

Table S2. DNA markers used in this study

A. Genomic DNA markers developed in this study

#	Marker	Cert.	Category	LG	Accession ID	SSR position	Source	Motif	Tag	Tagged forward primer	F Tm	tail	Tailed reverse primer	R Tm	Amp	Program
1	CTVR01	*	gSSR	LG7	AF506028	274544	Genomic sequence	(ctg)n	F9GAC	ctagatcaggagcagTAGAGTCCGACAGTGGTTC	58.91	gtttctt	gtttcttCAAACACTGTAATCAATGCAGC	59.30	305	56/32
2	CTVR04	**	gSSR	LG7	AF506028	274557	Genomic sequence	(tgtcgt)n	F9GCC	ctagatcaggagcagTAGAGTCCGACAGTGGTTC	58.91	gtttctt	gtttcttCAAACACTGTAATCAATGCAGC	59.30	305	56/32
3	CUBER403	*	gSSR	L05	GA975130	98	Citrus unshiu BAC end sequences	(taat)n	F9GTC	ctagatcaggagcagcTAACTTTCTTCTTCAATGGG	57.02	gtttctt	gtttcttTAATCTTCGTCGTAATGTGAC	56.49	251	58/32
4	CUBER410	*	gSSR	L05	GA977509	312	Citrus unshiu BAC end sequences	(aaac)n	F9TAC	ctagatcaggagcagcCAACCAACAGCTTTATCAATC	56.16	gtttctt	gtttcttTGTTTGGTTTACTGCTTGG	56.4	258	54/32
5	CUBER601	*	gSSR	L02	GA975859	111	Citrus unshiu BAC end sequences	(tgtaa)n	F9GTC	ctagatcaggagcagcCAATGACTGTGATAATGGTGC	57.27	gtttctt	gtttcttCTAGGAAAGTTTGTCTTCT	57.04	164	56/32
6	CUBER602	**	gSSR	L01	GA976278	99	Citrus unshiu BAC end sequences	(ttcctc)n	F9TAC	ctagatcaggagcagcGCCATTTCTTTCTTCTTCTC	56.73	gtttctt	gtttcttGACTGAAAGTCTTCAAAATC	56.87	232	54/34
7	CUBER903	*	gSSR	L07	GA976453	774	Citrus unshiu BAC end sequences	(ata)n	F9GCC	ctagatcaggagcagcCACTGCACAAATCATAAGTAG	58.03	gttt	gttttGAAGATAATGAGAGCCAAATC	57.43	175	56/32
8	CUBER918	*	gSSR	L09	GA974879	627	Citrus unshiu BAC end sequences	(tcc)n	F9GTC	ctagatcaggagcagcCAGGCTGTGTTCCTCAATG	62.34	gttt	gttttGGATACCCCGCAGTTT	62.38	101	56/32
9	CUBER920	*	gSSR	L04	GA977190	719	Citrus unshiu BAC end sequences	(atg)n	F9GTC	ctagatcaggagcagcCAATGACTGTGATAATGGTGC	59.06	gttt	gttttGGACTATCCCTTCAATG	58.87	164	56/32
10	CUBER925	*	gSSR	L05	GA975321	635	Citrus unshiu BAC end sequences	(atg)n	F9GAC	ctagatcaggagcagcCAATGACTGTGATAATGGTGC	57.06	gttt	gttttAGGTAACTTACGCTTGTGAG	56.65	167	56/32
11	CUBER935	**	gSSR	L06	GA976619	482	Citrus unshiu BAC end sequences	(tga)n	F9GAC	ctagatcaggagcagcTCTTGTGTTCTCAACATGAATA	59.61	gt	gtttTAGTTCCTCCCCCAATAT	58.93	178	58/32
12	CUBER939	*	gSSR	L01	GA975313	822	Citrus unshiu BAC end sequences	(tca)n	F9GCC	ctagatcaggagcagcTAAAGTATGAAAGTTGACGCA	58.21	gttt	gttttGGCAGGAGTACTGTGATA	57.8	215	60/32
13	CUBER951	*	gSSR	L01	GA976278	322	Citrus unshiu BAC end sequences	(ttc)n	F9AGG	ctagatcaggagcagcTTCCTCTTCCTTCCTCCTC	57.87	gttt	gtttTAGTATTCCTGACACTGATGA	57.74	161	56/32
14	GRW2011	*	gSSR	LG3	Scaffold3	8602126	Clementine v1.0	(TA)n(CT)n	F9GTC	ctagatcaggagcagcTCAACTCAGCCCTTCCAGTTT	59.83	gttt	gttttCGTGATCTAAGTGGGAAGTAT	61.38	122	54/32
15	GRW2015	*	gSSR	LG3	Scaffold3	43996493	Clementine v1.0	(TA)n	F9TAC	ctagatcaggagcagcATGTGACACAAAGAAATTTGTC	59.71	gttt	gttttATTCTTAATTAAGCTTAACAGGG	57.01	108	56/32
16	GRW3021	*	gSSR	L05	BUZY1863.g1	426	NCBI Trace Archive	(TGT)n	F9TAC	CTAGTACAGGACTACATCCCGCCTCTCTTTCT	61.75	gttt	gttttGGCTGGCTTTGACATPA	60.59	117	56/32
17	GRW3011	*	gSSR	LG3	Scaffold3	8606684	Clementine v1.0	(TAT)n	F9GAC	ctagatcaggagcagcCAGGACACAGCTTCAACAC	62.02	gttt	gttttAAAGCTTAGCCTCTCCACC	61.58	94	58/32
18	GSRI0509	*	gSSR	L05	BDG001000073	2983	Shimizu, T. et al. unpublished	(aga)n	F9GCC	ctagatcaggagcagcCGGACAGCAAAAATAACCTG	56.77	gttt	gttttATAAACAAGCAGTGTAGC	57.57	196	54/32
19	GSRI0517	*	gSSR	L05	BDG001000144	3275	Shimizu, T. et al. unpublished	(attatc)n	F9GAC	ctagatcaggagcagcGTCACTGATGTTATCAAC	57.17	g	gttttATTATGTGACGTGGAAAGC	58.08	163	54/32
20	GSRI0529	*	gSSR	L02	BDG001000234	2691	Shimizu, T. et al. unpublished	(ttaa)n	F9GTC	ctagatcaggagcagcTCTCCCTCTGTGCTTAAATC	56.92	gttt	gttttATTATTTCTTACCGTGGAGC	57.67	139	54/32
21	GSR2101	*	gSSR	L01	BUZY106502.bl	151	NCBI Trace Archive	(ta)n(ga)n	F9GAC	ctagatcaggagcagcAAATGAAATGTAATGACGGAGAT	57.07	gttt	gttttGAGATCTTATAATGAAAGCTCTC	57.07	113	54/34
22	GSR2103	*	gSSR	L01	BUZY123497.bl	527	NCBI Trace Archive	(ga)n	F9TAC	ctagatcaggagcagcAATGCAATGCACTCTTGTTC	59.26	gttt	gttttGACCAATCTAGTACTGCTTGG	58.48	221	56/32
