Supporting Files

Files S1-S3 are available for download at http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.111.001867/-/DC1.

File S1: R script containing all the commands necessary to run the analyses. Comments on commands are included in the file.
File S2 : Input file formatted for R/QTL package gathering all the genotypic and phenotypic information.
File S3 : Raw genotyping data for SSR and SNP markers used in the present study to build the linkage map.

Table S1 Description of the SSR markers used to build the linkage map in the Brook charr, *Salvelinus fontinalis*

	Marker	Primer F et R	Annealing Tempearature	Accession Number	Associated publication
1	BHMS206	CCAAATAACTGACAAGTGAG	54	AF256680	Timusk et al. 2011
		CAGAGGTTGATAATGGGG			
2	BHMS238	GATAATGCCTGGATGTGC	54	AF256682	Timusk et al. 2011
		CTAGAGCCGACCCTTTAC			
3	BHMS272	AGCTTGACAGCAGCTTGG	54	AF256690	Timusk et al. 2011
		TGCAATGCAGACTGACTG			
4	BHMS331	CAGCACCAGAACATAACC	54	AF256744	Timusk et al. 2011
		AGCCATCAACACTCCCTG			
5	BHMS377	TGGCTACAACAGGGATAC	54	AF256707	Timusk et al. 2011
		AGTCTCTTACATGGAGGC			
6	BHMS417/i/ii/iii/	ACATAGACCATGACGCTC	54	AF256752	Timusk et al. 2011
		TGACACGCTCTCTGATCC			
7	BHMS429	CCCCTGTCAAACGTCTTC	54	AF256719	Thorsen et al., 2005
		AGCACACTGGATTCAAGG			
8	BHMS465/i/ii	ACTCATCAACTGAGCCCC	54	AF256857	Timusk et al. 2011
		GTGATCTGTAGTTTTCCATC			
9	BHMS7.011	GGGACAGCTAATGGATCG	54	AF256834	Timusk et al. 2011
		GTTTTAGTAATCGGAGTGTG			
10	BX073647/i/ii	TATGGCTTTCCAAACCAAAG	54	BX073647	Timusk et al. 2011
		ACAGGGGGTTAACAGTGACA			
11	BX073974	TGTACGGAAAGATGGGCTCC	54	BX073974	Timusk et al. 2011
		CTCGAAGTCACCCAAACAGC			
12	BX076085	AAGACAGGAGATGAAGACACCG	54	BX076085	Timusk et al. 2011
		ATATGTCGTGGGAAACATGTAGG			
13	BX079862	TGTGAGAAGAACACGAGAGTTGG	54	BX079862	Timusk et al. 2011

		GAATGAGGTGTTAGAACGACTGC			
14	BX087664/i/ii	ATAGCCAGAGGGAAGCCTGC	54	BX087664	Timusk et al. 2011
		GCATCTCCAGCAGTCATTTGG			
15	BX299451	CCTGGTCTCCTTCACTTTCA	54	BX299451	
		CTGTGCTTACTGGGCAACTT			
16	BX305863	TACTGTACAGGATGGGTCTCTGC	54	BX305863	Timusk et al. 2011
		GGAGTACTACGTGTGAGGATTGG			
17	BX311224	CCGTGTGAAACCTGCATCC	54	BX311224	Timusk et al. 2011
		CCTTGGAATGCTTACCCTACC			
18	BX311884/i/ii	TGGACAACTTCAGCAAGGACC	54	BX311884	Timusk et al. 2011
		TGGTGACAGTTTCTGCTGAACC			
19	BX313739	CATGGAGTGTAAGGCAGGGC	54	BX313739	Timusk et al. 2011
		CGACAGATCAGCATCGCTGC			
20	BX318599	GATTTTCTGACCAGCACCTCC	54	BX318599	Timusk et al. 2011
		CCAACTGGACCCAGAACAGC			
21	BX319197	CGTCATCCATGTATGTTTCATGC	54	BX319197	Timusk et al. 2011
		GACAACTCACACATCCACATGG			
22	BX319411/i/ii	GCTGTGGCCCTCTGTCATACC	54	BX319411	Timusk et al. 2011
		GACATCAACGTGACACCAGGC			
23	BX861121/i/ii	CCTTCATCAAGGATGCAGCC	50	BX861121	Timusk et al. 2011
		TATGTTTCCCAGTACATACCGGG			
24	BX870052/i/ii	CAGATGAAATTGATCCAGATGACG	54	BX87005	Timusk et al. 2011
		GGAAGGGGATGATGTGATTGG			
25	BX873441	GAAGAGTTCCGGTCCATCGG	54	BX873441	Timusk et al. 2011
		CGTGCATGTAATTCAGCCTGC			
26	BX881655	AGAAAGACCTGGCAAGGACC	54	BX881655	Timusk et al. 2011
		CCTCTGGCACAAACTCCAGC			
27	BX890355/i/ii	ACTGAGAACACTTCAGCCAAGG	54	BX890355	Timusk et al. 2011

