

Development and Characterization of EST based SSR markers in Madagascar periwinkle (*Catharanthus roseus*) and their transferability in other medicinal plants

Supplementary data 1

Supplementary data sheet of SSR microsatellite markers developed in this study, table includes genbank accession no. of associated EST, SSR type, repeat motif, primer sequence, annealing temperature (T_m), percentage of GC, expected band size in *Catharanthus roseus*.

S.no	ID	SSR type	SSR motif	T _m	GC%	Forward Primer	Reverse Primer	Expected Product size
RG01	gil164561865	p3	(CTT)7	59.86	50	GGAACCAAGGATGTTAGAGTGG	CTGCAACGGTTACTAGAGAGTAGAGC	157bp
RG02	gil164561642	p3	(GAA)6	60.07	50	CCGAGTTCAGATCGGTGAAT	AACGCCTCACAACTTCCTC	194bp
RG03	gil164561321	p3	(AGA)9	60.43	55	GTAGCCGAGGAGGATGATT	AACAGAGGCTCCGAGCA	116bp
RG04	gil164556897	p3	(ATA)5	61.04	57	CGTCAAGACCTTACCCAGGAG	GTCTCCTCCGTCACCAGAAA	127bp
RG05	gil164556756	p3	(TGC)5	60.72	57	CTGCTAGGCATGGTGGTGTAG	GATCCCAGCGGTGACTCTTA	199bp
RG06	gil164556642	p3	(AAG)5	60.24	55	GTGGCAGACCCAACATTACC	GGAGCAAAGGCTGGTGTAAAC	149bp
RG07	gil164556449	p3	(GCA)5	60	57	GAGGAGGTGTCTCTCATGCTG	CGACCTCAACAGAAGGTTTCG	175bp
RG08	gil164555839	p3	(GCA)6	60.3	55	AGAAGGAAGTGGTGGTGTCTG	GTTTACAGGGGGAGGAGGAG	159bp
RG09	gil171846161	p2	(TA)7	60.59	61	CTGGGGCTCTTGGGTTTC	GCTGCTTCTTCTGCCGTCTC	282bp
RG10	gil164561674	p2	(AT)9	60.79	63	CGTCAGCTCAGCAGTGGAC	CTTCCTCTTACCCCTAGCC	241bp
RG11	gil164561349	p2	(AT)11	62.09	60	GGCACGAGGCATCCTTACTC	CCACAGCTCTGGTAGCTCCT	115bp
RG12	gil164561153	p2	(TA)10	61.32	61	GGACAAGCTGGAGCAGCA	CTGCAACCAGAGGCTTCC	111bp
RG13	gil164560959	p2	(TC)6	62.98	60	CCGGAGGTGATGAGTTCTG	GAGGCTGCTTTGGAGGAG	171bp
RG14	gil164560486	p2	(TC)6	61.28	60	GGAAGGCCGAGTACGAGAAG	CTACTACACCCACCCCATCC	210bp
RG15	gil164556819	p2	(AG)8	59.58	60	GAGAGAGAGAGAGCGGCAAG	GTGGGTCTCCCACAATAGCC	263bp
RG16	gil164554530	p2	(AG)8	59.43	60	GCCAAGCCAGAGAGAGAGAG	GTCACCGTACGGAGGTGTTTC	256bp
RG17	gil164554046	p2	(TC)7	59.9	61	GGCGGAGGAGCTCATGTA	CGGCACCGGAGAAGAAGA	169bp
RG18	gil164561715	p4	(AAGA)4	60.64	50	CATTCTCTTCTCGAGGCTTCTG	ACCCCATGACAGTCAAGATAG	280bp
RG19	gil171846227	p4	(TTTA)4	60	55	ACCTGAGGCGATTGTGTACC	CTTAGCTTTCTCAGCCTGCTCT	175bp
