Query  61    GAGCATGGAGAAGCGGCAATGTTTGCACAGTTCATCAAGTTTCATCATAAGATGCATGAT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   GAGCATGGAGAAGCGGCAATGTTTGCACAGTTCATCAAGTTTCATCATAAGATGCATGAT  200

Query  121   TAGAAAACTCACATGCATCTGCAAAATGATTTGGTTGAGCATATGTGAATTCGTGCCGAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   TAGAAAACTCACATGCATCTGCAAAATGATTTGGTTGAGCATATGTGAATTCGTGCCGAC  260

Query  181   AACCAATAGATGTATCGGTAACCTTTTCTTTTATATGTATTTGAGACAATTTAACGTTAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   AACCAATAGATGTATCGGTAACCTTTTCTTTTATATGTATTTGAGACAATTTAACGTTAA  320

Query  241   ACATGAAATATTTATGTAGTTTTTGAACTATGCAATGTTTTGTATTGATCATTTGTTAAG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   ACATGAAATATTTATGTAGTTTTTGAACTATGCAATGTTTTGTATTGATCATTTGTTAAG  380

Query  301   CTAGTATTAAATTTTATATGGTTTTCGATAAAGCAACCTAAAAATGGACACAAGTCTGTC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   CTAGTATTAAATTTTATATGGTTTTCGATAAAGCAACCTAAAAATGGACACAAGTCTGTC  440

Query  361   GCGCGAACGAAAAATGGGTCGGCACGTTGGGCGCACGACCGATCCAAATGAAGAACGGGT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GCGCGAACGAAAAATGGGTCGGCACGTTGGGCGCACGACCGATCCAAATGAAGAACGGGT  500

Query  421   TGAACATGTCGATCCAAACGGACAAAACACACGTCCATTGGAGTCGCCTTGCTAAATCCC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   TGAACATGTCGATCCAAACGGACAAAACACACGTCCATTGGAGTCGCCTTGCTAAATCCC  560

Query  481   GCAATCTGCAACGCGTCGGAACGAGGCATAGCATGACTGACGAAGGAGGAGTACGCGAGA  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   GCAATCTGCAACGCGTCGGAACGAGGCATAGCATGACTGACGAAGGAGGAGTACGCGAGA  620

Query  541   ACCACTTCTCTTCTCAAGCTCGAGTAGCATGTGAAAGAAAATCCCTTATAAGGAGGTTCA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  621   ACCACTTCTCTTCTCAAGCTCGAGTAGCATGTGAAAGAAAATCCCTTATAAGGAGGTTCA  680

Query  601   ACCCCCTCTAACTTTGGGAATCATACTAAACTTTCTATCATCCCTTGCCATGACACTTAC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCCCCTCTAACTTTGGGAATCATACTAAACTTTCTATCATCCCTTGCCATGACACTTAC  740

Query  661   ATGGATCCTTCAATTTTTACTTCTTTTGGAAATTGTTAGATGGACCAAGTTTGAAACCGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   ATGGATCCTTCAATTTTTACTTCTTTTGGAAATTGTTAGATGGACCAAGTTTGAAACCGC  800

Query  721   AGCACAGCCCTTTTGAAGTTCAAGCACCAAATCGCAGCATGAGTCTAAATTTGTGACCTG  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801   AGCACAGCCCTTTTGAAGTTCAAGCACCAAATCGCAGCATGAGTCTAAATTTGTGACCTG  860
```

```
Query  781   CGCCCAATATAACTCCCGGTTTGTATCTGCTCTGTCCACAGTGTGGTTACTGTTGGGAGG  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  861   CGCCCAATATAACTCCCGGTTTGTATCTGCTCTGTCCACAGTGTGGTTACTGTTGGGAGG  920

Query  841   AACGGATTCATTGATCAGCACTGCACACGCATCAATCTCCCGTCACGCTTCCAGCATAAT  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  921   AACGGATTCATTGATCAGCACTGCACACGCATCAATCTCCCGTCACGCTTCCAGCATAAT  980

Query  901   CTTACTCGAATCTAACGTTCTCCCCTCACGCTTGATCTAAGAAAGATCGTCTCCATCTCC  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  981   CTTACTCGAATCTAACGTTCTCCCCTCACGCTTGATCTAAGAAAGATCGTCTCCATCTCC  1040

Query  961   TAGTCTCCTAGACAGCACTCACCGCGCCATGCCTGCACCTTCAATTTCCCCCCTTCCATG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1041  TAGTCTCCTAGACAGCACTCACCGCGCCATGCCTGCACCTTCAATTTCCCCCCTTCCATG  1100

Query  1021  GACCACTTGGACCCCCTTGGCGCGTAAAACCTGTGCCAAGACCACAGGCTTTTCTGGGGA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1101  GACCACTTGGACCCCCTTGGCGCGTAAAACCTGTGCCAAGACCACAGGCTTTTCTGGGGA  1160

Query  1081  GCACACGGCACATGCGAGCTGCTGCGctcctccctcccgtcctccatccatctccatctc  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1161  GCACACGGCACATGCGAGCTGCTGCGCTCCTCCCTCCCGTCCTCCATCCATCTCCATCTC  1220

Query  1141  catctccatctccatctccatctccccaCAGATGAGATGAGATGAGGTGAGAGAGGTACC  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1221  CATCTCCATCTCCATCTCCATCTCCCCACAGATGAGATGAGATGAGGTGAGAGAGGTACC  1280

Query  1201  TGGCGGTATTTGGCGAGACCAGTCGACGCCGATCCCTCGCAATCATACAAAACTAGGAGT  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1281  TGGCGGTATTTGGCGAGACCAGTCGACGCCGATCCCTCGCAATCATACAAAACTAGGAGT  1340

Query  1261  ACTGAGGTGACGAGTGAGGCGAGGTCGGACGACGTACGTGGTACCGTTCTGCACTGTTGC  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1341  ACTGAGGTGACGAGTGAGGCGAGGTCGGACGACGTACGTGGTACCGTTCTGCACTGTTGC  1400

Query  1321  TGCCTGCGCGTTCTTTTATGCGTCTGCGCACCTGCTGCTCCCCTCTCGCCCCTGCATTCA  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1401  TGCCTGCGCGTTCTTTTATGCGTCTGCGCACCTGCTGCTCCCCTCTCGCCCCTGCATTCA  1460

Query  1381  CTCCCATCCATCCACCGATCGACCGATCTCGTACGGTTGTAGAGTCTCGTCCGACGGATT  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1461  CTCCCATCCATCCACCGATCGACCGATCTCGTACGGTTGTAGAGTCTCGTCCGACGGATT  1520

Query  1441  CCGATCGGTCGAGAGATCTGACGCCGCTACAGTGCCGAGCGGGCTCCTGCTACAAGAGGC  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1521  CCGATCGGTCGAGAGATCTGACGCCGCTACAGTGCCGAGCGGGCTCCTGCTACAAGAGGC  1580

Query  1501  AGCGGTGACCGGTGGAGGCTCCGTGCTGGGTGTGTGCGTGCGCCTCTCTgcttccgcttc  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1581  AGCGGTGACCGGTGGAGGCTCCGTGCTGGGTGTGTGCGTGCGCCTCTCTGCTTCCGCTTC  1640

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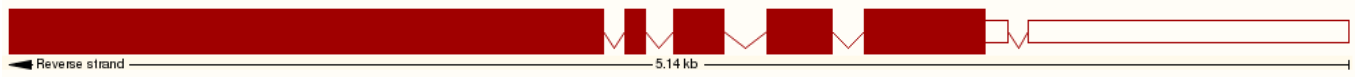
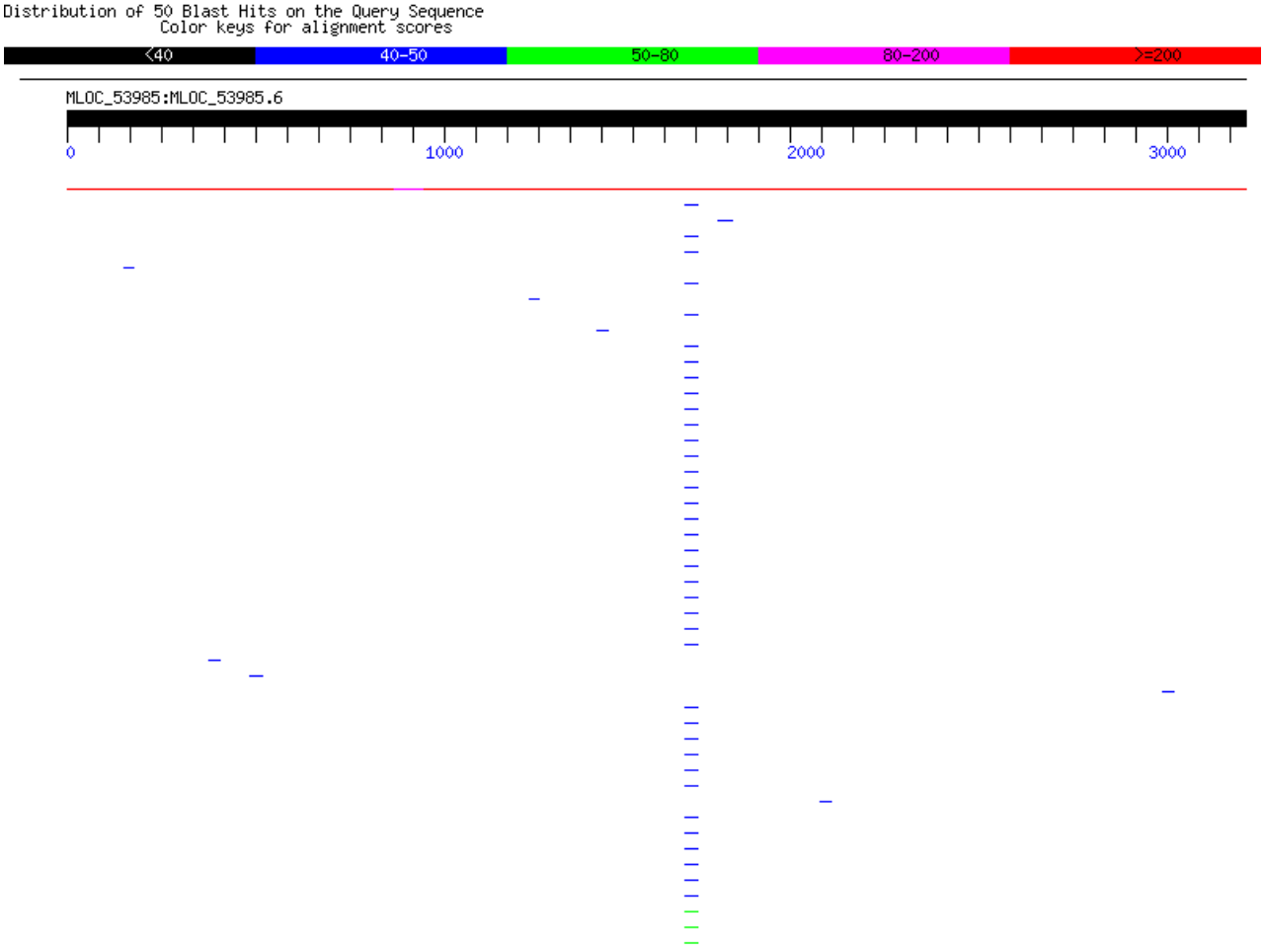
MLOC_53985

Ensebl plant data



Statistics
Exons: 6 **Coding exons:** 5 **Transcript length:** 4,578 bps **Translation length:** 1,087 residues
Type
Novel protein coding

WGS Morex contig match data



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           2,670,738 sequences; 1,868,648,155 total letters


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Length=3261
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

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  morex_contig_1704523 CAJW011704523                                  44.6     0.22


> morex_contig_38798 CAJW010038798 carma=3HL
Length=10413

 Score = 4109 bits (4556),  Expect = 0.0
 Identities = 2278/2278 (100%), Gaps = 0/2278 (0%)
 Strand=Plus/Minus

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Sbjct  1978  GCTGGGGGAATCTTATCTGGCACTTGGAGAGGCGTATAAAAATGATGGGCAGCTTCATCG  1919

Query  1644  TACTCTGAAAGTTGTGGAATTAGCTTGCATGGTTTATGGGTCTATGCCTAAACATCTAGA  1703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1918  TACTCTGAAAGTTGTGGAATTAGCTTGCATGGTTTATGGGTCTATGCCTAAACATCTAGA  1859

Query  1704  TGGTGATGAATTCATCTCATCCATGTCCAATAGTTCGCTGTGCCTGGAAGATGGTGATCT  1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1858  TGGTGATGAATTCATCTCATCCATGTCCAATAGTTCGCTGTGCCTGGAAGATGGTGATCT  1799

Query  1764  AAACTCAAGTCTTGTATTGGATGAAGCAGAATATTTCAAGAATGCAAAATGCTTTGGTTA  1823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1798  AAACTCAAGTCTTGTATTGGATGAAGCAGAATATTTCAAGAATGCAAAATGCTTTGGTTA  1739
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Query  1824  TGATGTTTCTGCTCAACAGTTGCCTCCAAACTATTTATTCTGGGCCAATGTGTGGATGCT  1883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1738  TGATGTTTCTGCTCAACAGTTGCCTCCAAACTATTTATTCTGGGCCAATGTGTGGATGCT  1679

Query  1884  TGTAGGTGATGTCTATGCAGAATATCACCGATTGGGCAGCCATCAAGCACCTGTGCTCCA  1943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1678  TGTAGGTGATGTCTATGCAGAATATCACCGATTGGGCAGCCATCAAGCACCTGTGCTCCA  1619

Query  1944  GGAGCAACAGCCTGAAGGTGAACTTAGGATGTCAAATGAAGTTGCAATGGAAGTCAAACG  2003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1618  GGAGCAACAGCCTGAAGGTGAACTTAGGATGTCAAATGAAGTTGCAATGGAAGTCAAACG  1559

Query  2004  TCTAAAGAGAAAACTGGGAAAAGATAAGCAGAATTGTGGAACATGCTCACTGATAAACTG  2063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1558  TCTAAAGAGAAAACTGGGAAAAGATAAGCAGAATTGTGGAACATGCTCACTGATAAACTG  1499

Query  2064  TAGTTGCCAAAGTGATAGGGCAAATAGTGGCAGTAGTGCAAGCAGTAGTAGTCCTGAGGC  2123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1498  TAGTTGCCAAAGTGATAGGGCAAATAGTGGCAGTAGTGCAAGCAGTAGTAGTCCTGAGGC  1439

Query  2124  CTCTACATTGCATGgaagaaagaaaaagaaaaaagCATCTGGCAGGAACATTCATTCACA  2183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1438  CTCTACATTGCATGGAAGAAAGAAAAAGAAAAAAGCATCTGGCAGGAACATTCATTCACA  1379

Query  2184  ATCTACTGAAATTAAAGAGAAACCTATTGCACAGGAAGCTACGGAAAGTTCTGAAGAAAC  2243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1378  ATCTACTGAAATTAAAGAGAAACCTATTGCACAGGAAGCTACGGAAAGTTCTGAAGAAAC  1319

Query  2244  TCAGCACAGCACGAATGATACTCGTCATGAGAAAAGGACGGTGGCAAATGCTGAACTTGA  2303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1318  TCAGCACAGCACGAATGATACTCGTCATGAGAAAAGGACGGTGGCAAATGCTGAACTTGA  1259

Query  2304  TTGTGATCATACCATGGAGAATCAGTCAAGTAATGCTGATGCTATTCCTGATAAACCTAA  2363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1258  TTGTGATCATACCATGGAGAATCAGTCAAGTAATGCTGATGCTATTCCTGATAAACCTAA  1199

Query  2364  TGATGATGTTTCCAGTGCGAGCGGTGGTATTTTCAAGTACCTTGGAGGTCCTAAACCAGG  2423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1198  TGATGATGTTTCCAGTGCGAGCGGTGGTATTTTCAAGTACCTTGGAGGTCCTAAACCAGG  1139

Query  2424  AGATACTGAATACAACTTGTGTTCTGCTATTCACTGCTATGGTGCAGCTAAGGGAGCCAT  2483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1138  AGATACTGAATACAACTTGTGTTCTGCTATTCACTGCTATGGTGCAGCTAAGGGAGCCAT  1079

Query  2484  GTTTGCATTTCCTATGCGCTCGGCAGAGTTCTCCACCATCCTTAAGAAAAGAGGTTGGGC  2543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1078  GTTTGCATTTCCTATGCGCTCGGCAGAGTTCTCCACCATCCTTAAGAAAAGAGGTTGGGC  1019

Query  2544  ATTCAATGAACTTGGTCGCATTAGACTTGAGAGTAAAAATCTGAGTAGTGCTGAGATTGC  2603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1018  ATTCAATGAACTTGGTCGCATTAGACTTGAGAGTAAAAATCTGAGTAGTGCTGAGATTGC  959

Query  2604  TTTTGCTGATGCCATTAGTGCATTTCAAGAGGTCTCTGATCACACAAATGTTATATTGAT  2663
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  958   TTTTGCTGATGCCATTAGTGCATTTCAAGAGGTCTCTGATCACACAAATGTTATATTGAT  899

Query  2664  CAATTGTAACTTAGCTCATGGTAGAAGAGCTTTAGCAGAGAAATTGGCGTCGAGGATAGA  2723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  898   CAATTGTAACTTAGCTCATGGTAGAAGAGCTTTAGCAGAGAAATTGGCGTCGAGGATAGA  839

Query  2724  AGAATTTCAGATGTATGATCTTCCTGAAGGCTCATATATGCAATCCGTGAAGTCTGCCAA  2783
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  838   AGAATTTCAGATGTATGATCTTCCTGAAGGCTCATATATGCAATCCGTGAAGTCTGCCAA  779

Query  2784  GTCGGAATATTTTCAAGCAATAAACTATTATACAGCAGCTAAGAGGCAACTGAAGTATGC  2843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  778   GTCGGAATATTTTCAAGCAATAAACTATTATACAGCAGCTAAGAGGCAACTGAAGTATGC  719

Query  2844  TATTGCTGACAATGAAGTTGATAAATCACTGTACAACGAAGTTTACACCCAGTATGCCCA  2903
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  718   TATTGCTGACAATGAAGTTGATAAATCACTGTACAACGAAGTTTACACCCAGTATGCCCA  659

Query  2904  TACCCACCTGAGGCTCGGAATGCTTTTGGCAAGGGAAAGCTTTTTAACTGGCAGCTACGA  2963
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  658   TACCCACCTGAGGCTCGGAATGCTTTTGGCAAGGGAAAGCTTTTTAACTGGCAGCTACGA  599
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Query  2964  AGGTGGACTTGTTGATGAATCATCTAACAGAACAGTTCTTGAGATTTCAGCAAGTGATGC  3023
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  598   AGGTGGACTTGTTGATGAATCATCTAACAGAACAGTTCTTGAGATTTCAGCAAGTGATGC  539

Query  3024  TTTTCGGGAGGCTTTGTCTACATATGAGTCCCTTGGTGAACTTCGCAAACAGGAGGCTGC  3083
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  538   TTTTCGGGAGGCTTTGTCTACATATGAGTCCCTTGGTGAACTTCGCAAACAGGAGGCTGC  479

Query  3084  CTTTGGCCATTTTCAGCTTGGTTGTTATCAAAGGGATCTGTGCTTGAAGTTCCTGGATTT  3143
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  478   CTTTGGCCATTTTCAGCTTGGTTGTTATCAAAGGGATCTGTGCTTGAAGTTCCTGGATTT  419

Query  3144  GGTTAACAAGGAGGTCAAACAGAAGAACGAGGATAAATTTCGTAAGAAAGCCAAGTGGTA  3203
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  418   GGTTAACAAGGAGGTCAAACAGAAGAACGAGGATAAATTTCGTAAGAAAGCCAAGTGGTA  359

Query  3204  TGGTTCGCTAGCAGAGAAGAACTGGCAGAAGGCTTTAGAATTCTATGGTCCGAAGACG  3261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  358   TGGTTCGCTAGCAGAGAAGAACTGGCAGAAGGCTTTAGAATTCTATGGTCCGAAGACG  301
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 Score =  843 bits (934),  Expect = 0.0
 Identities = 467/467 (100%), Gaps = 0/467 (0%)
 Strand=Plus/Minus

Query  1     ATGCACTCGGTTAGGGCAGAGGCATGTGATTGCCCACCAAGTCATCAACCATCACAGGAC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4044  ATGCACTCGGTTAGGGCAGAGGCATGTGATTGCCCACCAAGTCATCAACCATCACAGGAC  3985

Query  61    AAGCAAACAGCATCCATGTTGCATGGACCCTTCGGTCATATGGAGGGTTCCTTTGATTCG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3984  AAGCAAACAGCATCCATGTTGCATGGACCCTTCGGTCATATGGAGGGTTCCTTTGATTCG  3925

Query  121   TCCTCCTCTTCTAATTTTAGCACATCGCCGTATTTGGATCAGAATATCAGTAAAAGTAGA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3924  TCCTCCTCTTCTAATTTTAGCACATCGCCGTATTTGGATCAGAATATCAGTAAAAGTAGA  3865

Query  181   AAACCGTCACATGGTACTTGTGAAAGCCTGTACTGGGGTGCAAGGGAAAATAAGCAAAAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3864  AAACCGTCACATGGTACTTGTGAAAGCCTGTACTGGGGTGCAAGGGAAAATAAGCAAAAA  3805

Query  241   GTTCCAGGATCGGACCCTGTTAGGAAAACCACTCGTGTTGGTGAAACCCCCAATTGTGAG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3804  GTTCCAGGATCGGACCCTGTTAGGAAAACCACTCGTGTTGGTGAAACCCCCAATTGTGAG  3745

Query  301   GTGCAAGAATCTGAGAAGAGTAGGAGAGTGGGGAACAATGGATTTCGGAAGGTTTGCTTT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3744  GTGCAAGAATCTGAGAAGAGTAGGAGAGTGGGGAACAATGGATTTCGGAAGGTTTGCTTT  3685