		ACCCACTAGCTGCTACATTATGG			
28	CA060381	AGTGGTGAAGTGGGATGGGG	54	CA060381	Rise et al., 2004
		CCCGATGCTTTCTTCATGG			
29	CA061336	TGCCATGTTTATTGAAATGCC	52	CA061336	Rise et al., 2004
		GGATCCAAAGGAGAGACTCCTG			
30	CA344270	CACACTTCCTGGACCACTTCC	54	CA344270	Rexroad et al., 2003
		TTCAAACTAGGGATTTCGTTGC			
31	CA345149	ACCACCTCAGAGTGTCTTTCTCC	54	CA345149	Rexroad et al., 2003
		GACTTGACATACAAACGACGTGG			
32	CA350064	GACCTGGTTTCGGTGTCAGAGC	54	CA350064	Rexroad et al., 2003
		CCACTGTGAAGTTAGGTGTTCCC			
33	CA368462/i/ii	CGACAGACTCAGACCACTGTCC	56	CA368462	Rexroad et al., 2003
		CGACAGACTCAGACCACTGTCC			
34	CA376300/i/ii	TTAAGCACTAAGGGGAAGACGG	54	CA376300	Rexroad et al., 2003
		TGGGGTGGAAGCAAAGAGC			
35	CA378164	GAACGGGGTGTCGTAGATGG	54	CA378164	Rexroad et al., 2003
		CCCTGACCTGTCCTCTTTGG			
36	CL4778	GAGGATACTGCCATTCAACA	54	NA	
		ACGGTCCCACCTTACCATAAA			
37	Clock3-7C2-3	GAGTACTGCCCTGCAGGTTG	54	NA	Timusk et al. 2011
		TTGACCATGGCCCTCTTATG			
38	CR363293	TCCGCAACAAGTACGCTGG	54	CR363293	Timusk et al. 2011
		TTCTCTTCTGGCAACTTCAGACC			
39	Ogo4UW	GTCGTCACTGGCATCAGCTA	54	AF009796	Olsen et al., 1998
		GAGTGGAGATGCAGCCAAAG			
40	Omi30TUF/i/ii	AGAAGACGAAGTGGATGCTG	54	NA	Timusk et al. 2011
		GTCACCGTTTCTTTACCTGC			

41	Omi126TUF	TTAAAGGAAACACACGCATACG TTCACACGACCGTTGGTG	54	NA	Timusk et al. 2011
42	Omi179TUF	TTATCCTAGTGCCGGGTCTG ATGCAGCTTTTCAGTGGCTT	54	NA	Timusk et al. 2011
43	OkeSLINRA	GAAAATAACTATAGACATTGCTGG CGTCCTTACACTCCAGAGGG	54	NA	Sakamoto et al., 2000
44	OMM1195	GCGAGGTTAGGATACACACAT CTTCAGCCTGGAAACACAA	54	AF469980	Timusk et al. 2011
45	OMM1197/i/ii	CTAGGAGAACAAGAAGACCATCGC AGGACAGAAAGGAGGTAAAACGG	54	AF469982	Timusk et al. 2011
46	OMM1201	CCGGAAAAGCTAGGGAGAG CCCTTCTGTATCCATTCCGTT	54	AF469986	
47	OMM1205	AAACGGTGCCCTCCTTCCTCTATA CCCAAGCCAATAAAGCCCTTACAT	54	AF469990	Timusk et al. 2011
48	OMM1210	CATCAGACAGCACAGAGCAG GGAGGAGCAAGCCTTCTAAC	54	AF469994	Timusk et al. 2011
49	OMM1211	ACCCACTCTCCCACTCAGTATT GAAGGAGGCTTGGAAGTGTATC	54	AF469995	Timusk et al. 2011
50	OMM1220	CTCTGGGACAGACTTATCAC CTATTGGACGATGCACAC	54	AF470002	Timusk et al. 2011
51	OMM1228	CCCTTCCTGTGTGTCGTTGTT CAGGAGTCACTTGGCAGTAGGAG	54	AF470009	Timusk et al. 2011
52	OMM1237/i/ii	GTCAGAGTCGTGGGTATCAA CAGAGTTTCCACGGTCACT	54	AF470017	Timusk et al. 2011
53	OMM1238	CGGAAATACGGAGGCTACTGTTG CTTCTCCCTGGCATCTTTCATCAG	54	AF470018	Timusk et al. 2011
54	OMM1263/i/ii	CTGCATTCCAATACTCCACAG TGGACGAACACTGGATCAG	54	AF470029	Timusk et al. 2011

