

EST-SSR ID	contig ID	EST ID	nucleotide motif
FIR001	CL1811_CT2120	YC12RM1.SCF, LG0AAC2	di
FIR003	CL1986_CT2305	10RM1.SCF, LG0AAC31Y	di
FIR004	CL2055_CT2381	D19RM1.SCF, LG0AAC4Y	di
FIR008	CL9715_CT12724	05RM1.SCF, LG0AAD12Y	di
FIR009	CL8676_CT12289	0RM1.SCF, SSH2pl4F06.e	tri
FIR011	CL8796_CT10192	RM1.SCF_1°, LG0AAA13Y	tri
FIR013	CL95_CT128	F_1X, LG0AAB21YB08R	tri
FIR015	CL1987_CT2307	2RM1.SCF_1, LG0AAC31	di
FIR016	CL9715_CT13062	RM1.SCF_1X, LG0AAC2	tri
FIR019	CL8709_CT12308	AAD32YC15RM1.SCF, S	penta
FIR020	CL2208_CT2549	AAC17YO09RM1.SCF, L	di
FIR021	CL8450_CT11820	K20RM1.SCF, LG0AAD17	tri
FIR023	CL7391_CT8245	LG0AAC2YA15RM1.SCF	tri
FIR024	CL2027_CT2349	D23RM1.SCF, LG0AAC3Y	tri
FIR025	CL2149_CT2483	G03RM1.SCF, LG0AAC7Y	tri
FIR026	CL8597_CT9915	YL09RM1.SCF_1, LG0AA	di
FIR027	CL1065_CT11335	19RM1.SCF, LG0AAB21Y	tri
FIR028	CL344_CT11278	19RM1.SCF, LG0AAC6Y	di
FIR029	CL8131_CT9053	D4RM1.SCF, LG0AAC21Y	tri
FIR030	CL8905_CT10338	09RM1.SCF, LG0AAC3Y	di
FIR031	CL289_CT370	YD14RM1.SCF, SSH2pl4	di
FIR032	CL2100_CT2430	E12RM1.SCF, LG0AAC5Y	di
FIR033	CL1905_CT2223	LG0AAC10YA18RM1.SCF	di
FIR034	CL7866_CT8774	7YK21RM1.SCF, LG0AAE	tri
FIR035	CL4150_CT4690	SCF, LG0AAD19YM07RM	di
FIR036	CL8970_CT10420	SCF, LG0AAC26YP11RM	di
FIR037	CL8591_CT12225	11.SCF, LG0AAB3YD21R	di
FIR038	CL841_CT1029	G0AAB27YJ03RM1.SCF,	di
FIR039	CL9715_CT15911	gfp11B02.esd_2X, SSH6gfp	di
FIR040	CL9715_CT13496	LG0AAA6YD14RM1.SCF	tri
FIR041	CL9715_CT14266	8RM1.SCF_1X, LG0AAA1	di
FIR042	CL114_CT149	LG0AAC9YE15RM1.scf	tri
FIR043	CL1945_CT2263	YH24RM1.SCF, LG0AAB	di
FIR044	CL176_CT232	13RM1.SCF_1°, LG0AAA	tetra
FIR045	CL7722_CT8620	K18RM1.SCF, LG0AAC9Y	tri
FIR046	CL8612_CT12241	SSH09C03, SSH09B03, SS	di
FIR047	CL5663_CT6350	14RM1.SCF, LG0AAA13Y	tri
FIR048	CL4741_CT5330	07RM1.SCF, LG0AAB15Y	di
FIR050	CL9715_CT15579	YJ06RM1.SCF, LG0AAB3	di
FIR051	CL5767_CT6464	24RM1.SCF, LG0AAA16Y	di
FIR052	CL5762_CT6459	SH4pl1C02.esd, LG0AAC	di
FIR053	CL3760_CT4250	LG0AAD50YO18RM1.SCF	tri
FIR059	CL9715_CT12753	1RM1.SCF, LG0AAD26Y	di
FIR062	CL3867_CT11424	LG0AAB10YD15RM1.SCF	tri
FIR065	CL343_CT434	LG0AAC17YE02RM1.SCF	tri
FIR069	CL442_CT559	LG0AAA2YD20RM1_SCF	di
FIR073	CL9715_CT15319	LG0AAD42YJ13RM1_SCF	di

FIR074	LG0AAB16YP18RM1_SCF	LG0AAB16YP18RM1_SC	tri
FIR075	CL9715_CT14860_CN15535	LG0AAD50YG14RM1_SC	di
FIR077	CL9715_CT15814	01RM1.SCF_1X, LG0AAC	di
FIR079	CL9715_CT14899	LG0AAD6YJ17RM1.SCF_	tri
FIR081	CL9715_CT15372	7K10RM1.SCF, LG0AAB1	di
FIR085	CL8710_CT12309	88YN03RM1.SCF, LG0AA	di
FIR089	CL1559_CT1848	14RM1.SCF_1t, LG0AAI	di
FIR093	CL3557_CT4027	08RM1.SCF, LG0AAD18Y	di
FIR094	CL3557_CT4027	08RM1.SCF, LG0AAD18Y	di
FIR095	CL9715_CT14348	03RM1.SCF, LG0AAD33	di
FIR097	CL8461_CT12015	04RM1.SCF, LG0AAC9Y	tri
FIR103	CL9715_CT13265	AAD28YC14RM1.SCF_1	tri
FIR104	CL7333_CT8185	RM1.SCF_1, LG0AAD50Y	tri
FIR106	CL9715_CT15596	7RM1.SCF_1°, LG0AAB1	tri
FIR107	CL2247_CT2590	20RM1.SCF, LG0AAD11Y	di
FIR110	CL3839_CT4339	RM1.SCF_1, LG0AAD32Y	di
FIR112	CL3833_CT4333	20RM1.SCF, LG0AAD37Y	di
FIR125			
GOT004	CL7387_CT8241	TG end 514, LG0AAB25Y	di
GOT005	CL9089_CT10564	7_1a stackPACK526_CT_3	di
GOT008	CL269_CT345	AT end 128, LG0AAA16YN	di
GOT009	CL292_CT376	CF stackPACK526_CT_32	di
GOT011	CL112_CT147	7_1a stackPACK526_CT_3	di
GOT012	CL2328_CT2684	1X stackPACK526_CT_331	di
GOT014	CL8041_CT8960	26_CT_3623 start 36 11.00	di
GOT016	CL8480_CT12132	0 TC end 291, SSH3pl3B05	di
GOT017	CL9715_CT13938	LG0AAC31YM22RM1.SC	di
GOT018	CL8480_CT12132	F stackPACK526_CT_371	di
GOT021	CL594_CT740	0 AT end 146, LG0AAA6Y	di
GOT022	CL9715_CT13973	7 stackPACK526_CT_3843	di
GOT025	CL623_CT777	7_1a stackPACK526_CT_38	di
GOT029	CL8543_CT12196	SCF, LG0AAC30YH01RM	di
GOT032	CL7598_CT11556	start 104 10.00 AT end 123,	di
GOT035	CL8815_CT12348	26_CT_4077 start 84 9.50	di
GOT037	CL9715_CT16227	start 124 11.50 TC end 146	di
GOT038	CL9715_CT16227	start 124 11.50 TC end 146	di
GOT039	CL9715_CT16227	start 124 11.50 TC end 146	di
GOT040	CL6785_CT7581	GA end 499, LG0AAD11Y	di
GOT044	CL8656_CT12281	7 stackPACK526_CT_4266	di
GOT045	CL7826_CT8728	CF stackPACK526_CT_432	di
GOT046	CL9715_CT13633	526_CT_4346 start 255 7.5	di
GOT047	CL8918_CT10353	00 CT end 66, LG0AAD8Y	di
GOT054	CL9715_CT13634	CA end 86, LG0AAA15YI	di
GOT061	CL263_CT338	7C end 194, LG0AAA1YD0	tri
GOT062	CL296_CT380	26_CT_3243 start 52 7.67	Tri
GOT063	CL8645_CT9993	7 stackPACK526_CT_3282	tri
GOT065	LG0AAD15YB01RM	1TC end 187, LG0AAB16Y	Tri
GOT066	CL9715_CT14779	7 stackPACK526_CT_3327	tri
GOT067	CL351_CT443	7GC end 176, LG0AAA19Y	hexa
GOT071	CL6333_CT7084	7 stackPACK526_CT_3412	Tri