Query  361   TGGCAGTTCCACAATTTCCATATCCTCTTGGGTAGCGACTTGCTTATATTTAGCAATGAG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3684  TGGCAGTTCCACAATTTCCATATCCTCTTGGGTAGCGACTTGCTTATATTTAGCAATGAG  3625

Query  421   AAATATATTGCAGTCAGCTTACACCTATGGGATGTTTCAAGACAGGT  467
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3624  AAATATATTGCAGTCAGCTTACACCTATGGGATGTTTCAAGACAGGT  3578
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 Score =  459 bits (508),  Expect = 3e-126
 Identities = 256/257 (99%), Gaps = 0/257 (0%)
 Strand=Plus/Minus

Query  461   GACAGGTTACTCCATTGAACTGGCTAGAAGCTTGGCTTGACAATGTAATGGCAAGTGTGC  520
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3462  GATAGGTTACTCCATTGAACTGGCTAGAAGCTTGGCTTGACAATGTAATGGCAAGTGTGC  3403

Query  521   CAGAATTGGCCATATGTTATCATCAGAATGGTGTTGTCCAAGGCTATGAGCTTCTAAAAA  580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3402  CAGAATTGGCCATATGTTATCATCAGAATGGTGTTGTCCAAGGCTATGAGCTTCTAAAAA  3343

Query  581   ATGATGATATATTTCTACTTAAGGGTGTGTCCGATGATGGCACGCCTGCATTTCATCCAC  640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3342  ATGATGATATATTTCTACTTAAGGGTGTGTCCGATGATGGCACGCCTGCATTTCATCCAC  3283

Query  641   AGGTTGTCCAGCAAAATGGCCTAGCTGTCCTAAGGTTCCTTCAGAATAACTGTAAGCAAG  700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3282  AGGTTGTCCAGCAAAATGGCCTAGCTGTCCTAAGGTTCCTTCAGAATAACTGTAAGCAAG  3223
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Query  701   ACCCTGGTGCATATTGG  717
             |||||||||||||||||
Sbjct  3222  ACCCTGGTGCATATTGG  3206


 Score =  358 bits (396),  Expect = 8e-96
 Identities = 198/198 (100%), Gaps = 0/198 (0%)
 Strand=Plus/Minus

Query  717   GCTCTACAAAGGCGCTGAAGAAGATGTTGTGCAGTTATATGACTTGTCCATATTACCTGA  776
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3040  GCTCTACAAAGGCGCTGAAGAAGATGTTGTGCAGTTATATGACTTGTCCATATTACCTGA  2981

Query  777   AAAACATACTGCTGGTGATCATATATCTACGTGCAATCCTGTGTCTTCTTTAATGAACAA  836
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2980  AAAACATACTGCTGGTGATCATATATCTACGTGCAATCCTGTGTCTTCTTTAATGAACAA  2921

Query  837   GGGGAGAAGGGAATCACTCTTCTCTCTGGGCACACTCCTCTATCGTGTTGCTCATAGGAT  896
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2920  GGGGAGAAGGGAATCACTCTTCTCTCTGGGCACACTCCTCTATCGTGTTGCTCATAGGAT  2861

Query  897   GTCTTTATCGAAGGTACC  914
             ||||||||||||||||||
Sbjct  2860  GTCTTTATCGAAGGTACC  2843


 Score =  143 bits (158),  Expect = 3e-31
 Identities = 79/79 (100%), Gaps = 0/79 (0%)
 Strand=Plus/Minus

Query  908   AGGTACCTAGTAATAGAGCAAAATGTGCAAAGTTCTTCAGAAAATGTTTAGATTTCCTCA  967
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2740  AGGTACCTAGTAATAGAGCAAAATGTGCAAAGTTCTTCAGAAAATGTTTAGATTTCCTCA  2681

Query  968   ACAAGCAGGATCACCTGGT  986
             |||||||||||||||||||
Sbjct  2680  ACAAGCAGGATCACCTGGT  2662


> morex contig 1704523 CAJW011704523
Length=304

 Score = 44.6 bits (48),  Expect = 0.22
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

Query  1713  ATTCATCTCATCCATGTCCAATAGTTCGCTGT  1744
             |||| ||| ||||||||||||||| |||||||
Sbjct  57    ATTCTTCTAATCCATGTCCAATAGATCGCTGT  26


> morex contig 1559497 CAJW011559497 carma=7HL
Length=8269

 Score = 44.6 bits (48),  Expect = 0.22
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Plus

Query  1804  AATGCAAAATGCTTTGGTTATGATGTTTCTGCTCAACAG  1842
             |||||||||||  | |||| ||||| |||||||| | |||
Sbjct  4674  AATGCAAAATGATGTGGTAATGATCTTTCTGCTAATCAG  4712
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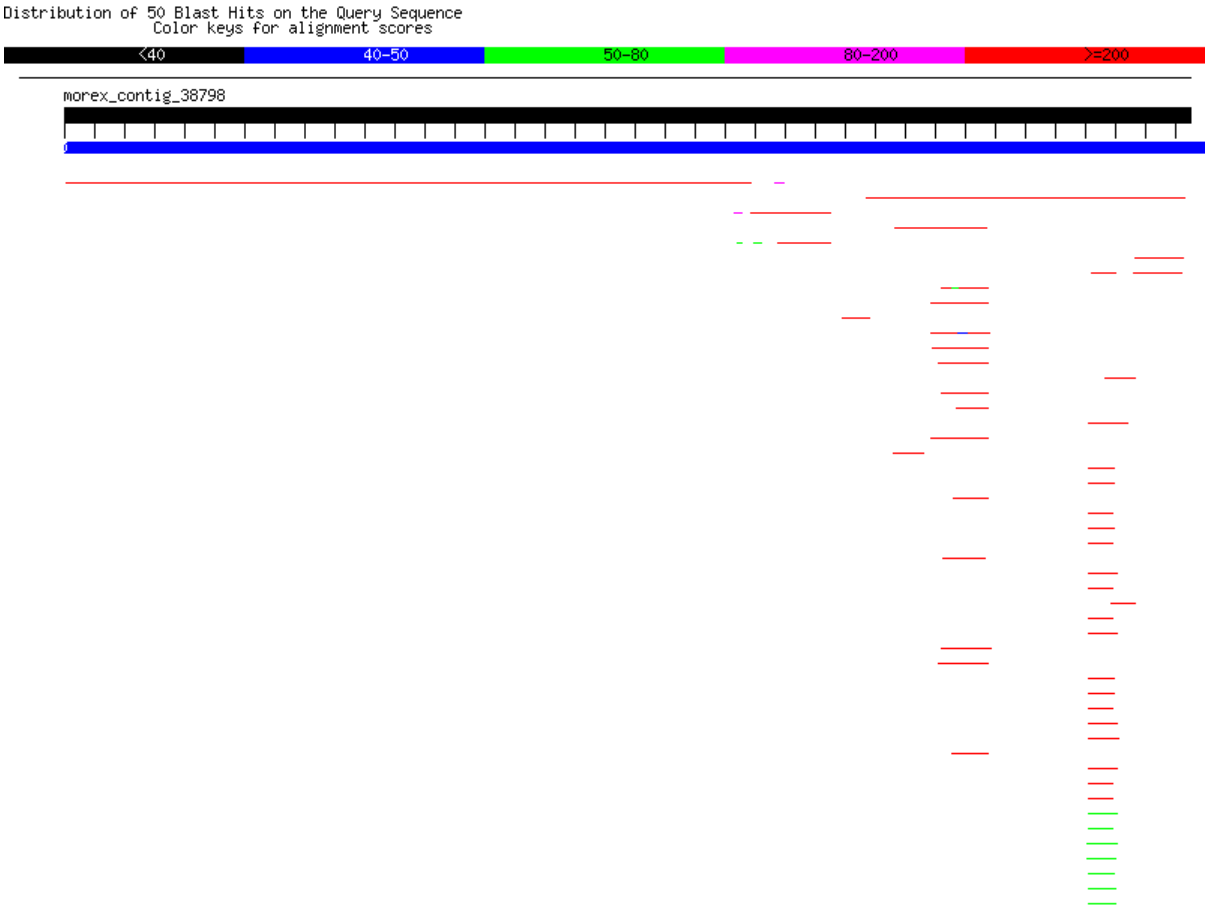

Query= morex_contig_38798 CAJW010038798 carma=3HL
Length=10413

Sequences producing significant alignments:	Score (Bits)	E Value
bowman contig 850578 CAJX010845683 carma=3HL	1.048e+04	0.0
bowman_contig_128375 CAJX010124260 carma=3HL	5126	0.0
bowman_contig_186994 CAJX010182639	1265	0.0
bowman_contig_145081 CAJX010140831 carma=3HS	955	0.0
bowman_contig_863858 CAJX010858963 carma=5HS	729	0.0
bowman contig 1999906 CAJX011994225 carma=3HS	605	1e-169
bowman contig 145856 CAJX010141606	464	2e-127
bowman_contig_886345 CAJX010881450 carma=5HL	462	8e-127
bowman_contig_895859 CAJX010890964	452	1e-123
bowman_contig_986 CAJX010000984 carma=3HL	452	1e-123
bowman_contig_852226 CAJX010847331 carma=2HS	446	6e-122

> bowman_contig_850578 CAJX010845683 carma=3HL
Length=7446

Score = 1.048e+04 bits (11620), Expect = 0.0
Identities = 6121/6333 (96%), Gaps = 59/6333 (0%)
Strand=Plus/Minus

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Query  24    TTCTAATCAGATGACATTATGCCGCTCGATTCTACACGCAACTACCCCCTCCATTCCGAA  83
             |||||||||||||||||| ||||||||||||| |||||||||||||||||||| ||||||
Sbjct  6279  TTCTAATCAGATGACATTGTGCCGCTCGATTCTGCACGCAACTACCCCCTCCAGTCCGAA  6220

Query  84    ATAAGTGTCGTCGTTTTAGTTTAAAATGTATGACAGGTAATGCACTTTCCGGATGCCAGA  143
             |||||||||||| ||||||||||||||||||||| ||||||| ||||||||||||||||||
Sbjct  6219  ATAAGTGTCGTGGTTTTAGTTTAAAATGTATGACGGGTAATACACTTTCCGGATGCCAGA  6160

Query  144   AAAGAATAATCATAACGAAGATCTAGCAGACTAAGCAACTAGAATAGAAGGAGATGGCAA  203
             |||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||
Sbjct  6159  AAAGAATAATCATAACGACGATCTAGCAGACTGAGCAACTAGAATAGAAGGAGATGGCAA  6100

Query  204   GCCAGGAAGAACATACCGCACTAGAGTGAAATGAATCAGAGATGCTAGTAGAAAGGGCAG  263
             ||| ||||| |||||||||| |||||||||| |||||||||||||||||||||||||||
Sbjct  6099  GCCTGGAAGCACATACCGCAATAGAGTGAAACGAATCAGAGATGCTAGTAGAAAGGGCAG  6040
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Query  264   ATTGCGCCATAAGGATGTTAAGAAACATGGTAGGATGCGTCTTCGGACCATAGAATTCTA  323
             |||||||||||||||| |||||||||| |||||||| ||||||||||||||||||||||
Sbjct  6039  ATTGCGCCATAAGGATGCTAAGAAACATCGTAGGATGAGTCTTCGGACCATAGAATTCTA  5980

Query  324   AAGCCTTCTGCCAGTTCTTCTCTGCTAGCGAACCATACCACTTGGCTTTCTTACGAAATT  383
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  5979  AAGCCTTCTGCCAGTTCTTCTCTGCTAGCGAACCATACCACTTAGCTTTCTTACGAAATT  5920

Query  384   TATCCTCGTTCTTCTGTTTGACCTCCTTGTTAACCAAATCCAGGAACTTCAAGCACAGAT  443
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5919  TATCCTCATTCTTCTGTTTGACCTCCTTGTTAACCAAATCCAGGAACTTCAAGCACAGAT  5860

Query  444   CCCTTTGATAACAACCAAGCTGAAAATGGCCAAAGGCAGCCTCCTGTTTGCGAAGTTCAC  503
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5859  CCCTTTGATAACAACCAAGCTGAAAATGGCCAAAGGCAGCCTCCTGTTTGCGAAGTTCAC  5800

Query  504   CAAGGGACTCATATGTAGACAAAGCCTCCCGAAAAGCATCACTTGCTGAAATCTCAAGAA  563
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5799  CAAGGGACTCGTATGTAGACAAAGCCTCCCGAAAAGCATCACTTGCTGAAATCTCAAGAA  5740

Query  564   CTGTTCTGTTAGATGATTCATCAACAAGTCCACCTTCGTAGCTGCCAGTTAAAAAGCTTT  623
             ||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  5739  CTGTTCTATTAGATGATTCGTCAACAAGTCCACCTTCGTAGCTGCCAGTTAAAAAGCTTT  5680

Query  624   CCCTTGCCAAAAGCATTCCGAGCCTCAGGTGGGTATGGGCATACTGGGTGTAAACTTCGT  683
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  5679  CCCTTGCCAAAAGCATTCCGAGCCTCAGGTGGGTATGGGCATACTGGGTGTAAACTTCAT  5620

Query  684   TGTACAGTGATTTATCAACTTCATTGTCAGCAATAGCATACTTCAGTTGCCTCTTAGCTG  743
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  5619  TGTACAGTGATTTATCAATTTCATTGTCAGCAATAGCATACTTCAGTTGCCTCTTAGCTG  5560

Query  744   CTGTATAATAGTTTATTGCTTGAAAATATTCCGACTTGGCAGACTTCACGGATTGCATAT  803
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5559  CTGTATAATAGTTTATTGCTTGAAAATATTCCGACTTGGCAGACTTCACGGATTGCATAT  5500

Query  804   ATGAGCCTTCAGGAAGATCATACATCTGAAATTCTTCTATCCTCGACGCCAATTTCTCTG  863
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5499  ATGAGCCTTCAGGAAGATCATACATCTGAAATTCTTCTATCCTCGACGCCAATTTCTCTG  5440

Query  864   CTAAAGCTCTTCTACCATGAGCTAAGTTACAATTGATCAATATAACATTTGTGTGATCAG  923
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |
Sbjct  5439  CTAAAGCTCTTCTACCATGAGCTAAGTTACAGTTGATCAATATAACATTTGTGTGATCCG  5380

Query  924   AGACCTCTTGAAATGCACTAATGGCATCAGCAAAAGCAATCTCAGCACTACTCAGATTTT  983
             |||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||
Sbjct  5379  AGACCTCTTGAAATGCACTAATAGCATCAGCAAAAGCAGTCTCAGCACTACTCAGATTTT  5320

Query  984   TACTCTCAAGTCTAATGCGACCAAGTTCATTGAATGCCCAACCTCTTTTCTTAAGGATGG  1043
             |||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||
Sbjct  5319  TACTCTCAAGTCTAATGCGGCCAAGTTCATTGAATGCCCAACCCCTTTTCTTAAGGATGG  5260

Query  1044  TGGAGAACTCTGCCGAGCGCATAGGAAATGCAAACATGGCTCCCTTAGCTGCACCATAGC  1103
             |||||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Sbjct  5259  TGGAGAACTCTGCCGAGCGCACAGGAAATGCAAACATGGCTGCCTTAGCTGCACCATAGC  5200

Query  1104  AGTGAATAGCAGAACACAAGTTGTATTCAGTATCTCCTGGTTTAGGACCTCCAAGGTACT  1163
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5199  AGTGAATAGCAGAACACAAGTTGTATTCAGTATCTCCTGGTTTAGGACCTCCAAGGTACT  5140

Query  1164  TGAAAATACCACCGCTCGCACTGGAAACATCATCATTAGGTTTATCAGGAATAGCATCAG  1223
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  5139  TGAAAATACCACCGCTCGCACTGGAAACATCGTCATTAGGTTTATCAGGAATAGCATCAG  5080

Query  1224  CATTACTTGACTGATTCTCCATGGTATGATCACAATCAAGTTCAGCATTTGCCACCGTCC  1283
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  5079  CATTACTTGACTGATTCTCCATGGTATGATAACAATCAAGTTCAGCATTTGCCACCGTCC  5020

Query  1284  TTTTCTCATGACGAGTATCATTCGTGCTGTGCTGAGTTTCTTCAGAACTTTCCGTAGCTT  1343
             |||||||||||| |||||||||||||||||||||||||||||||||||| ||||
Sbjct  5019  TTTTCTCATGACAAGTATCATTCGTGCTGTGCTGAGTTTCTTCAGAACTTTCCGTTGCTT  4960

Query  1344  CCTGTGCAATAGGTTTCTCTTTAATTTCAGTAGATTGTGAATGAATGTTCCTGCCAGATG  1403
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  4959  CCTGTGCAATAGGTTTCTCTTTAATTTCAGTAGATTGTGAACGAATGTTCCTGCCAGATG  4900
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Query  1404  ctttttttctttttctttcttcCATGCAATGTAGAGGCCTCAGGACTACTACTGCTTGCAC  1463
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Sbjct  4899  CTTTTTTATTTTTCTTTCTTCCATGCAATGTAGAGGCCTCGGGACTACTACTGCTTGCAC  4840

Query  1464  TACTGCCACTATTTGCCCTATCACTTTGGCAACTACAGTTTATCAGTGAGCATGTTCCAC  1523
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4839  TACTGCCACTATTTGCCCTATCACTTTGGCAACTACAGTTTATCAGTGAGCATGTTCCAC  4780

Query  1524  AATTCTGCTTATCTTTTCCCAGTTTTCTCTTTAGACGTTTGACTTCCATTGCAACTTCAT  1583
             ||||||||||||||||||||  |||||||||  ||||||||||||||||||||||||||||
Sbjct  4779  AATTCTGCTTATCTTTTCCCAATTTTCTCTTGAGACGTTTGACTTCCATTGCAACTTCAT  4720

Query  1584  TTGACATCCTAAGTTCACCTTCAGGCTGTTGCTCCTGGAGCACAGGTGCTTGATGGCTGC  1643
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Sbjct  4719  TTGACATCCTAAGTTCACCTTCAGGCTTTTGCTCCTGGAGCACCGGTGCTTGATGGCTGC  4660

Query  1644  CCAATCGGTGATATTCTGCATAGACATCACCTACAAGCATCCACACATTGGCCCAGAATA  1703
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Sbjct  4659  CCAATCGGTGATATTCTGCATAGACATCACCTACAAGCATCCACACATTGGCCCAGAATA  4600

Query  1704  AATAGTTTGGAGGCAACTGTTGAGCAGAAACATCATAACCAAAGCATTTTGCATTCTTGA  1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4599  AATAGTTTGGAGGCAACTGTTGAGCAGAAACATCATAACCAAAGCATTTTGCATTCTTGA  4540

Query  1764  AATATTCTGCTTCATCCAATACAAGACTTGAGTTTAGATCACCATCTTCCAGGCACAGCG  1823
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Sbjct  4539  AATATTCTGCTTCATCCAATACAAGACTTGAGTTAAGATCACCATCTTCAAGGCACAGCG  4480

Query  1824  AACTATTGGACATGGATGAGATGAATTCATCACCATCTAGATGTTTAGGCATAGACCCAT  1883
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Sbjct  4479  AACTATTGGACATGGATGAGATGAATTCATCACCATCTAGATGTTTAGGCATAGACCCAT  4420

Query  1884  AAACCATGCAAGCTAATTCCACAACTTTCAGAGTACGATGAAGCTGCCCATCATTTTTAT  1943
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Sbjct  4419  AAACCATGCAAGCTAATTCCACAACTTTCAGAGTGCGATGAAGCTGCCCGTCATTTTTAT  4360

Query  1944  ACGCCTCTCCAAGTGCCAGATAAGATTCCCCCAGCAAAAGAGCAAGTTTCCACAATTTAT  2003
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Sbjct  4359  ATGCCTCTCCAAGTGCCAGATAAGATTCCCCCAGCAAAAGAGCAAGTTTCCACAATTTAT  4300

Query  2004  GGTCCATTTTCAGTTTGGGTAGCCACTCCCTAATGTCGCAAACTTCAATGCAATCAACAT  2063
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Sbjct  4299  GGTCCATTTTCAGTTTTGGTAACCACTCCCTAATGTCGCAAACTTCAATGCAATCAACAT  4240

Query  2064  CGCCACATCTACATAAAGAGAAGTCAACAGGTCTCTCCCAAATGGTGTCTGCATTGTCAA  2123
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Sbjct  4239  CGCCACATCTACATAAAGAGAAGTCAACAGGTCTCTCCCAAATGGTGTCTGCATTGTCAA  4180

Query  2124  TACAATCATCCTGAGTGTTCTGCAGCTGCCGGTTCCACCTTAAAGATTTGATAGCTTGTG  2183
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Sbjct  4179  CACAATCATCCTGAGTGTTCTGCAGCTGACGGTTCCACCTTAGAGATTTGATAGCTTGTG  4120

Query  2184  ATACATGATGTATAGCTGCCAACTTAGAGGAGATAGCATCAGCAATTGGTTTTGATATCT  2243
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Sbjct  4119  ATACGTGATGTATAGCTGCCAGCTTAGAGGAGATAGCATCAGCAATTGGTTTTGATATCT  4060

Query  2244  GAGAGTTTCCAGCCTTACACATTAGCAAGCTATCATCAGAGACATCTTTTGTAGTTGAAG  2303
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Sbjct  4059  GAGAGTTTCCAGCCTGGCACATTAGCAAGCTATCATCAGAGACATCTTTTGTAGTAGAAG  4000

Query  2304  ATGCAGTACCAGTATCAACATGACCACGTGAAGATTCTGACTGTGAATACTCCAACATAC  2363
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Sbjct  3999  ATGCAGTACCAGTATCAGCATGTCCACGGGAAGATTCTGATTGTGAATACTCCAACATAC  3940

Query  2364  TATCTACGGCTGCTGGCTCATCCTTGCTTATCTCTGTCAAAACATCATCTTGCTTTGATG  2423
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Sbjct  3939  TATCTACGGCTGCTGGCTCATCCTTGTTTATCTCTGTCAATACATCATCTTGCTTTGATG  3880

