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Supplementary Material

Identification of quantitative trait loci underlying lodging of soybean across multiple environments

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Supplementary Materials

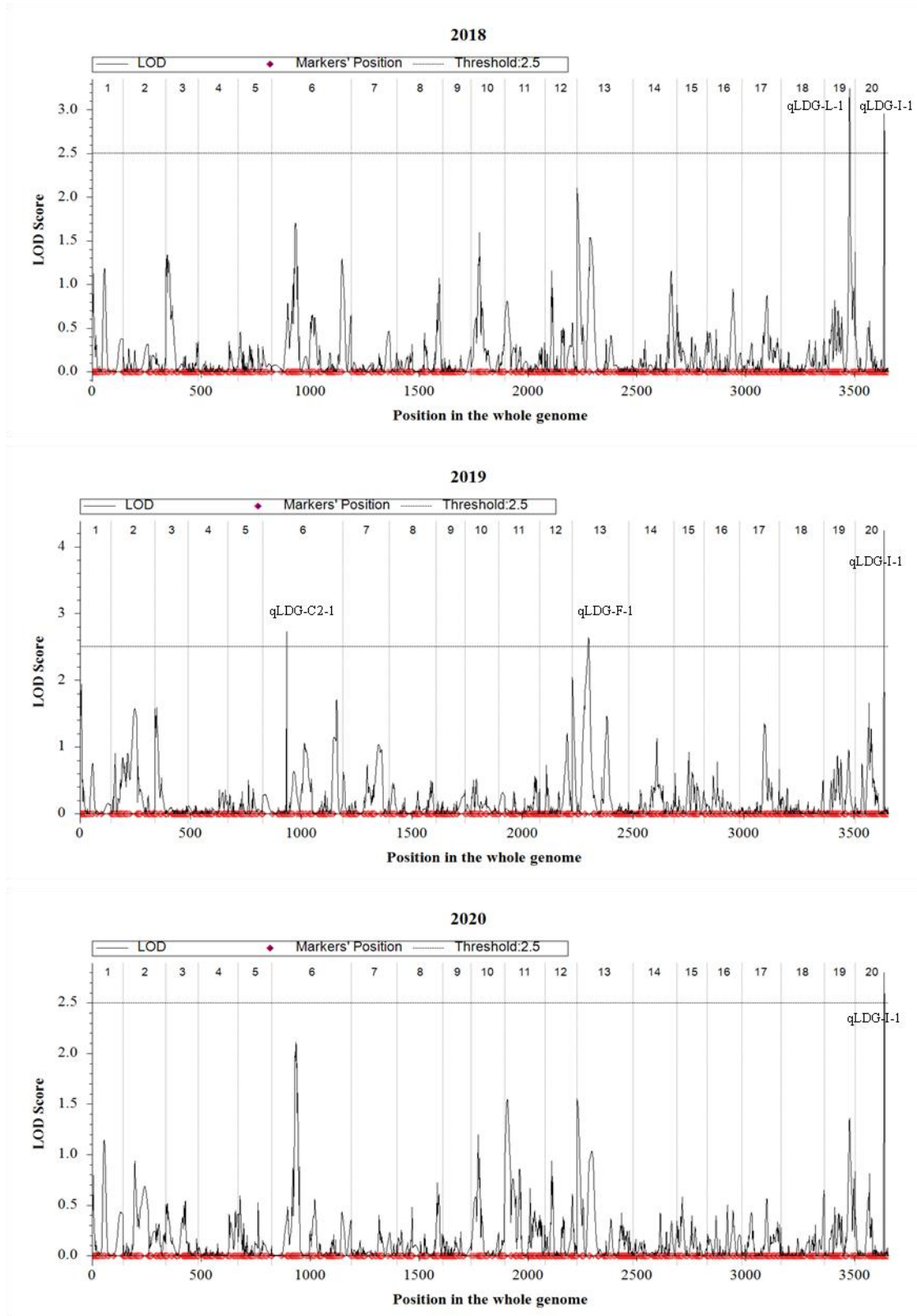


Fig. S1. Major QTL of lodging detected in ICIM-ADD model in a single environment

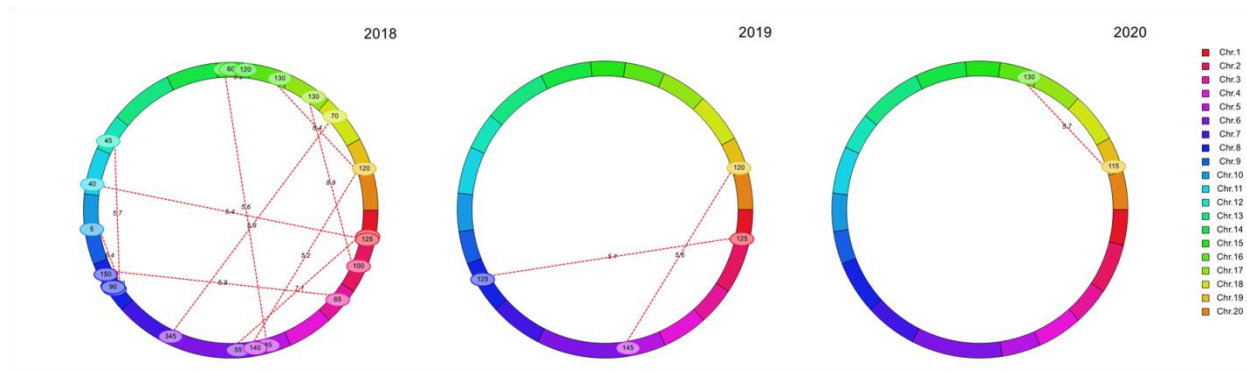


Fig. S2. Epistatic QTL of lodging detected in a single environment

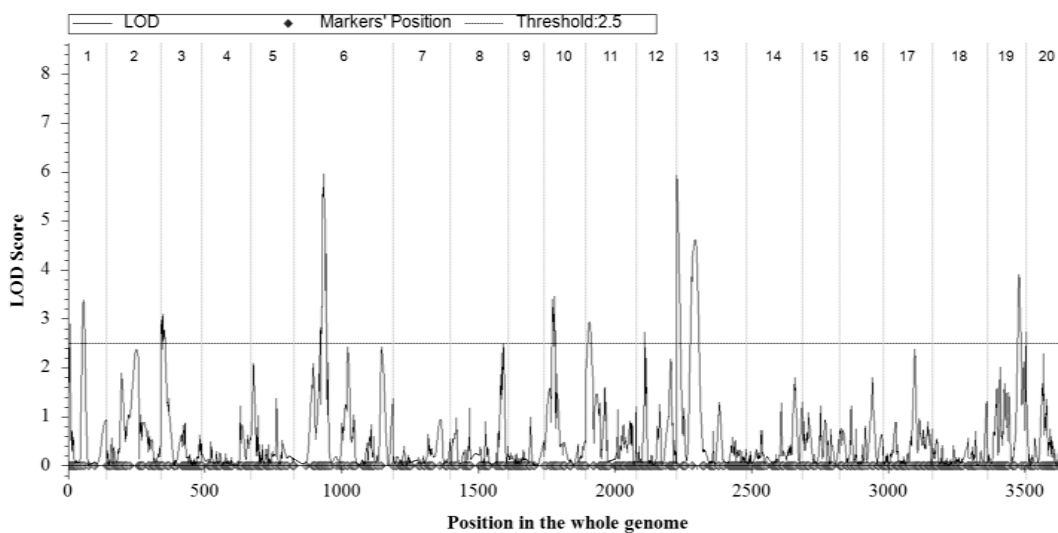


Fig. S3. Major QTL of lodging detected in ICIM-ADD model in QEI mapping

Table S1. Distribution of SNP markers on genetic linkage map

Chromosome	Makers	Total distance	Average distance	Max distance
1	260	141.81	0.55	44.27
2	261	197.62	0.76	33.37
3	291	149.55	0.51	22.64
4	277	181.34	0.65	22.65
5	248	155.86	0.63	19.28
6	281	363.99	1.30	43.73
7	286	209.24	0.73	26.94
8	258	211.25	0.82	34.93
9	281	130.33	0.46	34.93
10	256	152.35	0.60	24.89

11	224	187.08	0.84	28.00
12	278	146.38	0.53	14.80
13	284	255.46	0.90	36.31
14	236	202.94	0.86	18.97
15	244	138.17	0.57	24.43
16	286	159.24	0.56	12.95
17	283	181.11	0.64	11.38
18	252	199.89	0.79	8.62
19	213	141.14	0.66	23.58
20	242	151.46	0.63	11.91

