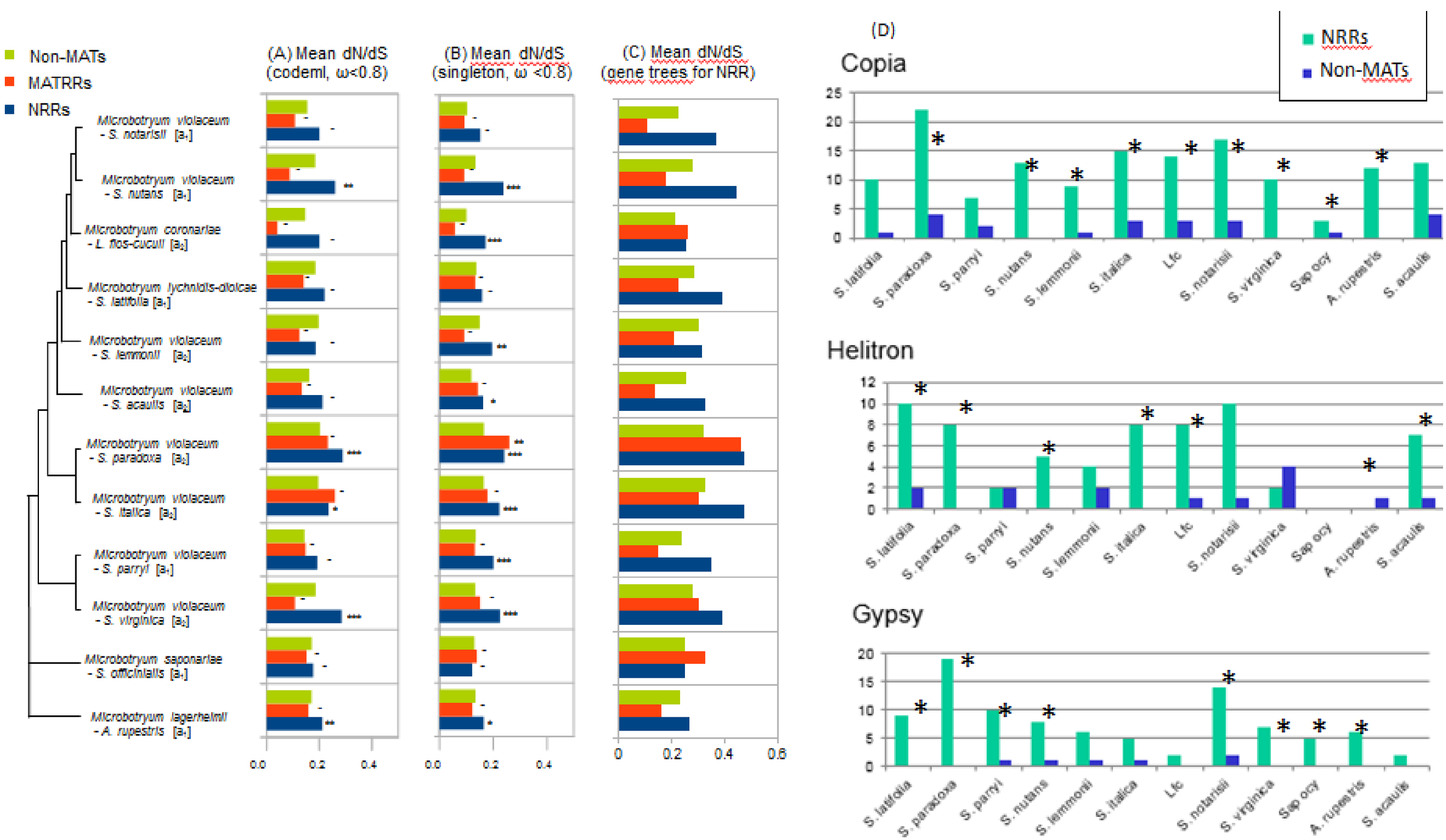

Figure S3. Degeneration evidence in non-recombining regions of the mating-type chromosomes in *Microbotryum*, in coding sequences and as accumulation of transposable elements. (A) and (B) Degeneration estimated by comparing mean non-synonymous vs synonymous substitutions (ω=dN/dS) across coding sequences (CDS) located respectively in non-mating-type chromosomes (non-MAT), NRRs (mating-type chromosome non-recombining regions) and MATRRs (mating-type chromosome recombining regions) in twelve haploid *Microbotryum* genomes (*i.e.*, either of a_1 or a_2 mating type), loci displaying dN/dS > 0.8 (i.e., nearly neutral and positively selected) being discarded from this analysis, (A) with the full frequency spectrum of substitutions used to compute dN/dS through a free-ratio branch model (Codeml, PAML), (B) with only singleton substitutions taken into account for focusing on recent events, or (C) using gene trees for NRR genes instead of species tree. (D) Transposable element (TE) contents of three families (Copia, Gypsy and Helitron) across contigs assigned respectively to non-mating-type chromosomes (non-MATs) and NRRs (mating-type chromosome non-recombining regions), in twelve haploid *Microbotryum* genomes (*i.e.*, either of a_1 or a_2 mating type). Results represent the proportion of sequences corresponding to TEs detected among 1,000 random 200-pb fragments in each compartment (non-MATs and NRR). Asterix indicate significant differences between non-mating-type chromosomes (non-MATs) and NRRs according to the Z test.