



Figure 2 – figure supplement 3: Frequency of transitions (excluding G:C>A:T in CG) and transversions per 1Mb window, binned per replication time, relative to the earliest replicating bin. Mutations are divided in 7 bins (left to right bins represent early to late replication timing events). Linear regression analysis was performed to assess whether observed increases were significant and independent of other genomic features. Bonferroni-corrected P -values were significant ($P < 2.0 \times 10^{-5}$) for transitions and non-significant for transversions. In none of the individual MMR-deficient genomes, transversions were significantly correlated to replication timing, whereas transitions correlated for each of the MMR-deficient genomes.