

Table S10 Polymorphic InDel/SSR markers developed on *qTN5.1* interval

Name	Forward 5'-3'	Reverse5'-3'	InDel sequence	InDel location
GSA05716	CTCCCAGATCTCTACGCCTC	TCTCGCCTTCTTTIATTC CC	(GACG)4	32903769
GSA05718	CATCTTTGACCGGGGACTAT	GTCATGTCGAGGTGGTG ACT	(AACA)4	32916473
InDel5-2	GCTGCTCTTTGGGATGAAGA	TGTATCCTGGCAGCTAA CCC	CTGTAAG	32991424
GSA05722	ATCAATTAACCCACCTTCGG	TTAGCATAGCACAACAG GGC	(TTCTT)3	32997779
Indel33.5	TGTCTGTTACCCGGTGTTCA	GTAATAAGGGGGTGG CACA	GGACCTTTCGTCCGC	33561365
Indel33.7	TTTGATTGCCTGTTTTGTGC	GCCCGTTTGTGTCGACT TAT	GCTGCGATCCGA	33710681
GSA05758	GTCCAAAAACACATGCAACC	GATCTAAGCATTTCTCG GGC	(TTTAT)3	34023602
Indel35.3	TAATGCGAAGTGAAGGCGTA	ACGTGCCAGATGACACT CAA	GAAATTAAAAGTTCCTCT	35326953
Indel35.9	CACAAACCAGTGCCCTACCT	AAACAAAGCGAGCCAT CTGT	GCAACA	35907713
Indel36.2	TGATGCATTACCTTTGGAA	TGGATGATTACGTGGCA TAAA	TTTCATCTCTCAAGTATTGCAAAAAGTGTG ACA	36204989
Indel36.8	TCACTCGATGGTACGACATGA	CCAGGCCAACTACCTCC TC	TGAGAGAGATGAGTGAGTCATTA	36890875
tIndel37.29	GGAAGTCATCGCCTTGGATA	GATGGATCGTGGAAG AAAT	TGATCAGCTTGTG	37297191
Indel37.3	GGGATGAAACCCTCCATTCT	CTAGGCCAGAGTCCATG TCC	TCTCTCTCTCTCTCTC	37338771
tIndel37.59	GCTGGGTCTCGTGGTATGTT	TAAGCCAAGCCAATCCT CAC	CAGTAATTGATTAAAGAGTGTAACATGG	37593001
IS5.1	TCGTCTGAGGGGACTACCAC	TGCTAGCATTCAAGTTCC GTG	AAAAGTTCTTCCTCAGTTTGACC	37598386
tIndel37.60	CTTTGGCGACGCTATTAAGC	ATACGGTCACCCTGAAG TGG	CATATCAA	37605318
tIndel37.72	AGCGACGAAATAGAGTGGGA	CCCAGCGGATTGTATCT TGT	ACATCCTC	37720222
IS5.3	ATGGTGTAATACGAGCGCC	GGCTCGGTTCTCTTGTG TTT	TCTAAATTATTG	37743134
tIndel37.76	GTGCAGGTGTTGATAGCGTG	TATTAGCCATGGTAAGC CGC	TTGGGGCGCGTGACTTTTGAACCC	37763147
tIndel37.79	TCACGTTGCAAGGCAAGTAG	AATCAAGGAGGAACTC AGCG	CATAGAAAATT	37792986
tIndel37.81	AAGCCGAGTATCGAGGTGTG	TGCAAACTGGTGCTTGG TAG	ACTGGCTGCATAATCTCC	37815880
tIndel37.92	AAATTCAGCTGATGGGATCG	CAAAAGCTCCAGACGCT ACC	CAAAAATTTG	37927163

