



Figure S3. Hitchhiking regions are enriched for deleterious SNPs. The log ratio of deleterious to neutral SNPs (DEL/NEU) after correcting for the number of potentially deleterious sites is significantly higher for hitchhiking (red) compared to non-hitchhiking windows (black). The adjusted log ratio of DEL/NEU was marginalized over the number of GC nucleotides in a codon ($j = 0, \dots, 3$) for presentation. The regression line $\beta_0 + \beta_1 * r + \beta_3 * h$ is shown for hitchhiking ($h = 1$) and non-hitchhiking ($h = 0$) regions. Sample size is indicated by circle size.