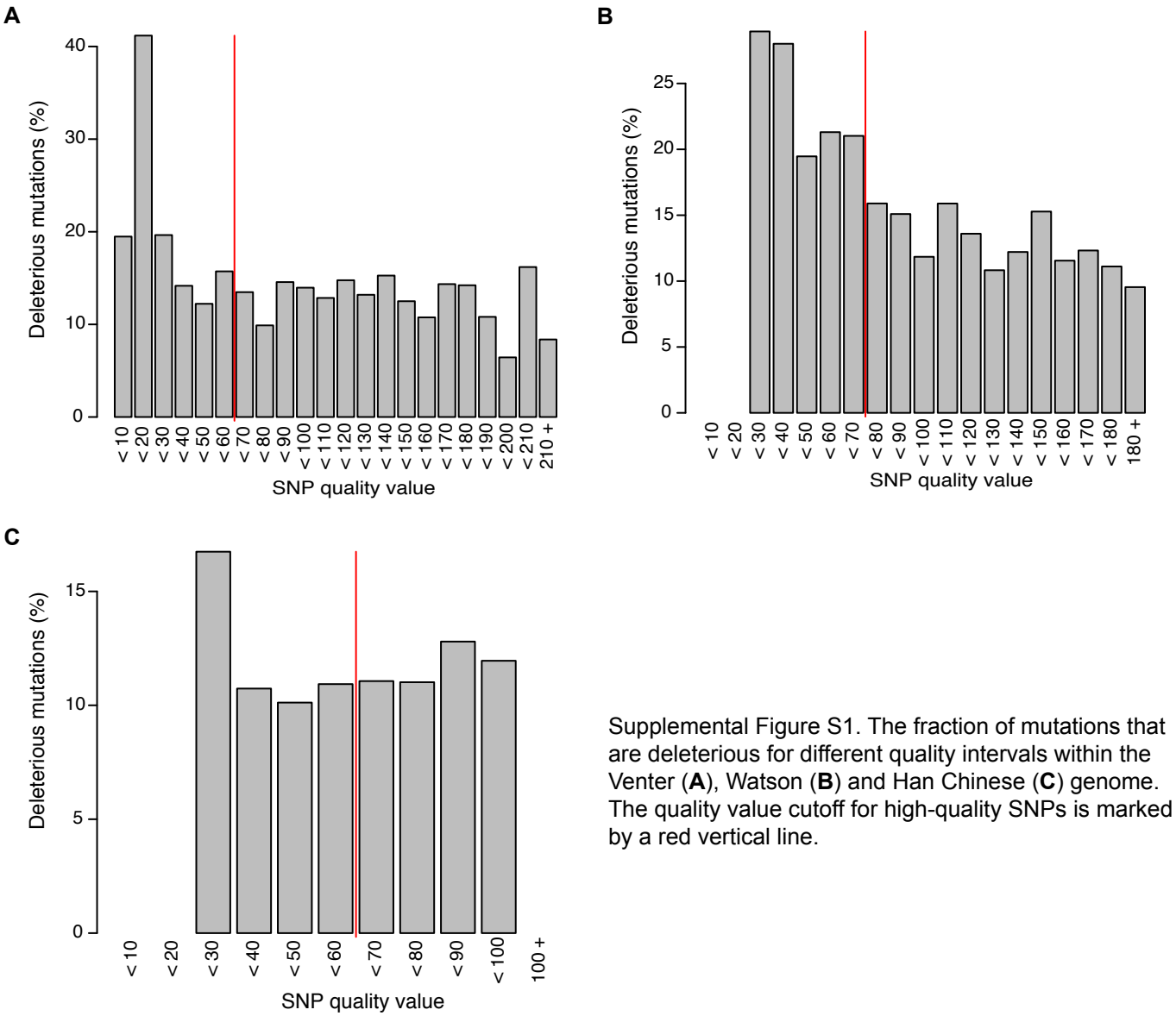
Supplemental Table S1 and Figures S1-S4

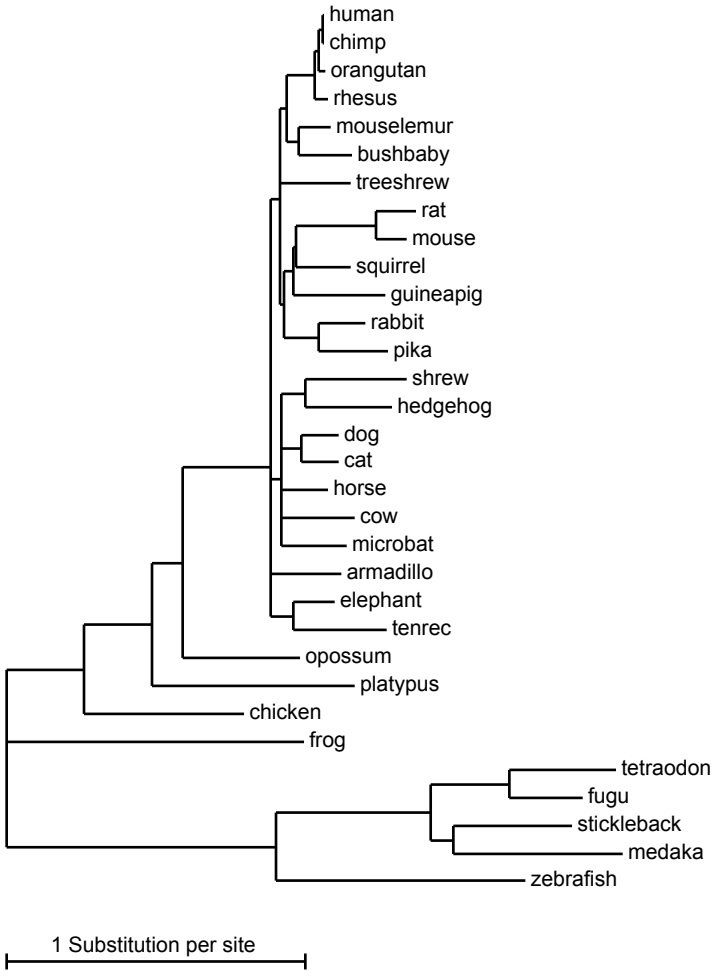
Supplemental Table S1. A sequence of filters used to identify deleterious mutations in the Venter genome.

Filter	Sites	Genes	Coding sequence (Mbp)	Heterozygotes (%)
Nonsynonymous SNPs	9708	5758	12.4	56
