

QTL mapping of soybean cyst nematode race 9: a generalized linear modeling approach

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Tab supplementary 1. Microsatellite markers (SSR) with segregation ratio 1:1 ($P < 0.05$ according to the Chi-square test) employed to map QTL for resistance to race 9 of the soybean cyst nematode

SSR	Linkage Group	GenBank Accession	Forward (5' → 3')	Reverse (5 → 3')
Satt454	A1	BH126628	GCTTTTCTTAGAACACAAATTACAAG	CAACCATGATAAATGTGAGTGAG
Satt545	A1	BH126713	CAATGCCATTCCATATTTGTT	CAATTGCCCTAGTTTTGATAG
Satt449	A1	CC453967	GCGTGCTTCTTATATTAGGTGTTAGT	GCGCATTGGAGTTTTTGCTTTT
Satt329	A2	BH126520	GCGGGACGCAAATTGGATTTAGT	GCGCCGAATAAAAACGTGAGAAGT
Satt233	A2	BH126434	AAGCATACTCGTCGTAAC	GCGGTGCAAAGATATTAGAAA
Sat_162	A2	BH126790	GCGTGGTTTTTCGCTGGATATA	GCGCATTTTCGTAACATATTTTTCAC
Satt632	A2	BH126793	GGGCTATGAAGGGAATGGAAAGGA	CCCATATTGAAGATTTGAAGTAAT
Satt207	A2	BH126413	GCGTTTTTCTCATTTTGATTCTAAAC	GCGATTGTGATTGTAGTCCCTAAA
Satt341	A2	BH126532	GCGGAGCTTACCAACATAAAAAAACT	GCGGTCCAACATTGAGGCAAGAATAC
Satt332	B1	BH126523	GCGCATCCAGGGCTTGCAACAAAG	GCGGTCCCTTATATATGGAAGATCA
Satt444	B1	BH146217	TGCAAAAATACGGGTTTATAAT	AGAGGAAGCGGAGACTAATAGAAG
Satt484	B1	BH126656	GCGTTTAATAAACTAATTTAATTGTACT	GCGTTCCCTTTCTCTCCTTTCTTTCTT
Satt416	B2	BH126595	TATAGCCCAGCAAAAAAAACAGAGAT	ATCAAAACCGACCAATGAACAAAAAAA
Sat_009	B2	CC453672	CACACGTATTGTCTTACCAC	CTCCGAGAAGCACGTA
Satt534	B2	BH126703	CTCCTCCTGCGCAACAACAATA	GGGGGATCTAGGCCATGAC
Satt556	B2	BH126723	GCGATAAAACCCGATAAATAA	GCGTTGTGCACCTTGTTTTCT
Satt476	C1	BH126648	TTTGCTGATTAATAAAACAAAAAACTG	TTGTTAGAATGGGGACTACTTCACTA
Satt180	C1	BH126388	TCGCGTTTTGTCAGC	TTGATTGAAACCCAACTA
Satt190	C1	BH126397	GGGAGTGTGAACTTACATTGTCT	GGGCCTTGAATTTTGTGCTAT

Satt277	C2	BH126473	GGTGGTGGCGGGTTACTATTACT	CCACGCTTCAGTTGATTCTTACA
Satt307	C2	BH126498	GCGCTGGCCTTTAGAAC	GCGTTGTAGGAAATTTGAGTAGTAAG
Satt202	C2	BH126409	GGAATGCATGAGTATTAACCTCTTAT	GGGCTAACGAACATGTAACCTTATCAAC
Satt371	C2	BH126558	TGCAAATAACTGGATTCACTCA	GAGATCCCGAAATTTTAGTGTAACA
Satt460	C2	BH126633	GCGCGATGGGCTGTTGGTTTTTAT	GCGCATACGATTTGGCATTTTTCTATTG
Satt357	C2	BH126546	CCTGAGCAATTCATACTCC	TAACCGATCCGATCCTTGACA
Satt316	C2	BH126507	GTGAGAACTAGCCAAGAATAGA	CAATTGTTTCCAAATGACACT
