

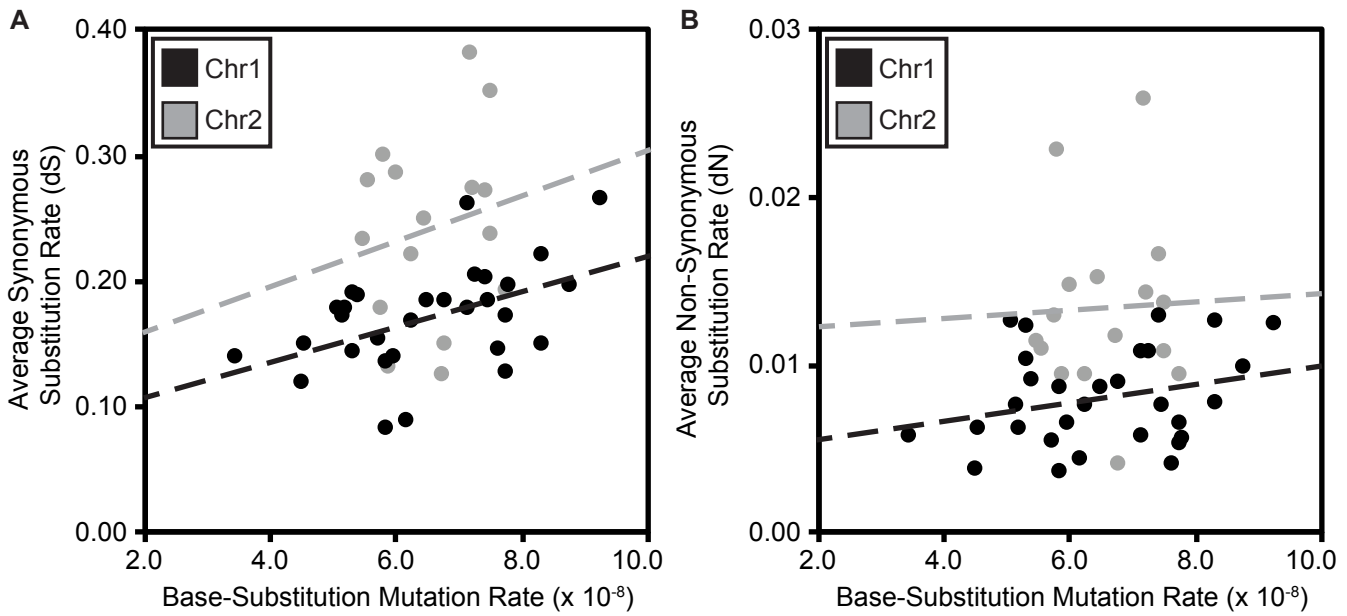
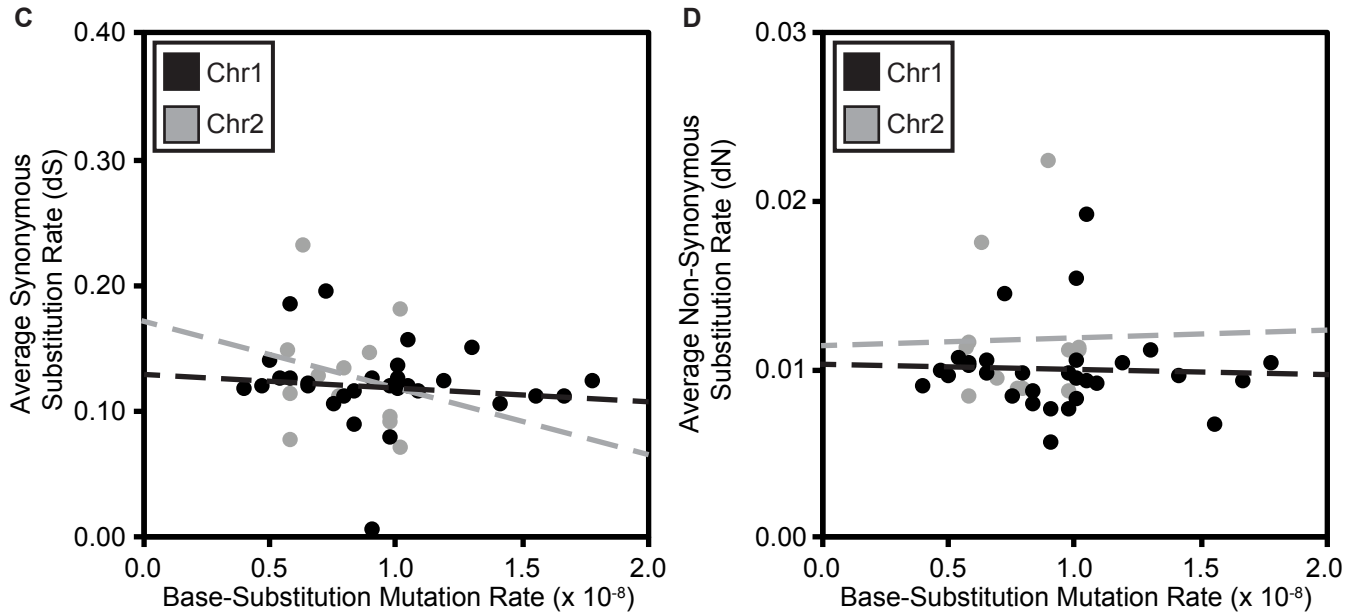
V. fischeri*V. cholerae*

Figure S6. Relationship between base-substitution mutation rates (bpsm) with average synonymous substitution rates (left panels) and average non-synonymous substitution rates (right panels) of genes. *V. fischeri*, top row, *V. cholerae*, bottom row, Average synonymous and non-synonymous substitution rates were calculated using the average rates of all one-to-one orthologs shared between *V. fischeri* ES114 and *V. fischeri* MJ11, or between *V. cholerae* 2740-80 and *V. cholerae* HE-16 within each 100kb interval. Synonymous and non-synonymous substitution rates for individual genes were calculated as described in (Yang and Nielsen 2000). In *V. fischeri*, only the relationship between bpsm rates and synonymous substitution rates on chromosome 1 is significant (A: Chr1 - $F = 8.32$, $df = 28$, $p = 0.0080$, $r^2 = 0.23$, Chr2 - $F = 0.56$, $df = 14$, $p = 0.4681$, $r^2 = 0.04$; B: Chr1 - $F = 2.14$, $df = 28$, $p = 0.1554$, $r^2 = 0.07$, Chr2 - $F = 0.03$, $df = 14$, $p = 0.8692$, $r^2 = 0.02$), and in *V. cholerae*, none are significant (C: Chr1 - $F = 0.43$, $df = 28$, $p = 0.5186$, $r^2 = 0.02$, Chr2 - $F = 0.49$, $df = 10$, $p = 0.5010$, $r^2 = 0.05$; D: Chr1 - $F = 0.02$, $df = 28$, $p = 0.8897$, $r^2 = 0.01$ 10⁻¹, Chr2 - $F = 0.01$, $df = 10$, $p = 0.9218$, $r^2 = 0.01$ 10⁻¹).