

Figure S1

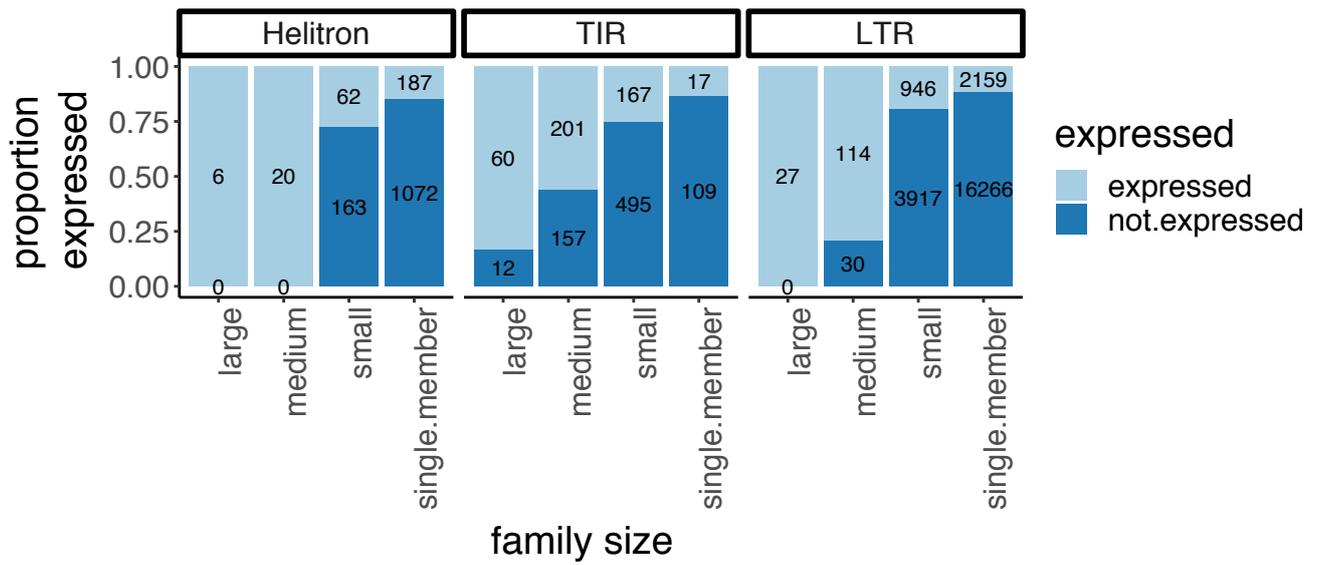


Figure S1: Breakdown of expressed TE families by family size. The proportion and count of TE families with (light blue) or without (dark blue) transcripts for helitrons (DH), TIRs (DT), and LTRs (RL). Families are categorized as small when they have 2-30 members, medium with 31-500 members, and large with > 500 members.

