

Primer code	Type	Primer sequence	Allele size range (kb)	N _A	He	PIC
25	RBIP	F:GAGAACTGAGAAGAGGGTC R:CTCCACCTTGACTTGAATC	0.2-0.4	9	0.83	0.81
40	RBIP	F:GAAAGGATTCTGAGCGTAG R:ATACTCTCCACCACTGTCA	0.5-1.0	5	0.63	0.56
41	RBIP	F:GAAAGGATTCTGAGCGTAG R:GTAATACTCTCCACCACTGTC	0.5-1.0	8	0.83	0.81
45	IRAP	F:TATGCTTCAACCTGAGGG R:GTTCAATTTCTGCTCGCTC	0.3-0.7	10	0.7	0.65
46	RBIP	F:GAAAGTCTAATGCCGAGG R:AATACTCTCCACCACGGT	0.2-0.7	9	0.7	0.65
54	RBIP	F:TCTCAGACATAGAACCCG R:AGTGATGGTAACCAACC	0.3-0.7	10	0.79	0.76
55	RBIP	F:GTGTCCACAAAGGATTCC R:TCTCCACAAGACCACTTC	0.15-0.4	8	0.73	0.69
62	IRAP	F:ATTTAGTGGCAGCCCTTC R:GACCTTTCTTTCCGCATC	0.1-1.0	15	0.84	0.82
67	RBIP	F:GACAACTTGAACGGACAAAC R:AGGGTAAAGGCTAAGGGAG	0.15-0.3	6	0.73	0.68
68	RBIP	F:GGGACAACTACATAACTTGG R:GCTGCCACTAAATCAGAG	0.3-0.7	11	0.83	0.81
69	RBIP	F:TCATTACCTATTGCTCTCC R:TGCTTCCTTGACAGTCTTAG	0.15-0.3	6	0.69	0.66
74	RBIP	F:TTCATACTCCGAGAG R:GGATGTCCATTAGAGGCT	0.15-0.2	4	0.43	0.4
76	RBIP	F:TGTGTGTGTGTCTGTCT R:AACCTCGTAGTTCGGGTA	0.3-0.5	5	0.78	0.74
78	RBIP	F:CATCCTGAATAGAGTCCCT R:ATCGGTATCCCTTAGCAC	0.15-0.3	4	0.57	0.52
83	RBIP	F:CTGTAGTATTCAAGGGTGG R:GAAGCCATTCTAAGGGTC	0.2-0.5	7	0.56	0.54
93	RBIP	F:CTCCTTGACTGTTGCCATTA R:GGGAAGAAACCCTGGATT	0.2-0.4	5	0.37	0.35
95	RBIP	F:CCTGAAGAAGAATGGTCC R:GTGGTAAGAAGTTGAAGCC	0.1-0.3	8	0.81	0.78
105	RBIP	F:TCTCAACTCCAATGGCAG R:TTCAGAGGCAGAAGCATC	0.15-0.3	7	0.8	0.77
138	IRAP	F:GCATTGTTGTCACAGTCAAG R:GCAAGTTACTCTTCATACCTGG	0.5-1.0	4	0.67	0.61
146	RBIP	F:ATCCCTTCTCTCCTTCCCT R:TCACCTTGATACTTGCCG	0.15-0.3	5	0.78	0.75
148	IRAP	F:GGTGTGGACAGATAGTAAGG	0.15-0.3	4	0.71	0.66

