

Figure S1

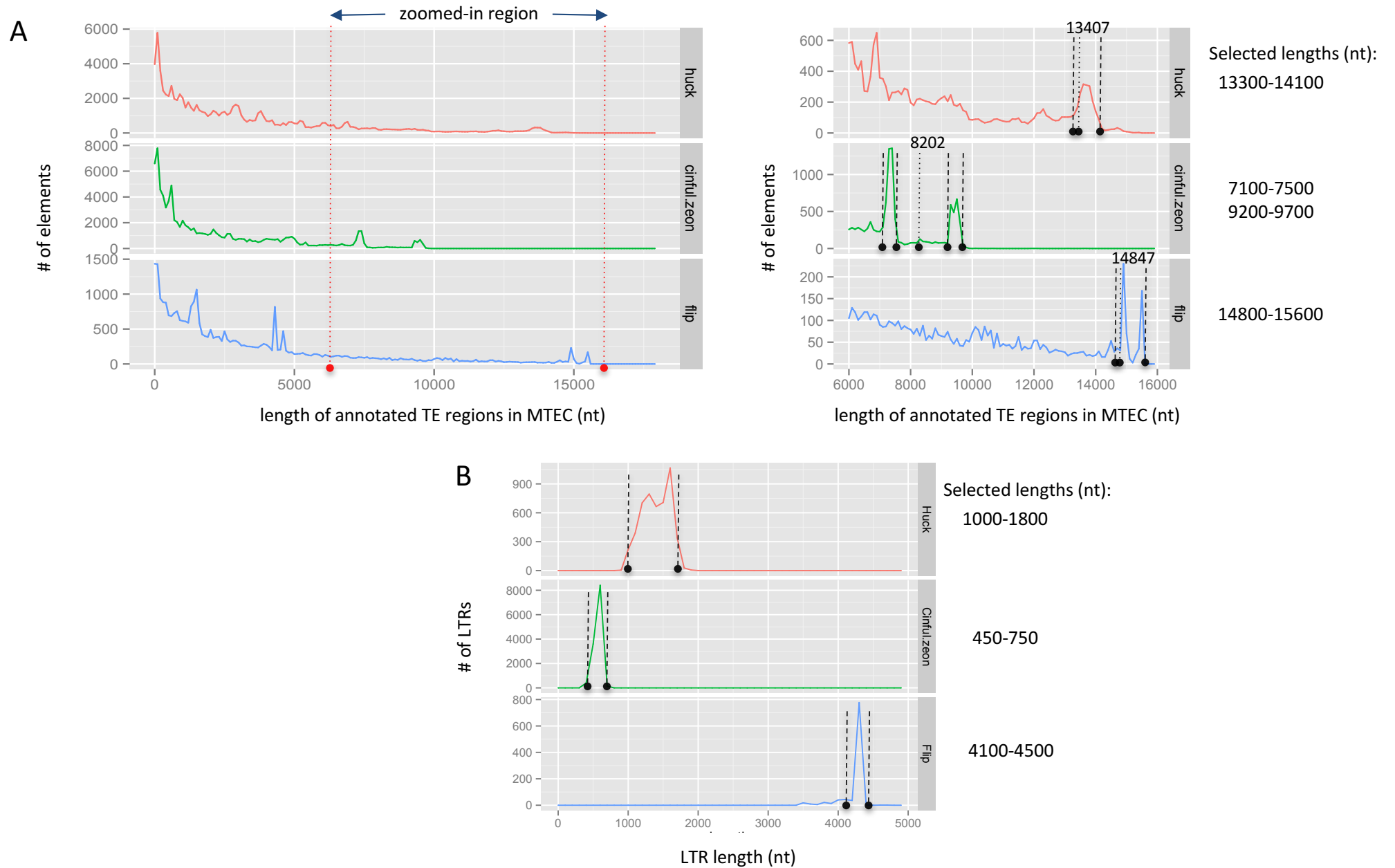


Figure S1. Gypsy TEs length analysis. **(A)** Frequency distribution of the lengths of annotated TE region according to the maze TE consortium. **(B)** Frequency distribution of LTR lengths. Thick dotted black lines indicate the full-length and LTR ranges used for each family, while the thin dotted black lines and number at the top of each plot in **A** show the Baucom et al. (2009) average.

