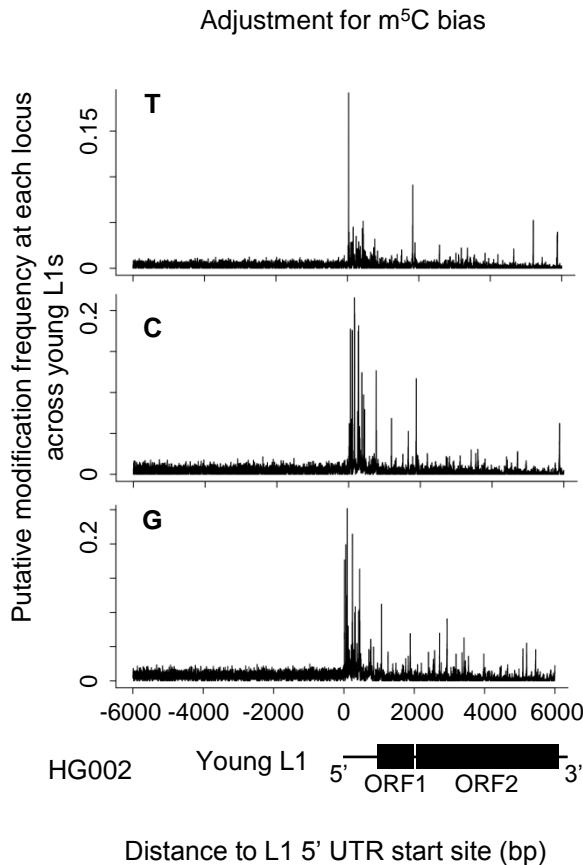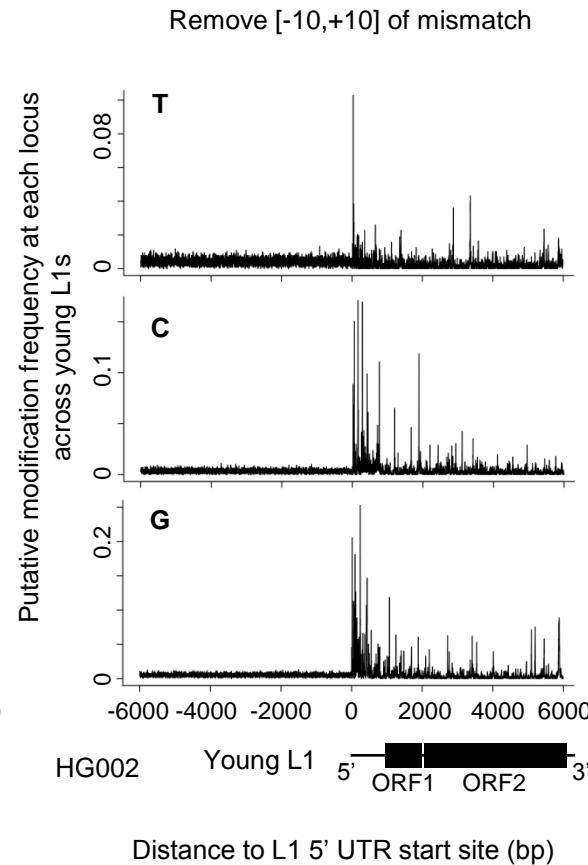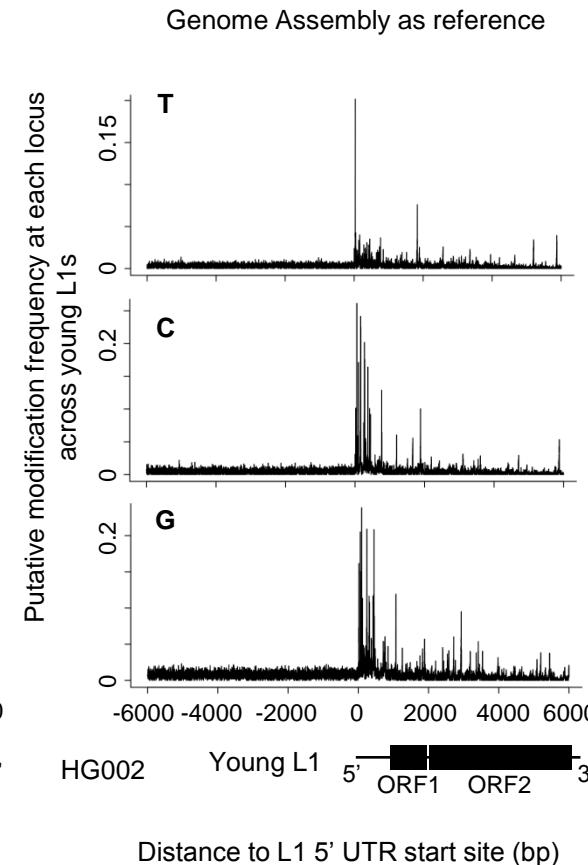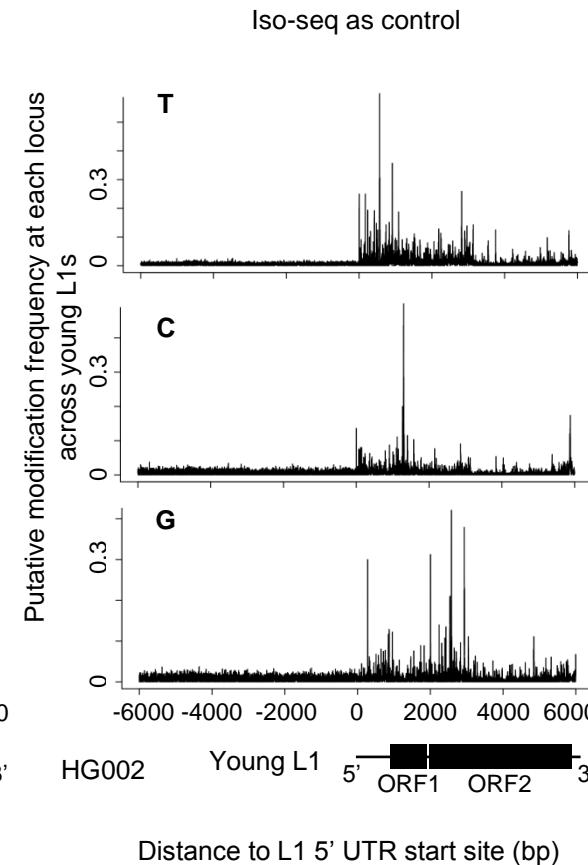**Supplemental Fig S10.** In addition to A's, T, C and G also show consensus patterns on human young L1s, after adjustment for multiple factors that may confound SMRT-seq based modification detection (as done for A's, Supplemental Fig S10). The consensus analyses (IPD ratio >3) were conducted for all three nucleotides across the +/-6,000bp beyond the 5' and 3' UTRs of Human young L1s with different adjustments: (**a**) adjustment for false positive modification calling due to neighboring m5C events **(Methods),** (**b**) adjustment for outlier effect resulting from sequencing errors in SMRT-seq **(Methods)**, (**c**) adjustment for SNP effect **(Methods)** and (**d**) adjustment for *in silico* control bias **(Methods)**.