55	OMM1290	GCCTCAGCACTGTCTTAA CGGAGGTCCCTAGAGA	54	AF470050	Timusk et al. 2011
56	OMM1329	GGGAAGTGTTCACCATTACACAAG CATCCAGGAACGCACCTTTA	54	G73564	Palti, Y et al., 2002
57	OMM1345	CCCTGGATTCTCCTGTTAG ACATAGACACAGCACTCATGG	54	G73576	Palti, Y et al., 2002
58	OMM1372/i/ii	CACTTCATGATGCCGAAAGCAG CCCCCATCATGACTCCTTCTAGTT	54	BV005159	Palti, Y et al., 2002
59	OMM1445	CTGCGTTATTGGTAGCTTGTG CCCGGTAATGTAGTTCCTGTC	54	BV079589	Timusk et al. 2011
60	OMM1459	GCAGGTATTCAGGTAGGTCAG AATGACCATGGAAAACAACAC	54	BV079593	Timusk et al. 2011
61	OMM1512	TTTCAAATCAGCCCAGGTTA AGGAAAAGGCAGGATGGTAT	54	BV212048	Coulibaly et al., 2005
62	OMM1579	CTAGGCTCTGTGAATCTGA GAAGGAATAAGACTGTCCG	54	BV212097	Coulibaly et al., 2005
63	OMM3015/i/ii	ACTCTTGCGCTGGTTGTATG GAAGAGTGTGAAAGTTTGGCTG	54	BV718488	Timusk et al. 2011
64	OMM3075	CATTTAATTGAGCTGGCCAC CCAGACAGTTCTGAGCAACC	54	BV676508	Timusk et al. 2011
65	OMM3095	CTTCCATTCAGGGTAGAGCAC CCAGGTGTGAAAGGGTTTG	54	BV676517	Timusk et al. 2011
66	OMM5000/i/ii	AACAGAGCAGTGAGGGGACTGAGA CAAGTGATGTTGGTGCGAGGG	54	CO805106	Timusk et al. 2011
67	OMM5007	AGATGCCTGTCGAGTGTTG GAGGAGCATCATTTAGAGACTACA	54	CO805113	Timusk et al. 2011
68	OMM5008	CTGTTTCGTTGTCCTCATATCAACC TCCATTATCCAATCAGGAGAGCTCTAT	54	CO805114	Timusk et al. 2011

69	OMM5014/i/ii	GGGTCTGAAAGGAGCATGG	54	CO805119	Timusk et al. 2011
		GGAACCTAACATGACGCAACA			
70	OMM5018	GAAGGAACGGAACAGAGTGGTAATCAC	54	CO805123	Timusk et al. 2011
		TCGGACAGGTAACTGGAACGGAT			
71	OMM5019	CATGCTGCCTCTCACCGTTTA	54	CO805124	Timusk et al. 2011
		AACACACCCAGCATCCAACC			
72	OMM5056	TCACCATCACCTTCATCGCCT	54	CA349207	Rexroad et al., 2003
		ACATGCTGCCCTTTGACGGAG			
73	OMM5060	TCTCGGGCCAAACCTTCTTATTGC	54	CA348688	Rexroad et al., 2003
		AGCCACTACATCTCCACGCCCTT			
74	OMM5061	GCGTTGGGAGAGAACAATACC	54	CA348688	Rexroad et al., 2003
		CCCATCACACCAGTTGCC			
75	OMM5074	TCGCTTTGGGTAGAAGTTGCCTTTAAC	54	CA348721	Rexroad et al., 2003
		AACATTAAGAACGAGTGGAATCACGC			
76	OMM5091	GCAGGAAAAACACCCAGATACAA	54	CA348850	Rexroad et al., 2003
		ACACTGGCTGGTGTCGTTACATTA			
77	OMM5102/i/ii	ATTCCAAATAACAGGTGCTACTGGTC	54	CA348955	Rexroad et al., 2003
		CTGGTTAACTAGGCAACTGATTGTGTC			
78	OMM5113	TCGGTAACAAGTCCTCTAGACCACA	54	CA349018	Rexroad et al., 2003
		CAGAGACCTAGACTGAGTCATGTCCTG			
79	OMM5146	GACAGATTCATGCAAGCCT	54	BV211874	Coulibaly et al., 2005
		CCTCACTACTTGCCAATCA			
80	OMM5147	CACTGTATGTTCTTACCCTG	54	BV211875	Coulibaly et al., 2005
		TATACTGGCTGAGTTCAACC			
81	OMM5155i/ii	GGACAGAACTGCCACTAAGTGTG	54	BV211883	Coulibaly et al., 2005
		GAGGAGACAGGGAAGAGCTATTG			
82	OMM5161/i/ii	CAAGTGTCCTTTGAGCAC	54	BV211889	Coulibaly et al., 2005
		AGCAACTGCTGACACTCC			

83	OMM5176	CCACTTGCTGCTTCTCTACATA	54	BV211902	Coulibaly et al., 2005
		AAGAACACCTAGCCAATAACCC			
84	OMM5179	CCCTGTCACATGGATGCT	54	BV211905	Coulibaly et al., 2005
		GATTTGGCAACCGAACAC			
85	OMM5312/i/ii/iii	ACTGTCAGCAGCAATACACT	54	BV21202	Coulibaly et al., 2005
		CCCATTTTCTCTTGTCACAC			
86	Omy6DIAS	CCACCAACTTCTTACATGAT	54	AF239042	Timusk et al. 2011
		CTATGGGGACAGCCGAATAA			
87	Omy21INRA/i/ii/iii	GCATTGGCGTAATGAGAAGG	54	NA	Gharbi et al., 2006
		CTGACGGACATATCAGCCC			
88	OmyRGT2TUF	ATAATGTGTCCCCAGGCAAG	54	AB087587	Sakamoto et al., 2000
		GAGGATGCGTCTTTGCATCT			
89	OmyRT16TUF	TGGCTGAGTTATACATGGAACG	54	NA	Timusk et al. 2011
		TCAATCAGGAGCAGTTAAAACA			
90	Otsclock1b_44_L_2	TGCTACTGTGGCAACCTTTG	54	NA	
		CCTGAGAGAGATGAGGGAGAGA			
91	Sal5UoG	TTTGCATTGAGCCTCTGTTG	54	NA	Timusk et al. 2011
		TGTTTCAGCTGCTATTAGGAAT			
92	Sal9UoG/i/ii/iii	TCACTGCTTCAAGGTATTTTTACTT	54	NA	Timusk et al. 2011
		AATTAGAGCTGCTAGGTCAGTGAG			
93	SalD25SFU	GATCTACACAGACCCCCACC	54	AF537305	McGowan et al., 2004
		CCGTTCTTCCAATAACTGCTC			
94	SalD39SFU	GGGGAGTCTGTGTTAAGTTGG	54	AF537310	McGowan et al., 2004
		TGAATGGACGTTCCTCTGAC			
95	SalE38SFU	CGCCTTGTCATACATTACACC	54	AF537309	McGowan et al., 2004
		CCGTTCTTCCAATAACTGCTC			
96	SalF41SFU	ATCCGCTATGAACCACAGG	54	AF537306	McGowan et al., 2004
		ACTGCTCCGGCAACTACAG			