GOT073			
PIE002	CL8464_CT12106	LG0AAD22YM14RM1	di
PIE004			
PIE011	CL1463_CT1735	LG0AAB9YA03RM1	di
PIE013	CL8920_CT10357	LG0AAB2YK05RM1	di
PIE014	CL9715_CT14153	LG0AAB9YK17RM1	di
PIE017	CL9715_CT14040	LG0AAA5YB14RM1	di
PIE020	CL1336_CT1599	LG0AAB6YF09RM1	di
PIE021	CL9715_CT13033	LG0AAD44YF01RM1	di
PIE022	CL9672_CT11206	LG0AAD34YN16RM1	di
PIE023	CL5733_CT6422	LG0AAD19YL11RM1	di
PIE027	CL639_CT11308	LG0AAB17YE03RM1	tri
PIE028	CL7587_CT8468	LG0AAD36YO24RM1	tri
PIE029	CL1345_CT1608	LG0AAB8YD20RM1	tri
PIE030	CL9715_CT14533	LG0AAB11YG06RM1	tri
PIE033	LG0AAB7YM23RM1	LG0AAB7YM23RM1	tri
PIE035	CL2905_CT3313	LG0AAD31YB09RM1	tri
PIE036	CL1420_CT1688	LG0AAA8YJ20RM1	tri
PIE037	CL1420_CT1688	LG0AAB8YN16RM1	tri
PIE039	CL4189_CT4728	LG0AAB21YG10RM1	tri
PIE040	CL5879_CT6589_CN5885	LG0AAB5YJ11RM1	tri
PIE041	CL9715_CT15766	LG0AAA9YB15RM1	tri
PIE042	CL9715_CT12753	LG0AAA3YC08RM1	tri
PIE043	CL9715_CT14040	LG0AAA17YB24RM1	tri
PIE051	CL8710_CT12309	LG0AAD31YJ06RM1	hexa
PIE053	CL1629_CT1924	LG0AAC23YI12RM1	hexa
PIE054	CL1124_CT1353	LG0AAB19YC23RM1	hexa
PIE059	CL2076_CT2406	LG0AAB19YG07RM1	hexa
PIE060	CL9715_CT14196	LG0AAC6YD22RM1	hexa
PIE061	CL9715_CT13656	LG0AAB12YC01RM1	hexa
PIE062	CL9715_CT15262	LG0AAD28YG04RM1	hexa
PIE063	CL6127_CT6864	LG0AAB2YH22RM1	hexa
PIE065	CL9258_CT12467	LG0AAB2YL23RM1	hexa
PIE066	CL1246_CT1493	LG0AAB3YD17RM1	hexa
PIE068	CL3535_CT4003	LG0AAD49YM08RM1	hexa
PIE069	CL9715_CT16449	LG0AAC11YE07RM1	hexa
PIE071	LG0AAB18YE17RM1	LG0AAB18YE17RM1	hexa
PIE075	CL98_CT131	LG0AAD14YG05RM1	hexa
PIE076	CL6971_CT7785	LG0AAD38YM09RM1	hexa
PIE077	CL4984_CT5590	LG0AAB7YA19RM1	hexa
PIE078	CL1367_CT1631	SSH10D01	hexa
PIE081	LG0AAB11YI19RM1	LG0AAB11YI19RM1	hexa
PIE082	CL5389_CT6039	LG0AAC2YH02RM1	hexa
PIE088	LG0AAD45YJ20RM1	LG0AAD45YJ20RM1	hexa
PIE089	CL3054_CT3472	LG0AAB9YM05RM1	hexa
PIE090	CL4327_CT4874	SSH07B10	hexa
PIE097	CL6946_CT7758_CN6904	WZ0AQPAC11YD13.r1	di
PIE099	CL4632_CT5204_CN4735	WZ0AQPAB13YK05.f1	di
PIE100	CL7542_CT8415_CN7528	WZ0AQPAB2YM04.f1	di
PIE101	CL895_CT1094_CN1023	WZ0AQPAB11YC04	di

PIE102	CL9715_CT14783_CN15426	WZ0AQPAC4YA03_1A.f1	di
PIE104	WZ0AQPAB11YF02	WZ0AQPAB11YF02.f1	di
PIE105	CL9715_CT14358_CN14787	WZ0AQPAB5YM16.f1	di
PIE111	CL9715_CT15708_CN16818	WZ0AQPAB7YJ13.f1	tri
PIE113	CL4598_CT5169_CN4705	WZ0AQPAB12YN24.r1	tri
PIE117	CL2_CT1_CN1	WZ0AQPAC7YI10.r1	hexa
PIE119	CL9715_CT13527_CN13453	WZ0AQPAB2YE14.f1	hexa
PIE120	CL369_CT470_CN466	WZ0AQPAA1YE10.f1	hexa
PIE122	CL330_CT419_CN425	WZ0AQPAC2YD13.f	hexa
PIE123	CL4545_CT11453_CN9963	WZ0AQPAB11YL06.f1	hexa
PIE125	CL9715_CT13796_CN13879	WZ0AQPAC7YM05.f1	hexa
PIE126	CL6932_CT7743_CN6893	WZ0AQPAB12YJ01.f1	hexa
PIE127	CL1874_CT2191_CN2056	WZ0AQPAA2YA01_1A.f1	hexa
PIE129	CL9715_CT13888_CN14026	Z0AQPAB2YP03_1A_2T	hexa
PIE130	CL8113_CT9034_CN8096	WZ0AQPAB7YA09.f1	hexa
PIE134	LG0AAC10YB10RM1	LG0AAC10YB10RM1	di
PIE135	CL8314_CT9254	LG0AAC10YF15RM1	di
PIE136	CL9715_CT15818	LG0AAC10YI11RM1	di
PIE137	LG0AAC11YA17RM1	LG0AAC11YA17RM1	di
PIE138	LG0AAC11YN15RM1	LG0AAC11YN15RM1	di
PIE141	LG0AAC12YL14RM1	LG0AAC12YL14RM1	di
PIE142	CL8429_CT11603	LG0AAC13YK24RM1	di
PIE144	CL9715_CT14431	LG0AAA10YF19RM1	di
PIE145	CL5590_CT6266	LG0AAA11YN24RM1	di
PIE148	CL9715_CT12927	LG0AAA15YH10RM1	di
PIE149	LG0AAA16YD10RM1	LG0AAA16YD10RM1	di
PIE150	CL326_CT414	LG0AAA18YH10RM1	di
PIE151	CL9715_CT16589	LG0AAA18YJ22RM1	di
PIE152	CL9715_CT16286	LG0AAA1YG07RM1	di
PIE153	LG0AAA1YM07RM1	LG0AAA1YM07RM1	di
PIE155	CL6949_CT7761	LG0AAA20YM22RM1	di
PIE157	CL9715_CT14229	LG0AAA3YH19RM1	di
PIE158	CL9715_CT15023	LG0AAA3YO24RM1	di
PIE159	CL6740_CT7533	LG0AAA4YC17RM1	di
PIE163	CL9715_CT12735	LG0AAA7YG23RM1	di
PIE164	LG0AAD10YC11RM1	LG0AAD10YC11RM1	di
PIE166	LG0AAD12YL24RM1	LG0AAD12YL24RM1	di
PIE167	LG0AAD13YK08RM1	LG0AAD13YK08RM1	di
PIE171	LG0AAC11YF14RM1	LG0AAC11YF14RM1	tri
PIE175	CL6970_CT7784	LG0AAC24YM02RM1	tri
PIE176	LG0AAC25YE10RM1	LG0AAC25YE10RM1	tri
PIE183	LG0AAC7YO22RM1	LG0AAC7YO22RM1	tri
PIE186	CL9715_CT12754	LG0AAA10YK14RM1	tri
PIE187	CL6947_CT7759	LG0AAA12YC08RM1	tri
PIE188	LG0AAA13YL17RM1	LG0AAA13YL17RM1	tri
PIE189	CL9715_CT12893	LG0AAA14YM03RM1	tri
PIE192	LG0AAA18YF05RM1	LG0AAA18YF05RM1	tri
PIE193	CL8676_CT12295	LG0AAA11YO03RM1	tri
PIE194	CL3284_CT3729	LG0AAC15YH13RM1	tri
PIE196	CL7448_CT8309	LG0AAA5YA18RM1	tri

PIE197	CL8516_CT12169	LG0AAC19YI11RM1	tri
PIE198	CL9715_CT14860	LG0AAD23YM20RM1	tri
PIE200	CL8918_CT10353	LG0AAA14YN15RM1	tri
PIE201	CL9715_CT15577	LG0AAC19YM15RM1	tri
PIE202	CL3870_CT4371	LG0AAD46YC03RM1	tri
PIE203	CL9715_CT16027	LG0AAA3YL21RM1	tri
PIE204	CL8705_CT12304	LG0AAC19YG19RM1	tri
PIE208	CL6771_CT7566	LG0AAC13YH15RM1	tri
PIE211	CL9715_CT14785	LG0AAA20YJ24RM1	tri
PIE212	CL5719_CT6408	LG0AAA19YD17RM1	tri
PIE214	CL9715_CT12746	LG0AAA19YG08RM1	tri
PIE215	CL209_CT272	LG0AAA15YF18RM1	tri
PIE216	CL459_CT11290	LG0AAA19YE22RM1	tri
PIE218	CL577_CT719	LG0AAD49YF07RM1	tri
PIE219	CL580_CT723	LG0AAA5YN24RM1	tri
PIE224	CL4857_CT5456	LG0AAA11YG16RM1	tri
PIE228	CL1245_CT1492	LG0AAB3YD06RM1	tri
PIE232	CL8824_CT10234	LG0AAC15YI19RM1	tri
PIE233	CL274_CT352	LG0AAC18YE17RM1	tri
PIE236	CL1338_CT1601	LG0AAA7YL07RM1	tri
PIE238	CL344_CT11278	LG0AAA18YN22RM1	di
PIE241	CL4561_CT5129	LG0AAB26YK19RM1	di
PIE242	CL8578_CT9892	LG0AAB5YF07RM1	di
PIE243	CL1629_CT1924	LG0AAC8YH13RM1	di
PIE244	CL9715_CT15579	LG0AAA14YE09RM1	di
PIE246	CL1479_CT1753	LG0AAB22YB17RM1	di
PIE247	CL8871_CT10298	LG0AAA16YC15RM1	di
PIE249	CL8788_CT12335	LG0AAB10YE17RM1	di
PIE250	CL8635_CT9980	LG0AAB17YD15RM1	di
PIE251	CL8462_CT12104	LG0AAD17YF05RM1	di
PIE252	CL9715_CT16273	LG0AAD25YI02RM1	di
PIE253	CL9715_CT14797	LG0AAD47YK13RM1	di
PIE255	CL8464_CT12114	LG0AAB17YB19RM1	di
PIE257	CL289_CT370	LG0AAA19YP10RM1	di
PIE258	CL419_CT532	LG0AAB5YD14RM1	di
PIE259	CL931_CT1135	LG0AAB10YC04RM1	di
PIE260	CL6097_CT6827	LG0AAB20YB20RM1	di
PIE262	CL1628_CT1923	LG0AAB25YB06RM1	di
PIE264	CL1824_CT2133	LG0AAC26YB13RM1	di
PIE265	CL1840_CT2154	LG0AAA20YB19RM1	di
PIE267	CL823_CT1012	LG0AAA12YL21RM1	di
PIE271	CL2700_CT3091	LG0AAB11YB03RM1	di
PIE275	CL8450_CT11842	LG0AAC16YF02RM1	di
POR001	CL4181_CT4720	4RM1.SCF_1, LG0AAD3	tri
POR002	CL9715_CT13317	9RM1.SCF, LG0AAD26Y	tri
POR003	CL2662_CT3047	M1.SCF, LG0AAD5YP03	di
POR006	CL9715_CT15579	L03RM1.SCF, LG0AAB16	di
POR007	CL9715_CT14883	RM1.SCF, LG0AAD39YEC	tri
POR008	CL883_CT1081	RM1.SCF, LG0AAD34YC	tri
POR009	CL8302_CT9239	02RM1.SCF, LG0AAD45Y	di

