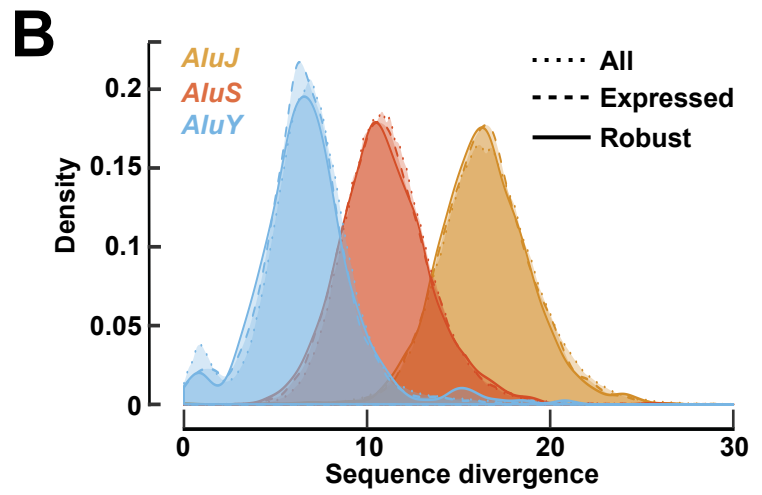
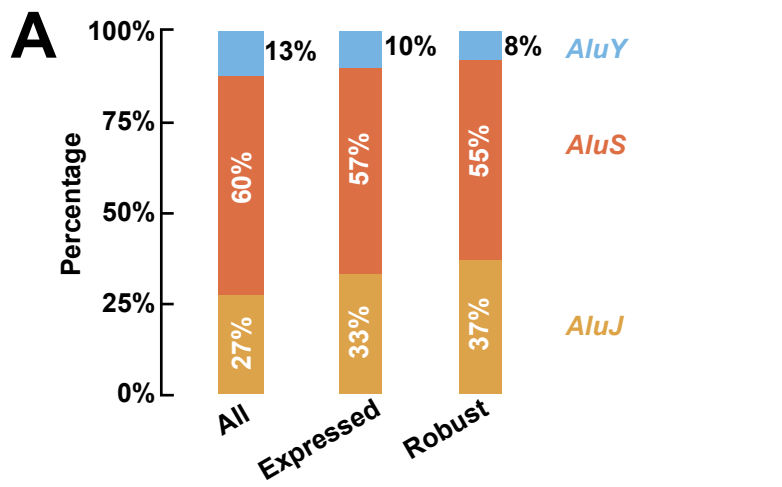
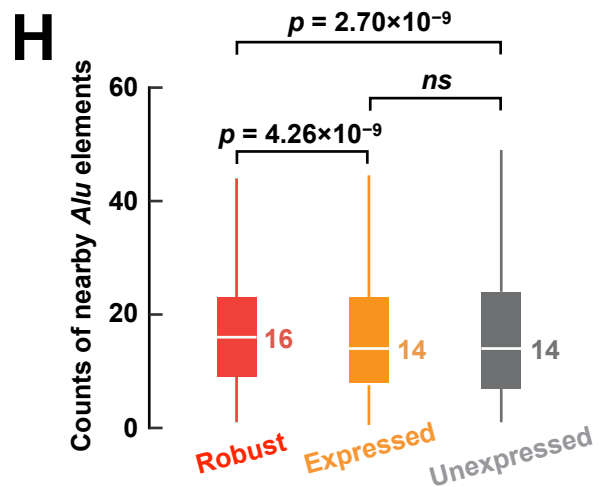
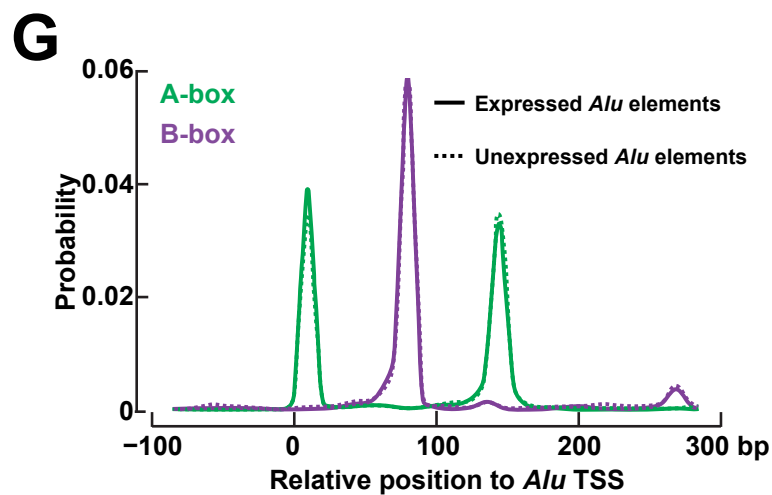
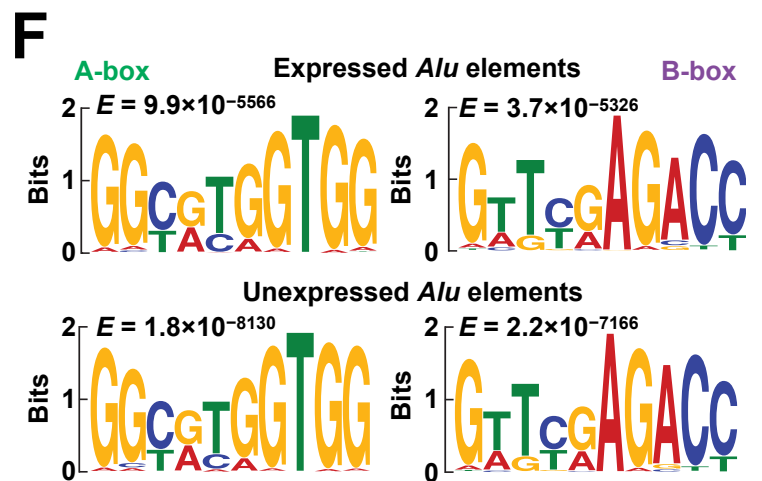
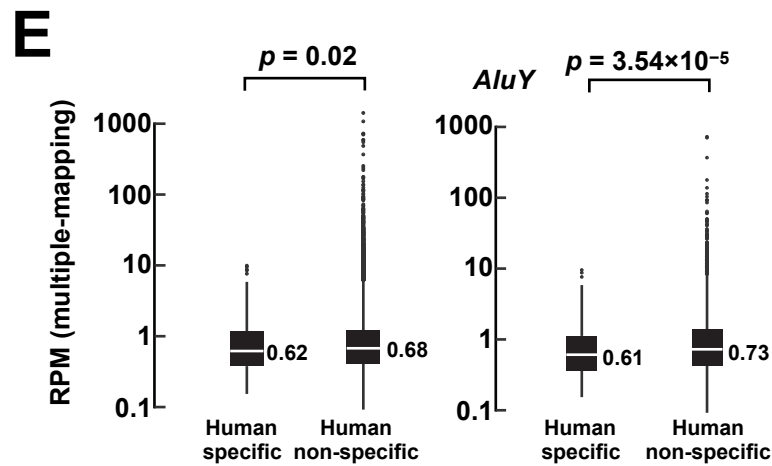
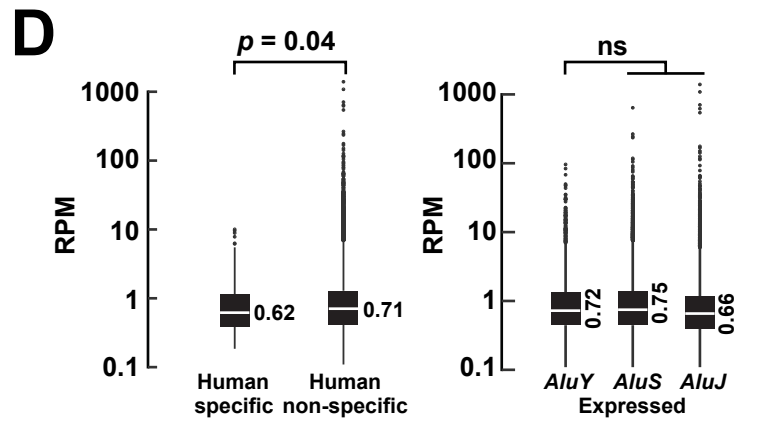


