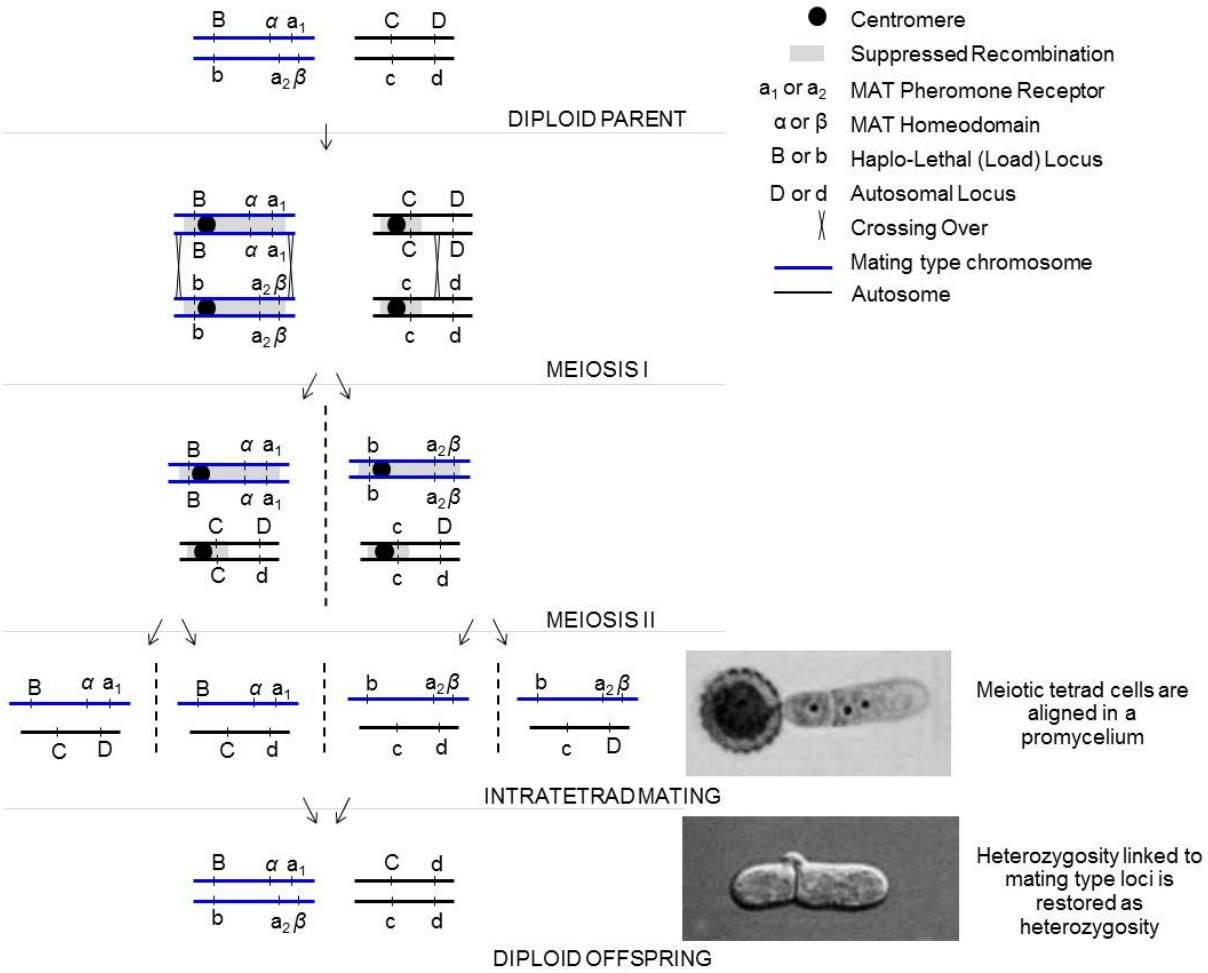

Figure S1: **Meiosis and intratetrad-mating (automixis) in *Microbotryum lychnidis-dioicae.*** A scenario with 2N number of 4 is shown, with a mating type (blue) and an autosomal (black) pair of homologous chromosomes. Mating type (MAT) is linked to the centromere. Mating type and linked loci (locus B) segregate at Meiosis I. Heterozygosity at loci linked to mating type, or that segregates a Meiosis I linked to other centromeres (locus C), is therefore restored by mating between cells from the same meiotic tetrad. This can shelters deleterious load loci linked to the mating type while purging heterozygosity at loci that segregate at Meiosis II due to crossing over (as shown for locus D).