Table S2. Primer design of candidate gene and internal reference gene

Gene	Sense primer	Anti-sense primer
Glyma.20G067800	GAAGGGCTATCAACGAAG	CAAACGGTAACCTGAACTG
Glyma.20G068000	CTTGTAATCCTTCATCTCCCTA	GTCCTCCAACCTTGTTCCTCT
Glyma.20G068100	CTCTGGTGGTGACCCTCT	AAATCGCTAACGCCTCTT
Actin 4	GATCTACCATGTTCCCAAGT	ATAGAGCCACCAATCCAGAC

Table S3. Epistatic QTL analysis in QEI mapping

QTL Name	Chromosome ^a	Position (cM) ^b	Markers (bp) ^c	Chromosome	Position (cM)	Markers (bp)	LOD	LOD (AA × E) ^e	PVE (%) ^f	PVE (AA × E) ^g	Add by Add ^h	AA byE ₀₁ ⁱ	AA byE ₀₂	AA byE ₀₃
qLD Ge-4	8	85	Chr08_667288- Chr08_47643176	10	5	Chr10_4560820- Chr10_5439167	6.1	2.19	16.09	3.13	-0.61	0.09	-0.03	-0.06
qLD Ge-7	5	85	Chr05_33560692- Chr05_34787808	15	30	Chr15_8536219- Chr15_10685118	12.2	2.27	26.07	0.17	-0.78	-0.08	0.02	0.06
qLD Ge-8	15	60	Chr15_12160646- Chr15_15187500	15	120	Chr15_23457758- Chr15_51536790	9.3	0.29	27.81	0.11	0.88	0.07	-0.02	-0.05
qLD Ge-11	5	145	Chr05_1325431- Chr05_9133252	19	120	Chr19_31468355- Chr19_50244060	10.3	1.27	24.81	0.1	0.75	0.06	-0.02	-0.04
qLD Ge-12	16	130	Chr16_3911525- Chr16_5144359	19	120	Chr19_31468355- Chr19_50244060	13.1	2.33	25.05	0.21	0.74	0.09	-0.06	-0.03
qLD	1	40	Chr01_5592710-	2	120	Chr02_8120252-	9.5	1.1	13.75	1.13	-0.55	-0.01	-0.0	0.07

