



Figure 1- figure supplement 3

Heatmap illustrating the varying size of the “initiation zone” at replication origins. Data is from the most efficient replication origins (n=1000, efficiency >0.5). Mapped sequencing reads for either the Watson strand (leftward moving forks, left of the origin) or Crick strand (rightward moving forks, right of the origin) are displayed for each replication origin. To allow comparisons across origins with different efficiencies, the mapped sequencing data for Watson or Crick reads +/- 25kb from each origin was mean centered and normalized such that sum of the squares of the values = 1.0. All origins are then ranked according the size of transition zone, with the smallest at the top.