POR010	CL200_CT261	LG0AAD24YM09RM1.SCF	di
POR011	CL9715_CT16543	21RM1.SCF, LG0AAC17	tri
POR012	CL9715_CT12606	RM1.SCF_1°, LG0AAD39	tri
POR014	CL3472_CT3937	2RM1.SCF, LG0AAD47Y	di
POR015	CL5009_CT5616	06RM1.SCF, LG0AAD30Y	di
POR016	CL7922_CT8832	LG0AAC21YJ23RM1.SCF	tri
POR017	CL6798_CT7595	3RM1.SCF, LG0AAD38YF	di
POR018	CL8795_CT12340	F, LG0AAC13YK20RM1.S	tri
POR019	CL3293_CT3740	13RM1.SCF, LG0AAD13	di
POR020	CL6888_CT7695	002RM1.SCF, LG0AAD36	tri
POR021	CL2699_CT3090	F_1X, LG0AAD51YI18RM	tri
POR022	CL9715_CT16129	E09RM1.SCF, LG0AAD37	di
POR023	CL6885_CT7692	11D11.esd, SSH2pl1D11.es	tri
POR024	CL2699_CT3090	F_1X, LG0AAD51YI18RM	di
POR025	CL4416_CT4972	0AAD38YF22RM1.SCF_	di
POR026	CL3270_CT3712	J07RM1.SCF, LG0AAA6	di
POR027	CL4996_CT5604	2RM1.SCF, LG0AAA5YO	di
POR028	CL9715_CT15579	YJ03RM1.SCF, LG0AAB2	tri
POR029	CL5742_CT11498	0RM1.SCF, LG0AAD40Y	tri
POR030	CL5416_CT11481	LG0AAD49YN03RM1.SCF	tri
POR032	CL6757_CT7551	F03RM1.SCF, LG0AAD48	di
POR033	CL3206_CT3639	17RM1.SCF, LG0AAD21	di
POR034	CL9715_CT15945	15RM1.SCF, LG0AAD3Y	tri
POR035	CL3118_CT3543	321RM1.SCF, LG0AAD18	di
POR036	CL8450_CT11793	2RM1.SCF, LG0AAD44YF	di
POR037	CL6798_CT7595	3RM1.SCF, LG0AAD38YF	di
POR038	CL9715_CT16129	E09RM1.SCF, LG0AAD37	di
POR039	CL9715_CT13317	04RM1.SCF, LG0AAD10Y	tri
POR040	CL119_CT157	04RM1.SCF, LG0AAD43	di
POR041	CL9715_CT14922	YK13RM1.SCF_1, LG0AA	di
POR045	CL9715_CT14066	08RM1.SCF, LG0AAD51Y	di
POR046	CL6098_CT6830	0AAD19YA19RM1.SCF_	tri
VIT003	CL2844_CT3248	LG0AAD38YB15RM1	di
VIT006	CL9715_CT15846	LG0AAD27YI20RM1	di
VIT007	CL2778_CT11390	LG0AAD27YG24RM1	di
VIT009	CL643_CT11311	SSH3pl4H01	di
VIT010	LG0AAD4YL04RM1	LG0AAD4YL04RM1	di
VIT013	SSH4GFp12D07	SSH4GFp12D07	tri
VIT017	CL8918_CT10353	LG0AAD45YL16RM1	tri
VIT018	LG0DAAD17YN19RM1	LG0DAAD17YN19RM1	tri
VIT020	CL2338_CT2696	LG0AAD7YO12RM1	di
VIT021	CL2346_CT2704	LG0AAA14YA15RM1	di
VIT022	LG0AAD15YB12RM1	LG0AAD15YB12RM1	di
VIT023	LG0AAD25YN12RM1	LG0AAD25YN12RM1	tri
VIT025			
VIT026	CL9715_CT13700	LG0AAC23YM16RM1	tri
VIT028	CL2370_CT2734	LG0AAD15YN04RM1	di
VIT031	CL109_CT143	LG0AAD16YA13RM1	di
VIT033	CL9715_CT15462	LG0AAD35YG22RM1	tri
VIT037	CL6567_CT7342	LG0AAD1YN19RM1	di

VIT043	CL9715_CT15561_CN16584	LG0AAD23YI21RM1	di
VIT046	CL829_CT1017	LG0AAB2YC16RM1	di
WAG002	CL6700_CT7490	LG0AAD49YO19RM1.SCF	di
WAG003	CL4182_CT4721	LG0AAA9YM01RM1.SCF	tri
WAG004	CL9715_CT13265	LG0AAD28YC14RM1.SCF	tri
WAG005	CL9715_CT14731	LG0AAC18YA03RM1.SCF	tri
WAG010	CL1847_CT2161	LG0AAC26YJ12RM1.SCF	tri
WAG011	CL9715_CT14301	LG0AAC27YK13RM1.SCF	di
WAG014	CL4144_CT4681	LG0AAB19YF15RM1.SCF	tri
WAG015	CL3867_CT11424	LG0AAA18YK14RM1.SCF	tri
WAG016	CL6482_CT7249	LG0AAB17YH02RM1.SCF	tri
WAG017	CL1126_CT1355	LG0AAA14YL12RM1.SCF	di
WAG018	CL6123_CT11517	LG0AAB21YH15RM1.SCF	di
WAG019	CL7244_CT8091	LG0AAC16YD02RM1.SCF	tri
WAG020	CL4523_CT5087	LG0AAB22YB03RM1.SCF	tri
WAG021	CL3384_CT3840	LG0AAD45YM20RM1.SCF	tri
WAG023	CL1295_CT1553	FSSH09C10	tri
WAG026	LG0AAB5YP15RM1.SCF	LG0AAB5YP15RM1.SCF	di
WAG027	CL7053_CT7876	LG0AAD41YH14RM1.SCF	tri
WAG031	CL3940_CT4444	LG0AAC9YK15RM1.SCF	tri
WAG032	CL561_CT702	SSH1GFpl2A10.esd	di
WAG040	CL8631_CT9973	LG0AAA15YB09RM1.SCF	tri
WAG041	CL1065_CT11335	LG0AAC24YF11RM1.SCF	tri
WAG042	CL9715_CT12525	LG0AAB26YO11RM1.SCF	tri
WAG043	CL9715_CT15163	LG0AAC24YF20RM1.SCF	di
WAG046	CL6994_CT7808	LG0AAB27YL21RM1.SCF	tri
WAG047	CL8433_CT11631	SSH5pl3H04	di
WAG049	CL352_CT446	LG0AAD32YG22RM1.SCF	di
WAG050	CL9715_CT14534	LG0AAC28YF11RM1.SCF	di
WAG052	CL9715_CT13450	LG0AAC19YH05RM1.SCF	tri
WAG053	SSH5pl2D02	SSH5pl2D02	tri
WAG054	CL9715_CT14717	LG0AAD32YH14RM1.SCF	tri
WAG057	CL5851_CT6560	LG0AAC23YG12RM1.SCF	tri
WAG059	CL1065_CT11335	LG0AAB25YH03RM1.SCF	tri
WAG060	CL5155_CT5775_CN5197	WZ0AQPAC14YJ04.f1	tri
WAG061	CL5337_CT5981_CN5356	LG0AAD16YO04.r1	tri
WAG062	CL9715_CT12543_CN11887	WZ0AQPAC5YN19.f1	tri
WAG063	CL9715_CT12543_CN11887	WZ0AQPAC6YO07.f1	tri
WAG064	CL4228_CT4771_CN4377	WZ0AQPAB7YN10.f1	tri
WAG065	WZ0AQPAA2YE04	WZ0AQPAA2YE04_1A.f1	tri
WAG066	WZ0AQPAA13YA14	WZ0AQPAA13YA14_1A.f1	di
WAG071	CL4282_CT4827_CN4422	WZ0AQPAA2YO12_1A.f1	di
WAG074	CL8739_CT10117_CN8765	WZ0AQPAA4YH18.r1	di
WAG078	WZ0AQPAB10YF21	WZ0AQPAB10YF21.f1	di
WAG079	CL5068_CT5680_CN5113	WZ0AQPAC11YN07.f1	di
gSSR ID	contig ID	EST ID	nucleotide motif
CQM13			di
CQM16			di

CQM4			di
F102			di
F104			di
KQMy50			complex
MCS1			tri
MCS11			complex
MSQ13			tri
MSQ16			Na
MSQ4			tri
PQRu3			di
PQRu5			di
PQRu6			di
PQRu9			di
PQRu10			di
PQRu13			di
PQRu16			di
PQRu19			di
PQRu2			di
PQRu20			di
PQRu22			di
SQS22			Na
TCS14			di
ZQP1/2			di
ZQP1/5			complex
ZQP102			complex
ZQP104			complex
ZQP105			di
ZQP108			di
ZQP110			di
ZQP119			di
ZQP15			di
ZQP16			di
ZQP36			di
ZQP46			di
ZQP58			di
ZQP62			di
ZQP64			di
ZQP7			di
ZQP9			di
ZQR101			complex
ZQR102			di
ZQR103			di
ZQR108			complex
ZQR11			di
ZQR111			di
ZQR112			di
ZQR121			di
ZQR15			di
ZQR18			di
ZQR19			di

