

Supplementary Tables

Supplementary Table 1 Primers used for the genotyping and the development of

CSSLs

Names	Chr.	Forward primer (5'–3')	Reverse primer (5'–3')	Position (Mb)
RM84	1	TAAGGGTCCATCCACAAGATG	TTGCAAATGCAGCTAGAGTAC	3.944672
RM8105	1	ATCAGCATTTTCAAGCCTAAG	GGCTGGCGTGTAGGATAC	4.051905
RM283	1	GTCTACATGTACCCTTGTGGG	CGGCATGAGAGTCTGTGATG	4.886049
RM259	1	TGGAGTTTGAGAGGAGGG	CTTGTTGCATGGTGCCATGT	7.445776
RM580	1	GATGAACTCGAATTTGCATCC	CACTCCCATGTTTGGCTCC	9.60565
RM8070	1	AAATGGACTCGCTCCTAAAC	AGGAGCGAATTTTATTGCTACT	9.605625
RM493	1	TAGCTCCAACAGGATCGACC	GTACGTAAACGCGGAAGGTG	12.423993
RM562	1	GGAAAGGAAGAATCAGACACAGAG C	GTACCGTTCCTTTGTCACCTTCC	14.77017
RM10986	1	TGGAGAGGAATGGGTGAGAAGC	CCTCTACAGTCCTCCACCAGAGG	18.93156
RM5422	1	CTTGCAGGGTTGCAATTAG	GAGGAGAGGATGAACATGAGG	20.413611
RM7056	1	GAAACGTGTAGCAGTACGCC	ACCAAGCTCTTCATCAACGG	24.770862
RM9	1	GGTGCCATTGTCGTCCTC	ACGGCCCTCATCACCTTC	24.983072
RM2318	1	CTTTTGCTCATCCATTCG	CCTCTTCATGCGATAAACAT	25.798911
RM7419	1	GAGGAGAAGAATGCTGGCTG	AGTGCTCACCGAGTCACTGG	29.458186
RM128	1	AGCTTGGGTGATTTCTTGAAGCG	ACGACGAGGAGTCGCCGTGCAG	32.494618
RM6950	1	GTCTGTGTCACTAACCATGCC	CATGGCGTCTCAACTACACC	36.265108
RM5389	1	TCTTGCATGAGAGCCAACAC	GCTATTGCGCGAGATTATCC	37.489316
RM5759	1	TTAACGGTCGGGAGTCAAAG	CATCGTCTTTGTCAGATGGC	40.77644
RM3482	1	TTGTTGTCAAGCTACGGTGG	CTGCTTCGTGATGTTGTTGG	41.475905
RM5536	1	GAATCCTGCAGGGATGAAAC	ATACTAATCCCGTCATCCGG	42.9627
RM3362	1	AAGTTGAAGCAGTCGCCAAC	GAATTGCGTGGGATATGGAC	44.839004
RM7451	2	TAATACGAGCAGCGATCGTG	GCTAATTGCAGCTTGTGTGCG	0.651977
RM5622	2	TCTTCGAAACAAGCAGCTCTAGG	GATAGGTCGGATGTGTGATTTGG	4.273744
RM5340	2	TGGGCCCTAAGTCATATTGC	ACCCAACGAGATGTACCTCG	7.512357
RM145	2	CCGGTAGGCCCTGCAGTTTC	CAAGGACCCCATCCTCGGCGTC	7.736086
RM5699	2	ATCGTTTCGCATATGTTT	ATCGGTAAAAGATGAGCC	9.010558
RM1234	2	ACACCAGAGTACATAGGCTAGAGG	ACTGCTGATGATCTGGCCAC	11.365401

