

TableS4 Details of all designed markers in the fine mapping region of A08

Primer Name	Forward Primer (5'→3')	Reverse Primer (5'→3')	Product Length(bp)	Start position(bp)
SSR1	ATCACCTTGATTGGCACACA	TAAACAAGCCATGCAAACA	209	7267
SSR2	GCATCAATTCATGGTGTCTT	TGAAATTTCCACTAAGGATGAA	235	7906
SSR3	AGGGAAAGAAGCTGAGAGGG	TTAACTTGGGCCAGATACAAA	198	8899
SSR4	TTTGCTTAAGTCTATTCGGTTGA	GGCTTGAGCTTAACCCGTTT	286	35886
SSR5	AATGACACTCTCCCAGCAGAC	TGAAGTGATGATATGGCACTTTG	169	36414
SSR6	TTCTCTGAGCTTCTGGGAT	GGGACGTCAAGTAAATTAATCCT	278	61694
SSR7	AAACAAAGTTGATGGCAAA	TTGGTTCGCTATCAATCTAAA	302	68265
SSR8	TTAAAGGTCCAACATCGCGT	TGCATGTATAGGTGAATCTTGAGG	251	78387
SSR9	GACCATGTTAATGACAACGATGA	TGCGCACTATCACATACCGT	182	79010
SSR10	ACCACATGACACATGGTAATTAGA	CCAATCAATGCCAGTCAACA	133	81310
SSR11	GAATTCCTCACAGCTCCAA	GTCTCGCTCGATTCTAGG	329	82272
SSR12	GGGCCATTAAGCAATAGGGA	GGGAACCAACGAAGTCAAGT	350	88280
SSR13	AAGCATAATAGCCCGTATGACAA	TTTAAACGGCTTACTTCATGTTGA	181	88901
SSR14	CAATCAAGATCTGAACAAAGTCG	GCTCAAGCTCGACCTGATCT	259	103185
SSR15	CTCTCCATTGCCATCACTT	TGGTTGGTATATGTAGTTGAGGGA	225	104037
SSR16	ATATGCATGGACGGATGGAT	CCGAGTTCGAAGCTGAAAGT	190	112969
SSR17	GTGCCAAGAACAAGGAGGAG	GTGCAATATTCATTGGACCG	296	114472
SSR18	CACGAGTGCTAATGGGACAA	ATCCAGGCAAAATGCGTACT	190	114727
SSR19	GCTAACACGCTCAGCAAGTG	TACTGGTGTCAACGATCCGA	293	115407
SSR20	TCGGATCGTTGACACCAGTA	ATCCTCCTCCTCCTCCTCT	195	115718
SSR21	ACGCATAAACGAAGTCAAGCA	AAATTCAGGAAAGTCAAGCA	322	115733
SSR22	ATTCGGATATGCTCAGTGCC	TTGATGGTTAGTGCAATCCG	312	130308
SSR23	CCAATTGGAGAACACAAATTA	CCTTGGGATTTAGGCTTTCC	251	133736
SSR24	GTTTGGTGGCTTTGGTTGGTT	CGAAGTCAAACCTATATTCTCCAA	224	135323
SSR25	TTTGGGAGTACAATTATGTGAAA	CAAATCATGCTAGTCCCTTTG	239	139953
SSR26	CTGTCGATCCCTCCGTGTT	GATTTCAATGCCTGATCGCT	313	141729
SSR27	TCGATGTTATATCAATTAGGTCATTC	CGACTTTAGATCTCATATGGCGT	273	144282
SSR28	AAATGCTCCGTTTCCATCG	CCTTACCTGATTCCCAA	267	178822
SSR29	TTTGGGAAATCAGGTGAAGG	AGCTGAATGAGCAGCAAATG	264	179193
SSR30	TGCAAAACCCAGTTATGTGT	GGTTAAAGGAGATGGGAGGG	250	189112
SSR31	GCGAATTTCTACTCTGCAA	CACACATCAAATCTAATTGGAATAC	251	201766
SSR32	CTCATCCTCTCCATTGGCAT	ATCAATTCACATCAAGCC	283	216626
SSR33	AAGACGATGAAGAGCACGGT	GAAAGTCCACAAGCTGTCC	205	217094
SSR34	AAATTGTTAAGTTTGGCCGC	CACTCTGCTCCACCATCAA	241	217621
SSR35	TGTCATTCTATCACAGCAGCA	TTGTTAGCAAGCATTGCTCG	282	219094
SSR36	TTGATAAATTCGATTGTTGATTG	CCCTAGATTGCAATGATGA	313	234864
SSR37	GGGAGGGACTATGAGCAGTTC	AAGTTAAGCCTCATCACATCAA	126	235763
SSR38	ATGCTTGAACCTGCCATTA	TCCCTCAGCAACAATTGAA	262	251584
SSR39	AAGATTCAAAGTTAGGACGTATGG	AAATCTTAAACTCTCGAAATGATTG	239	258303
SSR40	AGGGAAAGCGTTTCCAGTAA	ATGAATTCGGCTGTCACTC	325	266237
SSR41	CGAAGAGGCTGAAACCCATA	ATGTTGCAGTTGGTGTGAG	341	268367