RG20	gil164556358	p3	(AGC)8	59.75	55	AGCTGAACAAGGAGCTGAGG	GCGCCGGTCTTTCTTCT	104bp

RG21	gil164559832	p5	(TGAAA)4	60.24	50	CCCTTCCTGAGAGACTCAAATG	CCAAGCACTCTTCATCTCAGG	273bp
RG22	gil164553982	p3	(ATC)6	60.16	60	CGAGGAGGTGTTAGCAGAGC	GGAGAGATGATGGGCTGATG	278bp
RG23	gil164553785	p3	(TCT)8	59.83	60	GAGCCATAGCACCAGAGGTC	GGGTCAGCCCAGTAGCTGTA	118bp
RG24	gil164551888	p2	(TC)7	62.63	60	CACGAGGGGGTGGATTAGTG	GTAACCAGGAGGGGGTGTCT	203bp
RG25	gil164551881	p2	(TA)11	60.09	61	CACCCTTCTCCTGGCACAC	GTAGTGGCGGGAGGTGATAG	148bp
RG26	gil16658717	p2	(TC)14	59.82	61	GGACAGCGAGCTTTGAGC	GGAGGATGCCACACCAAG	126bp
RG27	gil164556759	p5	(TGAAA)4	60.89	50	GTTATGACGTGTGAAGCAGCAG	CCCAAGCACTCTTCATCTCAG	202bp
RG28	gil164555337	p5	(TCCTT)4	61.53	50	CTCTTGGTGATGCTAACAGAGACC	CCTTGATTCTTCCTTCCTCCT	172bp
RG29	gil164554532	p3	(GCA)6	59.02	55	GTGAAAGCCTCCGAAGAGTC	CTTCGGTAGCAAAGGGACTG	186bp
RG30	gil164554493	p3	(GAT)5	60.07	55	GGACCTCTGCCTGTTATGGA	CGCTCCCTTGCCAGAGTAA	205bp
RG31	gil164555592	p2	(TC)7	60.07	60	GCCTCCAGTTACCCTTCCTC	ACAGCAGGATCACCAAGACC	198bp
RG32	gil171846202	p2	(TA)6	59.85	55	CAAGAGCGAGCTAGGGAAGA	CTGGCGGGTACAACCTTAGA	124bp
RG33	gil164560173	p4	(GAGT)4	62.32	52	CTGTCTATGACTGGCTGTACAGTGG	CCAACTCACTCACTCACTCCAGTT	281bp
RG34	gil164554234	p4	(GAGT)4	61.07	52	AGGAGGAGCAAGGGTAAAAGC	CCAACTCACTCACTCACTCCAG	177bp
RG35	gil164554654	p4	(TGTT)5	60.75	52	GCAGTACAGTGTGAGCTTCTTC	GGCGATTCCATTGATCCTC	144bp
RG36	gil156628465	p2	(TG)10	59.73	50	GACATCATCCAGACTGAGAACG	CACACACACACACACAGAGTC	231bp
RG37	gil164559638	p2	(TC)7	60.41	52	GTTCTCTAGGAAGAGGAGAGGACAG	CGTTGAGAAGAGAAGGGTTGTC	205bp
RG38	gil164553409	p2	(TC)10	60.9	52	GTACCTGAGTGGCGTTATCCTCT	GTAGTATTCTGGCATCTCTGAGC	203bp
RG39	gil164553941	p4	(GCAG)4	60.12	52	GCCCCAAGAAGGTTGAACAG	GCTAGCCTTGATCTACTCCTTCC	113bp
RG40	gil164560951	p5	(TGAAA)4	59.91	50	GAGAGACTCAAATGTGCCTGTG	GATCATAGGCTTCTCCCCAAG	281bp
RG41	gil164553425	p5	(TCCTT)4	60.22	52	GAAGGTCTCCTGTCGTGTACTION	GGTCTCTGTTAGCATCACCAAGAG	178bp
RG42	gil164558595	p6	(AGTTGG)6	61.25	50	GGCTCTAATACGTTGCAGTACACC	GAAAGCTCCTGTCTCATCAACC	278bp
RG43	gil171846206	p3	(GAT)6	61.25	52	TCGGATGTCCCTCACCTTTAC	AAAGGAGGAAGAGGGTTGGA	122bp
RG44	gil164562150	p3	(AGC)7	60.08	50	CCTCCCACAGACGATCTACTACTT	GTCCAGCCATACTATTGCACTCC	124bp
