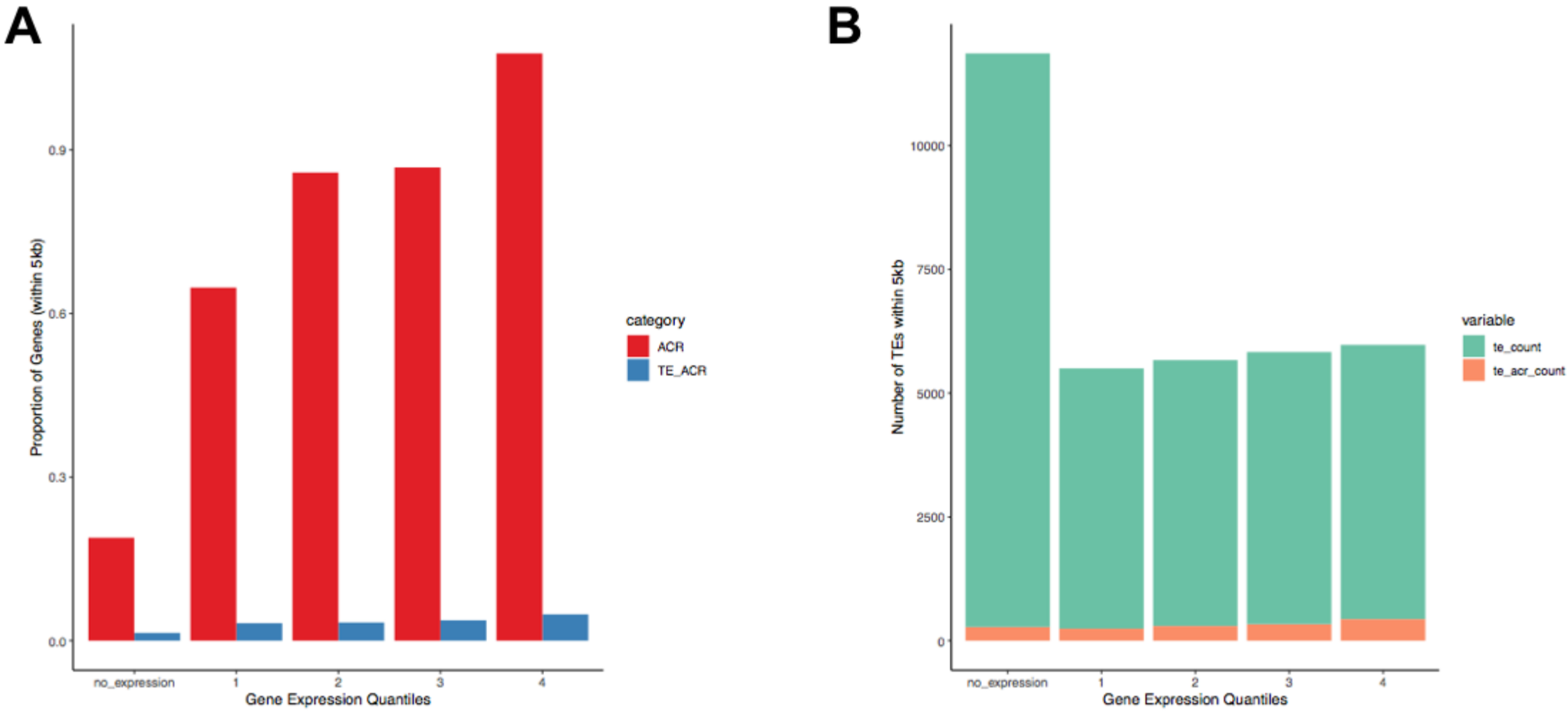

Figure S4: TE-ACRs and highly expressed genes. RNA-seq data from B73 seedling leaf samples were used to classify genes into no expression and 4 additional expression quantiles with 1 being the lowest expressed genes and 4 being the highest expressed genes (13,956 genes with no expression and 6,262 genes in each supplemental quantile). For each gene category we assessed the proportion of genes that have a defined ACR (red) or TE-ACR (blue) within 5kb (A) and the number of TEs (green) and TEs containing an ACR (orange) within 5kb of the gene (B).