97	Ssa0017BSFU	CGCAACAGGCTTAGTTAGAT CAACATTCAGTTCCCTTCAT	54	AF019154	Timusk et al. 2011
98	Ssa0033BSFU	ATTCTTGATCGTGGTCTTTG CCGTTCTTCCAATAACTGCTC	54	NA	Phillips et al., 2009
99	Ssa0072BSFU	TCCGAAGATAGGGGAGGTT ATAAACATCTGGGTGGCTGC	54	NA	Phillips et al., 2009
100	Ssa0080BSFU/i/ii	CTACTGCACAGCACCTGGAA CACAGAGCACCTCCTGAACA	54	NA	Phillips et al., 2009
101	TC126859i/ii	TTTTCTCCCTTTGACGACAG TGGTTGTGACTCGATGTCTG	54	NA	Phillips et al., 2009
102	C113	GGAGCCCAGACTATATTGACG CCTTGAAGTCTTGCCAGAT	64	NA	King TL, unpublished
103	B52	GCACACGAAACCAGTATATTTC TTGTCTTGGTGATTTCAGAGC	64	NA	King TL, unpublished
104	C28	CAGTTGAAGTGATTGGGTTAGC TCATCCTTAAAGCAGAATACCAC	64	NA	King TL, unpublished
105	C129	AGTGGGTACAACATACCTTTGG AGGTATTCACACCTCAGATTGG	64	NA	King TL, unpublished
106	C88	TAGTCTCTGGTGGGGAATAATG ATATCAGCCATAAGAGCTGGAG	60	NA	King TL, unpublished
107	C24	GCTACTGTTGGATTTCATCTCAG ATCACAGAGATGGGGTGATG	60	NA	King TL, unpublished
108	D100	ACCTTTGACCTGTACATCGTG CAGACCTAGACTAAAGCATCCG	60	NA	King TL, unpublished
109	D75	GTAGTGCCAAAACAGGTAGAGC CATCCTTATTCCAACCTCAATC	60	NA	King TL, unpublished
110	C86	ACCGATGGCCTTCAACAC ATAGGCCCCTACCTCAAACC	60	NA	King TL, unpublished

111	Sfo266	CTGGCAGCATTGTAAAGAAG	64	NA	Perry et al., 2005
		CTGGGTGATTTGACGACC			
112	Sco216	CCTTGTGAGAGCTAAGGTAGTG	64	NA	Dehaan and Ardren 2005
		GGAGGACATATTCCAACTTTG			
113	Sfo262	CCCATGTCAGTATTGGACTC	64	NA	Perry et al., 2005
		CTTCATGGGCAGAATGGAC			
114	Sco218	TTCTAACTGTTGGCACTCTG	60	NA	Dehaan and Ardren 2005
		GTGTGGTTGGGTGGTAAG			
115	SFO241	CTCCATTAGAAAGGGTTTG	60	NA	King TL, unpublished
		CCAGTCTTTAGTCAACGC			
116	SFO091	AAATAACAACAATATGTGAGAAC	60	NA	King TL, unpublished
		TATGCTGATATTGACTTTGG			
117	SFO308	CAGCAATGGGGCTGAAGTAG	60	NA	Perry et al., 2005
		GTCACTGTGTGAATCCTCC			
118	SFO269	GTAGATGAAACCTGATGG	60	NA	Perry et al., 2005
		GTTCTATGGTCACATACTG			
119	SFOD105	CAGGGAAAATGCTAATGTGC	60	NA	King TL, unpublished
		GGTTGTGTCGAATGGAGTTC			
120	Ssa85	AGCTGGGTCCTCCAAGCTAC	60	NA	King TL, unpublished
		ACCCGCTCCTCACTTAATC			
121	SFOC115	CAGTTTCTATCTCCAGGCAATC	60	NA	King TL, unpublished
		TTCTGAAAGCACTCAACATGG			
122	SSA197	GGGTTGAGTAGGGAGGCTTG	60	NA	O'Reilly et al., 1996
		TGGCAGGGATTTGACATAAC			
123	SFO12	GGTTTTGAAGAGTGACAG	60	NA	Angers et al., 1995
		CCCGTTTCACAATCAGAG			
124	SFO177	CGAATGTGGAGCTGAACTG	60	NA	Perry et al., 2005
		GGGTATTTGTACAATGGGT			

125	ONE8	AACATTCTGGGATGACAGGGGTA CTGTTCTGCTCCAGTGAAGTGGA	60	NA	Scribner et al., 1996
126	SFO226	GAGGGCTAGAGACTAGCTTCAG GCAGTGGAACAAATACCCAG	60	NA	Perry et al., 2005

McGowan, CR, Davidson, EA, Woram, RA, Danzmann, RG, Ferguson, MM and Davidson, WS, 2004. Ten polymorphic microsatellite markers from Arctic charr (Salvelinus alpinus): linkage analysis and amplification in other salmonids Anim. Genet. 35:479-481.