Figure S2

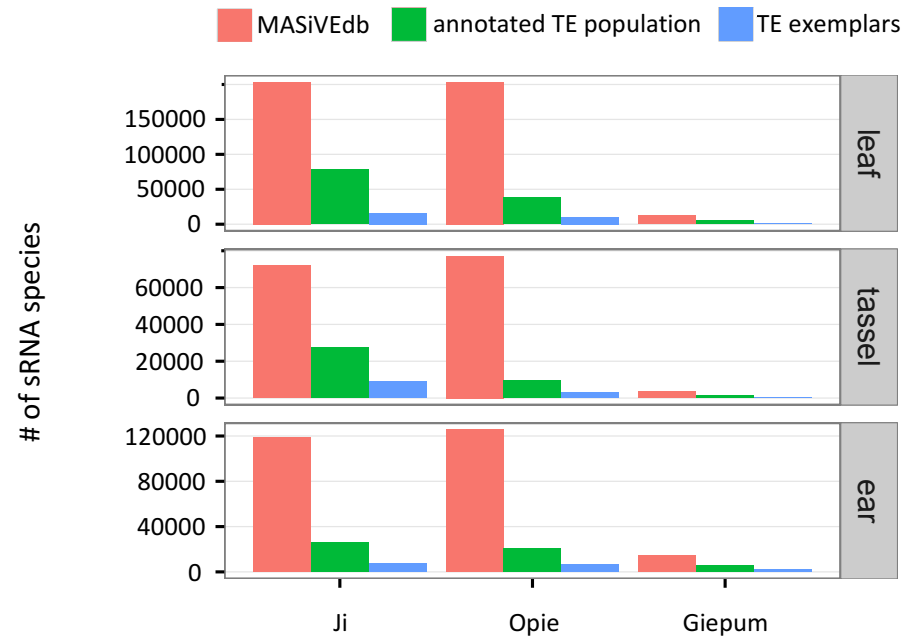


Figure S2. Total number of sRNA species that mapped to different datasets of the three *Copia* families .