RG45	gil164560957	p3	(TTA)20	59.75	55	GCGGCTCTGTTTCTGTCT	GAACATCTCCTCCCACAAGC	234bp
RG46	gil164560911	p3	(TCC)5	60.2	55	CAGTTGCACCACCAACTGTC	TTCCACCTCTCCAGTCTTG	149bp
RG47	gil164560771	p3	(AGA)6	61.87	55	GAATTCGGCACGAGGTAAGG	GCGATGTAGCGGAGTTCTCT	153bp
RG48	gil164560728	p3	(CAC)5	59.6	55	ATCAGCAGCTCCTCCGTAAG	CCTCCTCCGTCCTTGTGATAG	185bp
RG49	gil164560369	p3	(GAG)6	62.31	56	GTAGGACGCTGACGTACCACTTC	CCTCCACCACTTCCAAAACC	188bp
RG50	gil164560187	p3	(CTT)5	61.18	57	GTACTIONCTCCAGCCGTTGAGG	CGCCTTATCCTCAGAAGCAC	228bp
RG51	gil164558940	p3	(GTC)5	60.06	57	CAGAGCCGGTTAGAGTGACAG	GGCTCAGCTACAGCTTCTCC	114bp

RG52	gil164557800	p3	(GGA)7	59.67	60	CCATAGTCACGGAGGAGGAG	GTGAGGCATGGCTGAAAGTG	107bp
RG53	gil164557046	p3	(CCA)6	60.39	60	CTATGAGTCCGACCCACCAC	AGGGTGGATTCGAGAGAAAC	290bp
RG54	gil164555951	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CAGCCCTCATAACCTCTCGAC	126bp
RG55	gil164555298	p3	(TTC)5	60.29	55	CTTACTACCGCTGCCGACAT	CTCGGATCACTTGGAAGGAC	156bp
RG56	gil164553403	p3	(AAG)8	59.72	60	GCTGTACCTGGTCCTTCTG	CTCATCAAGGGCAGCAGACT	297bp
RG57	gil164553274	p3	(AGA)5	59.77	57	GTAGCCCTGCACCTGATACTG	GCCTCCTCAGCTTCCTTCTTC	169bp
RG58	gil164552057	p3	(TCT)7	59.01	55	GGCTCTTCTTCTTGACTGG	GACTAGGTTGCCACCACCTCT	174bp
RG59	gil164559865	p2	(TG)6	58.53	60	GTCCTGTGGACAGAGAGCAG	GTAGTGCCATCACGGACACC	128bp
RG60	gil164559804	p2	(AT)6	60.52	61	GAGCCGATGCCTGAAGTG	GAGGCAGGCAGTGCAGTAAG	157bp
RG61	gil164559720	p2	(TA)12	60.76	61	GGTGGTGCTGGTGCAACT	GGCCTCCACCTCCCTCATA	201bp
RG62	gil164559608	p2	(AT)6	60.21	60	GACTCCGCCTCCTTACCTTC	GGCTTCTGGGCTCTCCTT	154bp
RG63	gil164558210	p2	(TG)6	58.53	60	GTCCTGTGGACAGAGAGCAG	GTAGTGCCATCACGGACACC	128bp
RG64	gil164557304	p2	(CT)6	60.38	63	CGCAGAAGGCTCTCCTCTC	GCTTCCTTAGCTCGGACCTG	292bp
RG65	gil164557187	p2	(CT)6	59.4	61	GCCGGTCAAGAGCGTTAC	CTTCCGGTGTACCTTCCTC	211bp
RG66	gil164553479	p2	(TC)7	60.21	61	GCACGAGGAATCCACCAG	GGGGTGTCTTCCACAAG	294bp
RG67	gil164553256	p2	(GA)8	60.71	60	CCGACCTGGTACTGTTGCTC	CACCCCTGATCCTCCTAGC	275bp
RG68	gil164552939	p2	(TC)6	61.28	60	GGAAGGCCGAGTACGAGAAG	CTACTACACCCACCCCATCC	213bp
RG69	gil164552768	p2	(AG)9	61.22	61	CACTCCGTGCCCTTCT	CCTGGGCTCTCTCCTTCTC	283bp
