Supporting Information

Brueggeman *et al.* 10.1073/pnas.0807270105

Table S1. Primers used for genotyping and sequencing in the *Rpg5*/*rpg4* region

Primer	Primer sequence 5′-3′	Gene	Clone	Position	Amplicon, bp
R4-F1	TCAACCGCTTTCGCTCATATGCATG	HvRGA1		118,020	715
R4-R1	GAAGTTGCTCTTCCGGATCCTGATC			117,306	
R4-F2	TTGGCCGCTCGAATGGCAGCAGATC	HvRGA1		117,553	1,038
R4-R2	CCCGTGAATGAATGTGCGCAAATAG			116,515	
R4-F3	ATCTTGAGTGCGATGTGGTGAACAC	HvRGA1		116,750	909
R4-R3	TCCTACTAGTCCATACCAATCACAC			115,842	
R4-F4	GATGGAATGTGGTCTAGGACTGTAG	HvRGA1		115,984	1,060
R4-R4	TCTCTTTGCCTGGCAGATTCTTCTC			114,924	
R4-F5	GAATCCCCTGATAAGGCGATGGCTG	HvRGA1		115,174	1,003
R4-R5	CTGCGTCAGCTTGCCTCTCAACTTG			114,172	
R4-F6	GCTACTTGAAGGTGACTGCACACAG	HvRGA1		114,511	1,037
R4-R6	AACAGGTTTGCACTGCAGACAGTAG			113,475	
R4-F13	CTTGTGCACGGCCAAGATCCTGATG			113,606	1,010
R4-R13	ATCTGAGTGTTTCCAGCGAGACAAG			112,597	
R4-F14	CAAACAGGTGTGCTGCAAATGGTTG			112,757	953
R4-R14	CAAGAGAGAGGAGGCTGAGATGAAC			111,805	
R4-F15	ATATCCAGGATCCTACTGCACTGAC			111,967	1,007
R4-R15	GAAGAAGTCAAGGTCCGCAAGGAAG			110,961	
R4-F16	CGGAGGAAGTATTTCCTCACCCATC			111,068	1,052
R4-R16	AAGCAAAGTGCAACGGAAACAGCAG			110,017	
R4-F17	AGAAACTCCTTTCAAGGTCGGCCAC			110,098	935
R4-R17	CAAAAACCATGGAGTTGTACCCGAG			109,164	
R4-F18	GAGCAAGACTCTTAGGGCGTGTTTG			109,319	1,006
R4-R18	TAGGGGACAGGATTTGCAACTCTGG			108,314	
R4-F19	ACATTGTTGCACTTCAGTTGGGCTC			108,542	1,040
R4-R19	TTGTAGTGGAGAATGGAAGAGCCAC			107,503	
R4-F20	CTTTCGTGTATACAGCATGAGCTTG			107,663	1,016
R4-R20	CCGACGACGTGTTAGACGGAATGAC			106,648	
R4-F21	CTCCATTCGGACCGGATCATGATTC			106,820	887
R4-R21	TTTGCGTGTATACTCACATGAGTAG			105,934	
R4-F22	CGGATATAGGGAGAAGGGTTTGATG			106,152	897
R4-R22	GTCGTCCATCTTGTACACCACGAAC			105,256	
R4-F23	GAACTCCACTGCGAAATACTCGTAC	HvAdf2		105,544	790
R4-R23	CGCGTGAACCGTCAATCATACACAC			104,754	
R4-F24	CAGTTCTTTGTTGCAGCATCATCAC	HvAdf2		105,519	950
R4-R24	CTCGTCTAATCGTTGCCATTACGTG			104,570	
R4-F25	GCTAGCTTTGTGCCGTGCATGTATC	HvAdf2		104,707	1,029
R4-R25	AGATTCCGAGGGACATACATGCAAG			103,679	
R45-F1	GACGAAAAACCTGTCCGATCAGATC		RSB1156	117,897	2,150
R45-R1	TTGTGCAACTCGCAATTGAAGGTAC			120,046	
R45-F2	ACCCAGGTAAGAGGGACCATGTTAG		RSB1157	119,849	2,006
R45-R2	GGGCGTGACATAGAGAGGGATGGAG			121,855	
R45-F3	GAACGTTGCGAGCTGCACGTCCTAC			121,152	2,318
R45-R3	CAGCCTCTCAACAATGCCATGAATC			123,469	
R45-F4	CCACCCTTTACCAAGTATGTAGGTG		RSB1166	123,293	2,424
R45-R4	ATGCGTCGTGGCTGAAGCCTCGAAG			125,717	
R5-F1	CCGCCTACCACACCTCCGATTCCAC	Rpg5	RSB762	−302*	1,087
R5-R1	TCAGGTTTGATGGCTGTCTCTGGAG			+785*	
RpgQ-F3	TGTGCCGGATGCAGATCTGGACCTC	Rpg5	RSB762	492*	1,046
RpgQ-R3	TGAGGAGAGCGAACCAATGTACTTC			1,538*	
Rpg5-F4.2	CATCAATGTTCTAACATGGCGTATC	Rpg5	RSB762	1,396*	1,153
RpgQ-R4	GATCGAACTTGGGACATTCTGATGC			2,548*	
Rpg5-F5.2	GGTGTTGTCATGTACAGTTGATCAC	Rpg5	RSB762	2,351*	1,259