Query  2424  GTAAATTCTGAAGGCTCAACTGTGGAGACTCATCATCCAAGTCTGTAAGAGTAACTTCCG  2483
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Sbjct  3879  GTAAATTCTGAAGGCTCAACTGTGGAGACTCATCATCCAAGTCGGTAAGAGTAACTTCCG  3820

Query  2484  ATTCAAGCAGAAATGATTCTGTTGTCAGTTCCAACTCCTCATAACATTTAAGGATGAGCC  2543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3819  ATTCAAGCAGAAATGATTCTGTTGTCAGTTCCAACTCCTCATAACATTTAAGGATGAGCC  3760

Query  2544  TTGCAAACTGTTCATGAGCATATGCCCTGACAACCTAAAACATGAAAGAATAAATCTTGA  2603
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Query  2604 GACAAATTTCTCACCGAGAAAATAACAGACTTGTAGAACGGTGATATGATAGATAAGTAC  2663
            ||||||||||||||| |||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  3700 GACAAATTTCTCACTGAGAAAATAACAGACTTGTAGAACGGTGATGTGATAGATAAGTAC  3641

Query  2664 CAGGTGATCCTGCTTGTTGAGGAAATCTAAACATTTTCTGAAGAACTTTGCACATTTTGC  2723
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Sbjct  3640 CAGGTGATCCTGCTTGCTGAGGAAATCTAAACATTTTCTGAAGAACTTTGCACATTTTGC  3581

Query  2724 TCTATTACTAGGTACCTGCAAACATATAAGGCCTTTAACAATCAGTAAAGCTGTACAAAA  2783
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  3580 TCTATTACTAGGTACCTGCAAACATACAAGGCCTTTAACAATCAGTAAAGCTGTAC----  3525

Query  2784 GTACATGTTaaaaaaaaaaaaaaCTGTACATAGAGGTAAAGTAAGAGTGACAATTCCCTG  2843
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Sbjct  3524 -------------ATAAAGAAAACTGTACATAG------AGTAAGAGTGACAATTCCCTG  3484

Query  2844 GTACCTTCGATAAAGACATCCTATGAGCAACACGATAGAGGAGTGTGCCCAGAGAGAAGA  2903
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Query  2904 GTGATTCCCTTCTCCCCTTGTTCATTAAAGAAGACACAGGATTGCACGTAGATATATGAT  2963
            ||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  3423 GTGATTCCCGTCTCCCCTTGTTCATTAAAGAAGACACAGGACTGCACGTAGATATATGAT  3364

Query  2964 CACCAGCAGTATGTTTTTCAGGTAATATGGACAAGTCATATAACTGCACAACATCTTCTT  3023
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Sbjct  3363 CACCAGCAGTATGTTTTTCAGGTAATATGGACAAGTCATATAACTGCACAACATCTTCTT  3304

Query  3024 CAGCGCCTTTGTAGAGCTGAGAAAGCAAACCTTCAGTATAAGTGCACAGGAACTAGCATT  3083
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Sbjct  3303 CAGCACCTTTGTAGAGCTGAGAAAGCAAACCTTCAGTATAAGTGCACAGGAACTAGCATT  3244

Query  3084 GGTGGTTACCAGTCTAATGCTAAATAAATCAAGTTGTACATAAAAATATCTAGAGACTAA  3143
            |||||||||||||||||||||||||||||||||||| |||||||||| |||||||||
Sbjct  3243 GGTGGTTACCAGTCTAATGCTAAATAAATCAAGTTGTACTTAAAAATATCCAGAGACTAA  3184

Query  3144 AAGGTTGAATAGAAACATATCTAACACATGTTGACTATCATAAGTAGGTTCGAAAGCCAT  3203
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Sbjct  3183 AAGGTTGAATAGAAACATATCTAACACATGTTGACTATCATAAGTAGGTTCAAAAGCCAT  3124

Query  3204 ACCCAATATGCACCAGGGTCTTGCTTACAGTTATTCTGAAGGAACCTTAGGACAGCTAGG  3263
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Sbjct  3123 ACCCAATATGCACCAGGGTCTTGCTTACAGTTATTCTGAAGGAACCTTAGGACAGCTAGG  3064

Query  3264 CCATTTTGCTGGACAACCTGTGGATGAAATGCAGGCGTGCCATCATCGGACACACCCTTA  3323
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Query  3324 AGTAGAAATATATCATCATTTTTTAGAAGCTCATAGCCTTGGACAACACCATTCTGATGA  3383
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Query  3384 TAACATATGGCCAATTCTGGCACACTTGCCATTACATTGTCAAGCCAAGCTTCTAGCCAG  3443
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Query  3444 TTCAATGGAGTAACCTATCAAAAGCAATTTGACAGCAGAGAGAGTAAGACAATTTGTCAG  3503
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Query  3504 CAGAGAGAGTAAGGCAATTTGTCAACAGAGGGAGTAAGGAAAGAAAATATGAAGCCAAAT  3563
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Sbjct  2848 CAGAGAGAGTAAGGCAATTTGTCAACAGAGAGAGTAAGGAAAGAAAATATGAAGCCAAAT  2789

Query  3564 TAAACATAAAGCATACCTGTCTTGAAACATCCCATAGGTGTAAGCTGACTGCAATATATT  3623
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Sbjct  2788 TAAATATAAAGCATACCTGTCTTGAAACATCCCATAGGTGTAAGCTGACAGCAATATATT  2729

Query  3624 TCTCATTGCTAAATATAAGCAAGTCGCTACCCAAGAGGATATGGAAATTGTGGAACTGCC  3683
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Query  3684 AAAAGCAAACCTTCCGAAATCCATTGTTCCCCACTCTCCTACTCTTCTCAGATTCTTGCA  3743
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Sbjct  2668  AAAAGCAAACCTTCCGAAATCCATTGTTCCCCACTCTCCTACTCTTCTCAGATTCTTGCA  2609

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Sbjct  2608  CCTCACAATTGGGGGTTTCACCAACACGAGTGGTTTTCCTAATGGGATCCGATCCTGGAA  2549

Query  3804  CTTTTTGCTTATTTTCCCTTGCACCCCAGTACAGGCTTTCACAAGTACCATGTGACGGTT  3863
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Sbjct  2548  CTTTTTGCTTATTTTCCCTTGCACCCCAGTACAGGCTTTCACAAGTACCATGTGATGGTT  2489

Query  3864  TTCTACTTTTACTGATATTCTGATCCAAATACGGCGATGTGCTAAAATTAGAAGAGGAGG  3923
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Sbjct  2488  TTCTACTTTTACTGATATTCTGATCCAAATACGGCGATGTGCTAAAATTAGACGAGGAGG  2429

Query  3924  ACGAATCAAAGGAACCCTCCATATGACCGAAGGGTCCATGCAACATGGATGCTGTTTGCT  3983
              |||||||||||||||||||||||||||||||||||||||||||| |||||||| |||||||
Sbjct  2428  ACGAATCAAAGGAACCCTCCATATGACCGAAGGGTCCATGCAAAATGGATGCAGTTTGCT  2369

Query  3984  TGTCCTGTGATGGTTGATGACTTGGTGGGCAATCACATGCCTCTGCCCTAACCGAGTGCA  4043
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Sbjct  2368  TGTCCTGTGATGGTTGATGACTTGGTGGGCAATCACATGCCTCTGCCCTAACCGAGTGCA  2309

Query  4044  TCGCAAAGTTCTTCAAAATTGAAGGATCAGATCCTTTAGGTTGGTTATTTTGTCTTCTAA  4103
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Sbjct  2308  TCGCAAAGTTCTTTAAAATTGAAGGATCAGATCCTTTAGGTTGGTTATTTTGTCTTCTAA  2249

Query  4104  ATATCTTTTCACCTTCATCAACATCAGGCCTGCAACAGAATGTGGAGTGGATCATTAGCA  4163
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Sbjct  2248  ATATCTTTTCACCTTCATCAACATCAGGCCTGCAACAGAATGTGGAGTGGATCATTAGCA  2189

Query  4164  TTCACTACATTGAGTATGGTCGTTTTGAAGTAGTGAGCACCTTACCCGGAGTTTAAAATG  4223
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Sbjct  2188  TTCACTACATTGAGTATGGTCGATTTAAAGTAGTGAGCACCTTACCCTGAGTTTAAAATG  2129

Query  4224  AGTGTGTCTCCAATACGGCTAACAGCAATAGATACTTGTGCCTTAGAGTAAGGTATTTTA  4283
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Sbjct  2128  AGTGTGTCTCCAATACGGCTAACAGCAATAGATACTTGTGCCTTAGAGTAAGGTATTTTA  2069

Query  4284  AATATCTGCTTTAGAATATCAGTTGGAGCAATCACATCTATTTCATCGCCATATTCAGCT  4343
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Sbjct  2068  AAGATCTGCTTTAGAATATCAGTTGGAGCAATCACATCTATTTCATCGCCATATTCGGCT  2009

Query  4344  AGGCCTGACACGGCTAGTGCTTCACACTTCCTTGATAAGTTTTGGTTGAAAAGTCCACTT  4403
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Sbjct  2008  AGGCCTGACACGGCTAGTGCTTCACACTTCCTTGATAAGTTTTGGTTGAAAAGTCCACTT  1949

Query  4404  CCATACCGTAATCCTAAAGAATATGAAGAAACATATATCAACAGAAATGTATTGCATGCC  4463
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Sbjct  1948  CCATACCGTAATCCTGAAGAATATGAACAAACATATATCAACAGAAATGTATTGCATGCC  1889

Query  4464  AAAAAACTTTAATAATTTTGGACTACTGGACCATGTGGACAGTGGTGTGATAAGAACACT  4523
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Sbjct  1888  AAAAAACTTTAATAATTTGGGACTACTGGACCATGTGGACAGTGGTGTGATAAGAACACT  1829

Query  4524  GCATAGATGGTAATCGGCCGCATATTCGGTGCTAATGGGGAACCATCATGAATACCTGAT  4583
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Query  4584  CCAGAGGCCTGTCCGCACCATTATATGTTTAATCACCTGACTAATGCAATTAGTCGGATA  4643
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Query  4644  ACTTTTGTGCAATCACACAACGAACTCGTAAAGCCTAAAAAAGAACACAAGGTTTTTACC  4703
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Sbjct  1708  ACTTTTGTGCAATCACACAACGAACTCATAAAGCCTAAAAAAGAACACAAGGTTTTTACC  1649

Query  4704  AGATCTGCTGACATGAAGCAGAGCAATCACGGACCGGTACCATCGAAGATATCAGTACCA  4763
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Sbjct  1648  AGATCTGCTGACATGAAGCAGAGCAATCACGGACCGGTACCATCGAAGATGTCAGTACCA  1589

Query  4764  CCCCATGATGTCACCTAAAGCCTTTGAAACCTGTTTGTGTGCTGAATGGAATGCTTGCCT  4823
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Sbjct  1588  CCCCATGATGTCACCT-AAGCCTTTCAAACCTGTTTGTGTGCTGGATGGAATGCTCGCCT  1530

Query  4824  CCCAGTTTATCCCTTGAGCCGATGGAGTTAGAGCTTCTATTGGAAACAGCAAAGGGGAGG  4883
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Sbjct  1529  CCCAGTTTATCCCTTGAGCCGATGGAGTTAGAGCTTTTATTGGAAACAGCAAAGGGGAGG  1470
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Query  4884  TGGAGAGCTAAAAACGGGAATGGGAAGAAAGATGTACAAGGGGAAGGCGAAGGCTCACAT  4943
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Sbjct  1469  TGGAGAGCTAAAAACGGGAACGGGAAGAAAGATGTAGAACGGGAAGGCGAAGGCTCACAT  1410

Query  4944  ATCCAAAAGGGGAGGTGCTTCCTTATCTTATTACATAGGATCGCCTTTATCAACTGTTGT  5003
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Sbjct  1409  AACCAAAAGGGGAGGTGCTTCCTTATCTTATTACGTAGGATCGCCTTTATCAACTGTTGT  1350

Query  5004  TTGTTTGTTTGGAGTGGTTTGCTAGGCTTTCTACTAACCACCTCGACATTCTTTAGTTTG  5063
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Sbjct  1349  TTGTTTGTCTGAAGTGGTTTGCTAGGCTTTCTACTAACTACCCCGATATTCTTTGGTCAG  1290

Query  5064  TTTTTATTAATTCCAAATACACCAATGCATTAATAGCACACAGTTTTCCATATAATTGGT  5123
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Sbjct  1289  TTTATATTAATTCCAAATACACCAATGCATTAATAG--CACAGTTTTCCATATAATTGGT  1232

Query  5124  AGGCGGCACATTTAAGTCTGCCAACCATATTTTGTCTTCAGCAAAACTGGTGAACAGCAC  5183
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1231  AGGCGGCACATTTAAGTCCGCCAACCATATTTTGTCTTCAGCAAAACTGGTGAACAGCAC  1172

Query  5184  ATCACTTCCGCAAATTGTAGGAATGATGCGGCAGTGGCCTAGGTCGCATCCTGCGGGTAA  5243
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Sbjct  1171  ATCACTTCCGCAAATTGTAGGAATGATGCGGCAGTGGCCTAGGTCGCATCCTGCGGGTAA  1112

Query  5244  GTGCTGTTTCAGGTAATTAGAACCAGGTTAGTGGGCTGGAAGATAGACGTTGTCGGTAGC  5303
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Sbjct  1111  GTGCCGTTTCAGGTAATTAGAACCAGGTTAGTAGGCTGGAAGATAGACGTTGTCGATAGC  1052

Query  5304  AATAGGACGAGAGAAAATATGTTTCCTGCCTGCCTTTGAAGAATTCCCAAAATGATAAAA  5363
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Sbjct  1051  AATAGGACGAGAGAAAATAGGTCTCCTGCCTGCCTTTGAAGAATTCCCAACATGATAAAA  992

Query  5364  AATATTAGCTATTTCTATATCTCTAGCTTGCATAATCTTCTTCTGGACTCTTTCCTAATA  5423
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Sbjct  991   AATCTTAGCTATTTCTATATCTCTAGCTTGCATAATCTTCTTCTGGACTCTTTCCTAATA  932

Query  5424  TGCCTAACTCTCCTCCTGGATTATTAATTTATGTACTGTTCCTGCTGTGTGCCATGGACT  5483
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Sbjct  931   TGCCTAACTCTCCTCCTGGATTACTAACTTATGTACTGTTCCTGCTGTGTGCCATGGACT  872

Query  5484  ACTACAGTTTCACCTCCTGTGCTTTACACAGTTACACTACAGCATTGGTATCTCAAACAG  5543
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Sbjct  871   ACTACAGTTTCACCTCCTGTGCTTTACACAGTTACACTACAGCATTGTTATCTCAAACAG  812

Query  5544  ACTGATGTCCGTTATTTGAAAGGTTTTGCTGCTGCATGTACCACTGCAGCAA----TCAT  5599
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Sbjct  811   ACTGATGTCCGTTATTTGAAAGGTTTTGCTGCTGCATGTACCACTGCAGCAAAAGCTCAT  752

Query  5600  CGAATGAAAGGTATCATGAACATGAAATAGAAAATCCCAAAGCTGGTATAATCACTCTCT  5659
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Sbjct  751   CGGATGAAAGGTATCATGAACATGAAATAGCAAATCCCAAAGCTGGTATTTTCACTCTCT  692

Query  5660  CACAGTCTCTAACTTCTTACCTTAGATTTACACATTTACAAGGGTAATACTCACAAAAAG  5719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  691   CACAGTCTCTAACTTCTTACCTTAGATTTACACATTTACAAGGGTAATACTCACAAAAAG  632

Query  5720  AAGAATATTCAAAATATTTATTGCTAACCAAGCAAATATGCTTCAATAATAATTCACCAG  5779
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  631   AAGAATATTCAAAATATTTATTGCTAACCGAGCAAATATGCTTCAATAATAATTCACCAG  572

Query  5780  GTCATGTCACCTAGAGTTTTCACAGGTAGCATCCATCCACTGTAAATACCAAACATCATT  5839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  571   GTCATGTCACCTAGAGTTTTCACAGGTAGCATCCATCCACTGTAAATACCAAACATCATT  512

Query  5840  TAATTATATAGGGTGTGATTGAGAAAGCACTTGGATACATGTATATGCTTATCACACGCT  5899
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  511   TAATTATATAGGGTGTGATTGAGAAAGCACTTGGATACATGTATATGCTTACCACACGCT  452

Query  5900  AAAACAGTTATAATTTTAATAGCACACGCATGTTTTTACCATCAGTAATGCTGCATTATA  5959
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  451   AAAACAGTTATAATTTTAATAGCACATGCATGTTTTTACCATCAGTAATGCTGCATTATA  392

Query  5960  CTACAAACTGCCAAGAAGCCTAG-Attttttttt CACAATAAAACTATATTGACGAAGGC  6018
              |||||||||| |||||||||| || |||||||||||| |||||||| ||||||||||
Sbjct  391   CTACAAACTGCAAAGAAGCCTAGAATCTTTTTTTCACAATCAAACTATAATGACGAAGGC  332
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Query  6019  TCGACAGAGGTCACCTTCAGTACTCTTTGCATCCGTTGGGAAAACCTTCTCTGGGAGGTT  6078
             ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331   TCGACAAAGGTCACCTTCAGTACTCTTTGCATCCGTTGGGAAAACCTTCTCTGGGAGGTT  272

Query  6079  TGGAATCACGGGGAGTGTGTTGAGGTCGGTCTCCAGTGGCAGCATTTGATACCTTGGAGC  6138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  271   TGGAATCACGGGGAGTGTGTTGAGGTCGGTCTCCAGTGGCAGCATTTGATACCTTGGAGC  212

Query  6139  TCCAGTCCCAGTCCTGCAATATTTGTGACAACAAGAGCATGATTAAACTAGTGGTTCTCC  6198
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  211   TCCAGTCCCAGTCCTGCAATATTTGTGACAACAAGAGCATGATTAAACTAGTGGTTTTCC  152

Query  6199  TGACTCAGACATTTGCGGACAACGAGAAATCTCATTTGATAACAGTAACGTGTCGCTGTA  6258
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  151   TGACTCAGACATTTGCGGACAACGGGAAATCTCATTTGATAACAGTAACGTGTCGCTGTA  92

Query  6259  CACTTCCCAACATGATTTTCCCTATCCCGCaaaaaaaaCATGATTTTCCCTACATACTCT  6318
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  91    CACTTCCCAACATGATTTTCCCTATCCCGCAAATAAAACATGATTTTCCCTACATACTCT  32

Query  6319  TTACCTCATGATGTCCGAATGAAGAAgggggggg  6351
             ||| ||||||||||||||||  |||||||||
Sbjct  31    TTAGCTCATGATGTCCGAATGA--AAGGGGGGG  1


 Score = 77.0 bits (84),  Expect = 1e-10
 Identities = 61/72 (84%), Gaps = 1/72 (1%)
 Strand=Plus/Minus

Query  6581  CTCAG-CATTTGCGGACTAGAGGAAATTTCATTCGGTAACAGTTACGTGTCACTTTACAC  6639
             |||||  |||||||||||  |  ||||||  |||||  |  |||||||  |||||||  ||  |||||
Sbjct  148   CTCAGACATTTGCGGACAACGGGAAATCTCATTTGATAACAGTAACGTGTCGCTGTACAC  89

Query  6640  TTCCCAGCATGA  6651
             ||||||  |||||
Sbjct  88    TTCCCAACATGA  77


> bowman_contig_128375 CAJX010124260 carma=3HL
Length=2949

 Score = 5126 bits (5684),  Expect = 0.0
 Identities = 2909/2950 (98%), Gaps = 4/2950 (0%)
 Strand=Plus/Plus

Query  7419   TGACGAACGCCCACGGAGTCAGTGGAGAGTGCTAGACGCTTCTACCTCTCTCCCCTTTGG  7478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      TGACGAACGCCCACGGAGTCAGTGGAGAGTGCTAGACGCTTCTACCTCTCTCCCCTTTGG  60

Query  7479   GCCTGTCATGGAGCAGCGGCGGCTGCAGTGTTGTTACGGACGTCCGAGGAAGCCCAGTTT  7538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61     GCCTGTCATGGAGCAGCGGCGGCTGCAGTGTTGTTACGGACGTCCGAGGAAGCCCAGTTT  120

Query  7539   GTTCTTCTTTTACGGGGCCGTGACGGGCCCGTCTATGAATCATCCTATTCTTCGCCTTAA  7598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121    GTTCTTCTTTTACGGGGCCGTGACGGGCCCGTCTATGAATCATCCTATTCTTCGCCTTAA  180

Query  7599   GCGACGGATCGTCGCTAAATGTGCAGGCGGCCCCAGTAAAAACGTTGTTCTAAGAAAAGG  7658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181    GCGACGGATCGTCGCTAAATGTGCAGGCGGCCCCAGTAAAAACGTTGTTCTAAGAAAAGG  240

Query  7659   TATAATAGACTaaaaaaagaaaggaaaaaGATTCTTCTCAATCGGCGGATTACAACATTG  7718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241    TATAATAGACTAAAAAAAGAAAGGAAAAAGATTCTTCTCAATCGGCGGATTACAACATTG  300

Query  7719   CATCCATCATGTTTGTGGCCGTTGGATTGGATTTGATCGTTTGTTTGCTTAATGCACCTC  7778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301    CATCCATCATGTTTGTGGCCGTTGGATTGGATTTGATCGTTTGTTTGCTTAATGCACCTC  360

Query  7779   ACATGGCTATAGGAGCCCACATGTGTCTAGAAATATCTTATCTTCATGTCCTTATCCTCA  7838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361    ACATGGCTATAGGAGCCCACATGTGTCTAGAAATATCTTATCTTCATGTCCTTATCCTCA  420

Query  7839   TCTCCACAAAAGTCACGGCTCACTACTCGTCTTCTTCATGGATTAATCTCGTCACTCTCT  7898
              ||  |  ||||||||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  421    TCCCTACAAAAGTCACCGCTCACTACTCGTCTTCTTCATGGATTAATCTCGTCACTCTCT  480
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Query  7899   CTCAAGCATCCACACGTCGGCCGTTGTTCCATTCCATCCAATCCCTTGTGCGTCGGCGTT  7958
              |||||||||||||||||| || |||||||||||||||| ||||||||||||||||||||
Sbjct  481    CTCAAGCATCCACACGTCAGCGGTTGTTCCATTCCATCCTATCCCTTGTGCGTCGGCGTT  540