23	GSR2108	*	gSSR	L03	BUZY133352.bl	1069	NCBI Trace Archive	(atc)n	F9GTC	ctagatcaggagcagcTCTTACAGACTGCTCC	59.26	gttt	gttttAGCTTCTTCTTCCAC	59.23	176	56/32
24	GSR2129	*	gSSR	LG3	BUZY33352.bl	639	NCBI Trace Archive	(atc)n	F9GCC	ctagatcaggagcagcTCTGCTGCTTGTGTAATAGAG	61.03	gttt	gttttGGTTAGAGGCAACATTTCC	58.73	157	54/34
25	GSR2131	*	gSSR	L08	BUZY261862.g1	600	NCBI Trace Archive	(ac)n	F9GAC	ctagatcaggagcagcTCTTGTGAGTACAGTGTGAG	59.84	gttt	gttttGTTACTGACTGATAGTGTGAG	59.28	156	60/32
26	GSR2150	*	gSSR	L01	BUZY112333.g1	589	NCBI Trace Archive	(tcc)n	F9GTC	ctagatcaggagcagcGTTGATCTTCCCTTCTCCTC	58.16	gttt	gttttACTGTCTTCTTCTGCTACC	59.78	234	56/36
27	GSR3114	*	gSSR	LG7	BUZY25274.bl	204	NCBI Trace Archive	(atc)n	F9GTC	ctagatcaggagcagcATCCCGCTCTTCTGATATG	59.32	gttt	gttttAGTGTAGCAAAATAGTCGGT	59.03	155	56/32
28	GSR3121	*	gSSR	LG4	BUZY53309.g1	466	NCBI Trace Archive	(aag)n	F9TAC	ctagatcaggagcagcCCAGTAATCAGACAACTTAGG	58.52	gttt	gttttCGAAATCTGTTAGCTTAAGAG	58.81	156	54/32
29	GSR3126	*	gSSR	LG7	BUZY170281.g1	793	NCBI Trace Archive	(aac)n	F9GTC	ctagatcaggagcagcCGCCAACTGACAAAACAT	59.61	gttt	gttttGTACACAGACTCAACAA	57.45	209	56/32
30	GSR3128	*	gSSR	--	BUZY72931.g1	514	NCBI Trace Archive	(gaa)n	F9TCC	ctagatcaggagcagcCGGGTGTCTTCTTATGTC	58.79	gttt	gttttATGAGAGGCTCTAATCTTGG	59.27	127	56/32
31	GSR3136	*	gSSR	LG3	BUZY128287.bl	671	NCBI Trace Archive	(atc)n(gt)c)n	F9AGG	ctagatcaggagcagcGCCAGTCACTCTTCAATG	59.37	gttt	gttttCTTGAGTGAAGAAAGTGA	61.58	133	58/32
32	GSR3137	*	gSSR	LG8	BUZY232019.g1	765	NCBI Trace Archive	(aat)n	F9GAC	ctagatcaggagcagcGCCATCACTTGTATTCCT	58.22	gttt	gttttTAATCTGATGAGCGATCCT	57.57	163	56/32
33	GSR3138	*	gSSR	LG5	BUZY63372.g1	120	NCBI Trace Archive	(aat)n	F9GTC	ctagatcaggagcagcGCCTTGTCAACTGGAAATCG	61.82	gttt	gttttCTAAAGTCTGCTGTTGTGT	61.83	135	54/32
34	GSR3140	*	gSSR	LG5	BUZY59969.bl	213	NCBI Trace Archive	(aat)n	F9TCC	ctagatcaggagcagcCGGAGAAAGGAAATTTAGT	59.47	gttt	gttttGTGGTATGATGAGAGGAG	57.37	170	56/32
35	GSR3141	*	gSSR	LG8	BUZY111250.g1	389	NCBI Trace Archive	(att)n	F9GCC	ctagatcaggagcagcGGATATACCTGATTAAGTAGAG	57.25	gttt	gttttAATAGTAGGATCTGAGTTAC	57.07	144	56/34
36	GSR3105	*	gSSR	--	BUZY29671.g1	106	NCBI Trace Archive	(atctc)n	F9GCC	ctagatcaggagcagcTAATGCAATGAGCCCAAAAG	56.57	gtttctt	gtttcttCAACTATGAGAGGAGGAGG	57.18	116	60/32
37	GSR5112	*	gSSR	L08	BUZY9077.bl	1002	NCBI Trace Archive	(ata)n	F9GTC	ctagatcaggagcagcTCTGCTGACTCAAGACTAG	57.09	gttt	gttttCTTGCATCTTCTTCCAC	59.98	228	56/34
38	GSR5114	*	gSSR	L05	BUZY129906.g1	488	NCBI Trace Archive	(aaac)n	F9TAC	ctagatcaggagcagcTAGTAACCGTGAAGTGA	56.27	gtttctt	gtttcttAACTGTGAAAGTAAATGTGG	57.05	308	56/36
39	GSR5122	*	gSSR	LG3	BUZY155080.g1	1878	NCBI Trace Archive	(cgccc)n	F9GCC	ctagatcaggagcagcCACATGACTTCTTCTTTCAG	56.96	gtttc	gttttCTTCCOATTTCACTCCCAAG	56.81	253	56/32
40	GSR5127	*	gSSR	L03	BUZY8842.bl	463	NCBI Trace Archive	(caagc)n	F9GCC	ctagatcaggagcagcCACTTAAGTCTTCTTCTGCTC	56.57	gtttctt	gtttcttACGAGATGTCACACTTTTGG	56.87	179	54/32
41	GSR5129	*	gSSR	LG3	BUZY254533.g1	270	NCBI Trace Archive	(tgagc)n	F9AGG	ctagatcaggagcagcGCCTTGATAAAATTTCTGTC	56.79	gtttctt	gtttcttAAAACACTTCAAGATCCACC	56.77	260	56/34
42	GSR6101	*	gSSR	LG7	BUZY128935.g1	107	NCBI Trace Archive	(cgccga)n	F9GCC	ctagatcaggagcagcAATAAACAAGGAAAGG	57.04	gttt	gttttGTCAACATCCCATATAGCAAG	57.04	248	60/32
43	GSR6122	*	gSSR	L02	BUZY50477.bl	103	NCBI Trace Archive	(aaacga)n	F9GCC	ctagatcaggagcagcCTAAGAAGTGTGCTAGGTTG	57.15	gtttctt	gtttcttTGATGATCAAAAGACCTCC	57.15	213	54/32
44	GSR6129	*	gSSR	LG6	BUZY22109.bl	229	NCBI Trace Archive	(gaaggt)n	F9AGG	ctagatcaggagcagcGAGAAGAAAGTGAAGTGG	57.48	gtttctt	gtttcttAAAGTCAAAAGAAAGTGAAG	56.79	227	56/30
45	GSR6133	*	gSSR	LG6	BUZY106766.g1	443	NCBI Trace Archive	(ctgggg)n	F9GCC	ctagatcaggagcagcGTTTGTACTTCTTGTGCTG	57.22	gtttc	gttttTCTGGGCTTACTCTCAAT	57.22	256	54/32
46	GSR6135	*	gSSR	LG7	BUZY210038.g1	459	NCBI Trace Archive	(aggggt)n	F9AGG	ctagatcaggagcagcAGGTTTTACGATTTCCAG	56.96	gtttctt	gtttcttGAAACACAGTATGAGGTGAAG	56.96	178	56/32
47	NSX02	*	gSSR	LG3	scaffold_3	8740	Clementine haploid v.0.9	(TA)n(CA)n	F9GTC	ctagatcaggagcagcCACTACATCGCCATCAACC	60.66	gtttctt	gtttcttTACTCGTGGACTCATGACTC	61.46	143	54/32