Figure S3

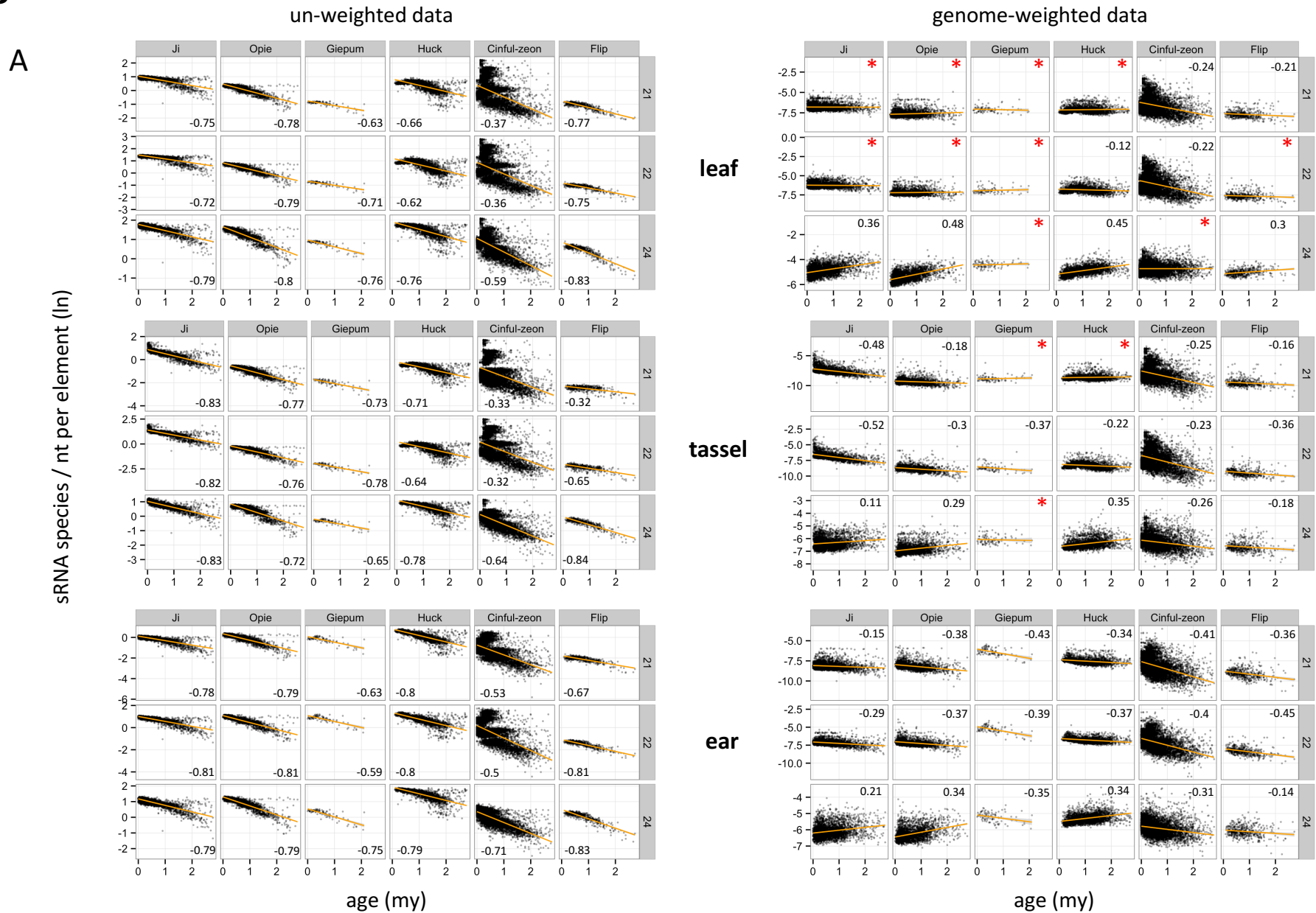


Figure S3. Relationship between TE age and sRNA mapping for leaf, tassel and ear tissues. The number of sRNA species (**A**) or expression (**B**) was calculated per nucleotide of full-length elements for each family, using un-weighted (left panels) and genome-weighted (right panels) approaches. Age is cutoff at 3 million years (my) to allow sufficient visualization of the x-axis. The Spearman r coefficient is shown for each plot, calculated for all elements and not only for those <3my. P values were <0.01, except those indicated by an asterisk.

Figure S3 (cont.)