Query  7959   GAGAAAGGAGGGGTCCCAGCTGCGGCTCTCCATGGATTAGTCTGTTCTCCTTCTGTAAGA  8018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541    GAGAAAGGAGGGGTCCCAGCTGCGGCTCTCCATGGATTAGTCTGTTCTCCTTCTGTAAGA  600

Query  8019   GGGGCTCGTCTCGGTAAGGTCCGGCGGCGTTGACGGGGAACTTGGCAGTTTCGATGCTCG  8078
              |||||||||||||||||||||||||| |||||||||||||||||||||||| ||||||
Sbjct  601    GGGGCTCGTCTCGGTAAGGTCCGGCGGGGTTGACGGGGAACTTGGCAGTTTCGGTGCTCG  660

Query  8079   CCGGCGGCACGACATTGCTATTCCCTCATCGGTGGTGAttttttttCTTGCAACATCCTC  8138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661    CCGGCGGCACGACATTGCTATTCCCTCATCGGTGGTGATTTTTTTTCTTGCAACATCCTC  720

Query  8139   CTTATTGTAAGAAAGATCCTACAACATCATCAATGTTGCAAAACTTTCATCCGTCAATAT  8198
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  721    CTTATTGTAAGAAAGATCCTACAACATCATCAATGTTGCAAAACTTTCATCCGTCGATAT  780

Query  8199   CTTTGTTTGaaaaaaaaCTGCAACACTACCTTTATTGTaaaaaaaaaTC--CGCAACACA  8256
              |||||||||||||||||||||||||||||||||||| |||||||||||   |||||||||
Sbjct  781    CTTTGTTTGAAAAAAAACTGCAACACTACCTTTATTGCAAAAAAAAATATTCGCAACACA  840

Query  8257   ACCTATGTTGTaaaaaaaTTCTGCAACATAACCTTTGTTGCATAAAAATTATGTGACACA  8316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841    ACCTATGTTGTAAAAAAATTCTGCAACATAACCTTTGTTGCATAAAAATTATGTGACACA  900

Query  8317   TTCATTATTATAAATGTTTCTGCAATAAAACTATTGTTGCAGGAATCTGCAACACCATCT  8376
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  901    TTCATTATTATAAATGTTTCTGCAATAAAACTATTGTTGCAGAAATCTGCAACACCATCT  960

Query  8377   CTGTTATAAATGTTTTTGTAACAAAGTCGTTGTTACGGAAATTAATAAGTGGGAAAGGGG  8436
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  961    CTGTTATAAATGTTTTTGTGACAAAGTCGTTGTTACGGAAATTAATAAGTGGGAAAGGGG  1020

Query  8437   ACAAGCAGGACGTGGCAGGAGATCGATCGGACGCTGACCGCACGTAGATCCAACGACCAT  8496
              |||||||||||||| |||||||||||||||||||||||||||||||||||| ||||
Sbjct  1021   ACAAGCAGGACGTGCCAGGAGATCGATCGGACGCTGACCGCACGTAGATCCAACGGCCAT  1080

Query  8497   CGAGGTGATGGATGTATAGCATACATCAACCGATGGATGCATAGCAGTCTCCAGAAAGGA  8556
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  1081   CGAGGTGATGGATGTATAGCATACATCAACCGATGGATGCATATCAGTCTCCAGAAAGGA  1140

Query  8557   AAGGGTAGAAAATCGTTAGCTGAGAAGAAACGTTAAACAAAAGAGGTTACAGATTAAGaa  8616
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141   AAGGGTAGAAAGTCGTTAGCTGAGAAGAAACGTTAAACAAAAGAGGTTACAGATTAAGAA  1200

Query  8617   aaaaaaa-caaaaaatactagtgatttaaaaaattgaattcaaaaaatgcagaattatga  8675
              ||||||| |||||||||||||||||||| |||||||||||||||| ||||||||||||
Sbjct  1201   AAAAAAAACAAAAAATACTAGTGATTTAAAAA-TTGAATTCAAAAAATGTAGAATTATGA  1259

Query  8676   aaatactcatgggtttaaaaaaCACACACATTTTGAAAATGTTCATCGGCTAAAATATAT  8735
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  1260   AAATACTCATGGGTTTAAAAAACACACACATTTTGAAAATGTTCATCGACTAAAATATAT  1319

Query  8736   TCATAAAATTAGGGAAACATCATGTATCCCAACCCGCGCGCCTGCCTCGGCGTTGTCCTC  8795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1320   TCATAAAATTAGGGAAACATCATGTATCCCAACCCGCGCGCCTGCCTCGGCGTTGTCCTC  1379

Query  8796   GCCTCCTGCAAGGGCAAGAAGGTAGACGTGATTTGAACATGGTCGGTGGTACTCGTTCCT  8855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1380   GCCTCCTGCAAGGGCAAGAAGGTAGACGTGATTTGAACATGGTCGGTGGTACTCGTTCCT  1439

Query  8856   TGATGTTATGGTTTCTGTCAGCAGAACTCTATCAATTTAATTCATACTTCTTACGATCCA  8915
              |||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||
Sbjct  1440   TGATGTTATGGTTTCTGTCAGCAGAACTCTATCAATTTAATTCGTACTCCTTACGATCCA  1499

Query  8916   AAATAAATGTTACACTTTTGGACTTGTTTTGGGGTTAGTTCAAAACAGCTACACTTTTTA  8975
              |||||| |||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  1500   AAATAAGTGTTACACTTTTGGACTTGTTTTGGGATTAGTTCAAAACAGCTACACTTTTTA  1559

Query  8976   TGGATAGGAGATGGTGATGCATCAGTTCACCTTACGTTACTTTGCTGGTTGTATTGTGAT  9035
              |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Sbjct  1560   TGGATAGGAGATGGTGATGCATCAGTTCACCTTACATTACTTTGCTAGTTGTATTGTGAT  1619
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Query  9036   TTTAGGTCACGGAAAAGCAAAAAGGATGCGCTCTTGGCTCTTGCTCTGTTTGGTTTGCAG  9095
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1620   TTTAGGTCACGGAAAAGCAAAAAGGATGCGCTCTTGGCTCTTGCTCTGTTTGGTTTGCAG  1679

Query  9096   TTTTTAAGTGACATTAATCATTAATATGAAAGTTTCAATGTAGGTCTAGGATGATAACGA  9155
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1680   TTTTTAAGTGACATTAATCATTAATATGAAAGTTTCAATGTAGGTCTAGGATGATAACGA  1739

Query  9156   CAATGATGAGATAGGTGGTTGTGCCAGTGCAACGAGCGTTCTTGCAGGGAGGGTGGTCAT  9215
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1740   CAATGATGAGATAGGTGGTTGTGCCAGTGCAACGAGCGTTCTTGCAGGGAGGGTGGTCAT  1799

Query  9216   TGAGACCTCGTGTGGAGGCATGACCTTGATGTTTAAATCTATCATTTTTAAGAAGTTGCT  9275
               |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  1800   TGAGACCTCGTGTGGAGGCATGACCTTGATGTTTAAATTTATCATTTTTAAGAAGTTGCT  1859

Query  9276   CCCCACTATTTTCTATTCTTTCACCATGCACAATGTCCACATCATCATAACGCCACGTCA  9335
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1860   CCCCACTATTTTCTATTCTTTCACCATGCACAATGTCCACATCATCATAACGCCACGTCA  1919

Query  9336   ACGTTTTCTCAACATGCAGGCTCCACCTCAGCAAGAAAAAGAAAAAGAAATCATTAGGTT  9395
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1920   ACGTTTTCTCAACATGCAGGCTCCACCTCAGCAAGAAAAAGAAAAAGAAATCATTAGGTT  1979

Query  9396   ACAATCTTAGTGGGTCATCAGAATTGTTTTAGGCGTTACATGCCACATCGGCCCTTTTTT  9455
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1980   ACAATCTTAGTGGGTCATCAGAATTGTTTTAGGCGTTACATGCCACATCGGCCCTTTTTT  2039

Query  9456   CGAACTCAACATTGTTTTTGTTAGAAACTAATTAGTAGATTAATTAATTAGCAAAGGGAT  9515
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  2040   CGAACTCAACATTGTTTTTGTTAGAAACTAATTAGTAGATTAATTAATTAGCAAAGGAAT  2099

Query  9516   GTGTCCAACCCGAACAGTTGTGTCTCTTCTCTCTCTTTATTGTCAACATGCATCTGTTTT  9575
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2100   GTGTCCAACCCGAACAGTTGTGTCTCTTCTCTCTCTTTATTGTCAACATGCATCTGTTTT  2159

Query  9576   GAAGGGATGTCTTCGAACAGACACCTCTTCTTCGCACCTTTTTCAGATGTATATATACTT  9635
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2160   AAAGGGATGTCTTCGAACAGACACCTCTTCTTCGCACCTTTTTCAGATGTATATATACTT  2219

Query  9636   GAGAATCAATAGAAACAAGAATAATGGTCCATTTACTTTCATTAATCTCGTTTTACTCTA  9695
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2220   GAGAATCAATAGAAACAAGAATAATGGTCCATTTACTTTCATTAATCTCGTTTTACTCTA  2279

Query  9696   ACACGTTATCAACGCGTGGCTCTCCGTTGAGAGAGAAAGGCCGGAGGGGCCGACGAGGAG  9755
               |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  2280   ACACGTTATCAACGCGTGGCTCTCCGCTGAGAGAGAAAGGCCGGAGGGGCCGACGAGGAG  2339

Query  9756   GCCTCTCAAGGACGCCTTCGACACACCGCGGCGCCCGATCCGTGGAGGAGAGCAGTGGTG  9815
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2340   GCCTCTCAAGGACGCCTTCGACACACCGCGGCGCCCGATCCGTGGAGGAGAGCAGTGGTG  2399

Query  9816   GAGTCTCCCGGTGTTCTCGCATGGACTAGTTGCGCCAGAAACCATGGCCTTCGGCGTGGT  9875
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2400   GAGTCTCCCGGCGTTCTCGCATGGACTAGTTGCGCCAGAAACCATGGCCTTCGGCGTGGT  2459

Query  9876   AGTTCTGCGACGGTCGGCGTCGTACTGGCTGGCAGGACAACGCTCATGCAATCGCTGTGG  9935
               |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  2460   AGTTCTGCGACGGTCGGCGTCGTACTGGCTGGCAAGACAACGCTCATGCAATCGCTGTGG  2519

Query  9936   CAAGGCAGGACAGCGAGATGCGACGCACACCCCAACGTAATTCACGGCCTAGAGGCAAGA  9995
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2520   CAAGGCAGGACAGCGAGATGCGACGCACACCCCAACGTAATTCACGGCCTAGAGGCAAGA  2579

Query  9996   AGCGCCACATCAGACATCACCGGCGGCAAGTCAACGCCAGGGCCAGCAGCGCACGCCGAT  10055
               |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  2580   AGCGCCACATCACACATCACCGGCGGCAAGTCGACGCCAGGGCCAGCAGCGCACGCCGAT  2639

Query  10056  GTGTCCTAGGCAGTGCATCAATCATCAATGAGAAGATGAGCATGCTTCTCACGCATACAT  10115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2640   GTGTCCTAGGCAGTGCATCAATCATCAATGAGAAGATGAGCATGCTTCTCACGCATACAT  2699

Query  10116  CCATTAAAGAAATCAATCACAAGAACAATGGCTTGGTTTACTTTTGTTATTTCTGACTTA  10175
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  2700   CCATTAAAGAAATCAATCACAAGAACAACGGCTTGGTTTACTTTTGTTATTTCTGACTTA  2759
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Query  10176  ACAAATTACTAATCGTCTTGTGATTGTCGAAttttttttCATGAACAGCGGTGCAATTGAT  10235
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  2760   ACAAATTACTAATCGTCTTGTGATTGTCGAATTTTTTTTCATGAACAGTGGTGCAATTGAT  2819

Query  10236  AGACGACCAAGGAACGCAAGAAGGCCGAGCGCGGCGATGATGATGGAATCCCGCGGCTCC  10295
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2820   AGACGACCGAGGAACGCAAGAAGGCCGAGCGCGGCGATGATGATGGAATCCCGCGGCTCC  2879

Query  10296  GCACGGCAACGCTCTGCGGACGCGACGAGCGGCTGGCAAATCGGAGCTACACGAGATTCT  10355
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  2880   GCACGGCAACGCTCTGCGGACGCGACGAGCGGCCGGCAAATCGGAGCTACACGAGATTCT  2939

Query  10356  AAGCAAGTTT  10365
              ||||||||||
Sbjct  2940   AAGCAAGTTT  2949


> bowman_contig_186994 CAJX010182639
Length=739

 Score = 1265 bits (1402),  Expect = 0.0
 Identities = 727/742 (97%), Gaps = 3/742 (0%)
 Strand=Plus/Plus

Query  6350  ggAGATAGTGTCCACCACCATTCTATGTTCCAGaaaaaaaTATCTAGATTATGCAGGTTT  6409
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  1     GGAGATAGTGTCCACCACCATTCTATGTTCCAGAAAAAA-TATCTAGATTATGCAGGTTT  59

Query  6410  GTAAATTGTAACCGCTACATTGATATACGGTGTGTTCATGATTCACTGGACCAGTCGTTG  6469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  60    GTAAATTGTAACCGCTACATTGATATACGGTGTGTTCATGATTCACTGGACCAGTCGTTG  119

Query  6470  CTAAAGCAGCAAGCAAGCCCGCAATCATCTCAGCATAGTCACTCTGCCCCCAAATATACC  6529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120   CTAAAGCAGCAAGCAAGCCCGCAATCATCTCAGCATAGTCACTCTGCCCCCAAATATACC  179

Query  6530  ATAACAATCAACTAACTGAAAGAGCGATTGACGTTTCATCTCCAGGCTCTGCTCAGCATT  6589
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  180   ATAACAATCAACTAACTGAAAGAGCGATTGACGTTTCATCTCCAGGCTCTACTCAGCATT  239

Query  6590  TGCGGACTAGAGGAAATTTCATTCGGTAACAGTTACGTGTCACTTTACACTTCCCAGCAT  6649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   TGCGGACTAGAGGAAATTTCATTCGGTAACAGTTACGTGTCACTTTACACTTCCCAGCAT  299

Query  6650  GAACGTGACTACACACTCGTTACTTGATGCTGTCCATTCTAGGTGGTAGGTTCCAACACA  6709
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  300   GAACGTGACTACACACTCGTT--TTGATGCTGTCCATTCTAGGTGGTAGGTTCCAACACA  357

Query  6710  AAATCTATGTTCTGCTAGTTTGTAAGTTGTAACAGTTACACTGAGATACCATGCATTCAC  6769
              |||||||||||||||||||||||||||||||| | |||| |||||||| ||||||||||
Sbjct  358   AAATCTATGTTCTGCTAGTTTGTAAGTTGTAACCGCTACATTGAGATACAATGCATTCAC  417

Query  6770  ATTCACTAGTCTGATCTTTGCTGCAAGCAGGACGCATCCAGTAACTGAAGAAGGGATTGA  6829
              |||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||
Sbjct  418   ATTCACTAGTCTGATCTTTGATGCAAGCAGGACGCACCCAGTAACTGAAGAAGGGATTGA  477

Query  6830  CATTGCATCTCCCAGGATCTACTATTCAAGCACCGTCTTAAGCCCTCACCAACGAATCAC  6889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  478   CATTGCATCTCCCAGGATCTACTATTCAAGCACCGTCTTAAGCCCTCACCAACGAATCAC  537

Query  6890  AACCAGGAACAATTCTAACTGTACAACCAAAGCAGATAGCGCTCTTCCCCAATCACATTT  6949
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| ||
Sbjct  538   AACCAGGAACAATTCTAACTGCACAACCAAAGCAGATAGCGCTCTTCCCCAATCACAATT  597

Query  6950  TAGCTCAAATTCGACACCACAGCCCTCCAAATCTCACAAGGACATTCAGCACGCAAGCTA  7009
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  598   TAGCTCAAATTCGACACCACAGCCCTCCAAATCTCACAAGCACATTCAGCACGCAAGCTA  657

Query  7010  TAAGCAATATAAACGCTCGGGTGATTCGGATTGAACAGCCTCCCGACGGATTCGACCAGG  7069
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  658   TAAGCAATATAATCGCTCGGGTGATTCGGATTGAACAGCCTCCCGACGGATTCGACCAGG  717

Query  7070  AGCCTGCATCAGAGCCCAACAA  7091
              ||||||||||||||||| |||
Sbjct  718   AGCCTGCATCAGAGCCCATCAA  739
```

```
 Score = 75.2 bits (82),  Expect = 4e-10
 Identities = 61/73 (83%), Gaps = 1/73 (1%)
 Strand=Plus/Plus

Query  6201  ACTCAGACATTTGCGGACAACGAGAAATCTCATTTGATAACAGTAACGTGTCGCTGTACA  6260
              |||||| |||||||||||  |   ||||| ||||| | ||||||| ||||||| || ||||
Sbjct  230   ACTCAG-CATTTGCGGACTAGAGGAAATTTCATTCGGTAACAGTTACGTGTCACTTTACA  288

Query  6261  CTTCCCAACATGA  6273
              ||||||| |||||
Sbjct  289   CTTCCCAGCATGA  301



> bowman contig 986 CAJX010000984 carma=3HL
Length=253

 Score =  452 bits (500),  Expect = 1e-123
 Identities = 252/253 (99%), Gaps = 0/253 (0%)
 Strand=Plus/Plus

Query  7192  ggaagcggaggggaggagggcgggggggtaggcggagtcgtcggtggggaccgggaggga  7251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGAAGCGGAGGGGAGGAGGGCGGGGGGGTAGGCGGAGTCGTCGGTGGGGACCGGGAGGGA  60

Query  7252  gCCCACGCGGAGGTAGCGCGCCGGCGGCGGCGCGGCGATCTCCAGCCGCCCCACGCACTG  7311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCCCACGCGGAGGTAGCGCGCCGGCGGCGGCGCGGCGATCTCCAGCCGCCCCACGCACTG  120

Query  7312  CATCTCGCCCGACGCGTCCATCGGAGCCGTCCTTCCTCCTCGCCGCCGGCGTCGGCTTGT  7371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATCTCGCCCGACGCGTCCATCGGAGCCGTCCTTCCTCCTCGCCGCCGGCGTCGGCTTGT  180

Query  7372  GGAGCTCGCTCGGATCGCGGCAGCGGCAGCGCGTTCCGTGCCCGGCTTGACGAACGCCCA  7431
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  181   GGAGCTCGCTCGGATCGCGGCAGCAGCAGCGCGTTCCGTGCCCGGCTTGACGAACGCCCA  240

