

Supplementary Table 1: Transcriptional and replicative strand asymmetries of Alu and L1 repeat subfamilies. Transcriptional and replicative strand asymmetry ratios are calculated as the occurrences in one orientation (leading or non-template) over the total number of occurrences in both orientations. Ratios above 0.5 indicate non-template and leading orientation preference, while ratios below 0.5 indicate template and lagging orientation preference for transcriptional and replicative strand asymmetries. Displayed p-values are from binomial testing with Bonferroni correction.

| Repeat Subfamily | Repeat transcriptional strand asymmetry ratio | Repeat transcriptional strand asymmetry p-value | Repeat replicative strand asymmetry ratio | Repeat replicative strand asymmetry p-value |
|------------------|---|---|---|---|
| AluJ | 0.472 | <0.001 | 0.534 | <0.001 |
| AluS | 0.449 | <0.001 | 0.531 | <0.001 |
| AluY | 0.459 | <0.001 | 0.525 | <0.001 |
| L1M | 0.373 | <0.001 | 0.542 | <0.001 |
| L1P | 0.409 | <0.001 | 0.523 | <0.001 |

Supplementary Table 2: Breakpoint transcriptional and replicative strand asymmetries of Alu and L1 repeat subfamilies. Adjusted transcriptional and replicative strand asymmetry ratios for breakpoints at repeats are displayed. Log₂(adjusted strand asymmetry ratios) above 0 indicate non-template and leading orientation preference, while log₂(adjusted strand asymmetry ratios) below 0 indicate template and lagging orientation preference for the breakpoints at Alu or L1 repeats. Displayed p-values are from binomial testing with Bonferroni correction.

| Repeat Subfamily | Breakpoint transcriptional strand asymmetry log ₂ (adjusted strand asymmetry ratios) | Breakpoint transcriptional strand asymmetry p-value | Breakpoint replicative strand asymmetry log ₂ (adjusted strand asymmetry ratios) | Breakpoint replicative strand asymmetry p-value |
|------------------|---|---|---|---|
| AluJ | -0.040 | >0.05 | 0.017 | >0.05 |
| AluS | -0.056 | <0.001 | 0.023 | <0.001 |
| AluY | -0.056 | <0.001 | 0.014 | >0.05 |
| L1M | -0.008 | >0.05 | 0.004 | >0.05 |
| L1P | -0.163 | <0.001 | 0.063 | <0.001 |