Zhang et al., Supplemental Figure S6



C

	B4	B3	B2	B1	B0
<i>AluY</i>	91	43	83	537	616
<i>AluS</i>	9	63	75	505	7,126
<i>AluJ</i>	3	21	28	218	4,545
Total	103	127	186	1,260	12,287



Supplemental Figure S6. Expressed *Alu* elements exhibit distinct genomic context and sequence features.

A. Compared with older *Alu* elements (*AluJ* and *AluS*), young *Alu* elements (*AluY*) accounted for a smaller proportion in expressed ($p\text{-value} = 4.38 \times 10^{-20}$, Chi-squared test) or robustly expressed ($p\text{-value} = 3.98 \times 10^{-14}$) *Alu* elements.

B. Sequence divergence distributions of all (dotted lines), expressed (dashed lines) and robustly expressed (solid lines) *Alu* elements in each *Alu* subfamily. The three distributions are indistinguishable from one another.

C. Summary of the evolutionary ages (branch) of all expressed *Alu* elements.

D. Human-specific *Alu* elements showed lower expression levels than non-human-specific *Alu* elements (left), and no significant differences were detected between the entire *AluY* and *AluS/J* subfamilies (right). Wilcoxon rank-sum test p -values are shown.

E. With permitting multiple-mapping reads, human-specific *Alu* elements showed lower expression levels than non-human-specific *Alu* elements (left), and human-specific *AluY* elements showed lower expression levels than non-human-specific *AluY* elements (right). Wilcoxon rank-sum test p -values are shown.

F. *De novo* motif analysis of the regulatory sequence elements (A-box and B-box) of expressed or unexpressed *Alu* elements.

G. The enrichment in A-box and B-box for expressed *Alu* elements is highly similar to the enrichment for unexpressed *Alu* elements.

H. The number of nearby (≤ 10 kb) *Alu* elements for robustly expressed (red), expressed (orange) or unexpressed (grey) *Alu* elements. Wilcoxon rank-sum test p -values are shown.