

General sequence properties of murine genes

	imprinted	maternally expressed	paternally expressed	autosomal
G+C content of genes	45.73%	45.73%	45.65%	45.89%
CpG_{obs}/CpG_{exp} of genes	0.24	0.22	0.32*	0.23
gene length (bp)	31058	44300	23787	16242
intron length (bp)	1262	1266	1262	1327
length of intergenic regions (bp)	36310	38969	28789	22296
coverage of introns with purely intronic PCSs	0.99%**	0.83%	1.79%	0.57%
purely intronic PCSs per 10 kb of intron per gene	2.02**	1.84	2.80*	1.26
coverage of intergenic regions with PCSs	1.25%	1.25%	1.18%	1.41%
intergenic PCSs per 10 kb per gene	1.93	1.54	1.99	2.46

Gene length: transcribed DNA sequence from most upstream transcriptional start site to most downstream transcriptional termination site; intergenic region: Sum of sequences upstream and downstream of a gene. For this, the distance between two genes was cut into two halves, each of these was assigned to the nearest gene.

Since features show a highly skewed distribution, medians are given instead of averages.

* $p < 0.01$, ** $p < 0.005$ for comparison with autosomes.