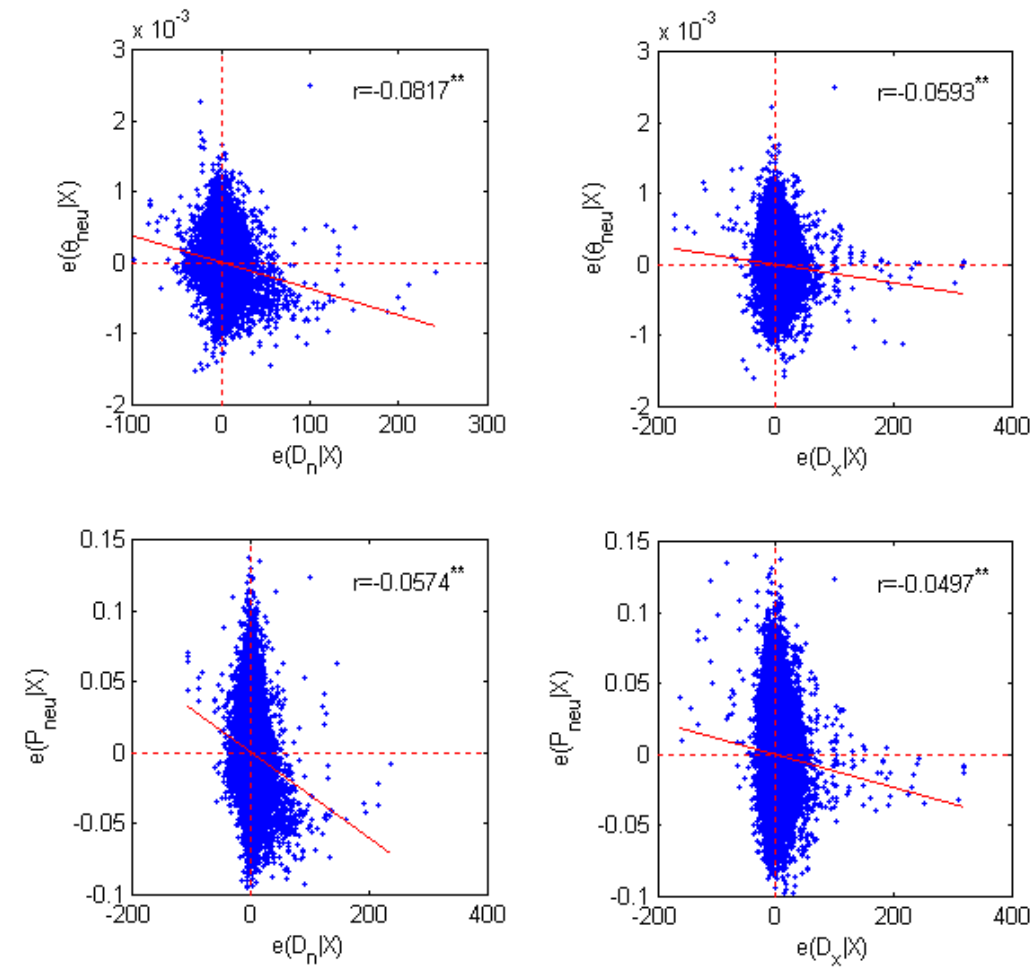


Figure S6. Residual-residual plots between functional divergence [i.e. the divergence at coding sites (D_n) or the divergence at conserved noncoding region (D_x)] and neutral polymorphism [i.e. the level of neutral polymorphism (θ_{neu}) and the level of normalized neutral polymorphism ($P_{neu} = \theta_{neu}/d_{neu}$)], after both have been adjusted for effects of GC content (GC), repeat density (RD), functional constraints [i.e. the number of codons (FD_n) and the number of conserved noncoding sites (FD_x)], and functional divergence (D_n or D_x , excluding the response variable under test). $e(Y|X)$ 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)