SSR42	TGCATGCCTGATAATAAGCAA	CAGGGTCTGTTTCAGAAATTT	202	268972
SSR43	AGTGAAGAGTCGAATTTGCCA	AGCTGAATAGTTTGATGCATTATTT	298	276049
SSR44	TCACCCACTGTAATCAGTGCTC	TGGGTTTGAGTGTGCTGAAG	173	278986
SSR45	GTGCCAAACAACAATCTCCC	TGCATGTGGAGTTGAACCAT	187	280568
SSR46	TGTTTGATGCGAGTTCACCT	CATGTGAACCTTCTATTGCTTT	254	282267
SSR47	CCCAACATTAGCGGTGTTAG	GTGAAACGGAGGGAACCTCA	137	291474
SSR48	AGCCCAATTAGCCCAACAAC	GATTTACAGGCTTTGTAGCCG	194	292801
SSR49	GGCTGAAATGGGTTAGGTCA	TTGAAAGTATTTACATCGGATAATGT	187	298359
SSR50	GGCTGAAATGGGTTAGGTCA	TTGAAAGTATTTACATGGGATAATGT	187	299425
SSR51	CACGGAAGTACACCCAACCT	GAGAAGCTACGAATGTCGGC	286	301593
SSR52	GGACTAAGACCATTACTACTCCATAG	TTGAAAGTATTTACATGGGATAATGT	273	302988
SSR53	CGGCCAGTTGAATAGGAAAC	GGCTAAGGCTACTCAATCGC	298	303757
SSR54	GCCTTAATCCTCAAATTTCCC	CCCTAAGTGCCATGTGTGTG	250	317941
SSR55	CGAACACACAAAGACCCAAA	TGAAATTCAAATATGAACACCCAAA	296	320488
SSR56	TGACCTTGACCCGAAATAA	AAATCAAAGTTTATTATGCCAAA	149	321626
SSR57	TGATATTGGCGTGGGAACCT	ATATTTGGCCCTCAACCTTT	287	322245
SSR58	TTGCAACTGTGGTACTTACAGC	GGCATGAAGGAATGCAGATT	165	329336
SSR59	CAGTCAGATTGATTGGACTGAGA	TTGTGCACACCATCACTTGT	322	341123
SSR60	TTCTGTCTGGGTTTGCTTT	CCGGAAGTTTAAGGTTGTGTC	281	342137
SSR61	CCGAACCACGTAATCCTTG	TGAGTACTCAATACTCAAACCTCG	227	349626
SSR62	AGCCCATTTGATGCAATCTG	GCCAAATCGAAATCGAGAAC	180	357760
SSR63	CCAAGCTCAAGAGGGAATTG	CGAATGGAATCGATGAAGGA	339	361419
SSR64	TAGCTCATCGGTCCCAGTTT	GCACGCTGCATACCTACAT	228	366943
SSR65	CACTCGGCCATAAATTGAT	CCGCCAACTTGGAATCTAC	289	372200
SSR66	CGGGCCATGAACATCTCTAA	ACAGTAACAGGCGGTATCGG	344	374080
SSR67	ATGCCAGTAGGTGTTGGTCC	GTCCAGGATACGGTGTGCT	337	375142
SSR68	ATGAGGAGGACGAGCAAGAA	CAGCCTGTGAATCTGATGA	255	377194
SSR69	ATGAGGAGGACGAGCAAGAA	TGCCTTCTCAGAATTCGCT	336	377214
SSR70	TTTATGATCCCTTACCCAA	GCATACAGCTGAATATATTAACACTCA	216	398847
SSR71	TGAAGGAAGAAGGGATAAATTCA	AGAGCCAAAGGGTAGTGGGT	154	419165
SSR72	TCGATGGTGTATTTGGCTCA	ATGCTTTGTTCCACAGACA	299	424052
SSR73	ATTGTCGGTACAGGAGGACG	TCCTTGTGCAAGAAGACGTG	221	424456
SSR74	AAATCCAAGAGAATTGAGTGATTA	GTTGCTACTTGCCACGTTGA	197	425765
SSR75	CATGTTAGTCGGTTGGTGACA	TGCAGATCACAGAGAATGGC	302	437510
SSR76	TGCCATTCTCTGTGATCTGC	ATGATTCCAACCCGATTCAA	176	437770
SSR77	CTGATTCTCAAGTGGCACGA	TTGCAAATTCATCTCCCTTTG	156	440278
SSR78	GGCACTTGGCATTGTTTCTT	ACGGCAAAGTTGACGGAATA	223	444245
SSR79	CCACAATCAAAGTTAATGCGTA	GAGCTCTAGTTTAGTCGGGTGG	225	446768
SSR80	TCAACTCAATGCACGAGGA	GCAAACAGCTCTGTGAACGA	125	455339
SSR81	CTGAAACCCCTCATTTCAGC	GGGTCTCTTCGCCGTAGTC	157	459808
SSR82	CCTTCCATGCATATTGGAAA	CAAAGCACCAATTTCAAGG	283	469010
SSR83	CACCTTGAAATGGGTGCTT	GCTTGGTGACCCTCTAGCTG	191	469261
SSR84	AGCTAGAGGGTACCAAGCA	CATCCCACTAGCAGCATTGA	162	469435
SSR85	TGTTAATCATGTGATTATTGAGTGTG	CATGAACTACCACGGGTTT	257	470082