Figure S2

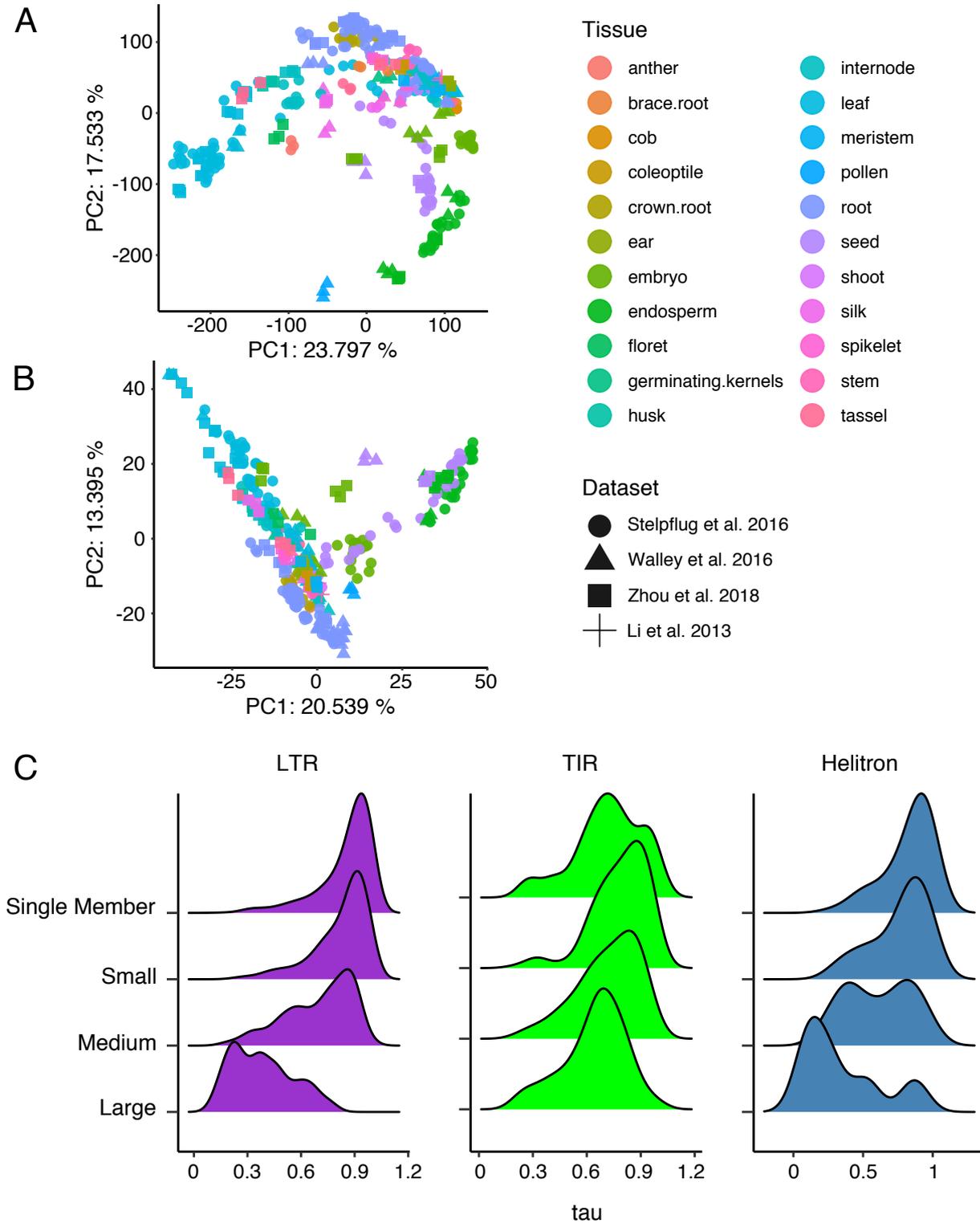


Figure S2: TEs contribute to transcriptome dynamics across development in B73. A-B. Principal component analysis was used to plot libraries based on similarity of gene (A) or TE (B) transcript abundance. C. The tissue-specificity of expression was estimated with the tau metric, where low values indicate constitutive expression and high values indicate tissue-specific expression. Tau densities were plotted for helitron (DH), TIR (DT) and LTR (RL) TEs based on family size. Families are categorized as small when they have 2-30 members, medium with 31-500 members, and large with > 500 members.