Ge - 14			Chr01_2812 1772			Chr02_8289 791	3						6	
qL D Ge - 15	2	160	Chr02_2931 747- Chr02_5212 093	2	195	Chr02_5140 92- Chr02_6421 69	7. 4 3	1.07	10. 11	1.08	0.5	0.06	- 0.0 1	- 0.0 5
qL D Ge - 16	1	40	Chr01_5592 710- Chr01_2812 1772	3	0	Chr03_3832 5793- Chr03_3838 6292	6. 2 5	0.04	8.5 4	0.05	0.45	0.04	- 0.0 4	0
qL D Ge - 17	3	60	Chr03_2969 4597- Chr03_4522 8398	3	75	Chr03_2969 4597- Chr03_4522 8398	5. 7 5	0.02	12. 16	0.01	0.57	0.04	- 0.0 1	- 0.0 3
qL D Ge - 18	1	55	Chr01_4142 188- Chr01_4142 259	4	145	Chr04_5093 882- Chr04_5368 082	5. 3 3	0.08	7.1 8	0.1	-0.4	- 0.06	0.0 6	0
qL D Ge - 19	2	165	Chr02_2931 747- Chr02_5212 093	4	180	Chr04_7152 78- Chr04_1952 616	6. 3 2	0.07	8.3 4	0.08	0.44	0.01	0.0 4	- 0.0 5
qL D Ge - 20	1	140	Chr01_5488 90- Chr01_5545 5938	5	150	Chr05_1325 431- Chr05_9133 252	5. 0 8	0.14	7.4 8	0.16	0.41	0.08	- 0.0 6	- 0.0 2
qL D Ge - 21	1	50	Chr01_4142 259- Chr01_5133 565	6	25	Chr06_2520 8683- Chr06_5048 8039	7. 8 2	1.5	23. 76	4.01	0.74	0.04	- 0.0 2	- 0.0 2
qL D Ge - 22	3	0	Chr03_3832 5793- Chr03_3838 6292	6	30	Chr06_2520 8683- Chr06_5048 8039	5. 4 7	0.1	12. 01	0.07	0.52	0.05	- 0.0 2	- 0.0 3
qL D Ge - 23	4	140	Chr04_5203 515- Chr04_5280 350	6	200	Chr06_1575 116- Chr06_4243 651	6. 1 3	0.3	8.9 9	0.28	0.44	0.10	- 0.0 9	- 0.0 1
qL D Ge - 24	6	215	Chr06_1142 649- Chr06_1583 974	6	290	Chr06_4831 0186- Chr06_4888 6700	5. 7 7	0.12	7.3 8	0.1	- 0.41	- 0.08	0.0 4	0.0 4
qL D	2	65	Chr02_4290 0067-	6	340	Chr06_1809 6007-	5. 5	1.74	17. 82	3.05	- 0.63	- 0.05	0.0 3	0.0 1

Ge - 25			Chr02_4319 6757			Chr06_4435 2903	7							
qL D Ge - 26	6	200	Chr06_1575 116- Chr06_4243 651	7	15	Chr07_3582 1740- Chr07_3695 4311	6. 6 4	0.04	11. 33	0.03	- 0.53	- 0.04	0.0 3	0.0 1
qL D Ge - 27	5	95	Chr05_3189 0671- Chr05_3303 5361	7	200	Chr07_4298 1974- Chr07_4439 4954	7. 1 2	0.04	11. 2	0.04	0.51	0	0.0 4	- 0.0 4
qL D Ge - 28	5	65	Chr05_3554 2368- Chr05_3555 5623	8	15	Chr08_8797 268- Chr08_1033 0165	6. 8 4	0.04	8.7 3	0.05	0.44	0.05	- 0.0 3	- 0.0 2
qL D Ge - 29	7	200	Chr07_4298 1974- Chr07_4439 4954	8	15	Chr08_8797 268- Chr08_1033 0165	5. 3 3	0.12	7.0 7	0.12	- 0.42	- 0.08	0.0 3	0.0 5
qL D Ge - 30	1	45	Chr01_5059 734- Chr01_5242 313	8	25	Chr08_7880 213- Chr08_8299 453	5. 2 8	0.06	7.1 7	0.06	-0.4	- 0.02	- 0.0 3	0.0 5
qL D Ge - 31	2	155	Chr02_5111 033- Chr02_5167 464	8	135	Chr08_4639 8037- Chr08_4643 6260	5. 5 1	0.05	6.8 4	0.05	- 0.39	0.09	- 0.0 3	- 0.0 6
qL D Ge - 32	3	140	Chr03_2223 095- Chr03_2322 848	8	145	Chr08_4093 6735- Chr08_4555 0328	5. 4 1	0.04	7.8	0.05	- 0.41	- 0.05	0.0 1	0.0 4
qL D Ge - 33	6	335	Chr06_1809 6007- Chr06_4435 2903	8	190	Chr08_2236 0573- Chr08_2241 2552	5. 7 7	0.03	11. 73	0.01	0.51	- 0.04	- 0.0 1	0.0 4
qL D Ge - 34	3	70	Chr03_2969 4597- Chr03_4522 8398	9	10	Chr09_2869 8027- Chr09_2880 3239	5. 3 4	0.12	10. 01	0.11	0.47	0	0.0 2	- 0.0 2
qL D Ge - 35	6	330	Chr06_1809 6007- Chr06_4435 2903	9	25	Chr09_3844 1024- Chr09_3847 2475	9. 5 2	2.06	17. 8	4.06	0.63	0.06	- 0.0 3	- 0.0 3
qL D	8	30	Chr08_3441 886-	9	55	Chr09_4112 5529-	5. 8	0.18	8.3 4	0.18	- 0.43	0.04	- 0.0	0.0 1