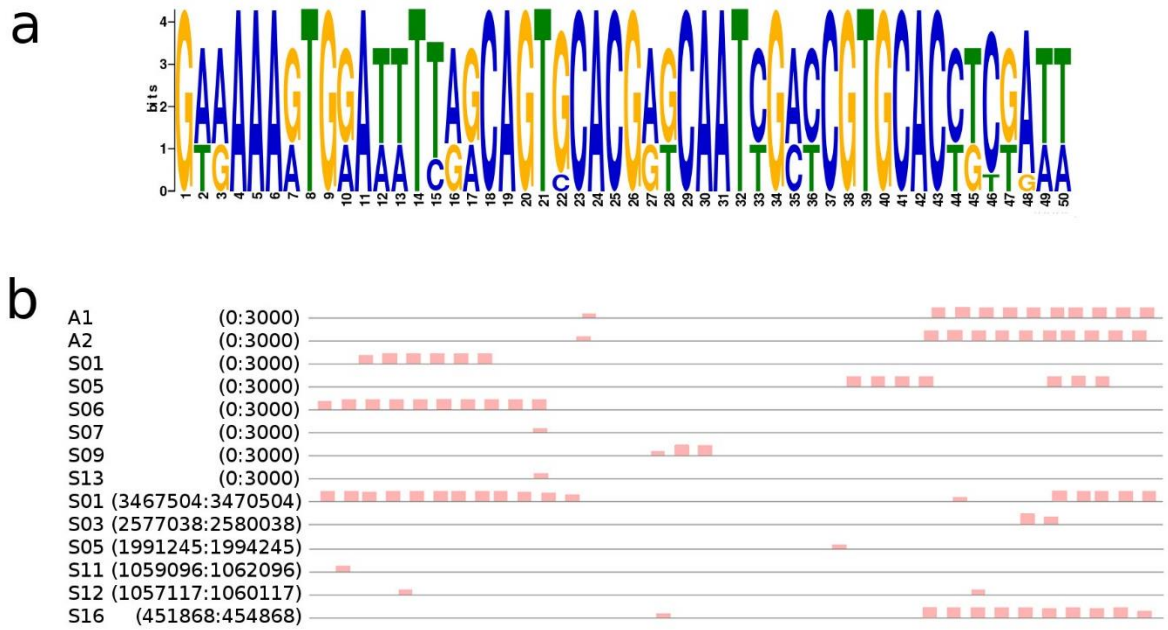

Figure S2: **Identification of sub-telomeric motifs in *Microbotryum lychnidis-dioicae*.** a) Consensus motif. b) Location in the 3000 bp of putative chromosomes edges. The genomic coordinates in bp are indicated in brackets.

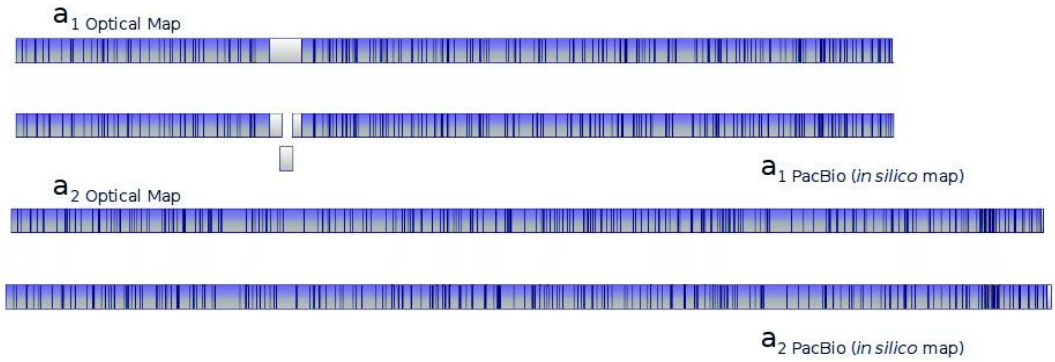

Figure S3: **Correspondence between the optical map and the PacBio assembly of the *Microbotryum lychnidis-dioicae* mating-type chromosomes.** The vertical lines within the chromosomes indicate restriction sites. Alignments compare restriction fragment sizes on single DNA molecules and from *in silico* sequences. Regions highlighted in blue indicate aligned optical map and *in silico* restriction site distributions, while regions in grey could not be aligned (*i.e.,* a_1 centromeres and a_2 telomeres).

