

Table S8: Pairwise correlations between variables for the CGS data after filtering CpG islands^a.

	Rec. rate	Genic content ^b	GC content ^c	Coverage ^d	d^e	# SNPs ^f	S_{norm}^g	π_{norm}^h	Average MAF	Tajima's D
Rec. rate		-0.0700	0.3884	0.2494	0.2491	0.3011	0.2001	0.2148	0.1012	0.0826
Genic content	1.0E-21		0.1374	0.2566	-0.3116	-0.1682	-0.0396	-0.0472	-0.0392	-0.0371
GC content	0	3.1E-79		0.1455	-0.0170	0.0893	0.0978	0.1085	0.0530	0.0449
Coverage	2.5E-262	3.1E-278	7.9E-89		0.0244	0.0871	0.0774	0.0786	0.0214	0.0075
Divergence	9.4E-262	0	2.0E-2	8.4E-4		0.3718	-0.0640	-0.0316	0.0790	0.0732
# SNPs	0	2.2E-118	2.4E-34	1.0E-32	0		0.8746	0.8241	0.1709	0.1567
S_{norm}	9.9E-168	6.3E-08	7.3E-41	3.5E-26	2.1E-18	0		0.9236	0.1491	0.1374
π_{norm}	1.4E-193	1.1E-10	6.5E-50	5.7E-27	1.6E-05	0	0		0.4674	0.4656
Average MAF	1.2E-43	8.8E-08	4.3E-13	3.4E-3	3.1E-27	3.5E-122	3.0E-79	0.0		0.9748
Tajima's D	1.4E-29	4.0E-07	8.8E-10	3.0E-1	1.4E-23	8.8E-103	3.9E-93	0.0	0.0	

Values of Spearman's ρ for each pair of variables are shown above the diagonal. P -values are shown below the diagonal.

^a. CpG islands were defined using the "CpG islands" track on the UCSC Genome Browser.

^b. The fraction of each 100 kb window that overlapped with a RefSeq transcript.

^c. Denotes the number of hg18-pantro2 alignable bases that were not Repeat Masked, not in CpG islands, and did not fall in phastCons regions that were G or C in hg18 divided by the total number of alignable bases within the window that were not Repeat Masked, not in CpG islands, and did not fall in phastCons regions.

^d. The number of bases per window that were alignable between hg18 and pantro2, were not Repeat Masked, not in CpG islands, and did not fall in phastCons regions, where all six individuals had sequencing data.

^e. Denotes the number of hg18-pantro2 differences that were not Repeat Masked, not in CpG islands, and did not fall in phastCons regions divided by the total number of positions within the window where differences could have been called (*i.e.* the total number of alignable bases that were not Repeat Masked, not in CpG islands, and did not fall in phastCons regions).

^f. Denotes the number of SNPs per window divided by the total number of bases where SNPs could have been called (*i.e.* the total number of alignable bases within the window that were not Repeat Masked, not in CpG islands, and did not fall in phastCons regions where all six individuals had sequencing data).

^g. Denotes the "# SNPs" divided by d .

^h. Denotes the average number of pairwise differences between sequences within a window divided by d .