

Primate segmental duplications: crucibles of evolution, diversity and disease

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Nature Reviews Genetics 7, 552–564 (2006)

The 'Total SD content' row of Table 1 in this Review was included in error, and the values that were given in this row are incorrect. The correct version of the table, without this row, is below.

Table 1 | **SD content of sequenced animal genomes**

	<i>Caenorhabditis elegans</i>	<i>Drosophila melanogaster</i>	Human	Mouse	Rat	Chicken	Chimpanzee*
SDs of >1 kb	4.3%	1.2%	5.2%	2.7%	1.6%	2.7%	N.D.
SDs of >10 kb	0.7%	0.1%	4.5%	2.2%	1.5%	0.3%	N.D.
SDs of >20 kb	N.D.	N.D.	4.0%	1.7%	0.9%	0.0%	~4.8%
Genome size	97	123	2,866	2,506	2,566	1,040	2,866

Data taken from REFS 2, 7 for pairwise segmental duplications (SDs) with >90% identity. *Given the fragmented nature of SDs in the draft chimpanzee genome, the duplication content can only be estimated indirectly on the basis of human duplication content, adjusting for detected differences in SD compared with chimpanzee whole-genome shotgun sequencing⁶. DNA not assigned to a chromosome was not included in these calculations. Consequently, in other genomes the estimate of recent duplication might rise as the quality of the sequence assembly improves. N.D., not determined.