



Figure S6: Repeat-induced point mutation (RIP) composite index per TE copy of *Zymoseptoria* species. Mean RIP composite index (CRI) frequencies of TEs estimated using a 50bp sliding windows approach as follows: $CRI = (TpA / ApT) - (CpA + TpG / ApC + GpT)$ for each TE copy per order from Class I and Class II. Regions of more than 4000 bp that are consecutively affected by RIP are considered to be LRARs (large RIP affected genomic regions).