SI Appendix

Homoeologous exchanges occur through intragenic recombination generating novel transcripts and proteins in wheat and other polyploids

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SI Materials and Methods

Plant materials, library construction and sequencing. The tetraploid wheat (DD) was produced by intergeneric hybridization between T. urartu (AA) and A. tauchii (DD) followed by colchicine-mediated genome doubling (1). A single S2 euploid individual seed was used as the founder to construct the tetraploid wheat population up to S12 (2). A total of 11 AADD individuals, including six euploid plants from S6, S9 and S12 generations and 5 compensated aneuploid plants with large-scale homoeologous exchanges (HEs) from S9 generation, were sampled and used in this study (Fig. S1). The 11 individual plants were karyotyped based on fluorescence in situ hybridization (FISH) and genomic in situ hybridization (GISH). All AADD plants and corresponding diploid parents (AA and DD) were grown in a glasshouse under normal conditions (25/20°C, 16/8 h, day/night). Young leaves collected from the trefoil stage plants were immediately frozen in liquid nitrogen. Genomic DNA was extracted by the CTAB methods. Total RNA was isolated using Trizol (Invitrogen) based on standard protocol. Library construction was carried out with standard protocols (Illumina, San Diego, CA, USA) for both DNA and RNA samples. Cluster generation and sequencing were performed on Illumina 2500 system with pair-end 150-bp read length. Clean data have been deposited in the SRA database (http://www.ncbi.nlm.nih.gov/sra/) with accession number PRJNA608801.

Publicly available data of other allopolyploid species used in this study. All publicly available sequencing data used in this study were downloaded from National Center for Biotechnology Information (NCBI) Sequence Read Archive collection (SRA). For diploid wheat progenitor, *Aegilops tauschii*, DNA methylation sequencing data by targeted capture (chromosome 3DL, ERR3149846, ERR3149847 and ERR3149848) and ATAC-seq data (ERR2927671, ERR2927672 and ERR2927673) were obtained.

For Brassica, whole-genomic re-sequencing data from *B. oleracea* (SRR3202040), *B. rapa* (SRR3203680) and 7 *B. napus* accessions (SRR1266094, SRR1266095, SRR1266021, ERR475359, ERR475361, ERR457868, ERR457756, ERR457816 and ERR457887) and RNA-seq data from *B. oleracea* (SRR8633040) and *B. rapa* (SRR8633039) and 2 *B. napus* accessions "Darmor-bsh" and "Yudal" (PRJNA362706), were obtained.

For banana, whole-genomic re-sequencing data from *M. balbisiana* (SRR6996488), *B. rapa* (SRR6996492) and 3 *Musa* triploid accession including "Pelipita" (SRR6996486, ABB), "FenJiao" (SRR6996487, AAB) and "Kamaramasenge" (SRR6996494, AAB) and RNA-seq data from *M. balbisiana* (SRR7006127), *M. acuminata* (SRR7006128) and "FenJiao" (SRR7006136), were also obtained.

For Arabidopsis, whole-genomic re-sequencing data from *A. arenosa* (SRR2040811) 15 *A. suecica* accessions (SRR3123759, SRR3123760, SRR3123761, SRR3123762, SRR3123763, SRR3123764, SRR3123765, SRR3123766, SRR3123767, SRR3123768, SRR3123769, SRR3123770, SRR2084154, SRR2084157, SRR2084158), were also obtained.

For rice, whole-genomic re-sequencing data and RNA-seq data from diploid parents (Nipponbare and 9311), diploid hybrids (N9 and 9N) and four segmental tetraploids, were download from SRA database with accession no. PRJNA514100.

For peanut (*Arachis hypogaea*), SNP information between A and B sub-genomes from 39 different varieties or accessions were downloaded from PeanutBase (https://peanutbase.org/data/public/Arachis_hypogaea/Tifrunner.esm.TVDM/).

Genome resequencing reads alignment and HE detection in synthetic tetraploid wheat (AADD). A total of 1.46 Tb (~17x per AADD sample) re-sequencing data was generated. Before reads alignment, an *in silico* tetraploid control dataset was constructed by mixing the diploid parental whole-genome sequencing data based on the ratio of the reference genomes size between A (*Triticum urartu*) and D (*Aegilops tauchii*). After removing low-quality reads (reads with Phred quality less than 10) using Trimmomatic (Bolger, et al. 2014), sequencing reads from both real and *in silico* tetraploid individuals were aligned to the combined AADD reference genome (merging the *T. urartu* and *Ae. tauchii* reference genomes (3, 4)) by Minimap2 (5) with default parameters. Considering that more than 85% genomic regions of AADD genome were TE-related regions, only uniquely mapped reads were retained for identification of HE events. PicardTools (v2.18.26) were used for sorting data, marking PCR duplication and adding RQ tags. Indel realignment was performed by GATK3 (https://software.broadinstitute.org/gatk/).

HE junctions were detected for each individual as follows. First, candidate HE junctions were detected by calculating the average depth of each 100 kb window at whole-genome level. Read depths were normalized by the whole-genome averaged depth. A slide-interval approach with 50 intervals (20 kb) with step-size of one interval was used to judge the depth difference between real and *in silico* individuals by Student's t-test. Intervals associated with significant difference of depth (p-value < 0.05) were flagged as "diff", the remaining intervals were flagged as "same". Intervals with identical flag were merged together and the joint of interval with different flag were treated as candidate HE junctions. Then, CNVkit (v0.9.6) (6) was performed to compare the copy number between *in silico* and real tetraploid individuals by scanning the candidate HE regions with 1kb-window size to shrink the HE junction size. Finally, each candidate HE junction was manually checked to confirm the exact joint. For HE junctions which were located in low reads-mappable region or when it was difficult to measure the exact location, HEs closest flanking regions that possessed different copy numbers were considered as the border of HE junctions.

For Brassica and banana, above method was used to identify original HE junctions.

Validation of HE junction based on SNPs-based methods. To validate HE junctions located in D genome of the AADD wheat tetraploid, first, re-sequencing reads from diploid *A*.

tauschii were aligned to D reference genome by Minimap2 with default parameter. PicardTools (v2.18.26) was used for sorting data, marking PCR duplication and adding RQ tags. Indel realignment was performed by GATK3 (https://software.broadinstitute.org/gatk/). SNP calling was performed by BCFtools. Only SNPs with mapping quality > 30, base quality >30, depth > 4 and the genotype equal to "1/1" were retained to generate the SNP list marked as "list 1", which indicated the inherent difference between our D genome and reference D genome. Second, sequencing reads from diploid T. urartu were aligned to D reference genome and performed SNP calling. This list was marked as "list 2", indicating the difference between our A genome and reference D genome. We removed SNPs occurring in "list 2" which also belonged to "list1", to generate a SNPs list, "list 3", which represented the difference between our DD and AA diploids. Then, sequencing reads from the in silico mix tetraploid were aligned to D reference genome and SAMtools mpileup was performed to assign the A-derived and D-derived reads based on list 3. In list 3, the SNP sites were kept if both A-derived and D-derived read depth > 4 and both A- and D-allele frequency belonged to the interval of [0.1, 0.9]. The filtered SNP list was marked as "list 4", representing the highconfident differences between our DD and AA diploids, including 5,870,921 SNP sites. Finally, sequencing reads from tetraploid individuals were aligned to D reference genome and samtools mpileup was performed to assign the A-derived and D-derived reads based on list 4. For each SNP site: (i) if all reads derived from A allele and the depth > 4, this site was flagged as "A-derived"; (ii) if all reads derived from D allele and the depth > 4, this site was flagged as "D-derived" and (iii) if the depth of both allele >4, this site was flagged as "heterozygous". Customized Python script was used to merge SNPs with same flag to generate different types of intervals (including AA-derive, DD-derived and heterozygous intervals, respectively). The junction between two adjacent intervals with different type was defined as HE junction. To avoid false positive derived from small interval and sequence elimination, HE junction that satisfied the following three conditions were retained: (1) The intervals on both sides of HE junction were large than 100kb; (2) The intervals on both sides of HE junction included at least 100 SNP sites and (3) the average sequencing depth of SNP sites in HE junction-related AA- and/or DD-derived intervals were larger than 1.5 fold of that in AA and/or DD subgenomes at whole genome level.

For Brassica, first, re-sequencing reads from diploid *B. oleracea* were aligned to *B. oleracea* (CC) reference genome to call SNP "list 1". Second, sequencing reads from diploid *B. rapa* (AA) were aligned to CC reference genome and performed call SNP "list 2". SNPs occurred in "list 2" that also belonged to "list1" were removed to generate SNPs "list 3". Then, sequencing reads from *B. napus* "Farmor-bzh" were aligned to CC reference genome and SAMtools mpileup was performed to assign the A-derived and C-derived reads based on SNP "list 3". Similar filtering criteria as for wheat were used to identify high-confident SNP "list 4" between AA and CC diploids (also between A and D subgenomes in *B. napus*). In total, we identified 2,063,999 SNP sites belonging to "list 4". Finally, sequencing reads from *B. napus* of different

accessions (including "H165", "Bristol", "Aburamasari", "Aviso", "Yudal" and "Kale") were aligned to CC reference genome and samtools mpileup was performed to assign the Aderived and C-derived reads based on list 4. Similar filtering criteria with wheat were used to flag SNP sites in "list 4" and customized Python script was performed to identify HE junctions.

For banana, first, re-sequencing reads from diploid *M. balbisiana* was aligned to *M. balbisiana* (BB) reference genome to call SNP "list 1". Second, sequencing reads from diploid *M. acuminata* (AA) were aligned to BB reference genome and performed call SNP "list 2". SNPs occurred in "list 2" that also belonged to "list1" were removed to generate SNPs "list 3". In total, we identified 1,513,073 SNP sites belonging to "list 3". Finally, sequencing reads from 3 triploid accessions were aligned to BB reference genome and samtools mpileup was performed to assign the A-derived and B-derived reads based on list 3. Similar filtering criteria with wheat were used to flag SNP sites in "list 3" and customized Python script was performed to identify HE junctions.

For Arabidopsis, first, re-sequencing reads from diploid *A. arenose* was aligned to *A. thaliana* reference genome to call SNP "list 1" (homozygous SNP). Then re-sequencing reads from tetraploid *A. suecica* including SRR2084154, SRR2084158 and SRR3123766 was aligned to *A. thaliana* reference genome. SNPs with mapping quality > 30, base quality >30, depth > 8 and the genotype equal to "0/1" were retained to generate the SNP list marked as "list 2", "list 3" and "list 4" (heterozygous SNP). SNP shared among all the four lists were generated to the final SNP site in "list 5". In total, we identified 271,627 SNP sites belonging to "list 5". Finally, sequencing reads from the remaining 12 *A. suecica* accessions were aligned to *A. thaliana* reference genome and identified HE junctions based on SNP "list 5". For Arabidopsis, the intervals on both sides of HE junction were large than 50kb.

For rice, the method descripted previously (7) were used to call SNP list between cv. Nipponbare (*japonica* rice) and cv. 9311 (*indica* rice). In total, 1,457,488 SNP sites between Nipponbare and 9311 were used for HE junction calling in synthetic rice tetraploid individuals.

For peanut (*Arachis hypogaea*), 825,960 SNP sites between A and B sub-genomes from 39 different varieties or accessions (8) were used to identify HE junctions.

For each species, the Bam files of each HE junction and 100 kb flanking region were deposited in the SRA database (<u>http://www.ncbi.nlm.nih.gov/sra/</u>) with accession number PRJNA625880.

Judgement of chromosome rearrangement flanking HE junctions based on

comparative genomic analysis in the synthetic tetraploid wheat (AADD). Chromosome rearrangement flanking HE junctions occurred in A sub-genome. To estimate if the rearrangements were attributed to HE or mis-assembly of A reference genome, chromosome sequences related to rearrangement flanking HE junctions in A genome were extracted and aligned to reference genomes of A sub-genome of wild emmer wheat (*T. turgidum* ssp. *dicoccoides*) and durum wheat (*T. turgidum* ssp. *durum*) and to D reference genome (*A.*

tauchii) by Minimap2 with "asm20" parameter. Only alignment hits with length large than 1000bp and alignment score large than 10 were retained. Dot plots between A genome and A sub-genome of emmer wheat, A sub-genome of durum wheat and D genome were performed and retrieved for structural variations, respectively.

Motif analysis. The 37 HE junctions from D subgenome were used for motif enrichment analysis by MEME Suite with classic mode (9). The candidate motif wide was set from 12 to 22 base pair. Motifs with E-value < 10e-10 were considered as candidate motifs. Genomic locations of motif were determined by FIMO (10) with q-value < 0.05. 3 kb flanking regions of each HE site was binned to 200bp non-overlapping windows to calculate the occurrences of each motif. Similar, as control, 37 random genomic regions with same size distribution were resampled with 1000 replicates using customized Python script. Bedtools coverage (11) was used to count motifs which overlapping with different genomic regions including promoter (upstream 2kb from gene region), gene and TE. For Brassica (104 HE junctions), rice (166 HE junctions) and peanut (26 junctions), similar methods were used to search HE-enriched motif and determine their genomic locations.

Identification of homoeologous gene pairs. Homoeolog pairs were identified by jcvi utility libraries (<u>https://github.com/tanghaibao/jcvi</u>) based on sequence similarity and genomic position of genes from homoeologous chromosomes. For wheat AADD segmental tetraploid, 13468 homoeolog pairs were identified between A and D reference genomes. For brassica, 25022 homoeolog pairs were identified between A and C reference genomes. For banana, 24497 homoeolog pairs were identified between A and B reference genomes. For rice, 24362 homoeolog pairs were identified between Nipponbare and 9311 reference genomes.

Validation of gene fusion on transcript level. Although not useful for validating HE sites in non-transcript genomic regions, RNA-seq data could be used for (i) testing gene fusion event on transcript level and (ii) narrowing down the resolution of HE events in transcript genomic regions (because of higher sequencing depth). Therefore, we also validated the HE interval using RNA-seq data based on the SNP list re-sequencing data. To test whether fusion transcripts occurred at the transcriptional level, Integrative genomics viewer (IGV) was performed to check if A-specific and D-specific SNP sites co-occurred in a single RNA-seq read or a single pair of RNA-seq reads (fusion-supporting reads). Furthermore, RT-PCR and Sanger sequencing were performed to obtain full-length fusion transcripts. For each fusion gene, 20 positive clones from diploid parents, control tetraploid and HE tetraploid were chosen for Sanger sequencing. MEGA7 was used for the alignment the results of Sanger sequencing. ORFfinder (<u>https://www.ncbi.nlm.nih.gov/orffinder/</u>) was used to predict the open reading frame of fusion transcripts.

For Brassica, banana and rice, above RNA-seq-based method was also used to validate gene fusion event at transcriptional level.

DNA Methylation data and ATAC-seq data analysis. After removing adaptor and lowquality reads, bisulphite-treated methylome reads were aligned to *A. tauschii* genome (for wheat data) or *B. oleracea* genome (for Brassica data) using Bismark software (12). Cytosine sites covered by at least 4 reads were retained further analysis. Methylation level of HE junctions and flanking regions (2Kb around) were calculated by CGmap Tools (13).

After removing adaptor and low-quality reads, ATAC-seq reads were aligned to *B. oleracea* genome using Bowtie2 (14) with 1-mismatch. Only uniquely mapped reads were retained for further analysis. Sequencing depth of HE junctions and flanking regions (2Kb around) were calculated by Bedtools (11).

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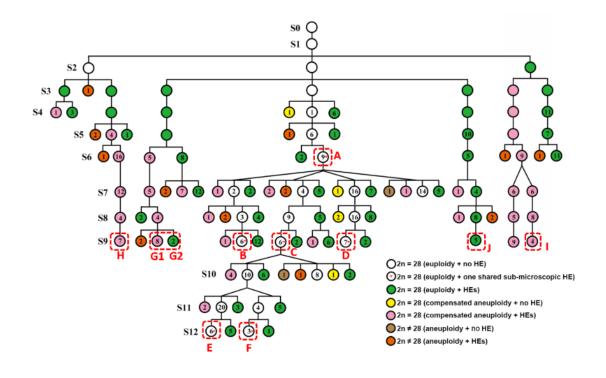


Fig. S1. Karyotypic composition of progenies of bona fide euploidy-descendants (being derived from one or more euploid parental individuals as indicated by the number of branches) in the synthetic tetraploid wheat (AADD) population from S0 to S12 generations. The seven different circles represent seven distinct karyotypic groups with numbers in the circles referring to individual numbers within a given karyotypic group. Circles within red dotted boxes denote the samples used in this study. Plants A-F (white circles with a red star) represent euploids at the cytological level, i.e., they did not contain numerical or structural variations including homoeologous exchange (HE). Sequencing of their genomes, however, showed that they all harbor a single sub-microscopic translocation between chromosomes 4A and 5D, and which most likely occurred in the S1 generation and then being vertically transmitted to, and shared by, all descendent plants. Because this translocation event occurred in regions including an ancient translocation between the long arms of chromosomes 4A and 5A in *T. urartu* (3), it was also a HE by definition. These plants (A-F), being sharing the same single sub-microscopic translocation, were thus represent ideal negative controls for the analysis of additional HEs in other plants.

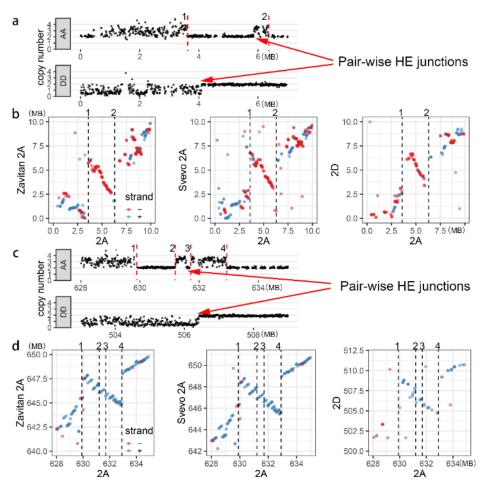


Fig. S2. Identification of HE-junction-related chromosome structural variation based on chromosome alignment among related wheat species. (a) and (c), two examples of candidate HE junction in A and D subgenomes. Regions between red dashed lines indicate the misordered genomic regions (large inversion) in A subgenome. Red arrows represent confident HE junctions in both chromosomes. (b) and (d), chromosome alignment among wheat species of corresponding regions in (a) and (c). Alignments between regions of A subgenome and syntenic regions in A subgenome of cv. Zavitan (wild emmer wheat, left), in A subgenome of cv. Svevo (durum wheat, middle) and D genome from *Ae. tauschii* (right) were shown. Red and blue dots indicate alignment hits in forward and reverse orientations, respectively. The black dashed lines and corresponding digits above them are identical with which occurred in (a) and (c). In each case, if the three comparisons in shared similar sequence-rearrangement patterns, it will be inferred that the reference sequence of *T. urartu* contains specific 'structure rearrangement', which is attributed to mis-assembly other than HE-induced structural variation.

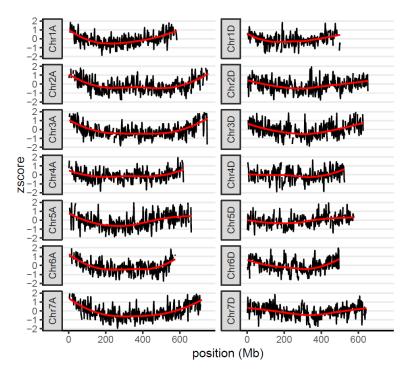


Fig. S3. Distribution of CCN motif in AADD genome. Genome was divided to 2Mb bins to count the number of CCN motif. X-axis indicates the chromosome position and y-axis indicates the Z-score transformed density of motif in each 2Mb bins. Red curves for each chromosome represent the fitting curves based on loess regression.

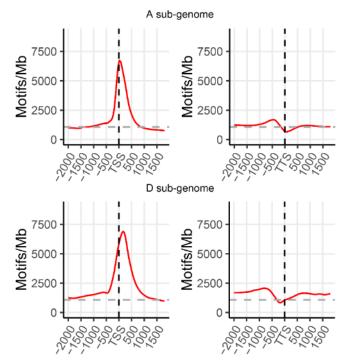


Fig. S4. Distribution of CCN motif in gene-related regions in A (a) and D (b) subgenomes. For each sub-genome, left panel represents the motif density flanking transcript start site (TSS) (2kb flanking regions), whereas right panel represents the motif density flanking transcript terminal site (TTS) (2kb flanking regions).

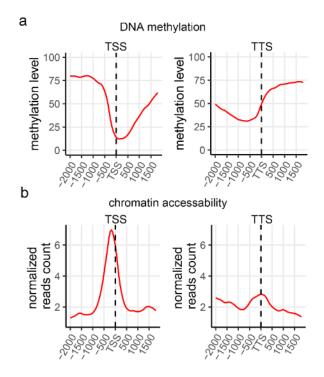


Fig. S5. Distribution of DNA methylation and chromatin accessibility in gene-related regions in *A. tauschii*. For both (a) DNA methylation and (b) chromatin accessibility, left panel represents the feature density flanking transcript start site (TSS) (2kb flanking regions), whereas right panel represents the feature density flanking transcript terminal site (TTS) (2kb flanking regions).

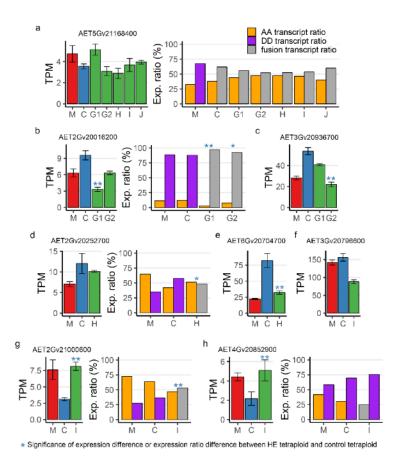


Fig. S6. Expression patterns of eight fusion genes in HE-related tetraploids. RNA-seq data of *in silico* mix (M), control tetraploid (C) and HE tetraploids (G1, G2, H, I and J) were aligned to *Ae. tauschii* reference genome to calculated total expression level. Meanwhile, SNP list between A and D subgenome were used to divide A-specific and D-specific reads to calculate relative expression ratio of A-derived transcript, D-derived transcript and fusion transcript in different samples. For each gene, left panel represents the total expression level and right panel represents the relative expression ratio of different expression (left panel, based on the results of DEseq2) or different relative expression ratio (right panel, based on Chi-squared test) compared with control sample (*: p-value < 0.05; **: p-value < 0.01). For (c), three types of transcripts (namely A-derived transcript, D-derived transcript and fusion transcript) generated simultaneously, calculating the relative expression level is not possible. For (e) and (f), only fusion transcript generated, namely the relative expression ratio of fusion transcript is equal to one.

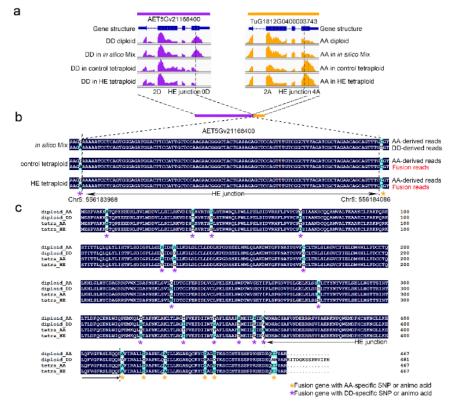
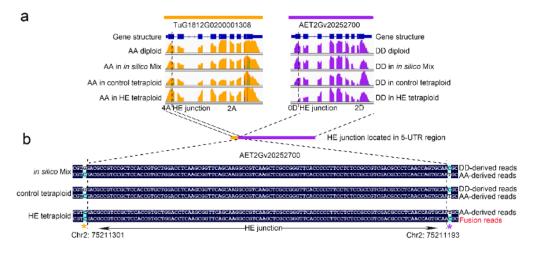


Fig. S7. Gene fusion event between HE-related homoeologous gene pairs. (a) IGV illustration of a candidate homoeolog fusion event based on RNA-seq reads depth. Each track (from up to down) represents the transcript structure and gene expression profile in diploid, in silico tetraploid, control tetraploid and HE-related tetraploid, respectively. Orange and purple indicate the profile of A and D subgenome genes, respectively. The position of HE junction were marked as dashed lines. The combination of number and letter flanking the HE junction represent the copy number of a given sub-genome in HE-related tetraploid (2A indicating 2 copies of A subgenome). (b) Validation of fusion transcript based on diploid-specific SNPs method. The tracks represent the consensus sequencing reads in *in silico* mix tetraploid, control tetraploid and HE-related tetraploid. Nucleotides without black background indicate high-confident SNPs between AA and DD diploid and used for genotyping the sequence reads. The asterisks in different colors under SNP positions indicate the origin of SNP (orange for A subgenome and purple for D subgenome) in fusion read. Region between adjacent asterisks of different colors represents HE junction, which position was also shown. (c) Predicted amino acid sequence of fusion transcript by ORFfinder

(<u>https://www.ncbi.nlm.nih.gov/orffinder/</u>) based on Sanger sequencing. Similar with SNPs in (b), amino acids without black background indicate high-confident variants between AA and DD diploid. The asterisks in different colors under variants positions indicate the origin of amino acid (orange for A subgenome and purple for D subgenome) in predicted fusion protein. Region between adjacent asterisks of different colors represents HE junction.



*Fusion gene with AA-specific SNP or animo acid *Fusion gene with DD-specific SNP or animo acid

Fig. S7. Gene fusion event 3.