Figure S3

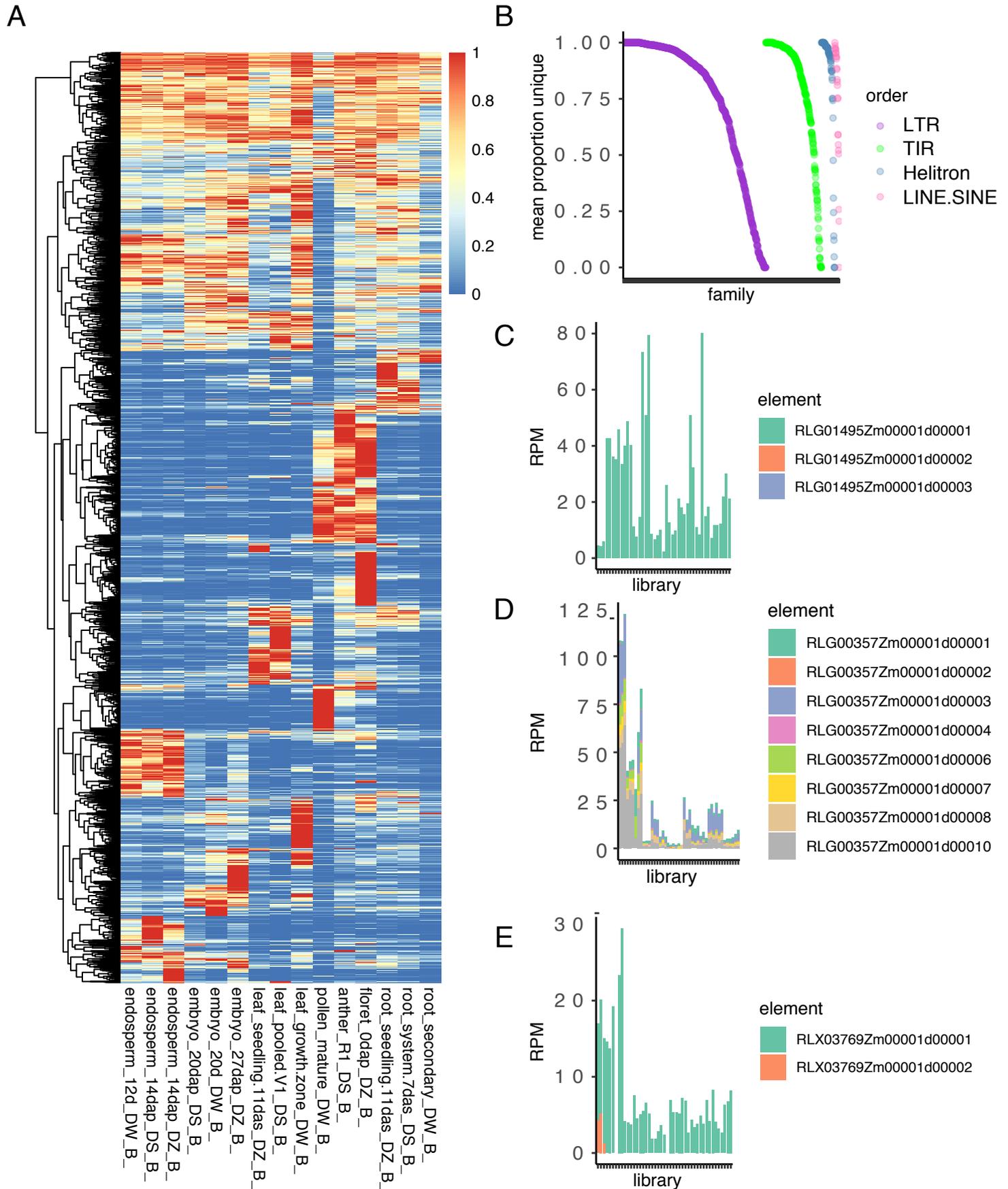


Figure S3: Dynamic transcript abundance patterns for expressed TE families in B73. A. Heat map showing the transcript abundance of all TE families detected in the tissue subset. Transcript abundance is normalized by row. B. Rank order plot of the proportion of reads per multi-member family ($N = 1176$) that are unique mapping. Proportions plotted are the average across all tissues with expression > 1 RPM, and the x-axis is ordered by TE order and proportion unique. C-E. Examples of unique per-element expression patterns for three TE families expressed in the development subset. Libraries are ordered along the x-axis as in A.

