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 ($\theta_{neu}$) 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 $\theta_{neu}$ and $P_{neu}$ here are based on the Perlegen data are in (a) and based on the Watson data are in (b).