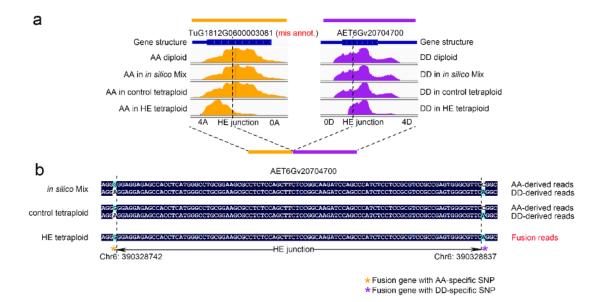
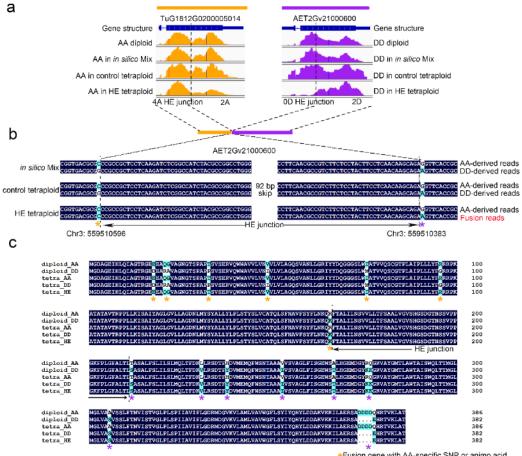
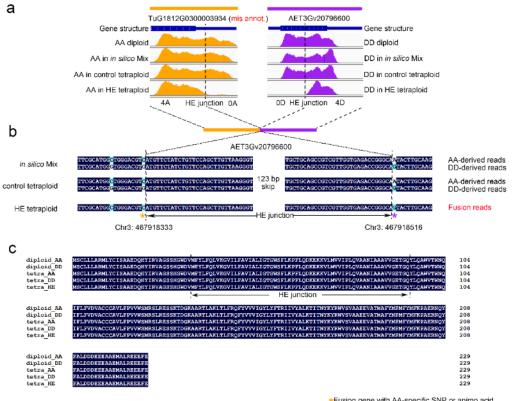


Fig. S7. Gene fusion event 4.



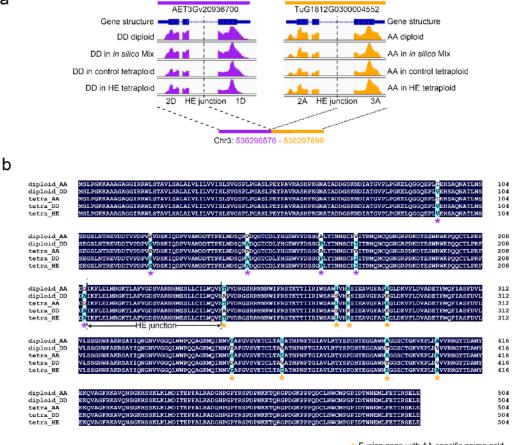
*Fusion gene with AA-specific SNP or animo acid *Fusion gene with DD-specific SNP or animo acid

Fig. S7. Gene fusion event 5.



*Fusion gene with AA-specific SNP or animo acid *Fusion gene with DD-specific SNP or animo acid

Fig. S7. Gene fusion event 6.



Fusion gene with AA-specific animo acid
 Fusion gene with DD-specific animo acid

Fig. S7. Gene fusion event 7.

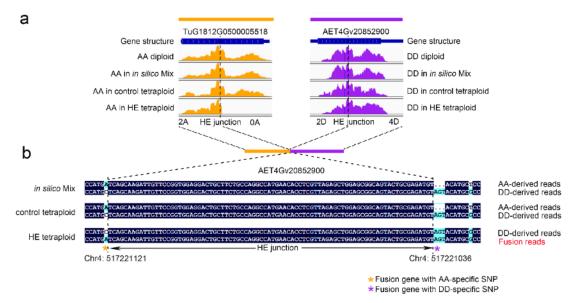


Fig. S7. Gene fusion event 8.

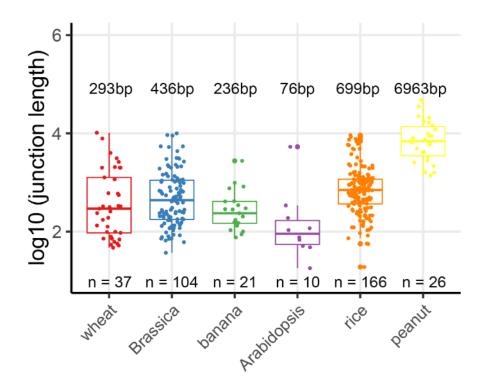


Fig. S8. Resolution of HE junctions based on diploid-specific SNP method in wheat, brassica and peanut. The number of HE junctions are shown above boxes. The median length of HE junctions are shown above of boxes.

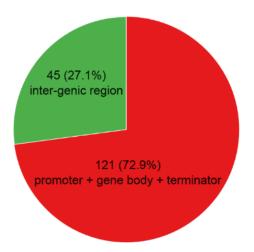


Fig. S9. Proportion of HE junctions including gene related regions (including promoter and terminator regions) and intergenic regions in the Nipponbare genome.

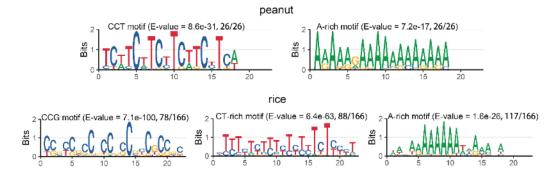


Fig. S10. HE-enriched motif logos in peanut and rice. Similar HE-enriched motif logos in Brassica was shown in Fig. 6b.

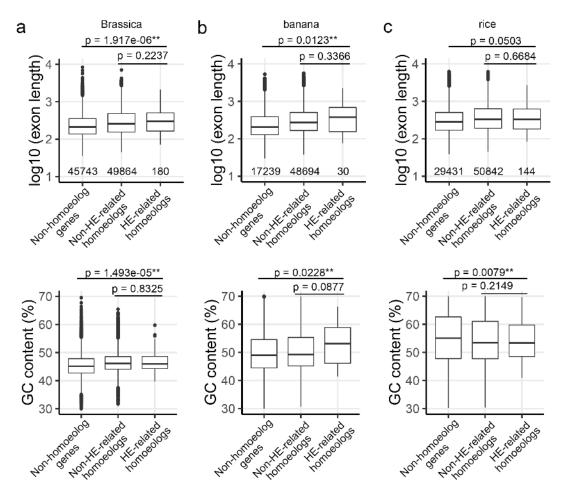


Fig. S11. Comparison of genomic features of HE-related homoeologs with non-HE-related homoeologs and non-homoeologous genes in (a) Brassica, (b) banana and (c) rice. For each species, up panel and bottom panel represent exon length and GC content, respectively, among three types of gene sets. The asterisks indicate significant differences between HE-related homoeologs and non-HE-related homoeologs or non-homoeologous genes (Mann-Whitney-U test; *: p-value < 0.05; **: p-value < 0.01).

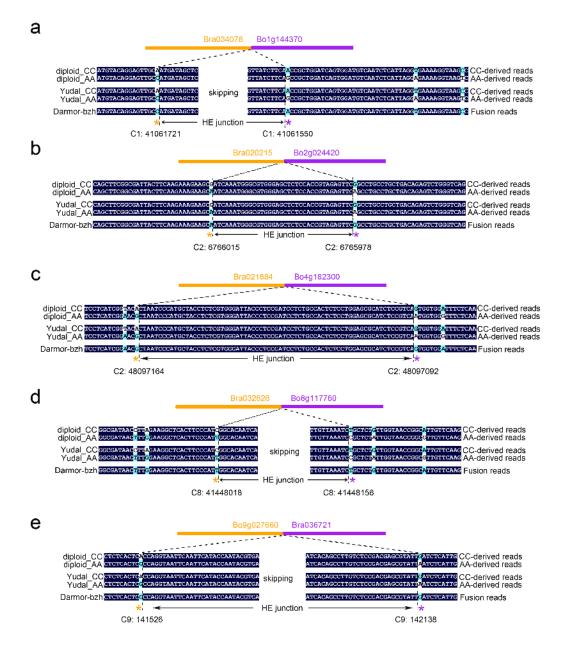


Fig. S12. Validation of gene fusion events based on RNA-seq data in Brassica. For (a) and (b), tracks represent the consensus sequencing reads in *B.oleracea* (CC) and *Brassica rapa* (AA), C and A subgenome in *B.napus* "Yudal" (control tetraploid) and HE-related tetraploid "Darmor-bzh". Nucleotides without black background indicate high-confident SNPs between AA and CC diploid and used for genotyping the sequence reads. The asterisks in different colors under SNP positions indicate the origin of SNP (orange for A subgenome and purple for C subgenome) in fusion read. Region between adjacent asterisks with different colors represents HE junction, which position was also shown. Other similar cases of HE-related gene fusion events in Brassica were shown in Fig. 6e.



Fig. S13. Validation of gene fusion events based on RNA-seq data in banana. For (a) and (b), tracks represent the consensus sequencing reads in *M.balbisiana* (BB) and *M.acuminata* (AA), B and A subgenome in HE-related triploid "Fenjiao" (control tetraploid). Nucleotides without black background indicate high-confident SNPs between AA and BB diploid and used for genotyping the sequence reads. The asterisks in different colors under SNP positions indicate the origin of SNP (orange for A subgenome and purple for B subgenome) in fusion read. Region between adjacent asterisks with different colors represents HE junction, which position was also shown. Other similar cases of HE-related gene fusion events in banana were shown in Fig. 6e.

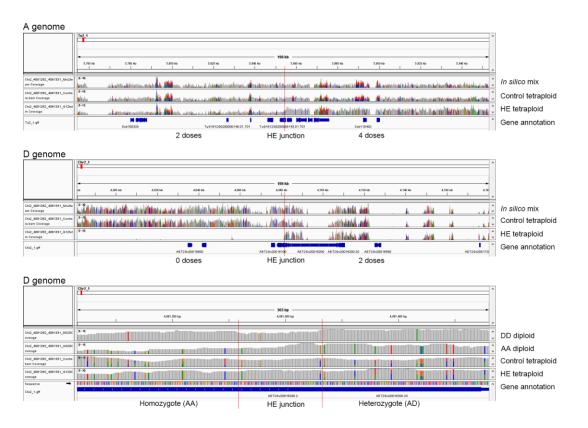
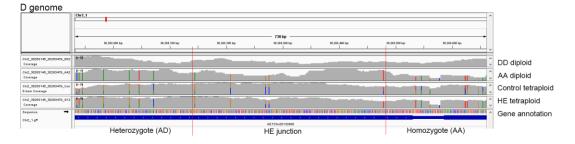


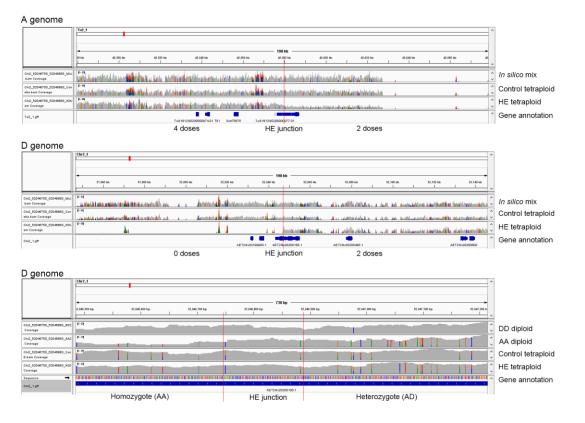
Fig. S14. IGV panels of HE junction regions in AADD tetraploid wheat (37 junctions). The top and middle panels show the sequencing depth around HE junctions in both A and D subgenomes, respectively. Red lines indicate the position of HE junctions and genome dosages are shown on both sides of HE junction. The bottom panel shows the genotypes (homozygote or heterozygote) around HE junction (region between red lines) based on SNP genotyping.

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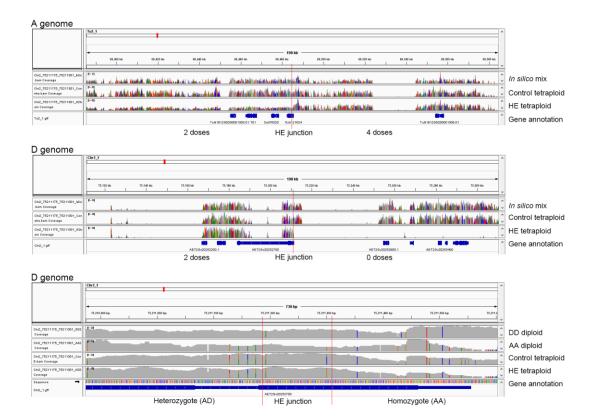
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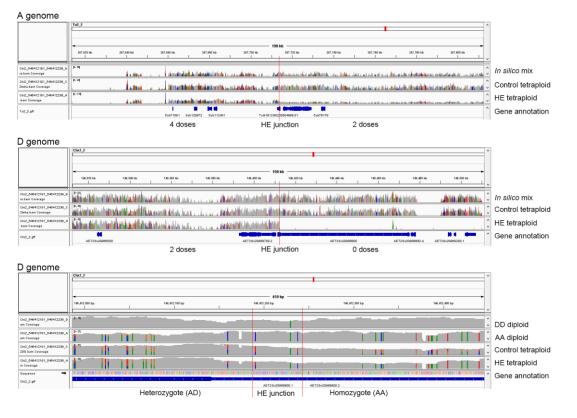
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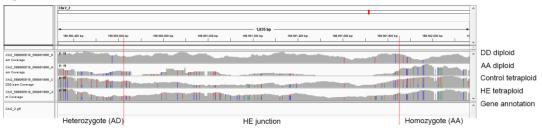
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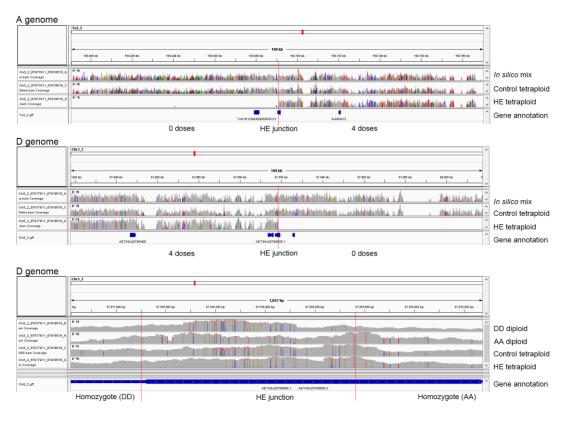
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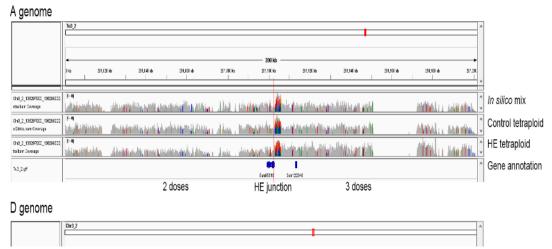
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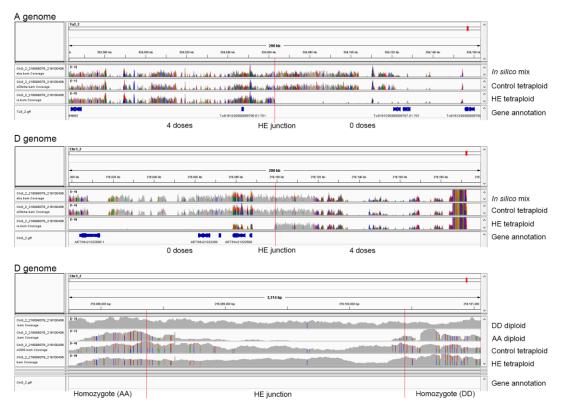
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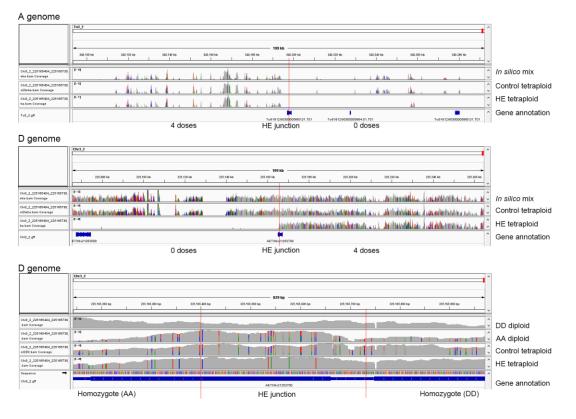
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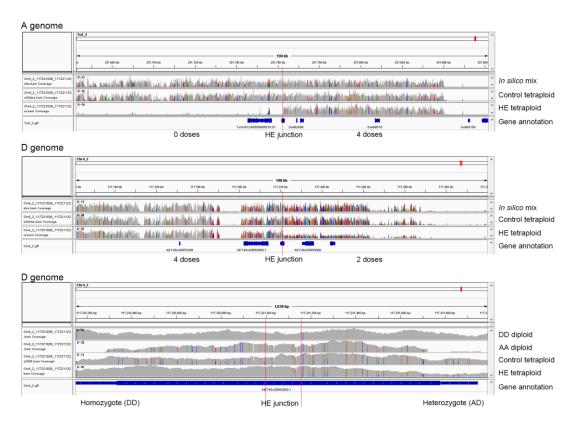
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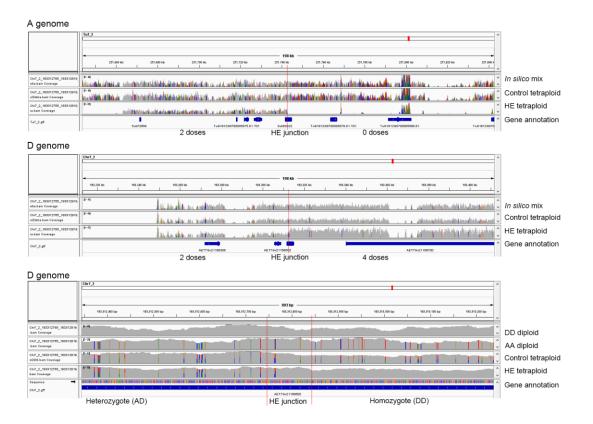
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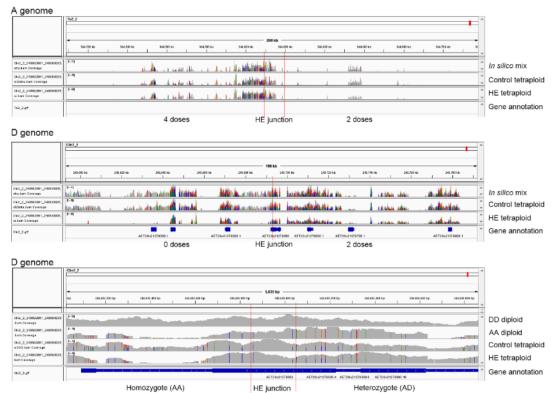
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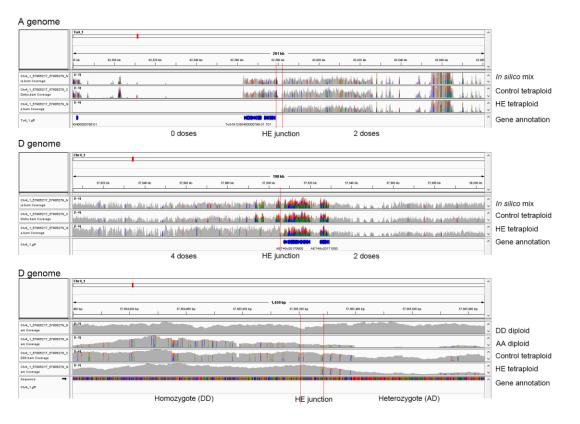
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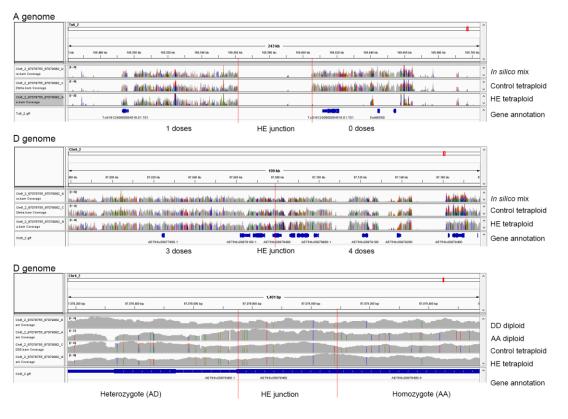
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HE junction 30.



HE junction 31.

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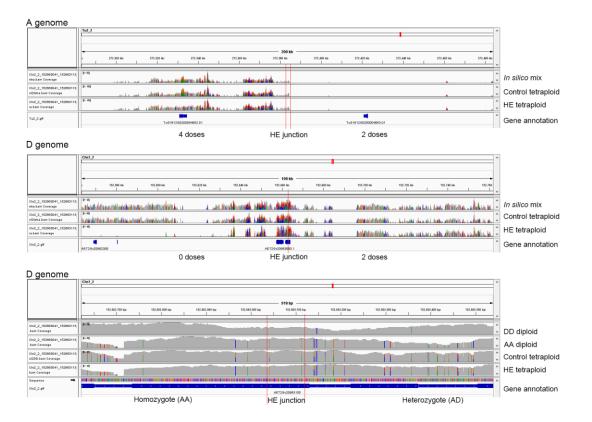
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HE junction 32.



HE junction 33.

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_	4 doses HE junction 2 doses		

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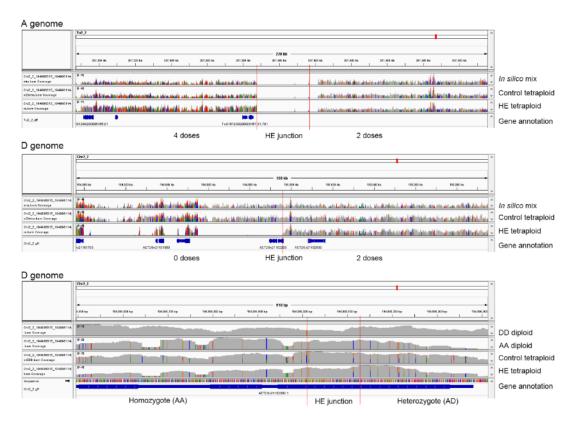
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HE junction 34.

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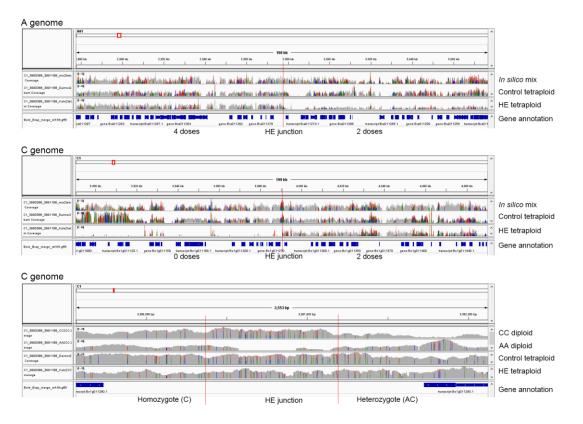
HE junction 35.



HE junction 36.

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a_1.#		Gene annotation
	Homozygote (AA) HE junction Homozygote (DD)	

HE junction 37.



IGV panels of HE junction regions in *Brassica napus* (104 junctions). The top and middle panels show the sequencing depth around HE junctions in both *B. oleracea* (C) and *B. rapa* (A) genomes, respectively. Red lines indicate the position of HE junctions and genome dosages are shown on both sides of HE junction. The bottom panel shows the genotypes (homozygote or heterozygote) around HE junction (region between red lines) based on SNP genotyping.

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Gene annotation

HE tetraploid

Homozygote (A)

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HE junction 2.

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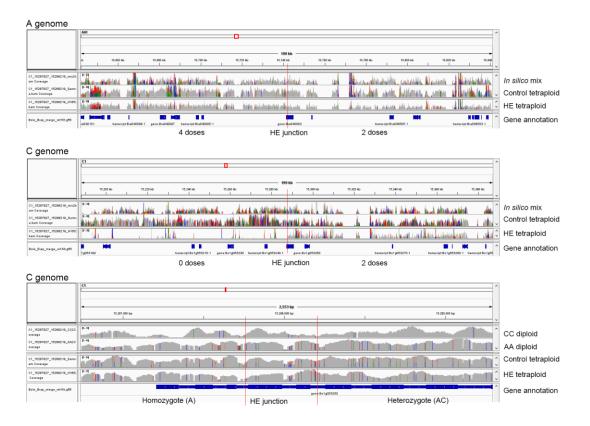
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HE junction 3.

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HE junction 4.



HE junction 5.

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HE junction 6.

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HE junction 7.

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C genome

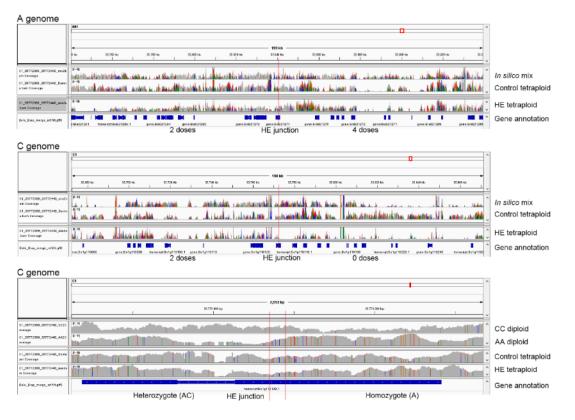
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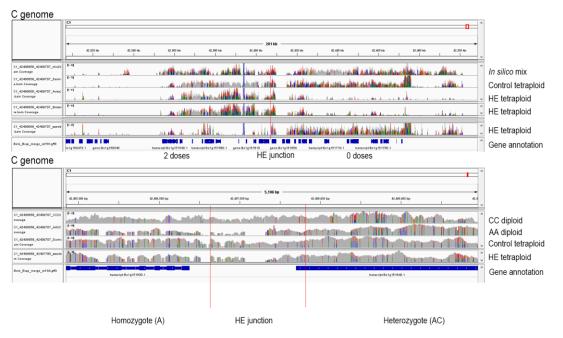
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HE junction 19.

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		Control tetraploid
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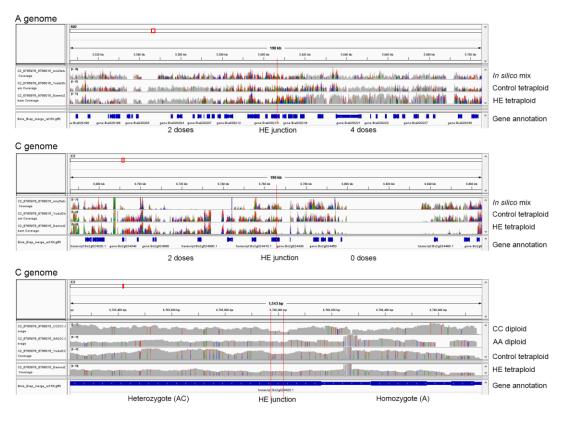
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HE junction 22.