ZQR2			di
ZQR20a			Na
ZQR25			di
ZQR30			di
ZQR31			di
ZQR39			di
ZQR4			complex
ZQR44			complex
ZQR49			di
ZQR5			di
ZQR58			di
ZQR59			di
ZQR5a			di
ZQR65			complex
ZQR7			di
ZQR73			di
ZQR74			di
ZQR75			di
ZQR8			di
ZQR87			di
ZQR96			di

motif type	repeat number	expected size (bp)
ag	9	160
tc	12	170
ct	18	160
tc	9	160
tta	6	150
ctt	5	172
cag	5	160
ac	10	135
ctt	11	230
gatct	5	220
ag	8	220
cac	6	210
aac	7	220
cct	6	230
atg	8	215
tc	11	215
gat	8	220
tc	8	225
aag	6	270
ag	7	150
tc	7	170
ta	7	170
ct	7	170
gaa	5	135
at	6	170
ac	7	150
ct	7	170
ag	7	130
ct	7	135
gga	15	185
at	6	170
gtt	5	135
tc	9	140
tgtt	5	135
caa	5	210
at	11	215
tcg	6	240
ct	9	210
tc	7	165
ga	11	170
tc	8	165
gtg	7	160
ga	15	160
ctc	7	160
ctt	9	190
tc	7	120
ta	13	170

caa	7	140
ga	9	160
ag	7	192
aag	8	205
ta	10	215
tg	8	200
ga	6	205
ag	6	190
ct	10	210
ct	14	180
gag	6	190
tct	7	195
ggt	7	225
tat	5	240
tc	12	280
ag	12	220
ct	9	250
TG	12	290
TC	8	179
TA	8	188
TC	7	226
TC	11	188
AC	12	205
TC	11	112
TC	8	145
CT	8	184
GA	8	273
AT	13	113
TA	6	197
GA	21	232
CT/GT	10_5	257
AT	10	143
GA	9	282
CT	11	260
CT (complex)	13	244
CT	11	105
GA	11	232
AT	12	178
CT (complex)	11	141
TC (complex)	9	167
A/CT (complex)	10_12	251
CT (complex)	9	166
CTG 6 (complex)	6	235
CTG 6 (complex)	11	187
CTG	5	230
CTT (complex)	6	237
GAA	10	238
CTCTCA	4	212
CTT (complex)	6	218

AG	12	170
AT	12	230
AT	10	230
AT	13	230
TC	12	180
TA	12	180
TC	7	170
AG	11	180
AG	11	180
AAG	7	170
CCA	7	170
TTC	5	180
TAC	5	180
TTC	7	170
AGA	7	170
CTT	9	170
CTT	9	180
CTT	8	170
TTC	8	180
ACC	6	170
GGT	5	170
AAG	7	180
ACCAAC	3	180
AAAGAA	3	174
GGTAGC	4	249
GAGCAC	6	172
CCAAAA	4	224
ACCCAC	3	170
AACACA	3	234
CACCCC	3	180
GGAATG	4	172
GGTGGA	3	231
CATCAC	4	236
TTTTGT	3	110
TATTTT	3	225
TATTTT	3	228
GAGGAA	3	172
AAGTGA	3	235
AAAAAG	3	233
GACAGG	4	174
CAGCAA	3	220
TCTTTC	3	180
TTAGGG	3	243
CAGCAA	3	180
TA	7	198
TC	9	198
ct	9	191
AT	13	150

ag	12	160
ct	13	211
AG	7	115
TGC	5	223
ACT	7	146
CCAGCA	3	113
CAGCAA	3	146
GTGGAG	3	174
GGCGGT	3	233
AAACAA	3	188
GGAAGC	3	170
AATCCG	3	239
ACACCA	3	135
ATTTT	3	231
TTTCGT	3	175
GA	13	170
CT	15	227
TG	8	228
TC	9	242
Ga	7	186
CT	20	157
TC	11	163
CT	12	218
TC	12	228
GA	10	174
AT	18	199
TG	11	154
AG	10	158
AG	11	247
TC	11	207
GA	11	227
CT	11	166
TA	12	242
TC	15	242
TC	16	220
AT	12	235
GA	12	132
TA	12	204
AGG	7	242
TCT	8	157
gga	8	171
gga	9	157
taa	9	182
aca	9	210
atc	8	108
gag	9	171
cat	8	134
TTA	8	216
TTC	7	209
GTG	8	220

CTA	6	187
CAT	6	205
CAA	5	120
CAA	7	82
GAA	8	118
ATC	8	118
CAA	7	115
ACC	12	295
CTT	8	302
TGG	7	180
CTG	5	200
GAG	6	200
GAT	10	150
TCA	6	130
ACC	7	120
TCT	5	160
AGA	8	190
TGG	10	170
CCA	8	160
GAA	10	200
AT	19	203
AG	14	204
TA	10	113
AG	15	220
GA	8	211
CT	11	104
GA	12	199
AG	13	281
AG	11	204
CT	13	83
AT	11	115
CT	10	212
AG	20	289
CT	12	160
TC	13	150
AC	10	120
AG	9	160
CT	16	180
AT	10	200
CT	14	250
AG	11	100
TC	11	190
AT	15	180
atc	5	120
agg	5	220
ct	8	130
tc	6	150
gca	7	128
gtg	5	146
ag	11	150

ct	12	165
ctt	9	220
cac	8	130
ct	8	180
ct	10	140
ggt	6	145
ct	12	140
act	6	130
ta	13	175
gat	8	126
aat	5	125
ct	15	160
ctt	6	170
ag	10	185
tc	10	120
tc	8	160
ga	10	130
aat	5	125
acc	9	160
ccg	8	120
ct	9	125
tc	10	210
ttc	7	160
at	11	199
at	18	155
ct	12	130
ct	15	140
cct	5	220
ga	11	230
ct	14	140
gt	7	150
cct	5	130
TA	10	164
AG	10	141
TC	14	137
AG	7	160
TC	10	147
AAC	7	161
CGG	6	101
(CCA)(AAC)	7	101
CT	10	149
GA	9	170
AG	11	177
ATA	6	136
CCA	8	163
AG	9	164
CT	9	110
(CTT)(CCT)CTT	9	111
TC	9	125

CA	7	115
CT	7	183
CT	16	250
CAA	6	260
TTC	7	270
TGG	6	141
CCT	6	210
CT	9	220
GAA	9	290
CCT	6	366
CCA	6	120
AC	6	140
GT	7	140
TTC	13	210
CAA	9	280
TTG	6	310
GCT	7	340
CT	11	180
CAA	6	260
CCA	6	158
CT	12	165
CGG	6	232
TGA	7	240
TGA	7	255
AG	13	270
TTC	8	180
CT	8	190
AT	19	185
AG	7	220
GAA	8	288
TTC	8	270
CCA	6	290
TAA	12	290
TGA	7	350
CAA	6	250
CAA	8	134
CAA	10	331
CAA	8	311
CAG	7	140
TGA	8	285
AG	14	180
AT	8	290
CT	6	220
CT	7	330
CT	13	200
motif type	repeat number	expected size (bp)
AG	14	191-221
		193-207

AG	17	207-228
(CCT)3 (CCG)(CCT)(CCA)(CCT)2		253
(GGC)8	8	180
(GGA)7(GGC)6	13	110
GCA		
GCG		
AG	18	239
AG	11	125
AG	15	214
AG	20	219
AG	19	209
AG	14	184
AG	17	207
AG	23	239
AG	15	181
AG	22	323
AG	16	
CA	22	
AG	16	97-117
(gt)16(ag)9	25	160-190
(ag)5aa(ag)13	18	184-244
(AG)16AT(GA)3	19	176-196
AG	13	213-237
AG	15	206-262
AG	24	64-98
AG	23	108-152
AG	19	147-164
AG	19	210-236
AG	13	190-222
AG	34	150-210
AG	4	113-145
AG	21	164-199
(AG)13(AAG)3	16	140-160
AG	12	182-210
(TC)20(AC)15	35	159
AG	29	263
CT	15	102
(GA)19(GGGA)3	22	105
CT	22	273
CT	19	128
AG	32	127
AG	23	236
AG	15	157
AG	41	258
AG	7	119

CT	22	153
	18	178
AG	32	135
AG	26	211
AG	31	190
CT	34	157
(GA)37GT(GA)7	44	192
(GA)29(TG)8	37	145
AG	22	273
CT	23	248
AG	20	126
CT	23	153
CT		248
(TC)21(TA)10	31	270
CT	17	150
CT	43	250
AG	23	124
AG	57	197
CT	31	139
CT	20	120
CT	20	172