RG70	gil164552746	p2	(AG)8	59.43	60	GCCAAGCCAGAGAGAGAGAG	GTCACCGTACGGAGGTGTTT	256bp
RG71	gil164552338	p2	(AT)12	59.82	61	GCTCAGAAAGCGCTGGAC	TTCTCCTGCCGGATAGGC	101bp
RG72	gil164552319	p2	(TA)11	60.09	61	CACCCTTCTGACACAC	GTAGTGGCGGGAGGTGATAG	148bp
RG73	gil164552190	p2	(TA)12	59.68	60	CAGGAGAGGCCACCAGATAC	GACCATCGGGTCCACTTCTC	210bp
RG74	gil164552183	p2	(CT)6	58.02	60	CCATAGAGGCTCCTCTCCTC	GCCTGTTCTGCCTCTGCTTC	150bp
RG75	gil171846154	p3	(ACC)5	60.27	61	AACCACCACCACCACCAG	ATCTGGGTCTCGGGTTC	135bp
RG76	gil171845887	p3	(CTT)10	60.14	60	CAGAGGAAGCCGAGAGTGTC	GCGGCTTCATTGGAGGAG	254bp
RG77	gil164561932	p3	(GCT)6	62.56	60	GGCACGAGGTGCACTCCTAT	GCCACCCCTACTCTGCTTTC	191bp
RG78	gil164561921	p3	(GCA)9	60.07	61	GGTGGTGGTGGTGGTGAT	CCTCCTTTGCTGCTGCTG	210bp
RG79	gil164561881	p3	(CAA)6	60.42	61	GGCCATGGAGGAGGAAAC	AGTGCCAGAGCCGGTACA	117bp
RG80	gil164561877	p3	(TAT)5	62.92	61	CGGCACGAGGAAAAGTGC	GGGCGAGCCATTGCTAAG	289bp
RG81	gil164561875	p3	(GAA)8	60.73	60	TCTTCTGCCCTACTCCTC	CTCCACAGCCAGAGAAGGTG	192bp
RG82	gil164561873	p3	(CTT)7	59.04	61	CTCCCGCCATTGTAGTC	ACCCCGAAGACGAAGAGG	122bp

RG83	gil164561867	p3	(TCA)7	59.62	61	CCTCGCCCTAAGGAAACC	ACCCGAACCGGAAGAAGC	144bp
RG84	gil164561866	p3	(AGG)5	60.57	60	GACCACCGACGAGTGTAAAG	GTCTCATAGACGCGGCACTC	156bp
RG85	gil164561774	p3	(GCT)5	62	61	ACCCCGGAAGCCCATATC	GCCACGAGACCTCTCAACTC	162bp
RG86	gil164561727	p3	(CTC)5	59.72	60	CTCCAACCGTGGTAGAGGAG	GGAGGAGGAGGAGTGGTTTC	106bp
RG87	gil164561696	p3	(AGC)6	60.1	60	CAGCAGCAGCAGCACTACTC	CTGGTCTCTGCTGGTTAGGG	246bp
RG88	gil164561316	p3	(CTT)5	59.92	61	CCTCCCCAACACCAACAG	CGGAGGTGGAAGAGGAAGAG	117bp
RG89	gil164561292	p3	(GAT)7	60.47	60	CCTCCTCCTTGCCTTCTCTC	CCTCGAGATGGGCTGCTA	107bp
RG90	gil164561186	p3	(GAT)5	61.25	60	GGCGAAGTAGAAGCCCTACG	ACCCAGGAGGGAGAGTAAC	289bp
RG91	gil164561100	p3	(CCA)6	62.3	60	GCCTGAGCCAACACCTTCTC	GTGGGGGTGGTGTGTGT	209bp
RG92	gil164561080	p3	(TCT)5	59.57	60	CCCGGTGTACAGAGGAGTTC	GACGGAGAGAAGGAGGAGGT	297bp
RG93	gil164560880	p3	(ATC)7	60.57	55	GCCCTTACTTTCTCCTGA	CTCTGCTTGTGCCACTGCTA	246bp
RG94	gil164560844	p3	(AGA)5	60.18	55	CAGCGGTAGCAGTAGCATCA	CCCAACCCTAATGTCCAGAG	230bp
RG95	gil164560584	p3	(AGA)5	60.18	55	CAGCGGTAGCAGTAGCATCA	CCCAACCCTAATGTCCAGAG	230bp
