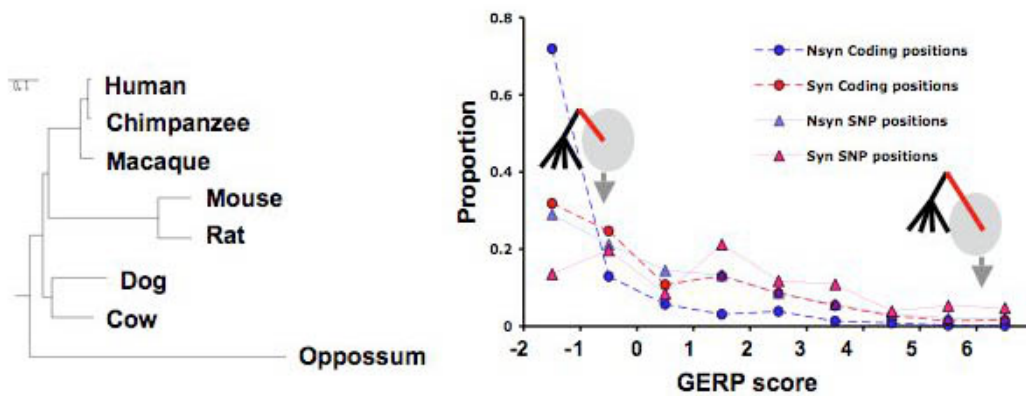


Additional File 2: GERP score distribution



Additional File 2: (A) The phylogenetic tree of the mammalian genomes used to calculate divergence rate. (B) Distribution of GERP score for coding SNP and non-SNP bases. The pattern is shown for synonymous and non-synonymous base positions. The coding SNP positions are more divergent than the coding non-SNP positions.