Query  7432  CGGAGTCAGTGGA  7444
              |||||||||||||
Sbjct  241   CGGAGTCAGTGGA  253
```

Tables summarising the primers used for the analysis of specific contigs/SNPs using KASPar® assays and Big Dye version 3.1 sequencing, including the 96-well optical plate sample reference for the KASPar® assays of the markers 11_20659, 11_10747, 11_20628 and 11_10515.

Table A177: A summary of the materials used for the delineation of *des8*. All information in the yellow boxes pertains to KASPar® assays and which primer was used and what region the genome (harbouring the chosen SNP between Morex and Bowman) according to the Morex x Barke consensus map (shown in red: Comadran *et al*., 2012), was analysed. All information in the lilac boxes pertains to Big Dye v3.1 sequencing (which primer was used to sequence a specific marker) and to what region of the in-house barley contig library the sequencing results for *des8* were compared to.

Barley marker	Rice homologue	Primer	Sequence	Morex contig v Bowman contig/ Morex x Barke in-house (JHI) map position.	SNP (Morex/Bowman)	Start sequence (position on contig).	Expt. Product size (bp).
MLOC_10987	LOC_Os01g65050	MLOC_10987_L02 (forward)	TTGCTACCGTCACGTATAATGG (designed using Primer3 sofware)	morex_contig_1560156 v Bowman_contig_855417 (page 543)	All SNPs in the contig	5381	6089
		MLOC_10987_R02 (reverse)	AGCGTGAATCGAAAGAATCC (designed using Primer3 sofware)			6089	
MLOC_4841	LOC_Os01g60900	MLOC_4841_L01 (forward)	GGGAGAGCGAGATACAGTGC (designed using Primer3 sofware)	morex_contig_135563 v Bowman_contig_126920 (page 552)	All SNPs in the contig (C/T)	3294	755
		MLOC_4841_R01 (reverse)	TTTCATCACGAGGCTGATCC (designed using Primer3 sofware)			4048	
MLOC_53985	LOC_Os01g65320	MLOC_53985_L01 (forward)	TCCAGGAACTTCAAGCACAG (designed using Primer3 sofware)	morex_contig_38798 v Bowman_contig_850578 (page 562)	All SNPs in the contig	422	760
		MLOC_53985_R01 (reverse)	CGAGCGGTGGTATTTTCAAG (designed using Primer3 sofware)			1181	
11_20628	LOC_Os 01g64770	Primer_11_20628	Unknown (KBiosciences® KASP primer).	3H 87.4 cM (Table A175: page 530)	T/A	N/A	N/A
11_10515	LOC_Os 01g64170	Primer_11_10515	Unknown (KBiosciences® KASP primer).	3H 88.8 cM (Table A176: page 532)	A/G	N/A	N/A
11_20659	LOC_Os 01g60230	Primer_11_20659	Unknown (KBiosciences® KASP primer).	3H 77.3 cM (Table A173: page 526)	T/C	N/A	N/A
11_10747	LOC_Os 01g60440	Primer_11_10747	Unknown (KBiosciences® KASP primer).	3H 82.19 cM (Table A174: page 528)	A/G	N/A	N/A

Figure A6: A depiction of the extracted leaf DNA from *des8* individuals (family) in the 96-well optical plates (plates 1 and 2), that were used in the KASPar® assays to ascertain the informative individuals using the markers 11_20659 and 11_10515. The plants were grown in the polytunnel (PT) in the year 2013 (13). The red coloured wells are empty and refer to *des8* seeds that failed to germinate.

des8_PT13_1	1	2	3	4	5	6	7	8	9	10	11	12
A	147_07_101_1	147_07_101_2	147_07_101_3	147_07_104_1	147_07_104_2	147_07_104_3	147_07_107_1	147_07_107_2	147_07_107_3	147_07_110_1	147_07_110_2	147_07_110_3
B	147_07_113_1	147_07_113_2	147_07_113_3	147_07_116_1	147_07_116_2	147_07_116_3	147_07_119_1	147_07_119_2	147_07_119_3	147_07_122_1	147_07_122_2	147_07_122_3
C	147_11_101_1	147_11_101_2	147_11_101_3	147_11_104_1	147_11_104_2	147_11_104_3	147_11_107_1	147_11_107_2	147_11_107_3	147_11_110_1	147_11_110_2	147_11_110_3
D	147_11_113_1	147_11_113_2	147_11_113_3	147_11_116_1	147_11_116_2	147_11_116_3	147_11_119_1	147_11_119_2	147_11_119_3	147_11_122_1	147_11_122_2	147_11_122_3
E	147_02_101_1	147_02_101_2	147_02_101_3	147_02_104_1	147_02_104_2	147_02_104_3	147_02_107_1	147_02_107_2	147_02_107_3	147_02_110_1	147_02_110_2	147_02_110_3
F	147_02_113_1	147_02_113_2	147_02_113_3	147_02_116_1	147_02_116_2	147_02_116_3	147_02_119_1	147_02_119_2	147_02_119_3	147_02_122_1	147_02_122_2	147_02_122_3
G	147_02_125_1	147_02_125_2	147_02_125_3	147_02_128_1	147_02_128_2	147_02_128_3	147_02_131_1	147_02_131_2	147_02_131_3	147_02_134_1	147_02_134_2	147_02_134_3
H	147_02_137_1	147_02_137_2	147_02_137_3	147_02_140_1	147_02_140_2	147_02_140_3	147_02_143_1	147_02_143_2	147_02_143_3	147_02_146_1	147_02_146_2	147_02_146_3

des8_PT13_2	1	2	3	4	5	6	7	8	9	10	11	12
A	147_03_101_1	147_03_101_2	147_03_101_3	147_03_104_1	147_03_104_2	147_03_104_3	147_03_107_1	147_03_107_2	147_03_107_3	147_03_110_1	147_03_110_2	147_03_110_3
B	147_03_113_1	147_03_113_2	147_03_113_3	147_03_116_1	147_03_116_2	147_03_116_3	147_03_119_1	147_03_119_2	147_03_119_3	147_03_122_1	147_03_122_2	147_03_122_3
C	147_04_101_1	147_04_101_2	147_04_101_3	147_04_104_1	147_04_104_2	147_04_104_3	147_04_107_1	147_04_107_2	147_04_107_3	147_04_110_1	147_04_110_2	147_04_110_3
D	147_04_113_1	147_04_113_2	147_04_113_3	147_04_116_1	147_04_116_2	147_04_116_3	147_04_119_1	147_04_119_2	147_04_119_3	147_04_122_1	147_04_122_2	147_04_122_3
E	147_06_101_1	147_06_101_2	147_06_101_3	147_06_104_1	147_06_104_2	147_06_104_3	147_06_107_1	147_06_107_2	147_06_107_3	147_06_110_1	147_06_110_2	147_06_110_3
F	147_06_113_1	147_06_113_2	147_06_113_3	147_06_116_1	147_06_116_2	147_06_116_3	147_06_119_1	147_06_119_2	147_06_119_3	147_06_122_1	147_06_122_2	147_06_122_3
G	147_06_125_1	147_06_125_2	147_06_125_3	147_06_128_1	147_06_128_2	147_06_128_3	147_06_131_1	147_06_131_2	147_06_131_3	147_06_134_1	147_06_134_2	147_06_134_3
H	147_06_137_1	147_06_137_2	147_06_137_3	147_06_140_1	147_06_140_2	147_06_140_3	147_06_143_1	147_06_143_2	147_06_143_3	147_06_146_1	147_06_146_2	147_06_146_3

Figure A7: A depiction of the extracted leaf DNA from *des8* individuals (family) in the 96-well optical plate (plates 4), that was used in the KASPar® assays to ascertain the informative individuals using the markers 11_20659 and 11_10515. The plants were grown in the polytunnel (PT) in the year 2013 (13). The red coloured wells are empty and refer to *des8* seeds that failed to germinate. A 96-well optical plate number 3 was not set up for KASPar® assays because the 96-well block (block 3) that was used to collect and store the *des8* plant material, pertained to many seeds that failed to germinate (empty wells) and therefore, would not have provided a sufficient number of samples to yield a reliable number of infomative individuals using the markers 11_20659 and 11_10515.

des8_PT13_4	1	2	3	4	5	6	7	8	9	10	11	12
A	147_09_101_1	147_09_101_2	147_09_101_3	147_09_104_1	147_09_104_2	147_09_104_3	147_09_107_1	147_09_107_2	147_09_107_3	147_09_110_1	147_09_110_2	147_09_110_3
B	147_09_113_1	147_09_113_2	147_09_113_3	147_09_116_1	147_09_116_2	147_09_116_3	147_09_119_1	147_09_119_2	147_09_119_3	147_09_122_1	147_09_122_2	147_09_122_3
C	147_09_125_1	147_09_125_2	147_09_125_3	147_09_128_1	147_09_128_2	147_09_128_3	147_09_131_1	147_09_131_2	147_09_131_3	147_09_134_1	147_09_134_2	147_09_134_3
D	147_09_137_1	147_09_137_2	147_09_137_3	147_09_140_1	147_09_140_2	147_09_140_3	147_09_143_1	147_09_143_2	147_09_143_3	147_09_146_1	147_09_146_2	147_09_146_3
E	147_09_149_1	147_09_149_2	147_09_149_3	147_09_152_1	147_09_152_2	147_09_152_3	147_09_155_1	147_09_155_2	147_09_155_3	147_09_158_1	147_09_158_2	147_09_158_3
F	147_09_161_1	147_09_161_2	147_09_161_3	147_09_164_1	147_09_164_2	147_09_164_3	147_09_167_1	147_09_167_2	147_09_167_3	147_09_170_1	147_09_170_2	147_09_170_3
G	147_09_173_1	147_09_173_2	147_09_173_3	147_09_176_1	147_09_176_2	147_09_176_3	147_09_179_1	147_09_179_2	147_09_179_3	147_09_182_1	147_09_182_2	147_09_182_3
H	147_09_185_1	147_09_185_2	147_09_185_3	147_09_188_1	147_09_188_2	147_09_188_3	147_09_191_1	147_09_191_2	147_09_191_3	147_09_194_1	147_09_194_2	147_09_194_3

Figure A8: A depiction of the extracted leaf DNA from *des8* individuals (family) in the 96-well optical plates (plates 8 and 9), that were used in the KASPar® assays to ascertain the informative individuals using the markers 11_20659 and 11_10515. The plants were grown in the polytunnel (PT) in the year 2013 (13). The red coloured wells are empty and refer to *des8* seeds that failed to germinate. 96-well optical plate numbers 5, 6 and 7 were not set up for KASPar® assays because the 96-well blocks (blocks 5, 6 and 7) that were used to collect and store the *des8* plant material, pertained to many seeds that failed to germinate (empty wells) and therefore, would not have provided a sufficient number of samples to yield a reliable number of infomative individuals using the markers 11_20659 and 11_10515.

des8_PT13_8	1	2	3	4	5	6	7	8	9	10	11	12
A	147_14_101_1	147_14_101_2	147_14_101_3	147_14_104_1	147_14_104_2	147_14_104_3	147_14_107_1	147_14_107_2	147_14_107_3	147_14_110_1	147_14_110_2	147_14_110_3
B	147_14_113_1	147_14_113_2	147_14_113_3	147_14_116_1	147_14_116_2	147_14_116_3	147_14_119_1	147_14_119_2	147_14_119_3	147_14_122_1	147_14_122_2	147_14_122_3
C	147_14_125_1	147_14_125_2	147_14_125_3	147_14_128_1	147_14_128_2	147_14_128_3	147_14_131_1	147_14_131_2	147_14_131_3	147_14_134_1	147_14_134_2	147_14_134_3
D	147_14_137_1	147_14_137_2	147_14_137_3	147_14_140_1	147_14_140_2	147_14_140_3	147_14_143_1	147_14_143_2	147_14_143_3	147_14_146_1	147_14_146_2	147_14_146_3
E	147_14_149_1	147_14_149_2	147_14_149_3	147_14_152_1	147_14_152_2	147_14_152_3	147_14_155_1	147_14_155_2	147_14_155_3	147_14_158_1	147_14_158_2	147_14_158_3
F	147_14_161_1	147_14_161_2	147_14_161_3	147_14_164_1	147_14_164_2	147_14_164_3	147_14_167_1	147_14_167_2	147_14_167_3	147_14_170_1	147_14_170_2	147_14_170_3
G	147_14_173_1	147_14_173_2	147_14_173_3	147_14_176_1	147_14_176_2	147_14_176_3	147_14_179_1	147_14_179_2	147_14_179_3	147_14_182_1	147_14_182_2	147_14_182_3
H	147_14_185_1	147_14_185_2	147_14_185_3	147_14_188_1	147_14_188_2	147_14_188_3	147_14_191_1	147_14_191_2	147_14_191_3	147_14_194_1	147_14_194_2	147_14_194_3

des8_PT13_9	1	2	3	4	5	6	7	8	9	10	11	12
A	147_15_101_1	147_15_101_2	147_15_101_3	147_15_104_1	147_15_104_2	147_15_104_3	147_15_107_1	147_15_107_2	147_15_107_3	147_15_110_1	147_15_110_2	147_15_110_3
B	147_15_113_1	147_15_113_2	147_15_113_3	147_15_116_1	147_15_116_2	147_15_116_3	147_15_119_1	147_15_119_2	147_15_119_3	147_15_122_1	147_15_122_2	147_15_122_3
C	147_15_125_1	147_15_125_2	147_15_125_3	147_15_128_1	147_15_128_2	147_15_128_3	147_15_131_1	147_15_131_2	147_15_131_3	147_15_134_1	147_15_134_2	147_15_134_3
D	147_15_137_1	147_15_137_2	147_15_137_3	147_15_140_1	147_15_140_2	147_15_140_3	147_15_143_1	147_15_143_2	147_15_143_3	147_15_146_1	147_15_146_2	147_15_146_3

KASPar® allelic discrimination plots (raw data) for the markers LOC_Os 01g60230 (11_20659) and 11_10515 and a table (raw data) showing the relationship between the genotype and the phenotype (determination of the informative individuals).

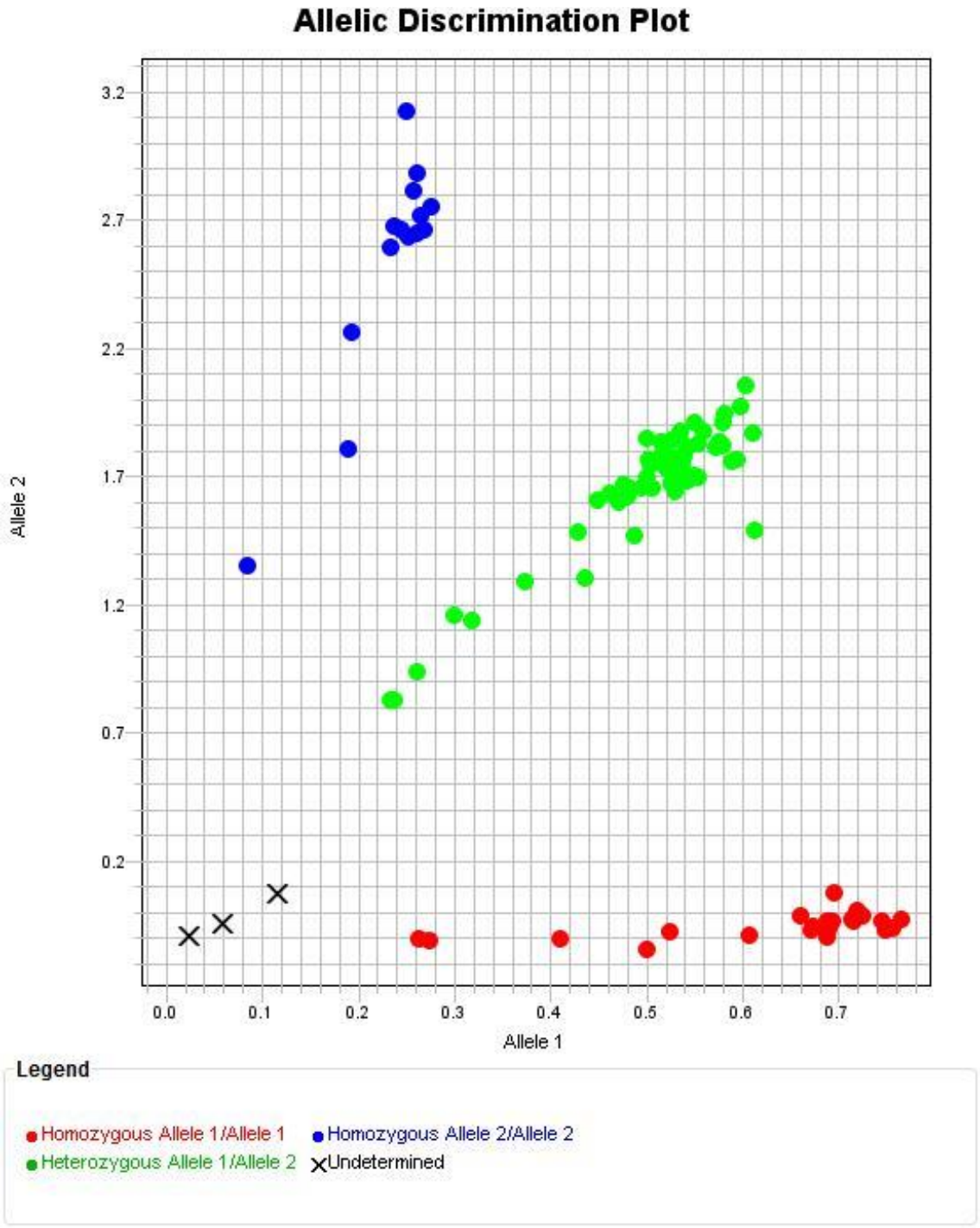

Figure A9: Allelic discrimination plot to attain informative samples for SNP marker 60230 using PT-13, plate 1 group. Allele 1/1 corresponds to the BW248 and allele 2/2 corresponds to the Morex allele.

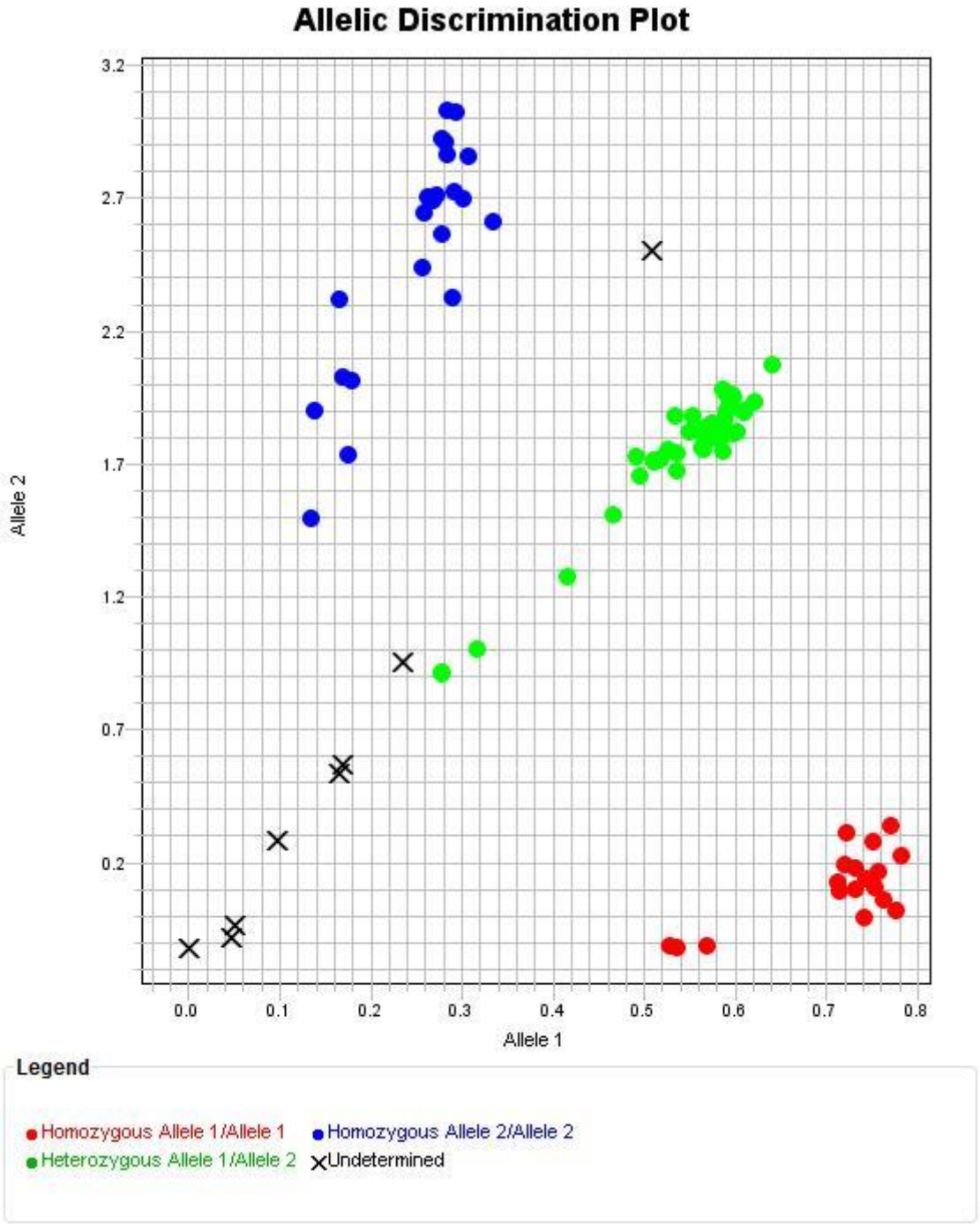

Figure A10: Allelic discrimination plot to attain informative samples for SNP marker 60230 using PT-13, plate 2 group. Allele 1/1 corresponds to the BW248 and allele 2/2 corresponds to the Morex allele.

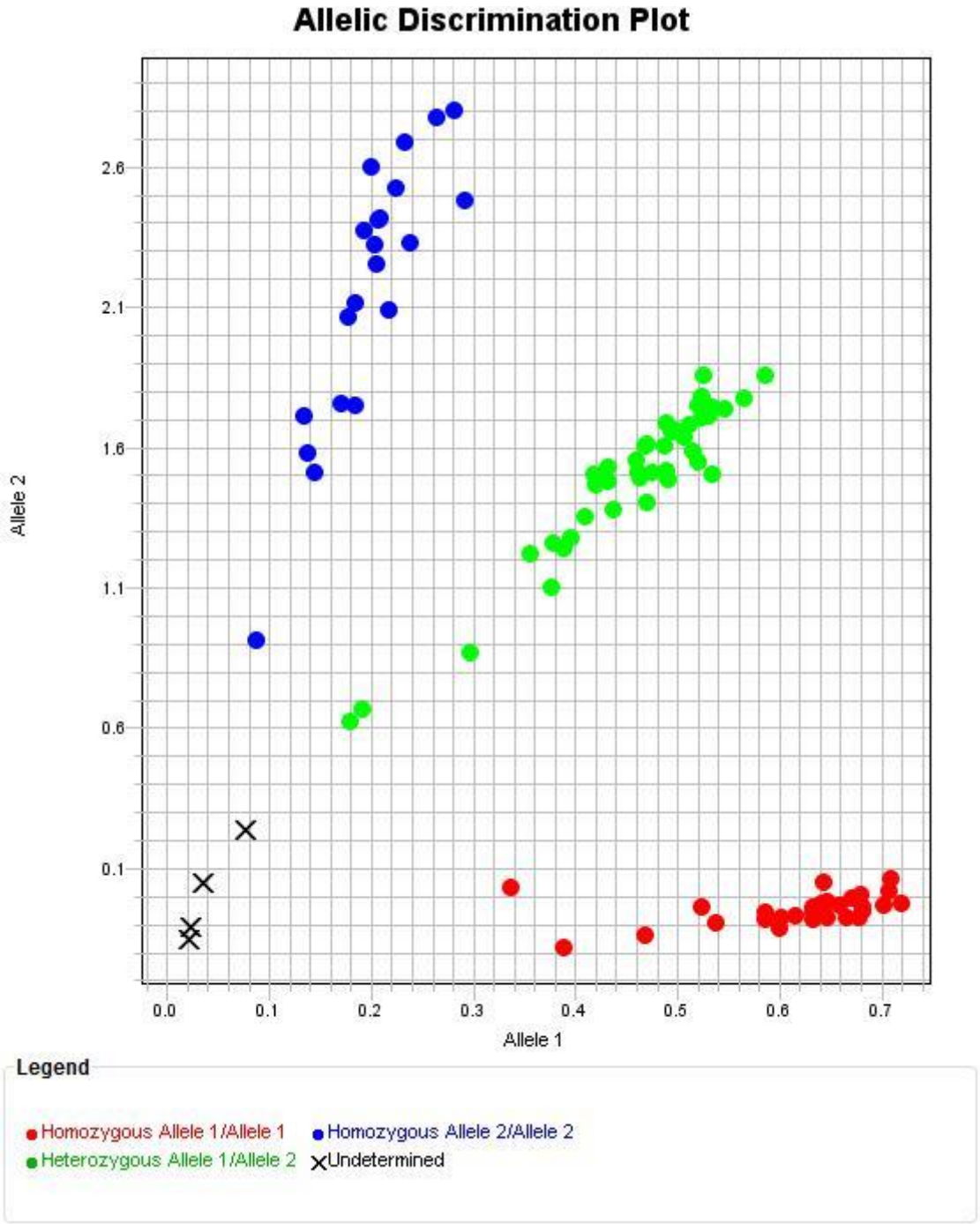

Figure A11: Allelic discrimination plot to attain informative samples for SNP marker 60230 using PT-13, plate 4 group. Allele 1/1 corresponds to the BW248 and allele 2/2 corresponds to the Morex allele.

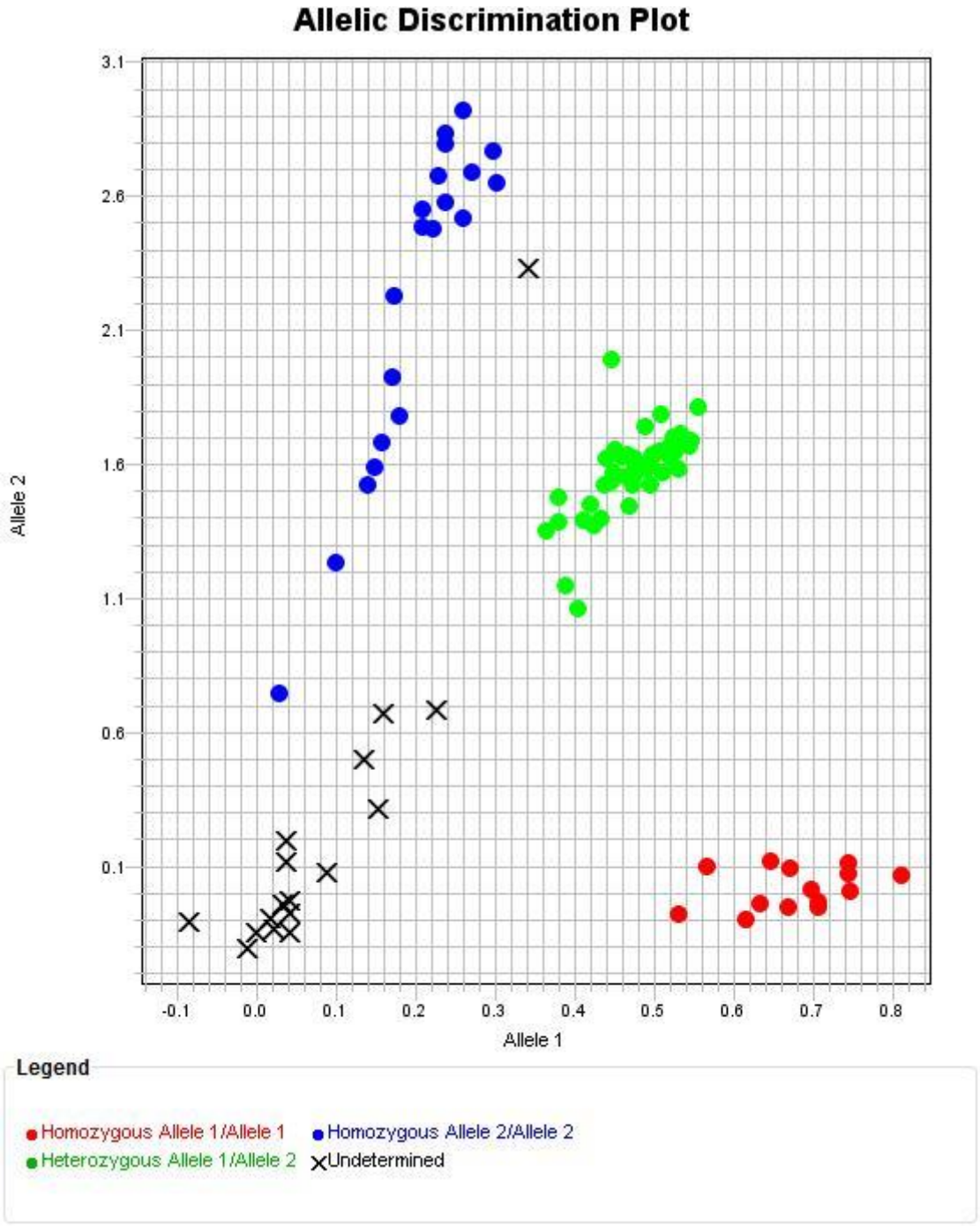

Figure A12: Allelic discrimination plot to attain informative samples for SNP marker 60230 using PT-13, plate 8 group. Allele 1/1 corresponds to the BW248 and allele 2/2 corresponds to the Morex allele.

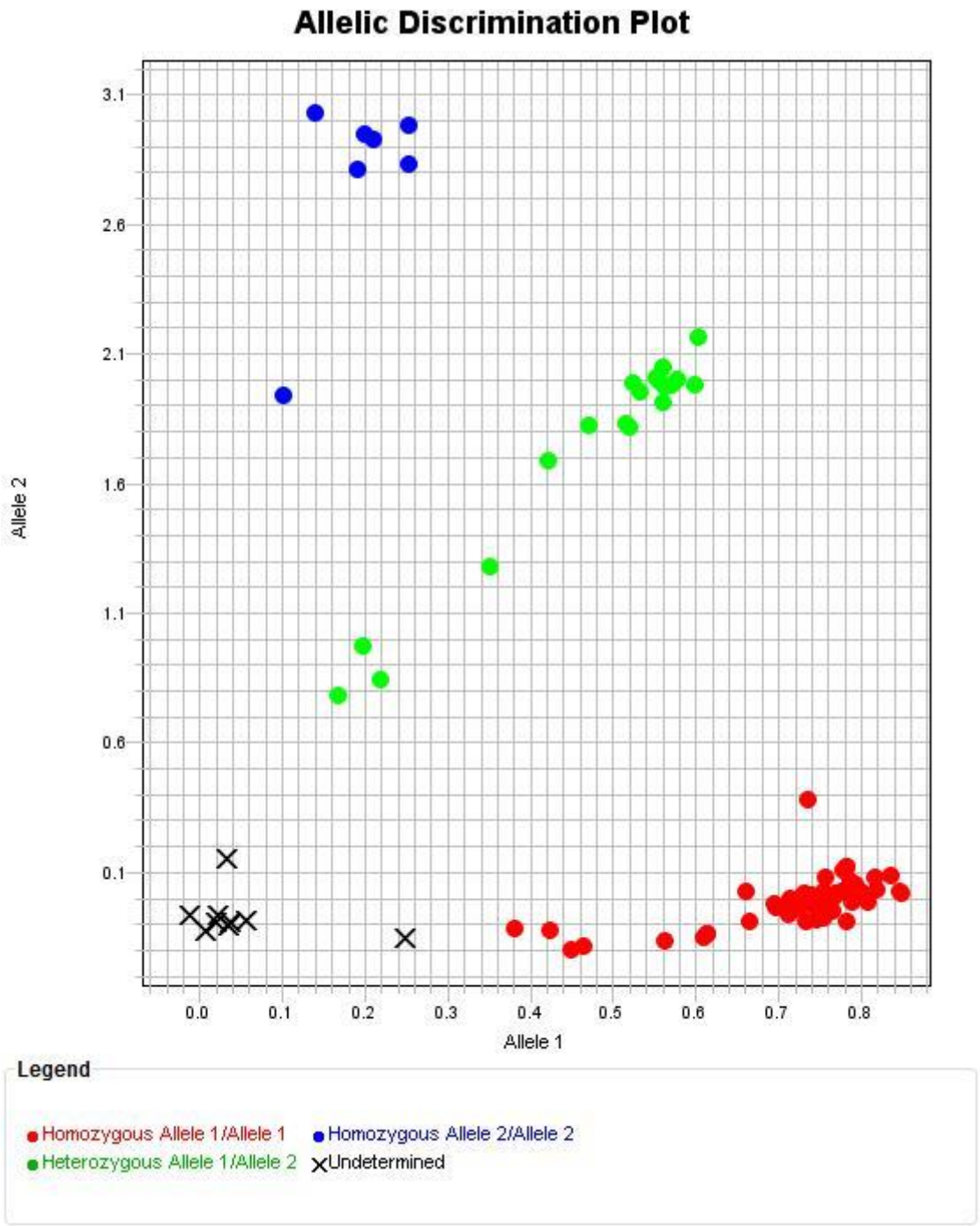

Figure A13: Allelic discrimination plot to attain informative samples for SNP marker 60230 using PT-13, plate 9 group. Allele 1/1 corresponds to the BW248 and allele 2/2 corresponds to the Morex allele.

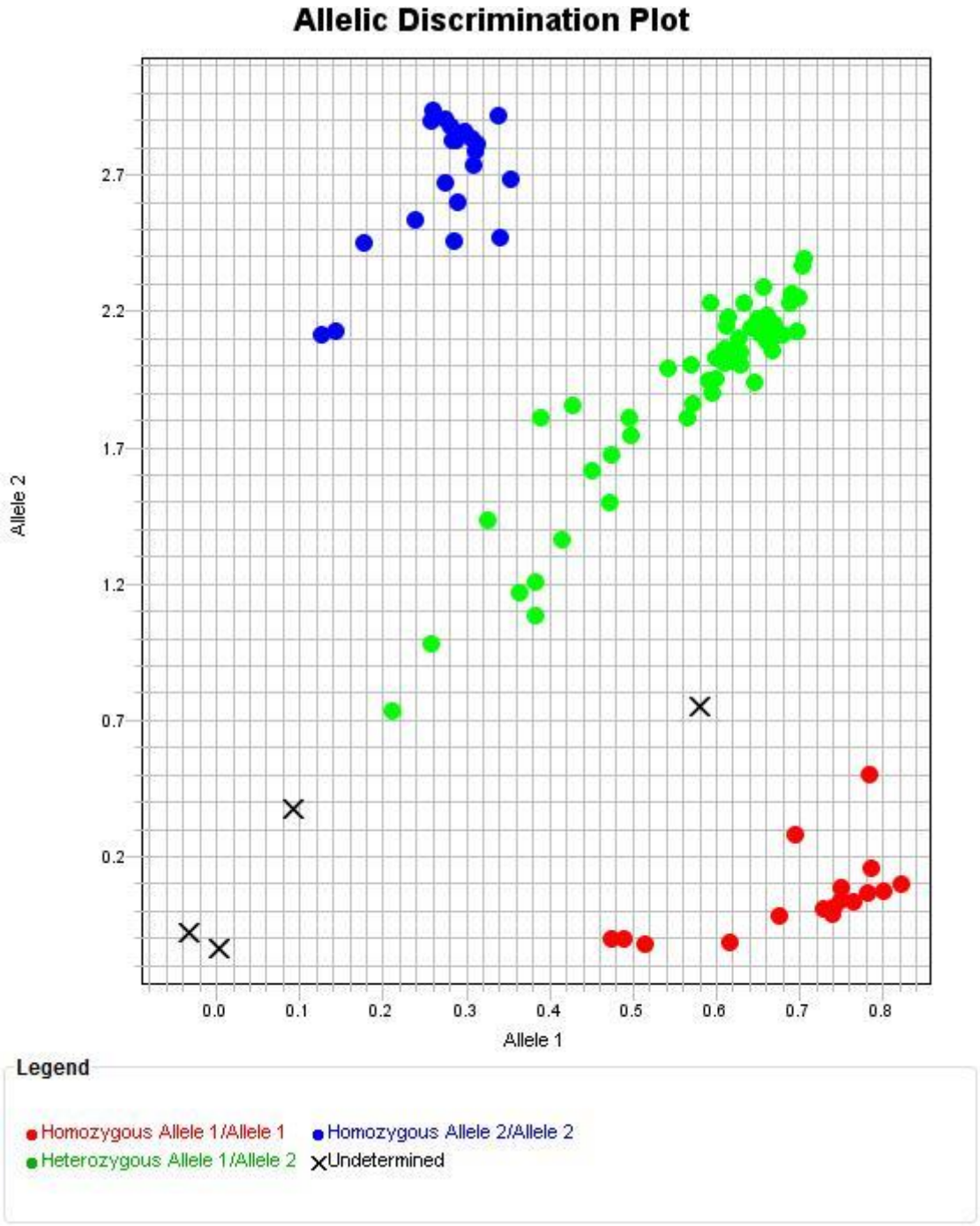

Figure A14: Allelic discrimination plot to attain informative samples for SNP marker 11_10515 using PT-13, plate 1 group. Allele 1/1 corresponds to the Morex allele and 2/2 corresponds to the BW248 allele.

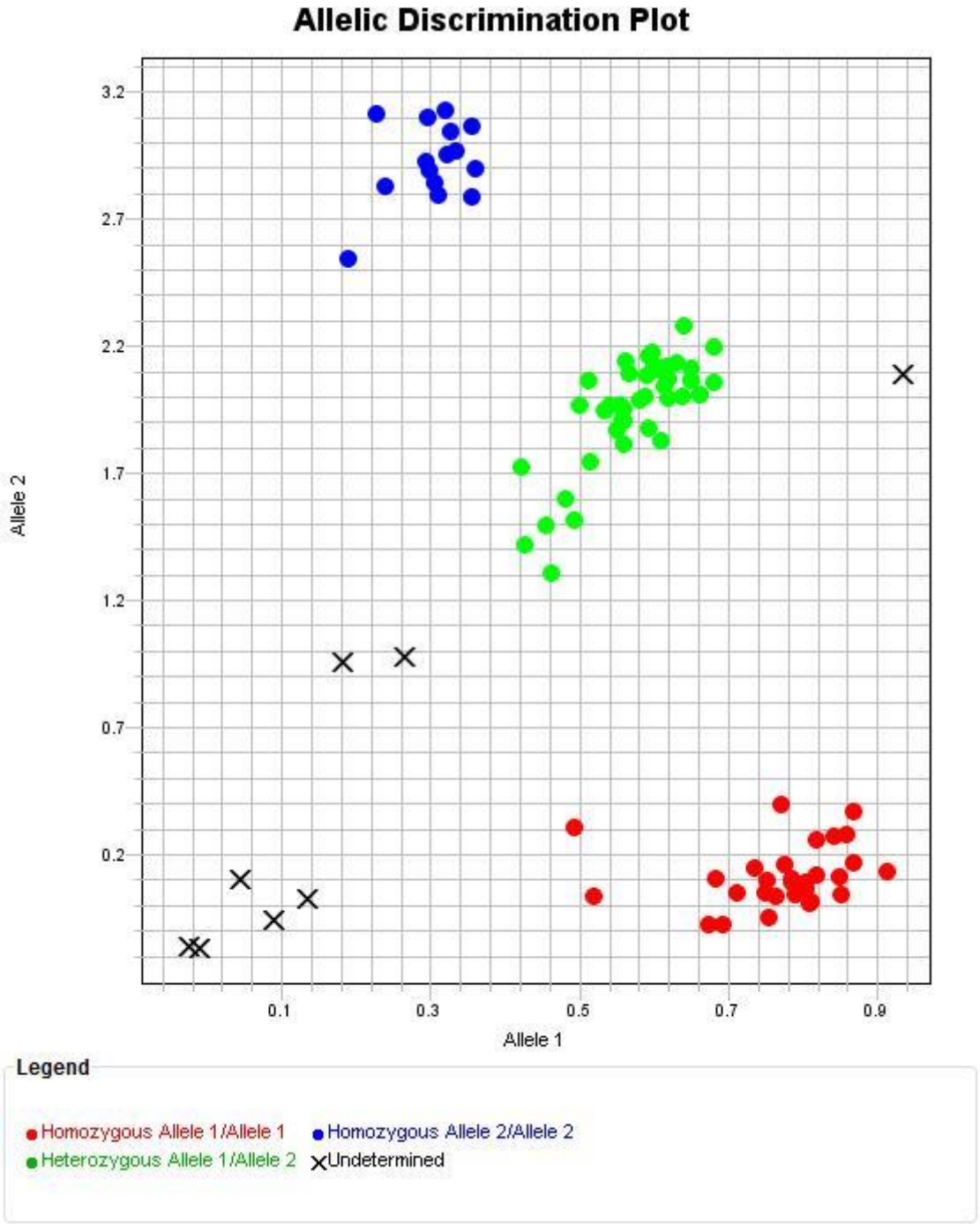

Figure A15: Allelic discrimination plot to attain informative samples for SNP marker 11_10515 using PT-13, plate 2 group. Allele 1/1 corresponds to the Morex allele and allele 2/2 corresponds to the BW248 allele.

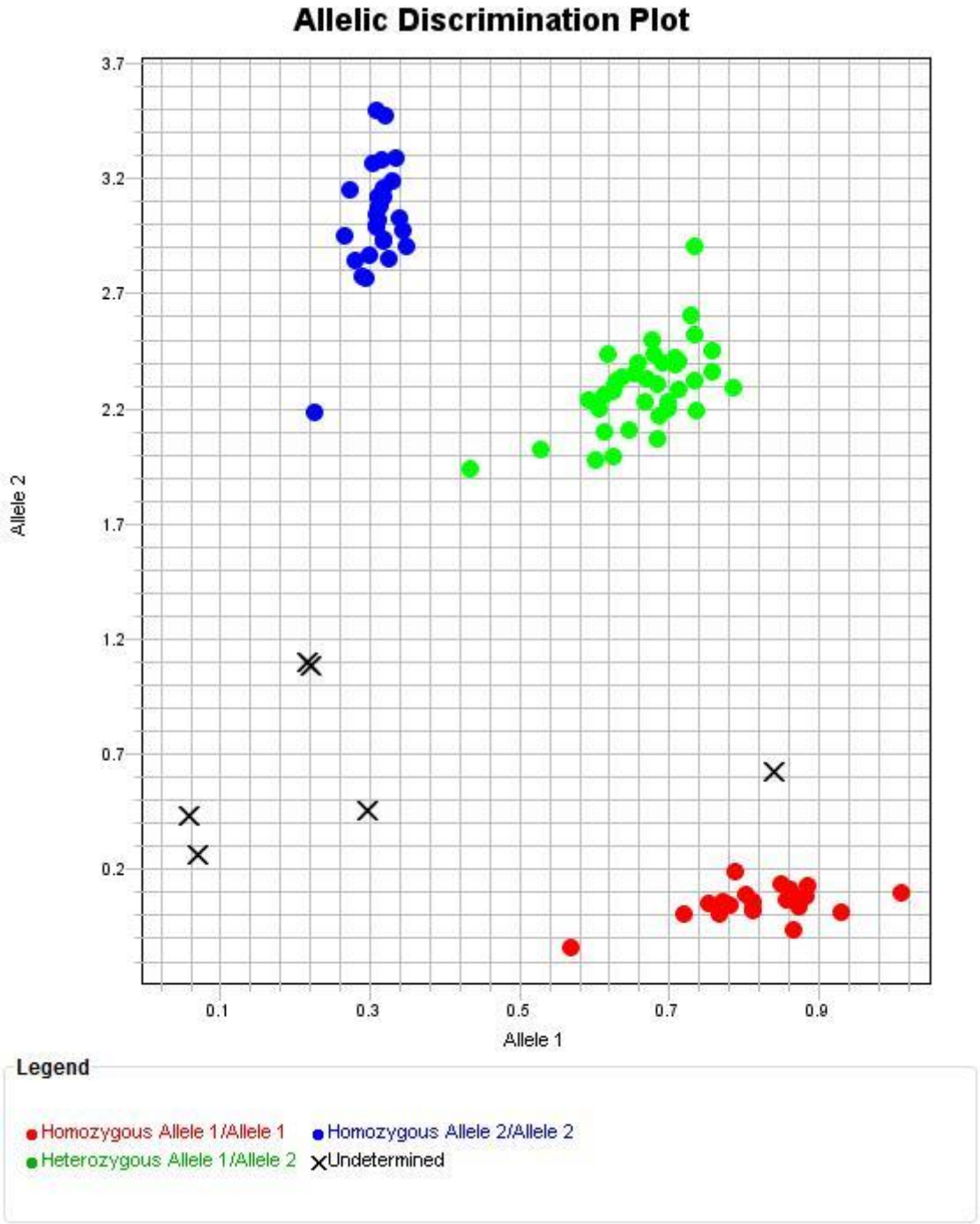

Figure A16: Allelic discrimination plot to attain informative samples for SNP marker 11_10515 using PT-13, plate 4 group. Allele 1/1 corresponds to the Morex allele and allele 2/2 corresponds to the BW248 allele.

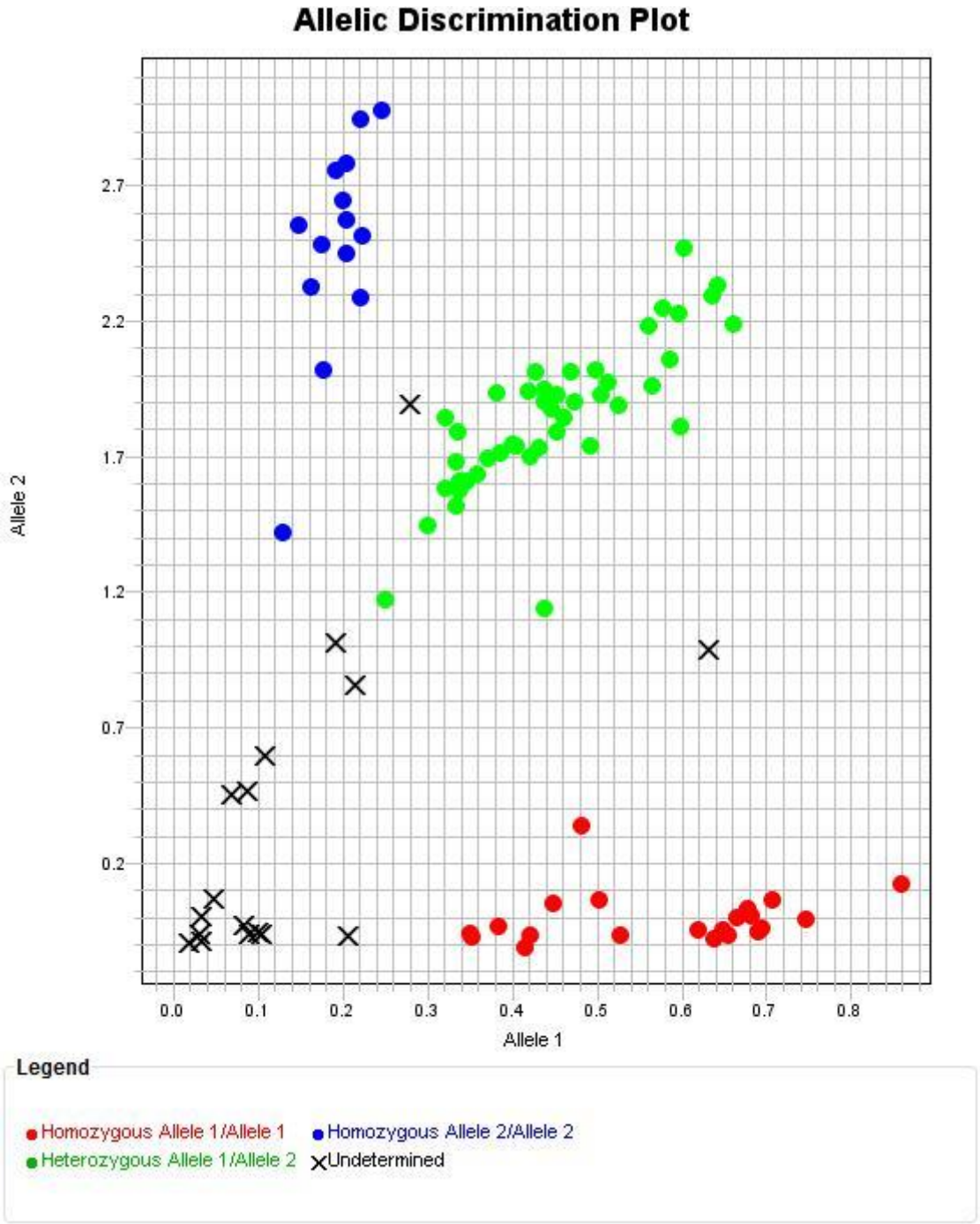

Figure A17: Allelic discrimination plot to attain informative samples for SNP marker 11_10515 using PT-13, plate 8 group. Allele 1/1 corresponds to the Morex allele and allele 2/2 corresponds to the BW248 allele.

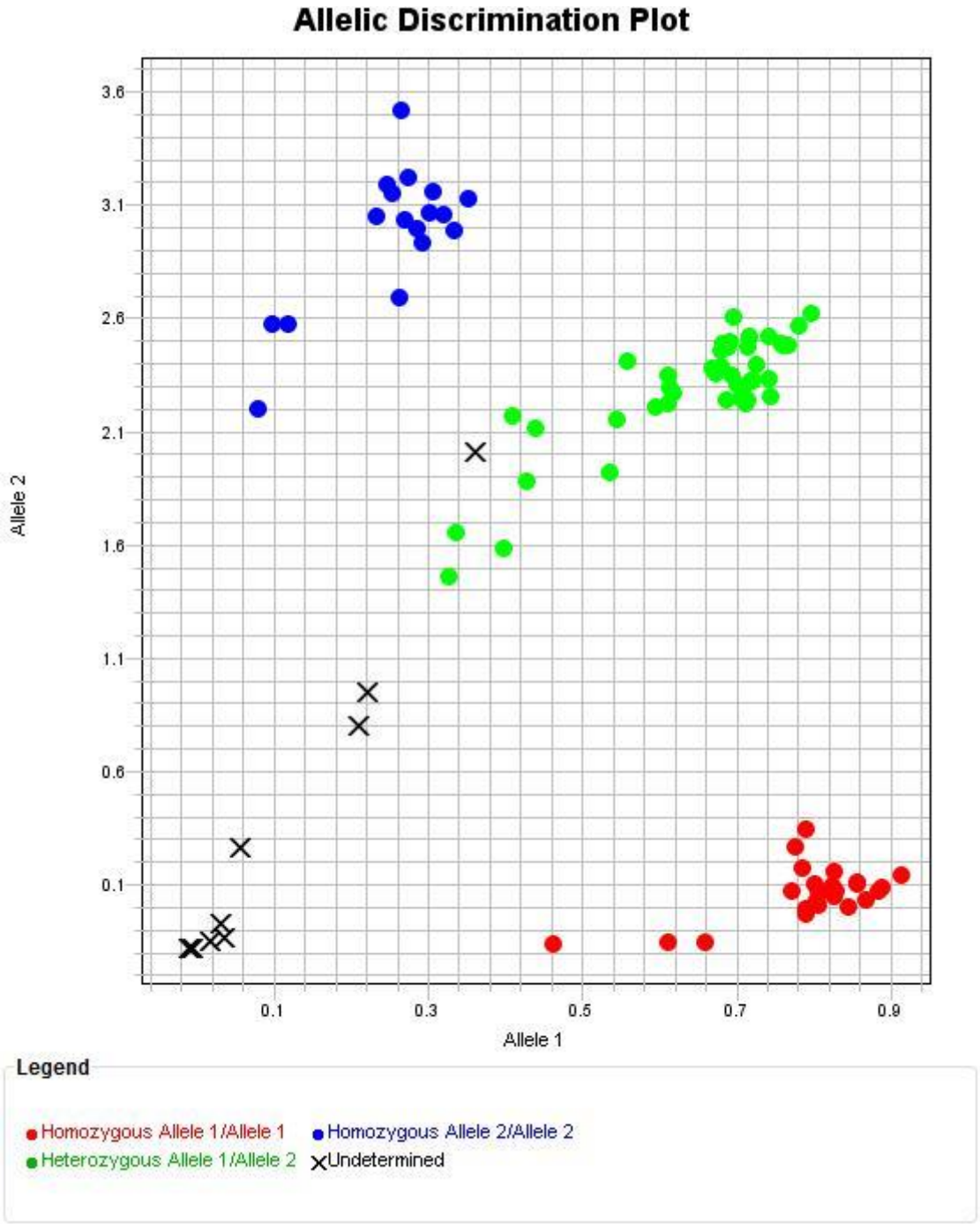

Figure A18: Allelic discrimination plot to attain informative samples for SNP marker 11_10515 using PT-13, plate 9 group. Allele 1/1 corresponds to the Morex allele and allele 2/2 corresponds to the BW248 allele.

Table A178: Raw data showing the relationship between the genotype and the phenotype (fertility) gained using a KASPar® for the markers LOC_Os 01g60230 (11_20659) and 11_10515 which flanked the 10cM *des8* region (78 showed recombination between these two SNP markers of which 48 were informative (involving a recombinant between a SNP homozygous for the BW248 and another heterozygous). Any cases in which the genotype was undetermined was due to the failure of seed germination of a particular member of the *des8* family (refer to 96-well plate reference Figures A6 to A8), or due to a lack of DNA in the wells.

Index	Plate	Well	Sample	LOC_Os1g64170 des8_11_10515	des8_LOC_Os01g60230	Phenotype	Row	Informatives
001	PT13_1	A1	147_07_101_1	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	2	
002	PT13_1	A2	147_07_101_2	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	1
003	PT13_1	A3	147_07_101_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
004	PT13_1	A4	147_07_104_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
005	PT13_1	A5	147_07_104_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
006	PT13_1	A6	147_07_104_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	int	
007	PT13_1	A7	147_07_107_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
008	PT13_1	A8	147_07_107_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
009	PT13_1	A9	147_07_107_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
010	PT13_1	A10	147_07_110_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
011	PT13_1	A11	147_07_110_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
012	PT13_1	A12	147_07_110_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
013	PT13_1	B1	147_07_113_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
014	PT13_1	B2	147_07_113_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	SS	2	2
015	PT13_1	B3	147_07_113_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
016	PT13_1	B4	147_07_116_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
017	PT13_1	B5	147_07_116_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
018	PT13_1	B6	147_07_116_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	

019	PT13_1	B7	147_07_119_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S?	6	
020	PT13_1	B8	147_07_119_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
021	PT13_1	B9	147_07_119_3	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	3
022	PT13_1	B10	147_07_122_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
023	PT13_1	B11	147_07_122_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
024	PT13_1	B12	147_07_122_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
025	PT13_1	C1	147_11_101_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
026	PT13_1	C2	147_11_101_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
027	PT13_1	C3	147_11_101_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
028	PT13_1	C4	147_11_104_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
029	PT13_1	C5	147_11_104_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
030	PT13_1	C6	147_11_104_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	?	4
031	PT13_1	C7	147_11_107_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