Olsen, JB, Bentzen, P, and Seeb, JE, 1998. Characterization of seven microsatellite loci derived from pink salmon. Mol. Ecol. 7: 1087-1089

O'Reilly P, Hamilton L, McConnell S, Wright J (1996). Rapid analysis of genetic variation in Atlantic salmon (Salmo salar) by PCR multiplexing of dinucleotide and tetranucleotide microsatellites. Canadian Journal of Fisheries and Aquatic Sciences 53: 2292-2298.

Phillips, RB, Keatley, KA, Morasch, MR, Ventura, AB Lubieniecki, KP, Koop, BF, Danzmann, RG and Davidson, WS, 2009. Assignment of Atlantic salmon (Salmo salar) linkage groups to specific chromosomes: Conservation of large syntenic blocks corresponding to whole chromosome arms in rainbow trout (Oncorhynchus mykiss) BMC Genetics 10:46

Palti, Y, Fincham, MR and Rexroad, CE, III, 2002. Characterization of 38 polymorphic microsatellite markers for rainbow trout (Oncorhynchus mykiss). Mol. Ecol. Notes. 2: 449-452

Perry GML, King TL, St-Cyr J, Valcourt M, Bernatchez L 2005. Isolation and cross-familial amplification of 41 microsatellites for the brook charr (Salvelinus fontinalis). Molecular Ecology Notes 5(2): 346-351.

Rexroad, CE, III, Lee, Y, Keele, JW, Karamycheva, S, Brown, G, Koop, B, Gahr, SA, Palti, Y, and Quackenbush, J. 2003. Sequence analysis of a rainbow trout cDNA library and creation of a gene index. Cytogenet. Genome Res. 102: 347-354

Rise, ML, von Schalburg, KR, Brown, GD, Mawer, MA, Devlin, RH, Kuipers, N, Busby, M, Beetz-Sargent, M, Alberto, R, Gibbs, AR, Hunt, P, Shukin, R, Zeznik, JA, Nelson, C, Jones, SR, Smailus, DE, Jones, SJ, Schein, JE, Marra, MA, Butterfield, YS, Stott, JM, Ng, SH, Davidson, WS and Koop, BF, 2004. Development and application of a salmonoid EST database and cDNA microarray: data mining and interspecific hybridization characteristics. Genome Res 14:478-490

Sakamoto,T, Danzmann, RG, Gharbi, K, Howard, P, Ozaki, A, Sokkean, K, Woram, RA, Okamoto, N, Ferguson, MM, Holm, L-E, Guyomard, R and Hoyheim, B, 2000. A microsatellite linkage map of rainbow trout (*Oncorhynchus mykiss*) characterized by large sex-specific differences in recombination rates. Genetics 155:1331-1345.

Scribner KT, Gust JR, Fields RL (1996). Isolation and characterization of novel salmon microsatellite loci: cross-species amplification and population genetic applications. Can J Fish Aquat Sci 53: 833-841.

Timusk, E. R., M. Ferguson, H. K. Mogahadam, J. D. Norman, C. Wilson *et al.*, 2011. Genome evolution in the fish family salmonidae: generation of a brook charr genetic map and comparisons among charrs (Arctic charr and brook charr) with rainbow trout. BMC genetics 68:12.

Thorsen, J, Zhu, B, Frengen, E, Osoegawa, K, de Jong, PJ, Koop, BF, Davidson, WS and Hoyheim, B, 2005. A highly redundant BAC library of Atlantic salmon (*Salmo salar*): an important tool for salmon projects. BMC Genomics 6:50

Table S2 Description of the Sequenom panel used to genotype the SNP markers in the F2 progeny