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HE junction 24.

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HE junction 25.

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	2 doses HE junction 0 doses	
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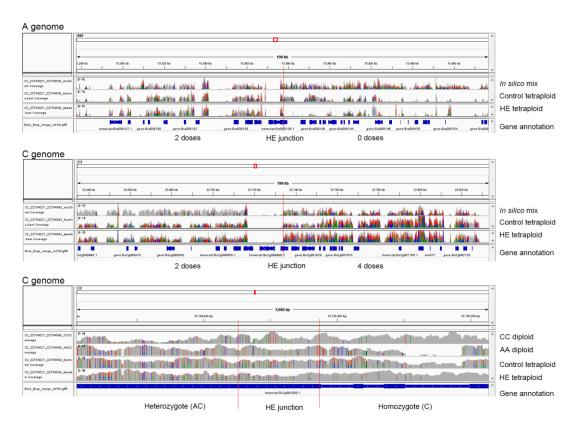
HE junction 26.

A genome		
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HE junction 27.

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HE junction 28.



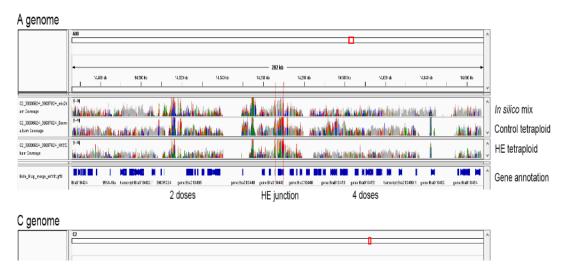
HE junction 29.

A genome		
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overage	i kan an in an in an an an ann an an ann an	
C2_23048525_23049745_Yudal	1 Mills In The Associate Devil - Although the second s	Control tetraploid
C2_23048525_23048745_Yedal m Coverage		
	Had an one of the second definition of the second definition of the second second second definition of the second	HE tetraploid
m Coverage C2_23048525_23049745_Damme		

HE junction 30.

A genome		
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C2_24507328_24507479_mix2b am Coverage	المتيمينة ومقدهان و وفر المتيني المطلوفة والي و	In silico mix
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C2_24597328_24597479_swede .bam Coverage	Canada a second a s	HE tetraploid
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	0 doses HE junction 2 doses	
C genome		
02_24597328_24597479_mix21		
am Coverage	📲 dá száladatok brihadaltoztóttotóttotótszátosás zek 🧠 Atalan, fesz száladból vészete Medeszettettékészészészéses 👘	In silico mix
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	4 doses HE junction 2 doses	
C genome		
	•	
	24399/301 bp 24399/3000 bp 24399/30	
C2_24597326_24597479_CC2C overage		CC diploid
C2_24597328_24597479_AA2C overage		AA diploid
C2_24597328_24597479_Barmi am Coverage		Control tetraploid
C2_24697328_24697479_swede m Coverage		HE tetraploid
Bale_Brap_merge_ref.filt.gfD	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Gene annotation
	Homozygote (C) HE junction Heterozygote (AC)	

HE junction 31.



HE junction 32.

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HE junction 33.

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HE junction 36.

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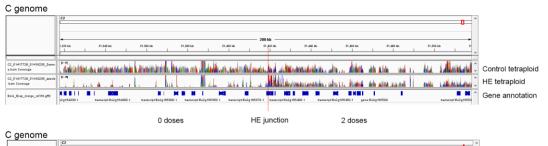
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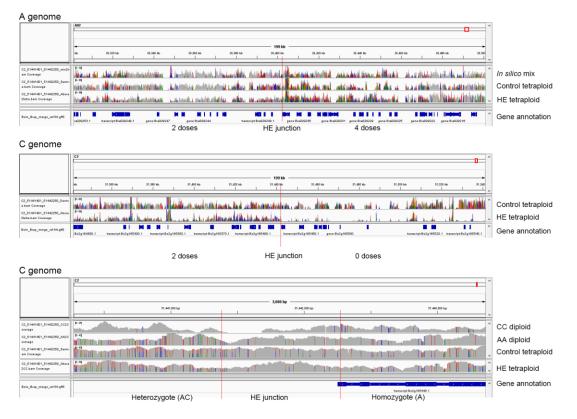
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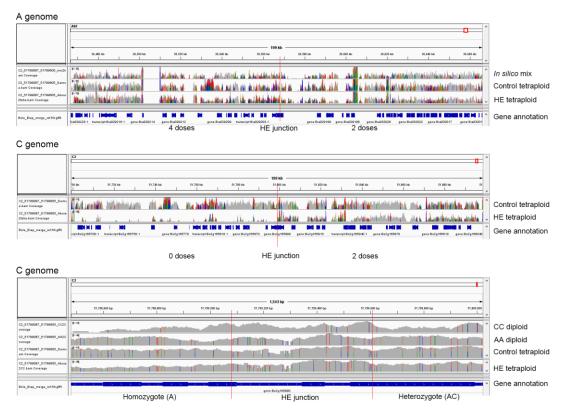


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HE junction 38.



HE junction 39.



HE junction 40.

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HE junction 41.

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HE junction 42.

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HE junction 43.

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4974207_4983198_CC2C0.1 * 4974207_4983198_AA2CC.4 #074207_4983198_Dame.2 #498 #074207_4983198_uwe4e2C #498 	and to the two sectors and the effective or the sector metric or the sector of the theory of the two sectors and the sector of t	AA diploid Control tetraplo

HE junction 44.

A genome		
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	- 199 bb	
C3_5851394_5851524_mix2tets Coverage C3_5851394_5851524_Damoi2 bam Coverage	Renternie het die seine werden in het werden die seine der enter het die seine die seine die seine die seine die Territer voor werden die deres seine die s	<i>In silico</i> mix Control tetraploid
C3_5851394_5851524_Aviss2te am Coverage	Part of the second seco	HE tetraploid
C3_5851394_5851524_Bristol25 .bam Coverage	F-H	
and converge	n na militeria da la caracteria da la caracteria da la caracteria da car	HE tetraploid
Bele_Brap_merge_ref.filt.gfD	NCD 1 N 1 N 1 N 1 N 1 N	Gene annotation
C genome	[0	
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C3_5851394_5851524_Avise2te am Coverage	المراجع ا	HE tetraploid
C3_5851394_5851524_Bristol21 .bam Coverage	12. ar ba dahar dalam	HE tetraploid
Bele_Bray_merge_set.fill.pf3 C genome	аде/1929	Gene annotation
genenie	a	
	- 1,898 kp	
	5,585,600 kp 5,850,600 kp 5,859,000 kp 5,859	
C3_6851394_6851524_CC2CC.i erage	PR	CC diploid
erage C3_5851304_5851524_AA2CC.1 erage		AA diploid
c3_5851384_5851524_Damo/2 Coverage		Control tetraploid
C3_5851394_5851524_Avise2C		HE tetraploid
Coverage C3_5851394_5851524_Bristol2C		
m Coverage		HE tetraploid
Bole_Brap_merge_ref.filt.g#3	Perella 2017/0	Gene annotation
	Heterozygote (AC) HE junction Homozygote (A)	

HE junction 45.

A genome		
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	19934	
	199 MD - 199	
C3_8247040_8247246_mix2tetr. Coverage	🕅 netakalas arkikais arkikais an da in jaman ol ninasis an haida in jaman in dia ka in da in d	In silico mix
C3_6247040_6247246_Damoi2 bam Coverage	ann ar haidh mala na ad dhana a ball a san a' chuanna an dhad danna (, , , na ku a bùirthin) , , , bha dù bh th' dhadh ti - A, , an anna an anna an anna an anna a' c	Control tetraploid
C3_8247040_8247245_H18521e m Caverage	🖾 salaadaadaadaa halaa ay aca, chaasaadaa madaadaa , miji , miji kadaadad tiradaa tiradahiina (- miji amini mini dini dabadaa 🕄	HE tetraploid
Bole_Brap_merge_ref.filt.g#3	Distribution No. N.	Gene annotation
	2 doses HE junction 4 doses	
C genome		
	19936	
	6.581.96 £.581.96 £.2	
C3_6247040_6247246_mix2tetr. Coverage	Taba suda at a satalin visit distan an a a a a a sata a ba da	In silico mix
C3_6247040_6247246_Damo/2 bam Coverage	an salah an dalam da na ang kana a	Control tetraploid
C3_6247040_6247245_Aburam: etra.bam Coverage	heiderstelen och atte hielder er heider her bliver att da och atte er blivere hielder det etter och atte besere station 🖉	
C3_6247040_6247246_H18521e m Caverage	an det a lande her standhein de her weiter van de en een de antersekende de een een de een een de her een een d	HE tetraploid
Bole_Brap_merge_ref.filt.g#3	Х ТИХ В Х Х ХОХ МА ВИ	Gene annotation
C genome	2 doses HE junction 0 doses	
	G	
	C342/30 kp	
C3_6247040_6247246_CC2CC.I etage		CC diploid
03_6247040_6247245_AA200.1		AA diploid
C3_6247040_6247246_Damar2 Coverage		Control tetraploid
C3_6247040_6247245_Yudal2C Coverage		HE tetraploid
C3_6247040_6247245_H1652C+ evenage		HE tetraploid
Bole_Brap_merge_vef.filt.g#3	Heterozygote (AC)	Gene annotation

HE junction 46.

A genome		
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	100.65	
C3_6367698_6367904_mix2tets. Coverage	an an the second s	In silico mix
C3_6367606_6367004_Damor2 bam Coverage	MINATE as which is the Minate Market of the Astronomy And Astronomy Astronomy And Astronomy A	Control tetraploid
C3_6367696_6367904_Avise2te am Coverage	stilling a strait in the limited the an and the sector balls while the addition and a second success and second straight and the second s	HE tetraploid
Bole_Brap_merge_ref.filt.g#3		Gene annotation
	4 doses HE junction 2 doses	
C genome		
5 genome	(G	
	+	
03_6367698_6367904_mix2tets Coverage	Disanden and the second stand with the second indication a day. If with a state defined a strategiest of the second state a second sta	In silico mix
C3_6367668_6367604_Damoi2 aam Coverage	📴 🖌 👘 e e e e e e e e e e e e e e e e e e	Control tetraploid
C3_6367698_6367904_Avise2te am Coverage	na sa	HE tetraploid
Bole_Brap_merge_ref.filt.gff3		Gene annotation
C genome	0 doses HE junction 2 doses	
	G	
C3_6367698_6367904_CC2CC.1 erage		CC diploid
C3_8367698_8367904_AA2CC.I erage		AA diploid
C3_6367698_6367904_Damo/2 Coverage		Control tetraploid
C3_8367698_8367904_Aviss2C1 Coverage	in the second	HE tetraploid
Sequence 🗕		
Bole_Brap_merge_ref.filt.g#3	### 849/10000 Homozygote (A) HE junction Heterozygote (AC)	Gene annotation
	The junction of the following state (16)	

HE junction 47.

genome		
8432818_6434256_mix2tets		In silico mix
rerage 6432816_6434256_Damor2 1 Coverage		Control tetraploid
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genome		
genome		
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5432816_6434256_mix2tets rerape	The make done with the full state is a state of the full state of the date of the state of the	In silico mix
6432816_6434256_Damor2 1 Coverage	perindent and a substantia and a	Control tetraploi
_0432810_0434250_H1052te Coverage	🗘 👘 🕴 👘 🖞 (sama a sa	HE tetraploid
ie_Brap_merge_ref.filt.g#3	E MENE E OL DEE MI HOURING MERSEN ET E MI OCHETHIGOTIE N Definition ματάσματο ματάσματο ματάσματο ματάσματο ματάσματο ματάσματο στατάσματο του ματάσματο που ματάσματο ματάσματο ματάσματο γ	Gene annotation
genome	0 doses HE junction 2 doses	
genome	<u>а</u>	
6432816_6434256_CC2CC.I	Number 1 and the state of the second state of the state of the second state of the sec	CC diploid
 6432816_6434256_AA2CC.I I*	The sense of the first first sense with the set of the line set of the set of	AA diploid
5432816_6434256_Damor2 erape	Stall and a stall with the stall and the sta	Control tetraploi
0432810_0434250_H1052C+ lage	in the contribution of the second second second from the second sec	HE tetraploid
_Brap_merge_ref.fill.g#3	gene 8/2/g/19020 bannerigt 8/2/g/19020 bannerigt 8/2/g/19020.1 bannerigt 8/2/g/19020.1	Gene annotation

HE junction 48.

A genome		
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_6725055_6727720_mix2tetr. tverage _6725055_6727720_Damor2 m Coverage _6725055_6727720_Bristol2t-	Entradistic disconsistività i dal , alcoherenziandori, allantat, dia ana e l'alla fina some una estativitativa da sua da da da plana antifessa di Industri ancontradori da sua canana anticaria, ancherenziandori e sua discontradori da da da da contra antifessa Industri ancontradori da canana anticaria, ancherenziandori e sua da	<i>In silico</i> mix Control tetraploid
am Coverage		HE tetraploid
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_6725055_6727720_Bristel2ti m Coverage	fillionentettersenterenterante almastata tal 🐜 de dad tal o 🔄 kas ku a 🧠 ku talifas a sassa ku talifas a sassa ku ta	HE tetraploid
ie_Brap_merge_ref.filt.g#3	M MC B B M K BN BN BN BN BN B B B B B B B B B B B	Gene annotation
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	- 3,791 bp	
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uge _6725055_6727720_Damei2 Iverage	na fi Dhall an Anna anna anna anna anna anna ann	AA diploid Control tetraploid
_6725055_6727720_Bristol2C Coverage	Citedard Antithe ball	HE tetraploid
		Gene annotation
ie_Brap_merge_ref.filt.gfD	Heterozygote (AC) HE junction Hemozygote (A)	Gene annotation

HE junction 49.

A genome		
	19936	
	199 40 3.741 kp 3.741 kp 3.651 kp 3.651 kp 3.661 kp 3.641 kp 3.641 kp 3.641 kp 3.641 kp 3.641 kp 3.541 kp 3.54	
C3_6924496_6924906_mix2tets. Coverage	💼 an the second s	In silico mix
C3_6024406_6924006_Damoi2 bam Coverage	Fillethistelik dewolftes Liebelsetheten verste aller franze and eller franketen er se asketelt das aller en beiter het en andere filmer het en andere filmer het en seine filmer het ein sekelste bie eine sekelste s	Control tetraploid
C3_6924496_6924906_Bristol25 .bam Coverage	Nill Alfred and a collected and a definition of the definition of	HE tetraploid
Bole_Brap_merge_ref.filt.g#3	N BC N B H H X X B BC N B B B BC BC 1 B L 1 B B N K W M B N B B 1 B 1 N B B N B B 1 B 1 B B B 1 B 1	Gene annotation
	4 doses HE junction 2 doses	
C genome		
e genenie	(C)	
C3_8924498_8924908_mix2tetri Coverage	🚰 die die de la company de la	In silico mix
C3_6924486_6924806_Damer2 bam Coverage	Simplificantes, a post change, freededings a grante protected dirities and demine a protected freeded directed	Control tetraploid
C3_6924486_6924806_Bristel2ti .bam Coverage	🕅 al data da	HE tetraploid
Bole_Brap_merge_ref.fil.gft3		Gene annotation
	algio19740.1 penebalgio19700 penebalgio19800 penebalgio2084 penebalgio2084 penebalgio20970 58058024 penebalgio20000 penebalgio2000 penebalgio2000	
C genome	0 doses HE junction 2 doses	
	- 1,396 bp	
C3_6924466_6924606_CC2CC.1 etage		CC diploid
C3_8924498_8924908_AA2CC.I		AA diploid
C3_6924486_6924886_Damo/2 Coverage	PH and the second statements and the second statement of the second statement	Control tetraploid
C3_6924496_6924906_Bristol2C m Coverage		HE tetraploid
		Gene annotation
Bole_Brap_merge_ref.filt.g#3	are Bulg20000.1	
	Homozygote (A) HE junction Heterozygote (AC)	

HE junction 50.

1 2.6024408_6024008_mix2tin Giverage 13.6024408_6024608_0amed am Galerage	an a	In silico mix Control tetraploid
5_6924406_6924006_8-Mix De tam Colevage	Viel effecte and the second	HE tetraploid
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	4 doses HE junction 2 doses	
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Jener		
1_0024696_0024800_w1x2510		
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na"per'ante'arge'arge	1 100 1 1 100 1 1	Gene annotation
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) genome	CELIBITE CALCULAR DE CALC	Gene annotation
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	Contract	Gene annotation CC diploid AA diploid
2 genome cr, server, second, second rep: mar: genome geno	Contract	Gene annotation CC diploid AA diploid Control tetraploid
C genome	Contract	Gene annotation CC diploid AA diploid Control tetraploid HE tetraploid

HE junction 51.

А	genome

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C4_48097092_48097184_mix2t am Coverage	l ha Maran Maley 👔 🖉 Maran Maran 🕹 Andrea 🗛 👘 🖉 👘 🖉 👘 🖓 An an Andrea Andr	În silico mix
C4_48097092_48097164_Yudal .ham Coverage		Control tetraploid
C4_48097092_48097164_Dame		Control tetrapiolo
a.bam Coverage	have a strang de alter and an anna a strang de alter a st	 HE tetraploid
		<u> </u>
Bale_Brap_marge_ref.filt.gfD		Gene annotation
and out out of a second s	ud21865.1 tansciptBid21880.1 tansciptBid21873.1 peneBid21875 tansciptBid21877.1 peneBid21880 tansciptBid21888.1 peneBid21880 peneBid21880 peneBid21888.1 peneBid21888.1	Gene annotation
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C genome

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2 doses HE junction 0 doses C genome

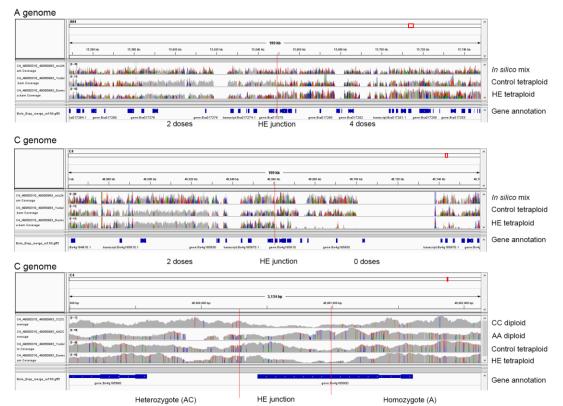
o genome					
	C4			^	
	48,0%,400 bp 48,0%,000 bp 48,0%,000 bp	43,007,000 bp 43,	197.203 bp #297.400 bp #2.57.505 bp	48,097,800 bp	
C4_48097092_48097164_CC2C overage	Filing and the state		a and a state of the second state of the secon	1	CC diploid
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C4_49007092_48097164_Yudal m Coverage		the state of the s	enterentiti di Chine entre anno essenti	·	Control tetraploid
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Bole_Brap_merge_ref.filt.gft3		c c c c c c c c c c c c c c c c c c c	τ. τ. τ	^	Gene annotation
	Heterozygote (AC)	HE junction	on Homozygote	: (A)	

Heterozygote (AC) HE junction

HE junction 52.

A genome		
	- 19936	
	1538140 15323140 1538140 1538140 1538140 1538140 1548140000000000000000000000000000000000	
C4_48671789_48672442_mix26 am Coverage	ก็ไม้สารการการการการการการการการการการการการกา	In silico mix
C4_48671789_48672442_Yudal .bam Coverage	🖓	Control tetraploid
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Dole_Drap_merge_ref.filt.g#3	NUMBER ANN ADMENT AND TERME AT A THE AT	Gene annotation
	pere Bio21940 pere Bio21940 taxes optimized at the second bio117321 taxes optimized at 172241 taxes optimized at 17224 ta	
C genome		
5 genome	[64	
C4_49871789_48872442_mix2t		
c4_48671789_48672442_mit20 am Coverage C4_48671789_48672442_Yudal	1 Lade sellans All a	In silico mix
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	0 doses HE junction 2 doses	
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C4_48871789_48872442_0020 overage	13 A A A A A A A A A A A A A A A A A A A	CC diploid
C4_48671789_48672442_AA2C overage	The second	AA diploid
C4_48671789_48672442_Yudal m Coverage	The search has a first the second	Control tetraploid
C4_48671789_48672442_Darmi am Coverage	ין אינעל דעל אינער איני אליינעל אינעל אינער אינער אינער אינער אינער אינער אינער אינער אווייער אינער אינער אינער	HE tetraploid
Bole_Brap_merge_ref.filt.g#3	A Concernence of the concernence	Gene annotation
	Homozygote (A) HE junction Heterozygote (AC)	
	Heterozygote (A) Heterozygote (AC)	

HE junction 53.



Heterozygote (AC) HE junction

HE junction 54.

A genome

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	14,000 W 15,000 14,000	
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04_49690019_49691040_0ami a.bam Coverage	Carl with said definition for the animal life as in the black of a strike see, between the stration of the second definition of the second s	HE tetraploid
Bale_Nep_recup_ref \$1, p10		Gene annotation
	4 doses HE junction 2 doses	

C genome

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C-1_42690810_426910-80_Yudal		ol tetraploid
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a kars Ceverage	- Construction of the second s Second second se	apiolu
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everage 04_48650010_48651340_AA20 overage 04_48650010_48651340_Vadat	Image: State of the state o	ploid

HE junction

Gene annotation

Heterozygote (AC)

Homozygote (A)

HE junction 55.

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_40744132_40744747_mic28	🖬 ne and an	In silico mix
_40744122_40744747_Dame: tam Coverage		Control tetraploi
- 20744130_40744747 june de em Generado	California ale and a second a second a second a second and the second and the second as a second as	HE tetraploid
		Gene annotation
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	4 doses HE junction 2 doses	
genome		
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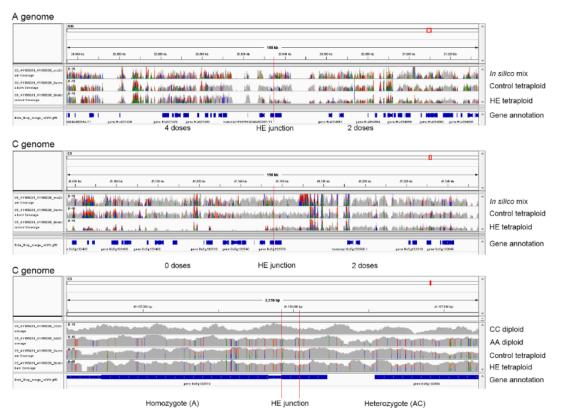
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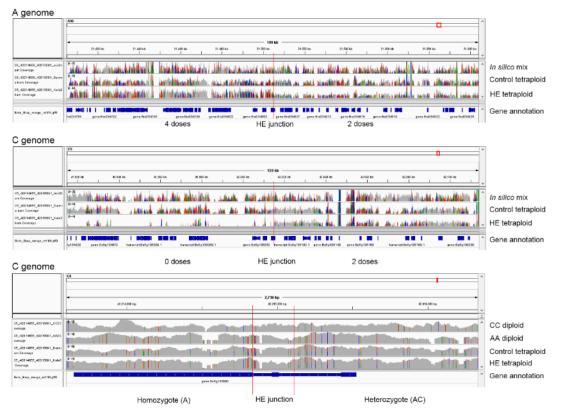
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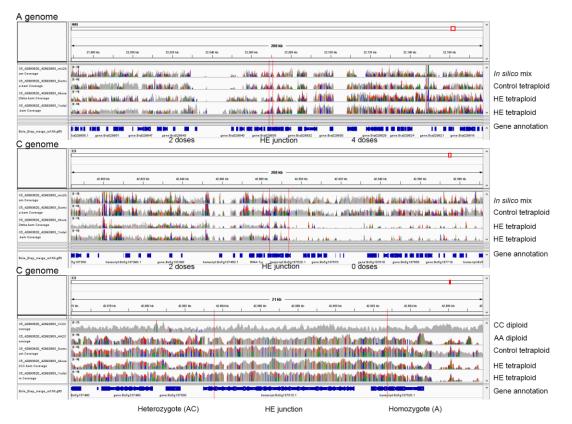
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HE junction 63.

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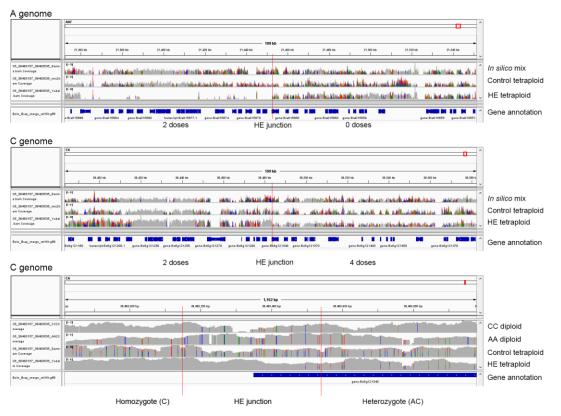
HE junction 67.

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HE junction 68.

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HE junction 69.



HE junction 70.

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HE junction 71.



HE junction 72.

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HE junction 73.

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08_38029713_38029713_Bristol a.bam Coverage	1997 - Anter ander and	HE tetraploid					
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00020713_00220713_00220 HH44 00220713_00220713_0420 HH44 _00220713_00220713_04020 HH42020713_00220713_0400 HH42020713_040220713_0400 HH42020713_040220713_0400 HH4204204 HH42044 HH4204204 HH4204	P NUMBER OF CONTROL ON CO	AA diploid Control tetraploid HE tetraploid					
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HE junction 74.

A genome

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08_38429400_38431592_mix21	
am Coverage	14
C9_38429460_38431692_swede	HE tetraploid
.bam Coverage	
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Heterozygote (AC)

HE junction

Homozygote (A)

HE junction 75.