48	NSX23	*	gSSR	LG3	scaffold_3	5899745	Clementine haploid v.0.9	(TAA)n	F9GCC	ctagatcaggagcagcAGATGATGCTTCCATCAAAATC	60.18	gtttctt	gtttcttGTTGTGTATTAATGACTTTGCAAT	59.67	246	54/32
49	NSX32	*	gSSR	LG3	scaffold_3	8574561	Clementine haploid v.0.9	(TTTGGA)n	F9GTC	ctagatcaggagcagcCTTTGTGGGAATGTGACAGA	60.74	gtttctt	gtttcttAAAGACTCGAATGCTGACCT	60.73	261	56/32
50	NSX34	*	gSSR	LG3	scaffold_3	8970241	Clementine haploid v.0.9	(TAA)n(ATC)n	F9GCC	ctagatcaggagcagcTATCCCACTGCAACAATCTAAT	60.65	gtttctt	gtttcttTTATGTTGCTTTATGACCCCAAT	59.83	259	54/34
51	NSX38	*	gSSR	LG2	scaffold_1	13148619	Clementine haploid v.0.9	(AT)n	F9GTC	ctagatcaggagcagcTCTGCTGCTCTTGTACTCT	59.48	gtttctt	gtttcttGCTTAAACAACAGCTCC	58.32	244	56/32
52	NSX39	*	gSSR	LG2	scaffold_1	13086339	Clementine haploid v.0.9	(TGA)n	F9TAC	ctagatcaggagcagcGTAAATGTAATCAATCCAGAT	57.64	gtttctt	gtttcttGCCATAAATCTTCTACTAGAT	58.29	202	56/32
53	NSX43	*	gSSR	L05	scaffold_1	12772252	Clementine haploid v.0.9	(TTCATGA)n	F9GAC	ctagatcaggagcagcTCTGCTGCTTCAATCTGCT	59.94	gtttctt	gtttcttAACTTAAACCTCAACTCAGCT	58.81	158	58/32
54	NSX48	*	gSSR	LG5	scaffold_1	11014805	Clementine haploid v.0.9	(CTATCT)n	F9AGG	ctagatcaggagcagcATGCTGCTCACTAAATGAGT	58.45	gtttctt	gtttcttTTGCTAAGGAGGATGGAAGT	58.04	128	56/32
55	NSX53	*	gSSR	L05	scaffold_1	9577531	Clementine haploid v.0.9	(ATT)n(TTV)n	F9GCC	ctagatcaggagcagcAATTTCAACTTCACTCCATCA	59.10	gtttctt	gtttcttGCTGTATTTGCAATGACTAT	58.00	187	56/32
56	NSX67	*	gSSR	LG5	scaffold_1	6050494	Clementine haploid v.0.9	(TATT)n	F9GAC	ctagatcaggagcagcCAGGATGCTCCTCACTTAGGA	60.82	gtttctt	gtttcttCGCTGTATCAACAAGTACTAAGA	60.48	173	54/32
57	NSX79	*	gSSR	LG5	scaffold_1	1989018	Clementine haploid v.0.9	(TAGT)n	F9GAC	ctagatcaggagcagcTAGCGGGTGTAGCTTCT	61.45	gtttctt	gtttcttTATCTATCAACAACCTTGTGCGAA	60.12	223	56/32
58	NSX82	*	gSSR	LG5	scaffold_1	11437282	Clementine haploid v.0.9	(TC)n	F9GCC	ctagatcaggagcagcGTGTAGCTTCAAGACTGAG	58.38	gtttctt	gtttcttGGCACTCAATACCTGCT	58.26	262	58/32
59	NSX84	*	gSSR	LG5	scaffold_1	6046416	Clementine haploid v.0.9	(TGCTAG)n	F9AGG	ctagatcaggagcagcTGAAGAAATGAAAGTCACTG	58.70	gtttctt	gtttcttGAGAAGAAATGTTAAGAGCCAAAG	60.63	174	56/32
60	NSX115	*	gSSR	LG7	scaffold_23	2031639	Clementine haploid v.0.9	(CTT)n	F9TAC	ctagatcaggagcagcCAATTAATGAAAGTGAAGG	58.12	gtttctt	gtttcttTCAACTGACTGACTTAATTTCTA	57.72	112	56/32
61	NSX119	*	gSSR	LG9	scaffold_27	158921	Clementine haploid v.0.9	(GT)n(AT)n	F9TAC	ctagatcaggagcagcCGACTCATCTTATCTCAAACTC	60.13	gtttctt	gtttcttTAGACTACAGATCCACAGC	58.27		

88	TSGR222		gSSR	LQ1	Scaffold_1	Clementine v1.0	(ttt)atn	F9CCG	ctagattaggaccgctTGAGACACTCCACTATAACMTT	57.49	gttttct	gttttct	TGGTGAGCGGGTGGTAA	57.97	196	58/32	
89	TSGR264	*	gSSR	LQ2	Scaffold_2	Clementine v1.0	(aa)tn	F9CCG	ctagattaggaccgctTAACACCACTCCACTAACTTCCA	59.72	gttttct	gttttct	TGGGAAACATTTAGACCTCCGCT	60.01	140	58/32	
90	TSGR265	**	gSSR	LQ2	Scaffold_2	Clementine v1.0	(ta[gc]n) (caa)n	F9CCG	ctagattaggaccgctACAGCTGCCACTAATTCATCC	57.94	gttttct	gttttct	TATCTCCAAAGACTCCAACCT	57.54	165	56/32	
91	TSGR271	*	gSSR	--	Scaffold_9	Clementine v1.0	(ata)n	F9CCG	ctagattaggaccgctCTTTAGAGCTCAGGCTC	59.18	gttttct	gttttct	ACTGCTGGTATGTAAGACCTT	59.42	202	56/32	
92	TSGR282		gSSR	LQ3	Scaffold_3	Clementine v1.0	(tttttc)n (tg)n	F9CCG	ctagattaggaccgctAGCAAATTAATTAACAGGCT	57.70	gttttct	gttttct	CTCTGAAATGGCTCTGCC	58.98	251	56/32	
93	NSX16	INDEL	--	scaffold_3	4098890	Clementine haploid v.0.9	CCATGTTAACTAAAGAGAATCTGTCTGCATCAACA/C	F9CCG	ctagattaggaccgctCCGCAATTAACACGAGG	58.11	gttttct	gttttct	LATGTTGCCGGTAATTTCTTGG	58.93	114	60/32	
94	NSX27	INDEL	LQ3	scaffold_3	7642393	Clementine haploid v.0.9	AC/AAAAAC	F9TAC	ctagattaggaccgctGAATCTCAATGACGACGGCA	59.61	gttttct	gttttct	CACATGTCATCTAGCCATCA	58.95	322	56/32	
95	NSX28		INDEL	LQ3	scaffold_3	8000304	Clementine haploid v.0.9	A/ACT	ctagattaggaccgctTTGGAGAATTTGAAACAGCAAA	57.07	gttttct	gttttct	TCGAGTTTACAGTTTCCACTTACAA	58.56	234	54/32	
