

Fig S3. Relationships among the levels of 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 ($P_{neu} = \theta_{neu}/d_{neu}$)]. Scatter plots display values of two variables in gray dots for **(a)** FD_n and θ_{neu} , **(b)** FD_x and θ_{neu} , **(c)** FD_n and P_{neu} , and **(d)** FD_x and P_{neu} . Red circles are average values for the pooled gray dots in 100 bins each containing 1% of the data points. The solid, green line shows the fit of a linear model. The values of θ_{neu} and P_{neu} here are based on the Watson data. The results derived from the Perlegen data are given in Fig. 2.