Satt079	C2	BH126324	AGTCGAAGATACACAATTAGAT	CTTTTAGACACAAATTTATCACT
Satt557	C2	BH126724	GCGGGATCCACCATGTAATATGTG	GCGACTAACCCTTTATTGAA
Satt286	C2	BH126480	GCGGCGTTAATTTATGCCGAAA	GCGTTTGGTCTAGAATAGTTCTCA
Satt376	C2	BH126563	GCTACGCATTTGGTTTGTTA	ACATGCAATACTTTTTTTTCAT
Satt147	D1a	BH126359	CCATCCCTTCCTCCAAATAGAT	CTTCCACACCCTAGTTTAGTGACAA
Satt267	D1a	BH126463	CCGGTCTGACCTATTCTCAT	CACGGCGTATTTTTATTTTG
Satt321	D1a	BH126512	CACCGTCGTAAAACTGTGTCGT	GCGTGTCAAAGAGTTTTAGACATC
Satt342	D1a	BH126533	GGTGCAAGGGAAAATGGAAATAA	GATACAACGTCGTGCTACTATCCAAATA
Satt370	D1a	BH126557	GCGGTAAAGGGAATTTGTAACCTGAA	GCGATCATGCATTTATTTGAGATA
Satt408	D1a	BH126588	GCGGTCCGTGCTGTTAATTCTATA	GCGTGATTTATTCATGATATATTTTTG
Satt482	D1a	BH126654	GCGCGTTAGTTTAAACGTAAAAGGAAAT	GCGTCACCTCAATGGATATTTATTTA
Satt507	D1a	BH126678	GCGCTCAGCCTTGTTAAATCACTT	GCGCTACTCTCGTGTCTGTTAGTTA
Satt531	D1a	BH126700	GCATGCAACTGAGGGAGCAGAT	GCCACAAATTATGCAGAATATA
Satt532	D1a	BH126701	GCGCCAATATTATCATGCTTTATGT	GCGTGTA AAAATCTTTGAATCTTGA
Satt189	D1b	BH126396	CCATACGCAGCATTAGAG	GCTATTTGCATGTTGAGAA
Satt600	D1b	BH126765	GCGCAGGAAAAAAAACGCTTTTATT	GCGCAATCCACTAGGTGTTAAT
Satt141	D1b	BH126353	CGGTGGTGGTGTGCATAATAA	CCGTCATAAAAAGTCCCTCAGAAT
Satt301	D2	BH126492	GCGAAACACTCCTAGTTGATTACAAA	GCGATATAATGCACAAAGAAATTAAGA
Satt574	D2	BH126740	GCGCCTCTCATATGGTAT	GCGGGGGGGAAATGTAGA
Satt389	D2	BH126574	GCGGCTGGTGTATGGTGAAATCA	GCGCCAAAACCAAAGTTATATC
Satt151	E	BH126363	ATTGCCTAATTTCTGTTTGTGTAA	CCAAAATTC AAGGCAGTGAC
Satt204	E	BH126411	GCCATCTTGTTACAATGCAGGTA	CCTTACTCACTCCATTGGCATAATA
Satt212	E	BH126418	CCAATCCAAACAAATCCACT	CAGCAATGATGATAATGAATGA
Satt263	E	BH126460	CACCCAATCATGATAGCATTTTAT	CTCATGGAATTGTCTTTCAGTTTC
Satt268	E	BH126464	TCAGGGGTGGACCTATATAAAAATA	CAGTGGTGGCAGATGTAGAA
Satt452	E	BH126626	GCGGTCGCTGCGTTCAATAT	GCGCCCAATTATCATGGTAGA
Satt602	E	BH126767	GCGGCGTTAGTGGAATAGA ACTA	GCGGGTATACCAAATGAGATAAT

Satt343	F	BH126534	CATGGCGGAAAGCGAAACA	TCCCAATTCACCTCTTCA
Satt516	F	BH126686	GCGTTAGCACTATTTTTTTACAAGA	GCGCCGTTCCCTCTTTACTTTAT
Satt193	F	BH126400	GCGTTTCGATAAAAATGTTACACCTC	TGTTTCGATTATTGATCAAAAAT
Satt490	F	BH126661	GCGGCACGAGTCAACTTTCTGTTTCCT	GCGGAAGAAGATTTTCGTTTTTAT
