

Table 1 | **Effective population size (N_e) estimates from DNA sequence diversities**

Species	N_e	Genes used	Refs
<i>Species with direct mutation rate estimates</i>			
Humans	10,400	50 nuclear sequences	145
<i>Drosophila melanogaster</i> (African populations)	1,150,000	252 nuclear genes	108
<i>Caenorhabditis elegans</i> (self-fertilizing hermaphrodite)	80,000	6 nuclear genes	41
<i>Escherichia coli</i>	25,000,000	410 genes	146
<i>Species with indirect mutation rate estimates</i>			
Bonobo	12,300	50 nuclear sequences	145
Chimpanzee	21,300	50 nuclear sequences	145
Gorilla	25,200	50 nuclear sequences	145
Gray whale	34,410	9 nuclear gene introns	147
<i>Caenorhabditis remanei</i> (separate sexes)	1,600,000	6 nuclear genes	43
<i>Plasmodium falciparum</i>	210,000–300,000	204 nuclear genes	148

For data from genes, synonymous site diversity for nuclear genes was used as the basis for the calculation, unless otherwise stated.

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