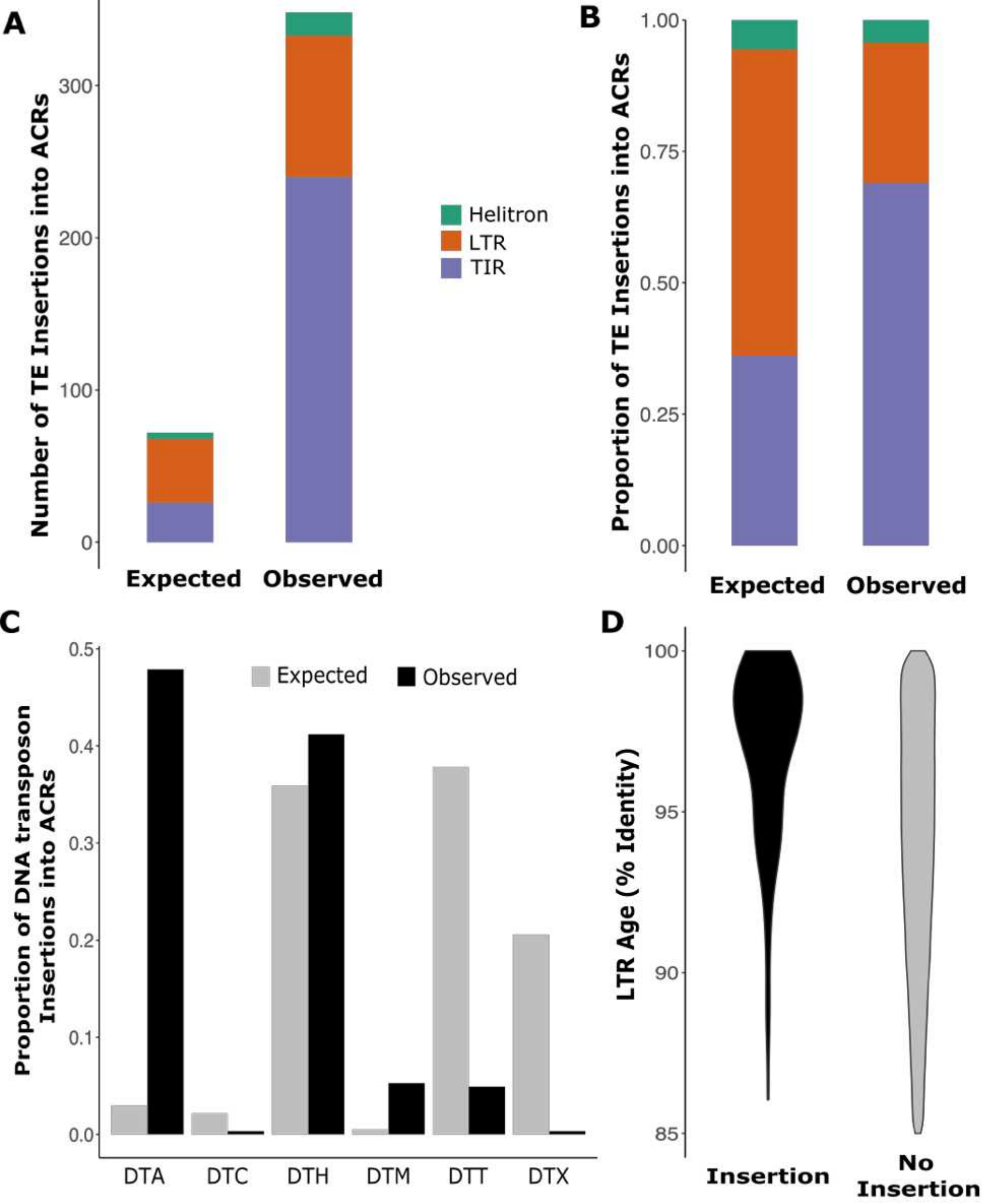

Figure S1: TE insertions by superfamily. A) Raw number of TE insertion into ACRs identified (observed) and a control set of random regions of the same size (expected). (B) The proportion of TE insertions into ACRs that are TIRs (purple), LTRs (orange), or Helitrons (green) relative to that expected by chance based on randomized regions of the same size. C) Proportion of DNA transposons that belong to each superfamily for observed (black) or expected based on randomized regions (grey) insertions into ACRs. D) LTR insertions (black) are younger on average than all LTRs in the genome (grey). LTR age is determined by percent identity of the LTR sequences (high % identity represents younger TEs).