



## Figure S11

**Mechanistic model is highly robust to simulation parameters.** (A) Randomly eliminating an ever larger fraction (x-axis) of DNase HS marks from the simulation of replication timing in GM06900 cells reduces the correlation (y-axis) of the model prediction with the empirical data only marginally when removing up to 50% of DNase sites. Beyond that, point, the correlation degrades gradually. Error bars represent standard error of the mean resulting from averaging the correlation value across 22 autosomal chromosomes. (B) DNA replication timing was predicted for K562 and GM06990 cells based on cell-specific DNase data. Different functions were used to mapping the amplitudes  $a(x)$  of the DNase signal at a location  $x$  in the ENCODE database to the probability  $p(x)$  of replication initiation at this DNase mark. No significant differences were seen between assigning a constant value  $p = 1$  or amplitude dependent values  $p(x) \sim a(x)$ ,  $p(x) \sim a(x)^2$ ,  $p \sim a(x)^{1/2}$ .