



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 $\pm 6,000$ bp 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**).