RM6374	2	TGAGGACGCTGATTGTCAAC	GCTGCCCTATTATTTACC	15.966863
RM13297	2	GATTTGGGCATGATCCTAAGAGG	GTGCATGGAACAATGGAAGAGC	19.443027
RM13345	2	CTTCTCCTGCTCCTCCCGATCC	CTTCCATGGCTGTCCGTCTTACC	20.19989
RM8254	2	AAAGGGACCCACTTGTGAGC	GTCGAGGATGGATCGATGG	20.606779
RM13423	2	GTTGGTGAATGGTGGAGTGAGC	ACCCACGTAATCCCATCCTCTCC	21.919407
RM5427	2	TGCTGTTGACACTTGACAGGTAGC	CACAATTATTGCGGCTCATCG	22.382841
RM5651	2	CATGCTGATGCGATTAAGACTGC	CTAACCTGTGCCTTGTGGATGG	24.431973
RM5631	2	CGTCCAAGAAATATTGCAGT	GTGAGACAGAATCCTTACGC	29.160357
RM3685	2	AAACGTATTAGTGCGCCAG	TCTCGCTTCTCCTCTCTCC	30.181744
RM208	2	TCTGCAAGCCTTGTCTGATG	TAAGTCGATCATTGTGTGGACC	36.028548
RM6312	2	TGCCTCCTTATCAATGGAGG	AGCAAAGCCTTGACAGAGAAG	36.27759
RM3372	3	CAAAGAATCCAAGGAGGCCAAAGC	ATGCCGATGAGCACCCAGAGG	1.435857
RM7072	3	CTAATCCTATTGATTTAGGG	AGTCTAGTGTCAACCTTCTC	2.548837
RM5474	3	GTGGGTTTGTGTTTGGAGAGACG	GTGTTGGTGAAGCATAGCAGTTGG	3.782596
RM7576	3	GTGGGAAGAAGAACATCAACTGG	GCACACAAGATAAACCCAATCAGC	6.106738
RM282	3	CTGTGTGCGAAAGGCTGCAC	CAGTCTGTGTTGCAGCAAG	12.459437
RM6959	3	TCCTATGGAGGATTGTTGCC	CGGAGGAGCAGAACAAAAAC	15.058968
RM1164	3	CGTTTCTCCGAGAAAAGTCG	CAAGGTGGTCGTTGAGGC	15.412771
RM7642	3	TTAGATCACGATACTCAGGGATGC	CGAAGAAAGAGAGCACGAAACG	19.268082
RM7370	3	GTAGCTGCATCTTGACAGTGC	CATCGGGCATAGTATGCATG	21.9107
RM6832	3	GTTGTAAATGCCTGAGTGC	AAAGAGCTAAACCGCTAGG	23.162608
RM16	3	GTGCGCCAGGAGTAGTTGTCTCC	GACGTGTACACATAGCCAAATCAT CC	23.88784
RM15456	3	AAGTAGGCGATGGCCAGGTACG	GGATCCTCGAGGTGAATGATCG	24.172259
RM3513	3	CAAACATGGCCTTGTAGTAGACG	CTGTGGCTATGCCTTTGGTTGG	25.874919
RM135	3	TCCATGCTCTTCAGCTTCTGG	GCTTCTACTGGAGGAGAGCAGAG G	28.179166
RM8277	3	AGCACAAGTAGGTGCATTTTC	ATTTGCCTGTGATGTAATAGC	29.57228
RM8210	3	GTCCCACATGTCAGGATG	ATCTGCTACTTGTGGAGGAG	33.092802
RM3346	3	AAGAACCAGAGCAAGATCGG	CTTCCAATTCGATCGCTAGC	34.175287
RM130	3	TGTTGCTTGCCCTCACGCGAAG	GGTCGCGTGCTTGGTTTGGTTC	34.244243
RM3564	3	CATAAACCGCTCGGCATTG	CTGACTCACAAGACAACAGGG	34.282475
RM3684	3	TATTTACCTTCTGCCACG	GAATGAGGTGGAGGATCGAC	35.474139
RM6712	3	GCGCATCATCACTTCATCAG	AGATGAGCCTATCAGCTGCC	36.08458
RM7585	4	CCTCCTCCCTCGACTACCTC	GGTGTGTCGGTGTGATATGC	0.219925

