

Table S1. Genotyping-by-sequencing (GBS) statistics for 96 samples

File Name	Sum
Number of total reads	715,257,004
Total length of reads (bp)	108,003,807,604
Number of trimmed reads	580,490,466
Average trimmed reads	6,046,776
Total length of trimmed reads (bp)	69,674,498,092
Number of mapped reads	535,702,448
Average length of trimmed reads (bp)	119.99
Total trimmed raw data	94.45%
Average number of mapped reads	5,216,741
Average number of mapped regions	125,718
Average depth of the mapped regions	14.75
Average length of the mapped regions (bp)	233.34

Table S2. Single-nucleotide polymorphism (SNP) filter criteria

Filter Criteria	Number of SNPs
Number of total SNPs	628,437
Missing data < 30%	61,967
MAF (minor allele frequency) > 25%	146,217
Missing < 30 % and MAF > 25%	11,020
Homozygous SNP in KC352	4,387
100kb window sized selection	1,643
Polymorphic SNPs between parents	1,639