96	NSX70	*	INDEL	--	scaffold_1	5092937	Clementine haploid v.0.9	A/ACAGCAAT	F9GCC	ctagattaggaccgctAAAGACTAGTGGACGCTCAG	59.50	gttttct	gttttct	TACAATGATTTGAAGCTCTCC	59.48	132	54/32
97	NSX87		INDEL	LQ5	scaffold_37	1669	Clementine haploid v.0.9	AGTT/AGTTAGACAATGTT	F9TAC	ctagattaggaccgctAGATCTCTCATAAAGCAATA	57.60	gttttct	gttttct	TGAGCAAGTGAACCTTAAACGA	58.30	132	56/32
98	NSX94	INDEL	LQ5	scaffold_37	1274730	Clementine haploid v.0.9	CAAGAG/CAAG	F9GCC	ctagattaggaccgctCAAGTCTCAACAAACCTTCTGT	60.60	gttttct	gttttct	GAATGTGGAAAGGGCTTCTTA	59.05	117	56/32	
99	NSX118		INDEL	LQ9	scaffold_27	27707	Clementine haploid v.0.9	TACGAGTATTA/TA	F9GTC	ctagattaggaccgctCGCTTCTGCAATGAGGTA	58.14	gttttct	gttttct	TGGTGGCTGGTGGAGTATGTA	61.48	142	58/32
100	NSX129	INDEL	LQ9	scaffold_27	326975	Clementine haploid v.0.9	CCA/GCACACTCA	F9GAC	ctagattaggaccgctCGCTTCTGCAATGAGGTA	58.53	gttttct	gttttct	TCGAAATTTACAGTTTCCACTTACAA	58.19	210	56/32	
101	NSX148		INDEL	LQ8	scaffold_16	3943508	Clementine haploid v.0.9	TTAATACGTGTAAT/TT	F9GTC	ctagattaggaccgctcAAGCTTAACTGGCTGCT	61.81	gttttct	gttttct	TTTGCGAACTGGATTTCTT	61.90	149	54/32
102	NSX161	*	INDEL	LQ8	scaffold_52	156369	Clementine haploid v.0.9	AATTCGAT/AATTCGATTTAAGGATTCGAT	F9GCC	ctagattaggaccgctcAGAAATCAAGTAACTGGCTTTTAT	57.65	gttttct	gttttct	TATCCCAAACTCCACTACATCT	59.47	101	56/32
103	NSX179	INDEL	LQ7	scaffold_68	414820	Clementine haploid v.0.9	AAAGTGCAA/*	F9TAC	ctagattaggaccgctcTTCCAAACATATTTCCACTCA	58.89	gttttct	gttttct	CTTTGAAGAGTCCGCAATATTA	57.44	251	54/34	
104	TS1A0A29		INDEL	LQ1	EY715084	473 EY715084	c/TC/CCTCTC/CTCTCCTCTC/CTCCTCTCA/A	F9TCC	ctagattaggaccgctCCTCTTGTCCACATTTCT	58.00	gttt	gttt	ACATCAACTCCGTAAGCAAG	57.61	222	54/34	
105	SSR07A05	*	EST/cDNA	LG2	CX663436		(cac)n	EST/cDNA	ctagattaggaccgctTCTTGAGCAATCTCATGTCTC	58.63	gttttct	gttttct	CAGGATTAGGCTATTGGCTG	58.28	140	56/32	
106	SSR07A07	*	EST/cDNA	LQ4	CX663643		(gaa)n	EST/cDNA	ctagattaggaccgctGCTCACTTAGGAAGAATCAG	57.74	gttttct	gttttct	TGGAGGTTCTTTATCTTCTTGG	56.90	176	58/34	
107	SSR07A14	*	EST/cDNA	--	CX666503		(att)n	EST/cDNA	ctagattaggaccgctacGCAATATGGCTTAAAGCT	59.46	gttttct	gttttct	CAGGCTCTTCTCATCATCCAC	57.86	141	54/32	
108	SSR07A17		EST/cDNA	LQ2	CX667444		(atg)n	EST/cDNA	ctagattaggaccgctGGCTCAATCATATAACAG	59.55	gttt	gttt	TCTCTCATCATTTCCCACTCG	59.14	223	56/34	
109	SSR07A19	*	EST/cDNA	LQ3	CX669071		(cat)n	EST/cDNA	ctagattaggaccgctGTTGGTTGTTTATCTCTCTGTG	55.78	gttttct	gttttct	GAAGATCAGAAAGATGATTGAG	56.48	129	56/34	
110	SSR07A23	*	EST/cDNA	LQ7	CX670335		(ca[ct]n)	EST/cDNA	ctagattaggaccgctcATGGCCAAACCAATATCC	59.38	gttt	gttt	CTAATTTCCGACATTTCCCTG	59.49	192	56/32	
111	SSR07A24	*	EST/cDNA	LQ9	CX670407		(aa)n	EST/cDNA	ctagattaggaccgctcCTTACAGGCTCTTCCACTACG	58.64	gttttct	gttttct	TAACATCTCACTACAGATCAGCA	58.86	168	54/34	
112	SSR07A20	*	EST/cDNA	LQ5	CX669338		(ttc)n (tac)n (gac)n	EST/cDNA	ctagattaggaccgctcCCTAATGACTTCATGACCTT	59.37	gttt	gttt	CCGATCTGGCATCTCTTGGC	58.83	201	58/32	
113	SSR07A21	*	EST/cDNA	LQ1	CX669454		(ct)n	EST/cDNA	ctagattaggaccgctcTGCTGTAATTTCCAGGCTC	62.45	gttt	gttt	CTATCTTCTGAGGCGCTC	57.23	137	54/32	
114	SSR07B05	*	EST/cDNA	--	CX936720		(gac)n	EST/cDNA	ctagattaggaccgctcCTTCCATCACTCACTGTTA	57.73	gttt	gttt	CCACAGCATCACTCAAA	60.05	177	58/32	
115	SSR07B08	*	EST/cDNA	LQ3	CB292573		(cgc)n	EST/cDNA	ctagattaggaccgctcTATTCGCTCAGCATCAGCA	62.53	gtttct	gtttct	CTAATCCGACATTTGGTAGTGG	60.31	192	54/30	
116	SSR07B09	*	EST/cDNA	LQ9	CB292707		(cgt)n	EST/cDNA	ctagattaggaccgctcTTTACAGCTGTTTGGTCTG	59.28	gtttct	gtttct	CCGTTGGATATCATGATGAGT	60.27	203	54/34	
117	SSR07B14	*	EST/cDNA	LQ7	CX183851		(ctt)n	EST/cDNA	ctagattaggaccgctcTTGCTCACTACTTGACTG	61.60	gttt	gttt	GGCTTTATGTCGGATCTG	61.36	215	56/32	
118	SSR07B27	*	EST/cDNA	LQ5	CX671829		(cct)n	EST/cDNA	ctagattaggaccgctcTACTTGGTACCAAGAAGAC	59.07	gtttct	gtttct	TGAGGCAAGAAAGTGTCTCT	60.49	191	54/32	
119	SSR07B25		EST/cDNA	LQ9	CX074011		(gaa)n	EST/cDNA	ctagattaggaccgctcAGGCTACTTCTAATCCATTTCT	60.86	gttt	gttt	GCCATTTGCTTCTTACTTACT	60.19	211	54/32	
120	SSR07B30		EST/cDNA	LQ5	CX665183		(ta)n	EST/cDNA	ctagattaggaccgctcCAGTAATGGAAGTGTTCCT	60.04	gtttct	gtttct	TGGCAAAACAAGTCTATTCCT	60.27	185	56/32	
