

Table S1 Chromosome level information. The reported number of SNPs for each chromosome reflects SNPs that are not fixed in both of the ancestral reference populations; percentage missing data due to failed genotyping; size of analyzing window used to combine information across chromosomes.

Chromosome	Number of SNPs	Missing data (%)	Analyzing window
1	32,417	0.75	7.52
2	35,221	0.69	8.17
3	32,005	0.62	7.43
4	29,117	0.65	6.76
5	28,179	0.70	6.54
6	33,862	0.72	7.86
7	24,676	0.73	5.73
8	25,025	0.67	5.81
9	20,914	0.65	4.85
10	21,755	0.76	5.05
11	20,494	0.77	4.76
12	21,398	0.74	4.97
13	17,564	0.63	4.08
14	14,552	0.77	3.38
15	13,856	0.75	3.22
16	13,402	0.81	3.11
17	9,348	0.90	2.17
18	14,246	0.74	3.31
19	5,733	1.12	1.33
20	10,553	0.87	2.45
21	6,403	0.74	1.49
22	4,309	1.16	1.00