Table 2. Analysis of synonymous mutations in the human lineage

	Genes	P	U	N	Test equilibrium, P vs. U*	GC	AT	GC=/AT=	Test equilibrium, GC vs. AT*
Overall	7,645	2,153	3,119	1,290	$P < 1 \times 10^{-10}$	2,640	3,369	553	$P < 1 \times 10^{-10}$
L1 (36.27% GC)	661	229	253	129	n.s.	283	274	54	n.s.
L2 (40.05% GC)	2,422	626	851	391	$P = 2 \times 10^{-9}$	762	948	158	$P = 3 \times 10^{-6}$
H1 (44.81% GC)	1,963	481	801	328	$P < 1 \times 10^{-10}$	613	857	140	$P = 1 \times 10^{-10}$
H2 (49.97% GC)	1,675	474	744	264	$P < 1 \times 10^{-10}$	563	795	124	$P = 1 \times 10^{-10}$
H3 (55.07% GC)	924	343	470	178	$P = 3 \times 10^{-6}$	419	495	77	$P = 0.005$

Mutations are assigned to the human lineage using chimpanzee and mouse orthologous sequences. Only codons with a single synonymous mutation among the human-chimpanzee-mouse comparison were used in the study. CpG dinucleotides were not used in the analyses. P, U, and N mutations define changes according to the set of favored and nonfavored codons in highly expressed genes (1): P, changes from a nonfavored to a favored codon; U, changes from a favored to a nonfavored codon; N, changes between two nonfavored codons. GC, AT, and GC=/AT= mutations correspond to AT-to-GC changes, GC-to-AT changes, and to changes between G and C or between A and T, respectively. n.s., not significant.

*Probability based on binomial distribution.

1. Comeron, J. M. (2004) *Genetics* **167,** 1293–1304.