121	SSR08A02	*	EST/cDNA	--	DY267483		(ttta)n	EST/cDNA	ctagattaggaccgctcTACCTATTCTTCTTGTCC	57.16	gttt	gttt	AACAGTGAATTTGACCGA	57.69	150	54/32	
122	SSR08A06	*	EST/cDNA	LQ1	DY304961		(ttta)n	EST/cDNA	ctagattaggaccgctcGTTATTTCAAGTATGTTGTCAG	57.50	gttttct	gttttct	TATAGGCCAACATCAATTTCCC	60.34	126	58/32	
123	SSR08A07	*	EST/cDNA	--	DY257192		(caga)n	EST/cDNA	ctagattaggaccgctcAATATTCAGCAGACAGACAG	59.99	gttttct	gttttct	TAATTTGCTTGTCTCGAGG	61.02	123	58/32	
124	SSR08A09	*	EST/cDNA	LQ2	CX663959		(cagg)n	EST/cDNA	ctagattaggaccgctcCATCTTGCATCAGACTCAC	60.08	gttttct	gttttct	LATGTTCTACATCAACTCTGCC	59.71	116	56/32	
125	SSR08A14	*	EST/cDNA	LQ2	DN618700		(aaat)n	EST/cDNA	ctagattaggaccgctcTCCGTCACATCATAGACTC	60.01	gttttct	gttttct	TGGGCTTTCTTCTTGTCTCT	60.88	186	58/32	
126	SSR08A15	*	EST/cDNA	LQ5	CX665717		(aaat)n	EST/cDNA	ctagattaggaccgctcATTTTCCGAAAGTGAAGT	59.51	gttt	gttt	ATTTCCCATATCTCCAAAT	57.25	141	58/32	
127	SSR08A16	*	EST/cDNA	LQ5	DN134966		(caga)n	EST/cDNA	ctagattaggaccgctcCATATTTCCAGGTAAGTCAAGT	59.51	gttttct	gttttct	TATTTCCATCACTCTGAAATG	57.23	145	56/32	
128	SSR08B02	*	EST/cDNA	LQ6	DY300589		(aat)n	EST/cDNA	ctagattaggaccgctcTCTGCTCAAGACTCTGCT	61.13	gttt	gttt	CATTTGAGCAAGAGCTGAAG	62.11	126	56/32	
129	SSR08B06	*	EST/cDNA	LQ9	DY298942		(cct)n	EST/cDNA	ctagattaggaccgctcTAACTGCTCCGATCAAGCTG	62.36	gttttct	gttttct	CCGCACTGGTAATCAAGCA	62.19	121	60/32	
130	SSR08B13		EST/cDNA	LQ9	DY295447		(cct)n	EST/cDNA	ctagattaggaccgctcTAACTGCTCCGATCAAGCTG	62.51	gttttct	gttttct	CCGCACTGGTAATCAAGCA	62.29	121	56/32	
131	SSR08B15	*	EST/cDNA	LQ7	DY292389		(acc)n	EST/cDNA	ctagattaggaccgctcACCATCACTTAACTCAAC	59.14	gttttct	gttttct	TAGCAGCATGACTTAATCCA	59.01	106	56/32	
132	SSR08B20	*	EST/cDNA	LQ9	DY291354		(att)n	EST/cDNA	ctagattaggaccgctcGCTGTACAAAGTGTGGTGG	61.07	gttt	gttt	ACAGTCCGAGACTTAGAC	62.95	152	56/32	
133	SSR08B21	**	EST/cDNA	LQ2	DY290555		(acc)n	EST/cDNA	ctagattaggaccgctcATGCTCACTCACTCACTTACT	58.95	gttt	gttt	CTTGGCGCTTTAGAAATG	59.51	130	60/32	
134	SSR08B22		EST/cDNA	LQ7	DY289533		(aat)n	EST/cDNA	ctagattaggaccgctcTTATCAATCACTCTGCTACC	58.94	gttt	gttt	ACGCGCATTCACTCTTAA	58.90	138	56/32	
135	SSR08B25	**	EST/cDNA	LQ9	DY289996		(aat)n	EST/cDNA	ctagattaggaccgctcGTTGACTCTCAAGAGATCTG	60.19	gttt	gttt	CTTCAAGCTCCGACGATTA	62.84	123	56/32	
136	SSR08B27	*	EST/cDNA	LQ6	DY288475		(ctca)n (ctcg)n	EST/cDNA	ctagattaggaccgctcCAACTCACTCACTCTGCTCTC	60.59	gttttct	gttttct	GCTTAATTTCACTACTCCGAG	62.97	101	60/32	
137	SSR08B28	*	EST/cDNA	LQ2	DY286595		(aat)n	EST/cDNA	ctagattaggaccgctcATCTCCACTCTTATGACTG	61.78	gttttct	gttttct	LATGTAACAAGTTCCTTGGCT	62.95	181	58/32	
138	SSR08B29	*	EST/cDNA	LQ6	DY285888		(cgg)n	EST/cDNA	ctagattaggaccgctcCTCTCAGCAGAGACTCAC	59.46	gttttct	gttttct	TGGGCTACTGATGACTG	58.93	160	56/32	
139	SSR08B31	*	EST/cDNA	LQ4	DY283748		(gag)n	EST/cDNA	ctagattaggaccgctcCACTGAAATATTTCAACAATCGAG	58.18	gttttct	gttttct	LATGTTCCGAAACAGTGAAGT	58.41	129	56/32	
140	SSR08B32	*	EST/cDNA	LQ6	DY281946		(aat)n	EST/cDNA	ctagattaggaccgctcATATTCATCTCCGCAAGTGT	59.28	gttt	gttt	GCCAACTCACTACTCTCAT	60.14	94	56/30	
141	SSR08B33	**	EST/cDNA	LQ2	DY287625		(cga)n	EST/cDNA	ctagattaggaccgctcCTCTCTCTCTCTCTA	57.84	gttt	gttt	ATGCTCACTCTCTCTCT	58.74	170	54/32	
142	SSR08B38	*	EST/cDNA	LQ3	DY283862		(cat)n	EST/cDNA	ctagattaggaccgctcACTCCTTTAAATTTCTCTGCT	57.63	gttt	gttt	CCGAAACAATCAAGAAATCTG	58.03	115	56/32	
143	SSR08B40	**	EST/cDNA	LQ2	DY280605		(aat)n	EST/cDNA	ctagattaggaccgctcACTCCCACTGTTTATGACTG	61.98	gttttct	gttttct	GCCTTTCGCTCACTGATA	61.97	171	56/32	
144	SSR08B44	*	EST/cDNA	LQ3	DY276228		(ctca)n (ctcg)n	EST/cDNA	ctagattaggaccgctcACTCCTTTAAATTTCTCTGCTG	57.87	gttttct	gttttct	CCGCAACAATCAAGTAACTG	58.22	118	54/34	
145	SSR08B47	*	EST/cDNA	LQ3	DY272433		(aat)n	EST/cDNA	ctagattaggaccgctcACTCCTTTAAATTTCTCTGCTG	57.87	gttt	gttt	GAATCCGAAACAATCAAGTAA	57.54	119	56/32	
146	SSR08B54	**	EST/cDNA	LQ2	DY268149		(cgg)n	EST/cDNA	ctagattaggaccgctcCATCTCACTCTCCACT	60.74	gttttct	gttttct	GCTTTCGCTCACTGATA	61.37	180	58/32	
147	SSR08B60	*	EST/cDNA	--	DY265343		(cgg)n	EST/cDNA	ctagattaggaccgctcATTCAATTTGGGGGTGAT	58.51	gttt	gttt	CTCCTCCAAATAGATAAGC	58.17	133	56/32	
