

Table s11 Polymorphic InDel/SSR markers developed on *qAB9.1* interval

Name	Forward 5'-3'	Reverse5'-3'	InDel sequence	InDel location
GSA08946	AGACGCGAATCCTGTT TTTC	CTTTGCTTTTTGCCACCAAC	(GCGCG)3	3952714
GSA08947	CTGCTCGGTTAGGGTG TTCT	ACTCCCTTGGATTGATTTG G	(TACACC) 3	3955831
Indel9-4	GAGCACGAGAAAGGA GATGG	CGCTAATCGACGCGTATTC T	ATGCAAC GAGGGGC GATTTGG CGCGCTG	4983165
Indel9-5	GACAATCACGCCACAC GTAG	TTCCGCTATAGCCTTGAAG C	TATACAA GA	5156043
GSA09012	GGCATGTCGTTAATCT GTGG	GTTCACTGGTGATGGACAG G	(AG)9	5292283
GSA09029	CTATGGTAGCCCATTTG GACC	GGATGGCTAGCACATAGTG G	(TGGGC)3	5625873
GSA09043	TGCTAACTACAGGGTG CAGAA	ACCAAACGATGCTAACTCC C	(AC)9	5868098
IS9.1	GAAATCGGGTGAAAAC AAAA	CCCTTAGAGAACGATGGCA G	AGTAACT CATGTCT	5952101
IS9.3	TAGAAAAACGCACAAG CACG	ATCCCCACTTTATTAGGCC G	CAGCTGC AGCCGCA GCACA	6209491
GSA09070	CGGTCTGCTCCATCTTT ACC	CAATAATTGATCGGGACGC	(GA)9	6356357
GSA09074	GGATGGAGTTCGGTTA AGGA	ATCTCTTTGGGACCAGATG C	(CAGGCA) 4	6366544
GSA09079	CAACCAAGTCGCTGAA AATG	AAAAGGAGAATACGCCGA GA	(AAAAG)3	6444464
bIndel6.600	ACGCACCCTCATATTT CGTC	AGGTGAGGAGAGACCGGG	CCCGCCT	6600417
IS9.5	CTCACCTCACTGCCAG TTCA	AAACATAAATGAGCCAC GG	CTTGTAC CTAAT	6635277
bIndel6.648	CGGAAGAGTTCTGGTT TTCG	GCAATCCATGGTTGATGAT G	ATTAAAA TCAG	6648905
bIndel6.685	AACTCGTGTGGGAGTT GGAT	TGATCCTCCTCAGAAGAGC C	CTTGTA	6685274
bIndel6.704	GGTGCTGCAGATCATG TGAC	AATTTGTGGACGAAACGA G	ACATCGG GCGTGAT CTAGGCC	6704294
bIndel6.747	AAAAATTGGAAGCCAA ATGC	AGAGAGGGTGAGGTTAGG CG	GGCCCCGA AGCCAAA T	6747643
bIndel6.773	CCTTCCCCGTTCTTATC CAT	ACATCTCCGTGAGGAACGT C	TGTACCC TCTCC	6773096
bIndel6.807	CAAATGGAAGGCTTTA GGCA	GGACACGCAAGCACTAGA CA	ACCATTTT AAATAGT T	6807585
bIndel6.833	GGGGAAAATCAATTTG CTGA	GCGAACACGACCCTGTAGT T	ACTAAAA TTTAGCTC	6833795
bIndel6.877	AAGACTGACATGACCA GGGG	GGATTCGCTGCAGCTCTAC T	TGGCTCG TACCGAA ACGGACG	6877420
bIndel6.902	TTAGCATCACGCATTG CTTC	AGGGTGCTGTACACATAC G	ACGTGGG GG	6902189
bIndel6.946	CCACTCCCACCATGTT ACCT	TAAAATGAGCCCTTGCCAA C	CTATGTCT GTTAATC TA	6946351