A genome		
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C genome	C	
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Bole_Brap_merge_ref.filt.gff3	NAMENA A DEPARTMENTER DE LA CONTRACTIONE DE LA CONT	Gene annotation
C genome	0 doses HE junction 2 doses	
	CI CA156 Bit P B-253 800 bp B-253 900 bp B-255 900 bp B-255 800 bp B-255 80	
C8_39529544_30529601_CC2C sverage C8_39529544_30529651_AA2C		CC diploid
overage C8_30529544_39529001_Damm< am Coverage		AA diploid Control tetraploid
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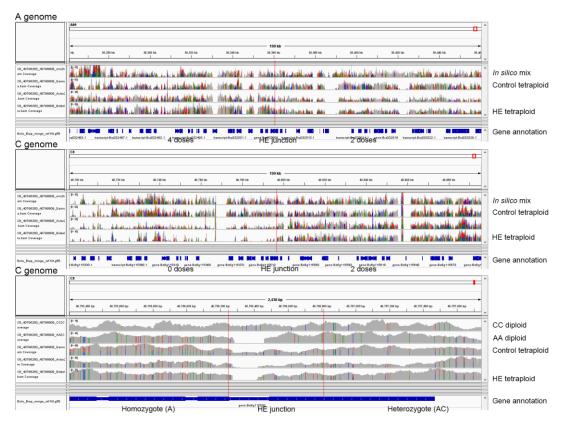
HE junction 76.

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HE junction 77.

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HE junction 78.



HE junction 79.

A genome				
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			F	
	•	4.872 bp		
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Bole_Brap_merge_ref.filt.g#3	s8g117310.1	transcript Be8g117320.1	gene:Bo8g117330	Gene annotation
	Homozygote (A)	HE junction	Homozygote (C)	

HE junction 80.

A genome		
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	2,1361bp	
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overage C8_41448018_41448155_Yuda1		AA diploid
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am Coverage		HE tetraploid
Dole_Drap_morge_ref.filt.g#3		Gene annotation
	Homozygote (A) HE junction Heterozygote (AC)	

HE junction 81.

A genome		
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Bole_Brap_merge_ref.fit.gfD	5anscipt.8v0;d02220.1	Gene annotation
	Homozygote (A) HE junction Heterozygote (AC)	

HE junction 82.

A genome		
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00_300006_300568_mix2tetba.b everage 00_300006_300568_Dame.2tet m Coverage 00_300006_300568_Kale2tetba. Coverage	laffelden zu "Millehit "nite Anderschatt" seinterfelden ist an "einen Millehit auf dem zum seinterfelden beschift ist dem konstelle einen " felden "	<i>In silico</i> mix Control tetraploid HE tetraploid
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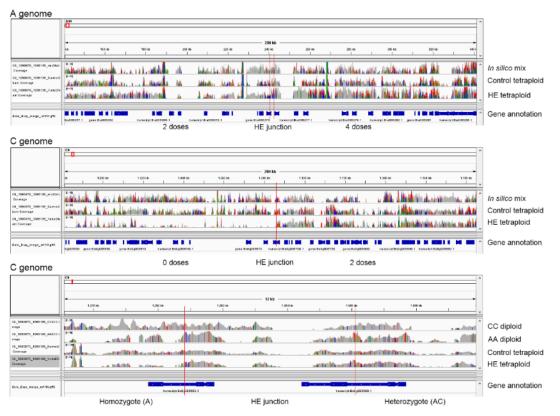
HE junction 83.

A genome		
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C genome	2 doses HE junction 4 doses	
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HE junction 84.

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Imperiation			
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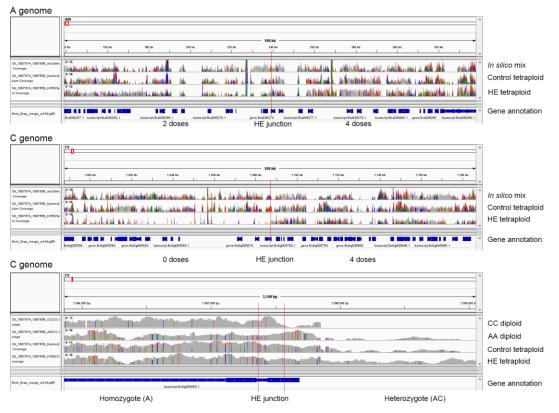
HE junction 85.



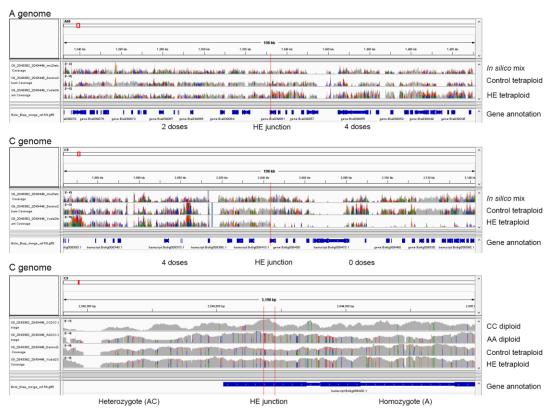
HE junction 86.

A genome		
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C9_1085741_1085938_Damo/2 Coverage		Control tetraploid
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	Homozygote (A) HE junction Homozygote (C)	

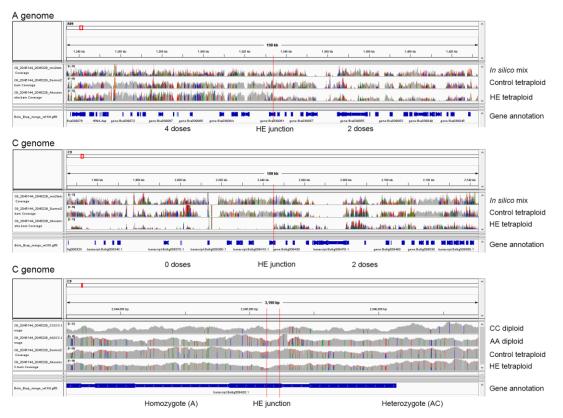
HE junction 87.



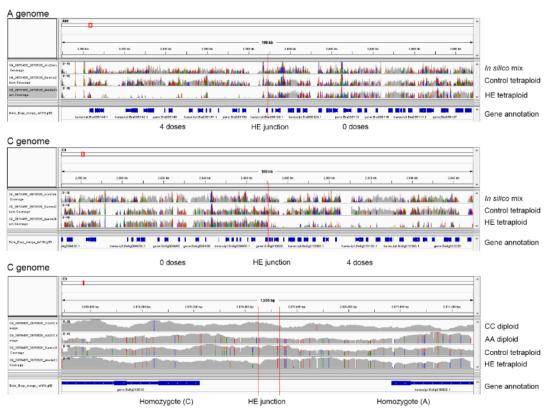
HE junction 88.



HE junction 89.



HE junction 90.



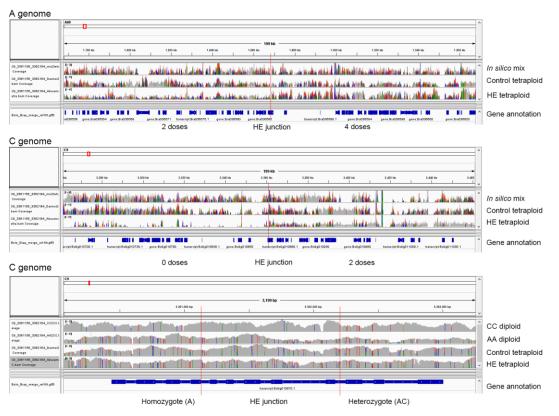
HE junction 91.

A genome		
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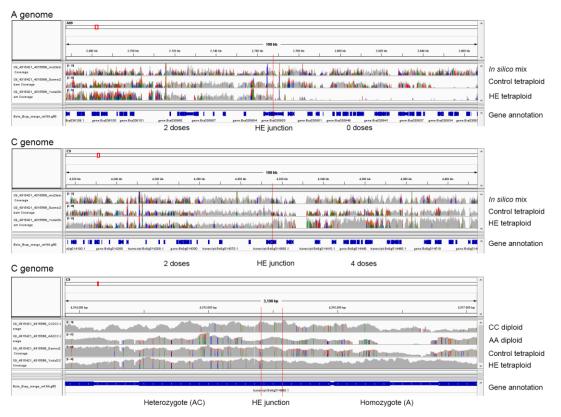
HE junction 92.

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HE junction 93.



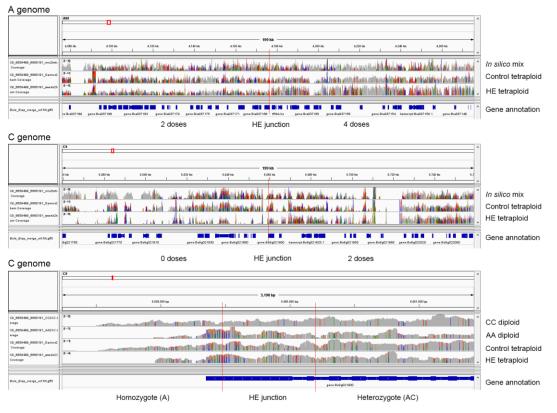
HE junction 94.



HE junction 95.

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	Homozygote (C) HE junction Heterozyg			
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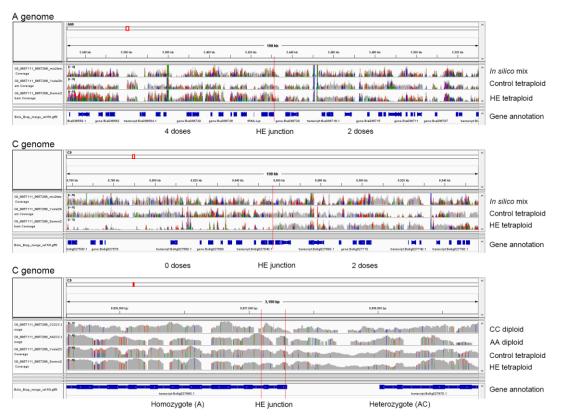
HE junction 96.



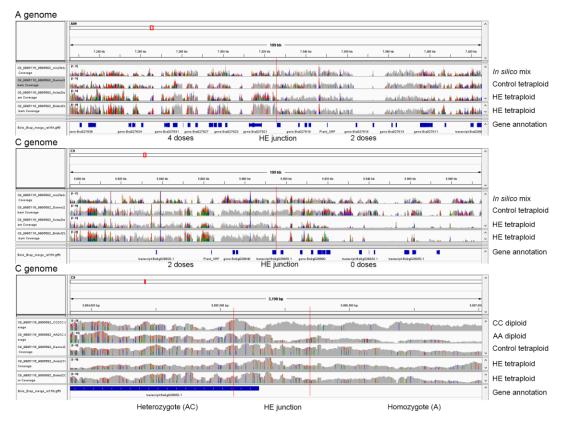
HE junction 97.

A genome		
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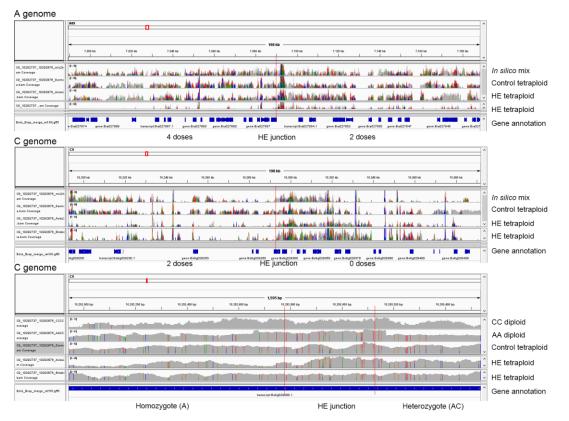
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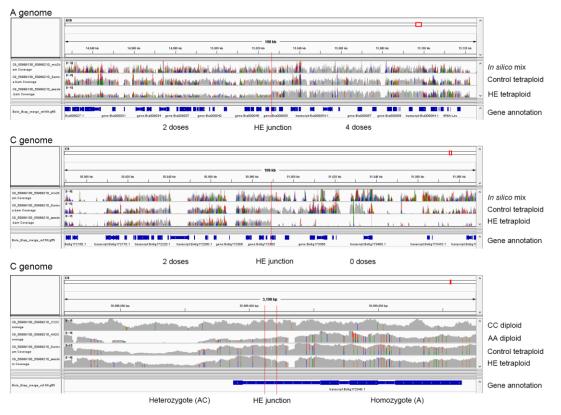
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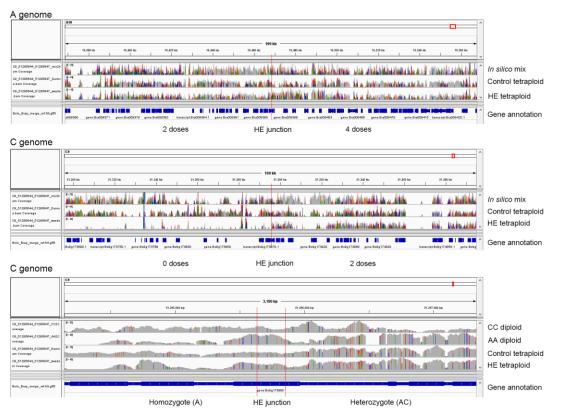
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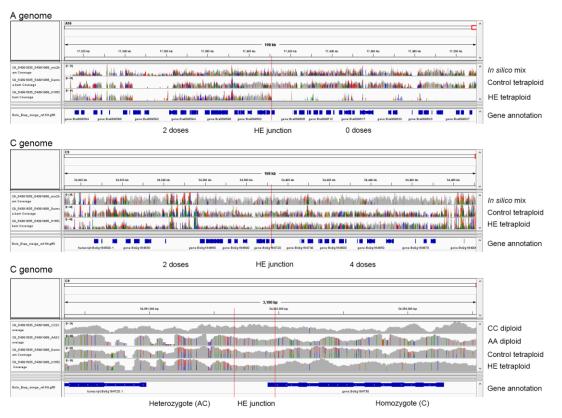
HE junction 101.



HE junction 102.



HE junction 103.



HE junction 104.

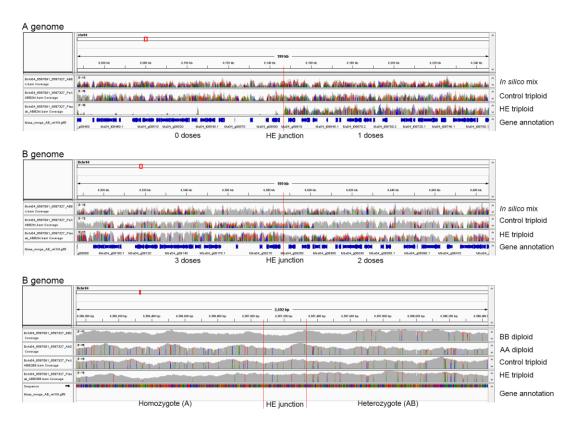


Fig. S16. IGV panels of HE junction regions in triploid banana (AAB and ABB, 21 junctions). The top and middle panels show the sequencing depth around HE junctions in both A and B subgenomes, respectively. Red lines indicate the position of HE junctions and genome dosages are shown on both sides of HE junction. The bottom panel shows the genotypes (homozygote or heterozygote) around HE junction (region between red lines) based on SNP genotyping.

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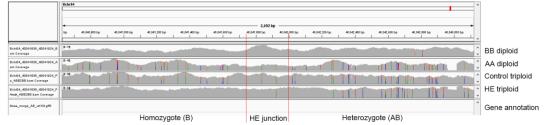
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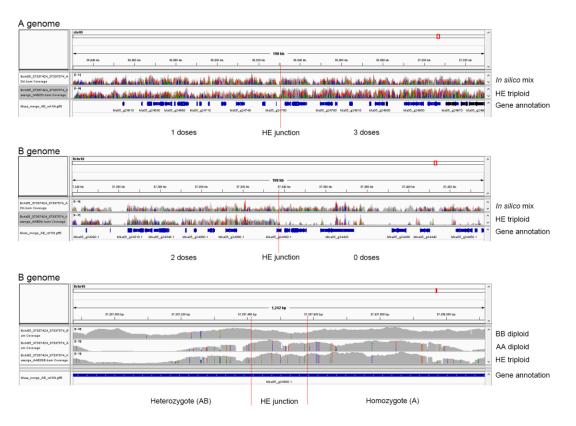
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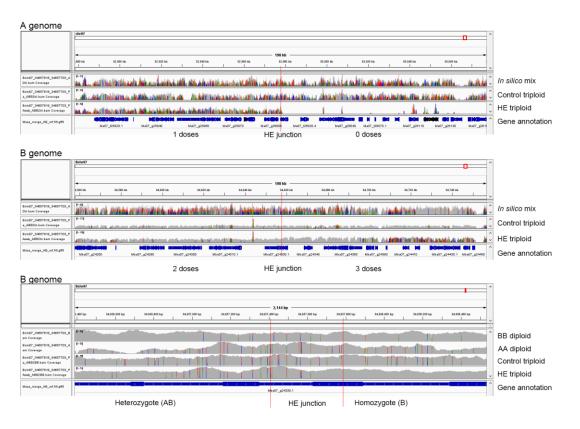
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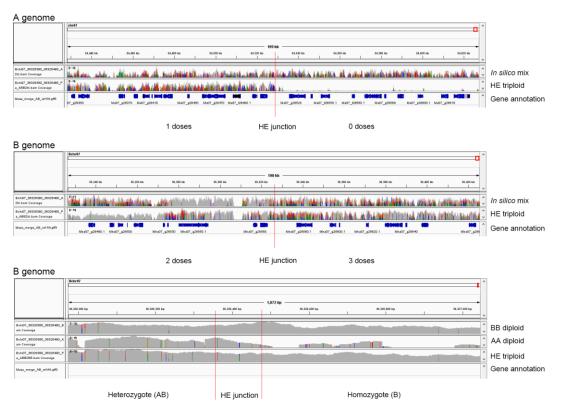
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HE junction 9.



HE junction 10.

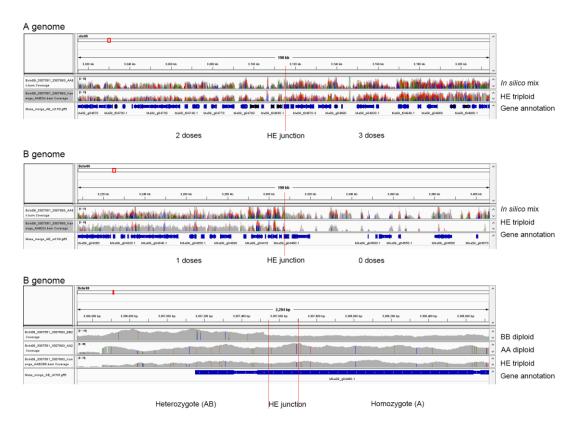
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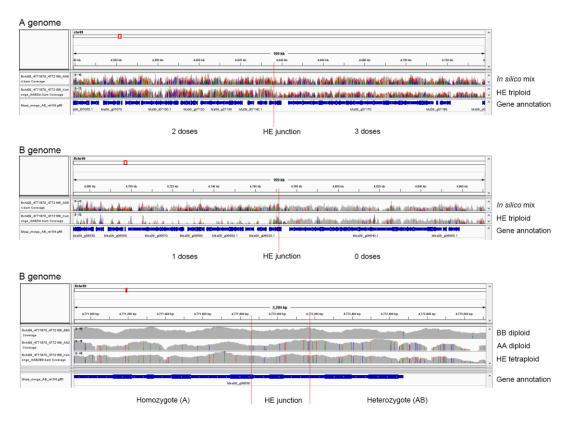
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HE junction 12.



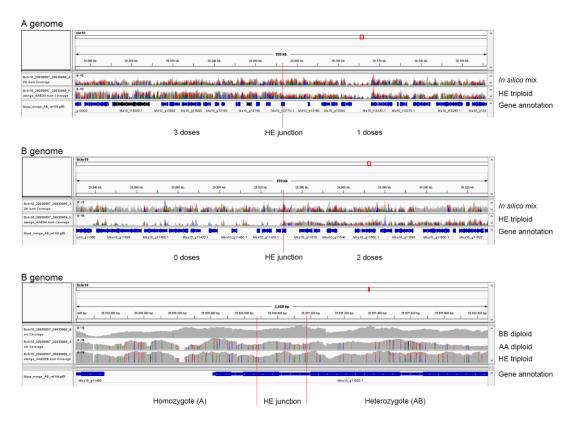
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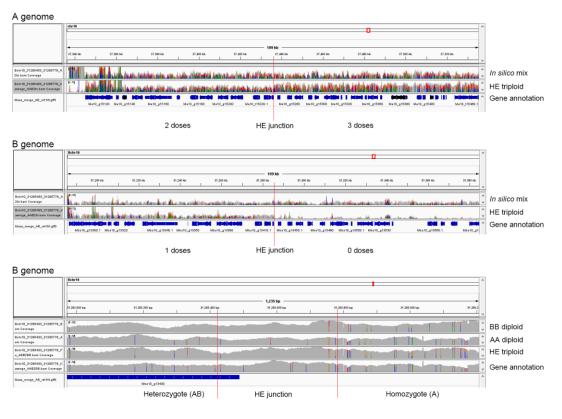
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3 genome		
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	+	
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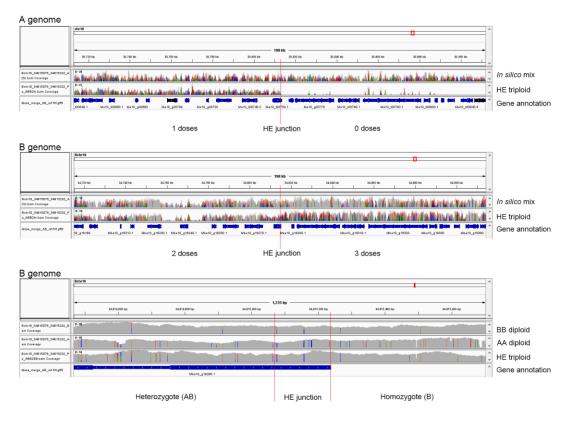
HE junction 15.



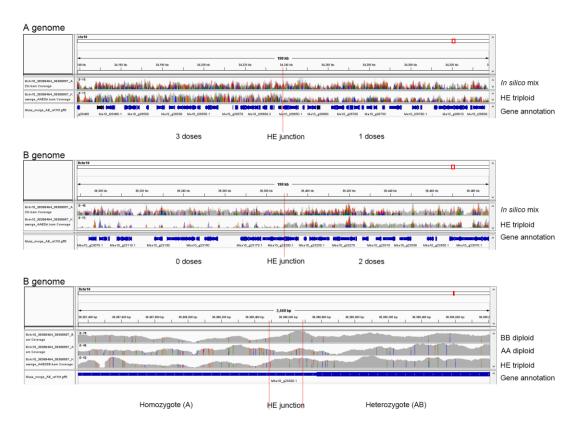
HE junction 16.



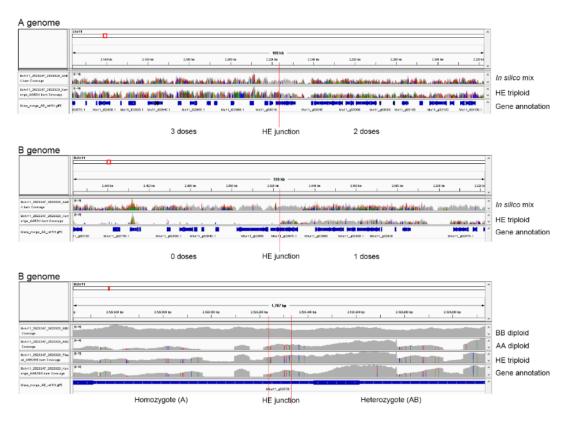
HE junction 17.



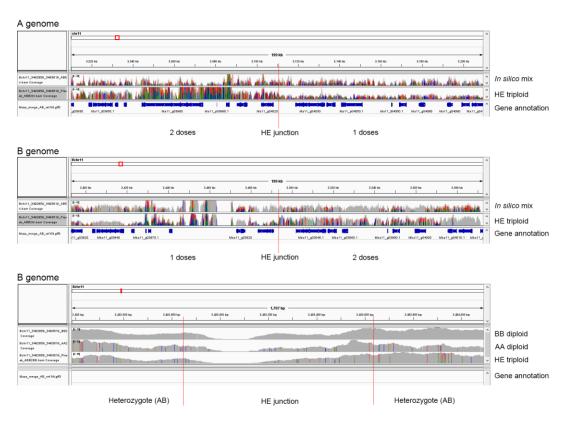
HE junction 18.



HE junction 19.



HE junction 20.



HE junction 21.

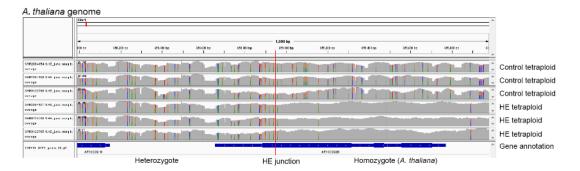
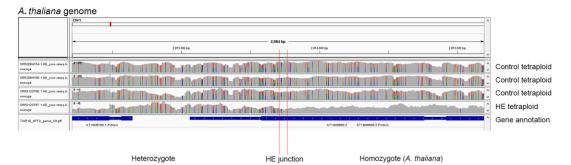


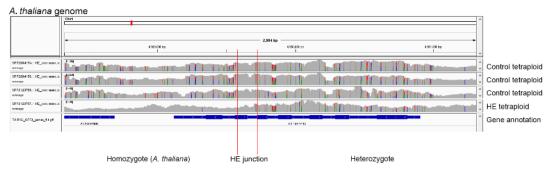
Fig. S17. IGV panel of HE junction regions in *Arabidopsis suecica* (9 HE junctions). The panel shows the genotypes (homozygote or heterozygote) around HE junction (region between red lines) based on SNP genotyping.

A. thaliana ge	enome	
	0e	
	4 1,900 kp *	
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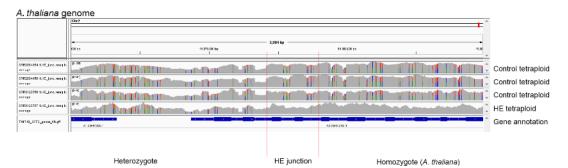
HE junction 2.



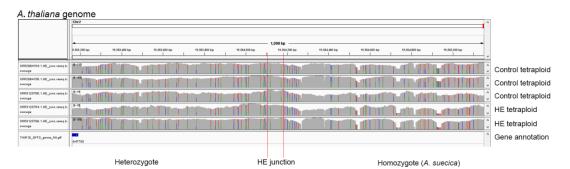
HE junction 3.



