Rozen et al., Table S5. The human Y-chromosome's X-degenerate genes show much lower variability at non-degenerate sites than at four-fold degenerate sites, in introns and in pseudogenes. This table is similar to Table 3 in the main text, except that rather than examining non-synonymous and synonymous sites, it examines non-degenerate sites—coding nucleotide sites at which any substitution would lead to a change in the encoded amino acid—and four-fold degenerate sites—coding sites at which any substitution would leave the amino acid unchanged. This analysis excludes two-fold degenerate sites, at which two of the three possible nucleotide substitutions would change the encoded amino acid while the third would leave it unchanged. For rows other than those with *P* values, the columns for introns and pseudogenes contain the same data as in main text Table 3.

	Non-degenerate	Four-fold degenerate	Intron	Pseudogene	Four-fold degenerate, intron, & pseudogene
Variant nucleotides	11	16	64	29	109
Invariant nucleotides	17,472	3,760	40,265	15,222	59,247
Total nucleotides	17,483	3,776	40,329	15,251	59,356
Proportion of variant sites	6.29×10^{-4}	4.24×10^{-3}	1.59×10^{-3}	1.90×10^{-3}	1.84×10^{-3}
P-values of proportions of variant versus invariant sites (Fisher's exact test, two sided)					
Non-degenerate vs. …		1.7×10^{-6}	2.4×10^{-3}	1.2×10^{-3}	1.8×10^{-4}
Four-fold degenerate vs. …			1.1×10^{-3}	1.4×10^{-2}	
Intron vs. …				0.42	
Nucleotide diversity	2.62×10^{-5}	2.34×10^{-4}	1.22×10^{-4}	9.8×10^{-5}	1.23×10^{-4}
P-values of differences in diversities (Wilcoxon rank sum test, two sided)					
Non-degenerate vs. …		1.6×10^{-8}	3.3×10^{-3}	1.0×10^{-3}	3.8×10^{-4}
Four-fold degenerate vs. …			2.5×10^{-4}	8.2×10^{-2}	
Intron vs. …				0.42	