



**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.