Sat_163	G	BH126791	GCGGTATATATGTTTGCAAGACATATT	GCGGAATCTCGCCCAGGAGGAACTT
Satt038	G	CC453951	GGGAATCTTTTTTTCTTTCTATTAAGTT	GGGCATTGAAATGGTTTTAGTCA
Satt130	G	BH126344	TAAACGAAATTTAGTTTTAAGACT	TGAATGGCTAAAAACGTGATT
Satt163	G	BH126374	AATAGCACGAGAAAAGGAGAGA	GTGTATGTGAAGGGGAAAAACTA
Satt217	G	BH126421	AATGATTTTGCGTATGTAAGATGA	GCGGATGACATTAATAGTTTTTAGA
Satt235	G	BH126436	GCGGGCTTTGCCAAGAAGTTT	GCGGTGAGGCTGGCTATAAG
Satt275	G	BH126471	GCGGGATAATTGGTTTTACGAAAATGC	GCGCCTAATCACCTAAAAAACGTTTA
Satt303	G	BH126494	AAAAGCGACGACCTATG	TGAACGTTCTATCAACACA
Satt309	G	BH126500	GCGCCTTCAAATTGGCGTCTT	GCGCCTTAAATAAAAACCCGAAACT
Satt356	G	BH126545	CATGCCTGGTCCATTTTG	TCAAGCCACGATAACAGTA
Satt427	G	BH126606	GCGAGTATCCACCCTTTTATAATAAT	TCTCCACGCCACCTTATTCCTCTCC
Satt564	G	BH126730	GCGCTTCCACCACAATAACA	GCGGCAGAGGACTGACAGCTA
Scct010	G	BH126786	CGCATGTGCAAGTAAC	TAGTTGGGGAGAAACAG
Satt293	H	BH126486	GCGCAGAAGGTTTGCATAAAAAGAAT	GCGGGCTAAAAAGTTGATGTAATGTG
Satt142	H	BH126354	GGACAACAACAGCGTTTTTAC	TTTGCCACAAAGTTAATTAATGTC
Satt302	H	BH126493	GCGAACTGTAGTTTACTAAAAATAAGTG	GCGGACTGAATTAATATTGGTGTGAATT
Satt317	H	BH126508	GCGAACAACTTTCTATACATGATAACA	GCGGGTATATTTTTGTACATAAGTTGGAA
Satt353	H	BH126542	CATACACGCATTGCCTTTCCTGAA	GCGAATGGGAATGCCTTCTTATTCTA
Satt354	I	BH126543	GCGAAAATGGACACCAAAAGTAGTTA	GCGATGCACATCAATTAGAATATACAA
Satt431	J	CC453966	GCGTGGCACCCCTTGATAAATAA	GCGCACGAAAGTTTTTCTGTAACA
Scct011	J	CC454081	CTCCGTTGCTGAT	TAAGCTGAATTAGTAAAA
Satt456	J	CC453968	GGGCCTTCGTTTGAGTTCATAG	GGGATCATTGGTTAATTGTTGTAAGA
Satt215	J	CC453956	GCGCCTTCTTCTGCTAAATCA	CCCATTCAATTGAGATCCAAAATTAC
Sat_366	J	CC453892	GCGGCACAAGAACAGAGGAAACTATT	GCGGACATGGTACATCTATATTACGAGTATT
Sat_394	J	CC453919	GCGGACAGTGTGCTCCTCATATAATAG	GCGTGACTCGGACTTGAAGATAATAATG
Sat_119	K	BH126289	TAGGCTTTC AATTTGCAGAACT	GTTAGGTGTCCAAGCAACTTA
Satt167	K	BH126378	GATTTACGGGACTTGGATTCAATA	AGCTACCCAATATGATACTCTACACAGT
Satt178	K	BH126386	GGGAAAATCTTTTCATATAGATG	GGGGTTGAGATATTTTGTTTCATAC
Satt196	K	BH126403	TTGGGAAATAGTGATTGAGGTA AAA	AAATCCCCATTGAATGAGAATAAG
Satt242	K	BH126443	GCGTTGATCAGGTCGATTTTTATTGT	GCGAGTGCCA ACTA ACTACTTTTATGA

Satt349	K	BH126539	GCGGGAACGAACGGGAAGAAGAAC	GCCATCCAATGTTTAGAAGAAC
Satt555	K	BH126722	GCGGTTGGCTTTGATGATGT	TTACCGCATGTTCTTGGACTA
