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 \( j = 0, \ldots, 3 \) for presentation. The regression line \( \beta_0 + \beta_1 * n + \beta_3 * h \) is shown for hitchhiking \( (h = 1) \) and non-hitchhiking \( (h = 0) \) regions. Sample size is indicated by circle size.