B

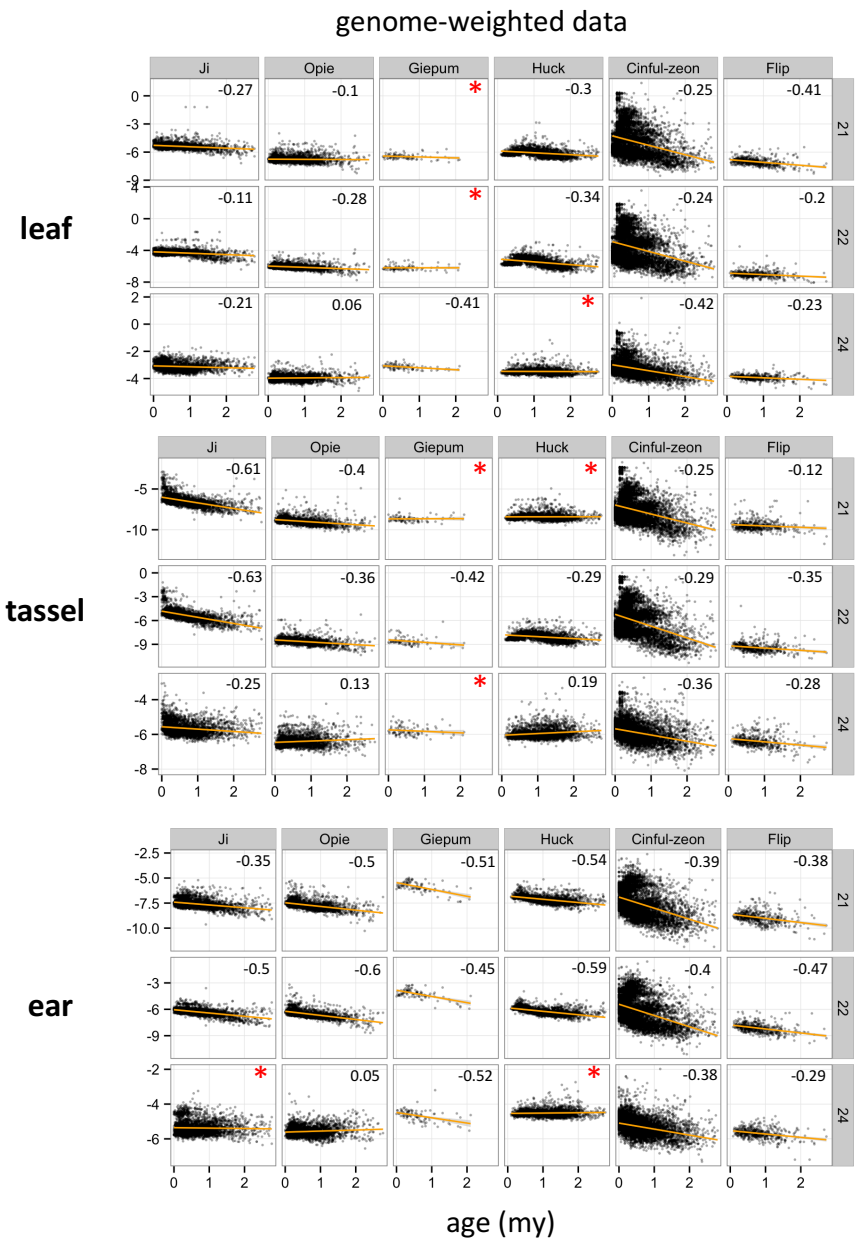
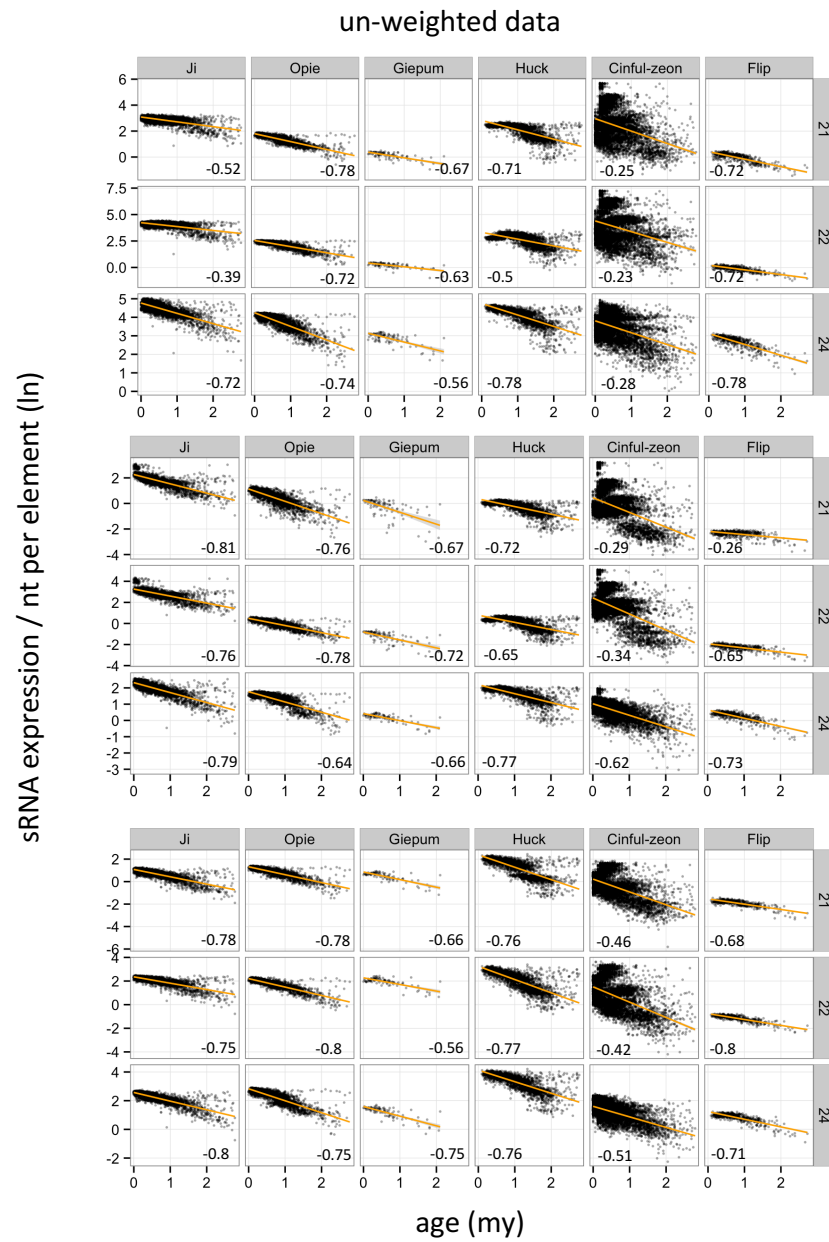


