



Figure S4: Divergence between the *Microbotryum lychnidis-dioicae* mating-type chromosomes. Synonymous divergence $dS \pm SE$ 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.