HE junction 4.



HE junction 5.



HE junction 6.

A. thaliana genome

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SRR3123760.1.HE_juno.reseq.b; overage) HE tetraploid			
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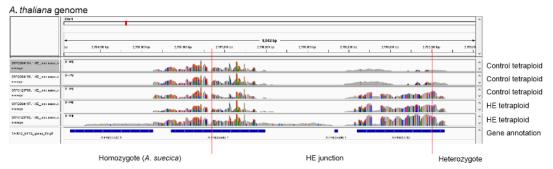
Heterozygote HE junction Homozygote (A. suecica)

HE junction 7.

A. thaliana genome

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	Listeren wete			
	Heterozygote	HE junction	Homozygote (A. suecica)	

HE junction 8.



HE junction 9.

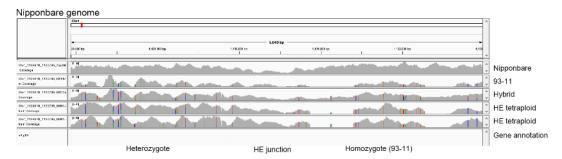
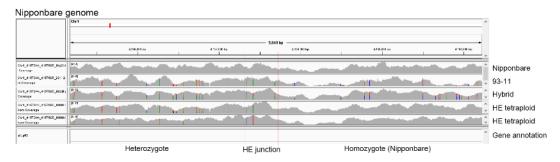
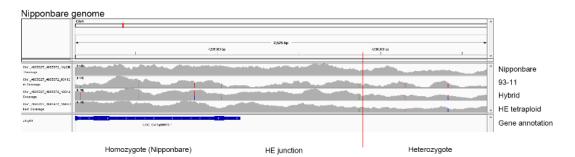


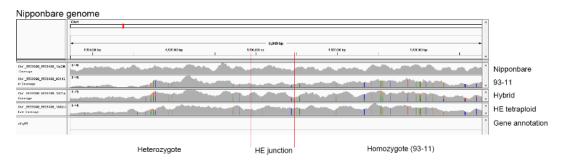
Fig. S18. IGV panel of HE junction regions in synthetic tetraploid rice (166 HE junctions). The panel shows the genotypes (homozygote or heterozygote) around HE junction (region between red lines) based on SNP genotyping between (Nipponbare and 93-11).



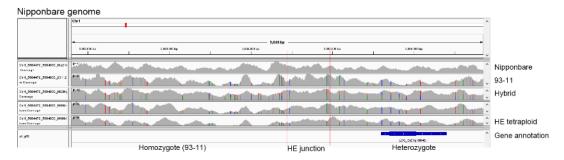
HE junction 2.



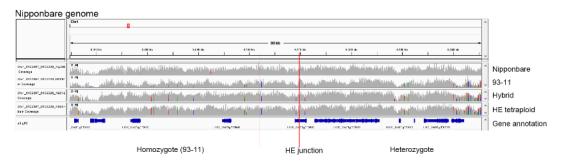
HE junction 3.



HE junction 4.



HE junction 5.



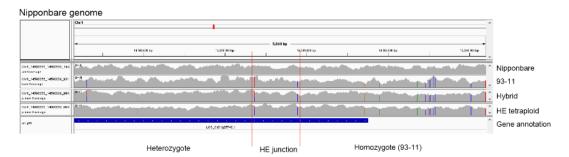
HE junction 6.

List Sectors Sectors Junctive 1 <t< th=""><th>Nipponbare</th><th>genome</th><th></th><th></th><th></th><th></th><th></th></t<>	Nipponbare	genome					
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HE junction 7.

Nipponbare	genome					
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21.813					ŕ	Gene annotation
	Homozygote (93-11)	HE junction		Heterozygote		

HE junction 8.



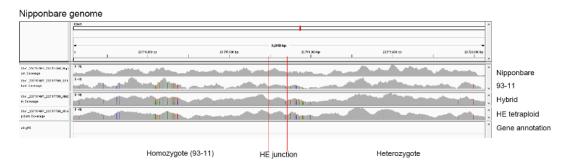
HE junction 9.

	Deri	^	
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(_1000070_100054'1_002 Severage			Hybrid
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с_1009070_10090F1_HV2 аль бонгар		dia and a second s	HE tetraploid
1583	Homozygote (93-11) HE junctio	Heterozygote	Gene annotation

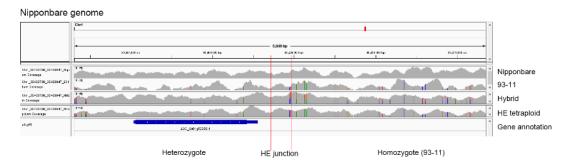
HE junction 10.

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_21223899_21234992_66M				1	HE tetraploid
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un.	Homozygote (93-11)		on Heterozygote		Gene annotation

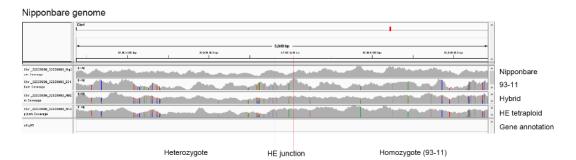
HE junction 11.



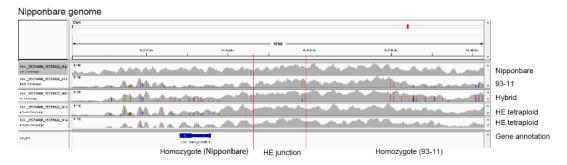
HE junction 12.



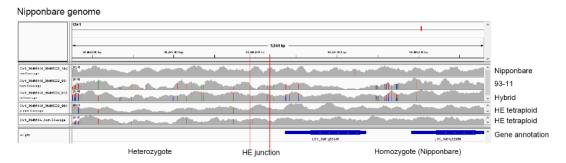
HE junction 13.



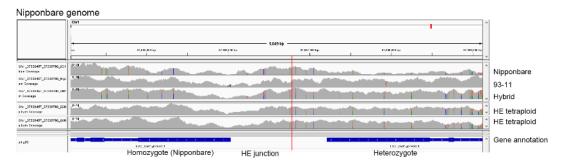
HE junction 14.



HE junction 15.



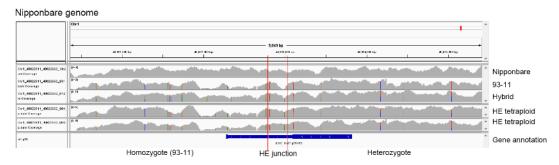
HE junction 16.



HE junction 17.

Nipponbare	genome	
Cbr1_40506040_40506220_666 am Coverage		Nipponbare
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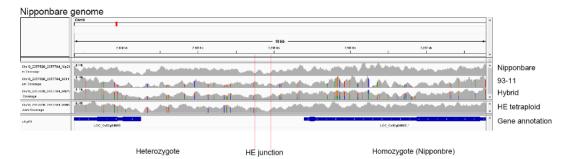
HE junction 18.



HE junction 19.

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HE junction 20.



HE junction 21.

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	Homozygote (Nipponbre)	HE junction	Heterozygote	

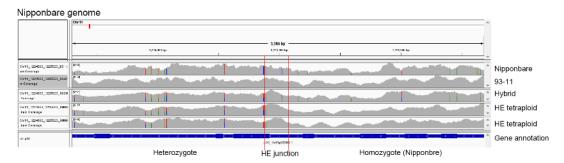
HE junction 22.

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HE junction 23.

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GA-13_14040844_14041837_5H iy kan Counage			in constant		1° Instanto i	HE tetraploid
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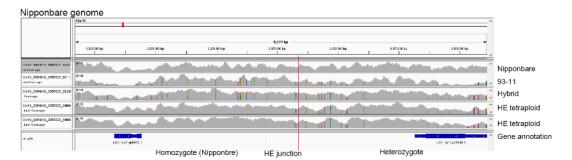
HE junction 24.



HE junction 25.

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	Heterozygote	HE junction	Homozygote (Nipponbre)	

HE junction 26.



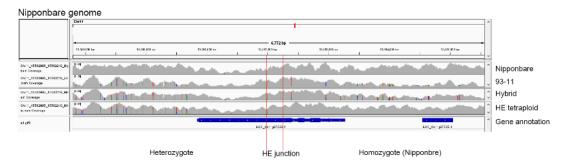
HE junction 27.

Nipponbare g	genome	
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HE junction 28.

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HE junction 29.



HE junction 30.

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	Homozygote (Nipponbre)	HE junction	Heterozygote	

HE junction 31.

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	Heterozygote	HE junction	Homozygote (Nipponbre)	

HE junction 32.

Nipponbare g	genome	
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	Heterozygote HE junction Homozygote (93-11)	

HE junction 33.

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	Chrtt			^
	- X/316 21/X16 X/326	13 kb 8./3	• • 20/Xi6 ¥.09.6 X.09.6	~
ылт_ансказац_ансказац_н. у Сахнари	The second s	and shares	and a product of the first of the first of the second product of the second second second second second second	Nipponbare
h11_28432840_28433866_23 are Converge	through a part of the first strength of the second strength of the	-	and a second different filler	93-11
r11_25402040_35400995_6H Sevenage		(Contraction)	and the second	, Hybrid
vil_30402040_304030905_88 Sam Governge		dia ang si		HE tetraploid
-1_28432840_28433006_22 524 Cave Up	ให้กับในไม่ชื่อข้างของในไม่เหตุสามีประกอบไป	in the state		JHE tetraploid
1,640		1		 Gene annotation
	Homozygote (Nipponbare)	HE junction	Homozygote (93-11)	

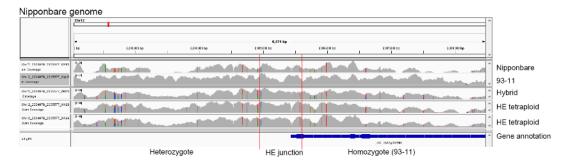
HE junction 34.

Nipponbare g		×	
		1004-0 1008-000-000-000-000-000-00-000-00-00-00-	
Charlo 1232308 1234691 Ny21 In Countyp			Nipponbare
0h12_1032000_1034434_0011 at Contage	la subdition and a state of the first of the subdivision of the	Martha the second s	93-11
CPU12_1032300_1034434_6H29 Generative			Hybrid
0+12_122208_1234091_0085 Jun towap	California and Michael Alice has a star ful	ومرود الأفاتات المرام فيشرف والمتشف والمتناف	HE tetraploid
Ching_1002000_1004404_66841 Joan Coverage	Tentenas activitation as a definit	🗘 🗤 an air Ailtean Anthraithean a chron à chuirtean 🕯	HE tetraploid
a1 (19	H	100 c317 graves	Gene annotation
	Homozygote (93-11) HE junc	ction Heterozygote	

HE junction 35.

Nipponbare g	genome	
	A	
	Κ/21 Ιφ Κ/22 Ιφ <	
Ca-12 Statement Statement (1977) are Coverage		Nipponbare
04-12_1437863_1437805_N92/ m George		93-11
0%42_407083_407608_9%2H Centrage		Hybrid
01-12_1407053_1407025_9910 her Gronge		HE tetraploid
0x-12_1407008_1407020_991M .hev Gevenge		HE tetraploid
มเมช		Gene annotation
	Heterozygote HE junction Homozygote (Nipponbare)	

HE junction 36.



HE junction 37.

Nipponbare g	enome				
	0ii)2				^
	4.780,981 to 4.780	6,424 hp	4,42,303 pp	2,493,300 kp. 2,494,300 kp.	~
0h12_4700920_4701191_01p21 m Develope	29				[^] Nipponbare
CHV12_4703928_4701191_6511 av Chvenge		in the	المرجلة والمرجلة والمرجلة	handhad hadh.	93-11
05-12_2200036_42031001_00036 05990056			and the first first of the second		, Hybrid
Chri2_4700920_4701191_6684 Ann Courage	51	in parts		he state data printing and	HE tetraploid
CH12_4780928_4781191_0084 Iven Countyp	19	in the second			HE tetraploid
دا و ا د	102_04/3Q29099			L00_01/2g00133	Gene annotatio
	Homozygote (Nipponbare)	HE junction	Heterozygote		

HE junction 38.

Nipponbare g	jenome		
	Ciri)	^	
Chil2_10101907_10102657_Ni bar Coverage		^	Nipponbare
CF / 2_18 10 1967_18 102007_83 Jum Coverage			93-11
СБ-С2_14-10-1162_14-162062_06 ам Сампара	in a data any data ang data ing		Hybrid
CF-12_19101067_19102667_08 p.taan Care age		-	HE tetraploid
1110	Loc extreme	^	Gene annotation
	Homozygote (93-11) HE junction Heterozygote		

HE junction Homozygote (93-11)

HE junction 39.

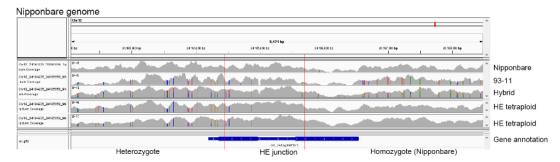
Nipponbare g	lenome			
	Chrt2		^	
	all 701.0X bp		4711,52 4613,57,52 4613,57,52 4	
Dar2_2001708_2001872_H bay Gwange				Nipponbare
0412_22781700_22781877_23 Juan Connage				93-11
CH12_22701709_22701077_28				Hybrid
CFv12_22701709_22701077_22 b.sem Coverage				HE tetraploid
al 510			*	Gene annotation
	Heterozygote	HE junctio	n Homozygote (93-11)	

HE junction 40.

Nipponbare g						
				1	^	
	4.45 25,01% MS 25	12 kb -	23 822 ha	22.034 ab	2,225 46	
0.9-12_22620125_22620710_1/k bars Coverage		a second and set with			م المراقعة المحمد الم	Nipponbare
сь по_завортна_завор7 по_ки Заам Сампара	P.N.	فمقاصف أسقاله	h dhalan in ha	1990 Automa	man na si a	93-11
0+12_20000140_20000210_50 am 0xee age		dadeddbiddi	in the factor of the	hini da an an tao an	t de trinsland 🕻	Hybrid
ice-12 concerner concerns An Ip have Deverage		التقار والتسوير ووالا	in ha ni di sina ma	the state of the state of the	ning had til 0	HE tetraploid
al gra	C_0412g00000.1 L0.0_0412g00000.1		C6_0+12#39900		_06_0x12g399.0	Gene annotation
	Homozygote (93-11)	HE junc	tion H	eterozygote		

Homozygote (93-11)

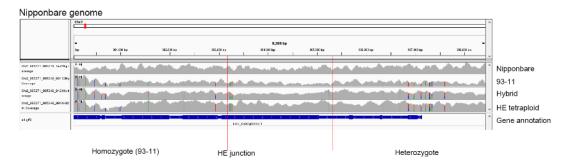
HE junction 41.



HE junction 42.

Nipponbare	genome					
	CH2				^	
	• 513.62kp	4,83 949 Xibp	13 bp 515.80 up	96.08	u •	,
Chi2_012255_014173_Mi221(p) rectage	PR Construction of the second second				- I	Nipponbare
Ch42_913355_914178_93115H (Coverage		with the second s		Contractory of the second	n	93-11
1942_015235_024123_04285_6 901 23 0			in the second second	n finan fi Tana si n	1	, Hybrid
сне "ного де на шени са в Сонарн		a di li ba collina a			10) HE tetraploid
a ju					· · · · · · · · · · · · · · · · · · ·	Gene annotation
	Homozygote (93-11)	HE junction		Heterozygote		

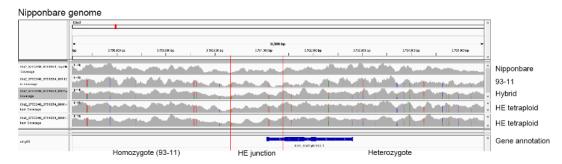
HE junction 43.



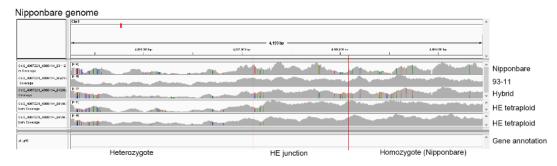
HE junction 44.

iipporibare i	genome		
	Chr2	· · · · · · · · · · · · · · · · · · ·]
		13110	
	2 800 to 2 800 to	2 300 ks 2.539 kb 2.539 kb 2.539 kb	
-27 2929228 299-007 00112 Levelage	والمتحدين والمراجع والمتعاقب والمتعاقب والمتعاقب والمتعاول والمتعاول والمتعاوي والمتعاوي والمتعاوي والمتعاوي	المتحالية والأربال ويرجعانه فالألالية ومنتجه والمقرار فالمتعاوين	Nipponbare
42_2070228_2004337_5\b2H	The state of the s	n a dia dia mandri amin'ny soratra amin'ny soratra amin'ny soratra amin'ny soratra dia dia dia dia dia dia dia 🖓	93-11
42_2070220_2004007_948254 ******	فترجيب المحاولة والألفان الأرابية والتعارية والمتحدين والمحاود والمحاول والمراكب والمحاكية ومنها والمحاكم والمحاك		Hybrid
62 2828238 288-537 00052 av Cavelage	والمتعاد المراجع والمراجع والمراجع والمعد المنافع والمعاد المتعادي والمحاد والمحادي والمحادي والمحادي والمحادي	and the second secon	HE tetraploid
N2_2878238_2884337_06H14 av Centege	1 and a structure participants of a primary inclusion of the plant of the structure of the	19 mellen att eine Jahren von Statistischer eine stern sicht aller einen der Statistischer	HE tetraploid
1 (12)	Lectorytem Loc corport Loc corport Loc corport	страни и следование исследниет иссле	Gene annotation

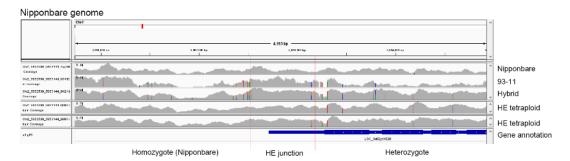
HE junction 45.



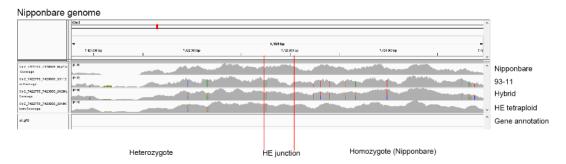
HE junction 46.



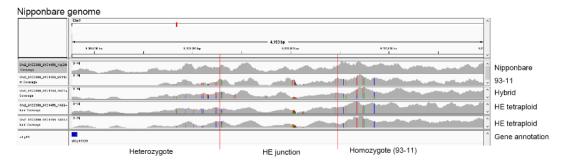
HE junction 47.



HE junction 48.



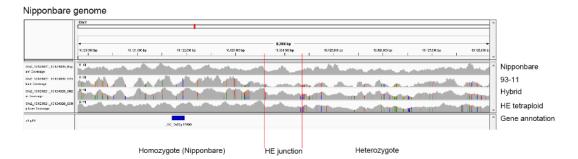
HE junction 49.



HE junction 50.

Nipponbare g	genome			
	Chr2			^
		16 kb 5.000 db 3.0	Ж Ia 24Ж ia 32514 - 32514 I I I I I I I I I I I I I I I I I I I	~
сьедникалакции синтера Сумпари		and a function of the		^ Nipponbare
CF-Q_0005766_0007604_00112 in Secondar	Shake a stopp of the Arth Statements	and a subject to the	والمحمول والمحافظ والمتحافظ والمحافظ والمحافظ والمحافظ والمحافظ والمحافظ والمحافظ والمحافظ والمحافظ والمحافظ	93-11
CH2_0005760_0007094_04233 Committee		na-k-k-na n		 Hybrid
D-2 DESUGE DESUGE DENV: hav Coverge		A. A. Barres		HE tetraploid
416		L00_0x02g17243		[^] Gene annotation
	Heterozygote	HE junction	Homozygote (Nipponbare)	

HE junction 51.



HE junction 52.

Nipponbare 9	0 0				
	4 18.02588.0pp 	4,193 bp	na 11 EMER her		
01/2_10323033_10324031_Mic ars Coverage	PX			Nipponbare	
Ciril_10225053_10024051_001 bars Coverage		distant 1		93-11	
040_10323833_10324031_402 m.Gwewge			لأمريد والمترجي والألفين والتقار فالمتحد والت	Hybrid	
сью_постного посмого т. смн р. Бала Соманда			0	HE tetraploid	
0.4.0_10322033_10324031_5189 p.5am Coverage			a dhu a bha an a bh	HE tetraploid	
al 31 0			~	Gene annotatior	
	Homozygote (93-11)	HE junction	Heterozygote/Homozygote (Nipponbare)		

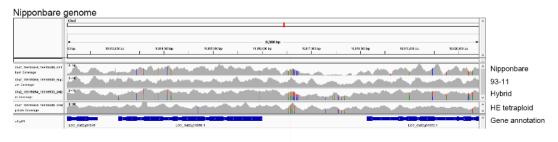
HE junction 53.

Nipponbare					*
	cc CK KA.P	4, 183 kg	11 M2 000 bp	qdCX BAP	v
Chie hieleros hielercan tale ara Constage	P-8				Nipponbare
Gh:2_11607203_11607405_931 Iven Dennage	P-2	and the second	وموركا التصحير وتشاكرهم	يد (ثلث (إفصفت بعدت	93-11
05-0_11607000_11607405_500 re Gevenue	Pre-	and the second	an a Constitution de Cilia	الأرائي حياته ويبر) Hybrid
05-0_11607000_11607485_5169 p.bara Governige	P-N	second the data) HE tetraploid
at gra					Gene annotation
	Heterozygote	HE junction	Homozygote	93-11)	

HE junction 54.

Nipponbare	genome		^	
	1.00K be 122600K be 12207300Ap 1220500Ap	3,3163р 112,818,10	•	
Chr2_10210096_10010554_H pt am Caratage	Manual Association and the second statements of the second statements o		^	Nipponbare
012_15518880_15518884_651 bay Gavenge	if he had a second state of the	here in the first part is a second in the first second		93-11
1942_13210000_13210664_402 m Coverage	The distribution of the data for the district of the district of the district of the district of the distribution of the distr	and the second state of the se	Ŷ	Hybrid
19-27_19230000_192306641_050 p.karn Contage	This is the second s	nindir (İbi Durs, aradı dır.dinarı, "	< >	HE tetraploid
a tu	2	105_0409(1721)	^	Gene annotation
	Heterozygote	HE junction Homozygote (93-11)		

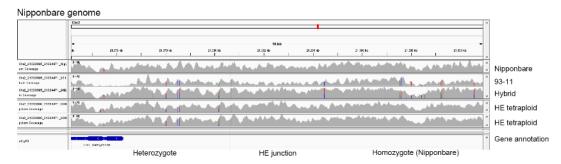
HE junction 55.



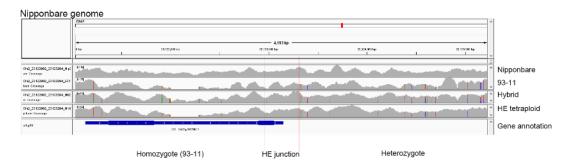
Homozygote (Nipponbare) HE junction

Heterozygote

HE junction 56.



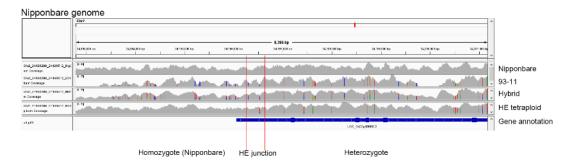
HE junction 57.



HE junction 58.

Nipponbare g	genome			
	Chr2			^
	• 22.011 X0 kp 22.012 X0 kp 22.012 X0 kp	И,386 Бр 24.014.00 Бр 24.01 I I I I	6431 kz 54013400 kz 24343,066 kp	<u>×</u>
the constant constant $\mu_{\rm F}$ as denoted	The second state of the second s			Nipponbare
0142_04010720_04019900_001 kay Cevrogr		and an and a second second		93-11
Chi2_34013723_34019930_H92 m Greenage		it, e.e. a constabilité	The shade the	Ĵ Hybrid
Chi2_2+013720_2+019900_H19 p.bem.Commage) HE tetraploid
0402_24010720_24010008_H10 p.kam.Comrage				JHE tetraploid
цв				Gene annotation
	Heterozygote	HE junction	Homozygote (Nipponbare)	

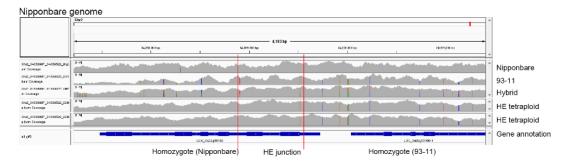
HE junction 59.



HE junction 60.

Nipponbare g	genome			
	Chr2		· · · · · · · · · · · · · · · · · · ·	•
	• 21.44 X33p 25.46	4,193 bp 1,893 bp 1,899 zz 25 46,5% bp	25 HP 408 12	
CH12_25448009_25448108_H p: art Chronage	14		and a second second second second second second second second second second second second second second second	Nipponbare
01/2_22445009_22440100_631 hav Gevenge	Condition and the second			93-11
01/2_25445009_25446106_162 m Coverage				Hybrid
terzyjst ensameljst energie pitem Coverage				HE tetraploid
al (†2		L01_0402p40110	L01_00074310	Gene annotation
	Heterozygote	HE junction	Homozygote (Nipponbare)	

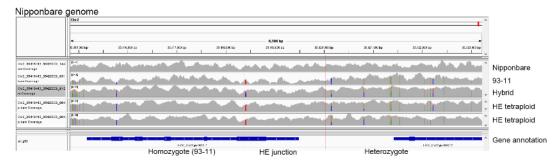
HE junction 61.



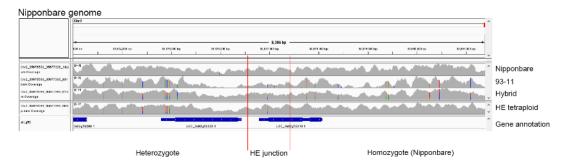
HE junction 62.

