Table 2. Average genomic recombination rates.

Species	Genetic map length (cM)[1]	Physical genome length (Mb)	Rate (cM/Mb)[1]	Natural log-transformed rate (cM/Mb)	Chakravarti et al. (1991) correction (cM/Mb)	Hall and Willis (2005) correction (cM/Mb)	Percent genome coverage[2]	Body weight (kg)[1,3]
Human	3615	3191	1.133	0.125	1.144	1.144	100	4.248
Baboon	2013	3100	0.649	−0.432	0.732	0.739	82.6	2.996
Macaque	2275	3100	0.734	−0.309	0.838	0.830	76.1	1.792
Mouse	1361	2600	0.523	−0.648	0.527	0.527	100	−3.912
Rat	1542	2800	0.551	−0.596	0.747	0.746	100	−1.204
Horse	2770	2700	1.026	0.026	1.128	1.122	93.1	6.273
Cat	3300	3000	1.100	0.095	1.348	1.295	53.5	1.386
Dog	3884	2500	1.554	0.441	1.604	1.603	99.9	2.996
Pig	2286	3000	0.762	−0.272	0.796	0.795	98.8	4.610
Sheep	3588	3000	1.196	0.178	1.260	1.258	94.5	5.298
Cow	3160	3000	1.053	0.052	1.070	1.070	100	6.620
Wallaby	829	3700	0.224	−1.496	0.309	0.291	53.8	1.386
Opossum	644	3500	0.184	−1.693	0.228	0.222	72.9	−2.303
CFTR	H_P^2=0.810	H_P^2=1.00	H_P^2=0.903	H_P^2=0.995	H_P^2=0.952	H_P^2=0.955	–	H_P^2=0.945
	P=0.041	P=0.001	P=0.0217	P=0.0187	P=0.0183	P=0.0161		P=0.0208
Mitochondria	H_P^2=1.00	H_P^2=1.00	H_P^2=0.996	H_P^2=0.998	H_P^2=0.995	H_P^2=0.993	–	H_P^2=0.998
	P=0.004	P=0.001	P=0.0083	P=0.0048	P=0.0072	P=0.0089		P=0.0050

[1] Sex-averaged.
[2] Percentage of the genome predicted to lie within 5 cM of a marker, assuming a random distribution of markers across the genome.
[3] Natural log transformed.