Figure S9. Results derived from the sliding windows of 600 kb. Correlations between functional density [i.e. the number of codons (FD_n) or the number of conserved noncoding sites (FD_x)], and 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}) or the level of normalized neutral polymorphism ($P_{neu}=\theta_{neu}/d_{neu}$)] are given. The results are based on the Perlegen data.

(e)

Level of neutral polymorphism, θ_neu (× 10⁻³)

FD_n (Number of codons)

(f)

Level of neutral polymorphism, θ_neu (× 10⁻³)

FD_x (Number of conserved noncoding sites)

(g)

Level of neutral polymorphism, P_neu = θ_neu/d_neu

FD_n (Number of codons)

(h)

Level of neutral polymorphism, P_neu = θ_neu/d_neu

FD_x (Number of conserved noncoding sites)