Nipponbare g				
	Chr2			^
	-	15 kb	-	
	130ka 25,132 do 25,134 do 35,131 ko	35.138 Hb	25,148 Ab 25142 ko 25.148 ko 26.563 kb	~
13-27 20137218 20133423 H p; 201 Develope		ay garage and the last	and the state of a state of a state of a state of a state of a state of a state of a state of a state of a state	Nipponbare
0542_30162218_30168403_661 hav Grenge	1-1	ويرجع أحجم وير	A state of the second stat	93-11
n Longo		hand a second second) Hybrid
(h42_05107210_05109420_044 p.bets Coverage		and a second second) HE tetraploid
(ha2_35137219_35139423_)453 p.barn Coverage	F-1	and the second states	and defining a field of the base of the ball) HE tetraploid
11.512	LOC_042457880 000_042457880 1			 Gene annotation
	Homozygote (Nipponbare)	HE junction	Heterozygote	

HE junction 63.



HE junction 64.



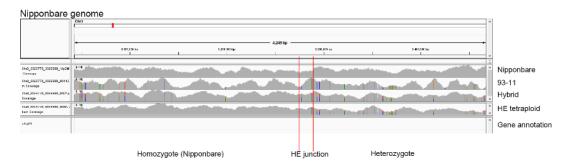
HE junction 65.

Nipponbare	genome								
	Dir3							^	
		16 kb							
	240 Ma 0075a 0045a 200 Ma	201	a.	300.06	380 16		10 d hás	•	
D-200812-00080-000-000-00 TANDA		1		January A.	and the second second		and the state of the state of the state of the state of the state of the state of the state of the state of the	^	Nipponbare
CH6_388243_388899_03112H1 Convege	ومعتقدتهم والمعرفان والتلك المتنبية فالتركي والمتحدث والمترك والمتركب والمتكر المتكري والمتحال والتكر			أمحي ومطاقة	Mitchen	. A.M.	h (na an the second sec		93-11
CH0_305243_300535_912M5.b	hill had a	-		de terre de	10 milliona	and h	li de de de de de de de de de de de de de		Hybrid
Ch0_000340_000508_9941972 m Devenge	The first sector to district the first first of the first sector first sector first first sector first first sector first first sector first			, ha ha she she	al barbara di	الأمريكي والم		\$	HE tetraploid
am	Long _ostay precs_1	L01_0403gD1110		2 4 LDG_0602g016201	L01_0403#	_		^	Gene annotation
	Heterozygote	HE junctio	n		Homozy	gote (Nip	ponbare)		

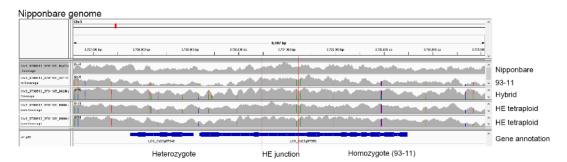
HE junction 66.

Nipponbare		
Сно_3237650_3230307_11(;2)И Селемиря	19 day day bar bar bar bar bar bar bar bar bar bar	Nipponbare
chuq_3037050_3034887_68113 m.Coverage	When a pairs in the first start of the start	93-11
анас, же жила с же жила с лага с у Соматира		Hybrid
0463_2227090_2228987_54684 kar Cornige		HE tetraploid
0445_3237450_3230397_44664 kar Greenge		HE tetraploid
-1 (19	Homozygote (Nipponbare) HE junction Heterozygote	Gene annotation

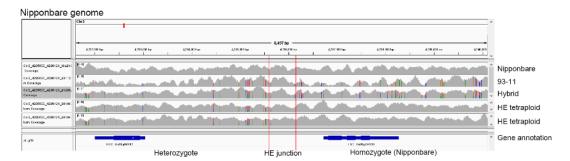
HE junction 67.



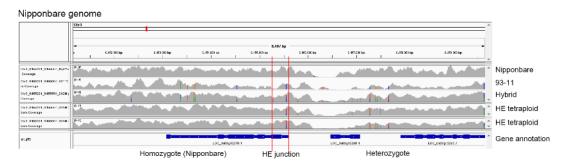
HE junction 68.



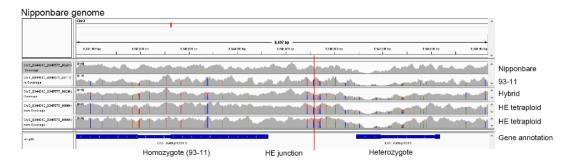
HE junction 69.



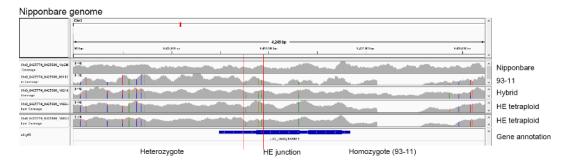
HE junction 70.



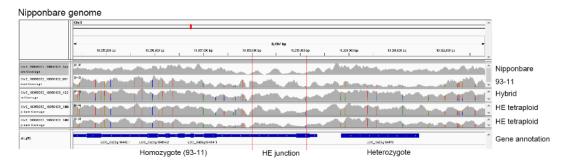
HE junction 71.



HE junction 72.



HE junction 73.



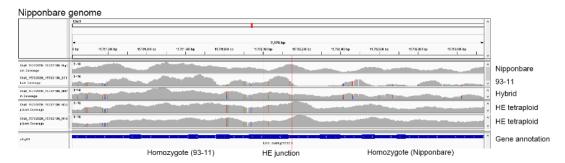
HE junction 74.

lipponbare g	genome				
	CIE3			^	
	и 12//Пер 12/ЮВа 12/ЮВа 1 I I I I	15 kb 12.413-do 12.413-do	12/31 lib 12/22 lib 12 60/14 I I I		
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ard_12417425_12418145_931 art Dansage	ne Line nearbailt ann ann an All a Bhailtean Ann	årill detertation.			93-11
сью_томпонал_томпетиц_сар в большде		in the state of th		ilulium en C	Hybrid
140_12417405_12410145_589 Chara Gaverage		i litta a tachada 🔒 👘		vivivi ni C	HE tetraploid
ala 12012428 12018118 AND Alaw Cavelage		hilderendersein,			HE tetraploid
e: Alex	L01_0409217301		6 6 6 6 6 U06_063ij2		Gene annotation
	Heterozygote	HE junction	Homozygote (93-11)		

HE junction 75.

Nipponbare g	genome					
	Chra	-			^	
		•				
			3.437 to			
	300 kp 13,744 000 kp 93,7151,000 mm	10,198,000 kps 10,207,0		58 (85 kg) 151 (70) (38 km 151 (77 (30 km	~	
снир_10785767_10787021_М р: им Семенари				······································	^	Nipponbare
044_12205707_12207021_651 bay Gavenge		and the second second second	Alternative sectors and			93-11
is at the second			a the second second second second second second second second second second second second second second second		¥	Hybrid
Ch48_12288787_12287021_00H # Auro Donnage	6.9	1 million have			Ĵ	HE tetraploid
cnus_15705707_15707021_6600 p.barn Doverage		The second			÷	HE tetraploid
a1 (#)	L01_000304030.1	.	L00_0403434210.1		^	Gene annotation
	Heterozygote	н	E junction	Homozygote (Nipponbare)		

HE junction 76.



HE junction 77.

Chr3	0		^^	
15,1% He	33 kb -	16 (20 ks	1 1 1	
Parisonal filler scher here einen state	Propagation and a grant state of the second s	The first second state of the second state of the second state of the second state of the second state of the s	and the second states of the second states of the second states of the second states of the second states of the	Nipponbare
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27	dan dan da karakar	والمرجع والأفراد والمعادية والمحافظ والمح	Manager and Market	Hybrid
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HE junction 78.

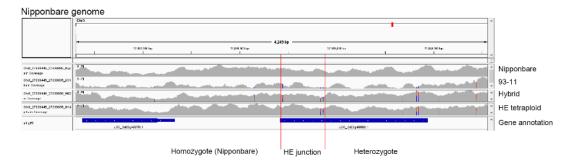
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HE junction 79.

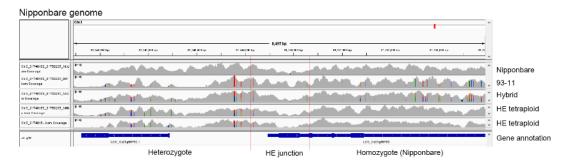
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Homozygote (Nipponbare) HE junction Heterozygote

HE junction 80.



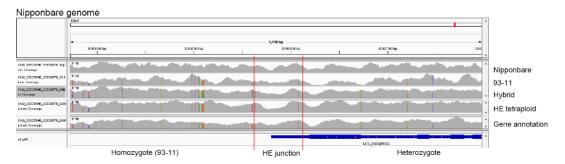
HE junction 81.



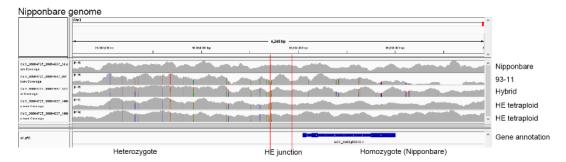
HE junction 82.

Nipponbare g	genome				
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	Homozygote (Nipponbare)	HE junct	ion	Heterozygote	

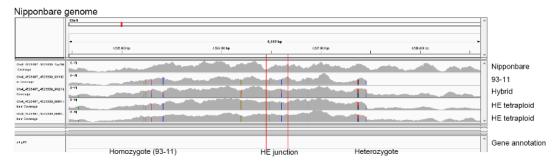
HE junction 83.



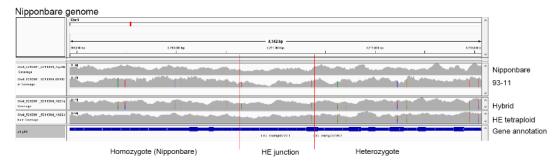
HE junction 84.



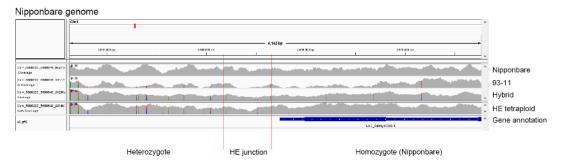
HE junction 85.



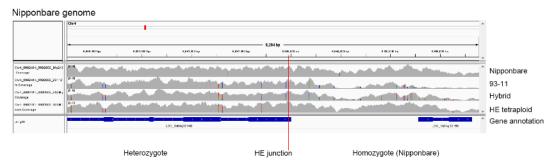
HE junction 87.



HE junction 88.

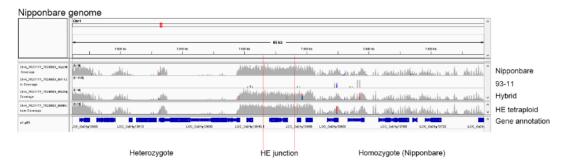


HE junction 89.

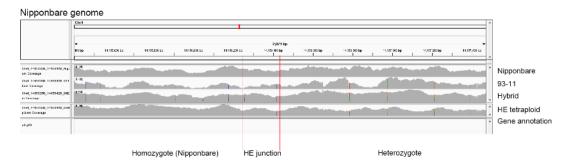


Heterozygote

HE junction 90.



HE junction 91.



HE junction 92.

Nipponbare g	genome	
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HE junction 93.

Nipponbare genome

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Heterozygote HE junction

Homozygote (93-11)

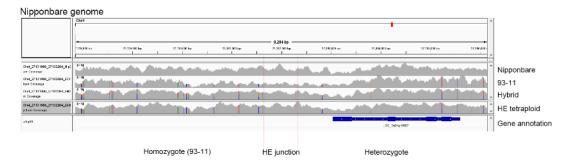
HE junction 94.

Nipponbare	genome			
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	Homozygote (93-11)	HE junction	Heterozygote	

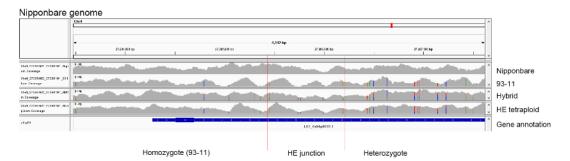
HE junction 95.

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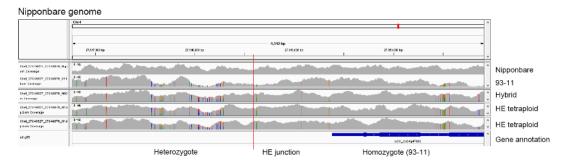
HE junction 96.



HE junction 97.



HE junction 98.



HE junction 99.

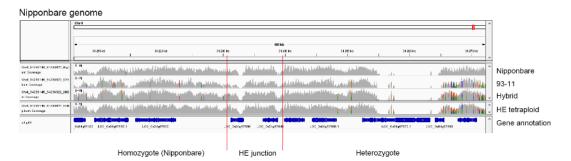
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		Homozygote (93-11)	HE junction	Heterozygote		

HE junction 100.

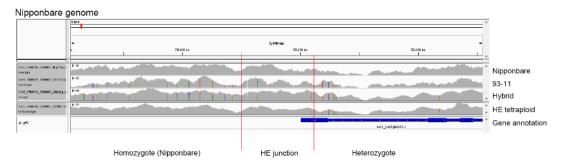
Nipponbare genome

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HE junction 101.



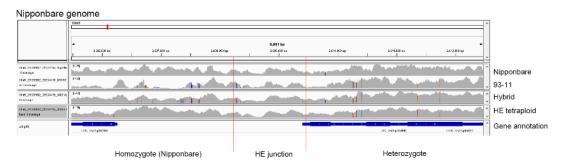
HE junction 102.



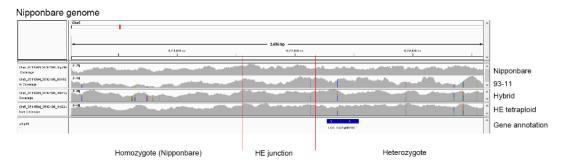
HE junction 103.

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	Heterozygote	HE junction	Homozygote (Nipponbare)	

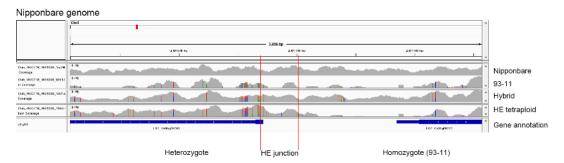
HE junction 104.



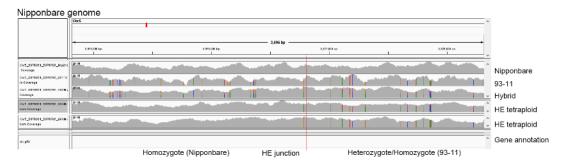
HE junction 105.



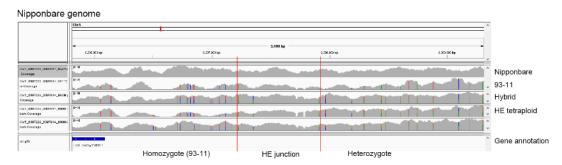
HE junction 106.



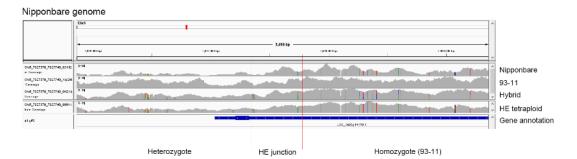
HE junction 107.



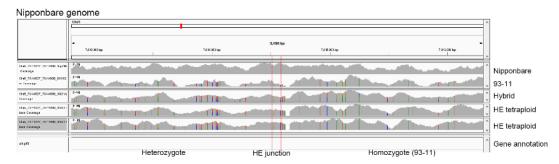
HE junction 108.



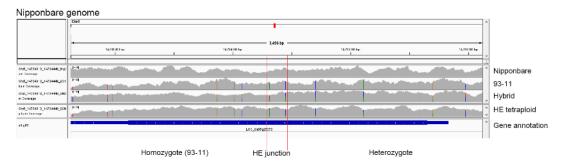
HE junction 109.



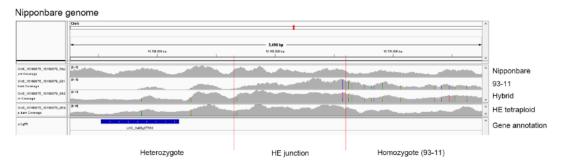
HE junction 110.



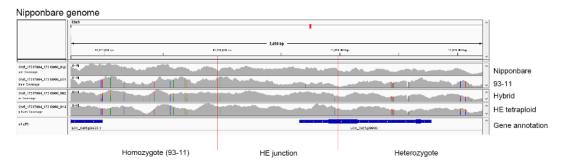
HE junction 111.



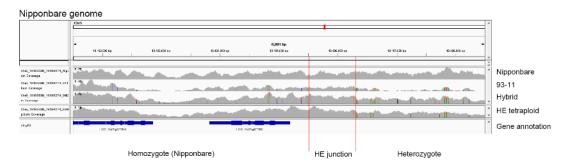
HE junction 112.



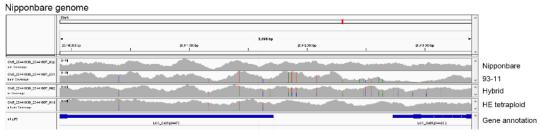
HE junction 113.



HE junction 114.



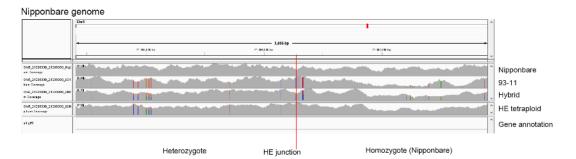
HE junction 115.



Heterozygote HE junction

Homozygote (Nipponbare)

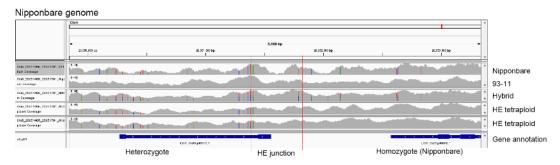
HE junction 116.



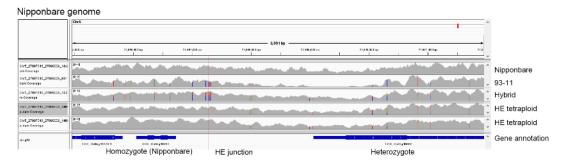
HE junction 117.

Nipponbare	genome					1
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0665_21550499_21553201_068 p.ham.Commun.	March and the second se				· ()	HE tetraploid
11.00					î	Gene annotation
	Heterozygote	HE junctio	n	Homozygote (Nipponbare))	

HE junction 118.



HE junction 119.



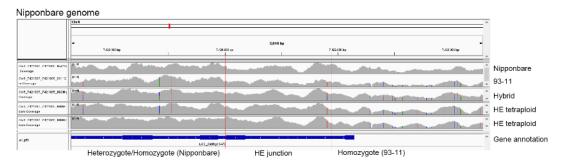
HE junction 120.

Nipponbare g	genome				
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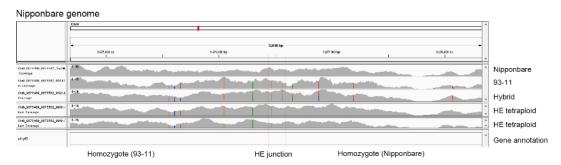
HE junction 121.

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. 7 0	Heterozygote HE junction	Homozygote (Nipponbare)	Gene annotation

HE junction 122.



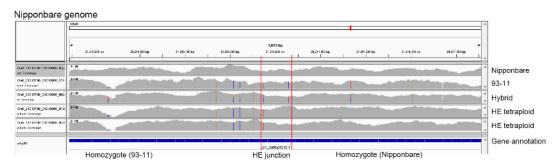
HE junction 123.



HE junction 124.

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642 6	Homozygote (Nipponbare)	HE junction	Homozygote (93-11)	rational recombase	Gene annotation

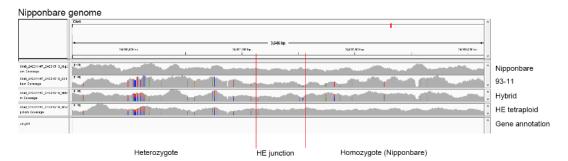
HE junction 125.



HE junction 126.

Nipponbare	enome ^{ENF}			•
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Chu6_21200092_21209255_H10 p.hem.Commun	P3) HE tetraploid
a1,412		о <mark>сазужно</mark>		Gene annotation
	Homozygote (Nipponbare)	HE junction	leterozygote	

HE junction 127.



HE junction 128.

Nipponbare	genome			
			1	^
	242278.046 242298.046 241299.66	24782Fr 2	2,795 us 72,795 us 72,795 us 72,795 us 72,795 us	~
CM6_240336 7_24035023_H pt am Directope	1986 and an an an an an an an an an an an an an	An and a second second	A design of the second second second second second second second second second second second second second second	[^] Nipponbare
0146_24033017_24035029_601 hav Gevenge		in provide the first of the	for the second plant, or shows a definition for the	93-11
снио, 2+43301-7_2+4350829_4682 т. Соннада		A flan Arbeiten		🕽 Hybrid
the Charles Constant Sciences (Line Constant)		te la companya de la	Constant and a second second second second second second second second second second second second second second	HE tetraploid
ata	LOC_COM # MAKE LOC_COM br>LOC_COM LOC LOC LOC LOC LOC LOC LOC LOC			Gene annotation
	Homozygote (Nipponbare)	HE junction	Heterozygote	

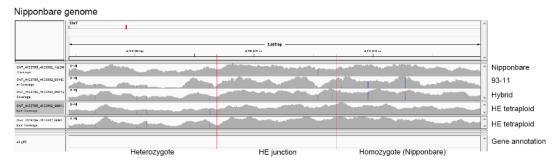
HE junction 129.

Nipponbare g	enome				-
	27 100 ks 	27,458 Mb		27.7336	
0.41_27156632_27166031_5846 am Goverage	P ^{-Q} A style strangers and a first strangers and a stranger strangers and a strangers and a strangers and a stranger		and the second state of th	and the second second second second second second second second second second second second second second second	Nipponbare
es e provins provenjike kari česniga	n n Inne an an Ardena Ardena Ardena an Ardena an Ardena an Ardena an Ardena	ihht.	والمركزة فالمحقمة فالمتحق فاستوجرن والتبر	underhäuten der Mittellich besonen so	93-11
and the second second second second	ner an an die ferste der bester die beste	ΎΥ.		and contributed to a second	Hybrid
0.40_27166633_27166031_546 p.5am Oswange	ha an tha the state of the second second	MT.		nderforward filliging and the	HE tetraploid
	ne alas de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra	Mi.		handdaad fillion braasse,	HE tetraploid
al 1970	Loc_party+4000 1 Loc_party+4000 Loc_party+4000. Heterozygote		HE junction Hom	ozygote (93-11)	Gene annotation

HE junction 130.

	Chi A	
	20.1 m 20	
а с 30041104 (30041127 1.) алб 11 бола хара		Nipponbare
et 28941084 28941271 081 n Concept		93-11
11_28341054_28341271_522 Coverage		Hybrid
al		HE tetraploid
el 200411284 20041223 MBS Sam Osverage	in	HE tetraploid
i ya	A	Gene annotation
	Homozygote (9311) HE junction Homozygote (Nipponbare)	Sene annotatio

HE junction 131.



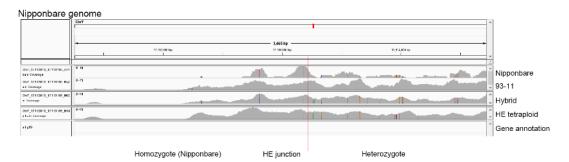
HE junction 132.

lipponbare g				<i>n</i> ,
	755,236 km 7,572,903 km 7,572,303 km 2,575	concites	2 726/2014 m 7,69/300 mm 9,697,900 kp	
N7_7170011_7170099_NIQON Xyonga	F8			Nipponbare
7.,7128011.,7128080,69110 Ссинар		and solar	his and the first second second	93-11
ar 21280 Y 212800 UN255 Sociaje			hard a start of the second second second second second second second second second second second second second	Hybrid
//_7170011_7170099_990154 у Саханда	17		till and an all the full the second	HE tetraploid
/7_7179311_7179939_66H342 • Самтада		الفعلامط	hiter and DDD hiters, and h	HE tetraploid
649			1	[^] Gene annotation
	Homozygote (Nipponbare)	HE junction	Heterozygote	

HE junction 134.

Vipponbare g	Cte?		· · · · · · · · · · · · · · · · · · ·	1
	- 10 13.07.001 80 16.177.003 80	K,830 bp *4.315 300 bp 16.315.00K bp	12.371.071 to %.371.074.07 to 12.371	
CAV_NERVED_NERVED_SAC an Consuge				Nipponbare
G 6 7_16374813_16376233_931 bare Converge	PC	and the second second second second second second second second second second second second second second second	I had a mathin has a submit	93-11
0.0_10074013_10070588_583 m Governge		A second s	hill have the state of process of the first	Hybrid
сь у _поската _поскола _мна р. 5 али Сружида				HE tetraploid
Ce 2, alberak 15, alberazio (1, 546) p. Sani Coverage				HE tetraploid
al 1940	LC LC _LC		LCC_017720000	Gene annotation
	Homozygote (93-11)	HE junction	Homozygote (Nipponbare)	

HE junction 135.



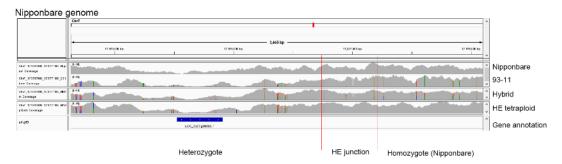
HE junction 136.

Nipponbare g		1
	€531bp	
01/7_17128236_17128644_Npc am Coverage		Nipponbare
0%7_17126296_17126644_091 bars Coverage	The descence with the first of the state of the distribution of the state of the state of the state of the	93-11
Chi7_17128038_17128644_042 m Cave age	in a star and a star in a star in a star of the star in the star in the star in the star of the	Hybrid
Chie_trises M_trises at pow p.kan Coverage		HE tetraploid
Gn7_17125236_171256-04_00% p.kam.Coverage	🗠	HE tetraploid
ی وا ی راند	UR, 647,670 11 101,647,670 1	Gene annotation
	Heterozygote HE junction Homozygote (Nipponbare)	

HE junction 137.