Forward primer	Reverse primer	linkage group assignment*
CCACTCTCTTCTCCCCTTC	ACTTGCTTTTCTTCCCAATTT	1
GGCTTCAGCTTTACGTCTGC	CAAAGGGCTCTACCTTGGTG	10
TCTCTCTCAGGGCAGCTTCT	AACCAAACCTCAGATCCAGATTCA	3
AATCAGCCGTGAGTTTCTCG	ACCGAAATCGAAGAGGGAGT	12
GCCGACGATTCCACACTACT	TCCCCAATGTTTCAATTCTACC	2
ATGATCCCCATAGCCTTGC	GCCGAGAAGAAGATCTCGAA	7
CGGGGAGGTTGATGAGTATT	AACACTGTCACCCCATAGC	2
ACCCTAAAACCCCAATCACC	CGGATCTTCGGCTATTCTTG	8
AAATGTGTGCTTGTTGTATGCAG	CCCAACAAATGATAATTAGAAGCA	2
AAGCAATTAGGTGGGCGAGT	TGTTCGCCATTTCTCTCTCTC	1
TGCCACCTTTTCTTCTCAT	ATTCACCTTACCCCATTC	11
CTCATCATCGGAGGTGGAGT	TTTGAGAAGAGGCGAGTCGT	6
CACACCCATCATCAAACACC	CGCTGGTAGGACCAGAACAT	10
CGCTTCTCCTCATCCTCAAG	CTCAAAAGGCACGATTCTCC	5
TTGGAAATGAGGATTGGAAGA	AAACCAAGTACACGGCAACA	10
CTTCATGCACCAATTCCTCA	GGCCATGTATGTGTGCAAAA	9
GCTCGAGGAGAAGAAGCTCA	GGGACTTTCACCTTAGCGATT	6
GGAAGAGTGTTTCGAAAGCA	CCAGCTCCTCCACAATAGCA	1
TGGCTTTTTGAGTGAAACGA	AGCGTGGACAGAATCTTTGG	10
GGACATATTTATCTAGGAGACGAGGT	ATGTCCCATAGCACAGAGCA	7
ACGAGTCCAACGGAAGTTGT	CACAACCTCACAAGGCAAGG	11
TGAAACTGGTCTCAGATTTTGTG	ACACTACACACACTTGCTCTTTTT	2
AAGCTTTCACCGACTTTCA	TGAAGTTGCGGAGAAGAGAGA	9
CACAAACCCAACATTTTCCA	TCAGTTCCATCAAAGCATCG	2
GCTAAGGTTCCGTGTTCCAA	GGCCAGCAACTAAACCAAGA	5
CCACCACACACATCTCTCTCA	CAAATCACCTTTTTTCGATTG	9
AACGATTCCAGCCTTGTCAT	CTTGGGTTGGAGTCATCTGG	9
CACACAAAACAAAACGCACA	ATGAGGTCGTCATCCTCTGG	??
GAGCCTCTTTCATCGCTCAC	TCAACACCCCAAACTCCAT	1
GAAACGGAAACGCAAACG	GAGCAGAGGGCTAAACTCCA	1/11??
TTAGCAATGGGAAATCAATCA	CAAGACATTTGGTCTTTTGTGC	8
CCCCATTTACGTTTGTTTGT	CCCGAACGACTAAATGAGCTA	6
TTCTCCATTTACACGCTTC	ACGACATCGTTTTGGAGCTT	7
TGTCCTTGTTTCCTACAAGGTG	TGCCGAAACTAGTCCTCAA	8
TGAACCCGTCGAATAAGACC	GTGAGCGAGTTCTCATGCTG	9
GTTTTGGGGCATTTTGTGAC	GGCTAGTCTAGTGTGGGGCTTT	8
AACCCATTTGAGGTTTTTGC	CCGAAAAAGAAAACCCACCT	3
TGCACCAAAATTGGAGGATG	TTGATGCAAGGTGCAGTTTC	2
ATGGGTGTTGCTATGGCTGT	CGCATTTAGCACCCAAAAAC	10
CCTTAAGGGAAAGCATGTCG	TGGTTTGACAGGAAGCCTTG	3
TTTGGTCCAAATCTCTTTTCTC	TCGCCATTAAATTAACAACCAA	8
AGTTTCCCCACATTTGTTGC	TACCATGCACCAAGCAATTC	5
GGTGGTTTCCGTGAGCATAG	TTGCCACACCTTCTCGTTAG	12
GCTGAAGCTGTGCTTTTCC	GAAGGCGAAGTAGTCGGTGA	5
ATTCCCATGCATCAAAATCC	TCCTTCAGTTTGAGAGCTCCTT	2
TACCCCATTTGACCATTCTT	GGAATTGTGAGAAAGGATAGAGG	7
TCGCTGAGAAAAGAAACAAAAA	GAATTTCTGGGAAAGCGTGA	1

TTCACAAACAAAACCTCCACA	AAAAAGAAACATGAATTGAGGAAA	3
GCAAGCAGCAGACTGTGTGT	CTCAAACCTCACTTGGGAATCG	3
TTTAATTCCGGCGAGTTTTG	TCTTTCGCTTGTTGCTTTTT	1
ACAACAAAACCCACCGAAAT	CGATTTTCGCACATGAGATGA	2
TGCATGCTAAACGGTGTTTT	TCATGACCAAATCAAAGCAGA	8
TTCCAATTTCCCAACTGCTT	TCTGCTTCAGCCACTTTTCA	3
AGCGACTAACCCAACTTCCA	GCGGATTTCGATAGCATTTTT	7
TGTCCGAAACCGTCATTACA	AAAGCAGCGATACGAAGCAC	2
CAAAAGCCTCTCACTCTTGAGC	TCAAACCCAAACAAAACGAA	2
TCCCACCTTCCCTCTCACAC	TGGAATATGGAAGTGGGTTCA	7
ACACTCACACCATTTCCACA	TTTTGTTCATCGCCATCCATA	2
AGTAACAGCCCACCAAAGC	CAAACGAGTCCTTCCCTTCA	2
TTAACTCGGTTTGCGACTCA	AGCACGTGACTCGACCTGTA	11
GGGTGAACATGGTGGAGATT	GAGAAAACCACACCTCACAAGA	5
CTTGTTGGTTGCTGGAGTGA	TTCAGTTTTCAAAGCCTGTCA	5
ACTTGCTCGCTTCAACCTTC	ATTCCTCCTCATCAGGCTCA	6
TCTCTTCTATAATCCTCTCTCAAGGTC	GCGCCAGAGTGAAACAAAGT	2
		2
GGGCATATTGATCGCTTAGG	TGAGCATTTCATACATTCCATGAT	7
TCCCTCTGCAAAACGTAACC	AGATTTTGGCGAGGATTGTG	12
GCGCGACACATTTCATTAAC	TCACATTGCCAGCATCAAAT	1
CACCTCACTAAGCAACCTGTCA	TTTTGGAGGCGGAGATAATG	12
CCCCACCGTCTACTCTCAAA	GCGTTCACCACGTCCATAAT	1
TGATGATCCCAAACCACAAA	AAGGCTGCAGGACTTTTCAA	6
CCCAATACTCCCAATGAAGTC	TGAGAGCCTGAGGAAGAAGC	12
TTGTGTTCTCCGTCTGTGGA	ATGCTGTCCCTCCCATTAAA	8
GAGTTCCTCGCCGTATTG	CCCAAGGTGTACTTGCCACT	1
AGGTTACCATGGTGTTTTTGG	TTTCCCCAGATGGTGTCAAT	7
AGAAAGTTCCAGGGAAAGCA	CTTCGTCCCCAGTTGAATGT	3
GCCTTGCCAATCCATTAAAA	TACAAGGCTCTTGGCAGCTT	8
ACACTCCCAACAGCCTCAAC	TCTTTGCTTGCCATCTCCTT	1
TCGCCCTTACTAGGGGAATC	GCACCTTGAACAACCCACTT	6
TTACAGCCATTCCCTTTGCT	AGACGAGGCTGAGCAAGTGT	12
GGAAAAGCAGGTACACACATACA	CCTTTGCCCTGAAAACCTCAC	11
CCATCCTTTTCATTCTTTCCA	TGTTGTTGTTGCTGTTGTCG	5
GGGTCTGCTTTGATTCTTCA	GGGTTC AACATTGTCGCTTT	4
CCATCCTTTTCATTCTTTCCA	TGAAGAATCAAAGCAGAACCCTA	5
AAGGCACTCGTCGCTTTCTA	ACCGATTTGAAGCTCGAGAA	6
TCCCATTTGAAGTCACGGTTAG	AATGAAAAGACAAATGGAGATGTT	2
TCAACAAAACCCATTAAACCAA	GGATCGGAGTGAAATGGAGA	10
TGCACTTCCTTTGTGCTTTG	TGAGGTGTGTGTTGTGCTGA	7
AACCCAAACCCAAACCTTTC	TGGTGAATTCGAGGTGTTGA	4
CACCCACACACACAAACACA	TTCGCCATGTACACGTTCTC	12
GACGACTCGACGGAAAGAAC	AAACCAAAAGCATCCCCTG	10
TCAGCTGAAGCATCAACCAC	AACACATGGCAACAAGCAAA	2
TGACAAATGTTGGGAAACCA	AACCAGAGGGCTGGTAACCT	6
AATGCAGGCATGACCTCTCT	TCAACCCGACTACGGAGAAC	5
TCCCTAGATGATGGGGATGA	TTTTACGTCGGCCAACTTTT	2
TGCAAGGCTACAACTAGACGA	TGGCTTCTCTCTGGGACTGT	9
AGGCTGTGTTGCCTCTGAC	CACGTTGGTGTGGAGAGAGA	10