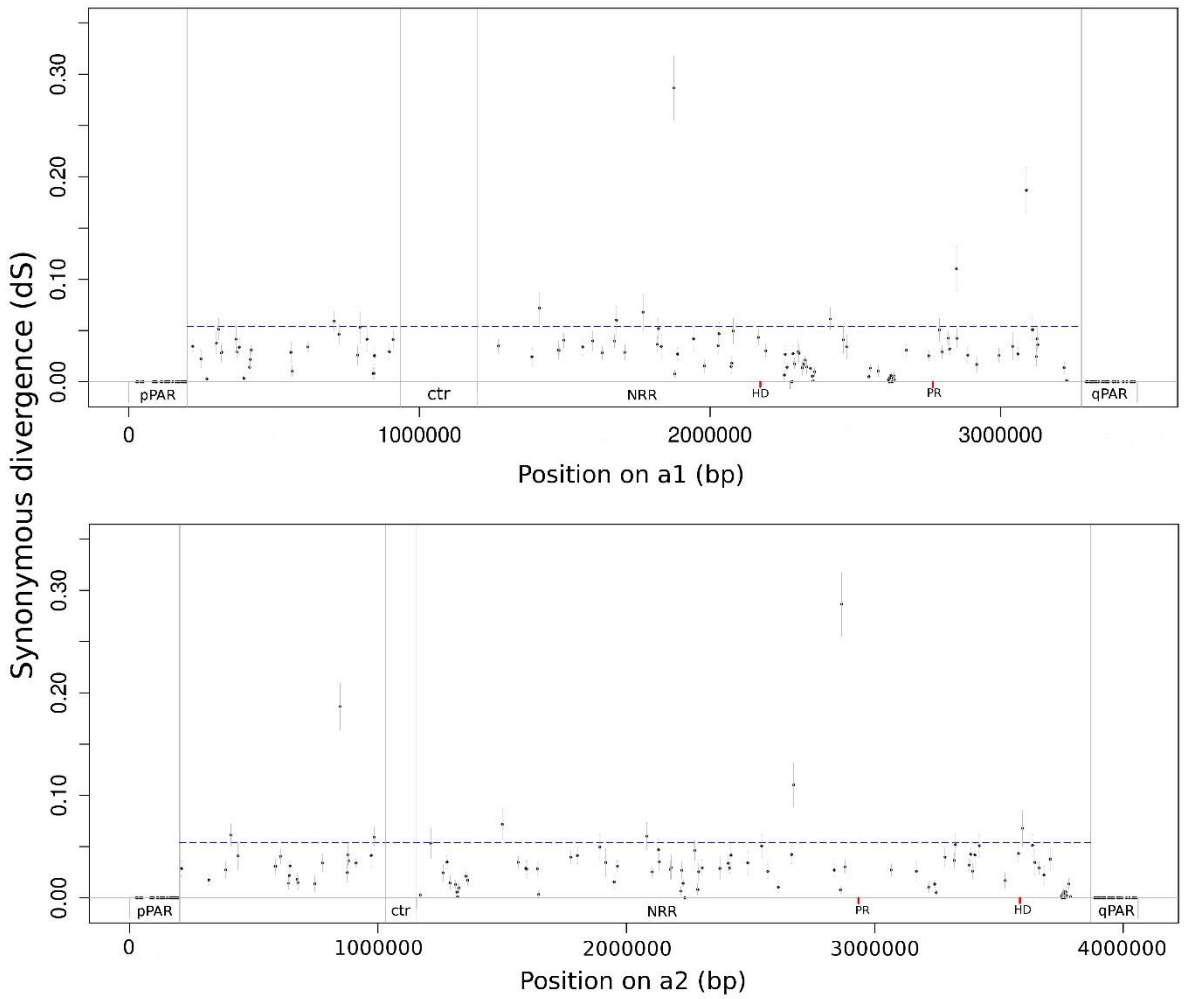

Figure S4: **Divergence between the *Microbotryum lychnidis-dioicae* mating-type chromosomes.** Synonymous divergence dS ± SE is plotted against the genomic coordinates of the a_1 (A) or a_2 (B) alleles, for predicted genes with a gap-free codon alignment of more than 1000 bp. The boundaries between the pseudo-autosomal region (PAR) and the non-recombining regions (NRR) are indicated, as well as the locations of the mating-type loci (*PR*: pheromone receptor gene; *HD*: homeodomain genes). The mean value of dS in the NRR is shown as blue dotted lines.

