Figure S2. Residual-residual plot between recombination rate (RR) and neutral polymorphism [i.e. the level of neutral polymorphism ($\theta_{\text{neu}}$) or the level of normalized neutral polymorphism ($P_{\text{neu}}=\theta_{\text{neu}}/d_{\text{neu}}$)] 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 $\theta_{\text{neu}}$ and $P_{\text{neu}}$ here are based on the Perlegen data are in (a) and based on the Watson data are in (b).

(a)

(b)