Technology	Panel	Marker Name	Oligo_Forward	Forward_oligo_Sequence	Oligo_Reverse	Reverse_Oligo_Sequence	Oligo_Probe	Probe_Sequence
sequenom	SEQ010	sf000032_01CT	sf000032_01CT_GA_F	ACGTTGGATGGGCGTCCCTGTTGAATTATC	sf000032_01CT_GA_R	ACGTTGGATGGGCACACCCTTCTTTATCAC	sf000032_01CT_GA_Pa	CTTTATCACACACACTATTACTG
sequenom	SEQ010	sf000124_02CT	sf000124_02CT_AG_F	ACGTTGGATGGCCCAGTTGCCTATAGATTC	sf000124_02CT_AG_R	ACGTTGGATGGTCTCCCTTATTCCCTTTGC	sf000124_02CT_AG02_P	CCTTATTCCCTTTGCACCAGTTTGTTAG
sequenom	SEQ010	sf000178_01CT	sf000178_01CT_GA_F	ACGTTGGATGCTTGCCACTTTTCCTGGTAG	sf000178_01CT_GA_R	ACGTTGGATGCTTGTCTGGGACAAACTGAG	sf000178_01CT_GA_Pa	GGGACAAACTGAGATACGA
sequenom	SEQ010	sf000191_01AG	sf000191_01AG_GC_F	ACGTTGGATGGACCTCTGTTTTACCGTGAG	sf000191_01AG_GC_R	ACGTTGGATGGGCACTTCTTTGTATTGTGG	sf000191_01AG_GC02_Pa	CCACTTGATAGGCAGCCA
sequenom	SEQ010	sf000228_01AC	sf000228_01AC_TA_F	ACGTTGGATGTACAACAATTGTTCCCACCC	sf000228_01AC_TA_R	ACGTTGGATGGTTCCCACAATCAACCACTG	sf000228_01AC_TA_Pa	TGCTCCAATCACAGGT
sequenom	SEQ010	sf000327_02AC	sf000327_02AC_GA_F	ACGTTGGATGATGAGTGACAGACGAGCTAC	sf000327_02AC_GA_R	ACGTTGGATGTGCCTTGGTAGTCTATTCTC	sf000327_02AC_GA_Pa	AAGACAAAGACTAACAAGTTAATTAC
sequenom	SEQ010	sf000657_01CT	sf000657_01CT_TC_F	ACGTTGGATGTTTCACACACTGTTCGAGGG	sf000657_01CT_TC_R	ACGTTGGATGCGGTTTTGAACCGATGAAGC	sf000657_01CT_TC_Pa	AAAAAATGTTCGAGGGTTTCTATG
sequenom	SEQ010	sf000679_01CT	sf000679_01CT_TC_F	ACGTTGGATGGGATATTTTAGTGACATCGG	sf000679_01CT_TC_R	ACGTTGGATGCCAGTGTGACAAAGGTTATG	sf000679_01CT_TC_Pa	CATTGTAATATGTGTATGTAGGCCTAGTA
sequenom	SEQ010	sf000810_03CT	sf000810_03CT_CT_F	ACGTTGGATGCCTAAACACAGAAACAAGGG	sf000810_03CT_CT_R	ACGTTGGATGTGAAGTATGCAAGGAGGGAG	sf000810_03CT_CT02_P	GGCAAGGAGGGAGTTTATCACAGA
sequenom	SEQ010	sf000878_01AG	sf000878_01AG_CT_F	ACGTTGGATGACGTTAGTTGGGTGCAAGGG	sf000878_01AG_CT_R	ACGTTGGATGAACAAACTAGGCTAGCTCCC	sf000878_01AG_CT02_P	CCCCTAGTTAACTCTGGAAAATAGGA
sequenom	SEQ010	sf000891_02AC	sf000891_02AC_CA_F	ACGTTGGATGCAGAAATCCTACACTCGTCC	sf000891_02AC_CA_R	ACGTTGGATGTCCTTCTTTAAAGAGGCAGG	sf000891_02AC_CA02_Pa	GGAGAGACGGAAGATTC
sequenom	SEQ010	sf000961_01AC	sf000961_01AC_CT_F	ACGTTGGATGCCCCTCAAGGATAGAAGAAC	sf000961_01AC_CT_R	ACGTTGGATGACTGTAATACAGAAACCAGC	sf000961_01AC_CT_P	ACCCAGCTATTCTCTGAATGTACAATT
