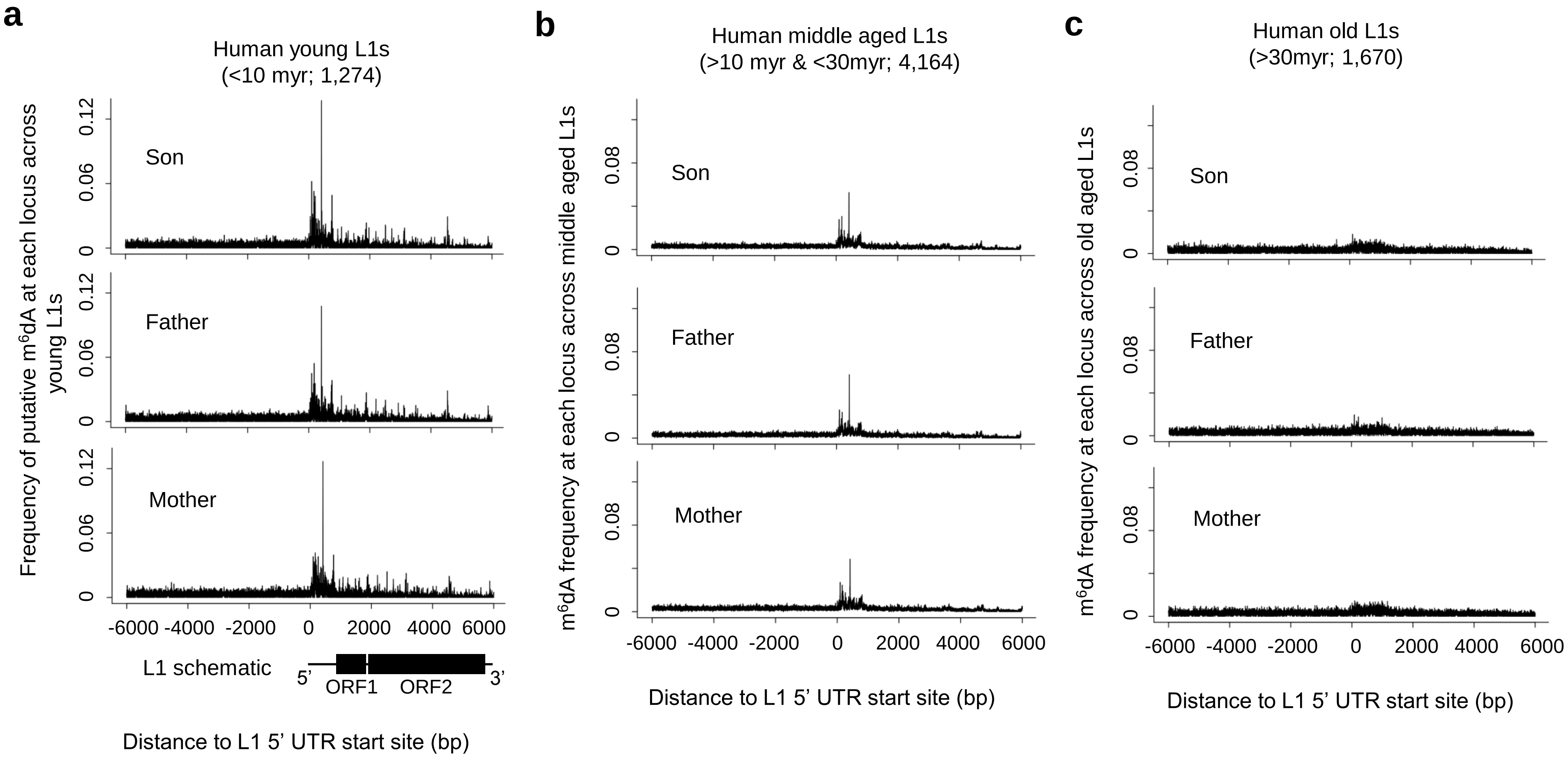

Supplemental Fig S8. Adjustment of false positive m^{6}dA due to neighboring m^{5}C events on Human young full-length L1s. We analyzed an *E. coli* methylome and estimated that putative m^{6}dA sites (IPD ratio > 3) called in the hLCLs data correspond to an FDR of < 0.016 with respect to A's that are positioned in the vicinity (+/-10bp) of m^{5}C sites. Based on this estimation, we used IPD ratio of 3 as the cutoff to plot the consensus of putative m^{6}dA events at each locus (adjusted by the frequency of A's) across 1,274 young (evolutionary age<10 million years) L1s **(a),** 4,164 middle-aged (evolutionary age >10 & <30 million years) L1s **(b)**, and 1,670 old (evolutionary age >30 million years) L1s **(c)** for the three hLCL lines. Consistent across the three hLCL lines, m^{6}dA is enriched at young full-length L1s, compared to middle-aged and old L1s, specifically in the promoter and proximal region.