bIndel6.975	CATGCATCTTTTTGCGT TTG	TTCATGAGTGGCTTCTGCA C	GGCTTTTC TGCAC	6975104
			AAAGATT TTGTCTTA	
bIndel7.044	ATCCATCAACAGGGGT TTCA	AACTTTTTGCTTGCTTCCGA	TCAAGTT ATAGTGG AATTACC AAC	7043977
			AGGCGGT TCTAGCT	7089670
bIndel7.089	GCCGTGTACAACTGTG ATGC	ATGCTAGCTTCCCTTGACG A	CAACACT TTGTGTGT	
bIndel7.127	CTAATGACCGTTTCAG CCGT	TTCTATGTTGCGCAAGCCA T	CATCGTC	7127302
			AGCCGCG GGCCGCG	7163320
bIndel7.163	TCCTTATCTGATTTCGTG CCC	AATGGATCCTGGCCTTCTC T	G	
bIndel7.236	GCGCTTGCCATATCTAT GAGC	CCACGGGTTCATATTTAC C	AAGCGAG CCCAAC	7236214
bIndel7.264	ATAGACGCATGCATCA GTGG	TCAAGCCATTGCCTACAAC A	TAAGTTG GAA GATAATC	7264640
bIndel7.336	AAACAGACCCAACCAG ATGC	TCGTACGAGCATTGATCAG C	CTCAGGA GTAAACA	7336939
			TCTTACA AC	7454205
bIndel7.454	GTTGGGTGAAGGTGAT TTGC	CCAGCTCTTGCTTCTATGG C	AACGGTT GCAGG	7465289
bIndel7.465	AGATGGGCTGTTGGAT CAAG	GGGGAAGTGAGCAGAGAC AT	GGACATC AATT AAGCGGC	7502553
bIndel7.502	TGATCATGACAAGAAC AAGGAGA	GATGTGGGTGTTTGACGCT A	GTGCTAT TTAAGCC	7520026
bIndel7.520	AGCACGCAATTGTGTT TCAC	TCTTCGGCGAGAGACGTG	GGAAGGA AGCAAGA	7537451
bIndel7.537	CTCTTCTCCCATTCCTC CCC	CTTCCTCAAGGCAACAGAC C	TAAAGTC TTAA	7546739
IS9.8	AGCTGTGGTGTTCAT AGGA	TGGTGAGGATCAAAGGGA AG	CCTGCAC CA	7548746
bIndel7.548	CGATCCGGTTATTTGC GTAT	CAGGAGTTAGGGATGCCAG A	TGACCTA GAG	7553391
bIndel7.553	CATTGTTGAATTTGCC GTGT	ACCCGCAAGCTATTTATTG G	TCTCATC AGGGCTG CTGCTTAT CTTATTA	7601405
bIndel7.601	GCGCTTTGGTTATTTGC GTA	TGGGTGTACCATCTCGTTG A	TTGTCTTG CTCTGTAT TCCCTAG	7712158
bIndel7.712	TGATTGCATTGAAAA GTGC	AGACGCATAAGGATGACAT GG	GGTGTCC AGATAAA TTGTGTGT	7828419
bIndel7.828	AGGGGCATTAGGAGAT CGTT	CCTTTCTGAGACTGGCAGG A	(CTG)6	7986584
GSA09147	GCATGCTTGCTAGCTT GTTC	GTTGCCACGGCCTATAAGT T	ATGAGGT TATCCAG TATC	8171937
bIndel8.171	TCCGTGTGCTAGTTCA TTCAA	GAGAGTGGCTGTGAGCCTG T	CTGCATT GGATACA TAT	8526738
bIndel8.526	GCTTTGCTGATCCGTT AGGT	ACGCATAGGAGTGCCAGA AG	(CT)9	8819170
GSA09177	GATGTTACCCATCCAC CTCC	GTGATGTGCGTGTGTTGA A		

Indel9-8	ACGTCCTGTATTCTGG TGGC	TACAAGTCAAGGAGACCG GG	AGTTG	9777012
GSA09217	GGGAAAGGGATTCTAG CCTT	CTCCATATCCCACTGCGA G	(GCGGG)3	9808803
GSA09231	AACAACGATGAGATCA ACCG	ATTAAGCATCACCACCACC A	(TGCG)4	10043525
GSA09258	GAATCGACAATGGGAC CCTA	ACGGTGTGTGGCTTTTGT (GAGAG)3	10632716	
GSA09285	GGAATCGAGTGCACGT ACC	CAAGAAGCCTCCAACCTC C	(G)19	11276237
Indel11.7	GACACACCATTGTTGG ATGC	GCTCATGGAATGATTCTCC A	TTCCTCTG GCACTGG TA	11779666
Indel12.2	TGTCGAAAACCTTGACC GATG	CTTGCAGATTCAAGATAGC AATAA	CTCTATAT GTT	12233238
Indel12.5	TGGATTGTTGCTCCAT ACCC	TTTTAGGCTTCGTTgttcca	CAAATAT ACTAG	12518184
GSA09347	GTTGTTGCGGAGTTGA TGAC	TCCAACCAACGACCACTTT A	(CGACTT)4	13041266
Indel9-3	TCGACACGTACGAGTT TGCT	AACATCGTGAGGAAGAAC CG	CGGCCT	13374183
GSA09371	ATGCGTGCGAGAGTAT TGAA	TGAATTCCAGAGCGAAGAT G	(TGTT)4	13697126
GSA09375	CGAAGCTTGCCTCCAA CTAT	AACAACCCATACCTTGCAC A	(CCTG)4	13929239
GSA09377	GTCTCGCAGGTCTCAA ACAA	AGGATATTAACCCCGTCGA A	(GAGCC)3	14025056
GSA09407	GCCTTTCTTTGGTTTCT TGC	GCTTCCCGCTCATAAACT C	(CT)9	14894681
GSA09455	TAGTACCTCGTGCGGT CGT	GGCAATCTGGGAGATGAG AT	(GCACT)3	16898238

Note: Markers beginning with the capital letter GSA are SSR marks, and the rest are indel markers.