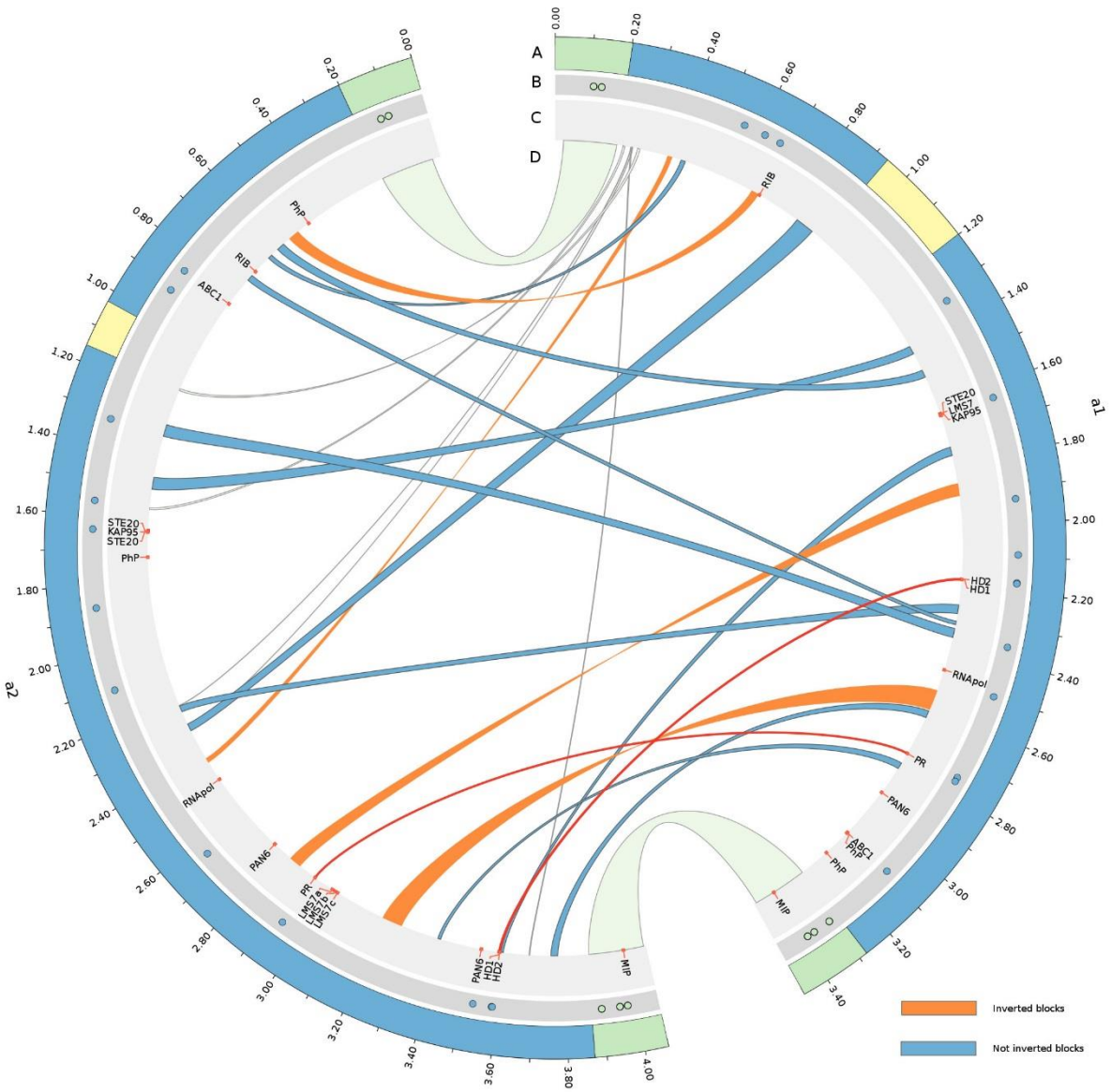

Figure S5: **Rearrangements between the main syntenic blocks of genes common to a_1 and a_2 *Microbotryum lychnidis-dioicae* mating-type chromosomes.** Tracks A to D show the location of different genomic elements, as follows: A – Structure of the chromosomes, with the pseudo-autosomal regions (PARs) in green, the non-recombining regions (NRRs) in blue, and the centromeres in yellow. B – Location of loci shown to be linked (blue circles) or unlinked (white circles) to mating-type by previous segregation analyses in *M. lychnidis-dioicae* {Abbate, 2010 #87;Petit, 2012 #86;Votintseva, 2009 #84}. C – Location of the genes related to the mating-type function: pheromone receptor and homeodomain genes (in red), the other genes likely involved in mating (*STE12, STE20*, and the precursors of pheromones, *PhP*) and the genes located around the pheromone receptor gene in the closely related *Sporidiobolus salmonicolor* {Coelho, 2010 #156} (*KAP95, RNAPol, RIB* and *ABC1*). D – Links between syntenic blocks of shared genes larger than 10 kb.

