



Figure S4: Relationship between base-substitution mutation (bpsm) rates in 100 Kb intervals on the right replichore with concurrently replicated 100 Kb intervals on the left replichore for $A:T > G:C$ (A) and $G:C > A:T$ (B) bpsms in MMR-deficient *Vibrio fischeri* and C) $A:T > G:C$ and D) $G:C > A:T$ bpsms in MMR-deficient *Vibrio cholerae*. Only the relationship between $G:C > A:T$ bpsm rates of concurrently replicated regions on chr1 is significantly positive (Vf: $A:T > G:C$: Chr1 - $F = 1.77$, $df = 13$, $p = 0.2067$, $r^2 = 0.12$, Chr2 - $F = 3.26$, $df = 6$, $p = 0.1209$, $r^2 = 0.35$; $G:C > A:T$: Chr1 - $F = 13.32$, $df = 13$, $p = 0.0029$, $r^2 = 0.51$, Chr2 - $F = 0.17$, $df = 6$, $p = 0.6947$, $r^2 = 0.03$; Vc: $A:T > G:C$: Chr1 - $F = 0.24$, $df = 13$, $p = 0.6313$, $r^2 = 0.02$, Chr2 - $F = 1.74$, $df = 4$, $p = 0.2574$, $r^2 = 0.30$; $G:C > A:T$: Chr1 - $F = 28.99$, $df = 13$, $p = 0.0001$, $r^2 = 0.6904$, Chr2 - $F = 0.15$, $df = 4$, $p = 0.7209$, $r^2 = 0.04$).