

Supplementary Table 3 - Human-chimpanzee nucleotide substitution rates in coding sequences and introns of X-degenerate genes and pseudogenes. Much of this data is represented graphically in Figure 2a.

	sequence classification	# of substitutions	# of sites	subst./site	p-value (vs. introns; z-test)
genes	coding	321	29481	1.09	<0.00001 ^a
	non-synon.	159.5	17478	0.91	<0.00001 ^b
	introns	17798	1115515	1.60	
pseudogenes	coding	393	19015	2.07	<0.0003 ^c
	introns	5536	319908	1.73	

^aFor the 16 X-degenerate genes, the coding sequence substitution rate (K_{coding}) is significantly lower than the intron substitution rate (K_{intron}).

^bFor the 16 X-degenerate genes, the rate of non-synonymous substitutions within the coding sequence (K_a) is significantly lower than K_{intron} .

^cFor the 11 X-degenerate pseudogenes, K_{coding} is significantly higher than K_{intron} . The higher G+C content of (former) coding vs. intron sequence (50.9% vs. 40.3%) likely accounts for the elevated substitution rate.