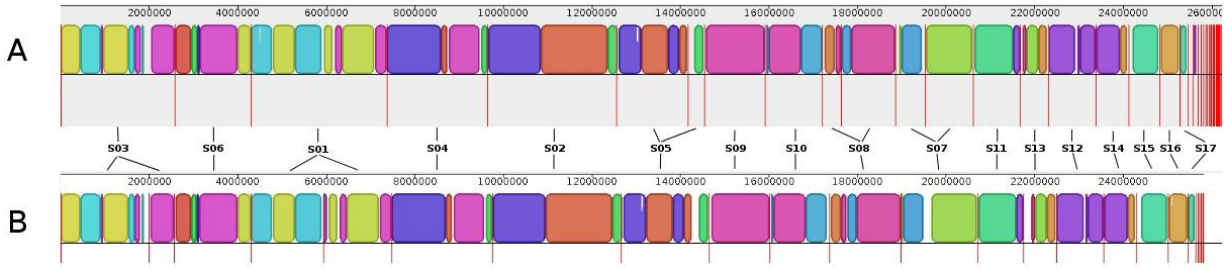

Figure S6: Autosomal contigs from the a_1 and a_2 assemblies, aligned with Mauve {Darling, 2010 #146}, illustrating their synteny. The contigs of a_1 (A) and a_2 (B) are separated by vertical red lines and the locally collinear blocks (LCBs) are represented as colored blocs. A couple of a_1 contigs were split into two contigs in the a_2 assembly (i.e., at position 2MB and 6MB), and conversely (at 14MB and 18MB). In these cases where an autosomal contig was larger in the a_1 or in the a_2 assembly, the largest contig was selected to resolve the final reference assembly (Figure 2). Contig names are indicated as in Figure 2, except the S18 that is one of the small contigs at right. The few short degenerate contigs at right were disregarded, likely resulting from the incorrect editing of reads.

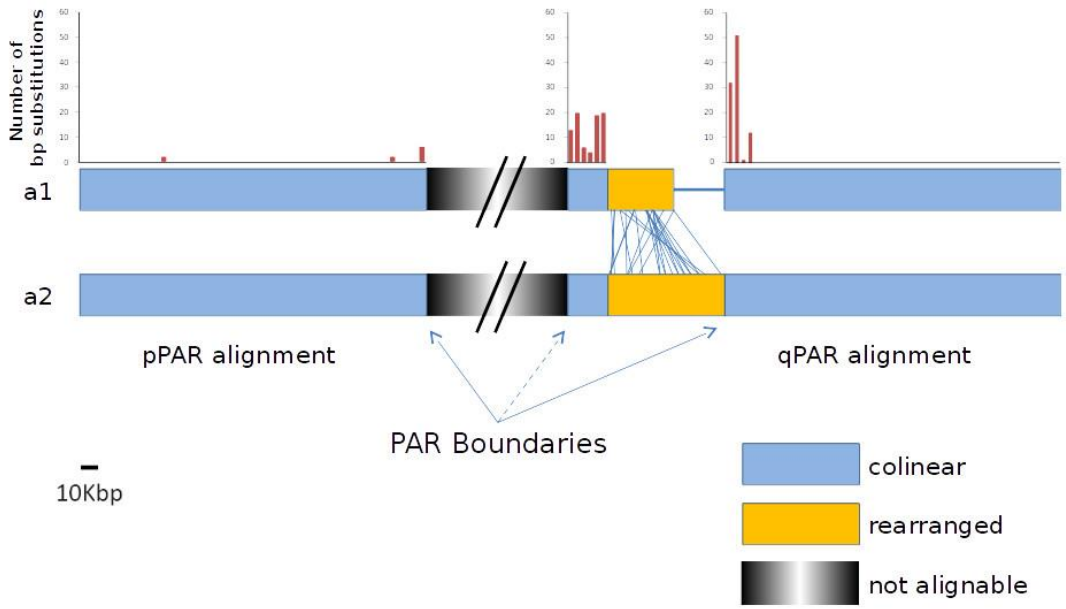

Figure S7: **Map of the base-pair substitutions in pseudo-autosomal regions of the *Microbotryum lychnidis-dioicae* mating-type chromosomes**. A collinear region of 23 kb in the non-recombining region is identified close to the qPAR boundary.

File S1

Available for download as a .txt file at http://www.genetics.org/content/suppl/2015/06/03/genetics.115.177709.DC1