

Table S2 Summary of nucleotide variation and the results of neutrality tests

Loci	<i>L</i>	<i>L</i> (Nonsyn)	<i>n</i>	<i>S</i>	π (Total)	π (Syn)	π (Nonsyn)	Tajima's <i>D</i>	Fu and Li's <i>D</i> *	Fu and Li's <i>F</i> *	<i>R_M</i>
BAC3											
Region 1	788		47	15	0.00442			0.06980	-1.59581	-1.22483	0
Region 2	730		47	22	0.00892			0.99867	-0.98068	-0.35328	0
Region 3	704		47	15	0.00662			1.15529	-1.14373	-0.43869	0
Total & Mean	2222		47	52	0.00660			0.85048	-1.46773	-0.75261	0
BAC6											
Region 1	730		48	7	0.00358			1.75357	0.47188	1.03243	0
Region 2	856		48	5	0.00205			1.36207	0.14404	0.61076	0
coding	284	230.84	48	1	0.00015	0	0.00018	-1.10686	-1.82907	-1.87498	0
Region 3	822		48	13	0.00409			0.44574	-0.00424	0.17222	0
Region 4	1593		48	7	0.00146			1.24840	1.24435	1.46202	0
coding	390	322.828	48	1	0.00127	0	0.00160	1.63398	0.54673	0.99290	0
Region 5	803		48	9	0.00249			-0.04505	0.04647	0.01976	0
Coding total	674	538.667	48	2	0.00080	0	0.00100	0.34973	-0.88132	-0.60235	0
Total & Mean	4804		48	41	0.00251			1.04035	0.49422	0.82158	1
BAC7											
region1-1	690		41	13	0.00425			-0.10908	-0.42852	-0.38201	0
region1-2	632		41	5	0.00092			-1.28932	-2.60755*	-2.57393*	0

region2-1	634	41	14	0.00439	-0.47203	-0.75364	-0.77967	0
region2-2	621	41	7	0.00315	0.48952	0.50634	0.587	0
region2-3	642	41	3	0.00187	1.46587	0.91296	1.25162	0
region2-4	2016	41	24	0.00361	1.00215	-0.37521	0.10916	2
region2-5	674	41	4	0.00149	0.18386	-0.04461	0.02828	0
region2-6	644	41	2	0.00127	1.28561	0.76847	1.06458	0
region2-7	661	41	11	0.00266	-0.95722	-1.83954	-1.82918	0
region3-1	509	41	9	0.00619	1.44836	1.3588	1.62925	1
region3-2	767	41	15	0.00445	-0.08479	-1.48049	-1.20371	1
Total & Mean	8491	41	107	0.00317	0.25972	-0.74551	-0.4592	7

L : Length

n : Number of sequences

S : Number of segregating sites

R_M : Minimum number of recombination event