RM335	4	GTACACACCCACATCGAGAAG	GCTCTATGCGAGTATCCATGG	0.679949
RM518	4	CTCTTCACTCACTCACCATGG	ATCCATCTGGAGCAAGCAAC	2.021865
RM16535	4	ACGCGGTAGTCCTCTTCAATGTCTG	GGCGCCAACCCCTTCTACTACC	8.064346
RM16626	4	ACATGATTGCTGGCTTGCTTACC	GCCACGCAGTGTGTTTCAGC	12.77457
RM401	4	TGGAACAGATAGGGTGTAAAGGG	CCGTTTCAACAACACTATAACAAGC	13.210938
RM273	4	GAAGCCGTCGTGAAGTTACC	GTTTCCTACCTGATCGCGAC	24.446998
RM3839	4	AATGGGACCAGAAAGCACAC	AAAAAGAGCATGGGGGCTAC	24.488594
RM3367	4	GGATCCATCCATCCACTGAC	GGATATGTGCTGCTGTGTGC	24.683536
RM252	4	TTCGCTGACGTGATAGGTTG	ATGACTTGATCCCGAGAACG	25.762798
RM241	4	GAGCCAAATAAGATCGCTGA	TGCAAGCAGCAGATTTAGTG	27.441089
RM7187	4	CAGCGAACGTGGTGTCTTC	CCCACACCAACTTCTCGC	28.049175
RM3687	4	CTCCTGAGAAGTGGGGACTG	AGTCCTCCATGCATGTGACC	31.882179
RM3306	4	CCTTTTACCTTTCATAGCAA	ACAAGAAGATGGTGAGTGAT	33.471066
RM280	4	ACACGATCCACTTTGCGC	TGTGTCTTGAGCAGCCAGG	35.574685
RM7302	5	AGGAGGAAGAAGAGATTGCC	CCCACACGAGATGAGATTGG	1.955936
RM267	5	TGCAGACATAGAGAAGGAAGTG	AGCAACAGCACAACCTTGATG	2.859504
RM7444	5	AATGGTACTACCGCCAGTGC	GGATTGTGATGTTCTGAGG	3.337511
RM5874	5	GAAAAGATCCTGGCTCGTTG	GCATCATCGCCAGAGCTC	3.509995
RM3777	5	TGCTTATGTCGCAAGACTAG	ATCTCACCTTCCCTACAA	4.152113
RM6082	5	AACCCTAGAATCGGCGCTG	CACCGATGACAACGAGGAC	8.910967
RM249	5	GGCGTAAAGGTTTTGCATGT	ATGATGCCATGAAGGTCAGC	10.787644
RM7568	5	GAAGCCAAGCCAGTTGAGTC	ATGTGGAAGAACATCTCGCC	19.497387
RM305	5	TACTGCCAAAGGCGAGCTTC	GTGAGAGGCTACAGCTAACC	21.013816
RM5970	5	CCCATCTGGTTCACCTTAC	AGGAGCAGCCTTTTGTCTTC	24.056029
RM421	5	AGCTCAGGTGAAACATCCAC	ATCCAGAATCCATTGACCCC	24.086294
RM274	5	CCTCGCTTATGAGAGCTTCG	CTTCTCCATCACTCCCATGG	26.97217
RM480	5	GCTCAAGCATTCTGCAGTTG	GCGCTTCTGCTTATTGGAAG	27.45768
RM8109	6	CATTGTTAAGTGCATAATTGG	ACCATGACATGGCACATT	0.485951
RM7420	6	TGAAGGAAGGAAGGACGATG	ACAAAGCAAGCACCCAGAAG	3.950725
RM253	6	TCCTTCAAGAGTGCAAACCC	GCATTGTCATGTCGAAGCC	5.425517
RM276	6	CTCAACGTTGACACCTCGTG	TCCTCCATCGAGCAGTATCA	6.23015
RM5531	6	TTTGTGTTGGTAAGTTGCTTC	TTAAGGAGAGTGTTTTCTTTCTC	7.176959
RM3183	6	GCTCCACAGAAAAGCAAAGC	TGCAACAGTAGCTGTAGCCG	12.516179
RM6818	6	GTCGCATTCTGCTCCACC	ACCATTTCCAGATGACTCGG	17.459525