032	PT13_1	C8	147_11_107_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
033	PT13_1	C9	147_11_107_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
034	PT13_1	C10	147_11_110_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
035	PT13_1	C11	147_11_110_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
036	PT13_1	C12	147_11_110_3	Homozygous Allele 1/Allele 1	Undetermined	Fertile	?	
037	PT13_1	D1	147_11_113_1	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	5
038	PT13_1	D2	147_11_113_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
039	PT13_1	D3	147_11_113_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	6
040	PT13_1	D4	147_11_116_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
041	PT13_1	D5	147_11_116_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
042	PT13_1	D6	147_11_116_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
043	PT13_1	D7	147_11_119_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
044	PT13_1	D8	147_11_119_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
045	PT13_1	D9	147_11_119_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	6	7
046	PT13_1	D10	147_11_122_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
047	PT13_1	D11	147_11_122_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
048	PT13_1	D12	147_11_122_3	Undetermined	Undetermined	Fertile	?	
049	PT13_1	E1	147_02_101_1	Heterozygous Allele	Heterozygous Allele 1/Allele	Fertile	6	

050	PT13_1	E2	147_02_101_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	SS?	6	
051	PT13_1	E3	147_02_101_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
052	PT13_1	E4	147_02_104_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
053	PT13_1	E5	147_02_104_2	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS	6	8
054	PT13_1	E6	147_02_104_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
055	PT13_1	E7	147_02_107_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
056	PT13_1	E8	147_02_107_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
057	PT13_1	E9	147_02_107_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	2	
058	PT13_1	E10	147_02_110_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
059	PT13_1	E11	147_02_110_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
060	PT13_1	E12	147_02_110_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	SS	2	
061	PT13_1	F1	147_02_113_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
062	PT13_1	F2	147_02_113_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
063	PT13_1	F3	147_02_113_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
064	PT13_1	F4	147_02_116_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
065	PT13_1	F5	147_02_116_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
066	PT13_1	F6	147_02_116_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	9
067	PT13_1	F7	147_02_119_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
068	PT13_1	F8	147_02_119_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
069	PT13_1	F9	147_02_119_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
070	PT13_1	F10	147_02_122_1	Undetermined	Homozygous Allele 2/Allele 2	Fertile	6	
071	PT13_1	F11	147_02_122_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
072	PT13_1	F12	147_02_122_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	SS	6	10
073	PT13_1	G1	147_02_125_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	11
074	PT13_1	G2	147_02_125_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	2	
075	PT13_1	G3	147_02_125_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
076	PT13_1	G4	147_02_128_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
077	PT13_1	G5	147_02_128_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
078	PT13_1	G6	147_02_128_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
079	PT13_1	G7	147_02_131_1	Heterozygous Allele	Heterozygous Allele 1/Allele	Fertile	2	

				1/Allele 2	2			
080	PT13_1	G8	147_02_131_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
081	PT13_1	G9	147_02_131_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
082	PT13_1	G10	147_02_134_1	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS	6	12
083	PT13_1	G11	147_02_134_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
084	PT13_1	G12	147_02_134_3	Undetermined	Undetermined	Fertile	2	
085	PT13_1	H1	147_02_137_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
086	PT13_1	H2	147_02_137_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
087	PT13_1	H3	147_02_137_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	13
088	PT13_1	H4	147_02_140_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
089	PT13_1	H5	147_02_140_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
090	PT13_1	H6	147_02_140_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
091	PT13_1	H7	147_02_143_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
092	PT13_1	H8	147_02_143_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
093	PT13_1	H9	147_02_143_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
094	PT13_1	H10	147_02_146_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
095	PT13_1	H11	147_02_146_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	14
096	PT13_1	H12	147_02_146_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
097	PT13_2	A1	147_03_101_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
098	PT13_2	A2	147_03_101_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
099	PT13_2	A3	147_03_101_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
100	PT13_2	A4	147_03_104_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
101	PT13_2	A5	147_03_104_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
102	PT13_2	A6	147_03_104_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
103	PT13_2	A7	147_03_107_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
104	PT13_2	A8	147_03_107_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
105	PT13_2	A9	147_03_107_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	6	15
106	PT13_2	A10	147_03_110_1	Undetermined	Undetermined	Fertile	2	
107	PT13_2	A11	147_03_110_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
108	PT13_2	A12	147_03_110_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
109	PT13_2	B1	147_03_113_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
110	PT13_2	B2	147_03_113_2	Heterozygous Allele	Heterozygous Allele 1/Allele	Fertile	2	

				1/Allele 2	2			
111	PT13_2	B3	147_03_113_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
112	PT13_2	B4	147_03_116_1	Homozygous Allele 1/Allele 1	Undetermined	Fertile	6	
113	PT13_2	B5	147_03_116_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
114	PT13_2	B6	147_03_116_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	6	16
115	PT13_2	B7	147_03_119_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
116	PT13_2	B8	147_03_119_2	Undetermined	Undetermined	Fertile		
117	PT13_2	B9	147_03_119_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
118	PT13_2	B10	147_03_122_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	6	17
119	PT13_2	B11	147_03_122_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
120	PT13_2	B12	147_03_122_3	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	18
121	PT13_2	C1	147_04_101_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
122	PT13_2	C2	147_04_101_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
123	PT13_2	C3	147_04_101_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
124	PT13_2	C4	147_04_104_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	19
125	PT13_2	C5	147_04_104_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS?	?	
126	PT13_2	C6	147_04_104_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	20
127	PT13_2	C7	147_04_107_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
128	PT13_2	C8	147_04_107_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS?	2	
129	PT13_2	C9	147_04_107_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
130	PT13_2	C10	147_04_110_1	Heterozygous Allele 1/Allele 2	Undetermined	Fertile	6	
131	PT13_2	C11	147_04_110_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
132	PT13_2	C12	147_04_110_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS?	6	
133	PT13_2	D1	147_04_113_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
134	PT13_2	D2	147_04_113_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
135	PT13_2	D3	147_04_113_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
136	PT13_2	D4	147_04_116_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS?	6	
137	PT13_2	D5	147_04_116_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	2	21
138	PT13_2	D6	147_04_116_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	22
139	PT13_2	D7	147_04_119_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
140	PT13_2	D8	147_04_119_2	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	23

141	PT13_2	D9	147_04_119_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
142	PT13_2	D10	147_04_122_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
143	PT13_2	D11	147_04_122_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
144	PT13_2	D12	147_04_122_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
145	PT13_2	E1	147_06_101_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	SS?	6	
146	PT13_2	E2	147_06_101_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	SS?	6	24
147	PT13_2	E3	147_06_101_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	?	6	25
148	PT13_2	E4	147_06_104_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
149	PT13_2	E5	147_06_104_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
150	PT13_2	E6	147_06_104_3	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS	?	26
151	PT13_2	E7	147_06_107_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	2	
152	PT13_2	E8	147_06_107_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
153	PT13_2	E9	147_06_107_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
154	PT13_2	E10	147_06_110_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
155	PT13_2	E11	147_06_110_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
156	PT13_2	E12	147_06_110_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
157	PT13_2	F1	147_06_113_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
158	PT13_2	F2	147_06_113_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
159	PT13_2	F3	147_06_113_3	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	2	
160	PT13_2	F4	147_06_116_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
161	PT13_2	F5	147_06_116_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
162	PT13_2	F6	147_06_116_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	27
163	PT13_2	F7	147_06_119_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
164	PT13_2	F8	147_06_119_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
165	PT13_2	F9	147_06_119_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
166	PT13_2	F10	147_06_122_1	Undetermined	Undetermined	Fertile	2	
167	PT13_2	F11	147_06_122_2	Undetermined	Undetermined	Fertile	2	
168	PT13_2	F12	147_06_122_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
169	PT13_2	G1	147_06_125_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
170	PT13_2	G2	147_06_125_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
171	PT13_2	G3	147_06_125_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	

172	PT13_2	G4	147_06_128_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	?	
173	PT13_2	G5	147_06_128_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
174	PT13_2	G6	147_06_128_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
175	PT13_2	G7	147_06_131_1	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	2	
176	PT13_2	G8	147_06_131_2	Homozygous Allele 1/Allele 1	Undetermined	Fertile	2	
177	PT13_2	G9	147_06_131_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
178	PT13_2	G10	147_06_134_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	2	
179	PT13_2	G11	147_06_134_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	28
180	PT13_2	G12	147_06_134_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
181	PT13_2	H1	147_06_137_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
182	PT13_2	H2	147_06_137_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	2	
183	PT13_2	H3	147_06_137_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
184	PT13_2	H4	147_06_140_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	29
185	PT13_2	H5	147_06_140_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
186	PT13_2	H6	147_06_140_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
187	PT13_2	H7	147_06_143_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	30
188	PT13_2	H8	147_06_143_2	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	2	
189	PT13_2	H9	147_06_143_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
190	PT13_2	H10	147_06_146_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
191	PT13_2	H11	147_06_146_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
192	PT13_2	H12	147_06_146_3	Undetermined	Undetermined	Fertile	2	
193	PT13_4	A1	147_09_101_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
194	PT13_4	A2	147_09_101_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	SS	2	31
195	PT13_4	A3	147_09_101_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
196	PT13_4	A4	147_09_104_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
197	PT13_4	A5	147_09_104_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
198	PT13_4	A6	147_09_104_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1		2	
199	PT13_4	A7	147_09_107_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1		2	
200	PT13_4	A8	147_09_107_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
201	PT13_4	A9	147_09_107_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
202	PT13_4	A10	147_09_110_1	Heterozygous Allele	Heterozygous Allele 1/Allele	Fertile	2	

				1/Allele 2	2			
203	PT13_4	A11	147_09_110_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
204	PT13_4	A12	147_09_110_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
205	PT13_4	B1	147_09_113_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
206	PT13_4	B2	147_09_113_2	Undetermined	Undetermined			
207	PT13_4	B3	147_09_113_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
208	PT13_4	B4	147_09_116_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
209	PT13_4	B5	147_09_116_2	Undetermined	Undetermined			
210	PT13_4	B6	147_09_116_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
211	PT13_4	B7	147_09_119_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
212	PT13_4	B8	147_09_119_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
213	PT13_4	B9	147_09_119_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
214	PT13_4	B10	147_09_122_1	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS	2	32
215	PT13_4	B11	147_09_122_2	Undetermined	Homozygous Allele 2/Allele 2	Fertile	2	
216	PT13_4	B12	147_09_122_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
217	PT13_4	C1	147_09_125_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
218	PT13_4	C2	147_09_125_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
219	PT13_4	C3	147_09_125_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
220	PT13_4	C4	147_09_128_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
221	PT13_4	C5	147_09_128_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
222	PT13_4	C6	147_09_128_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	33
223	PT13_4	C7	147_09_131_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
224	PT13_4	C8	147_09_131_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
225	PT13_4	C9	147_09_131_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
226	PT13_4	C10	147_09_134_1	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	6	
227	PT13_4	C11	147_09_134_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
228	PT13_4	C12	147_09_134_3	Undetermined	Undetermined			
229	PT13_4	D1	147_09_137_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
230	PT13_4	D2	147_09_137_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
231	PT13_4	D3	147_09_137_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
232	PT13_4	D4	147_09_140_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
233	PT13_4	D5	147_09_140_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	

234	PT13_4	D6	147_09_140_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
235	PT13_4	D7	147_09_143_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	?	
236	PT13_4	D8	147_09_143_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