148	SSR08B62	*	EST/cDNA	LQ5	DY257536		(aaagtg)n (aaagtg)n	EST/cDNA	ctagattaggaccgctcTGACTCAAGTATGAGAGAG	59.13	gttt	gttt	ACTGTTCTGCTTGTTCAG	61.43	145	54/32	
149	SSR08B64	*	EST/cDNA	LQ4	CV716381		(ctt)n	EST/cDNA	ctagattaggaccgctcTCAATGTTCTTCTCAACAAG	58.71	gttt	gttt	GATGGGAATAGCTCTCT	57.98	147	54/32	
150	SSR08B66	*	EST/cDNA	LQ8	CV711633		(cga)n	EST/cDNA	ctagattaggaccgctcAGAGACAATCAACCGAC	58.47	gttt	gttt	AAAGCAACAATTTCTCTC	57.96	111	58/32	
151	SSR08B68	*	EST/cDNA	LQ3	CV709642		(atggga)n	EST/cDNA	ctagattaggaccgctcTATGGAGGTATGATCAG	57.76	gttt	gttt	GGCTACTTCCCAATTTCCC	59.95	125	58/32	
152	SSR08B75	*	EST/cDNA	LQ4	CX296800		(gttt)n	EST/cDNA	ctagattaggaccgctcCTTAGAGATTTGAGTGAAGTCA	58.59	gttt	gttt	GATACCAACAACGAGTTC	58.12	191	54/34	
153	SSR08B78	*	EST/cDNA	LQ7	CX639446		(aat)n	EST/cDNA	ctagattaggaccgctcAGGCGCATTTCACTCTTAA	58.80	gttttct	gttttct	TTATCAATACTCTGTGTACC	58.71	142	56/32	
154	SSR08B82	*	EST/cDNA	LQ6	CX677953		(ctt)n	EST/cDNA	ctagattaggaccgctcTGGCAAAAGGGTCAAGAG	61.83	gttt	gttt	CAAGCTCACTCACTCACT	58.93	169	56/32	
155	SSR08B85	*	EST/cDNA	LQ5	CX076164		(cga)n	EST/cDNA	ctagattaggaccgctcTCTGCTCAAGTCTTCCC	61.79	gttttct	gttttct	GCTTCAAGTCTTCTGAG	58.71	153	54/32	
156	SSR08B85	*	EST/cDNA	LQ7	CX072241		(ctg)n	EST/cDNA	ctagattaggaccgctcAGAGTGGCTTGAATTAACACTGA	60.10	gttttct	gttttct	LAATGGAGGAGTGGCTATG	61.07	191	60/32	
157	SSR08B88	*	EST/cDNA	LQ6	CX044303		(gca)n	EST/cDNA	ctagattaggaccgctcACTCGCTGATGATCATTTAGT	59.72	gttttct	gttttct	CCGCAACTCATCATGCTCAT	60.14	115	56/36	
158	SSR08B90	*	EST/cDNA	LQ8	CX934959		(aaag)n	EST/cDNA	ctagattaggaccgctcGAACCAACTTACACCGAC	60.81	gttttct	gttttct	ACTGAGTGAATTCGCAACA	59.83	174	56/30	
159	SSR08B92	*	EST/cDNA	LQ8	CF509535		(aac)n (agc)n	EST/cDNA	ctagattaggaccgctcCTAAGCAAGTGTCTCACTC	59.63	gttttct	gttttct	T				

179	TSRF116	*	EST/cDNA	L63	DC895047	EST/cDNA	(aac)n(gac)n	F9GCC	ctagatattaggacgcacAGGCCAAGAACTGACAATATCC	60.87	gttt	gtttATCCATTTGGTCCCTACCATC	60.87	174	56/30
180	TSRF120	*	EST/cDNA	L62	CX295530	EST/cDNA	(aag)n	F9GTC	ctagataggagcgtcAGCTCGAGAGAGGGGAGAAAC	60.65	gttt	gtttATTCCCTGTCCAGTAAATAGC	60.65	197	60/32
181	TSRF124	*	EST/cDNA	L67	EY705148	EST/cDNA	(agg)n	F9AGG	ctagatattaggacagcAGTGGAGTTACAGCCAAACCCAG	61.05	gttt	gtttCTGTAATTTGGAGTGAAGGTTG	61.05	235	60/32
182	TSRF136	*	EST/cDNA	L65	PC877062	EST/cDNA	(acc)n	F9AGG	ctagatattaggacagcAGTGGAGTTACAGCCAAACCCAG	60.99	gttt	gtttGGGGGTATATAAAGAGGAGG	60.99	213	56/32
183	TSRF138	*	EST/cDNA	--	DY272315	EST/cDNA	(aca)n(ata)n	F9GTC	ctagataggagcgtcACAGAGTGTGAAACTGTGTCC	60.78	gttt	gtttATATCCCGCAATACAGAGCATG	60.78	177	60/32
184	TSRF144	*	EST/cDNA	L62	DN618162	EST/cDNA	(acc)n	F9TAC	ctagatcaggactacACAGATAGTAGACCTCGAAAG	60.99	gttt	gtttAAACTTCTCTCGTGTCCCG	60.99	222	60/32
185	TSRF157	*	EST/cDNA	L67	DY262980	EST/cDNA	(agc)n	F9TAC	ctagatcaggactacGTTGTGTAGAGTTACAATCT	61.20	gtttttt	gttttttCAAGGCTGGTGTATCAGATG	61.20	293	56/32
186	TSRF160	*	EST/cDNA	--	EY683407	EST/cDNA	(agc)n	F9CCG	ctagatattaggacccgTCAGAAAGAAATCATGCGCCG	61.05	gtttttt	gttttttGAGCTGAACATTTTGGCAAGG	61.05	214	54/32
187	TSRF161	*	EST/cDNA	L68	EY651421	EST/cDNA	(agc)n	F9GAC	ctagatcaggacgacGCTGAAATGGCAAAACAGAGC	60.44	gtttttt	gttttttGGCAACAATCTTCCCAAGTC	60.44	253	56/32
188	TSRF162	*	EST/cDNA	L67	DY266884	EST/cDNA	(agcc)n	F9TAC	ctagatcaggactacTTCAGTTTCAAAGAGGCCGAG	61.06	gtttttt	gttttttCACTTTCCCACTTCCCTCATC	61.06	190	58/32
189	TSRF164	*	EST/cDNA	--	DY265747	EST/cDNA	(agccaa)n	F9GCC	ctagatattaggacccgTTCAGTACACAGGGCCATCG	61.12	gtttttt	gttttttGGGACTTGTTCGGTTATCCAG	61.12	229	54/32
190	TSRF167	*	EST/cDNA	--	EY863111	EST/cDNA	(att)n	F9GCC	ctagatattaggacccgGCTGCTGATGATGATAAATCCAG	61.48	gtttttt	gttttttTCAGCAAAAACCAAGCTCC	61.48	175	58/32
191	TSRF169	*	EST/cDNA	L69	PC913104	EST/cDNA	(ata)n	F9GAC	ctagatcaggacgacGTGTAAACAGAGGATTCATGG	60.84	gtttttt	gttttttAGATTAABAAATGGCCGTTCGG	60.84	310	56/32
192	TSRF172	*	EST/cDNA	L64	DY297851	EST/cDNA	(ata)n	F9AGG	ctagatattaggacagcGTGATACGCTTCCCAACAC	60.91	gtttttt	gttttttGGCTGGCAACATTAATCTC	60.91	268	56/32