Primer	Primer sequence 5′-3′	Gene	Clone	Position	Amplicon, bp
Rpg5-R5.3	CTATCTGAGATCTAACCGTGTATTG			3,609*	
RpgQ-F6	AGATGCACCTATCTGCATCGAGCAC	Rpg5	RSB762	3,422*	1,017
RpgQ-R6	ATGTCGAGCCTGAGACTACTGACAC			4,438*	
QK-F2	CCCCATACTTCAAATTACACTTCGCTGCC	Rpg5	RSB762	4,237*	1,016
R5-R7.3	GCAACCTTCATTCTGACAGACCATG			5,253*	
RQ4K-F1	CTATTCAGAAGTATGCACTGACCAG	Rpg5	RSB762	5,024*	1,160
RQ4K-R1	GCACCGCAACTCCTGTGTGTTCGAC			6,183*	
RQ4K-F2	ACGCCTCCGAGGAGGAGGTTTACAG	Rpg5	RSB762	5,994*	985
RQ4K-R2	GCTTTGGTTCAGCCGAACAGACGAG			6,978*	
RQ4K-F3	GCTTGGGGATGCAAGCATAGAGCTG	Rpg5	RSB762	6,776*	1,001
RQ4K-R3	CACGCCAAAGCTATACACATCACTC			7,776*	
R54K-F4.2	TGCATCTATCTGCTCATGCAAGGAG	Rpg5	RSB762	7,303*	1,082
RCR1	AACAATATTCACCTGCGGCACCAAC			8,384*	
HvPP2C-R2	CCCGAGGTTTGCGATGAAGAGAGTC	HvPP2C		156,716	
HvPP2C-R4	ACGACCTGTATGATGCCTTTCACTC	HvPP2C		156,901	
RpgQ-J17	TCTGGCCCATCTTGAGAGACTTGAG	Rpg5	RSB762	3,073*	
RpgQ-F11	AGGATGACGCTACATACTCAGCGAG	Rpg5	RSB762	242*	
Rpg5-F13	GAGGGACACGGTCCCGGTGAAGATG	Rpg5	RSB762	333*	
Rpg5-F14	CAGTCCTGATTCCGCTTCGCTTGAG	Rpg5	RSB762	297*	
Rpg5-F15	GGATCCCCCCATCACGGCTTTGCTC	Rpg5	RSB933	267*	2,080
R5i-R1	GTAGTTGGTGTCAACAGGTTGGATC			2,346*	
Rpg5-F16	ACCTCGGTGCCACGCCCAAATGGTG	Rpg5	RSB762	512*	
Rpg5-F17	ACCACTGTGGTCAGTAGTCCAGTAG	Rpg5	RSB762	−390*	
Rpg5-F18	TCCTCGTATTCAGCGAGGAGTGATG	Rpg5	RSB762	−84*	
Rpg5-F19	GCCTCCCCTGGACTATTCGCTC	Rpg5	RSB762	−121*	
Rpg5-F20	ATGTCGTCGAGGTCGGGAGCTCCTC	Rpg5	RSB762	−145*	
ADF3-F1	ATCATACGAGCAGCTCCTGTC	HvAdf3		161,306	701
ADF3-R1	AACCAAGCACTCAATTCTCGAAGAG	HvAdf3		160,609	
ADF3-F1	ATCATACGAGCAGCTCCTGTC	HvAdf3		−79**	660
Q ADF3-R1	CGATCCCATGCGCAGGTATGCCAAG	HvAdf3		580**	
5112-F1	AGTCATGGAGGTGTACACGTACGTG			161,422	976
5112-R1	ATATGATTTCTGGTCGTCCGTCCTG			162,398	
5112-F2	ACGGATTGATTACGTGAAACATCAG			162,191	945
5112-R2	CTTCTCCTCCCTCAAGTCTTTCTTG			163,136	
