

**Supplementary Table 8. Estimation of imputation error rate.** The imputed SNPs in the long-range phasing step was compared against the SNPs called from the sequencing data. We excluded SNPs where we found missing alleles.

HJ Descendant	Imputed SNPs	SNPs with missing information	Concordant Alleles	Discordant Alleles	Discordant proportion
HJD_5_109	132207	12293	239748	80	0.00033
HJD_6_310	350094	24497	651157	37	0.00006
HJD_5_136	349796	22610	654324	48	0.00007
HJD_6_274	350332	36070	628451	73	0.00012
HJD_7_487	263300	14330	497916	24	0.00005
HJD_4_43	131228	21076	220234	70	0.00032
HJD_6_363	349909	19159	661449	51	0.00008
HJD_5_103	350133	18326	663565	49	0.00007
HJD_6_335	350604	21759	657492	198	0.00030
HJD_7_525	131858	7760	248159	37	0.00015
HJD_5_125	131574	19122	224817	87	0.00039
HJD_6_333	132288	9200	246146	30	0.00012
HJD_7_442	131636	7095	249059	23	0.00009
HJD_6_388	349828	76147	547304	58	0.00011
HJD_7_443	131935	7540	248770	20	0.00008
HJD_5_118	130960	17016	227851	37	0.00016
HJD_7_532	131746	15347	232784	14	0.00006
HJD_6_233	350108	16498	667186	34	0.00005
HJD_4_46	349392	29740	639244	60	0.00009
HJD_5_108	349966	21307	657259	59	0.00009
Total			9062915	1089	0.00012