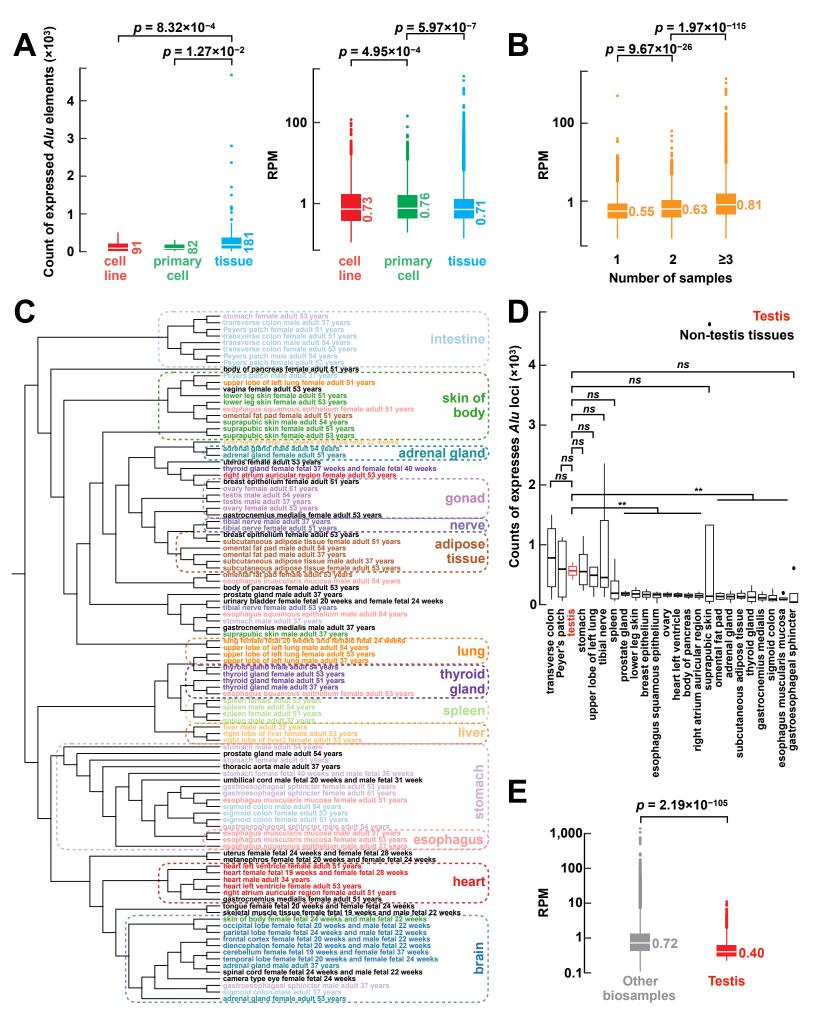
## Zhang et al., Supplemental Figure S5



## Supplemental Figure S5. Genome-wide identification of expressed *Alu* elements across 155 biosamples.

- A. Tissues (blue) contained more expressed Alu elements than cell lines (red) and primary cells (green), while the Alu elements expressed in primary cells (green) had higher expression levels than the Alu elements expressed in cell lines (red) or tissues (blue). Wilcoxon rank-sum test p-values are shown. B. Robustly expressed Alu elements (expressed in  $\geq 3$  biosamples) showed higher expression levels (measured by RPM) than Alu elements only detected in one or two biosamples. Wilcoxon rank-sum test p-values are shown.
- C. Hierarchical clustering of tissue biosamples by *Alu* expression profile.
- D. Counts of expressed *Alu* loci between the testis (red) and non-testis tissues (black). Permutation test FDR adjusted *p*-values are shown.
- E. *Alu* elements expressed in testis showed lower expression levels (measured by RPM) than *Alu* elements detected in other biosamples. Wilcoxon rank-sum test *p*-values are shown.