InDel5-4	ACTCGGTTTGCTCATTGCT	CTGGAGCCACACAACCTT	TCTTTGTTGATTTATGCTTTCAAGCTA	37936135
Indel38.0	GTCTGATTACCCCTCCCAAA	TCA TGCCAATCCTTTTCAAC	GAAACGAGCAAATGGAAGC	38008285
tIndel38.35	TTTGTGTTGTGCAAGCGTAGC	ACC GGATGAGCAGAGTAGG	TATCCATCGAGGCGACGTCACAAAAAAA	38351123
tIndel38.38	CATGTATGCCTCATCACGCT	TCCG ATCTCGTTGGTCATTAG	A CAAAC TGCCCCGGCTCCACACAG	38387073
tIndel38.42	CGGTAACCGCCTAAGTAGCA	CCG ATGGAATTGGGAGGGA	AATTGATTGATAATTTACTAGCAT	38421936
tIndel38.60	TTCAGCTTTTCAGCCGATTT	TAGG TGAATAGACGATGCAG	TCAGACGAACACGCAGACGAACGCG	38605633
Indel38.6	CTATCAAGCAGCCCCACCTA	GCAG AAATTCAATGCCATGGG	TTGTTTGTA	38611695
tIndel38.63	GCCAGCCTCAGCTAGTCAGT	TGT ATTGTATTGACACCCT	GTCACCTACTGC	38639474
tIndel38.69	TCGGGAACGAGAAGAAGAAA	CGG CGGGGTCATCAAGCAGT	GAATCAGA	38695030
tIndel38.74	GTATGAACCGTCGAACCGAT	ATT GAGGACTTCTTCTGTTG	TTCCAAAC	38744639
tIndel38.77	GGCCTTAATGCCACAGTTCT	CCG ATCCGATGTGACAGGGC	GTGATGAAAGTGTAGCCTTAAAAATTAC	38773050
tIndel38.83	GGCCTTCTGAAGTTGACAGC	TAA AGCAAAGAGCCAGAGA	TACTCTCC	38831992
tIndel38.94	CCCCCTGAAATAAAGGTTTTG	CGAG CCTTCTCGACAAAAGCA	TATATTAAGTTTGTTC	38943493
tIndel38.98	GCAGCCTGTACCCAATCACT	ACA AGAGCCTCCATGTCACA	ATCACCCAT	38980729
IS5.7	GGACCCAAAAGAGAACCCTC	TCC TTGCTCTCAAGGACTTC	CACTTG TAGACATAGGAGTTGCTACTGGC	39036674
tIndel39.10	GTCAACAGGTCAGTTCGGGT	GGT GGGTGTAGTTTCCCCTG	TT CCAGACGCGCAGGTAGCTGCT	39106053
tIndel39.19	TCGAGAGTGCTCCTCAGACA	GTT GAAGCGACGACCTAGT	TCTGCGCGGAAGCGCAGGGG	39190778
tIndel39.26	TGTTTGATTACCGCTCCCTC	GACC CTTGGGACAGTGGGAGT	TGCTAGGAC	39262760
tIndel39.29	CCAATCCCGCCTAACTTGTA	AGC GCTGTGGCAAAGCTCCT	CTCCGATTCCAAT	39293760
tIndel39.35	CATGGAAGCAACCACACAC	ATC GATGCAAGCTTTGTGTC	TTTAGTAAGACAAGACAGA	39356510
IS5.8	GATGAACGCGTGAATCATTG	GAA CCGAACAACACCAACA	GTGCATCATCCTGACTTGTTTCTTATGCC	39442804
tIndel39.44	GCTCGTCCTAGTTTCGAGTCC	CAAG CCAGATCCAGTACCACC	AC GTGATTGTACA	39449852
tIndel39.48	CTTGTTTTGGGTGGGAAGAA	ACC TCCACCGGCTAGCAGAT	ATCAATCTAT	39481874
		TAC		

tIndel39.55	CAAGCGGGCTATCTGCTTAG	CGCCTGTAAGAACTCTG CCT	ATTGCCCTATCATGGAG	39551626
tIndel39.62	ACAAAGCTGTTAACCCACCG	GAGAAGAAGTTCGGCG TGTC	CCACTTGATCG	39620294
tIndel39.69	GGCATATTCTGCTTCCCTCA	ACACACCATGTTAGCAC CCA	GGTTACATTAAGCTAAGCTCT	39690270
tIndel39.75	AAATTCATGGGAGGCAGTTG	ATTGCACGGTGGTGGTT TAT	TAATCCATTA	39750019
tIndel39.80	TCGCGAATTAGACTCCATTTG	AGCACTACTGCATGTGA GCC	CCTTACCATGTGTCCA	39806844
IS5.9	GGCATTGCAGGTGAATAGGT	TGGCAATGTTCTCAGTC AGC	TGATCTGAAGATTTTTTTTTTCGTGAATAA	39821719
tIndel39.85	AATCCTCTGCGAATTCATGG	AAGTGTACCAACTCGCA CCA	GGCATGGTACATGTAA	39854168
tIndel39.89	CTGCAAACATTTTCAGTGGC	TACAAGTTAGCCAGGGC AGC	AAACCGTCTG	39890041
tIndel39.95	CGTCCTTCAGTCCTCTGCTT	AATCATCAAGGGCGAGT GAC	ACACTAGTATCACTGTATCCAATAGCTTT	39953710
tIndel40.07	AGCACAACACAAGCACGAAG	TGCTTTGGTGCAGTGCT ATC	AAAATCATTGCTCACCAT	40075796
tIndel40.20	AGTTCACATAAGCATCCCGC	TCTCTGTTTCGTGTGGGC ATA	AAAATTAGT	40204975
IS5.10	CGAAGTAAGTGTGCGTGCAT	CGTCAACATTGGAACAC GAC	ACACATCCCCGCAGCT	40113943

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