sequenom	SEQ010	sf000970_01AC	sf000970_01AC_GA_F	ACGTTGGATGAGGAAGCGATGAGTTAGGAC	sf000970_01AC_GA_R	ACGTTGGATGAAATGGCAACTCGGTTGAGG	sf000970_01AC_GA_Pa	TAAACTCGGTTGAGGGAGGGAGATA
sequenom	SEQ010	sf001181_01CT	sf001181_01CT_GA_F	ACGTTGGATGTGTGCAGTGATCCACAGTTC	sf001181_01CT_GA_R	ACGTTGGATGCAAACACACACACAAACCCC	sf001181_01CT_GA_Pa	GTTCTGTTGGAGCATTG
sequenom	SEQ010	sf001661_01AC	sf001661_01AC_GT_F	ACGTTGGATGTCAGAATCCAGGGCTTGAAC	sf001661_01AC_GT_R	ACGTTGGATGGGGTACTTCAGAGCCAAATG	sf001661_01AC_GT02_P	TGTGTTGGGTTCAGAGAAT
sequenom	SEQ010	sf001740_01GT	sf001740_01GT_GA_F	ACGTTGGATGCCAAAGCCCAACAAAAAAGG	sf001740_01GT_GA_R	ACGTTGGATGGAGTTTCCTGAAAGTTCAC	sf001740_01GT_GA_Pa	TGAAAGTTCACATTAGACTCTAG
sequenom	SEQ010	sf002175_02GT	sf002175_02GT_TC_F	ACGTTGGATGTGCCTGACATCTGAACTCTG	sf002175_02GT_TC_R	ACGTTGGATGTTTTCACAGTGGCGGAACGG	sf002175_02GT_TC02_Pa	AGCGGAACGGGCCAATG
sequenom	SEQ010	sf003063_01AC	sf003063_01AC_CA_F	ACGTTGGATGACCCTCAGCCTATCATATCC	sf003063_01AC_CA_R	ACGTTGGATGGCAGTACCTACATTGTGTCC	sf003063_01AC_CA_P	GGTAGCAAATGTTGCTACAGCAACAATGAG
sequenom	SEQ010	sf003084_01AG	sf003084_01AG_AG_F	ACGTTGGATGCCATGGCTCTCTCTATAGAC	sf003084_01AG_AG_R	ACGTTGGATGGCAATATGGGGTAACACAAG	sf003084_01AG_AG_P	CAGCATTATTACTGGTACAATTAATGCATA
sequenom	SEQ010	sf003407_01AG	sf003407_01AG_TC_F	ACGTTGGATGTGCAGGCCATTCCAAAAAGC	sf003407_01AG_TC_R	ACGTTGGATGCTGCCCATTCTGAAGAAACG	sf003407_01AG_TC02_Pa	CCTGAGCATGTTATTACCTGACAAGAA
sequenom	SEQ010	sf003601_01GT	sf003601_01GT_CT_F	ACGTTGGATGGTAAAGTAGCTGGTGCCTTG	sf003601_01GT_CT_R	ACGTTGGATGAGCCCCGGATTTATGTATGC	sf003601_01GT_CT_P	ACAGTAGCAACAAACCCCT
sequenom	SEQ010	sf003621_01AC	sf003621_01AC_TC_F	ACGTTGGATGGAGCCATAGGTAATGTCCAG	sf003621_01AC_TC_R	ACGTTGGATGCATTCCTACCGGAGTGTAAC	sf003621_01AC_TC02_Pa	CCAACTCTGTTTGAGATGTC
sequenom	SEQ010	sf003698_01AT	sf003698_01AT_GT_F	ACGTTGGATGTTGGTTGAAGGGAAAGGCTG	sf003698_01AT_GT_R	ACGTTGGATGAACACAGTGCCTTCTCACTC	sf003698_01AT_GT_Pa	TCTCACTCACCCTAAAACAAAT
sequenom	SEQ010	sf003713_01AG	sf003713_01AG_TA_F	ACGTTGGATGCGATTCAGACACATCTATGG	sf003713_01AG_TA_R	ACGTTGGATGTAGATAGCAGATCTCGGAAG	sf003713_01AG_TA_Pa	CTACTCCACATGTGATGTTAAT
sequenom	SEQ010	sf003724_01CG	sf003724_01CG_TC_F	ACGTTGGATGCTGGCTTTGCTTGTAAACCC	sf003724_01CG_TC_R	ACGTTGGATGGGAAAAATCTGCATGGTTTAC	sf003724_01CG_TC_Pa	CCCCCCATCTGCATGGTTTACCCATTG