193	TSRF184	*	EST/cDNA	L61	EY884078	EST/cDNA	(atc)n	F9GCC	ctagatattaggacagcGTGGCTCTTATACCTGGGAG	61.04	gtttttt	gttttttATACATCATCTGATCAGAGGAC	61.04	258	56/32
194	TSRF187	*	EST/cDNA	--	EY650146	EST/cDNA	(atc)n	F9GTC	ctagataggagcgtcTAACGGAGGAAACAGGAG	61.12	gtttttt	gttttttCACTGCTGATGGTTAGGACG	61.12	237	62/32
195	TSRF191	**	EST/cDNA	L63	CF507794	EST/cDNA	(atg)n	F9GAC	ctagatcaggacgacGTTGTTCTTCCACCCACAC	61.72	gtttttt	gttttttTAGACGCACATCAATCGAAGG	61.72	187	54/32
196	TSRF192	*	EST/cDNA	L65	CX672882	EST/cDNA	(atg)n	F9TAC	ctagatcaggactacAGCGAAGAAAGCAAGAAATAG	61.19	gtttttt	gttttttGGCTCTTATCCCTTCCCAAG	61.19	179	56/32
197	TSRF194	*	EST/cDNA	--	CX637983	EST/cDNA	(atg)n	F9TAC	ctagatcaggactacGTGGTGTATACGACTATGC	61.47	gtttttt	gttttttAGTTTATTCATCGAGCCGAG	61.47	172	58/34
198	TSRF195	*	EST/cDNA	L63	FC927104	EST/cDNA	(atgaaa)n	F9AGG	ctagatattaggacagcAGTGGAGTTGATGCTCAGATG	61.19	gtttttt	gttttttCTTCCGATGTCACCAATTC	61.19	167	58/32
199	TSRF198	*	EST/cDNA	L63	EY849742	EST/cDNA	(atgggg)n	F9GAC	ctagatcaggacgacTGGCAATGCAACAACAATCTC	61.00	gtttttt	gttttttTAGAAAGGAGGAAAGCAATGAGT	61.00	167	56/32
200	TSRF204	*	EST/cDNA	L65	EY673751	EST/cDNA	(caa)n	F9GCC	ctagatattaggacccgTTCATCCGTTTTCACAGCTC	61.13	gtttttt	gttttttGCTTCAAAACCCAGATTTCTC	61.13	207	56/30
201	TSRF208	*	EST/cDNA	L67	EY776018	EST/cDNA	(caa)n	F9GTC	ctagataggagcgtcCTCCAAACCAAACCTCTC	61.19	gtttttt	gttttttGTGGGTATGAAGTTCCTGGT	61.19	214	62/32
202	TSRF211	*	EST/cDNA	L67	EY879492	EST/cDNA	(caacag)n	F9GAC	ctagatcaggacgacGAGTGAACAAGCAAGCTGTC	60.93	gtttttt	gttttttAAACCCCTTTTAGCACCAGAG	60.93	243	60/32
203	TSRF215	*	EST/cDNA	L63	CF507794	EST/cDNA	(cac)n	F9AGG	ctagatattaggacagcGTTTACATGATGAAAGGGGG	61.72	gtttttt	gttttttTAGACGCACATCAATCGAAGG	61.72	247	60/32
204	TSRF218	*	EST/cDNA	L61	CV174512	EST/cDNA	(cag)n	F9CCG	ctagatattaggacccgTCTGACCATCTTTCACAGCTG	61.41	gtttttt	gttttttATTTGAAGACGGGTATGGCC	61.41	204	56/32
205	TSRF219	**	EST/cDNA	L68	EY651421	EST/cDNA	(caa)n	F9GAC	ctagatcaggacgacGTGATGAGAGGACTGTCG	61.62	gtttttt	gttttttGTGTCCTCCATCAACGCG	61.62	267	56/32
206	TSRF225	*	EST/cDNA	L64	EY741460	EST/cDNA	(cag)n	F9AGG	ctagatattaggacagcGTTCTCCATCCCAACAC	60.65	gtttttt	gttttttTCGCGATAGCCTAATCAGG	60.65	151	54/32
207	TSRF229	*	EST/cDNA	--	PC913104	EST/cDNA	(cag)n	F9TAC	ctagatcaggactacAAAGATTCACCAACCTCTCC	61.10	gtttttt	gttttttCACTGCTGATGATGAGGACG	61.10	289	56/32
208	TSRF230	*	EST/cDNA	L68	CB293840	EST/cDNA	(cag)n	F9GTC	ctagataggagcgtcGTAAGATCCTTCCACACCTC	60.91	gtttttt	gttttttGAAAGCTGTGTTGTGCTCACC	60.91	230	60/32
209	TSRF234	**	EST/cDNA	L68	CB293840	EST/cDNA	(cag)n	F9CCG	ctagatattaggacccgATAAGTGGGAGTGGAGTTC	61.47	gtt	gttTCTTGTCTGCTGATATGG	61.47	203	60/32
210	TSRF237	*	EST/cDNA	--	DC886823	EST/cDNA	(ctcggg)n	F9GTC	ctagataggagcgtcAACCAATACCCACAGAAAC	61.21	gtttttt	gttttttCTAATGGGCTTTGGAGATGG	61.21	186	54/32
211	TSRF238	*	EST/cDNA	--	EY770405	EST/cDNA	(caggtt)n	F9GCC	ctagatattaggacccgATCCGGCTCCCTGAAAAGAG	60.85	gtttttt	gttttttGCATTAACAGGCTCTTCTCTC	60.85	183	54/32
212	TSRN214	*	EST/cDNA	L62	DY271862	EST/cDNA	(can)n	F9TCC	ctagatcaggactccCGCAACAGAGGATAAACAGAC	60.62	gtttttt	gttttttTCTTCTTAAACAGGCTCTTCTG	59.94	145	60/32
213	TSRP06	*	EST/cDNA	L66	DY281841	EST/cDNA	(gaa)n	F9GAC	ctagatcaggacgacAACAGCAAAACAGCAAA	61.94	gtttttt	gttttttCAAGTACATGAACAGCCAC	59.40	208	60/32
214	TSRP07	*	EST/cDNA	L62	EY812469	EST/cDNA	(agj)n	F9GTC	ctagataggagcgtcATCCAACTTATATTTGCTCAT	58.29	gtttttt	gttttttTGACCTATCATGAAGACACA	59.63	161	60/32

B. SSR markers used in this study

#	Marker	Cert.	Reference	LG	Accession ID	Tag	Tagged forward primer	tail	Failed reverse primer	Amp	Program
215	C1BE0246	*	1)	L65	ET089421	F9GCC	ctagatattaggacccgATTGGTGTGTGTTGAGGTTG	gtttttt	gttttttCGTGACAGAGATGATGTT	233	56/32
216	C1BE0447	*	1)	L66	ET091388	F9CCG	ctagatattaggacccgCACAAAGAGGATACCCACAA	gtttttt	gttttttCGTCAAGAGAGGAGATGATG	326	56/32
217	C1BE1644	*	1)	L63	ET097780	F9GCC	ctagatattaggacccgACAGAAGAGGAGCCATATTT	gtttttt	gttttttTCAGAGAGAACCCGAGAAAG	383	56/32
218	C1BE2165	*	1)	L67	ET102021	F9GTC	ctagatcaggagcgtcAATCACTCTCAACACCCAG	gtttttt	gttttttTAATGCAAAATAACTACCATTC	286	56/32