Ge - 36			Chr08_7871 477			Chr09_4148 0450	8						5	
qL D Ge - 37	7	25	Chr07_2058 6808- Chr07_3010 4874	9	65	Chr09_4167 2691- Chr09_4214 9772	5. 0 6	0.02	6.3 5	0.01	- 0.38	- 0.02	- 0.0 1	0.0 3
qL D Ge - 38	4	0	Chr04_1851 0829- Chr04_1852 4173	9	70	Chr09_4213 4679- Chr09_4350 6159	5. 2 4	0.01	7.5 6	0.01	- 0.41	- 0.01	0 0	0.0 1
qL D Ge - 39	2	110	Chr02_7158 639- Chr02_4168 9128	9	90	Chr09_4490 1931- Chr09_4794 4242	6. 5 5	0.16	13. 13	0.12	0.54	0.06	- 0.0 6	0
qL D Ge - 40	1	25	Chr01_2757 0711- Chr01_2775 7687	9	115	Chr09_2003 1546- Chr09_4799 2641	6. 1 6	0.08	13. 89	0.06	- 0.59	- 0.04	0.0 5	0
qL D Ge - 41	5	10	Chr05_3906 3431- Chr05_3926 8957	1 0	40	Chr10_1278 5119- Chr10_1315 4062	6. 3 1	0.02	7.4 1	0.02	- 0.41	- 0.04	0.0 2	0.0 2
qL D Ge - 42	2	85	Chr02_7158 639- Chr02_4168 9128	1 0	140	Chr10_4856 5588- Chr10_4860 4685	6. 1	0.02	9.0 3	0.03	- 0.45	- 0.03	0.0 3	0
qL D Ge - 43	6	145	Chr06_8950 528- Chr06_1101 1941	1 0	150	Chr10_4882 1422- Chr10_5056 2136	5. 7	0.01	10. 47	0.01	0.48	0.02	- 0.0 2	0
qL D Ge - 44	1	135	Chr01_5488 90- Chr01_5545 5938	1 1	80	Chr11_9994 040- Chr11_1022 3209	8. 6 5	1.13	16. 94	1.11	- 0.61	- 0.06	0.0 6	0
qL D Ge - 45	6	15	Chr06_2520 8683- Chr06_5048 8039	1 1	150	Chr11_3091 5623- Chr11_3160 1728	5. 5 4	0.09	15. 73	0.06	0.59	0.04	- 0.0 5	0.0 1
qL D Ge - 46	7	190	Chr07_4258 8703- Chr07_4282 2722	1 1	155	Chr11_3160 1728- Chr11_3195 7128	6. 9 6	0.08	9.0 1	0.08	- 0.45	- 0.06	0.0 5	0.0 1
qL D	8	205	Chr08_1786 1113-	1 1	185	Chr11_3421 6740-	5. 0	0.12	7.5	0.11	- 0.41	- 0.04	- 0.0	0.0 7

Ge - 47			Chr08_2151 4962			Chr11_3433 2014	6						3	
qL D Ge - 48	1 0	45	Chr10_1545 7230- Chr10_2412 6301	1 1	185	Chr11_3421 6740- Chr11_3433 2014	5. 7 6	0.34	6.9 6	0.4	0.38	0.10	- 0.1 2	0.0 2
qL D Ge - 49	9	110	Chr09_2003 1546- Chr09_4799 2641	1 2	55	Chr12_1279 5935- Chr12_1338 7126	5. 9 4	0.2	12. 54	0.14	0.52	0.06	- 0.0 7	0.0 1
qL D Ge - 50	8	130	Chr08_4607 9506- Chr08_4611 4145	1 2	75	Chr12_1118 8539- Chr12_2050 2781	6. 8 7	0.06	8.9 8	0.04	- 0.47	- 0.04	0.0 5	- 0.0 1
qL D Ge - 51	1 1	125	Chr11_1511 8639- Chr11_1603 7605	1 2	145	Chr12_1742 588- Chr12_1818 403	5. 0 9	0.01	6.5 9	0.01	0.38	0	- 0.0 1	0.0 1
qL D Ge - 52	2	70	Chr02_4277 1486- Chr02_4287 6053	1 3	0	Chr13_4204 7985- Chr13_4477 6547	5. 8 4	0.31	6.8 3	0.33	- 0.38	- 0.10	0.1 1	- 0.0 1
qL D Ge - 53	1 2	35	Chr12_3374 4934- Chr12_3439 5711	1 3	0	Chr13_4204 7985- Chr13_4477 6547	5. 9 4	0.09	7	0.07	-0.4	- 0.06	0.0 6	0
qL D Ge - 54	9	25	Chr09_3844 1024- Chr09_3847 2475	1 3	10	Chr13_4204 7985- Chr13_4477 6547	7. 3 1	0.01	10. 6	0.01	0.49	0.01	0.0 1	- 0.0 2
qL D Ge - 55	6	295	Chr06_4833 8765- Chr06_4898 5703	1 3	20	Chr13_4204 7985- Chr13_4477 6547	8. 2 1	0.11	11. 19	0.11	- 0.51	- 0.04	- 0.0 2	0.0 6
qL D Ge - 56	4	40	Chr04_4964 5786- Chr04_5012 0374	1 3	45	Chr13_3916 2381- Chr13_4214 7095	6. 6 5	0.12	12. 65	0.09	- 0.53	- 0.07	0.0 3	0.0 4
qL D Ge - 57	5	70	Chr05_3496 3403- Chr05_3542 8112	1 3	105	Chr13_1381 0558- Chr13_1691 9466	1 0. 2 4	2.21	15. 29	2.24	0.59	0.10	- 0.0 7	- 0.0 3
qL D	7	15	Chr07_3582 1740-	1 3	135	Chr13_1921 2498-	8. 7	0.03	13. 11	0.02	- 0.54	- 0.01	0.0 3	- 0.0

