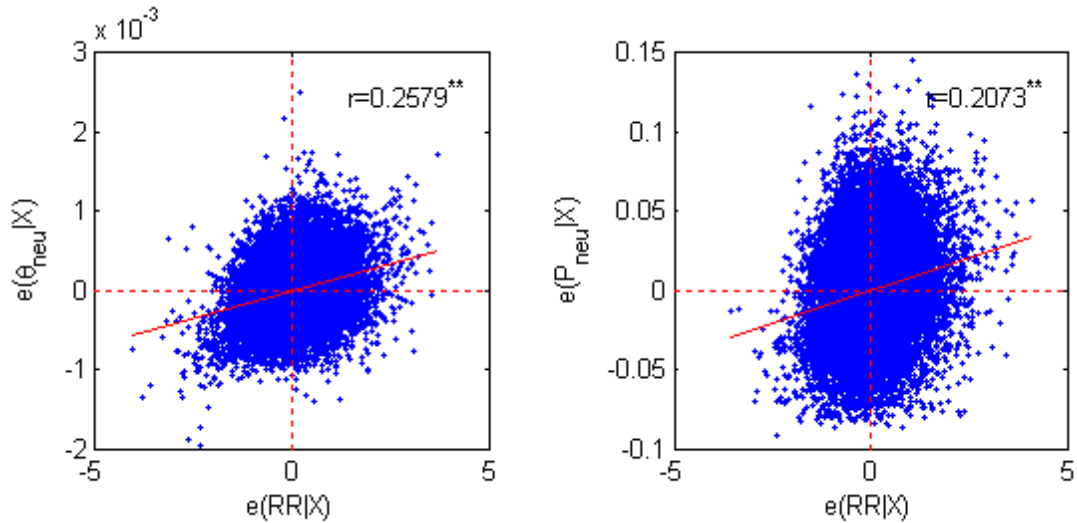Figure S2. Residual-residual plot between recombination rate (RR) and neutral polymorphism [i.e. the level of neutral polymorphism (θ_{neu}) or the level of normalized neutral polymorphism ($P_{neu}=\theta_{neu}/d_{neu}$)] after statistically removing the effects of GC content (GC), repeat density (RD), functional divergences [i.e. the divergence at coding sites (D_n) and the divergence at conserved noncoding region (D_x)], and functional constraints [i.e. the number of codons (FD_n) and the number of conserved noncoding sites (FD_x)]. $e(Y|X)$ is the difference between the observed value of the response variable, Y, and the value suggested by the regression model of Y on several predictor variables X={GC, RD, D_n, D_x, FD_n, FD_x}. The values of θ_{neu} and P_{neu} here are based on the Perlegen data are in **(a)** and based on the Watson data are in **(b)**.

(a)

(b)