



**Supplementary Figure S1. Relationship between mutation rate and GC content.**

Linear fit between observed mutation rate and GC content of the 1000bp surrounding a site. Each point represents multiple genomic sites placed in discrete bins (width = 0.005) based on each site's GC content. Observed mutation rate for each point was calculated as the number of observed mutations divided by the total number of callable sites-generations in that bin. The shaded grey area around the line represents the 95% confidence region.