Satt418	L	BH126597	GCGAAAGCACATATGGGTTTGAAT	GCGAGGGCATATATATGATGAGGTA
Sat_134	L	BH126304	GCGATGAGGAAAGGTGATAGTGAACCTTG	GCGCTCAGCTTGCATATATAAAATAATA
Satt497	L	BH126668	GCGGTTTTGGATTGACTTTGTTGA	GGCTCAATTAGAGCATGCAACATC
Satt446	L	BH126621	CCGCATAAAAAACACAACAATA	GCGGGCAAATTTGACCTAACTCACAAC
Satt523	L	BH126693	GCGATTTCTTCCTTGAAGAATTTTCTG	GCGCTTTTTTCGGCTGTTATTTTTAACT
Satt527	L	BH126697	GCGGTTACATCTTGCAAATAAATTAAC	GCGGAATTTTGCACATAAATTAATAACT
Sct_010	L	BH126771	TCCCAAAGCATTGAG	TATGCACGGAAGAGGA
Satt238	L	BH126439	GCGCCATTTAATGATTTATTTA	GCGGAAAGAAGAGGAAGAAAG
Satt150	M	BH126362	AAGCTTGAGGTTATTCGAAAATGAC	TGCCATCAGGTTGTGTAAGTGT
Satt175	M	BH126384	GACCTCGCTCTCTGTTTCTCAT	GGTGACCACCCTATTCCTTAT
Satt245	M	BH126445	AACGGGAGTAGGACATTTTATT	GCGCCTCCTGAATTTCAAAGAATGAAGA
Satt250	M	BH126448	CGCCAGCTAGCTAGTCTCAT	AATTTGCTCCAGTGTTTTAAGTTT
Satt463	M	BH126636	TTGGATCTCATATTCAAACTTTCAAG	CTGCAAATTTGATGCACATGTGTCTA
Satt536	M	BH126704	GCGCCACAGAAATTCCTTTTTCTA	GCGCCATAAGGTGGTTACCAAAGA
Satt551	M	BH126718	GAATATCACGCGAGAATTTTAC	TATATGCGAACCTCTTACAAT
Satt590	M	BH126756	GCGCGCATTTTTTAAGTTAATGTTCT	GCGCGAGTTAGCGAATTATTTGTC
Sat_084	N	CC453683	AAAAAAGTATCCATGAAACAA	TTGGGACCTTAGAAGCTA
Satt237	N	BH126438	GCGTGATTTCAATCCTTTTTTC	GCGGTTGTCCTGTTAGAACCT
Satt387	N	BH126572	GCGTTACGTTTCACTATTTATTTAACAT	GCGGCAGGCTAGCTACATCAAGAG
Satt485	N	BH146218	GCGAATACGCATAAAAAAATCAACAAGA	GCGAAAAGAAAATTTAAAAAAAATATAT
Satt530	N	BH126699	CATGCATATTGACTTCATTATT	CCAAGCGGGTGAAGAGGTTTTT
Satt549	N	BH126716	GCGGCAAACTTTGGAGTATTGCAA	GCGCGCAACAATCACTAGTACG
Satt345	O	BH126535	CCCCTATTTCAAGAGAATAAGGAA	CCATGCTCTACATCTTCATCATC
Satt478	O	BH126650	CAGCCAAGCAAAAGATAAATAATA	TCCCCACAAGAGAACAAGAAGGT
Sat_108	O	CC453689	AAAAATCTATTTACTTTGAGTCTA	TTGAAAGAGTCACGTCTATTCTAT
Satt550	O	BH126717	CGTCAATTAAGCAAAAATGTGA	GCGCGGATGAGCGTTCGTTTTTA
Satt173	O	BH126382	TGCGCCATTTATTCTTCA	AAGCGAAATCACCTCCTCT
Satt358	O	BH126547	GCGGCGCTTTATGTAACAATACGATTT	GCGAGTAAAAGCAGAGTGCGGAGTA
Satt479	O	BH126651	GCGCTTTCAAAAAGTAACAATTAATGAAA	GCGGGAATTGGTTAATCTCATCGTGAC
Sat_274	O	CC453808	GCGCCGATCTTTAGTGAGGTTACAAGT	GCGTTCAGCGAGTCCAGAAATAG
Satt188	O	BH126395	GCGTTTTAATTTTAATTTATTATTTTC	GCGCTGTCTTAATTGGAGATAC