Figure S4

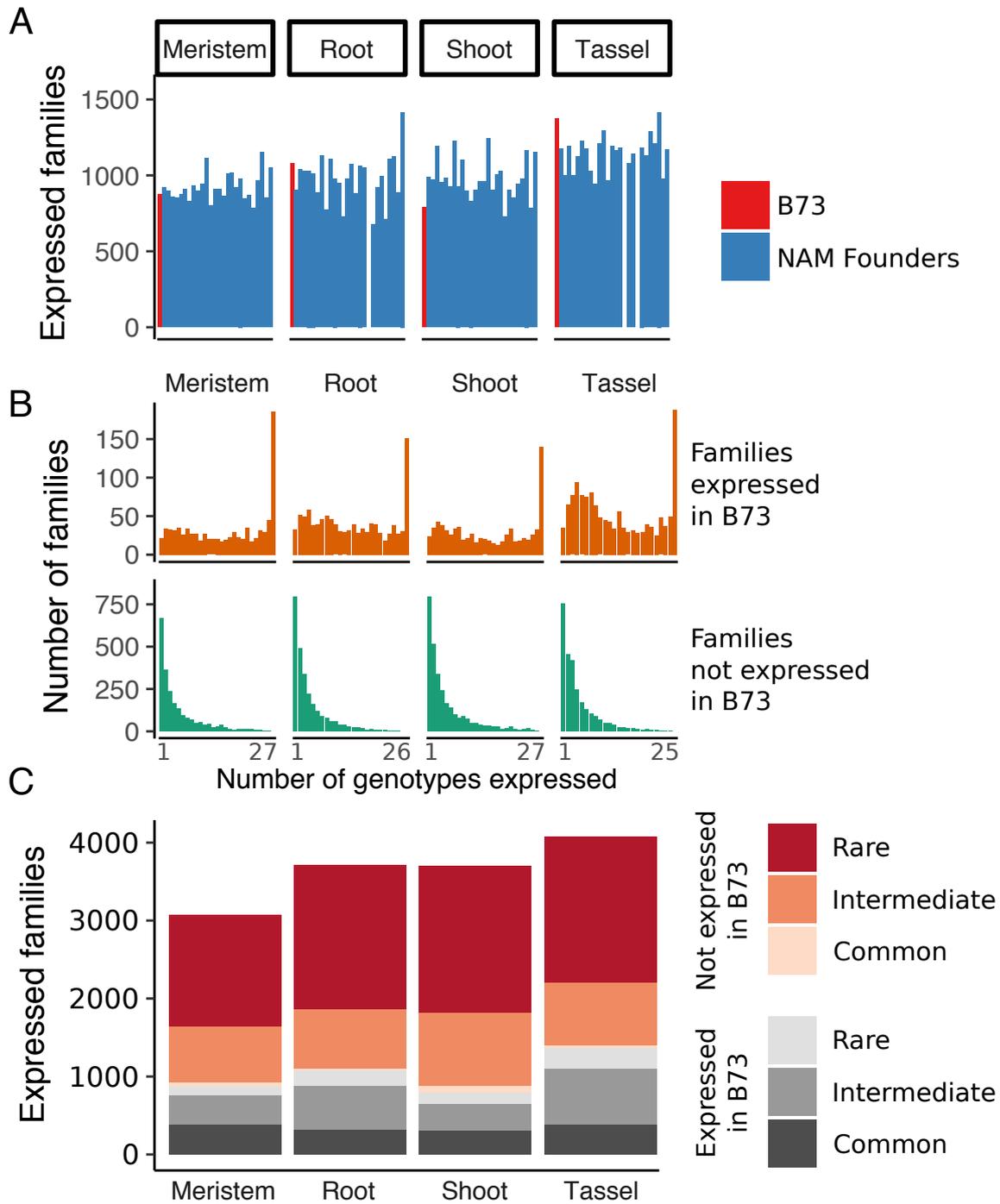


Figure S4: TE transcripts across tissues are dynamic across genotypes. A. The number of TE families expressed (RPM \geq 1) is similar in B73 and the other NAM founder lines. B. TE families expressed in B73 also tend to be expressed in a large number of lines, while families not detected in B73 tend to be expressed in few lines. C. Breakdown of TEs detected in any genotype, with rare families detected in $<$ 5 genotypes and common families detected in at least 20 genotypes.