Nipponbare g	genome			
	Uhr L			^
	• 19 70-20165 - 19 70-20165 - 9-00 ХОЗфр. 	1,733 Bp 17 18038 bp 17 18039 bp	т, лая жовр – 17.408 жовр – 12.466.200 во 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	~
CH/7_17179910_17100039_H p1 att Chrystops		the second second second second second second second second second second second second second second second s		^ Nipponbare
0947_17179910_17180099_631 barr Gevenge				93-11
1947_17178918_17188888_982 m Coverage) Hybrid
15-0-17 1700 N_17 160000_0150 p.kan Leonage	1.4) HE tetraploid
al (#3				Gene annotation
	Homozygote (Nipponbare)	HE junction	Heterozygote	

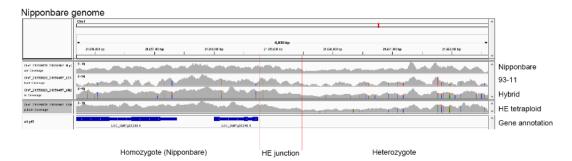
HE junction 138.



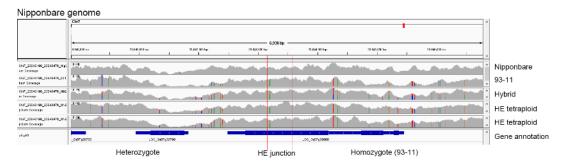
HE junction 139.

Nipponbare g	enome				^
		6,930 hp 10 19,43,00		13 4555K bp 15,455,000 bn	v
CH/7_15400002_15401000_04 p1 av Ch/Atage			والمتحرب والمربي والمحري والمحاوي	The second second second second	[^] Nipponbare
1947_19480082_19481088_931 bay Osyanga	for the first sector in the sector is a sector of the sect	Interaction and the	man that had	all with at the first the start has	93-11
CH/7_10400002_10401000_082 m Severage		here and here	and the second second second second second second second second second second second second second second second	an diarity discontinue da daris.) Hybrid
Ch/7_12400002_12401000_0119 p.k.em.Coverage	Noted that the state of the sta	no-n-dha	and the second second second second second second second second second second second second second second second		< >
ch/7_154e0060_154e1060_84ve a barn Coverage			second second from the		HE tetraploid
11 543					Gene annotation
	Homozygote (Nipponbare)	HE junction	Hetero	zygote	

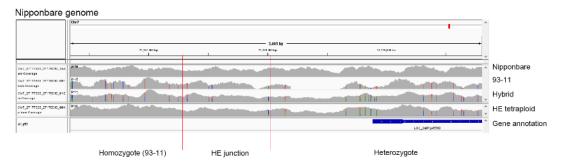
HE junction 140.



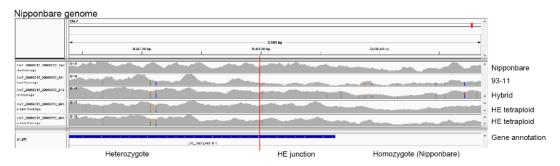
HE junction 141.



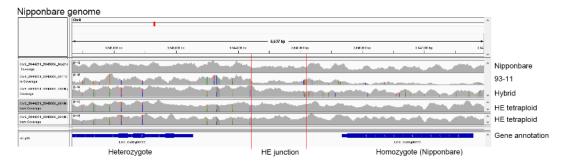
HE junction 142.



HE junction 143.



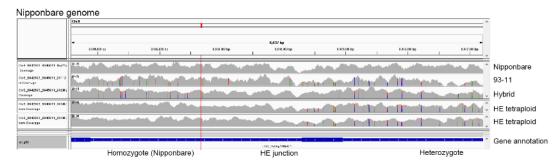
HE junction 144.



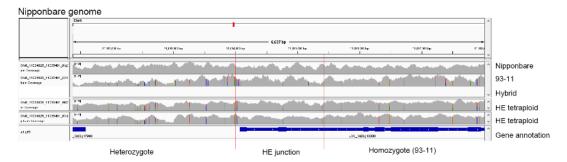
HE junction 145.

Nipponbare	Chr3		×	
	Criti 2005pp Criti 2005pp Criti 2005pp Criti 2005pp Criti 2005pp	6,637 bp	4 *37.0K kp 0 *158.00 m 4.72	
0.48 6125021 6126276 542H Cavelage	1-11		(han a faile and a second second second second second second second second second second second second second s	Nipponbare
040_6125024_6125276_60112 n Develop	and the state of t	and the particular a	The second	93-11
340_6126324_6126276_49244 Seconda			Ministry and a state of the second second second second second second second second second second second second	Hybrid
040_6129224_6128276_19824 htt://www.sec.	in the second of the second second second second second second second second second second second second second		all the discovery defined the address of the	HE tetraploid
4110	Concentration Concentration		L00_00910493.1	Gene annotatior
	Heterozygote	HE junction	Homozygote (93-11)	

HE junction 146.



HE junction 147.



HE junction 148.

Vipponbare	Uni 8				^
			- 3,318.bp	- 	9
chas tocalitio tocalizat Alg: an Dominge	5-21		and the second second second second second second second second second second second second second second second		Nipponbare
0x0_10404110_10405251_001 hav Cavrage	P-4				. 93-11
nak_tizizinin_tizininin_ake n Comage					Hybrid
сыв токалто токалот иза и кат Скалада					HE tetraploid
chull_19+04110_19405251_013 p.b.em.Ck+erage					HE tetraploid
11 (12)	5 - 5	5 5 1 5 1 5	Loc_ocayp1+011	Loc_cumpri-012 100_cumpri-012	Gene annotati
	Homozygote (93-11)	н	E junction	Heterozygote	

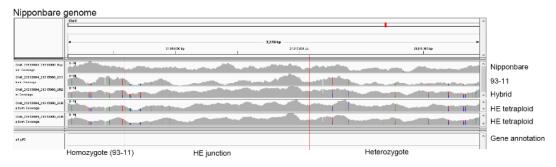
HE junction 149.

Nipponbare g	genome			
	Clea		^	
		3,3158 kgs 23.654.698 ss	20.47 X0.10p 20.4	
Co.4. 20000002 20000024 And an Oceange	P-8		· · · · · · · · · · · · · · · · · · ·	Nipponbare
044_20635602_20636024_931 here Concept			The second secon	93-11
сь « "Ляражса "Лярана» ("152 га боланда				Hybrid
G44 20026422 20026224 005 p.baw Caveuge	P.9.			HE tetraploid
0x6,0000501,0000614,005 p.5am Governge	PR			HE tetraploid
мция			 < 8 < 6 < < < < < < < < < < < < < < < <	Gene annotation
	Heterozygote	HE junction	Homozygote (93-11)	

HE junction 150.

Nipponbare	jenome			
	4 	21.247.000 bps	- 3,319360	
Chie provinsie provinske kaal	p.q			Nipponbare
0645_21246705_21247244_931 Isan Danmage	PR		The second second second second second second second second second second second second second second second se	93-11
019_21248763_2124734_362 m Generate		handhildin.		Hybrid
0140_21246753_21247344_5469 p.5am Garanga				HE tetraploid
NL270			^	Gene annotatior
	Heterozygote	HE junction	Homozygote (93-11)	

HE junction 151.



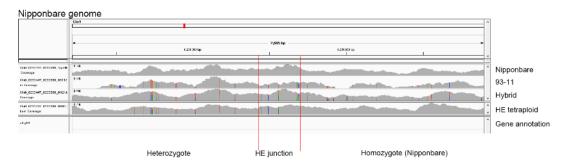
HE junction 152.

Nipponbare g	genome		-
		- 5,5771-p 	<u>.</u>
CA-4	Pitte		Nipponbare
G44_23667122_23667242_031 hart Donney	Phase and the day day of	the state of the second second second second second second second second second second second second second se	93-11
014_23657122_23657342_912 rs Governge	Photo and the state of the state of the		, Hybrid
G4-8 2000/122 2000/242 005 p.kaw Caveuge	Property and the second s		HE tetraploid
al 1940			Gene annotation
	Heterozygote HE	junction Homozygote (93-11)	

HE junction 153.

Nipponbare				_
	Chris			
	1.05500 bp	2,685 bp	500,000 km	
снир_55522906_5600217_11(рай Саханира	Fill			Nipponbare
040_0001000_0000017_00113 m Exempte		particular and the second	In a shine was shown	, 93-11
Chr9_5503996_5600217_19256 Coverage				Hybrid
chu9_5522596_5600217_hNB2- har Granapa	أنبوع بالتلاذات ويجرعهم والترك			HE tetraploid
040_0000006_0000217_44004 kay Cevelage	A Charlen and Charles and Charles			HE tetraploid
11 (17)	L00_069910074		800_00-	Gene annotation
	Heterozygote	HE junction	Homozygote (Nipponbare)	

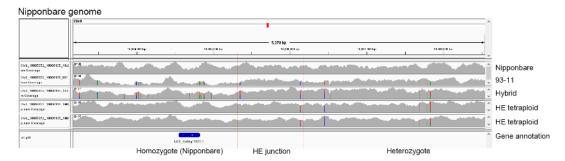
HE junction 154.



HE junction 155.

Nipponbare g	genome		
		*	
	1,427,873 pr 7,4258 pr 7,441,593 pr 7,442,931 pr 7,442,93	1,214,300 (a	
icale presidente presidente da general Economia			Nipponbare
GNG_7461224_7461010_03112 m Coverage	Patra da manda de de la como de de la como de secono de sec	and the second	93-11
ova_versov_versov_assec bars Coverage	[20] Defit [1] (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	.	Hybrid
ickal_vaerosk_vaerono_aasa . bara Coeerage		C	HE tetraploid
at grite	כל כל ל ל ל ל ל ל ל ל ל ל ל ל ל ל ל ל ל	^	Gene annotation
	Homozygote (Nipponbare) HE junction Heterozygote		

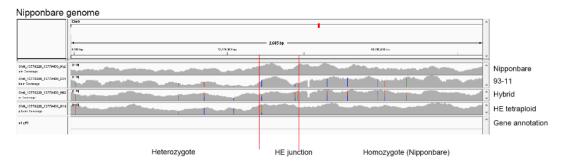
HE junction 156.



HE junction 157.

	genome					
		12,142.HD	121860 121660 5.03¢ 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
h/9_12143200_12144050_11p; m Devenue		ara ng	أسمعه ومرجعه فبالرجع التوسية فاللغان فستسترج والوالية متعاصر ومر	Nipponbare		
NO_12143280_12144880_021 av Caverage		a constantino a		93-11		
249_12143200_12144090_H92				Hybrid		
249_12143200_12144050_1458 them Coursep				HE tetraploid		
a ta			Lee congress :	Gene annota		
	Heterozygote	HE junctior	Homozygote (Nipponbare)			

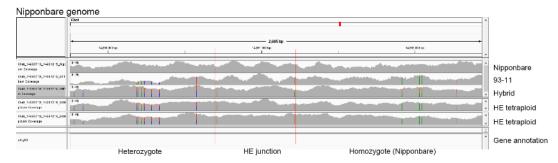
HE junction 158.



HE junction 159.

lipponbare g	(1+1)							^	
	-	12.509 de	4.012 	42 kb	13.520 Ha	1	12.38 Hz		
046_13911151_13910050_555 en Coverage	PTS-CEPTER	and and a substance of the	an an an an an an an an an an an an an a	an an an an an an an an an an an an an a	والمتحرب أكر	Alexandra Maria	A MARKAN AND AND A D	non a trainin 🗅	Nipponbare
ave_taernist_taereess_eer aan Coverage	PERMIT	and definition of the second second	والارتبع ومرجعه والملطان	Manager and a line to serve a	والأبر والأبر	and the first first	and Real Providence	the states a	93-11
os a _ valenninin_ valenskabi_ sab n Goveringe	6.0	port of the second of the	Alternation of the of	والمراثبين أأأ فتتخذ والمعار	a dha an fha	والإخاذة المدمن	11.11 (J. 111)	a Anni Alban 🗘	Hybrid
046_13911151_13910050_5N9 . barn Gevenige	Particular (A)	أمكري والإحمار فيالمعلمات كماري	Manager and the second second second	the second states and s	, de la della	ب المعالما المعمور	and the solution	a hana dan 🗘	HE tetraploid
al 1970	e_ocayzzas	LD1_0406453380	LOE_040935589.1	100_049433410		101_040653480	Loc_cas gaves	LD1_0406533488	Gene annotation
		Homozygote	(Nipponbare)	HE junction		Heterozy	gote		

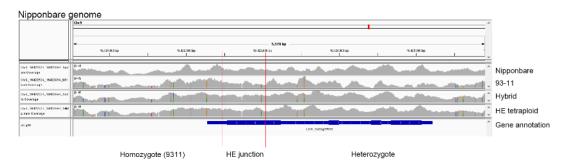
HE junction 160.



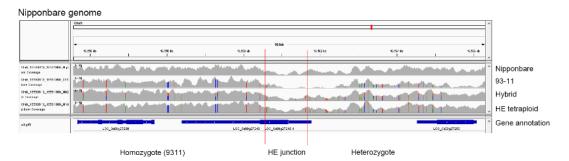
HE junction 161.

Nipponbare g		
	Dana Carala Car	
	- 2,005 bp	
INACTIONNAL TRANSPORTANTS an Dewinge	14	Nipponbare
Child_15021226_15021411_651 halv Cavenge		93-11
снир_тероторы_теротит_уние те Семпада) الالتين من القام ومسيح من عن الألب (تعميناً) بلك و جامع مثلًا أو من من الألب من مثلًا الأن من معا	Hybrid
is all the state of the state o		HE tetraploid
ська тасетель тасета" и на µ burn Econogo		HE tetraploid
a tu	· · · · · · · · · · · · · · · · · · ·	Gene annotation
	Homozygote (Nipponbare) HE junction Homozygote (93-11)	

HE junction 162.



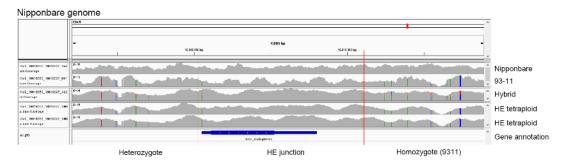
HE junction 163.



HE junction 164.

Nipponbare g	genome			
	Chr9			
		5,370 hp		
	17,698,000 km	17,650,000 kgs	17,085,000 kp 07,000 km	
<u> </u>	EA and a set a			-
Ch.0_17524301_17525206_H p: av: Develope	The second state of the second state of the second state of the second state of the second state of the second	and the state of the second		Nipponbare
0149_17094081_17085280_651 bay Coverage	na an an an an an an an an an an an an a			93-11
1240_1789-081_1789/281_182 In Coverage	na an an an an an an an an an an an an a		had been been an an an and the first of	Hybrid
040_17834381_178342386_00H p.t.am.Connage	Thursday, and the second state of the second s			HE tetraploid
Cr.0_17234361_17235286_00M p kaon Connage	in the second se		hand here a discourse on a second second billing	HE tetraploid
41,013	-		1	Gene annotation
	Homozygote (9311)	HE junction	Heterozygote	1

HE junction 165.



HE junction 166.

Table S1. Chromosome positions of HE junction in wheat A and D subgenomes.

Chr. D	Start D	End D	Chr. A	Start A	End A	Samples	Type ¹	Rank
Chr2	4081262	4081331	Tu2	5854113	5854181	G1 G2	match	pair1
Chr2	30263145	30263479	Tu2	29920319	29920639	G1 G2	match	pair2
Chr2	52046750	52046883	Tu2	45579512	45579643	Н	match	pair3
Chr2	74158600	74158914	Tu2	67784015	67785007	G1 G2	match	pair4
Chr2	75211175	75211301	Tu2	68485323	68485447	Н	match	pair5
Chr2	506421129	506421186	Tu2	631557463	631557518	Н	match	pair6
Chr2	546412191	546412238	Tu2	667713487	667713532	Н	match	pair7
Chr2	559510166	559510721	Tu2	677566210	677566761	I	match	pair8
Chr2	588960618	588961886	Tu2	713427396	713428374	J	match	pair9
Chr3	374870371	374872997	Tu3	488565520	488567696	J	match	pair10
Chr3	396392710	396392948	Tu3	511130697	511130934	I	match	pair11
Chr3	467917911	467918516	Tu3	593690522	593691126	I	match	pair12
Chr3	536297000	536299000	Tu3	651100682	651102829	G1 G2	match	pair13
Chr3	618098378	618100436	Tu3	734062498	734064366	Ι	match	pair14
Chr3	625165404	625165730	Tu3	743197205	743197529	G1 G2	match	pair15
Chr4	517221028	517221122	Tu5	651762614	651762704	I	match	pair16
Chr5	556183988	556184086	Tu4	604288955	604289052	all	match	pair17
Chr5	561442633	561443226	Tu4	607815658	607816345	G1	match	pair18
Chr6	29626000	29628000	Tu6	28046771	28048534	G2	match	pair19
Chr6	390328742	390328999	Tu6	475223901	475224157	Н	match	pair20
Chr6	478071000	478073000	Tu6	557158220	557160221	G1 G2	match	pair21
Chr6	479733727	479734020	Tu6	559593480	559593770	G2	match	pair22
Chr7	583312765	583312819	Tu7	651742736	651742789	Н	match	pair23
Chr2	643692861	643693035	Tu2	744609000	744619000	I	no match	pair24
Chr3	449708292	449711421	Tu3	575953875	575962554	I	low res.	pair25
Chr4	493497185	493497257	Tu5	623025000	623028000	I	no match	pair26
Chr2	39105736	39116042	Tu2	39705000	39708000	Н	low res.	pair27
Chr4	57905217	57905279	Tu4	62579600	62582000	G1 G2	no match	pair28
Chr7	569559483	569567346	Tu7	643189000	643207000	J	shift(12.7Mb)	pair29
Chr2	639513469	639514631	Tu2	737648000	737652000	G1 G2	no match	pair30
Chr6	487078755	487079082	Tu6	569561000	569606000	G1	shift (387kb)	pair31
Chr3	555267182	555267373	Tu3	670210000	670212000	G1 G2	shift (427kb)	pair32
Chr2	552663041	552663113	Tu2	672383000	672385000	Н	no match	pair33
Chr3	436186321	436186399	Tu3	561990000	561993000	I	shift (49Mb)	pair34
Chr4	5910000	5914000	Tu4	8834000	8838000	Н	shift (77kb)	pair35
Chr2	594996015	594996114	Tu2	707387000	707417000	J	shift (94Mb)	pair36
Chr3	4490649	4490701	Tu3	5453000	5471113		no match.	pair37

¹ indicates the match types of HE junctions between A and D sugbenome. match: HE junction pairs were well aligned; shift: HE junctions from D subgenome were not aligned to those from A subgenome but in the same chromosome, content in brackets represent the genomic distance between the alignment hit and HE junction of in A subgenome; no match: HE

junctions from D subgenome were not aligned to A subgenome; low res.: HE junction with low resolution and not used for alignment.

	Total HE junctions	Well-aligned HE junctions
Group 1	0	0
Group 2	14	9
Group 3	10	6
Group 4	2	0
Group 5	0	0
Group 6	5	4
Group 7	2	1
4A and 5D	2	1
5A and 4D	2	2
All	37	23

Table S2. Number of HE junctions in different homoeologous groups in AADD tetraploids

Primers	Sequences
AET5Gv21168400-F	CACTCCGTGAGGAACCG
AET5Gv21168400-R	GAGGATTTGCCATCTGTGA
AET2Gv20016200-F	CAGGATGGGGATTCAAGA
AET2Gv20016200-R	ACTGTAACAGATTCAAGGCACT
AET2Gv20252700-F	CGCTCTACCTGCTCTTCG
AET2Gv20252700-R	CAGATACGCCGCTTCAGT
AET6Gv20704700-F	GGCCACCATCCTGGAGAACAT
AET6Gv20704700-R	GCTCTGGGTGTAGGCGAACTGC
AET2Gv21000600-F	GGGCGATGCGGGTGAAA
AET2Gv21000600-R	TCAAGGTAGTGCTGGTAGATGTAGGA
AET3Gv20796600-F	CCGACGATCTACGCCTTCT
AET3Gv20796600-R	CCCTCGCAGCAACACTCTA
AET3Gv20936700-F	ATGCGGCCATGAGTTTG
AET3Gv20936700-R	CTCCCTCTAGTTCGCTTCG
AET4Gv20852900-F	GTCCTCATCTTCCCCTTCTTCG
AET4Gv20852900-R	AGTTCTTCTTGGCTCTTGCTTCC

Table S3. Primer sequences for validating full-length fusion transcripts by Sanger sequencing

Table S4. Chromosome positions of 104 HE junctions in eight *Brassica napus* accessions (based on the position in C genome of *B. oleracea* and A genome of *B. rapa*).

Chr. C	Start C	End C	Chr. A	Start A	End A	Samples	Type ¹
C1	3990388	3991188	A01	2977924	2978111	Kale	match
C1	11735922	11737262	A01	7858737	7859586	Kale	match
C1	11865844	11866094	A01	7960324	7960579	Kale	match
C1	14151827	14152506	A01	10002456	10003132	H165	match
C1	15287827	15288219	A01	10741934	10742323	H165	match
C1	15853350	15853654	A01	11095573	11095878	Aviso, Bristol	match
C1	16121876	16122339	A01	11324456	11324918	Aviso, Bristol	match
C1	34309991	34310187	A01	21441244	21441437	H165	match
C1	34409828	34410006	A01	21530833	21531013	Kale	match
C1	35772368	35772440	A01	22840197	22840467	Swede	match
C1	37350795	37351421	A01	23795409	23796028	Aviso, Bristol	match
C1	39617623	39618660	Scaffold000164	42911	43947	Bristol	other_chr
C1	39966798	39969099	A01	26526111	26528203	Darmor	match
C1	40849674	40849952	A01	27396486	27396777	Darmor	match
C1	41061550	41061721	A01	27559695	27559865	Darmor	match
C1	41321910	41322147	A01	27714087	27714320	Darmor	shift (3kb)
C1	41749893	41752893	A01	28002805	28005720	Yudal	match
C1	42406658	42409707	Scaffold000229	48896	51211	Aviso, Bristol	other_chr
C1	42406658	42407785	Scaffold000229	50818	51211	Swede	other_chr
C1	43065473	43066124	A01	25557481	25558127	Swede	match
C2	494539	495291	A02	1700901	1701616	H165	match
C2	2414523	2417669	A02	2817850	2820774	Yudal	match
C2	3492502	3493594	A02	3612871	3613053	Aburamasari	match
C2	6765978	6766015	A02	5606300	5606417	Darmor	match
C2	7698382	7698643	A02	6055332	6055592	Darmor	match
C2	7831687	7831943	A02	6149124	6149379	H165	match
C2	10349704	10351053	A02	7379461	7380768	Aburamasari, swede, Yudal	match
C2	11408303	11408364	A02	7837983	7838043	Aburamasari, swede, Yudal	match
C2	22734221	22734342	A02	13377573	13377691	Swede	match
C2	23048525	23049745	A02	13554306	13555525	Darmor	shift (6kb)
C2	24597326	24597479	A02	14332176	14332306	Swede	match
C2	38035924	38037924	A08	14565897	14569316	H165	other_chr
C2	39469355	39469526	A02	18187047	18187225	Kale	match
C2	41046507	41047022	A02	19229213	19229718	Kale	match
C2	42209256	42214691	A02	21071121	21073404	H165	match
C2	50793193	50794281	A02	25881931	25883040	Darmor	match
C2	51312311	51312407	A02	26296470	26296560	Darmor	match
C2	51417726	51419235	Scaffold000490	5076	6337	Swede	other_chr
C2	51441401	51442250	A02	26401130	26401979	Aburamasari, Yudal	match
C2	51799087	51799605	A02	26567316	26567863	Aburamasari	match
01							

C3	2006236	2008479	A03	1672744	1673744	Aburamasari	match
C3	2317136	2322567	A03	1865672	1867972	Aburamasari, Yudal	match
C3	4874207	4883188	A03	3880693	3888275	Swede	match
C3	5851394	5851524	A03	4682354	4682487	Aviso, Bristol	match
C3	6247040	6247245	A03	4911997	4912159	H165	match
C3	6367698	6367904	A03	5017476	5017680	Aviso	match
C3	6432816	6434256	A03	5068737	5070176	H165	match
C3	6725055	6727720	A03	5317319	5319125	Bristol	match
C3	6924496	6924906	A03	5447284	5447687	Bristol	match
C4	332560	334644	A05	244419	246516	Kale	match
C4	48097092	48097164	A04	15032101	15032172	Darmor	match
C4	48671789	48672442	A04	15394477	15395129	Darmor	match
C4	49060310	49060983	A04	15648440	15649120	Darmor	match
C4	49690619	49691040	A04	16087023	16087443	Darmor	match
C4	49744132	49744747	A04	16121435	16122058	Swede	match
C4	50961650	50961766	A04	17103791	17103906	Kale	match
C5	40730725	40731829	A05	20650702	20651411	Bristol	match
C5	41155931	41156036	A05	20934550	20934654	Bristol	match
C5	41830248	41830334	A05	21373620	21373882	Kale	match
C5	42014855	42015091	A05	21504892	21505111	Kale	match
C5	42718082	42718260	A05	21964626	21964802	Kale	match
C5	42883620	42892863	A05	22068769	22078022	Yudal, Aburamasari	match
C5	43079621	43079870	A05	22213585	22213833	Aburamasari, Yudal	match
C5	44628034	44628532	A02	23231824	23232375	Aviso, Bristol	other_chr
C5	45313958	45314187	A05	23467203	23467419	Swede	match
C5	46030229	46032365	A02	26802762	26804822	Swede	other_chr
C5	46416349	46416426	A05	23623171	23623446	Yudal	match
C6	38384984	38385261	A07	21359722	21359998	Yudal	match
C6	38483157	38483535	A07	21452115	21452484	Yudal	match
C8	35753612	35756743	A09	32062424	32062911	H165	match
C8	35853527	35854117	A09	32171396	32171965	H165	match
C8	37493119	37497467	A09	33644447	33647886	H165	match
C8	38028713	38029713	A09	34119912	34120709	Bristol	match
C8	38429460	38431592	A09	34453620	34454711	Swede	match
C8	39529544	39529661	A09	35237812	35237928	Bristol	match
C8	40140326	40140458	A09	35725845	35725976	Aviso, Bristol	match
C8	40558577	40558852	A09	36150008	36150282	H165	match
C8	40796260	40796808	A09	36360984	36361401	Aviso, Bristol	match
C8	41227220	41229135	A09	36732348	36734330	Aburamasari	match
C8	41448018	41448156	A09	36914218	36914355	Darmor	match
C9	141476	141594	A09	1037680	1037803	Darmor	match
C9	300095	300568	A09	901176	901509	Kale	match
C9	593138	593365	A09	629747	629974	Aviso, Bristol	match
C9	908000	918000	A09	397099	403042	swede, Yudal	match

C9	1080870	1086136	A09	240441	242307	Yudal	match
C9	1085741	1085938	A09	240637	240833	Swede	match
C9	1087374	1087558	A09	238966	239153	H165	match
C9	2043382	2043448	A09	1332047	1332112	Yudal	match
C9	2045144	2045228	A09	1333816	1333899	Aburamasari	match
C9	2870455	2870526	A09	2589483	2589553	Swede	match
C9	3014517	3014760	A09	2698977	2699219	Aburamasari	match
C9	3360366	3360818	A09	1869180	1869618	Yudal	match
C9	3361156	3362184	A09	1867829	1868824	Aburamasari	match
C9	4315421	4315568	A09	2767361	2767507	Yudal	match
C9	4502543	4503520	A09	2919760	2920408	Yudal	match
C9	6659489	6660191	A09	4175893	4176566	Swede	match
C9	8684926	8685180	A09	5319971	5320224	Darmor	match
C9	8857111	8857268	A09	5431010	5431189	Darmor	match
C9	9895116	9895692	A09	7325629	7326202	Aviso, Bristol	match
C9	10292737	10292876	A09	7089358	7089494	Aviso, Bristol	match
C9	50989130	50989210	A10	15026481	15026556	Swede	match
C9	51295644	51295847	A10	16468542	16468744	Swede	match
C9	54391835	54391968	A10	17410729	17410860	H165	match

Table S5. Chromosome positions of 21 HE junctions in three banana triploid accessions (based on the position in B genome of *M. balbisiana* and A genome of *M. acuminata*).