High quality SNPs	7534	4879	10.7	53
SNPs within alignments	5645	3756	8.9	52
Derived allele in Venter	3832	2755	6.7	75
dN not equal to dS (P < 0.001)	1012	886	2.3	76
dN < dS	942	827	2.2	77
Not observed in other eutherian mammals	796	700	1.9	78

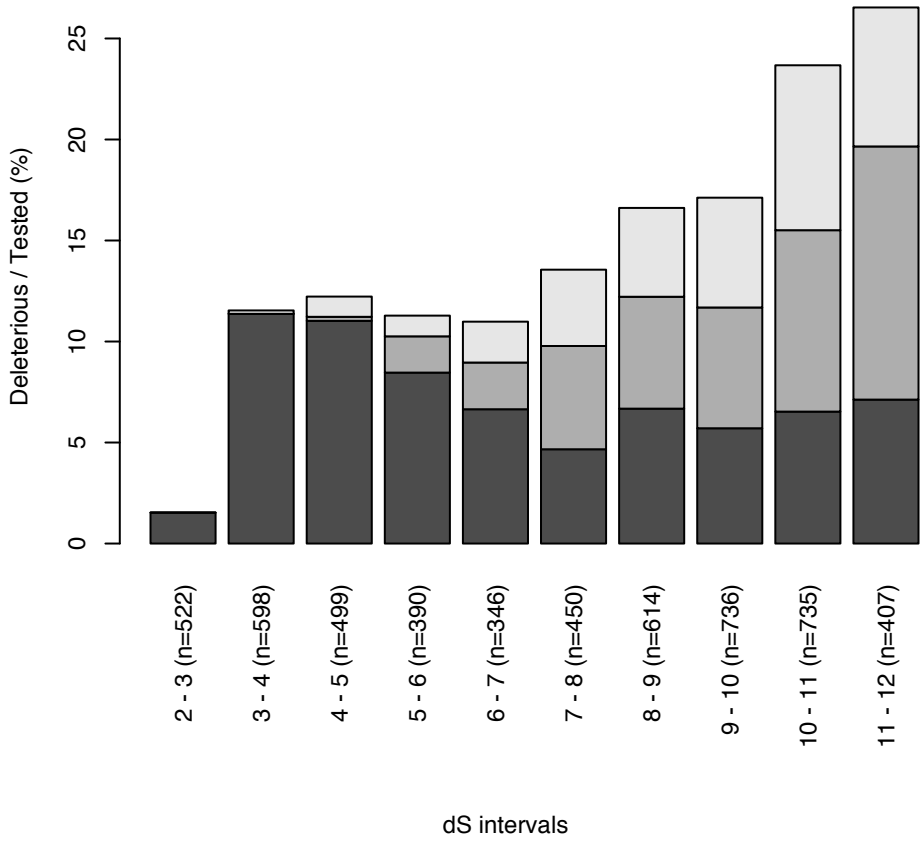
Filters were applied cumulatively from top to bottom.