RM3	6	ACACTGTAGCGGCACTG	CCTCCACTGCTCCACATCTT	20.37742
RM1370	6	AAACGAGAACCAACCGACAC	GGAGGGAGGAATGGGTACAC	29.410606
RM340	6	GGTAAATGGACAATCCTATGGC	GACAAATATAAGGGCAGTGTGC	29.477203
RM6811	6	GGTGATCACCAGCAACACAC	AGCGTGTGACTTCATTGCAC	30.106848
RM3509	6	GTGGTACATCCTCAAGGATCG	GTTGAGGAAGGGGGCTAGAG	31.849017
RM5463	6	AGTGCCTGTTTGTTCCTCTTCG	CATGGTCAGAGCAAGTTAGTGTGG	31.86304
RM427	7	TCACTAGCTCTGCCCTGACC	TGATGAGAGTTGGTTGCGAG	2.711983
RM6872	7	GGATGAACACTGATGATGGC	ACCTCCACCACGATATCCAC	4.692642
RM3583	7	TACAATTTGGCGACCTCCTC	GGATGCCATGTCATCATCTG	8.078023
RM542	7	TGAATCAAGCCCCTCACTAC	CTGCAACGAGTAAGGCAGAG	13.373244
RM6449	7	CAAGAGCAGCAGCTTGACAG	GCGTAGGGACTAGGAGAGGG	16.071109
RM7110	7	GCGATCTCTGTGTTTATTG	ATTAACCGTTGAGATGGTG	17.514477
RM5380	7	CCACCCTGTTTTCATCTCGC	ATGGCGATACCACCACTCTC	20.022445
RM346	7	CGAGAGAGCCCATAACTACG	ACAAGACGACGAGGAGGGAC	21.705279
RM7564	7	ATGCATGTGAGCATGCTAGC	AAATACCACTCCTGCTCCCC	23.417266
RM5623	7	TCACGTCCTCGTACAGGATG	CTCAAGAAGCTCTGGATCCG	23.77082
RM1132	7	ATCACCTGAGAAACATCCGG	CTCCTCCCACGTCAAGGTC	24.645713
RM8261	7	GACGACTGGATGGTACGAC	TGCTTCTCCTGCAAACAC	26.52775
RM5426	7	GAGAGTAGTGGCTGTTCCGC	GCGGTTTCGATCTCTACGAG	26.591728
RM6216	7	GGAGCGCATGTGGAAGTC	GTTGAACTGATGAAACCCCG	27.057741
RM3555	7	TGGAAGTTTCTGGCGATAG	TGGTTGGACTGAAAAGTCCC	28.551757
RM1306	7	TGCCAATTACCTTCCCGTAC	TGCTCCGTATTGCTGCTATG	29.6082
RM248	7	TCCTTGTGAAATCTGGTCCC	GTAGCCTAGCATGGTGCATG	30.001194
RM408	8	AATTGCCCAACGAGCTAACTTCC	TGAGCTGTTTGTGCTCTTCTACTTC G	0.125301
RM152	8	GAAACCACCACACCTCACCG	CCGTAGACCTTCTTGAAGTAG	0.682983
RM6356	8	TTATCTGCCACCTGAGTCCC	ACTTGGCGACTCTGATCTGC	1.560934
RM6863	8	GCTGCAGAATTAAGGAGAAC	TGCTCAAATAATCAGCTCC	2.011435
RM22491	8	TTGAGCGACGCAAATAACTACCC	CGGACGTGTTCACTTCATCATAGG	4.504859
RM310	8	CCAAAACATTTAAAATATCATG	GCTTGTTGGTCATTACCATTC	5.115845
RM22694	8	TTAGCTGTATTTAGCCCGACATAGCC	CGCCGGTTCTTCTCCTTAGG	8.969204
RM7027	8	AGGACCTGGACTTTATGGGC	CCTGCACTGCTCCACAGTAC	15.93567
RM6215	8	CAGCAGAGAGATGACGCAAG	AAACCCAAAACCTCGTCTC	19.153771
RM342	8	CCATCCTCTACTTCAATGAAG	ACTATGCAGTGGTGTACCC	20.048272