RG96	gil164560513	p3	(CAA)5	60.62	55	CTCCCTCCGACAAGAAACT	AGGTGGAGGAGGAGGAGGT	242bp
RG97	gil164560282	p3	(AGA)5	59.8	55	GAAGAAGACCGAGTCGGATG	TGCTCCTTCTCCCCTTTCTC	120bp
RG98	gil164560245	p3	(AGA)6	60.96	55	GCATCACCAAGACGAGAAGC	GATCGTGTCTTCACCGTGT	188bp
RG99	gil164560188	p3	(CCG)6	59.69	55	CTAGTCAAATCCGCCACCTC	ATGGCGTGTACTTCCAGTCC	116bp
RG100	gil164560065	p3	(GAA)5	60	55	CCAGAGTTGGTCTGGTGTT	CTGATGCCACCAATCAC	173bp
RG101	gil164560012	p3	(AAG)5	60.91	55	TGGAAGTGTGATGGCTGTGAG	GCTGAGCCACCAGGTTGTAT	203bp
RG102	gil164560001	p3	(GTC)5	60.11	55	ATCACCTGTGTTCGGAGAG	CAAGTAGCCGGCTCAATCTC	286bp
RG103	gil164559870	p3	(AAG)5	59.95	55	GAGGAAGTTGATCGGAGCAG	GCCCTCTGACCTTTCTCTT	144bp
RG104	gil164559634	p3	(GAA)7	60.05	55	CTAACACCAGCTGAGGCACA	GGGGCTAACAGCAGTGAAG	155bp
RG105	gil164559489	p3	(TAC)5	60.05	55	GAGGTGATTCTCCCCACTCA	GCCCATGCCTTGACGAT	230bp
RG106	gil164559337	p3	(CGG)5	60.01	60	CGAGTACGGAGACAGGAAGC	GAGTAGCTCGTGGAGCCTTG	228bp
RG107	gil164559308	p3	(AAC)7	60.18	55	AAAGGCTACACCACCACAGC	GGTGTCACTCATGCCCTGTT	117bp
RG108	gil164559180	p3	(AGA)5	60.14	55	GCCCTGCACCTGATACTGTT	GCCTCCTCAGCTTCTTCTT	166bp
RG109	gil164559110	p3	(CTG)5	60.66	55	GTGCACAAGGATAGCCAAGG	AGCAGCAGCAGGACTCTTGT	155bp
RG110	gil164559086	p3	(GAT)6	59.99	55	CACTCGTCTTTGCTCCCTTC	AGACCCACCGGAAAACACTAC	265bp
RG111	gil164559032	p3	(GAA)5	59.85	55	GTGCAAGTCCTGCAAAAGTTC	TAGCCCCATACACTCCTTGG	139bp
RG112	gil164558933	p3	(TTC)5	59.32	55	GAATTCGGCACGAGGAAG	GGGTGAGGATTCGGAGAGAT	108bp
RG113	gil164558918	p3	(AGA)5	60.33	60	CTCGGAAGGAGGAGGAGAACC	CTGGCGAAGTGAAGAGAACC	183bp

RG114	gil164558862	p3	(TCA)5	59.77	55	CTGCCGCTAGAGCTTACGAT	GAAGAAGAAGGCTGCGGTTG	226bp
RG115	gil164558789	p3	(GAT)5	60.38	55	GCTCAGCAGATGAGGGTGAT	CCTCCTCCTCGTCTTCTCT	105bp
RG116	gil164558738	p3	(GCA)5	59.8	55	CTCCTCGGATAAGCGATGTC	ACCAGCAGCACCACCTATTG	261bp
RG117	gil164558687	p3	(AAT)6	59.85	60	GGCACGAGGCTCTCTCTCTA	ACCTCAGCTGACTTGCTGCT	281bp
RG118	gil164558403	p3	(TTC)6	60.33	55	GGATGGGACACCAATCAGAG	AACACGACCGCCTTGTGTAG	131bp
RG119	gil164558244	p3	(GAA)7	61.16	60	GGGAGGACGAAGTGGAGAAG	CGGACTCCTCATCGAAACTC	180bp
RG120	gil164558138	p3	(GAA)6	59.78	55	GGAGGAAGCAGAGGGAGAAT	AGTAACAGTGGTGCCGCTCA	144bp