Ge - 58			Chr07_3695 4311			Chr13_2031 6402	9							2
qL D Ge - 59	1 1	30	Chr11_1843 4- Chr11_3268 0	1 3	140	Chr13_2040 3941- Chr13_2201 6619	5. 2 2	0.08	6.6 3	0.1	0.39	0.07	- 0.0 5	- 0.0 2
qL D Ge - 60	1 0	10	Chr10_5531 006- Chr10_6761 404	1 3	175	Chr13_2454 5749- Chr13_2769 3748	5. 2 9	0.15	7.3 3	0.17	- 0.43	- 0.08	0.0 9	- 0.0 1
qL D Ge - 61	1	45	Chr01_5059 734- Chr01_5242 313	1 3	205	Chr13_2856 4438- Chr13_2893 7494	6. 3 1	0.05	8.0 8	0.05	0.42	- 0.02	0.0 5	- 0.0 3
qL D Ge - 62	3	0	Chr03_3832 5793- Chr03_3838 6292	1 3	250	Chr13_3451 9992- Chr13_3480 8457	5. 2	0.11	6.3 9	0.16	0.38	0.08	- 0.0 4	- 0.0 4
qL D Ge - 63	1 3	35	Chr13_3916 2381- Chr13_4214 7095	1 4	5	Chr14_1244 32- Chr14_1285 42	6. 7 5	0.07	10. 33	0.07	0.48	0.05	- 0.0 4	- 0.0 1
qL D Ge - 64	4	130	Chr04_6374 605- Chr04_4630 6648	1 4	10	Chr14_6530 10- Chr14_7649 88	5. 4	0.07	7.4 4	0.09	0.42	0.05	0.0 1	- 0.0 6
qL D Ge - 65	1	25	Chr01_2757 0711- Chr01_2775 7687	1 4	50	Chr14_3760 081- Chr14_3801 945	6. 2 4	0.16	8.0 6	0.15	0.42	0.01	0.0 7	- 0.0 8
qL D Ge - 66	1 4	15	Chr14_1295 374- Chr14_1479 058	1 4	55	Chr14_4028 410- Chr14_4393 707	7. 0 6	0.05	8.8 7	0.03	- 0.46	- 0.05	0.0 1	0.0 4
qL D Ge - 67	1 0	30	Chr10_6698 754- Chr10_1032 9848	1 4	70	Chr14_4956 367- Chr14_6008 788	5. 0 9	0.06	6.9	0.06	0.39	0.03	- 0.0 5	0.0 2
qL D Ge - 68	7	70	Chr07_7873 044- Chr07_1517 4544	1 4	115	Chr14_1240 4901- Chr14_1266 6428	7. 2 7	1.02	12. 89	2.01	- 0.54	- 0.03	0.0 1	0.0 2
qL D	8	45	Chr08_3441 886-	1 4	120	Chr14_1374 0225-	6. 4	0.23	8.2 8	0.22	- 0.44	- 0.11	0.0 4	0.0 7