		1
CTCCTCCATTTCCTCAATTCA	TCGCTTGTGGTACATCTTGG	1/4??
		11
CACCAAAAATTTCTTCGCTTATG	TGAGCTACAAGGTTTACATCCCTA	8
TGGTGTAGTGAAGGAACAAATAAAA	CAGGAAGCTGTGACATGATGA	5
AACAACCAAAATCGATACATGAAA	GTAGCTGCCGCTTGAGATTG	7
CGCCACTTTTCGTTTCTTTT	GCATTGTACCATCAGGGTGA	1
GCAGAGGCTCTTCTAAATACAGAACT	GGGAGGTTTCTGGGAGAGAT	1
CACCTCTCTTTCCTTCTTTAGCA	CCCAGATAAGAGAACCCCAT	3
GTTTCGGTGCATGTGTTTGAC	CGAAAGATCAGGGAAGTAGAGA	11
GGTCTCTCTTATTTTCTCTTCTCG	TGTGAAGAAGAACAAGACCCTTT	8
CCATCTTTAACCCCTCAGC	AGGGATTATGGGAGCGAGAG	3
GAACATGTTGAAAGCCAATTCA	GGATTGGGGAAATGGGATAG	9
TCACGTGGTTTGTCTGCTTTT	CAATACTGTTTTTCGGCAATGA	5
ACGGCCAGTTAACCCCTCCT	TTCATTTTGTGATGGACGA	5
AAGCGACTTCTCCTGTCTGG	CCATGCAACAACCAATGAT	11
GCAGTAAAACCGAAACCACAA	AGATTTCTTCAGCGGCCTTT	6
TGACCTCTGAATTCCAAGAACC	TATGAAGGTGTTGATTCCCTTTT	11
AACCCCTTGTTCTCCAGCTT	TGCAAAGCGTTGTACAGATACC	11
CCTCACCCCTCTGCGGTCT	CAGAAAGGGCTGCAAAGC	12
GAGAGAGAGAGAGACAAAGAAGAAAA	AAATTCTCCGCCACATTGAG	11
TCAGGCTTTGCTTCTTCTCC	GGAAAGCATGCGGTAATTGT	10
CCCAGGGGAAGATTTGGTAG	TAAGCCCTTCACCATCTTTTG	12
CACACAAACAAACCCAGAAAGA	GCATTGTACCATCAGGGTGA	1
TCAAAACCAAAAGCCAAAACC	GCAGCTTCCAAAAGATCACC	3
GAGCTGCATATTTTCCTTAGTCA	GAACTCTTCTCTTCATCTTCTGC	10
AGCTAGCCCTGATCGATGTC	CTGTGAAAGTGCCACTGGAG	8
GAGAGATGGAGCACGAGCA	GGGTCAGGACCATCTTCTTGT	9
CCCTCCACATTCACTTCTCTATC	TTTTCCGGTGACCTTGAATC	2
CTTCACCCTCTTACTCTGCAATC	GGGGATCAGCTGGCTTTG	8
TGTTCTCCCAAGAAAAGAGTTT	TCGGGGACTTTGAGAACTTG	8
CTCACCGTTTCTTCCACGTC	GGATTGGGTGAAGAGTTTGC	??
TGTCAATGGGAGCTGGTTTT	TAACCCGAAGGTCCAACATT	3
AAAGCGCTCGGAGATTGATA	GACAAGAGTGCGAGTCTGGA	66
GAGGGTCGTCGAGTGCTTT	CCCTCTCCTGATAGGCAAGA	2
CATGTAGGATGGGGGTATACG	CGAAATGTCACTGTTGGCTA	6
GTCGGCGATGAGAGGAAAG	GGAGACATAGTTCCAACCTCAAGC	6
GTGCGCTTCAGAGGAACACT	CCAATCCCAATCTCTTTCGT	3
CGATTTCCCTCAGGATTGAGC	TTGCCGATCTCGATTCTCTT	1
TTGAGACCAAGGAGCCCTAA	ATCTGGGTCCAAATCCACAA	2
TCTTCCATCTATTACGTTTTTACGA	TGCCCATAGAAGCAACTCAA	4
GCAGAAGAACGGAAGAAGCA	ATCCCGACTACCTCGAGCAT	9
GAATTCGATTTTTGATCGAAGC	GAGCAGAGTCCGGTTGTGAC	4
AGAATGGCCTGTACTTTCCTG	CATACTGGAGTCCTGGCAGAG	4
CGCCCTTAGACCAGGATTTT	TTGAGTCTTGCTTGCCATTG	12
GAAACGTTCTGTGAGGGA	GGAAAGCTGGGAAACCAAG	8
ACTCCAGTCCACATTCCAAC	CGTAGCTGAGAAAAGATGGTG	8
GGCTACCGACTACTACCACTTC	CGGTGGACCCAATATGTAAC	8
GCCAGAAATCCATTTCTCCAAC	TTGTATTTTCCGGTGTGGTC	5
GCGACAGTCACAATTAAGCTAC	CACCCAATTTTCAATCTGTG	8

ACCTTCCATGCTCAAAGATG	GCTGGTGATACAAGTGTTTGG	11
AGTTCCTCTCCTCACCAAGG	CTCTCTGATTCTCCGCTCTC	3
CGCTAGGGTTTTGGTAATAAG	CTCTTCGCCTTTCTCTGTTG	10
TGCTAATCTTGAACGGAAGC	CAACCTCTCCAACACATTCC	6
ATCCCCAACCCAACAATC	GGAAGGTCGTTTGGATTTC	12
CCCTTGCCTGATGATTCC	CCTTTACAACCAACCAGGTG	2
ACTGCTCCTCTACGATGGTC	GCTTGTACTGGATGGGAATG	9
ACGTAACGATTTCGATTGTGC	TTGCCAAACTTTTCAAGAGC	5
TCTCTGTTCCAAATGTTACCG	TAACCGTAACCGACTCATCC	1
GAAAAAGCCTCCACTGTTCC	GGTGTGGGTGTCTTTCTTG	11
AATACAAATCGCAGGAGGTG	CTAACCCATCGTTCATGGAG	6
ACCGAAAGAAAAGCAGTGAG	TAGTCGCGGAAGAAAGAGAG	12
CTTTTGGGGATGATCTGTTG	AGGATCCTTTGAATGGGAAG	7
TGTAATTCAACGATCGAGGTC	AACCCGCTGAAATAACGAG	8
CCTCCCTAGGGTTTTACAGC	CACTCGTTGATCCAAATTCC	3
ACGGTGATGCCGATTTTG	TCCTCCTCAGAAACCCACTC	2
TTGTCTACCTTTATCAAACATCATG	CAAATACGAGAATACCACAGCAAC	3
TTATCCACTCTGCGGACATG	ATACACAGCCAGACCCATCC	2
TCTCCTACCACCAAAACAAGG	CACTTCTCTAACCCCATCAGC	7
TGACGAAGACAACAAATCTACAG	CCCTAAAACTAAGGGTCTCACTC	3
CGCTGTTCTAGTTTTTGC	TTGTCTGGTCTTTGCGTGTG	6
CCTCTTGTTAAATGATGGTTCAAAG	TTTGCTTGCCCAAATACTTTC	2
TGCAAGGTGGGAACCTTGAT	CGGCATTAAAAGAGCCTTCTC	11
TCTCTGATAATGGTGGGTGTTG	AGTGGAGTTTCTGGGGGAAT	3
GGTGTGAAGTTTTTGTTTCC	ATCCTTTGGTGGGTGTGG	10
ATTTTGTTCCAATCACATCAGA	TCGCCTGTCTTCAAATTATGTC	8
CATGACCCCATGACTTGTTG	CAGCCTCAATATGGGCATTA	2
TGGGATTAGGGGTTAGGG	TGGATGCGGTTCTTCTTGTT	2
TGTACCTCTTTCCTCTCTCTAAACT	GAATTTCTAAACCACTAGCATTGAC	2
TTCTGTGGTAGTATGAAAATCTCAA	GATGCCATACACATAAGCATGA	3
CCAGAAAATCAAGGCTGCTC	ACAACCTACTCATCACCCTGA	8
TCTTTGCTTCCTACACAGCTTTT	CCCAGTTTTACAGGCATCT	8
ATGGTTGCGGTGGAGGTA	CTCTGGTAGTAGGGGCACTTG	4
TGCGAAGATGGAGGAAGA	CAAACGAAATCAGAGAACGAAA	3
AGAGGCATGTGGAACCAAG	CAAGCATAGGTGGTGGAAACC	3
CCAGCCCTGCTTATTTTCAG	TGTTTGGGGGACTTTTCTTG	7
TGGTCTCCTACCCCTTTTC	TTGTTCTGTTTCATACCCGTGA	2
GCACCTAATGGAGGGAGA	GATTAAGATCCAGGCCGATT	7
GATGCAAGGGCTACGG	CAACATGAGGATCGGCTAAAG	2
ATTTGTCCACCGAGGTTTACG	CTTGGAATGTGGGTTTTGG	8
GACATAAAGATGGGCATGG	GGCAGCATCTCCCTAATGTT	4
TAAAGATGGGCATGGTCAGG	TCCCTAATGTTGGTGATGTCC	4
CCATCACAAAACGCGCTATC	CACGCTCATATACACCCAAATG	10
TTCTCAGCCCTTCGATCAAC	TTTGTTGGTGGTCTTTGTTGG	10
CTACCAACAGAAGACGCAATG	AATTGATGCAGATGGGGAAG	4
CAACGTGAAGTCAAGCGATG	CAGGCGGTGACAGAGGAG	3
TTGAAAGTGGTCGAAATGGAG	GGCTTAGGGAGAGGGTCAAG	3
AGACAATGGCGATACCTTGG	CCCCAATGTTTCAATTCTTCC	2
GCTTCCAATTTCCAAATCC	TGGAGGGACGTACTTTCGAG	4
GTCTGCGTGTCTCAACTTCG	CACAGCACTCTCACCACAGC	12

