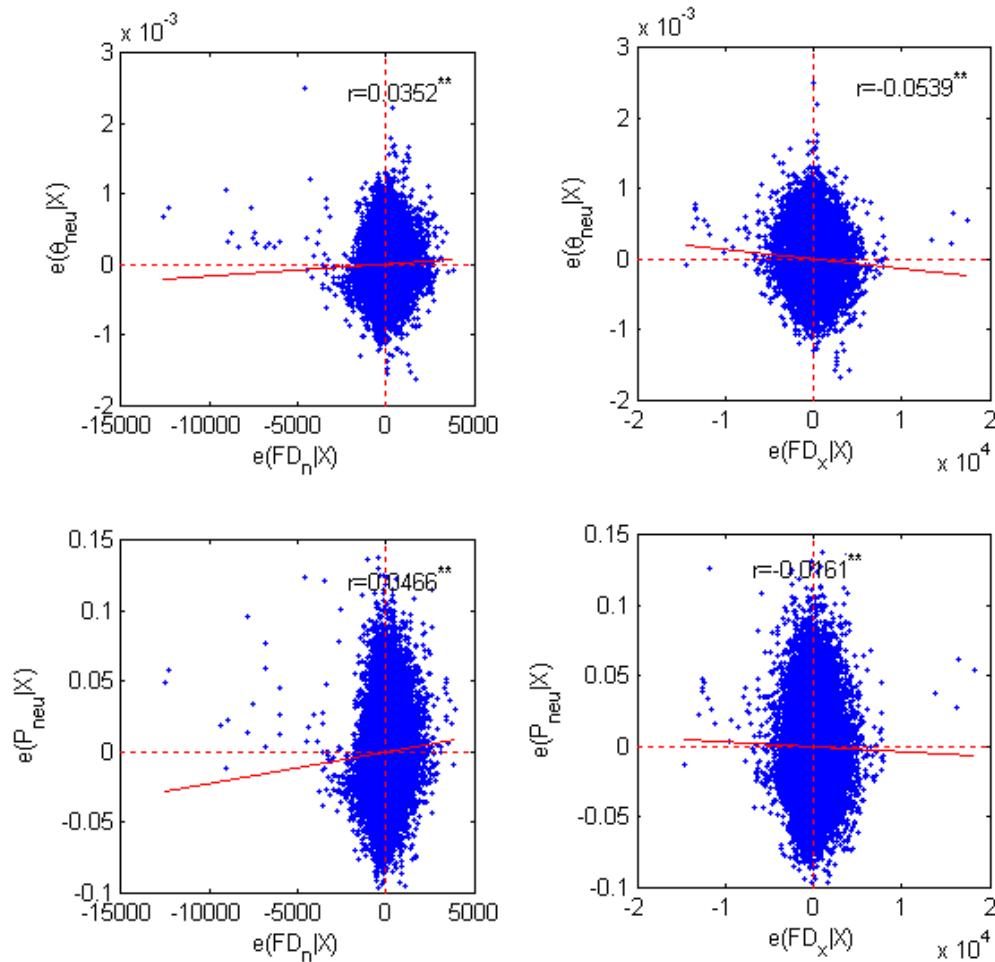Figure S4. Residual-residual plots between functional density [i.e. the number of codons (FD_n) or the number of conserved noncoding sites (FD_x)] and neutral polymorphism [i.e. the level of neutral polymorphism (θ_{neu}) or the level of normalized neutral polymorphism ($P_{neu}=\theta_{neu}/d_{neu}$)], after both have been adjusted for 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 density (FD_n or FD_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)