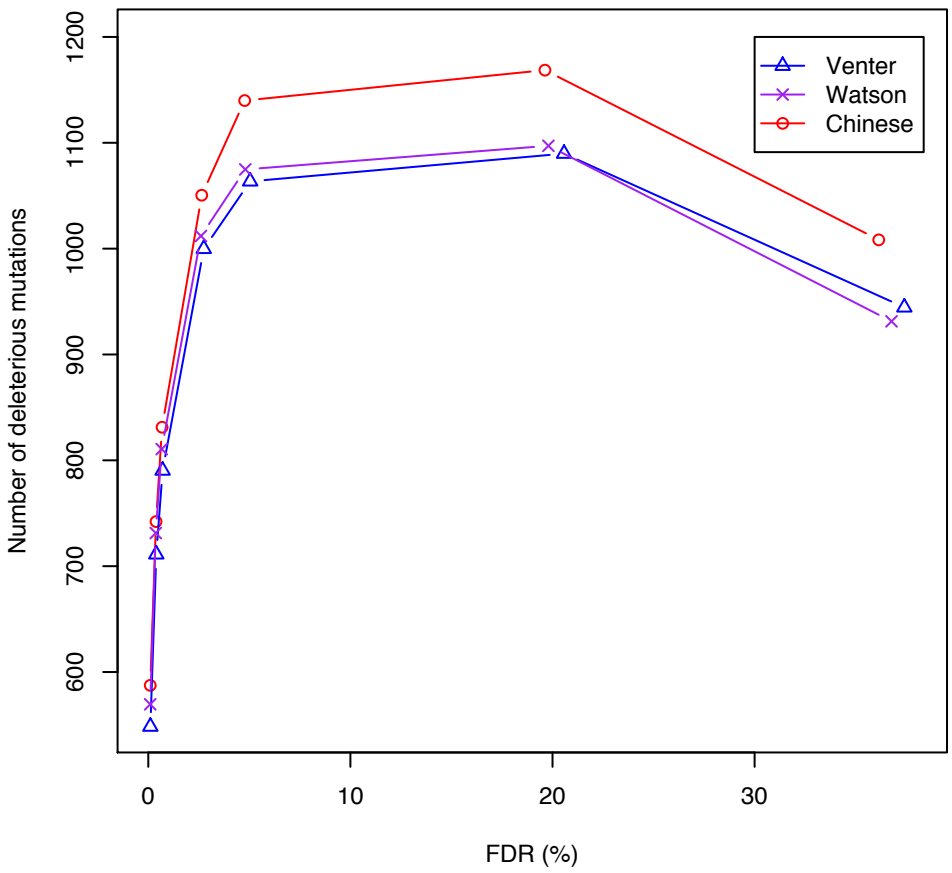
Supplemental Figure S1. The fraction of mutations that are deleterious for different quality intervals within the Venter (**A**), Watson (**B**) and Han Chinese (**C**) genome. The quality value cutoff for high-quality SNPs is marked by a red vertical line.



Supplemental Figure S2. Phylogenetic tree showing the 32 vertebrate species used in the comparative genomic dataset. Scale bar shows the synonymous substitution rate.



Supplemental Figure S3. The percentage of mutations predicted to be deleterious as a function of the total synonymous substitution rate (dS). Each bar represents a different dS interval and sample sizes are denoted by n. Dark gray shows deleterious mutations at perfectly conserved sites, medium gray shows sites where all eutherian mammals are perfectly conserved but at least one vertebrate outside of Eutheria is different, and light gray shows deleterious mutations at all other types of sites.



Supplemental Figure S4. The estimated number of deleterious mutations as a function of the false discovery rate (FDR). The number of deleterious mutations was estimated by the number of mutations predicted to be deleterious at a P-value cutoff of 0.0001, 0.0005, 0.001, 0.005, 0.01, 0.05, 0.1 minus the number of false positive predictions expected due to multiple testing. The false discovery rate was calculated by the estimated number of deleterious mutations (true positives) divided by the total number of mutations predicted at each P-value cutoff. For example, at a P-value cutoff of 0.1, 1,509/5,645 mutations were predicted to be deleterious in the Venter genome, 0.1*5,645 = 564 of these are expected to be false positives. This leads to a false discovery rate of 564/1,509 = 37%.