

Table 2 | Percentage of non-coding DNA in selected sequenced genomes

Species name		Genome size (Mb)	Fraction of genome (%)				Source of gene annotations
Common	Scientific		Genic	Exonic	Non-coding		
				Intronic	Intergenic		
Yeast	<i>Saccharomyces cerevisiae</i>	12.2	73.5	72.9	0.6	26.6	Saccharomyces Genome Database (June 2008 build)
Nematode worm	<i>Caenorhabditis elegans</i>	100.3	59.2	28.1	31.2	40.8	WormBase (WS190)
Fruitfly	<i>Drosophila melanogaster</i>	168.7	48.2	18.3	30.0	51.8	FlyBase and Berkeley Drosophila Genome Project (BDGP; release no. 5)
Human	<i>Homo sapiens</i>	3,107	45.1	2.8	42.3	54.9	UCSC Genome Browser Known Genes table (hg18)

The genic fraction consists of both exonic and intronic sequence. The exonic fraction consists of both coding sequence (CDS) and 5' and 3' UTRs. Strictly speaking, UTRs are non-coding, so the exon fraction is a slight overestimate of the fraction of coding sequence in the genome.