RG121	gil164558101	p3	(TGC)5	59.81	55	AGGCATGGTGGTGTAGATCC	GATCCCAGCGGTGACTCTTA	194bp
RG122	gil164557958	p3	(GCA)5	60.4	55	TAGCAAACCTGGCTGGAGGTC	GCTGCTGCTGCATGTACTGT	239bp
RG123	gil164557828	p3	(GGA)7	60.06	57	CCTAGGCACTCACGTCTTCTG	CATCACAGACCCCATTTCTC	208bp
RG124	gil164557550	p3	(GGA)6	59.77	55	GCACTACTCTTGCTGCGATG	CTCTCCTCCTCCTCCTC	243bp
RG125	gil164557544	p3	(TTC)11	61.42	55	CAACGAGGATTCCTCCACT	GGCGCGGTTTCTCATAGGTA	113bp
RG126	gil164557273	p3	(TGG)7	59.93	55	GGGACCGACCTAGTCAATCA	AGGCCCTAACTCCCCTGTTA	129bp
RG127	gil164557043	p3	(CCT)5	60.34	65	CTCCTCCTCCTCACCTCTC	CTGTATCTCCCTCGCAACC	121bp
RG128	gil164556917	p3	(AAG)7	59.11	55	GGAATCGGTGGTGATGGT	GGGTGTTCTTCTGAGCTTCC	129bp
RG129	gil164556901	p3	(CAG)7	59.81	55	ATCAGTGGGGCTACACATC	ATACCTGCCTACCAGCACCA	115bp
RG130	gil164556804	p3	(AGG)5	60.21	55	CCATGGCTCCTCCAGAACTA	CTCCTCCTCCTCCCTTCT	113bp
RG131	gil164556520	p3	(GAA)5	62.92	57	CGACACCGAAATCGAGCAG	CAGCAGATAAACCCCACTC	227bp
RG132	gil164556379	p3	(GCA)6	59.68	55	GCTCCCGAAGACTCAAGAGA	CGGTAGACAAACCGTCCAGT	209bp
RG133	gil164556129	p3	(AAG)7	60.25	55	AGGAACAGGGCTCTTGAGGT	CTCCAACCTCCAGGAAGACCA	277bp
RG134	gil164555996	p3	(AAG)7	60.25	55	AGGAACAGGGCTCTTGAGGT	CTCCAACCTCCAGGAAGACCA	277bp
RG135	gil164555947	p3	(CAA)5	60.49	55	TAACGCGAGCTGCTCTCAG	CCACCAGCTACAATGCTCAG	112bp
RG136	gil164555665	p3	(ATG)5	60.36	55	GCATCGACGAGAGGAACCTA	ACTCCCTGTCTCGAGGGTCT	153bp
RG137	gil164555652	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CATAACCTCTCGACGGAACC	119bp
RG138	gil164555538	p3	(ATC)6	62.53	55	GCGCCCAATGTGAAAAGG	GGAGAGATGATGGGCTGATG	231bp
RG139	gil164555485	p3	(AGA)9	59.92	55	CCCATCTCTGGGGACTAACA	GCGTTCTAACTGGGGAGGA	295bp
RG140	gil164555462	p3	(ATC)5	59.84	55	CAAACCAGACAGGGAAGCTC	AGACCAGACCAGACCACCAC	268bp
RG141	gil164555444	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CATAACCTCTCGACGGAACC	119bp
RG142	gil164555404	p3	(ATG)6	60.2	55	GAATTCGCGACGAGGTTG	CCAGGAGAAAGCAACAGGAC	116bp
RG143	gil164555393	p3	(CAT)6	60.8	55	GGCGAAGTTGCTGGTATCTG	GCCGGGAATCCCTATAA	169bp
RG144	gil164555341	p3	(TTC)8	59.96	55	GGTTTCCCCCATTTCCAC	GGGCAGGAAAAACAGCAG	264bp

RG145	gil164555320	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CATAACCTCTCGACGGAACC	119bp