219	C1BE2227	*	1)	L68	ET100673	F9TAC	ctagatcaggactacAGAAACCAAGTCACTCACAG	gtttttt	gttttttTAGAGAAGGATGAGGATGAGG	176	54/32
220	C1BE4265	*	1)	L62	ET106965	F9AGG	ctagatattaggacagcACACTGCTAAACCGACAC	gtttttt	gttttttTACTACTCAACAGCAACAGGAA	254	56/32
221	CX0004	*	2)	L65	CK933007	F9CCG	ctagatattaggacccgAAACCCCACTTCAAGCAAC	gtttttt	gttttttGAAAGGAGGCTTTGATGTC	276	56/30
222	CX0010	*	2)	L61	BQ623170	F9TAC	ctagatcaggactacAACCGAAGTGAAGGAACT	gtttttt	gttttttACATTCATGGCCACATCTCA	228	58/32
223	CX0035	*	2)	L63	CD575772	F9GTC	ctagataggagcgtcCACTTAACAGAAACCAAAACA	gtttttt	gttttttCAAAAAGGGGTGCAAAAGAA	189	56/34
224	CX2004	*	2)	L62	CF653229	F9CCG	ctagatattaggacccgAAACCGCCGAAACTTTTACA	gtttttt	gttttttGGAAATCCCAAGAAAGTTGG	202	56/32
225	CX2018	*	2)	L62	CF507198	F9GTC	ctagataggagcgtcAAGAGATCGAAAGGCAAGAGA	gtttttt	gttttttTTGAGATTGATGTGAGCCG	179	56/32
226	CX2021	*	2)	L62	CK739933	F9TAC	ctagatcaggactacAAGTCACTGCTTTAGCACTTTGA	gtttttt	gttttttCAAGTTGCCAATTCAGGAGG	147	58/32
227	CX2040	*	2)	L63	CK932713	F9CCG	ctagatattaggacccgACAGCTCCCACTTTCTTT	gtttttt	gttttttGATGATGTTTTCCTGTCGCG	112	56/32
228	CX3001	*	2)	L63	CO913029	F9GAC	ctagatcaggacgacAAACAACTCTTCAAGAGGCG	gtttttt	gttttttGAGACTCAACCAAGCAACCA	432	56/32
229	CX3040	*	2)	L69	CNI90783	F9TCC	ctagatcaggactccAAGCGATGCAACAGATACCC	gtttttt	gttttttCAGCAGCAACAGCTCTTCA	308	60/32
230	CX4005	*	2)	L63	CK938465	F9AGG	ctagatattaggacagcACACCAAACTTGGCCCTC	gtttttt	gttttttTGAAGATGGATGTCGGTATA	372	54/34
231	CX4008	*	2)	L64	CK933430	F9GAC	ctagatcaggacgacACCTCACTCACCACACTCC	gtttttt	gttttttTGAGGCTAGGCACTGGTTT	394	58/32
232	CX4040	*	2)	L62	CF834831	F9TAC	ctagatcaggactacGAAAGAGGCAAGAATACCG	gtttttt	gttttttTGCACTTCTCATGCCAAAATA	368	56/32
233	CX5022	**	2)	L67	CD574077	F9TAC	ctagatcaggactacCTCTCGATCCACTGCAAAACA	gtttttt	gttttttTAGCCAGCCAAAGCAACTTAA	255	56/32
234	CX5039	*	2)	L67	CF833361	F9AGG	ctagatattaggacagcTCCGCAATAATTTCAATTTATTA	gtttttt	gttttttTCGATGAATTCGGAGGATC	443	56/32
235	CX6024	*	2)	L66	CE9505	F9AGG	ctagatattaggacagcAGGCTGCTCTTCTCTCTC	gtttttt	gttttttTCTCGGATTTGTGAGTTTG	203	56/32
236	CX6035	*	2)	L67	CD573989	F9GTC	ctagataggagcgtcCTTGGCCAGGGTCTCACTCTC	gtttttt	gttttttCTCGGACTCAGGTTACCAT	258	56/32
237	CX6037	*	2)	L67	DR909803	F9TAC	ctagatcaggactacGAAAGGGAATGATGGCAACA	gtttttt	gttttttTGTCTTCAACCCCTCTCCAT	177	58/32
238	CX6F21	*	2)	L61	DN621499	F9GAC	ctagatcaggacgacTACAAGTTCGCCAGTTATCCCG	gtttttt	gttttttTACTTGACCCGCTTAGGAGTGAC	163	58/32
239	CX6F32	*	2)	L65	CF506971	F9TAC	ctagatcaggactacACCCCTCTTGTGGCAGTCTTT	gtttttt	gttttttACAAAAGAAAGGAGTTGACCGGTA	166	56/32
240	F02	*	3)	L65	BQ623425	F9TAC	ctagatcaggactacAAACAGTGTAGCTGCACTTTTCAAC	gtttttt	gttttttGATCAAGAGGACTTGGCCATCTC	178	56/32
241	F03	**	3)	L65	CK912164	F9AGG	ctagatattaggacccgCAGGATGAGGATGAAAGA	gtttttt	gttttttCTGTGCTGATTTCTTCTCAC	146	54/32
242	F16	**	3)	L63	DR909803	F9GAC	ctagatcaggacgacGCTTCAACCTCTCCATCTTCTCTC	gtttttt	gttttttGGGACTTATGGCAACATTAACGCA	172	52/34
243	F21	*	3)	L61	DN621499	F9GTC	ctagataggagcgtcCTCAAGATTCGCCAGTTATCCCG	gtttttt	gttttttTACTTGACCCGCTTAGGAGTGAC	163	52/34
244	F40	*	3)	L67	CV716690	F9GCC	ctagatattaggacccgTGTGTTTACAGAGGCAAGCAAG	gtttttt	gttttttCTGCAAGGAGCTTCTTACTCAA	104	56/32
245	F50	*	3)	L64	CNI83579	F9GAC	ctagatcaggacgacAGGACGATTTCAAGTTCAGACTTG	gtttttt	gttttttTGACAAAATCGAAGAGATCAAGC	165	54/34
246	F79	*	3)	L62	BQ624534	F9GCC	ctagatattaggacccgCTGGCTGCAAGACTTCTGTGTAG	gtttttt	gttttttATAGATGTGGCAAGCAGAGCAAG	176	58/32

Cert: certified markers by error check with trio sets. *) certified and used for genetic analysis. **) certified, but rejected from genetic analysis due to overlap to other certified marker. No symbol: not certified due to error on certain trio.
Category: gSSR - designed from genomic SSR, EST/cDNA - designed from public EST or cDNA sequence. INDEL: genomic indel.
LG: Linkage group of this marker on one or two cross population(s).
Source:
Tag: type of BS tag (Shimizu and Yano, 2012).
Tail: pig tail sequence (xxxx).
Amp: amplicon size with tag sequence.
Program: anneal temperature/PCR cycles

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