SSR86	TGTTGTTAAATTGCTTACTTGGA	TCGATACCTACCAAGGTTTGAA	310	485966
SSR87	TTATTATCCGCCAAACAGC	AAC TTGGCAGGTGGATTGAT	325	486744
SSR88	TCCTATTGCTGGCGAGATT	AAGTGGCCTGACCATACAC	316	490174
SSR89	TGAACGTATACGAAGATTGGTT	AAGTGGCCTGACCATACAC	253	490296
SSR90	AATGCCTTACCTTTGAAATGC	TGGACTTGTTCTTCTTGTTGC	136	491476
SSR91	AACAGGAGCATTGATGCAAA	GCTGTGAAGCTGAGGCTAT	306	498723
SSR92	GTATCTGCAAGGGTGGAGGA	AAGATACGCAATGGCAAAGC	203	520481
SSR93	TTTGAGTTTAAATTGAACGGATTT	TCTTGGTGGTGGAGTTCACA	160	544219
SSR94	TGTGAACTCCACCACCAAGA	TTCACTACCATCATTCCGGGA	259	544357
SSR95	TGTGAACTCCACCACCAAGA	TTCACTACCATCATTCCGGGA	259	544421
SSR96	GGGCAAATGCAATACGAGT	AACCAATCAGCATAGCCAC	275	546417
SSR97	TTGTTTCGCAACGAATTAATG	TTAACCTTACTCCTTCGAACCAT	237	547865
SSR98	AATTGTGGGATCTGCTGCAT	TGGCGTGGACATGTACCTTA	323	551918
InDel1	GGCTGCCACCCCC	CCTCACATTTAACGTCAAGCTCAC	356	76294
InDel2	CCAAACATCCATGTGGACCAATTTG	GGTAATAACTGTCTTTATGAGCCCTTTTC	360	501736
InDel3	CATCAACGTGGCAAGTAGCAACA	CCCAGGGGCAAAAAAATTTGGG	372	525615
InDel4	GCCCCTCCAGATTTGCCTC	GGTCCAAATTGTCTAAAATAAATCCGTAGAGAC	565	531453
InDel5	CGAATCCTGAACCCCAAACCTAAAC	CATCACCATGGCAACAACCTCC	376	532619
InDel6	CGCGAGGACTAAAATTTGAAAGTTTGA	GGTAAGGATTGGGGCATTAACTGG	178	534201
InDel7	CCATAATTAGAGTTTCACGTGATAAATTGTACC	GAGTTTTGTGTCACCACTCAATCG	256	534829
InDel8	GGCTTGTGCAGCCATTGTG	TCGTGCATTA AAAAGAACATGCTAGG	377	640157
InDel9	GATTCCCTTTCATCAAATATTCTATGTTAGCG	ACTCAAATACTTAGTATACCATATTAGCCTCTTTC	536	650514
InDel10	AGTAGGTGCTACAAAATCAGCTCC	CTGTTTTAGCATTTTGGGTGCTCTTTTC	327	664027
InDel11	CACAACATTTAGTAAATAGAAATTTGGGCAATCC	GGTTATTGACTTGAAGAGGGGGG	252	666443

Note: markers in highlight are polymorphic between two mapping parents.