RM223	8	GAGTGAGCTTGGGCTGAAAC	GAAGGCAAGTCTTGGCACTG	20.740837
RM7356	8	CCAAGGACACATATGCATGC	GCAATTCATGGCGCTGTTC	21.370836
RM210	8	TCACATTCGGTGGCATTG	CGAGGATGGTTGTTCACTTG	22.562614
RM6976	8	CTCATGGGGCTTCTTCCC	CCCATTGGATAGAATCCCAG	23.646402
RM256	8	GACAGGGAGTGATTGAAGGC	GTTGATTTCCGCAAGGGC	24.361373
RM447	8	CCCTTGTGCTGTCTCCTCTC	ACGGGCTTCTTCTCCTTCTC	26.637802
RM6845	8	GTGACGGCAAGAGGAAGAAG	GTTTCGACAGGAACGCCAC	27.650919
RM264	8	GTTGCGTCTACTGCTACTTC	GATCCGTGTCGATGATTAGC	28.014637
RM6196	9	GGGCACGGACTACCAAAGGAAGC	ATCAGGCCCAGCACCCAAACC	6.015762
RM444	9	GCTCCACCTGCTTAAGCATC	TGAAGACCATGTTCTGCAGG	6.492145
RM219	9	CGTCGGATGATGTAAAGCCT	CATATCGGCATTCGCCTG	8.454131
RM6051	9	AGGCTGATCCAAGATCCATG	CCCGGAGGCTGATTCTTG	13.436113
RM3700	9	AAATGCCCCATGCACAAC	TTGTCAGATTGTCACCAGGG	16.082099
RM7048	9	CAACCCTAATTCACGCTC	GACTTCACTGGCACTGGATG	17.590063
RM6570	9	CGATCCGCATCTCGAATC	CCTCCAAGGTCTCATCTC	19.230946
RM3164	9	TCCTCCTGCTAGCTGCCTAG	TCGCCTTCCTTTTCACTCAC	19.575415
RM5661	9	GTTGCTGGGCTTGATCTTTG	CTGTCATGGCCCCTCATTAC	19.615442
RM160	9	AGCTAGCAGCTATAGCTTAGCTGGA GATC	TCTCATCGCCATGCGAGGCCTC	20.442399
RM215	9	CAAAATGGAGCAGCAAGAGC	TGAGCACCTCCTTCTCTGTAG	22.021245
RM2144	9	ACATTATGAAACGGAGGAAG	GAAATGATGCATCAGCATTAA	23.041633
RM7492	10	AGATGGTTGCCAAGAGCATG	GTCACGTGGCGATTTAGGAG	0.034023
RM6370	10	TTGACAAGCCACACACACAG	GTCCTCCCTTGGTTCTTTCC	0.324488
RM216	10	GCATGGCCGATGGTAAAG	TGTATAAAACCACACGGCCA	5.01684
RM5348	10	AATCCGATAGGAGTACCGCC	AAGTGTATGGGCTGGAATGG	8.754129
RM25294	10	GGGATTACTATGCGGATTAGG	ACTTGGAGAAAGAAAGCAGAGG	12.090313
RM8201	10	TCTGTTTATAAGCGCAGCAC	GCCGGCGAGCTACTACTAC	14.190714
RM5620	10	TCGACTTGAAGCATCACACC	TCTGAAATGTCAAGTGGGCC	17.932217
RM3773	10	CTGGATGAAAGGATACAACA	CACATTATCTGTCAAGGTCC	20.42206
RM3451	10	CGGCGAGATAACAATTCTCC	GCGTGATGATATGGTATCGG	22.09748
RM228	10	CTGGCCATTAGTCCTTGG	GCTTGCGGCTCTGCTTAC	22.769983
RM333	10	GTACGACTACGAGTGTACCAA	GTCTTCGCGATCACTCGC	22.898952
RM6824	10	GAGAGAACCTGGTGGTGGAG	AGTGGTAGAAGATCCGAGATCG	23.57011
RM286	11	GGCTTCATCTTTGGCGAC	CCGGATTACGAGATAAACTC	0.383856