5112-F3	GACCAACTCGAAGAAGGAGGACAAG			163,062	1,028
5112-R3	CGGTGGTCGTCATAAATAAGACGAC			164,090	
5112-F4	AAAAGTGGACGCTCAATGCGTCGAC			163,911	985
5112-R4	GCATGCTACTACTCGGCTGACTGTG			164,896	
5112-F5	CTCACCGTTGGACGGTCAAGCTGAC			164,739	1,008
5112-R5	AGTTGCACGTTTGAACTACCATCAG			165,747	
5112-F6	TTGGATTAGTTGTTCGACCATCGAC			165,590	1,008
5112-R6	ATTTGTATAAGCAATGTTGGTAGTC			166,598	
5112-F7	TTGAACACATGGTCAACATATTTTC			166,467	1,038
5112-R7	GGGCCACCGACACTGTAGCACTC			167,505	
5112-F8	GTAGCTGGACCGGCTCATGACCATC			167,435	1,070
5112-R8	TTAGCTTCATCTACGAGTCGAGCAC			168,504	
5112-F9	CTAACAGACGGTGGTGGAGGAAACG			168,461	1,017
5112-R9	TTGAATGATGACTCTAATGGTGTTG			169,477	
5112-F10	AGACTTGCATGCCTTTGCTAAGTAC		RSB1090	169,343	1,351
5112-R10	CCCCAAAACTCCATGCTTGGTACTC			170,693	
5112-F11	TCCGCTGAGAATTGGCATCCCCTACTAC		RSB1172	170,348	1,804
5112-R11	CCGCCTAGCATGCATTTGTCTCCAGTG			172,151	
5112-F17	CAGGCACTCGAGCAACAATCGTCAC		RSB1192	172,015	1,696
5112-R17	TGGTAAGCCTGGACCGTTTATACAG			173,710	
5112-F13	CGCCCGACGAAAGAGAACGACAATG		RSB1159	173,659	1,330
5112-R13	GGGCCACCGACACTGTAGCACTC			174,989	
5112-F14	CGCGTGCTTGCTGTTTTGTGGGTAC		RSB1161	174,659	1,482
5112-R14	GGCCCTTGCTCTGAAATGCTAATAAA			176,141	

The column labeled Clone refers to the plasmid clones generated by or containing the PCR amplicon. Positions designated with an asterisk (*) are determined by the first nucleotide of the *Rpg5* start methionine codon, and positions designated with a double asterisk (**) are determined by the first nucleotide of the HvAdf3 start methionine codon from Q21861 genomic sequence (GenBank accession no. EU878778). All other positions are determined by the Morex genomic sequence (GenBank accession no. EU812563). Amplicon refers to the size of the PCR fragments generated with the specified primer pair.