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**Appendix S2.** Parameters used for analysis programs.

**A.** Parameters used for mapping Illumina read to the 59,493 carrot EST (2) consensus sequences with Mosaik:

|  |  |
| --- | --- |
| hash size (-hs) | 15 |
| number of mismatches allowed (-mm) | 4 |
| alignment mode (-m) | all |
| maximum hash positions per seed (-mhp) | 100 |
| alignment candidate threshold (-act) | 20 |

**B.** Parameters used for preliminary filtering with a custom Perl program:

|  |  |
| --- | --- |
| gigaBayes quality | ≥ 0.99 |
| distance from either end of sequences | ≥ 20 nt |
| read coverage for most abundant allele | ≥ 15 (10)\* |
| read coverage for second most abundant allele | ≥ 15 (10) |
| amount of sequence on either side of the SNP in the output file | 100 nt |
| Isolation range | 100 nt |
| amount of sequence on either side of the SNP that cannot contain any other SNPs on one side | 30 nt (22 nt) |
| maximum number of other nearby SNPs within range of isolation range on one side | 10 (20) |
| amount of sequence on either side of the SNP that cannot contain any other SNPs on other side | 25 nt (3 nt) |
| maximum number of other nearby SNPs within range of isolation range on other side | 3 (20) |

**C.** Parameters used for megablast alignment of EST contig against whole genome assembly:

|  |  |
| --- | --- |
| low complexity filtering | off |
| e-value | ≤1 |
| amount of sequence flanking SNP on each side used for alignment (and blast hit must include SNP location) | 50 nt |

\*Parameters in parentheses were applied to develop the list of SNPs included in the high priority list, see table S6 (Priority 1 and 2).