RM1812	11	CAGCTAGTGAGCTCCTAGTG	GCTAACCCACCAACTTATTC	2.391251
RM6544	11	ACCACTATGCACCCTTCGTC	GAATGCTCTGCTTCGTTCC	3.841072
RM167	11	GATCCAGCGTGAGGAACACGT	AGTCCGACCACAAGGTGCGTTGTC	4.060463
RM5704	11	AACGAATGATTAACATCTA	AAGCAGAGTCAACATATTTA	5.464507
RM26281	11	AACAAATCCACATGACGATGC	GCCCTAGTCAGTCCCTCTGTAATCC	6.474595
RM3625	11	CTTGCAATTCAATTGCTTAC	GGTGGCCTAGTGAAACTAAA	6.652024
RM4862	11	CAACTTTCTGGCATAAACTA	TGGTGAAAGATATTTTCAGAC	10.030624
RM6091	11	GCTGTCCTGTCCTGAATCC	TGGTAGGCTGGTGACATGC	15.692774
RM229	11	CACTCACACGAACGACTGAC	CGCAGGTTCTTGTAATGT	20.701889
RM1341	11	AACCTGGAGGTGCTGGTCTC	TTTCTCCCCCAACCAC	22.011871
RM26999	11	CGGCTTCGGCTTCTTCTCC	GACACTCCCGTTTGTATAACTGTTG C	24.483447
RM27154	11	TAGTCGGGCATCTCCTCTCC	GTTACCTCCGATGAAGGCAAGG	27.073314
RM1233	11	TTCGTTTTCTTGTTAGTG	ATTGGCTCCTGAAGAAGG	28.848416
RM224	11	ATCGATCGATCTTCACGAGG	TGCTATAAAAGGCATTCGGG	29.515977
RM1880	12	ACCACTAAATAAGCACATAC	GGCATCATACATTAATAAC	0.747083
RM20	12	ATCTTGTCCTGCAGGTCAT	GAAACAGAGGCACATTTATTG	0.970514
RM6296	12	TCTTGCCTCGCTAGGGTTAG	CCCACGTTTCTTGTCTC	3.200759
RM27706	12	ACTCCCTCCGACCATCATCC	ATACGGGAACCCTCACGCTACC	5.029946
RM2935	12	CAGCAAATTTGTTACTTATG	TGCTATGTTTTTTATAACG	7.425146
RM101	12	GTGAATGGTCAAGTGACTTAGGTGG C	ACACAACATGTTCCCTCCCATGC	8.828479
RM27902	12	TATTCGTCGTCGTCTCGTCATCC	GTTGACGTTGACATTTGCAGTGG	9.596568
RM1337	12	GTGCAATGCTGAGGAGTATC	CTGAGAATCTGGAGTGCTTG	11.935058
RM1261	12	GTCCATGCCAAGACACAAC	GTTACATCATGGGTGACCCC	17.681919
RM7344	12	GACTGCCTCAGCCTTTTCAC	CGACGCCATATATGCCTTTC	18.094758
RM277	12	CGGTCAAATCATCACCTGAC	CAAGGCTTGCAAGGGAAG	18.46385
RM519	12	AATTTCCGCGAAATCAGCATCC	TCATCTGGACAGTCGAGGTACGC	20.077119
RM7376	12	TCACCGTCACCTCTTAAGTC	GGTGGTTGTGTTCTGTTTGG	23.680867
RM1103	12	CAGCTGCTGCTACTACACCG	CTACTCCACGTCCATGCATG	23.776938
RM5609	12	CGCCAGTGTCGAATATGATG	TCTTGGTGCAGTAGGTGCAC	24.204806
RM6953	12	ATGTCTCAACGGACGTAGGC	CTTGATGCAAGAACTGCTGC	26.38981
RM17	12	TGCCCTGTTATTTCTTCTCTC	GGTGATCCTTTCCCATTTCA	27.214867

