Supplementary data file 2: Filtering criteria used to identify the final set of high confidence SNPs

Total Reads/Read Pairs	226,467,750 / 113,233,875
~Reads/Read pairs per individual (million)	3.1/1.55
Reads mapped to reference	119,392,038
Reads failed to map to reference	98370816
Reads supressed due to mapping to multiple positions	8,704,896
Reported SNPs from Varscan (default settings)	98042
SNPs after filtering to exclude monomorphic and >35% missing values	16,417
Biallelic/Triallelic SNPs	16,323/94
Biallelic SNPs grouping into LGs at 0.2/18 (RF/LOD)	9,817
Grouped at LOD >=6 using 'independence LOD' function of JoinMap 4.1	7806
High confidence SNPs with read depth >20	6,072

In total, the paired end Illumina sequencing yielded 226,467,750 reads (113,233,875 read pairs). After de-multiplexing, on average 3.1 million reads (~1.5 million read pairs) per individual were obtained. In total 119,392,038 (53%) of the total 226,467,750 reads aligned to the reference set allowing three mismatches, 8,704,896 reads (4%) were suppressed as they mapped to more than one region in the reference set and 98,370,816 reads (43%) failed to align. Using VarScan.v2.2.11 with the default settings, 98,042 SNP variants were reported. The filtering criteria adopted to exclude monomorphic markers and markers with large number of missing values (>35%) yielded 16,417 SNPs. Out of these 16,323 SNPs were bi-allelic and 94 of them were tri-allelic. Of the 16,323 biallelic SNP variants, the majority were of transition types: C/T (30%) and A/G (30%) and the remaining were of transversion types: C/G (15%), G/T (10%), A/C (9%) and A/T (6%) respectively. 9,817 out of 16,323 SNPs grouped into seven linkage groups at a recombination fraction (RF) vs LOD score threshold of 0.2/18. For the framework map only 7806 markers that grouped at LOD >=6 using 'independence LOD' function of JoinMap 4.1 were carried forward. An additional round of filtering for SNPs from alignments with a read depth of > 20 reduced the number to a set of 6072 high confidence SNPs.