Ge - 69			Chr08_7871 477			Chr14_2261 4667	1							
qL D Ge - 70	2	70	Chr02_4277 1486- Chr02_4287 6053	1 4	145	Chr14_4365 9325- Chr14_4538 5242	5. 9 3	0.07	9.4 7	0.07	0.46	0.06	- 0.0 4	- 0.0 2
qL D Ge - 71	6	305	Chr06_4690 4753- Chr06_4898 5703	1 4	200	Chr14_4816 3434- Chr14_4899 4584	5. 9	0.33	7.6	0.39	- 0.41	- 0.12	0.1 1	0.0 1
qL D Ge - 72	4	110	Chr04_4612 9829- Chr04_4630 6648	1 5	10	Chr15_6082 551- Chr15_6770 751	7. 8 5	0.14	10. 34	0.17	- 0.48	- 0.06	0.0 9	- 0.0 3
qL D Ge - 73	1 3	0	Chr13_4204 7985- Chr13_4477 6547	1 5	20	Chr15_7857 370- Chr15_8198 387	7. 6 8	0.13	8.3 9	0.08	0.45	0.08	- 0.0 3	- 0.0 5
qL D Ge - 74	1 0	30	Chr10_6698 754- Chr10_1032 9848	1 5	30	Chr15_8536 219- Chr15_1068 5118	6	0.05	9.3 6	0.04	0.46	0.04	0	- 0.0 4
qL D Ge - 75	6	195	Chr06_4243 651- Chr06_4503 483	1 5	50	Chr15_1134 2488- Chr15_1216 0646	5. 1 2	0.29	6.8 8	0.33	- 0.38	- 0.12	0.0 3	0.0 9
qL D Ge - 76	8	15	Chr08_8797 268- Chr08_1033 0165	1 5	55	Chr15_1216 0646- Chr15_1518 7500	9. 4 8	1.23	15. 42	1.19	0.59	0.07	- 0.0 9	0.0 2
qL D Ge - 77	1 1	125	Chr11_1511 8639- Chr11_1603 7605	1 5	120	Chr15_2345 7758- Chr15_5153 6790	9. 8 1	0.03	20. 01	0.03	0.68	0.04	- 0.0 2	- 0.0 2
qL D Ge - 78	2	20	Chr02_4600 6453- Chr02_4615 3743	1 5	130	Chr15_2345 7758- Chr15_5153 6790	5. 1 5	0.09	9.2 4	0.06	- 0.46	- 0.04	0.0 4	0
qL D Ge - 79	4	5	Chr04_1852 2469- Chr04_4941 5449	1 6	10	Chr16_3429 8390- Chr16_3520 1284	6. 4 7	0.16	9.0 3	0.16	- 0.44	- 0.06	0.0 8	- 0.0 2
qL D	7	35	Chr07_1893 7475-	1 6	10	Chr16_3429 8390-	6. 3	0.14	7.7 5	0.16	- 0.41	- 0.06	0.0 9	- 0.0

Ge - 80			Chr07_1910 1902			Chr16_3520 1284	3							3
qL D Ge - 81	6	320	Chr06_4435 2903- Chr06_4689 1844	1 6	25	Chr16_3280 3794- Chr16_3301 2657	6. 1 1	0.11	7.9 1	0.15	- 0.41	- 0.08	0.0 6	0.0 2
qL D Ge - 82	1 3	5	Chr13_4204 7985- Chr13_4477 6547	1 6	40	Chr16_3146 8256- Chr16_3149 6527	6. 4 6	0.08	9.2 8	0.11	- 0.45	- 0.06	0 6	0.0 6
qL D Ge - 83	1 5	10	Chr15_6082 551- Chr15_6770 751	1 6	40	Chr16_3146 8256- Chr16_3149 6527	7. 0 9	0.26	8.7 3	0.32	- 0.44	- 0.11	0.1 1	0
qL D Ge - 84	8	175	Chr08_2321 1701- Chr08_3661 3506	1 6	65	Chr16_2947 1775- Chr16_3074 1434	6. 2 7	0.04	8.2 3	0.05	0.43	0.04	- 0.0 1	- 0.0 3
qL D Ge - 85	1 1	105	Chr11_2510 6737- Chr11_2710 5086	1 6	65	Chr16_2947 1775- Chr16_3074 1434	6. 4 9	0.16	9.3 1	0.16	0.46	0.05	- 0.0 9	0.0 4
qL D Ge - 86	1 4	160	Chr14_4662 8593- Chr14_4668 4931	1 6	65	Chr16_2947 1775- Chr16_3074 1434	5. 0 9	0.16	6.7	0.18	0.38	0.06	- 0.0 9	0.0 3
qL D Ge - 87	5	130	Chr05_6820 615- Chr05_1051 8929	1 6	95	Chr16_7966 285- Chr16_2590 9507	7. 4 8	0.15	9.8 9	0.17	- 0.47	- 0.08	0.0 6	0.0 2
qL D Ge - 88	1 0	5	Chr10_4560 820- Chr10_5439 167	1 6	120	Chr16_5621 107- Chr16_6162 282	8. 6 6	0.05	11. 89	0.07	0.51	0.05	- 0.0 1	- 0.0 4
qL D Ge - 89	2	100	Chr02_7158 639- Chr02_4168 9128	1 6	130	Chr16_3911 525- Chr16_5144 359	5. 0 5	0.02	8.2 4	0.03	- 0.47	0.01	- 0.0 2	0.0 1
qL D Ge - 90	3	65	Chr03_2969 4597- Chr03_4522 8398	1 6	130	Chr16_3911 525- Chr16_5144 359	7. 7 7	2.02	19. 07	3.02	- 0.66	- 0.03	0.0 1	0.0 2
qL D	6	315	Chr06_4435 2903-	1 7	30	Chr17_3917 9633-	6. 8	0.11	10. 07	0.09	0.48	0.05	- 0.0	0.0 2