		R:GAGTTGGTAGGTTGAGTTTG				
149	RBIP	F:CTAAATGGAGGGAAGAGAGA R:GTGACAACCTTGAGTGCCA	0.2-0.3	5	0.74	0.7
152	IRAP	F:CTTATCTCCCTCAACAAGC R:CTACAGAAATGGCGACTTC	0.15-0.2	3	0.61	0.53
153	IRAP	F:CAGCAACATAACGAGAACG R:CCGAGAGAAATGAGAGAGAAAGT	0.4-0.7	8	0.77	0.75
155	RBIP	F:CTTGTTGCGTTAGTGTGC R:AACTGGGATGGTCCGTAT	0.5-1.0	6	0.72	0.68
169	IRAP	F:GTGAATGTGTGTGTGTGC R:CTTTGAGCAAGTGTGTAGGT	0.3-0.5	7	0.83	0.81
170	RBIP	F:GTGACGAGAAGAAGAAAAGG R:CACAGATTTACCACTGGC	0.2-0.3	4	0.69	0.63
183	RBIP	F:T TACTAATCCCACCACCC R:GACGAAGGAGAAGAGAATG	0.3-0.5	5	0.73	0.68
196	RBIP	F:GATTGTTCCGATTCAGGC R:AGGACTTGCTGGATTGG	0.2-0.4	6	0.78	0.75
209	RBIP	F:GTCTCACACACAAGATTCC R:GGTGGTTAGGGAGGTTAT	0.15-0.4	7	0.84	0.82
210	RBIP	F:GTCTCACACACAAGATTCC R:GGTGGTTAGGGAGGTTAT	0.15-0.3	6	0.72	0.67
226	RBIP	F:GCTTCAAGTGTGGTGGAT R:AACGCAACCCTTCTCTCT	0.2-0.3	5	0.68	0.63
229	RBIP	F:ATCGGAATGGACTCTACC R:GTGTATGCGTATGTGTGAG	0.1-0.3	10	0.83	0.81
277	RBIP	F:TCAGATGGAGTTGTGAGG R:GAGGCTAAACCCTACGAT	0.2-0.3	3	0.62	0.54
280	RBIP	F:GAACTGTATGTGTCCAAGG R:CCAGGAAGAGAACAAGAC	0.2-0.3	4	0.68	0.63
281	RBIP	F:AGAGGAAGAAGACAACCG R:GTCACAAAGGATGAGGGT	0.15-0.3	4	0.45	0.42
283	IRAP	F:CCCGAATCTAAGGTCAAAGT R:CACGCAAGAAACACATCAC	0.15-0.5	10	0.86	0.84
284	IRAP	F:ATTTGGACCAGGCACACT R:AAGCACTCCGTCATCGTA	0.1-0.3	6	0.7	0.65
286	IRAP	F:CGGATGATACGAAAGTGAG R:GCTTCTGTTGTTAGCCCAT	0.3-0.5	4	0.66	0.6
290	RBIP	F:ACTAAGGTTCCAGGCTGT R:GACTCATCCAACAATCCC	0.2-0.4	3	0.4	0.37
293	RBIP	F:CGGCAAGGTAGAGAGAAGT R:AATGGGCTTTGGAGTAGG	0.1-0.3	8	0.79	0.76
300	IRAP	F:CTCTCACACATACACAAAGG R:ATCTGGAGTTCTGGAAGTC	0.2-0.5	5	0.7	0.66
301	RBIP	F:CAAGCACGGTAAGTTAGC	0.2-0.4	4	0.68	0.62

		R:CGAGTTCAAGAGCACCTT				
302	RBIP	F:AAAGAGGACAAAGACCCG	0.3-0.5	3	0.5	0.38
		R: TAGTCAACGCACATACGC				
324	IRAP	F:GGTATCAGAGCCTGGTTAG	0.2-0.3	4	0.56	0.5
		R:AAACAGTCCTCAGTTCCTC				
336	IRAP	F:GAGGAAGTAGACGCTTATTG	0.2-0.4	5	0.76	0.72
		R:GTTGGTGGTGTCAATCAC				
350	RBIP	F:TCACAGAGTTTGAGTCCC	0.15-0.4	7	0.84	0.82
		R:GAAGAAGAAGGTGGGTTC				
Mean				6.21	0.70	0.66

NA: number of alleles, He: expected heterozygosity, PIC: polymorphic information content, RBIP: retrotransposon-based insertion polymorphisms, IRAP: inter-retrotransposon amplified polymorphisms.