RG146	gil164555239	p3	(AAT)8	60.11	55	CACGAGGACAAGGAGGTGAT	GAGGACCTGCCATATCTCA	100bp
RG147	gil164555196	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CATAACCTCTCGACGGAACC	119bp
RG148	gil164555156	p3	(GAA)7	59.55	55	GACCAAGACGACCAAGGTTTC	CTTCTGGACATCCCTCCGTA	291bp
RG149	gil164555055	p3	(ATC)5	60.59	55	CACGAGGGGGAAGCTCTATT	AGACCAGACCAGACCACCAC	264bp
RG150	gil164555030	p3	(CTC)5	59.83	55	CCCAGCAAGGAGAATACGAG	TGAACAGAGGAGGAGGAGGA	127bp
RG151	gil164554941	p3	(GCA)6	59.02	55	GTGAAAGCCTCCGAAGAGTC	CTTCGGTAGCAAAGGGACTG	186bp
RG152	gil164554835	p3	(TCT)8	59.83	60	GAGCCATAGCACCAGAGGTC	GGGTCAGCCCAGTAGCTGTA	118bp
RG153	gil164554454	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CATAACCTCTCGACGGAACC	119bp
RG154	gil164554434	p3	(TCT)10	60.17	55	GCCCCTCTCTTGCTTATTCC	CCTATCTGGAGGACCATTGC	257bp
RG155	gil164554198	p3	(CTT)6	59.88	55	GGCAGGAGGAAACAGCTAAC	GTGGGAGCAGAGGAAAGTCA	251bp
RG156	gil164554069	p3	(GCA)6	59.02	55	GTGAAAGCCTCCGAAGAGTC	CTTCGGTAGCAAAGGGACTG	186bp
RG157	gil164554056	p3	(TCT)10	60.17	55	GCCCCTCTCTTGCTTATTCC	CCTATCTGGAGGACCATTGC	257bp
RG158	gil164554041	p3	(GAA)8	60.29	55	GGTAGATCCGACGGAGGAAT	GGAGGAAGAGCAATGGCAAG	129bp
RG159	gil164554021	p3	(GAA)7	60.03	60	GAGGGGGTATCGAAGAGGAG	GAACCTTGGTCGTCTTGGTC	121bp
RG160	gil164554015	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CATAACCTCTCGACGGAACC	119bp
RG161	gil164554002	p3	(TCT)7	60.14	55	GTGCTGACCTGGTGCTATT	AGCCCTGTTCTCCTGTAGCA	189bp
RG162	gil164553987	p3	(GAT)5	59.51	55	GACCATGGGTCTGAAGAAG	CTCCTCCATTGCAGTGTCTCT	235bp
RG163	gil164553697	p3	(GAA)6	60.81	55	GCACGAGGCAGTAATCGAAC	ATTCCTCCGTCGGATCTACC	202bp
RG164	gil164553612	p3	(ATC)6	60.16	60	CGAGGAGGTGTTAGCAGAGC	GGAGAGATGATGGGCTGATG	278bp
RG165	gil164553591	p3	(TCT)10	59.79	55	CGAGGCTTCTCATCCATAG	TAAGCAAGAGAGGGGCAGAC	258bp
RG166	gil164553502	p3	(GAA)7	60.62	55	ACGAGGGAAAGGTGAGGAAG	GGGAGGCACATCATAACCAC	283bp
RG167	gil164553495	p3	(TCT)7	60.17	55	GCCCCTCTCTTGCTTATTCC	CATAACCTCTCGACGGAACC	119bp
RG68	gil164553337	p3	(AGA)5	59.83	55	CCGAGCTGAAGATAACTGG	CGAACCATGCAGCAAAGC	110bp
RG169	gil164553248	p3	(AAT)11	60.71	55	AGGCGTACCTGGTTGTAGCA	CTTGGTGGATCGTGTACGTG	291bp
RG170	gil164553239	p3	(TAT)6	60.13	55	GCTCCTGCTTCAGTTTCAGG	TTCCCCCTACCACTACAAC	188bp