237	PT13_4	D9	147_09_143_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	?	34
238	PT13_4	D10	147_09_146_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	35
239	PT13_4	D11	147_09_146_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
240	PT13_4	D12	147_09_146_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	?	
241	PT13_4	E1	147_09_149_1	Undetermined	Undetermined			
242	PT13_4	E2	147_09_149_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
243	PT13_4	E3	147_09_149_3	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS	2	36
244	PT13_4	E4	147_09_152_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
245	PT13_4	E5	147_09_152_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	6	37
246	PT13_4	E6	147_09_152_3	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS	6	38
247	PT13_4	E7	147_09_155_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
248	PT13_4	E8	147_09_155_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
249	PT13_4	E9	147_09_155_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
250	PT13_4	E10	147_09_158_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
251	PT13_4	E11	147_09_158_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
252	PT13_4	E12	147_09_158_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
253	PT13_4	F1	147_09_161_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
254	PT13_4	F2	147_09_161_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
255	PT13_4	F3	147_09_161_3	Undetermined	Undetermined			
256	PT13_4	F4	147_09_164_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
257	PT13_4	F5	147_09_164_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
258	PT13_4	F6	147_09_164_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
259	PT13_4	F7	147_09_167_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	Fertile	6	
260	PT13_4	F8	147_09_167_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
261	PT13_4	F9	147_09_167_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
262	PT13_4	F10	147_09_170_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2		2	
263	PT13_4	F11	147_09_170_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
264	PT13_4	F12	147_09_170_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	SS	6	39

265	PT13_4	G1	147_09_173_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	SS	6	40
266	PT13_4	G2	147_09_173_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
267	PT13_4	G3	147_09_173_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	?	
268	PT13_4	G4	147_09_176_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
269	PT13_4	G5	147_09_176_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
270	PT13_4	G6	147_09_176_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
271	PT13_4	G7	147_09_179_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
272	PT13_4	G8	147_09_179_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	?	
273	PT13_4	G9	147_09_179_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
274	PT13_4	G10	147_09_182_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
275	PT13_4	G11	147_09_182_2	Homozygous Allele 2/Allele 2	Undetermined	SS	?	
276	PT13_4	G12	147_09_182_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	6	41
277	PT13_4	H1	147_09_185_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	42
278	PT13_4	H2	147_09_185_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	43
279	PT13_4	H3	147_09_185_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
280	PT13_4	H4	147_09_188_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
281	PT13_4	H5	147_09_188_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	6	44
282	PT13_4	H6	147_09_188_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
283	PT13_4	H7	147_09_191_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	6	45
284	PT13_4	H8	147_09_191_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS?	6	
285	PT13_4	H9	147_09_191_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
286	PT13_4	H10	147_09_194_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	?	2	
287	PT13_4	H11	147_09_194_2	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS?	?	46
288	PT13_4	H12	147_09_194_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
289	PT13_8	A1	147_14_101_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
290	PT13_8	A2	147_14_101_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
291	PT13_8	A3	147_14_101_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
292	PT13_8	A4	147_14_104_1	Undetermined	Undetermined			
293	PT13_8	A5	147_14_104_2	Undetermined	Undetermined			
294	PT13_8	A6	147_14_104_3	Undetermined	Undetermined			
295	PT13_8	A7	147_14_107_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
296	PT13_8	A8	147_14_107_2	Homozygous Allele	Homozygous Allele 1/Allele	SS	?	

				2/Allele 2	1			
297	PT13_8	A9	147_14_107_3	Homozygous Allele 1/Allele 1	Undetermined	Fertile	?	
298	PT13_8	A10	147_14_110_1	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	2	
299	PT13_8	A11	147_14_110_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
300	PT13_8	A12	147_14_110_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
301	PT13_8	B1	147_14_113_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	47
302	PT13_8	B2	147_14_113_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
303	PT13_8	B3	147_14_113_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
304	PT13_8	B4	147_14_116_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
305	PT13_8	B5	147_14_116_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	2	48
306	PT13_8	B6	147_14_116_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
307	PT13_8	B7	147_14_119_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
308	PT13_8	B8	147_14_119_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
309	PT13_8	B9	147_14_119_3	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	2	
310	PT13_8	B10	147_14_122_1	Undetermined	Homozygous Allele 1/Allele 1		?	
311	PT13_8	B11	147_14_122_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
312	PT13_8	B12	147_14_122_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
313	PT13_8	C1	147_14_125_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
314	PT13_8	C2	147_14_125_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
315	PT13_8	C3	147_14_125_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	Fertile	6	
316	PT13_8	C4	147_14_128_1	Undetermined	Undetermined			
317	PT13_8	C5	147_14_128_2	Undetermined	Homozygous Allele 1/Allele 1	SS	2	
318	PT13_8	C6	147_14_128_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
319	PT13_8	C7	147_14_131_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	6	
320	PT13_8	C8	147_14_131_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	6	
321	PT13_8	C9	147_14_131_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
322	PT13_8	C10	147_14_134_1	Undetermined	Undetermined			
323	PT13_8	C11	147_14_134_2	Heterozygous Allele 1/Allele 2	Undetermined	?	?	
324	PT13_8	C12	147_14_134_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
325	PT13_8	D1	147_14_137_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	6	
326	PT13_8	D2	147_14_137_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
327	PT13_8	D3	147_14_137_3	Homozygous Allele	Homozygous Allele 1/Allele	SS?	6	

				2/Allele 2	1			
328	PT13_8	D4	147_14_140_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
329	PT13_8	D5	147_14_140_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	?	
330	PT13_8	D6	147_14_140_3	Undetermined	Heterozygous Allele 1/Allele 2	Fertile	?	
331	PT13_8	D7	147_14_143_1	Undetermined	Undetermined			
332	PT13_8	D8	147_14_143_2	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	SS?	6	49
333	PT13_8	D9	147_14_143_3	Undetermined	Undetermined			
334	PT13_8	D10	147_14_146_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
335	PT13_8	D11	147_14_146_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
336	PT13_8	D12	147_14_146_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
337	PT13_8	E1	147_14_149_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
338	PT13_8	E2	147_14_149_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
339	PT13_8	E3	147_14_149_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
340	PT13_8	E4	147_14_152_1	Undetermined	Homozygous Allele 2/Allele 2	Fertile	?	
341	PT13_8	E5	147_14_152_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
342	PT13_8	E6	147_14_152_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
343	PT13_8	E7	147_14_155_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
344	PT13_8	E8	147_14_155_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
345	PT13_8	E9	147_14_155_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
346	PT13_8	E10	147_14_158_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
347	PT13_8	E11	147_14_158_2	Homozygous Allele 1/Allele 1	Undetermined	Fertile	?	
348	PT13_8	E12	147_14_158_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S?	?	
349	PT13_8	F1	147_14_161_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	Fertile	?	
350	PT13_8	F2	147_14_161_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
351	PT13_8	F3	147_14_161_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	?	50
352	PT13_8	F4	147_14_164_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
353	PT13_8	F5	147_14_164_2	Undetermined	Undetermined	Fertile	6	
354	PT13_8	F6	147_14_164_3	Undetermined	Undetermined	Fertile	6	
355	PT13_8	F7	147_14_167_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
356	PT13_8	F8	147_14_167_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
357	PT13_8	F9	147_14_167_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	2	51
358	PT13_8	F10	147_14_170_1	Undetermined	Undetermined	Fertile	?	
359	PT13_8	F11	147_14_170_2	Undetermined	Undetermined	SS	6	

360	PT13_8	F12	147_14_170_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
361	PT13_8	G1	147_14_173_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	?	52
362	PT13_8	G2	147_14_173_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
363	PT13_8	G3	147_14_173_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
364	PT13_8	G4	147_14_176_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
365	PT13_8	G5	147_14_176_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
366	PT13_8	G6	147_14_176_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
367	PT13_8	G7	147_14_179_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	6	53
368	PT13_8	G8	147_14_179_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	?	
369	PT13_8	G9	147_14_179_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	2	54
370	PT13_8	G10	147_14_182_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
371	PT13_8	G11	147_14_182_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
372	PT13_8	G12	147_14_182_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
373	PT13_8	H1	147_14_185_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
374	PT13_8	H2	147_14_185_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	SS	2	
375	PT13_8	H3	147_14_185_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
376	PT13_8	H4	147_14_188_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	55
377	PT13_8	H5	147_14_188_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
378	PT13_8	H6	147_14_188_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
379	PT13_8	H7	147_14_191_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
380	PT13_8	H8	147_14_191_2	Homozygous Allele 2/Allele 2	Undetermined	SS	6	
381	PT13_8	H9	147_14_191_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
382	PT13_8	H10	147_14_194_1	Homozygous Allele 2/Allele 2	Undetermined	SS	2	
383	PT13_8	H11	147_14_194_2	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
384	PT13_8	H12	147_14_194_3	Homozygous Allele 2/Allele 2	Undetermined	S	2	
385	PT13_9	A1	147_15_101_1	Undetermined	Undetermined			
386	PT13_9	A2	147_15_101_2	Undetermined	Undetermined			
387	PT13_9	A3	147_15_101_3	Undetermined	Undetermined			
388	PT13_9	A4	147_15_104_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	56
389	PT13_9	A5	147_15_104_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	int	
390	PT13_9	A6	147_15_104_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	57
391	PT13_9	A7	147_15_107_1	Homozygous Allele	Homozygous Allele 1/Allele	Fertile	2	58

				1/Allele 1	1			
392	PT13_9	A8	147_15_107_2	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	6	59
393	PT13_9	A9	147_15_107_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	60
394	PT13_9	A10	147_15_110_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	61
395	PT13_9	A11	147_15_110_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	62
396	PT13_9	A12	147_15_110_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	int?	
397	PT13_9	B1	147_15_113_1	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	int	
398	PT13_9	B2	147_15_113_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	int	63
399	PT13_9	B3	147_15_113_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
400	PT13_9	B4	147_15_116_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
401	PT13_9	B5	147_15_116_2	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	S	6	64
402	PT13_9	B6	147_15_116_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	int?	
403	PT13_9	B7	147_15_119_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	int	
404	PT13_9	B8	147_15_119_2	Undetermined	Undetermined	Fertile	2	
405	PT13_9	B9	147_15_119_3	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	65
406	PT13_9	B10	147_15_122_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	?	
407	PT13_9	B11	147_15_122_2	Undetermined	Undetermined	Fertile	2	
408	PT13_9	B12	147_15_122_3	Homozygous Allele 1/Allele 1	Homozygous Allele 2/Allele 2	Fertile	2	
409	PT13_9	C1	147_15_125_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
410	PT13_9	C2	147_15_125_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	int	66
411	PT13_9	C3	147_15_125_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
412	PT13_9	C4	147_15_128_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
413	PT13_9	C5	147_15_128_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
414	PT13_9	C6	147_15_128_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
415	PT13_9	C7	147_15_131_1	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	67
416	PT13_9	C8	147_15_131_2	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	Fertile	2	68
417	PT13_9	C9	147_15_131_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	69
418	PT13_9	C10	147_15_134_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2		?	70
419	PT13_9	C11	147_15_134_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
420	PT13_9	C12	147_15_134_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	2	
421	PT13_9	D1	147_15_137_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	int	
422	PT13_9	D2	147_15_137_2	Heterozygous Allele	Homozygous Allele 2/Allele	Fertile	6	71

				1/Allele 2	2			
423	PT13_9	D3	147_15_137_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	72
424	PT13_9	D4	147_15_140_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	73
425	PT13_9	D5	147_15_140_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	74
426	PT13_9	D6	147_15_140_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
427	PT13_9	D7	147_15_143_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	75
428	PT13_9	D8	147_15_143_2	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2	S?	int?	76
429	PT13_9	D9	147_15_143_3	Heterozygous Allele 1/Allele 2	Undetermined	Fertile	2	
430	PT13_9	D10	147_15_146_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	6	
431	PT13_9	D11	147_15_146_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	77
432	PT13_9	D12	147_15_146_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
433	PT13_9	E1	147_08_101_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
434	PT13_9	E2	147_08_101_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
435	PT13_9	E3	147_08_101_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
436	PT13_9	E4	147_08_104_1	Undetermined	Undetermined			
437	PT13_9	E5	147_08_104_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
438	PT13_9	E6	147_08_104_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
439	PT13_9	E7	147_08_107_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	
440	PT13_9	E8	147_08_107_2	Undetermined	Undetermined			
441	PT13_9	E9	147_08_107_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
442	PT13_9	E10	147_08_110_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	S	int?	