CAAGTACCACACCCACAACC	GAAAGAGCACTGCCTCCAAC	2
GGTGCTGTGTTGGTAACTGC	GTTCTGAAGCCGAATCCATAC	3
ACAACATGTGCCAAAACCTGC	TCGATGATGTGGTTGTTGATG	4
ACCTCAACCTCAACCACCAC	GAGGGCAAAATGGTCTCTTG	5
GGGAAGAGAGAAAGAGATGGAAG	CATTTCTGAAAAGCCCAATATG	11
ATCGCCGGAAAAACCATAC	AGTCATATTCGGGATTCATGG	12
GCCATGGCTTACACCACTTC	ACACGTCGGCAAGCAAGTAG	8
ATCCACCAATTCCCACACTC	CTCGTCGTAAAGGCGAAGTG	7
CATCATGAAGACCACACACG	CCCCAACAGTCCTCACACAG	2
GTGTCCACAACCGGACTTTC	TCGGAGAAGCCTCTTTTCC	6
AGAAGCAGCAACAACAGCAA	CCTTTGCTTCAGGCTCAGTT	11
ACGAAATGGAGCTGTTGACC	TCTCCTTCTCTTCTGCCATGA	12
ACCATTACCAAAACCTTCAAC	TCTTTTTTGAAGGATTGATGAGA	4
TCAGTTTTTGCACCGAAAGA	CCAGCTCCCACTCCAAAAT	4
CAACAGAGTCTGGTAGCGAAA	CCAGTCATGCATGTTCTTCG	7
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TGGAGGAGCACTGCATATTG	CACTGTGGCTGGAGCATCTA	4
CATCTCCACCACCAAAACCT	TGATGAATCTGCCAGCTCAG	??
CATCAATATCCATGGCAGCA	GAAGCTGGGAAAGAAGCAGA	10
TCAATCCCATCTTCCTGCTC	TCTATGCGATTCCGCTTACC	12
CTTTGGTAGCATTTCCTGTGC	TTCCCCCATTTGTGCTAAAC	1
AATTTTGATGGGCACTTTGC	CACCTCAGCCTTTTGTTGAC	2
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GGGGTCAGTAGGCAAGTCTTC	GAGCTGCATATTTTCCTTAGTCAG	10
AGCACCCAAAAACCCTAAGC	TCCTTGGTGAGGTTCCAGAG	10
CGCCATAATACCTGCCTTTC	ACTTCAGATCCGCCATTGAC	5
ACCGCATTAGGCACTCAATC	TCCTTGACCCCTCATAGTG	2
GCTTTCACCTTTGAGAGAACTTG	TGGCTATGAACTCAGCAATCC	8
GCTGTAAGCAACACAATAAACG	TCAAAGGCTTCTGGCTCATC	11
GATTTGAATTTCCACACACAAAC	TGTGTGTGATGATTAACGATGATG	9
GAGGATATTATCAATTGCAGCTC	TTCCAACTGAGTGAGCCTAGC	6
CCAGACACTTCACACCTCCAC	AAGGGCTAAGAAAAGCACCAG	3
TCAACCAAGTGAGTTTCTTAGG	TTCTGTCCAGTCCACTCTGC	6
GCCAACGAGAGCTAAGTTGC	GCAAGGTCAAGGTCAGGGTA	11
TCTCGATCTCAAAACAAAACCA	TTTGATTTGTTTAAGGAAAATTGGA	2
TGGCTTTATGACACCTTTCG	CCTTTGGCATTTAGCATCAAA	8
TTCTTACTCCTTTCCCACTTC	TGGCTGTTCCAAATCTTCAA	6
CCTCAAACGCAAGACACTCA	CGGTCAGTGGTAATGGGAAT	8
GCGCAGAGTCAGAGTTCCTT	ACGAGAATCAAGCGCAAAAT	9
GCTCAGATTTGCCAACACAA	TGTGGGCATGTGTGTTCATA	2
CCAACCATCAAGGCCATTAC	GTGCGAACAGATCCCTTGTC	3
CACACTACCAACCCTACCC	GTGCGGTTGTAGACGGAGAT	2
GCAGCAATACCAACACAATGA	GGAGCAGATAAGCTTCCCTTT	11
TCCCTCTTAAACGCAACTCAA	TTTGATCTGTTGTGGCTGT	2
CGAAGGAAAAGCCAAAAGAA	GCATTCAGTGCAACAAGTCC	1
CTCGCTCTCCTCCCCTAATC	AGCTTTGATCGAGTCCGAAA	3
CTATGGCTGTACCATGTGC	AGCACCCAAAAACCCTAAGC	10
ATACACAGCCACAGCAGCAA	CCGATACTGCATAGCCATC	2
AGGGGTCATCAGAGTTGGTG	ATCCCTCAGTCTTCCCGAAC	8
GGAGGCTTGTGTAGGACTCG	AGGGCTCTCTCGTTTCACCT	8

GAAATCTGAACCCAGGTGGT	TTCAACCAAGAAGAACAAGAAGAA	10
ATCCTTCAACGCCCTTTAGC	GGCAAGCTTAGAAACGGAGA	3
TCAGCAGCACCAACAGAATC	TCGACAGTCTTGCAGTGTCC	6
TTCCCACACATCAATTTTTCC	TGAGACGTAAAGAGCCAATCCT	5
GCAAAGCAAAGCAAAACACA	CCCCAATCATACAAATTCAA	1
AGCAACAGCAGAGCCAAAAT	CAGCGGCTTTGAGGTAATTC	6
CCCATATCCCTCTACGAAAGAA	CTGGAGATGACATAGTGTCTCAA	6
TCCCTTCCCTTCCTGCTATT	CCACGCGAGTAGTGAATCAA	6
ATCACAAACCCCAACCCATA	GCCATCCTTAAACCCCTTTG	2
CAAATCCGCTCAACTTGTCA	ACCATCGTCTCCAACATCAA	12
AAGTCAAACCTTGCACAATCC	GAACCCGACCCATGTAATTG	6
CTTATCTTTCCGGCCTGCTT	CGAGCTGTTCTTGAAGGTTG	2
TCGACTTCATCCCCATCTTC	CATACGGACCACTTGCCTCT	2
GCCCCGATTATTTCTCTG	TGAGCCTCAACCAAAACAAA	6
CACACAAACCCATATGATCTGAA	TCTCTTTCGATCCCTTCTGC	7
CAATCCCCACATCCAAGTTT	TTGCTGTTGCTTGTTTTTGC	10
AGGCCAGTTCATCCTTACA	TGGTAATCCAACCTCAAGCTG	6
TCTTCAAAACCCCTTCAACG	TGAGGATGCCATAACCATCA	10
TGGGTTGTGTCTCTCAATGG	AAGCCTGCAATGAAGCTGAT	4
CTCACTCCAACTCCGAAGC	CTAACCTCCCACCTCCATT	5
GCTACTCTCACCGCACCATT	GAGCCAGATGGGTCACAGAG	3
TCTCTTACAACCCAGTACTTCCA	ACCCTACAGGTGCCTCTCTG	2
TGCGTCTCAATCACTCTCTCTT	TCGATCCGTGAAAATCTGAA	6
GCGGGCAGGTTTGGTCTAT	CACAACAACAACCTGTGCTG	7
TCGGTCCGAAAACACAATTA	GAAAATGGATAGACAAAGCCTCA	1
CCCATATCCCTCTACGAAAGAA	CTGGAGATGACATAGTGTCTCAA	6
GCCTGCTTTTTGTTCCAGAT	CGAGCTGTTCTTGAAGGTTG	2
CGAAGGAAAAGCCAAAGAA	GCATTCAGTGCAACAAGTCC	5
CATCATACGACCCGAAAACC	TCTTCTGCTCCTCTCCCCTA	1
TGAAACCCAGAGGCAGAGAT	CCAATTGCCAAAGAAAAGAG	2
CACCTTCTGTTGCGTTGTGT	TGTGACATTCTCCCTTTCC	9
CCTGTAGCCAAACCTGTGGT	TTGTTGATACGGTGGTGGTG	6
GCAGTATCCAAACAGACCCTAA	GCTTTGCTCTAAACAGCAACTT	4
CCACATCTCCCCAAAACAAT	TGCCACATTTTCCCTGTATG	7
ACCCTTTCCTCTTCCCAAAG	GGAAATCGGAAATCGGAAAT	1
CTGCTGCTGCTTCTTCCTCT	GCGATCCGTAGGGTTAGGTC	7
CACGTGCATGTAAAGGTGCT	CTGTGTCTGTGATGCGTGTTT	12
GCCATGGCTTACACCACTTC	ATCAACAGAGCGGGTTTGTC	8
GATCCGAATCCGAAACTGAA	GTTACGAGCGAGGACGTTGT	4
TGATGCGTTTGTGTTTGTG	CCAACAACATGTGCCAAAAC	4
CCAAACACGGCTTACAAAGAA	CCGCTCGAGGCTTTTCTAGT	2
GCCGATCCTCGATCTGATAC	CGCTGAGACCTTCTTCAACC	7
TTCTGGGAAAGTAGCTTTGGA	TTCAACGCAGACTTGGTTTG	3
AATGCGAACGACATGAACAA	CTCTCGTCGGAGACTCAACC	5
		9
CCACCTAAACCAAACCCTCA	TGTTGCCAATACCGATTCTT	1
CGGAGTTGGTAGGCTCGAT	CTCTCCCTCACTCTCCCTCA	6
GCCACCCACCACTTTACAA	TTGAAGCTTGAGGAGATGAA	8
CATGAAGAACACACACGATGC	TTCGGTGAACTTGAAGTAGGC	2
GAAGCCACCAAAAGCTCTGT	GAGTGAAATGAAAAACCCAGA	12