Figure S4

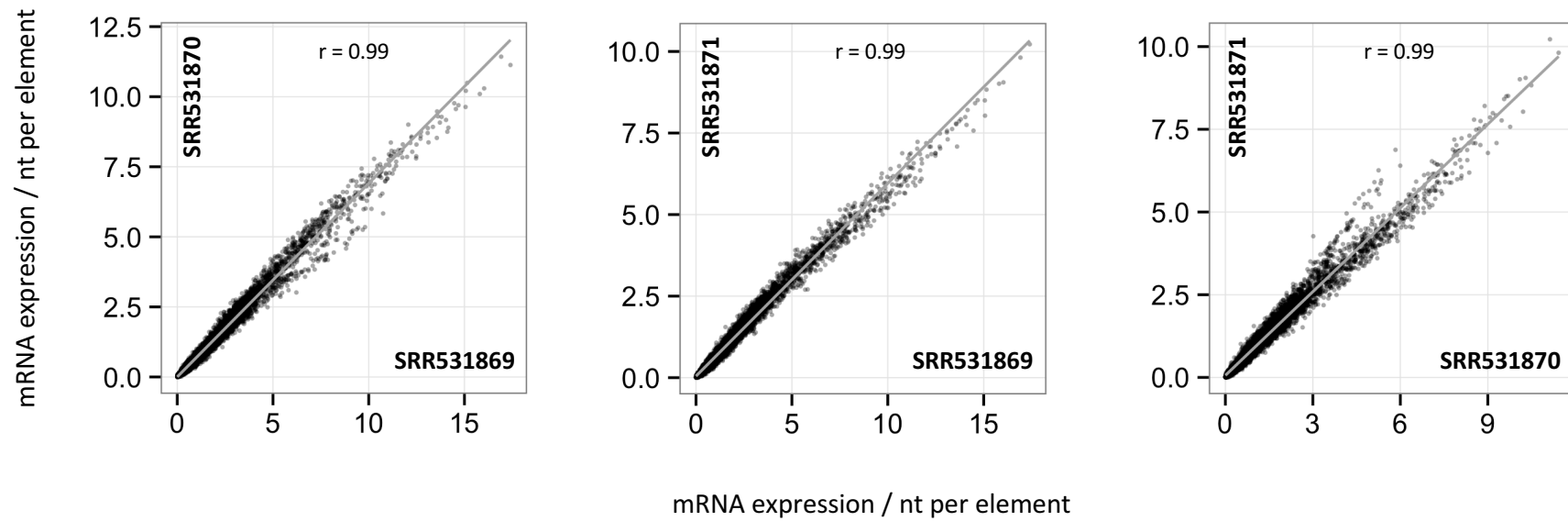


Figure S4. Mapping patterns of three leaf replicate mRNA libraries to individual elements using un-weighted data. The Spearman r coefficient is shown for each plot. P values were <0.01 in all cases.