

Name ^a	Chr ^b	Location (cM)	Effect ^c	Minor allele frequency	Genetic variance	% of phenotypic variance explained	Estimated effect in multiple regression
M1	1	20.00	0.62	0.28	0.15	3.50	0.61
S1	1	31.87	0.01	0.44	0.00	0.00	0.06
S2	1	33.16	0.00	0.30	0.00	0.00	0.04
M2	1	40.00	0.56	0.07	0.04	0.91	0.62
S3	1	50.37	0.06	0.46	0.00	0.04	0.08
S4	1	52.50	0.05	0.40	0.00	0.03	0.07
S5	1	62.21	0.00	0.29	0.00	0.00	0.02
M3	1	77.23	0.37	0.29	0.06	1.29	0.42
S6	1	86.68	0.01	0.30	0.00	0.00	0.09
S7	1	93.99	0.01	0.47	0.00	0.00	0.01
S8	2	2.25	0.01	0.39	0.00	0.00	0.06
S9	2	6.52	0.07	0.38	0.00	0.06	0.09
M4	2	27.41	0.35	0.44	0.06	1.38	0.44
M5	2	30.00	0.33	0.21	0.04	0.82	0.25
S10	2	32.49	0.04	0.41	0.00	0.02	0.07
S11	2	45.71	0.01	0.09	0.00	0.00	0.07
S12	2	48.22	0.04	0.08	0.00	0.01	0.06
M6	2	48.62	0.37	0.40	0.07	1.50	0.39
M7	2	74.91	0.50	0.18	0.07	1.63	0.46
S13	2	89.04	0.12	0.22	0.01	0.12	0.15
S14	2	93.54	0.25	0.32	0.03	0.61	0.22
S15	2	95.66	0.02	0.29	0.00	0.01	0.12
S16	2	97.83	0.13	0.41	0.01	0.19	0.14
S17	3	0.70	0.03	0.00	0.00	0.00	- ^d
S18	3	7.89	0.01	0.46	0.00	0.00	0.04
M8	3	14.91	0.30	0.40	0.04	0.98	0.27
S19	3	21.07	0.02	0.26	0.00	0.00	0.00
S20	3	29.81	0.07	0.29	0.00	0.04	0.05
M9	3	60.00	0.68	0.07	0.06	1.29	0.70
M10	4	3.21	0.61	0.39	0.18	4.01	0.64
S21	4	3.44	0.08	0.32	0.00	0.06	0.10
S22	4	3.88	0.02	0.23	0.00	0.00	0.02
S23	4	10.00	0.01	0.04	0.00	0.00	0.06
S24	4	16.35	0.00	0.36	0.00	0.00	0.11
S25	4	19.84	0.07	0.47	0.00	0.05	0.10
M11	4	36.93	0.34	0.24	0.04	0.95	0.37
S26	4	69.56	0.00	0.08	0.00	0.00	0.01
M12	4	76.06	0.58	0.41	0.16	3.70	0.58
M13	4	96.49	0.29	0.19	0.03	0.59	0.38
M14	5	5.15	0.18	0.21	0.01	0.24	0.25
S27	5	12.98	0.09	0.44	0.00	0.10	0.09
S28	5	28.64	0.00	0.13	0.00	0.00	0.05
S29	5	68.39	0.12	0.44	0.01	0.15	0.17
S30	5	68.48	0.00	0.43	0.00	0.00	0.02
S31	5	72.54	0.00	0.12	0.00	0.00	0.06
S32	5	77.02	0.13	0.25	0.01	0.14	0.15
S33	5	80.00	0.08	0.11	0.00	0.03	0.05
S34	5	82.14	0.01	0.36	0.00	0.00	0.08
M15	5	93.50	0.75	0.26	0.22	4.97	0.75
S35	5	98.32	0.01	0.45	0.00	0.00	0.02

^aQTL labelled M are major QTL, known to be detectable in this dataset based on the results from our multiple regression. QTL labelled S are secondary QTL that were not detected, with the significance threshold used, in our multiple regression.

^bChromosome.

^cAverage effect of allelic substitution (absolute value).

^dCould not be estimated because the QTL was fixed in the population.