



Supplemental Fig S9. The consensus pattern of A's in the young full length L1 remain after rigorous filtering of possible confounding factors. The consensus analyses (IPD ratio >3) were conducted across the +/-6,000bp beyond the 5' UTRs of human young L1s with different adjustments: **(a)** adjustment for outlier effect resulting from sequencing errors in SMRT-seq (**Methods**), **(b)** adjustment for SNP effect, i.e., heterozygous genotype at certain loci (**Methods**) and **(c)** adjustment for *in silico* control bias (**Methods**).