Supplementary Table 2 Primers used for the fine mapping of *qSH1*^{JCQ}

Names	Chr.	Forward primer (5'–3')	Reverse primer (5'–3')	Position (Mb)
H6	1	GCCATCGCCGCAACATAAA	GCCTTCGGTTGGTCACTTGG	37.254933
RM5389	1	TCTTGCATGAGAGCCAACAC	GCTATTGCGCGAGATTATCC	37.489335
H8	1	GAGGCGAACGAAAGTCAC	GATCAATTTTATCTAACGGT	37.842191
H15	1	ACAGGGACGATCATGTATGG	AGTCTTTGCGTCAGTAGTAGC	38.141138
Jm36	1	GCAAACGCACGCAAGCGAC	GGTTTCCGTGCTGGGAGTTGA	38.157727
Jm1	1	GATGAAAGAAAGCGGTGGTC	CACTCTTCTATCTTATCATTGTCCC	38.164145
H16	1	CGGATGACACGGGATGAG	TTCGCAAATAGAAAGAGGG	38.237034
Jm23	1	GGTGCGAAGACAGACAAAG	CGTCGAACCTAACGAAAGA	38.255949
Jm26	1	ATAAATCGACCTAGCACAA	TCATCGGTCAAACATCAAG	38.357387
H23	1	GTGGGACCCGGTTTCAGT	GAGCGATATGGCTAGGAGATG	38.751828
H24	1	CAGGCACGATCACGGAAAG	CTCGAAATGGGAGTCTTCAAAT	39.031549

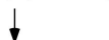
Supplementary Table 3 Primers used in the quantitative RT-PCR of the seed shattering related genes

Genes	Chr.	Forward primer (5'–3')	Reverse primer (5'–3')
<i>qSH1</i>	1	AGGCTTGACACGCAACCAGGTATC	TCTCCACCATTGGCTTCCACAAC
<i>OsCPL1</i>	7	TGCCAAGAAGAAGAAGTCTGTTGG	TGCGGATATCAACTTCCTTCCAC
<i>sh4</i>	4	GCCAGAACCAGTGCAATGACAAG	TCGTAGTCGCGGACCTTCTGTAG
<i>SH5</i>	5	CTGTTTCGGTTCTTCGTGCATGG	GCTTATCGCTGTCAGTTGGATACG
<i>SHAT1</i>	4	CTATGGCGTTCGACCTTGACTG	GGTTCGAGTTCTGGTCGAACTTAG

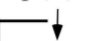
Supplementary Figures

Supplementary Figure 1 Breeding scheme for the development of CSSLs. The CSSLs were developed from the *japonica* landrace rice Jiucaiqing in the *indica* rice IR26 background. MAS: Marker assisted selection.

Jiucaiqing (P1) \times IR26 (P2)



F₁ \times P2



BC₁F₁ \times P2



BC₂F₁ \times P2



BC₃F₁ \times P2



BC₄F₁ \times P2



BC₅F₁



BC₃F₂ BC₄F₂ BC₅F₂ \rightarrow CSSLs

MAS



BC₅F₃