	(based on the position in B genome of <i>W. balasiana</i> and A genome of <i>W. acuminata</i>).							
Chr. B	Start B	End B	Chr. A	Start A	End A	Samples	Type ¹	
Bchr04	6587091	6587327	chr04	6146789	6147023	FenJiao	match	
Bchr04	37744538	37747294	chr04	32298270	32299199	FenJiao	match	
Bchr04	40041836	40041924	chr04	34572494	34572581	FenJiao	match	
Bchr05	37337424	37337574	chr05	36930151	36930295	Kamaramasenge	match	
Bchr06	448664	449081	chr06	446637	447053	Pelipita	match	
Bchr06	37939967	37940074	chr06	34352094	34352195	FenJiao	match	
Bchr06	38491637	38492463	chr06	34869521	34870340	Pelipita	match	
Bchr07	32999005	32999152	chr07	31552034	31552163	Pelipita	match	
Bchr07	34657417	34657703	chr07	32977979	32978265	FenJiao	match	
Bchr07	36326380	36326480	chr07	34528141	34528384	Pelipita	match	
Bchr09	654679	654882	chr09	552362	552565	Pelipita	match	
Bchr09	3307561	3307693	chr09	3114861	3114991	Kamaramasenge	match	
Bchr09	4771870	4772168	chr09	4639024	4639321	Kamaramasenge	match	
Bchr09	35336812	35337797	chr09	39158712	39159668	FenJiao	match	
Bchr10	29235499	29235909	chr10	25413320	25413728	FenJiao	match	
Bchr10	29930687	29930969	chr10	26072695	26072976	Kamaramasenge	match	
Bchr10	31285433	31285778	chr10	27435983	27436327	Kamaramasenge	match	
Bchr10	34815076	34815232	chr10	30812846	30813001	Pelipita	match	
Bchr10	38388494	38388667	chr10	34238777	34238949	Kamaramasenge	match	
Bchr11	2523247	2523323	chr11	2223384	2223459	Kamaramasenge	match	
Bchr11	3492859	3493619	chr11	3110017	3110517	FenJiao	match	

Table S6. Chromosome positions of 166 HE junctions in four synthetic rice tetraploid individuals (based on the position in genome of Nipponbare and 9311).

_			Obr 0211				Tupol
Chr. Nip	Start Nip	End Nip	Chr. 9311	Start 9311	End 9311	Samples	Type ¹
Chr1	1129918	1130735	9311_chr01	1184035	1184831	99NN-3, 99NN-7	match
Chr1	4157344	4157685	9311_chr01	4353397	4353736	NN99-4, NN99-8	match
Chr1	4985027	4985872	9311_chr01	5108472	5109321	NN99-8	match
Chr1	5536090	5536438	9311_chr01	5670451	5670798	NN99-8	match
Chr1	5684479	5684930	9311_chr01	5825188	5825638	NN99-8	match
Chr1	6102367	6109226	9311_chr01	6291653	6298511	NN99-4	match
Chr1	8332955	8333710	9311_chr01	8809221	8809975	NN99-4, NN99-8	match
Chr1	10636446	10637172	9311_chr01	11272652	11273337	99NN-3, 99NN-7	match
Chr1	14590366	14590889	9311_chr01	15554627	15555148	99NN-3, 99NN-7	match
Chr1	19986079	19986411	9311_chr01	21398260	21398592	NN99-4, NN99-8	match
Chr1	21203888	21204092	9311_chr01	22665214	22665417	99NN-3, 99NN-7	match
Chr1	23717497	23717750	9311_chr01	25599562	25599814	NN99-8	match
Chr1	30408738	30408947	9311_chr01	32855527	32855737	NN99-8	match
Chr1	32806839	32806983	9311_chr01	35290081	35290224	NN99-4	match
Chr1	35054686	35055822	9311_chr01	37642338	37643472	NN99-4, NN99-8	match
Chr1	36466146	36466229	9311_chr01	39053787	39053869	99NN-3, 99NN-7	match
Chr1	37636457	37636760	9311_chr01	40166663	40166965	99NN-3, 99NN-7	match
Chr1	40595040	40596220	9311_chr01	43331519	43332693	99NN-3, 99NN-7	match
Chr1	40822811	40822992	9311_chr01	43620665	43620843	99NN-3, 99NN-7	match
Chr1	42024667	42033150	9311_chr01	44896269	44903327	99NN-3, 99NN-7	match
Chr10	2357528	2357794	9311_chr10	2433505	2433770	99NN-7	match
Chr10	9919537	9920695	9311_chr10	9719676	9720818	99NN-7	match
Chr10	11006519	11008450	9311_chr10	10799253	10801183	99NN-3, 99NN-7	match
Chr10	14940844	14941607	9311_chr10	15439859	15440620	NN99-4, NN99-8	match
Chr11	1224893	1225023	9311_chr11	1311212	1311341	NN99-4, NN99-8	match
Chr11	1458320	1459347	9311_chr11	1563533	1564559	99NN-7	match
Chr11	3354848	3355306	9311_chr11	3615392	3615850	NN99-4, NN99-8	match
Chr11	6505875	6506847	9311_chr11	6764486	6765358	99NN-3	match
Chr11	8989586	8990682	9311_chr11	8803805	8804892	99NN-3, 99NN-7	match
Chr11	15562005	15562218	9311_chr11	15894881	15895093	NN99-4	match
Chr11	16453477	16454189	9311_chr11	16976700	16977412	NN99-4	match
Chr11	17387697	17388993	9311_chr11	18070010	18071305	NN99-4, NN99-8	match
Chr11	25277115	25278035	9311_chr11	26875583	26876499	99NN-3, 99NN-7	match
Chr11	26432840	26433995	9311_chr11	27929386	27930533	99NN-3, 99NN-7	match
Chr12	1032308	1034434	9311_chr12	1021608	1023736	99NN-3, 99NN-7	match
Chr12	1437869	1437925	9311_chr12	1454193	1454248	99NN-3, 99NN-7	match
Chr12	2304970	2305577	9311_chr12	2268447	2269037	NN99-4, NN99-8	match
Chr12	4760928	4761191	9311_chr12	4714751	4715012	99NN-3, 99NN-7	match
Chr12	18101987	18102657	9311_chr12	17023965	17024636	NN99-4	match
Chr12	20781709	20781877	9311_chr12	19238131	19238298	99NN-3	match
Chr12	23920185	23920710	9311_chr12	22333373	22333894	NN99-8	match

Chr12	24184905	24185658	9311_chr12	22588876	22589592	99NN-3, 99NN-7	match
Chr2	913255	914179	9311_chr02	944414	945336	99NN-7	match
Chr2	983271	985248	9311_chr02	1018721	1020700	99NN-3	match
Chr2	2878228	2884337	9311_chr02	3115332	3121447	99NN-3, 99NN-7	match
Chr2	3760348	3761354	9311_chr02	4018044	4019050	99NN-3, 99NN-7	match
Chr2	4367221	4368114	9311_chr02	4715322	4716217	99NN-3, 99NN-7	match
Chr2	5862539	5863144	9311_chr02	6429265	6429868	99NN-3, 99NN-7	match
Chr2	7422756	7423008	9311_chr02	8012608	8012859	99NN-3	match
Chr2	9100300	9101456	9311_chr02	9802304	9804123	NN99-4, NN99-8	match
Chr2	9885768	9887894	9311_chr02	10422434	10424560	99NN-7	match
Chr2	10123621	10124329	9311_chr02	10673088	10673795	99NN-7	match
Chr2	10323633	10324031	9311_chr02	10854561	10854957	NN99-4, NN99-8	match
Chr2	11687200	11687495	9311_chr02	12306927	12307221	NN99-4	match
Chr2	12218696	12219554	9311_chr02	12766873	12767730	NN99-8	match
Chr2	18815954	18816533	9311_chr02	19304579	19305157	99NN-3	match
Chr2	21380695	21384471	9311_chr02 9311_chr02	21958751	21962526	99NN-3, 99NN-7	match
Chr2	23122982	23123294	9311_chr02 9311_chr02	23685187	23685498	NN99-4	match
Chr2	24013723	24015938	9311_chr02	24582986	24585195	NN99-4, NN99-8	match
Chr2	24196299	24015950	9311_chr02 9311_chr02	24759135	24759347	NN99-8	match
Chr2	24190299 25445009	25446106	9311_chr02 9311_chr02	25960455	25961543	NN99-8	match
Chr2	23443009 34368907	34369522	9311_chr02 9311_chr02	23900433 34805513	34806126	99NN-3, 99NN-7	
Chr2	34308907	34309522	9311_chr02 9311_chr02	35625106	34800120	NN99-4, NN99-8	match match
GIIIZ	33137210	30139423	9311_01102	33023100	33027309	111199-4, 111199-0	match
Chro	25/10/12	25420000	0.211 obr 0.2	25020576	25021101		motob
Chr2	35418413	35420009	9311_chr02	35929576	35931191	99NN-3, 99NN-7	match
Chr2	35676588	35677386	9311_chr01	423747	424522	99NN-7	other_chr
Chr2 Chr3	35676588 386243	35677386 388586	9311_chr01 9311_chr03	423747 449557	424522 450974	99NN-7 99NN-3, 99NN-7	other_chr match
Chr2 Chr3 Chr3	35676588 386243 3237650	35677386 388586 3238887	9311_chr01 9311_chr03 9311_chr03	423747 449557 3344116	424522 450974 3345722	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8	other_chr match match
Chr2 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773	35677386 388586 3238887 3398880	9311_chr01 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353	424522 450974 3345722 3517459	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7	other_chr match match match
Chr2 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513	35677386 388586 3238887 3398880 3731195	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500	424522 450974 3345722 3517459 3850181	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8	other_chr match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630	35677386 388586 3238887 3398880 3731195 4236121	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267	424522 450974 3345722 3517459 3850181 4325758	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7	other_chr match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291	35677386 388586 3238887 3398880 3731195 4236121 6455554	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626	424522 450974 3345722 3517459 3850181 4325758 6600888	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7	other_chr match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8	other_chr match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8	other_chr match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 NN99-4	other_chr match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8	other_chr match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 NN99-4 NN99-4, NN99-8 99NN-3, 99NN-7	other_chr match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8	other_chr match match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029 16731513	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138 16732914	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628 18213603	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736 18215003	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 NN99-4 NN99-4 NN99-4 NN99-4 NN99-8 99NN-3, 99NN-7	other_chr match match match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029 16731513 24300330	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138 16732914 24300822	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628 18213603 27056630	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736 18215003 27057121	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7	other_chr match match match match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029 16731513 24300330 27618636	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138 16732914 24300822 27624348	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628 18213603 27056630 30587227	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736 18215003 27057121 30590573	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8	other_chr match match match match match match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029 16731513 24300330 27618636 27838445	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138 16732914 24300822 27624348 27838835	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628 18213603 27056630 30587227 30792106	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736 18215003 27057121 30590573 30792495	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-8 NN99-4	other_chr match match match match match match match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029 16731513 24300330 27618636 27838445 31749168	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138 16732914 24300822 27624348 27838835 31750285	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628 18213603 27056630 30587227 30792106 34957957	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736 18215003 27057121 30590573 30792495 34959073	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4 NN99-4 NN99-4	other_chr match match match match match match match match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029 16731513 24300330 27618636 27838445 31749168 32617863	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138 16732914 24300822 27624348 27838835 31750285 32619300	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628 18213603 27056630 30587227 30792106 34957957 35821512	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736 18215003 27057121 30590573 30792495 34959073 35822935	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 NN99-4, NN99-8	other_chr match match match match match match match match match match match match match match match match match match
Chr2 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3 Chr3	35676588 386243 3237650 3398773 3730513 4235630 6455291 8344310 9425774 10358060 12417425 13765767 15792029 16731513 24300330 27618636 27838445 31749168	35677386 388586 3238887 3398880 3731195 4236121 6455554 8345575 9425896 10359106 12418116 13767021 15792138 16732914 24300822 27624348 27838835 31750285	9311_chr01 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03 9311_chr03	423747 449557 3344116 3517353 3849500 4325267 6600626 8521968 9713531 10825823 13329537 13768839 17059628 18213603 27056630 30587227 30792106 34957957	424522 450974 3345722 3517459 3850181 4325758 6600888 8523233 9713652 10826846 13330218 13769747 17059736 18215003 27057121 30590573 30792495 34959073	99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4, NN99-8 99NN-3, 99NN-7 99NN-3, 99NN-7 NN99-4, NN99-8 NN99-4 NN99-4 NN99-4	other_chr match match match match match match match match match match match match match match match match match

Chr4	1795488	1795507	9311_chr04	2268764	2269081	NN99-4	match
Chr4	4526487	4526609	9311_chr04	3849208	3849329	99NN-7	match
Chr4	5210661	5211364	9311_chr04	4579387	4580091	NN99-8	match
Chr4	5608200	5608648	9311_chr04	4952638	4953076	99NN-3	match
Chr4	6692414	6692909	9311_chr04	6031861	6032355	99NN-7	match
Chr4	7621177	7628603	9311_chr04	6847456	6848963	99NN-3	match
Chr4	14156258	14156420	9311_chr04	13343773	13343934	99NN-3	match
Chr4	19991419	19992451	9311_chr04	19475440	19476470	99NN-3, 99NN-7	match
Chr4	23024048	23030179	9311_chr04	22968677	22974808	NN99-8	match
Chr4	23077402	23082258	9311_chr04	23022044	23026900	99NN-3	match
Chr4	26790491	26796353	9311_chr04	27285169	27291029	99NN-3	match
Chr4	27131669	27132284	9311_chr04	27643140	27643754	99NN-7	match
Chr4	27285452	27286191	9311_chr04	27824211	27824950	NN99-8	match
Chr4	27948627	27949076	9311_chr04	28516860	28517308	NN99-4, NN99-8	match
Chr4	28201453	28202465	9311_chr04	28757241	28758248	99NN-3	match
Chr4	30281846	30282502	9311_chr04	30965072	30965728	99NN-3	match
Chr4	34230146	34239322	9311_chr04	35223316	35232493	99NN-3, 99NN-7	match
Chr5	758518	759097	9311_chr05	777958	778531	99NN-7	match
Chr5	1120146	1121800	9311_chr05	1196244	1197860	99NN-3, 99NN-7	match
Chr5	2608352	2609415	9311_chr05	2810677	2811737	NN99-8	match
Chr5	3511584	3512136	9311_chr05	3646067	3646618	NN99-4	match
Chr5	4830718	4831000	9311_chr05	4911035	4911323	NN99-4	match
Chr5	5376361	5376786	9311_chr05	5497807	5498232	99NN-3, 99NN-7	match
Chr5	6397229	6397914	9311_chr05	6462184	6462835	NN99-4	match
Chr5	7927370	7927740	9311_chr05	8189957	8190326	99NN-3	match
Chr5	7944527	7944600	9311_chr05	8206516	8206688	NN99-4, NN99-8	match
Chr5	14734313	14734449	9311_chr05	14980352	14980487	99NN-7	match
Chr5	16168675	16169578	9311_chr05	16285485	16286381	99NN-7	match
Chr5	17317984	17318960	9311_chr05	17603786	17604763	NN99-4	match
Chr5	18185538	18186274	9311_chr05	18592228	18592963	99NN-7	match
Chr5	20441630	20441687	9311_chr05	20972731	20972787	NN99-4, NN99-8	match
Chr5	21096330	21096333	9311_chr03	33155295	33155353	99NN-3	other_chr
Chr5	21550499	21553231	9311_chr05	22216186	22217353	99NN-7	match
Chr5	26951405	26951791	9311_chr05	27655586	27655971	NN99-4, NN99-8	match
Chr5	27897316	27898009	9311_chr05	28509997	28510691	NN99-4, NN99-8	match
Chr6	297212	299550	9311_chr06	227091	229427	99NN-3, 99NN-7	match
Chr6	5536745	5541462	9311_chr06	5667184	5669712	NN99-4, NN99-8	match
Chr6	7421037	7421905	9311_chr06	7739798	7740665	NN99-4, NN99-8	match
Chr6	9676469	9676562	9311_chr06	9865994	9866086	99NN-3, 99NN-7	match
Chr6	10922005	10926880	9311_chr06	10963059	10967934	99NN-3, 99NN-7	match
Chr6	21210749	21210860	9311_chr06	21241968	21242078	NN99-4	match
Chr6	21398092	21399255	9311_chr06	21424364	21425526	NN99-4	match
Chr6	24031147	24031513	9311_chr06	24084373	24084738	NN99-4	match
Chr6	24233617	24235823	9311_chr06	24279539	24281744	NN99-4	match

Chr6	27159932	27168661	9311_chr06	27621283	27628557	NN99-4, NN99-8	match
Chr6	28341054	28341271	9311_chr06	28884301	28884509	NN99-4, NN99-8	match
Chr7	4108705	4109662	9311_chr07	3859853	3860813	99NN-3, 99NN-7	match
Chr7	6042827	6044024	9311_chr07	5875674	5876869	NN99-4, NN99-8	match
Chr7	7178011	7178699	9311_chr07	6920679	6921365	99NN-3, 99NN-7	match
Chr7	16374813	16376299	9311_chr07	15444918	15446444	NN99-4, NN99-8	match
Chr7	17112810	17113185	9311_chr07	16119189	16119579	NN99-4	match
Chr7	17128236	17129544	9311_chr07	16141812	16143120	99NN-3, 99NN-7	match
Chr7	17179918	17180039	9311_chr07	16191719	16191839	NN99-8	match
Chr7	17376768	17377185	9311_chr07	16395612	16396024	NN99-8	match
Chr7	19480082	19481088	9311_chr07	18271054	18272071	NN99-8	match
Chr7	21658823	21659457	9311_chr07	20296530	20297163	99NN-3	match
Chr7	23843198	23843476	9311_chr07	22453708	22453985	NN99-4, NN99-8	match
Chr7	27177326	27178010	9311_chr07	25754806	25755493	99NN-7	match
Chr7	28868015	28868560	9311_chr07	27372995	27373539	99NN-3, 99NN-7	match
Chr8	5644251	5645069	9311_chr08	5626399	5627210	99NN-7	match
Chr8	6125024	6126276	9311_chr08	6245419	6246670	NN99-8	match
Chr8	8942693	8945911	9311_chr08	9445282	9448476	99NN-3, 99NN-7	match
Chr8	11034025	11035401	9311_chr08	12250322	12251696	NN99-8	match
Chr8	19464110	19465251	9311_chr08	21584746	21585534	NN99-4, NN99-8	match
Chr8	20635802	20636924	9311_chr08	22728137	22729259	99NN-3, 99NN-7	match
Chr8	21246798	21247244	9311_chr08	23338474	23338919	NN99-8	match
Chr8	21813604	21815060	9311_chr08	23934617	23936072	99NN-3, 99NN-7	match
Chr8	23657122	23657342	9311_chr08	25990865	25991084	99NN-7	match
Chr9	5599596	5600217	9311_chr09	5365432	5366052	NN99-4, NN99-8	match
Chr9	6230447	6230680	9311_chr09	6089856	6090089	99NN-7	match
Chr9	7481224	7481910	9311_chr09	7359392	7360077	99NN-7	match
Chr9	10805352	10806135	9311_chr09	10045490	10046272	NN99-4, NN99-8	match
Chr9	12143280	12144850	9311_chr09	11361572	11363141	NN99-4	match
Chr9	13779228	13779433	9311_chr09	13085281	13085485	NN99-8	match
Chr9	13911151	13918860	9311_chr09	13221169	13228876	NN99-4	match
Chr9	14980713	14981215	9311_chr09	14177249	14177752	99NN-3, 99NN-7	match
Chr9	15021225	15021411	9311_chr09	14212809	14212994	NN99-4, NN99-8	match
Chr9	16422504	16422984	9311_chr09	15655571	15656038	NN99-4	match
Chr9	16560613	16561309	9311_chr09	15781313	15782009	NN99-8	match
Chr9	17694381	17695286	9311_chr09	16989111	16990015	99NN-3, 99NN-7	match
Chr9	18618052	18619097	9311_chr09	17933762	17934806	NN99-4, NN99-8	match
	-						

Chr	Chr Start End Samples			
Chr1	658958	658976	SRR2084157, SRR3123760, SRR3123765	
Chr1	732181	732288	SRR2084157, SRR3123760, SRR3123765	
Chr1	2813704	2813752	SRR3123767	
Chr1	4929662	4929738	SRR3123767	
Chr2	19379436	19379776	SRR3123767	
Chr2	19564121	19564172	SRR3123764, SRR3123769	
Chr4	1068487	1068604	SRR3123760, SRR2084157	
Chr4	2240257	2240325	SRR2084157, SRR3123760	
Chr4	2786695	2792022	SRR2084157, SRR3123760	

Table S7. Chromosome positions of 10 HE junctions in *Arabidopsis suecica* individuals (based on the position in genome of *A. thaliana*).

Chr. B	Start B	End B	Samples
Arahy.12	117668999	117704310	Amonticola
Arahy.12	117817965	117822170	NC3033, N423, N421, N464, N692, N705, N693, N689, N717,
			N734, N726, N725, N711, N745, N709, N713
Arahy.12	118256778	118258164	TR, N744, N657, N625, N683, N675, N665, N663, N431,
			N741, N435, N733, N704, N702, N743, N700, NM, N730,
			N690, N740, N723, N751
Arahy.13	146343047	146347951	All samples
Arahy.14	77162579	77168419	N431, N741, N423, N421, N435
Arahy.14	90393195	90440728	N431, N741, N423, N421, N435
Arahy.14	137403639	137406947	N744, N709
Arahy.14	138862257	138863838	Amonticola
Arahy.14	139404845	139413753	Amonticola
Arahy.14	139899365	139905900	N733, N745
Arahy.14	140466186	140468348	N733
Arahy.14	140572534	140582341	N657, N700, N717, N725, N711, N745
Arahy.14	140582345	140589736	NC3033, N625, N683, N665, N663, N704, N702, N693, N713
Arahy.14	141430181	141442130	NC3033, N657, N625, N683, N675, N665, N663, N704, N702,
			N693, N700, N717, N713
Arahy.15	6306066	6308629	All samples
Arahy.16	3202449	3210486	TR, N683, N689, N700, N717, N734, N690
Arahy.16	146245083	146267448	NC3033, N683, N665, N431, N741, N423, N692, N743, N713
Arahy.16	151628012	151636887	NC3033
Arahy.16	152284902	152286523	TR, N713
Arahy.16	152723849	152730064	Amonticola
Arahy.16	152819251	152836728	TR, N657, N625, N683, N675, N665, N663, N464, N704,
			N705, N743, N689, N700, N734, N713, N723
Arahy.16	153003860	153007978	Amonticola, N744, N431, N741, N423, N421, N435, N692,
			N733, N702, N693, N717, NM, N726, N725, N711, N730,
			N745, N709, N690, N740, N751
Arahy.17	1438055	1452535	All samples
Arahy.17	1839088	1855636	N733
Arahy.17	2291088	2312052	N733
Arahy.18	1127952	1130739	All samples

Table S8. Chromosome positions of 26 HE junctions in *Arachis hypogaea* individuals (based on the position in B genome of *A. hypogaea*).

Table S9. Genomic feature of HE-junction-related motifs in wheat, Brassica and rice. A-rich motif

	Promoter			
	(up-stream 2kb of TSS)	UTR and intron	Exon	Intergenic region
Brassica	10 (28%)	14 (40%)	5 (14%)	6 (18%)
Rice	26 (22%)	24 (21%)	11 (9%)	56 (49%)
CTT- or CT-r	epeat motif			
	Promoter			
	(up-stream 2kb of TSS)	UTR and intron	Exon	Intergenic region
Brassica	13 (13%)	19 (19%)	61 (61%)	9 (8%)
Rice	21 (24%)	25 (28%)	5 (6%)	37 (42%)
CCN-repeat	motif			
	Promoter			
	(up-stream 2kb of TSS)	UTR and intron	Exon	Intergenic region
Wheat	6 (19%)	4 (13%)	17 (55%)	4 (13%)
Rice	14 (18%)	13 (17%)	18 (23%)	32 (42%)