Ge - 91			Chr06_4689 1844			Chr17_3937 2790	5						7	
qL D Ge - 92	1 0	130	Chr10_4697 1304- Chr10_4844 8324	1 7	55	Chr17_3748 3706- Chr17_3812 4550	6. 0 2	0.02	8.2 3	0.03	- 0.43	- 0.03	0.0 2	0.0 1
qL D Ge - 93	1 3	40	Chr13_3916 2381- Chr13_4214 7095	1 7	55	Chr17_3748 3706- Chr17_3812 4550	5. 8 4	0.1	11. 84	0.1	0.52	0.07	- 0.0 5	- 0.0 2
qL D Ge - 94	8	70	Chr08_9334 53- Chr08_1090 639	1 7	70	Chr17_3672 8291- Chr17_3684 2695	7. 6 9	0.04	9.5 2	0.04	0.46	0.02	0.0 2	- 0.0 4
qL D Ge - 95	1 5	0	Chr15_5188 502- Chr15_5211 328	1 7	70	Chr17_3672 8291- Chr17_3684 2695	8. 4 7	0.14	9.9 5	0.15	0.47	0.09	- 0.0 4	- 0.0 5
qL D Ge - 96	2	95	Chr02_7158 639- Chr02_4168 9128	1 7	85	Chr17_1425 0670- Chr17_3382 8522	9. 6 4	0.26	21. 08	0.16	- 0.68	- 0.09	0.0 5	0.0 4
qL D Ge - 97	1 4	70	Chr14_4956 367- Chr14_6008 788	1 7	125	Chr17_1177 1847- Chr17_1236 2378	7. 3 2	0.02	9.7 1	0.05	0.48	0.04	- 0.0 2	- 0.0 2
qL D Ge - 98	1 2	55	Chr12_1279 5935- Chr12_1338 7126	1 7	165	Chr17_8293 917- Chr17_8304 154	6. 5 8	0.07	8.0 4	0.09	- 0.42	- 0.06	0.0 4	0.0 2
qL D Ge - 99	1 6	155	Chr16_7626 01- Chr16_9214 88	1 7	170	Chr17_7239 329- Chr17_7918 931	8. 1 4	0.43	11. 15	0.48	0.5	0.14	- 0.0 5	- 0.0 9
qL D Ge - 10 0	7	5	Chr07_3683 1967- Chr07_3886 4073	1 7	175	Chr17_6349 671- Chr17_7256 590	6. 7 7	0.05	9.9 9	0.07	- 0.47	- 0.06	0.0 4	0.0 2
qL D Ge - 10 1	1 6	80	Chr16_1709 2151- Chr16_1809 4195	1 8	35	Chr18_5461 2343- Chr18_5509 7079	5. 4 9	0.04	7.0 5	0.04	-0.4	- 0.04	0.0 2	0.0 2

qL D Ge - 10 2	6	200	Chr06_1575 116- Chr06_4243 651	1 8	65	Chr18_5357 0314- Chr18_5375 3657	1 0. 1 9	0.33	13. 7	0.3	- 0.55	- 0.11	0.0 8	0.0 3
qL D Ge - 10 3	1 4	115	Chr14_1240 4901- Chr14_1266 6428	1 8	70	Chr18_5316 1911- Chr18_5332 4929	6. 9 7	0.07	8.5 6	0.08	- 0.44	- 0.06	0.0 2	0.0 4
qL D Ge - 10 4	4	165	Chr04_2640 223- Chr04_3532 366	1 8	85	Chr18_5147 5419- Chr18_5166 6883	6. 2 9	0.08	8.4 4	0.05	0.45	0.04	- 0.0 6	0.0 2
qL D Ge - 10 5	1 5	0	Chr15_5188 502- Chr15_5211 328	1 8	90	Chr18_5127 1242- Chr18_5128 3338	5. 0 6	0.04	5.3 9	0.01	0.39	0.05	- 0.0 3	- 0.0 2
qL D Ge - 10 6	7	195	Chr07_4258 8703- Chr07_4282 2722	1 8	95	Chr18_5034 2597- Chr18_5167 4025	6. 1 8	0.19	8.1	0.2	- 0.42	- 0.09	0.0 2	0.0 7
qL D Ge - 10 7	2	160	Chr02_2931 747- Chr02_5212 093	1 8	100	Chr18_4942 0693- Chr18_5021 4161	7. 4 7	0.03	10. 95	0.04	-0.5	- 0.04	0	0.0 4
qL D Ge - 10 8	8	185	Chr08_2242 9410- Chr08_2247 5225	1 8	100	Chr18_4942 0693- Chr18_5021 4161	5. 5 7	0.07	7.3 1	0.09	0.4	0.07	- 0.0 4	- 0.0 3
qL D Ge - 10 9	1 2	110	Chr12_4877 574- Chr12_6472 915	1 8	120	Chr18_1295 0561- Chr18_5065 5078	9. 1 3	0.18	18. 83	0.13	- 0.64	- 0.07	0.0 5	0.0 2
qL D Ge - 11 0	1	45	Chr01_5059 734- Chr01_5242 313	1 8	135	Chr18_9169 264- Chr18_1212 3610	8. 4 1	0.11	11. 16	0.11	-0.5	- 0.03	- 0.0 4	0.0 7

