

Table S2. Information of 20 pairs of sequence related amplified polymorphism (SRAP) primers

SRAP primers	Forward//Reserve primer sequence (5'-3')	Polymorphic fragments	Size range of amplified fragments (bp)	PIC	NA	NE	H	I
Em1Me18	TGAGTCCAAACCGGAAG // GACTGCGTACGAATTATT	5	200-800	0.704	1.899	1.487	0.302	0.461
Em4Me1	TGAGTCCAAACCGGATA // GACTGCGTACGAATTTGA	4	200-500	0.664	1.647	1.392	0.232	0.348
Em4Me2	TGAGTCCAAACCGGAGC // GACTGCGTACGAATTTGA	7	500-1200	0.800	1.989	1.634	0.368	0.546
Em4Me8	TGAGTCCAAACCGGTGC // GACTGCGTACGAATTTGA	4	100-800	0.659	1.858	1.585	0.334	0.491
Em5Me21	CTGGCGAACTCCGGATG// GACTGCGTACGAATTAAC	7	200-1200	0.829	1.929	1.476	0.298	0.459
Em5Me22	GGTGAACGCTCCGGAAG // GACTGCGTACGAATTAAC	4	200-1200	0.697	1.545	1.411	0.225	0.326
Em5Me23	AGCGAGCAAGCCGGTGG // GACTGCGTACGAATTAAC	3	100-800	0.589	1.717	1.541	0.299	0.433
Em5Me24	GAGCGTCGAACCGGATG // GACTGCGTACGAATTAAC	3	100-500	0.592	1.303	1.246	0.133	0.189
Em5Me30	GACCAGTAAACCGGATG // GACTGCGTACGAATTAAC	1	200-1200	-	-	-	-	-
Em10Me9	TGAGTCCAAACCGGAAT // GACTGCGTACGAATTCAC	6	100-500	0.801	1.889	1.777	0.409	0.579
Em10Me25	CAAATGTGAACCGGATA // GACTGCGTACGAATTCAC	3	200-1200	0.590	1.535	1.345	0.202	0.3001
Em10Me31	CAGGACTAAACCGGATA // GACTGCGTACGAATTCAC	2	200-1200	0.373	1.576	1.407	0.238	0.348

Table S2. Continued

SRAP primers	Forward//Reserve primer sequence (5'-3')	Polymorphic fragments	Size range of amplified fragments (bp)	PIC	NA	NE	H	I
Em13Me24	GAGCGTCGAACCGGATG // GACTGCGTACGAATTCTA	3	100-1200	0.583	1.556	1.423	0.233	0.337
Em13Me30	GACCAGTAAACCGGATG // GACTGCGTACGAATTCTA	4	200-1200	0.690	1.535	1.410	0.222	0.321
Em14Me32	ATCAGTCGGACCGGATT // GACTGCGTACGAATTCTC	2	200-1200	0.330	1.565	1.400	0.234	0.342
Em15Me5	TGAGTCCAAACCGGGAT // GACTGCGTACGAATTCTT	1	200-800	-	-	-	-	-
Em15Me8	TGAGTCCAAACCGGTGC // GACTGCGTACGAATTCTT	8	200-1200	0.836	2.000	1.660	0.381	0.563
Em15Me23	AGCGAGCAAGCCGGTGG // GACTGCGTACGAATTCTT	3	100-800	0.584	1.353	1.279	0.152	0.218
Em17Me24	GAGCGTCGAACCGGATG // GACTGCGTACGAATTGTC	9	200-500	0.874	1.859	1.664	0.365	0.526
Em19Me12	TGAGTCCAAACCGGACG // TGTGGTCCGCAAATTTAG	8	200-800	0.805	1.879	1.434	0.156	0.211
Total		87						
Average		4.35		0.667	1.702	1.476	0.266	0.389

PIC, Polymorphic information content; NA, Observed number of alleles; NE, Effective number of alleles; H, Nei's gene diversity; I, Shannon's information index.