Figure S5

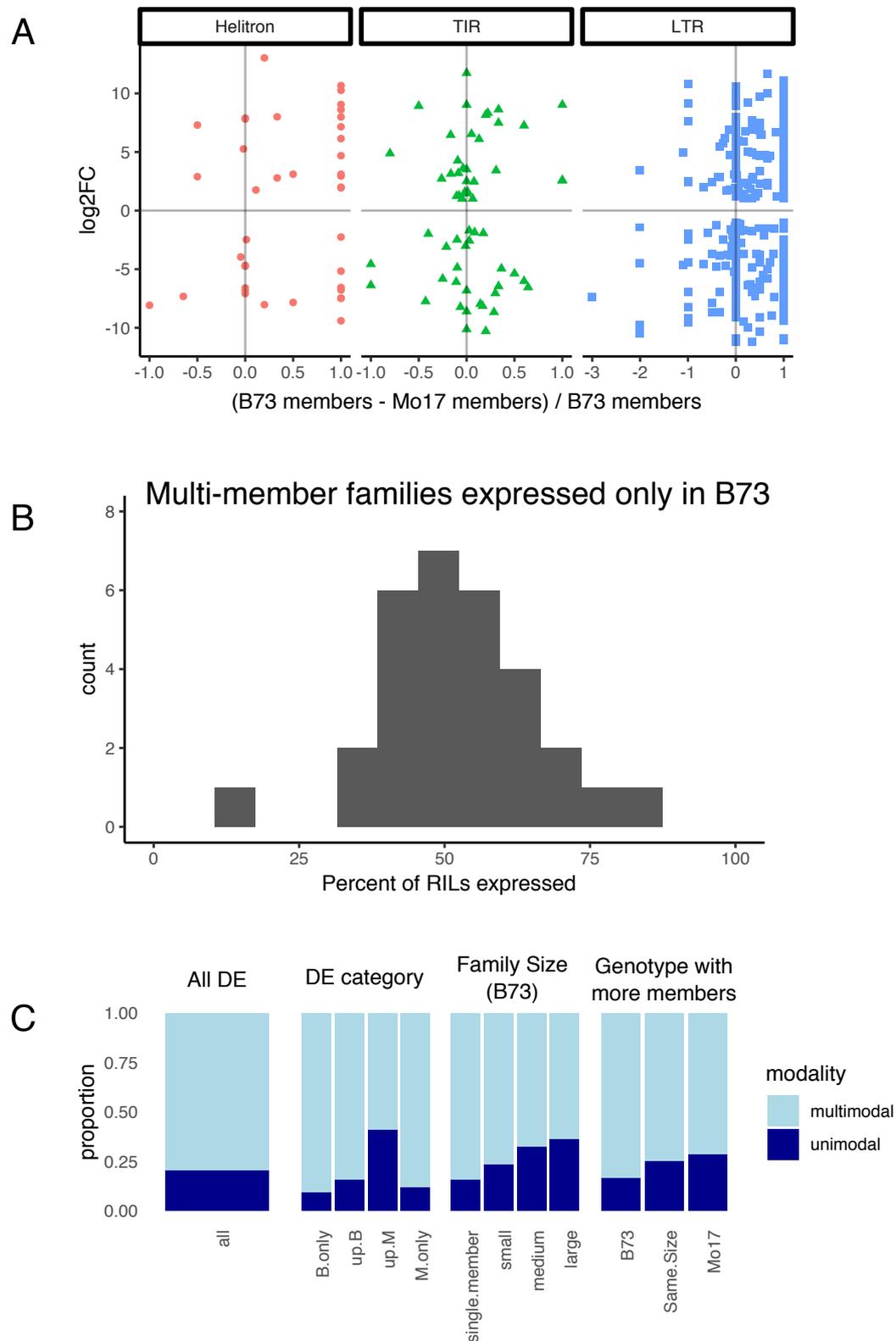


Figure S5: TE transcript dynamics across Recombinant inbred lines. A. Differentially expressed TE families were plotted, showing little relationship between the difference of members per family in the two parents and the expression difference observed. B. For multi-member TE families expressed specifically in B73 (N =), the percent of RILs with detectable transcripts (RPM > = 1) is shown. The peak at 50% suggests segregation of a single expressed locus among lines. C. The proportion of TEs in each group that segregate as a unimodal distribution among RILs.