qL D Ge - 11 1	3	65	Chr03_2969 4597- Chr03_4522 8398	1 8	145	Chr18_7449 305- Chr18_7636 909	6. 8	0.17	13	0.15	- 0.53	- 0.07	0	0.0 7
qL D Ge - 11 2	1 7	30	Chr17_3917 9633- Chr17_3937 2790	1 8	175	Chr18_3680 464- Chr18_5084 724	8. 3 5	0.01	10. 66	0.01	- 0.49	0	0.0 2	- 0.0 2
qL D Ge - 11 3	5	35	Chr05_3732 2109- Chr05_3735 6351	1 8	185	Chr18_2560 852- Chr18_3087 777	5. 4 2	0.01	7.0 8	0.01	-0.4	- 0.03	0.0 1	0.0 2
qL D Ge - 11 4	1 7	100	Chr17_1339 2060- Chr17_1386 6024	1 9	0	Chr19_4472 2900- Chr19_4508 2406	5. 3 2	0.03	6.6 1	0.04	- 0.38	- 0.04	0.0 1	0.0 3
qL D Ge - 11 5	1	45	Chr01_5059 734- Chr01_5242 313	1 9	15	Chr19_4319 4427- Chr19_4457 6364	1 3. 4 8	1.2	17. 24	0.05	0.62	0.04	- 0.0 1	- 0.0 3
qL D Ge - 11 6	2	80	Chr02_4168 9128- Chr02_4218 6533	1 9	15	Chr19_4319 4427- Chr19_4457 6364	5. 5 2	0.01	8.2 6	0.02	- 0.43	- 0.03	0.0 2	0.0 1
qL D Ge - 11 7	3	135	Chr03_3170 068- Chr03_3516 529	1 9	40	Chr19_4066 2747- Chr19_4066 3854	5. 0 8	0.57	6.3 4	0.68	0.36	0.17	- 0.1 2	- 0.0 5
qL D Ge - 11 8	1 3	45	Chr13_3916 2381- Chr13_4214 7095	1 9	105	Chr19_3146 8355- Chr19_5024 4060	7. 4	0.16	16. 41	0.1	-0.6	- 0.07	0.0 5	0.0 2
qL D Ge - 11 9	1 4	60	Chr14_4604 584- Chr14_4726 462	1 9	105	Chr19_3146 8355- Chr19_5024 4060	6. 5 5	0.12	12. 2	0.09	0.52	0.07	- 0.0 4	- 0.0 3

qL D Ge - 12 0	1 0	55	Chr10_3805 8098- Chr10_3836 3190	1 9	110	Chr19_3146 8355- Chr19_5024 4060	5. 2 5	0.01	12. 2	0.01	0.52	0.02	- 0.0 1	- 0.0 1
qL D Ge - 12 1	1 9	25	Chr19_4225 0834- Chr19_4308 9572	1 9	110	Chr19_3146 8355- Chr19_5024 4060	8. 9	0.14	15. 07	0.1	0.58	0.07	- 0.0 4	- 0.0 3
qL D Ge - 12 2	1 8	20	Chr18_5551 4239- Chr18_5632 3759	1 9	120	Chr19_3146 8355- Chr19_5024 4060	7. 3 9	0.24	14. 22	0.2	0.56	0.09	- 0.0 6	- 0.0 3
qL D Ge - 12 3	9	25	Chr09_3844 1024- Chr09_3847 2475	1 9	140	Chr19_5041 7070- Chr19_5051 5701	5. 4 6	0.02	7.1 2	0.01	-0.4	- 0.04	0.0 3	0.0 1
qL D Ge - 12 4	8	150	Chr08_4093 6735- Chr08_4555 0328	2 0	5	Chr20_4151 8902- Chr20_4282 3180	9. 8 6	0.33	19. 3	0.24	- 0.65	- 0.10	0.0 7	0.0 3
qL D Ge - 12 5	7	195	Chr07_4258 8703- Chr07_4282 2722	2 0	10	Chr20_4151 8902- Chr20_4282 3180	6. 9 5	0.08	9.2 7	0.1	- 0.46	- 0.07	0.0 3	0.0 4
qL D Ge - 12 6	1 5	45	Chr15_1134 2488- Chr15_1216 0646	2 0	25	Chr20_4007 9906- Chr20_4060 7484	7. 9 2	0.03	10. 62	0.05	0.49	0.04	- 0.0 1	- 0.0 3
qL D Ge - 12 7	1 4	200	Chr14_4816 3434- Chr14_4899 4584	2 0	70	Chr20_3563 5820- Chr20_3607 1570	6. 5 6	0.13	7.5	0.13	0.44	0.08	- 0.0 6	- 0.0 2
qL D Ge - 12 8	1 1	180	Chr11_3375 8875- Chr11_3382 8052	2 0	110	Chr20_3363 9229- Chr20_3393 1061	5. 7 6	0.04	8.1	0.03	0.43	0.02	0.0 2	- 0.0 4

qL D Ge - 12 9	9	95	Chr09_2003 1546- Chr09_4799 2641	2 0	130	Chr20_2362 3977- Chr20_2467 4689	8	1.05	10. 02	0.07	0.47	0.05	- 0.0 5	0
qL D Ge - 13 0	1 6	140	Chr16_2884 746- Chr16_3071 707	2 0	140	Chr20_4268 595- Chr20_4366 687	6. 0 8	0.07	7.4 9	0.07	- 0.41	0	- 0.0 5	0.0 5

^aChromosome

^bGenetic position

^cPhysical position of SNP makers

^dLOD score for additive and QEI effect

^eLOD score for QEI effect

^fPhenotypic variation explained by additive and QEI effect

^gPhenotypic variation explained by QEI effect

^hEpistatic effect between two QTL

ⁱEpistatic effect between two QTL affected by individual environment