GATGGGTTGAGCGGACTATC	CAACCAAAATGGAACATCG	4
ACATCACATGCTGGGGAAAT	GCCAAGTGCTATCAGTGCAA	7
AACTCCAATTTTTCGGACCC	CTTCAGCCCTAGATTGCGAG	6
AGCAAATCAAAACCTCACCG	CTGGTCTCTGGGTTTGTG	2
AAAGCAATTCAACTGGGACG	ACGACACCGTTTGTTCCTTC	2
TTTAAGTGTGGGAAGCCTGG	TTTCGGTCAGGACCATAACG	2
TGCAGATGGCAAAGCTACAC	AAGGTGGCAGATTCTGTTGG	2
AAAAACCCCATTTCCACCCTC	TTTGAGAAACTTTGGCCACC	1
CCGAGCTTCAATTCCTCGAG	TCTTATGCAGAAGTGGGATGG	8
GCTGAAGCTGTGTCTTTTCC	ACTCATTGAAGACGAACCCG	5
CCCATGACCTCATCCTCAAC	GTGAGCCGTATAATCGGACG	4
AACTCTCAACTTCCCTCGCC	TTCGAGAAAAAGGGTGGTTG	5
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ACAGAACACGGAGGAGTTGG	CTGCAAAATCGGCTTAGCTC	2
AGATCAGGATGTGGAGGTGC	AAATCCAAACCCCCAGTTTC	10
ACCATCCTCTGATGCTGCTC	GTAAGGAAGAGACCGTGGGG	8
GGTAGCTTGACGAAGTTGG	CTTGCAGCTCCCTGGTAGTC	8
CTCCTAGCTCCGTCGTGAAG	CACCGACTCATGTTCCACAC	??
AGCCGCAGCCTCTCTGAGC	ACTTTGGTCTTGCCGAAGT	5
CCAACAGCAACAGCAACATC	AAGTAGGTCACGCCGAATTG	1
GGGGACTCTGGAGTTGTGC	AGGCTGTGTGAGAAGGTTGG	2
AGAAAGAGAAAGAAGGCGGC	GCATGCCCATACCCATTAAC	1
ACCGGAGACCTGCGATTAC	TTGGGACTTTCCACTTAGCG	6
TAAAAGCTTCTGGCCCAATG	GCTGCACAGAAGAAGAAGCC	4
GCCACAGGCAAATAACAAC	AACTCAGGCATGGGCTACAG	5
GCGTATAGGAAGCAGCATGG	ACCCATTCTGTTGAACCACAC	2
ATGCACCGTGGTAAGCATTC	TCTTGCAATGACCACACCTG	12
GCAGAAAATGTGCAAGAGGG	ACCAACACAACCAAGCAAGG	??
TTGCAATTACAAGCAGCAGG	AACTCCAGGTGGACTGTTGG	2
CTTGAGTCGGTTATGGCTGG	TGATGACTGAAGCGACGAAG	2
AGGGGGTGGAAGATCCTATG	GCTTAGTGAAGTTGCGAGGC	??
AACAGCTCATCCAAGATGCC	AGGACGAGGCTTCTTGTTC	2
ATACCAGTCTCGCAAGCCC	TGGCTCAGATGCTGTCTCAC	6
TAATCACCGGAGAGACCTGC	GTCATGGCAAAGGTCGAAAC	6
TTGGGACTAGACCATCCACC	ATGGACAGCCAAGCCATTAG	9
TCTTTCTCTCTCCTCACCGC	TGAGGGGATTGTAGTAGGCG	??
GCTCTCTTACGCACCCAGTC	ACAACCTCAACTCCCATTC	2
CATTCATGGCGTACCACAAC	AGCCATTGGTTTGAAGATTG	2
ACTCAGCAGCAGCATCAAAG	CTGATTGGGAGGAGCATAGC	9
TCAGCACCTGTGAACATTCC	GTCCCTCCCTTTCAGAGTCC	8
AACCTGTTTGGCTTCGTGTG	AACAAAAGATTGGGAGGTGC	1
CAATAATTGCATGGAGGAGTC	TCTTGATTTTGTCACTGCTTG	1
GCCCTACATGGGTGACAATG	ACAGCTTTCCTGGAGAGAG	2
CTCAAGAATCCGTTACACG	TGAAGCTGCACTAACATGGC	??
CAAAACGACAAGGAAGGAGC	CTAACACTGGCTGCTGTTGC	11
Forward primer	Reverse primer	linkage group assignement*
ACA CTC AGA CCC ACC ATT TTT CC	TGG CTG CAC CTA TGG CTC TTA G	6
TTG CCT ATC CTG CC CCG TAT CAC	GGA ACA ACT AGA GAG AAC CAA GTC AG	9

GTT CCT CTA TCC AAT CAG TAG TGA G	TCT CCT CTC CCC ATA AAC AGG	4
CGG GCT TTG GAT ACG GAT TC	CCC GAT TTC CCT TCC CTG CT	6
GAC CGA AGA AGA CCC TAC CTC AG	TCC GTA TCC ACC TGC GAA TCC TC	11
CCGGAGGCGACACCACC	CAAGGAGCGCCAGATGATGA	11
CGGCTTCGGTTTCGTC	TTAGCTTTTACGCAGTGTCG	8
TTTGATTGATATAATTGATCGCT	CTCTCGCTCTGCACGTGACTCA	8
TCCCCAAATTCAGGTAGTGT	ATACCCAGCTCCCATGACCA	1
CTTTGCGCAGGTCCATTAC	CTACAAGTTACATGCCCAATCA	10
TTTTGTGTCATCCGGTATTA	TTTAGCATCACATTTCCGTT	9
GATTCCATTGTCAACTGCGAAGA	AAAACACACAGCCGATTACTA	1
GGCTTCACATTGAGAACGTTG	ATTTTATATTAGCATAAGGGTG	5
TAAGTGGCTAGATAATCAG	GCCAACAAATTTAACTATCCAT	??
TGGTTGTTTTGCTTTATTCAGCC	CCAATCCACCCTTCCAAGTTCC	6
TGGCGCTCACTCCGAGAT	CCAAGCGCAGCCCATCACTAAC	2
GGG CAA CAT TCA AAT GTA TCT A	ATA TGG TCC CGA TTA ATT C	2
CGA TGT GGG ATT TTG ATT TT	CGA TTT TGA ACA CCT TCT TC	9
GATCTCAAGTCAAAAGGTGTC	CGAGGTTGTTGTTCATCATTAC	4
AAA CCT CCA CCA AAA CAT TC	TCC TCC GCT CAC TCA CCA TT	5
GCA ACA CCC TTT AAC TAC CA	GCT TGA GAG TTG AGA TTT GT	7
CGC TTT TGA CTT TCC TAC CTT	CAA CAA TGA AAG GGA GAA AGC	9
GAT GGT ACA GTA GCA ACA TTC	CAC CAC TAC CGC TGT GAG ATA G	2
		7
CCT CTT TTG TGA ATG ACC AAG	CTA GCC ACA ATT CAG GAA CAG	2
GAT CTC TTG TGT GCT GTA TTT	GGA GGC TTC CTT CAA CCT ACT	8
GAT CAA CAA GCC CAA GGC AC	GAT CAG TGA TAG TGC CTC TC	2
CAT CGA CTC ATT GTT AAG CAC	CGA TTT GAT AAT GAC ACT ATG G	9
CTT TTT GGA AGC CGC TTC CGT A	TAG AAA GCC CAA AAC CAA AAC C	6
ACT GTG GTG GTG AGT CTA ACA TGT AG	GAT CAA AAT TTG GAA TAT TAA GAG AG	2
TCT CCC ATG TAA GTA GCT CTG	CCC CTA TTG AAG TCC TAG CCG	2
TCT TTT TCC TAA TCT CAC CTG	CTG CAA GAT TCG GAC AAG CAA	5
TCT AGA GGA GCT TTC CTT TAC AC	CTT GAG CAT GGA ATC CTA TG	10
TGA AGC CCT TGT CAA CAT GC	CTT CAC TGG CTT TTC CTC CT	2
CTT ATA GGA GAC ATG CCC AG	CGC ACG ACC GAC CTA GGT A	??
GTC TGG ACC TAG CCC TCA TG	GCA ATT ACA GGC TAG GCT GG	7
GCC ATG AAC AAC GGA GGT ATC TAG	CCT GCA CAA TCA AAT CCT TCA CTT	1
GAC TTG TAA CAC CTT AAG CAT TAT CT	GCC TAC ACT CTT CAA TCT ACA TGA	3
GAA TGG TCA TGC ACA CGG	CTT CCC TCC CAT GTA TTT ATT G	10
GAA CCT TGA TCA TAC GTG GAG A	AAG AGA GCA AAT TTA GAG TGA TGT	7
GTA GGT CAA AAC CAT TGG TTG ACT	CCT TGA ACT CGA AGG TGT CCT T	10
GGT GGT GAT GTT TCT TTA ATT TTG	CAT CCA AAC CTC TGC GAT CT	11
GTG GTC AGA GAC TCG GTA AGT ATT C	TTC TTG CTT TGG TGC GCG	12
GTA CCC AAG ATG TAA AAT CAC CC	GGC ATG TGT ATT GAA AGC TGT A	9
GTG GTA TCT ATA TCT TGC CAA AGG	CCT CCT AAC AGT AAC ATT CTA CGA	9
GTT GCT ACC AAA CTT GTG TGA A	TTG TGG TGT TTT ATG TTT GTA CC	11
ND	ND	9

GCA GCC GTG GAT GTG GAA T	AAT TTT GAA ACA CCA ATA AAA ACG G	10
GCA ACA CTC AGC CTA TAT CTA GAA	CCA TTA AAA GAA GCA GTA TTT TGT	1
GTT AGA ACC AAT GTA CCA AAG TCC	GAT ATG AAA GAT TCT TAT TCC ATC C	10
GAC ACC AAA CAA ATG AAA T	TGC TCC GTC ATA ATC TTG CTC TGA	12
GCA ACC AAA CAA ATG AAA T	CTT AGT TTG GTT GGG AAG AT	9
GAC CTA AGC CAA AGT GTG GGC	CAC CGC TGG AAT TTT AAG GGA	5
GTA ACT ATG ATG TGA TTC TTA CTT CA	CGT CTA TAA GTT CTT GGG TGA	11
GAA ATC TCA CCT GCT CCC TAT C	ACC CTT GTA GTC ATG TTC GTT G	7
ND	ND	7
GTA TGT GAG TGT TTG TGG TTT GG	TGA AGA GTA AGA CCA TTC ACA TCA	6
GTT ATT CAC TCC CAGTGT TCG C	AAG AGA ATG AGA AAT GGG GGG	2
GCC ATT GAA ACT CTC GAC CTC TT	AAC AAT GAA CTC ATC AAT CCA ACA	2
GTA TGT GAG TGT TTG TGG TTT GG	TGA AGA GTA AGA CCA TTC ACA TCA	8
GTC AGG TGA CCA TTC AAA CCT AGA A	CAG TGG TGT CAA CTC CTC CCA G	10
GTG CAT TTC TTT TAT AGC ATT CAC	CAA CTT GGT GTT CGG ATC AA	2
GCA CAC CCA CGT CGT TCT TAG	CAT GCC TAG TGG AGT CGA GAC C	5
GCT ATC ATC CAT CCC CCA ACA	TTT ATG TAG TGA GTA GTG GGG GTC	1
GTC CGA GAA TCA TCA TTA AAG G	ACC GCC TAT CTC AAC CAG AG	5
GCT CTC ATT AAC CAT TCT CTC TCT	CAA TGA TGG CAA TGG CAA	12
GTT GTC AGC AGT GGG ATG GGT A	TCC CAC CAC TTT GGT CTC TCA	2
GGT TGG GAA AAG GAG ATC AGA	CCC AGT CAC ATC CAC TAC TGT CC	10

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