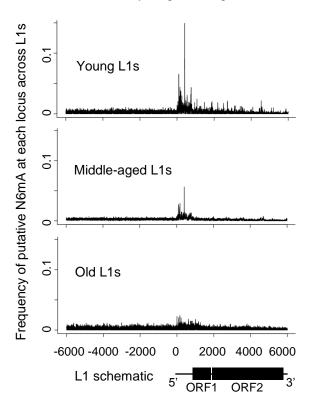
HG002 Genome Assembly as reference

Human young, full length L1s



Distance to L1 5' UTR start site (bp)

Supplemental Fig S6. Mean IPD ratio of A sites (adjusted by the frequency of A's) across 1,274 young (evolutionary age<10 million years), full-length (>6,000bp) L1s. The consensus analyses (IPD ratio >3) were conducted across the +/-6,000bp beyond the 5' UTRs of human young L1s (top panel), middle-aged L1s (middle panel) and old L1s (bottom panel) using *de novo* genome assembly (Zook *et al.*).