443	PT13_9	E11	147_08_110_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	int?	
444	PT13_9	E12	147_08_110_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
445	PT13_9	F1	147_08_113_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	int?	
446	PT13_9	F2	147_08_113_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	
447	PT13_9	F3	147_08_113_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2	
448	PT13_9	F4	147_08_116_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	
449	PT13_9	F5	147_08_116_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
450	PT13_9	F6	147_08_116_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
451	PT13_9	F7	147_08_119_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2	
452	PT13_9	F8	147_08_119_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2	
453	PT13_9	F9	147_08_119_3	Heterozygous Allele	Homozygous Allele 1/Allele	Fertile	2	

				1/Allele 2	1		
454	PT13_9	F10	147_08_122_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
455	PT13_9	F11	147_08_122_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
456	PT13_9	F12	147_08_122_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
457	PT13_9	G1	147_08_125_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
458	PT13_9	G2	147_08_125_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
459	PT13_9	G3	147_08_125_3	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	int?
460	PT13_9	G4	147_08_128_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
461	PT13_9	G5	147_08_128_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
462	PT13_9	G6	147_08_128_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
463	PT13_9	G7	147_08_131_1	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
464	PT13_9	G8	147_08_131_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
465	PT13_9	G9	147_08_131_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
466	PT13_9	G10	147_08_134_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	SS	2
467	PT13_9	G11	147_08_134_2	Undetermined	Undetermined		
468	PT13_9	G12	147_08_134_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
469	PT13_9	H1	147_08_137_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
470	PT13_9	H2	147_08_137_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
471	PT13_9	H3	147_08_137_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
472	PT13_9	H4	147_08_140_1	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
473	PT13_9	H5	147_08_140_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
474	PT13_9	H6	147_08_140_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
475	PT13_9	H7	147_08_143_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
476	PT13_9	H8	147_08_143_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	Fertile	2
477	PT13_9	H9	147_08_143_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
478	PT13_9	H10	147_08_146_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	2
479	PT13_9	H11	147_08_146_2	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1	SS	2
480	PT13_9	H12	147_08_146_3	Undetermined	Homozygous Allele 1/Allele 1	Fertile	2

Raw data representing the relationship of the genotype with the phenotype using only the informative individuals for further KASPar® assays and Big Dye v3.1 sequencing (previous data for the dermination of the informative individuals is also included).

Table A179: Raw data representing the relationship of the genotype with the phenotype using only the informative individuals for further KASPar® assays and Big Dye v3.1 sequencing, to delineate *des8* to a sub-cM interval (previous data for the dermination of the informative individuals is also included). All DNA pertaining to the informative individuals was removed (and stored at -20°C) from the first set of 96-well plates (Figures A6 to A8). This informative DNA was sampled and pooled into a single 96-well plate for the remaining markers 11_20628 and 11_10747 (one plate per marker) for further KASPar® assays, including Big Dye v3.1 sequencing of the markers MLOC 10987, MLOC 4841 and MLOC 53985 (one plate per marker). The new 96-well plate references (which well was used) are shown in the table (the old well references from the pilot (determination of the informative individuals) KASPar® assay are also shown).

				LOC_Os01g60230	LOC_Os01g60440	LOC_Os1g60900	LOC_Os1g65320	LOC_Os1g65050	*des8*	LOC_Os01g64770	LOC_Os1g64170
Plate	Old plate ref	New plate ref	Sample	des8_LOC_Os01g60230	des8_LOC_Os01g60440	MLOC4841_R01	MLOC_53985_R01	MLOC_10987_R02	Phenotype	des8_11_20628	des8_11_10515
PT13_1	E5	H01	147_02_104_2	Heterozygous Allele 1/Allele 2	Undetermined	A/G	G	C	SS	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_1	F6	A02	147_02_116_3	Homozygous Allele 1/Allele 1	Undetermined	G	G/T	C/G	Fertile	Undetermined	Heterozygous Allele 1/Allele 2
PT13_1	F12	B02	147_02_122_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G?	C	SS	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_1	G1	C02	147_02_125_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G/T	C	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_1	G10	D02	147_02_134_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	G	Undetermined	C	SS	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_1	H11	F02	147_02_146_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_2	A9	G02	147_03_107_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	A/G	T	G	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_2	B6	H02	147_03_116_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G/T	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_2	B12	B03	147_03_122_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	A/G	G/T?	C/G	Fertile	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2
PT13_2	E2	H03	147_06_101_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G/T	C/G	SS?	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_2	E6	B04	147_06_104_3	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	G	G/T?	C	SS	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2

PT13_2	G11	D04	147_06_134_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	Undetermined	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_2	H4	E04	147_06_140_1	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2	A/G	G/T	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_1	B2	B01	147_07_113_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G?	C	SS	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_1	B9	C01	147_07_119_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	A/G	G/T?	C/G	Fertile	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_9	E1	F10	147_08_101_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	A/G	G	C/G (I think thi sis C)	Fertile	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_4	A2	G04	147_09_101_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G	C	SS	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_4	B10	H04	147_09_122_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	G	G	C	SS	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_4	E3	D05	147_09_149_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	G	Undetermined	C	SS	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_4	E6	F05	147_09_152_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	A/G	G	C	SS	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_4	F12	G05	147_09_170_3	Homozygous Allele 1/Allele 1	Undetermined	G	G	C	SS	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_4	G1	H05	147_09_173_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Undetermined	T	G	SS?	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_4	H2	C06	147_09_185_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	G/T	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_4	H5	D06	147_09_188_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	A/G	Undetermined	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_4	H7	E06	147_09_191_1	Homozygous Allele 1/Allele 1	Undetermined	Undetermined	Undetermined	Undetermined	Fertile	Undetermined	Heterozygous Allele 1/Allele 2
PT13_4	H11	F06	147_09_194_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	A?HET?	G	C	SS?	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_1	C6	D01	147_11_104_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	G	Undetermined	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_1	D1	E01	147_11_113_1	Heterozygous Allele 1/Allele 2	Undetermined	A/G	Undetermined	C/G	Fertile	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2
PT13_1	D3	F01	147_11_113_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	A	T?	G	Fertile	Undetermined	Homozygous Allele 1/Allele 1
PT13_1	D9	G01	147_11_119_3	Homozygous Allele 1/Allele 1	Undetermined	G	G?T	C/G	Fertile	Undetermined	Heterozygous Allele 1/Allele 2
PT13_8	D8	A07	147_14_143_2	Heterozygous Allele 1/Allele 2	Undetermined	A/G	G/T?	C/G	SS?	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_8	G1	D07	147_14_173_1	Homozygous Allele 1/Allele 1	Undetermined	A/G	Undetermined	C/G	Fertile	Undetermined	Heterozygous Allele 1/Allele 2
PT13_8	G7	E07	147_14_179_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	A/G	G/T	C/G	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_8	G9	F07	147_14_179_3	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2				Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_8	H4	G07	147_14_188_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2				Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1

PT13_1	H3	E02	147_02_137_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_2	B10	A03	147_03_122_1	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_2	C4	C03	147_04_104_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_2	C6	D03	147_04_104_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1
PT13_2	D5	E03	147_04_116_2	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_2	D6	F03	147_04_116_3	Heterozygous Allele 1/Allele 2	Undetermined	Fertile	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1
PT13_2	D8	G03	147_04_119_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_2	E3	A04	147_06_101_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	?	Undetermined	Homozygous Allele 1/Allele 1
PT13_2	F6	C04	147_06_116_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1
PT13_2	H7	F04	147_06_143_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1
PT13_1	A2	A01	147_07_101_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_4	C6	A05	147_09_128_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_4	D9	B05	147_09_143_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_4	D10	C05	147_09_146_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_4	E5	E05	147_09_152_2	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_4	G12	A06	147_09_182_3	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_4	H1	B06	147_09_185_1	Heterozygous Allele 1/Allele 2	Undetermined	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_8	F3	B07	147_14_161_3	Heterozygous Allele 1/Allele 2	Undetermined	Fertile	Undetermined	Homozygous Allele 1/Allele 1
PT13_8	F9	C07	147_14_167_3	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_9	A4	H07	147_15_104_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Undetermined	Heterozygous Allele 1/Allele 2
PT13_9	A6	A08	147_15_104_3	Heterozygous Allele 1/Allele 2	Undetermined	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_9	A7	B08	147_15_107_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1
PT13_9	A8	C08	147_15_107_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1

PT13_9	A9	D08	147_15_107_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_9	A10	E08	147_15_110_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1
PT13_9	A11	F08	147_15_110_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1
PT13_9	B2	G08	147_15_113_2	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2
PT13_9	B5	H08	147_15_116_2	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	S	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_9	B9	A09	147_15_119_3	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_9	C2	B09	147_15_125_2	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2
PT13_9	C7	C09	147_15_131_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Heterozygous Allele 1/Allele 2	Homozygous Allele 2/Allele 2
PT13_9	C8	D09	147_15_131_2	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_9	C9	E09	147_15_131_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1
PT13_9	C10	F09	147_15_134_1	Heterozygous Allele 1/Allele 2	Heterozygous Allele 1/Allele 2		Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1
PT13_9	D2	G09	147_15_137_2	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2	Fertile	Homozygous Allele 1/Allele 1	Heterozygous Allele 1/Allele 2
PT13_9	D3	H09	147_15_137_3	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_9	D4	A10	147_15_140_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Homozygous Allele 1/Allele 1
PT13_9	D5	B10	147_15_140_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_9	D7	C10	147_15_143_1	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2
PT13_9	D8	D10	147_15_143_2	Heterozygous Allele 1/Allele 2	Homozygous Allele 1/Allele 1	S?	Homozygous Allele 2/Allele 2	Homozygous Allele 2/Allele 2
PT13_9	D11	E10	147_15_146_2	Homozygous Allele 1/Allele 1	Homozygous Allele 1/Allele 1	Fertile	Homozygous Allele 2/Allele 2	Heterozygous Allele 1/Allele 2

Meetings and conferences attended

Biosciences Graduate Research School. Student Symposium. 14th to 15th April, 2014.

British meiosis meeting, Edinburgh. 24th and 25th March, 2014. "Can we use the chromatin modifying chemical trichostatin A to influence crossover distribution and frequency in barley?"

Abstract:

Can we use the chromatin modifying chemical trichostatin A to influence crossover distribution and frequency in barley?

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In barley, meiotic crossover (CO) distribution is skewed to the distal regions of the paired chromosomes. This restricts recombination to these regions thereby reducing the potential genetic variation that can be exploited in plant breeding programmes. The aim of this project is to develop experimental strategies that will enable the frequency and distribution of meiotic crossovers to be modified.

One potential route to modifying crossover distribution and frequency is through the use of chemicals that may alter chromatin organisation. Recently, we showed that an Arabidopsis line MCC1, which over-expresses a GCN5-related histone acetylase, exhibited an alteration in CO distribution relative to wild-type plants (Perella *et al*., 2010). This effect could be phenocopied with the histone deacetylase inhibitor trichostatin A. This suggested a potential route to modify recombination in barley.

Preliminary studies were carried out to develop a procedure that would enable inhibitors to be administered at the appropriate developmental stage via the transpiration stream. As the first step, meiotic chromosome spreads were prepared from anthers at sequential developmental stages. This enabled a correlation between anther length and meiotic sub-stage to be established. In order to develop a protocol to effectively deliver chemicals to the meiocytes via the transpiration stream, the thymidine analogue bromodeoxyuridine (BrdU) was injected into anthers at the appropriate stage. This enabled a meiotic time course to be established, as BrdU is incorporated into the meiocytes during meiotic S-phase. The duration of the meiotic pathway from the beginning of G2 through to tetrad formation was then determined by analysing chromosome spreads from anthers taken at specific time-points post-BrdU application. This revealed that the meiotic pathway takes ~43h of which prophase I occupies ~40h. Based on this information, trichostatin A in a range of concentrations from 100ng/ml to 1,000ng/ml was administered and led to a significant reduction in CO frequency in a dose dependant manner. At a concentration of 1000ng/ml we found a mean CO frequency of 9.2 compared to 14.64 in WT but this

resulted in complete loss of fertility. At a concentration of 100ng/ml, we observed a mean CO frequency of 13.48 (*) and fertility was reduced to ~80% of WT, allowing for fertile seeds to be harvested. We are currently examining the progeny of these lines to investigate the frequency and distribution of CO's using a SNP genotyping assay.
(*) is significant at 5% level.