sequenom	SEQ010	sf003897_01CT	sf003897_01CT_GA_F	ACGTTGGATGGGGAATCATAGGCAATGAGG	sf003897_01CT_GA_R	ACGTTGGATGGGCGTAGTCGGTACTTTATG	sf003897_01CT_GA02_Pa	CCATACCTCCAGCTTGACT
sequenom	SEQ010	sf003919_01CT	sf003919_01CT_CT_F	ACGTTGGATGCAGTCCCTTGGTATAATGGC	sf003919_01CT_CT_R	ACGTTGGATGGAATCCTGACCAGAGTAGTG	sf003919_01CT_CT_P	ACTGACCAGAGTAGTGACCCAATT
sequenom	SEQ010	sf004030_01AG	sf004030_01AG_AT_F	ACGTTGGATGGAGGAAAGACAGTGGGAAAG	sf004030_01AG_AT_R	ACGTTGGATGGGCTGGTCTAGCCTATTTAG	sf004030_01AG_AT_P	TGGATTCAAACATGTGAGC
sequenom	SEQ010	sf004070_25AC	sf004070_25AC_GA_F	ACGTTGGATGCACAAATTTCTGGGTCTGGG	sf004070_25AC_GA_R	ACGTTGGATGAGCTGTTAGCAGAAAGCTGG	sf004070_25AC_GA_Pa	ATCAATCAATCACACTCACTT
sequenom	SEQ011	sf000071_02CT	sf000071_02CT_CA_F	ACGTTGGATGCAGATTAGGCCTAGACAACG	sf000071_02CT_CA_R	ACGTTGGATGCACAGGTACTAAGAGTGTGC	sf000071_02CT_CA_Pa	GGACTAAGAGTGTGCTGAAATT
sequenom	SEQ011	sf000078_02AG	sf000078_02AG_AT_F	ACGTTGGATGAGGGAAAGGGTTTTAAGCGG	sf000078_02AG_AT_R	ACGTTGGATGGCCACATTAACATACACCTG	sf000078_02AG_AT_P	GACCTACAGAAGAAAATAAAATAAGC
sequenom	SEQ011	sf000137_01AG	sf000137_01AG_TA_F	ACGTTGGATGTTCGAAACGCAATCACCGAG	sf000137_01AG_TA_R	ACGTTGGATGACTGAATTGACGGGATCAGC	sf000137_01AG_TA_Pa	AGACATGGAGTCCTATACTAT
sequenom	SEQ011	sf000324_05AC	sf000324_05AC_CA_F	ACGTTGGATGTCTGGAAACTGCGTTCTACC	sf000324_05AC_CA_R	ACGTTGGATGAGACAGCGGATTTGAGACAG	sf000324_05AC_CA_P	GTCTCCACACTTTACTTCCT
sequenom	SEQ011	sf000390_01AC	sf000390_01AC_TC_F	ACGTTGGATGCACAGGTATACTGTTGGTCG	sf000390_01AC_TC_R	ACGTTGGATGACCATGGTACTCATGACTGG	sf000390_01AC_TC_Pa	TGGAGGGCTTTGACAT
sequenom	SEQ011	sf000397_07CG	sf000397_07CG_CG_F	ACGTTGGATGTTGCCTGTTTGAGTGTTTGG	sf000397_07CG_CG_R	ACGTTGGATGCAAAGACTAAACAACAGCCC	sf000397_07CG_CG_P	GTTGAGCACCAACCACAA
sequenom	SEQ011	sf000428_01AT	sf000428_01AT_AT_F	ACGTTGGATGACCGTATGTTATGCAGCCAG	sf000428_01AT_AT_R	ACGTTGGATGCTGGACAATCTAAGCACTGG	sf000428_01AT_AT02_P	ACATTAAGCATGGTAGGCTATATAA
sequenom	SEQ011	sf000584_01GT	sf000584_01GT_GA_F	ACGTTGGATGGGGACTCCACACATTACAAA	sf000584_01GT_GA_R	ACGTTGGATGAACTAACAGTTAGCATGGTG	sf000584_01GT_GA_Pa	GAGAAAAGCTGAACAAAGTAATTTTCTA
sequenom	SEQ011	sf000854_01CT	sf000854_01CT_GT_F	ACGTTGGATGCGGTGTCTGCGATGATTTAG	sf000854_01CT_GT_R	ACGTTGGATGTCTCCCTCCTCTCAATCTTC	sf000854_01CT_GT02_P	CACGTCGGCTCAGCATCA
sequenom	SEQ011	sf001086_01CT	sf001086_01CT_TC_F	ACGTTGGATGTACTGTCACGACCAACACTC	sf001086_01CT_TC_R	ACGTTGGATGATTTACACCCCAGGTCTAAC	sf001086_01CT_TC_Pa	TAACCCAGGTCTAACATACCT
sequenom	SEQ011	sf001184_01CT	sf001184_01CT_TC_F	ACGTTGGATGTCTCTCAACAGCAAGAAGGG	sf001184_01CT_TC_R	ACGTTGGATGCACTGCTCAGACGCTCTTTG	sf001184_01CT_TC02_Pa	CCAACACATTACTTGCTCATCAATATT
sequenom	SEQ011	sf001284_01AG	sf001284_01AG_GT_F	ACGTTGGATGGCTATTCCCCAAGTTTCCTC	sf001284_01AG_GT_R	ACGTTGGATGCGGCCGTTCTTTAAATTACC	sf001284_01AG_GT_Pa	CTTTTCCTCAAAGCCACA
sequenom	SEQ011	sf001770_01AG	sf001770_01AG_AG_F	ACGTTGGATGAGGCACTGGTGTCTTTGTTC	sf001770_01AG_AG_R	ACGTTGGATGTCACGCTTAACTAAGGTCGG	sf001770_01AG_AG_P	TAAGGTCGGCCCCTAT
sequenom	SEQ011	sf002024_02AC	sf002024_02AC_AG_F	ACGTTGGATGGCTATCTCTGGATAGAGAGG	sf002024_02AC_AG_R	ACGTTGGATGCCTGTGTGTTTGTACATGCG	sf002024_02AC_AG_P	TTGGCTTCCAGTTATACTACCAC
sequenom	SEQ011	sf002033_01AG	sf002033_01AG_TA_F	ACGTTGGATGAGTTGAGGTTGGAGGAGTAG	sf002033_01AG_TA_R	ACGTTGGATGGAAACTACACCTACTGTCAC	sf002033_01AG_TA_Pa	GGAGTAGTGATTGTCATTGG
sequenom	SEQ011	sf002155_01CT	sf002155_01CT_AG_F	ACGTTGGATGGTACCACCTTGATTGTCACG	sf002155_01CT_AG_R	ACGTTGGATGATGAAGCCTGATATTCCAAC	sf002155_01CT_AG02_P	CTCTTTTTAATCAAACATTCCATTTGCA
sequenom	SEQ011	sf002948_01CG	sf002948_01CG_GT_F	ACGTTGGATGAAGGTCAGAGCAGTGTTTCC	sf002948_01CG_GT_R	ACGTTGGATGATCTGAGCGGTAGATCTAGG	sf002948_01CG_GT02_P	CGACTCAGAAACGTTGGT
sequenom	SEQ011	sf003141_03AC	sf003141_03AC_TA_F	ACGTTGGATGTGTTGGATGCCTTTGTTCGG	sf003141_03AC_TA_R	ACGTTGGATGCTGACAGACTCCACTTTTCC	sf003141_03AC_TA02_Pa	AGTCCACTTTTCCCAGCGCAT
sequenom	SEQ011	sf003197_01AG	sf003197_01AG_GA_F	ACGTTGGATGCAGAGCACCTATGATGTGAC	sf003197_01AG_GA_R	ACGTTGGATGAGCCTCCTTTACGAGTTACC	sf003197_01AG_GA02_Pa	GGGGTACCTCCCCATTGTCCGTCTGATTC
sequenom	SEQ011	sf003589_01AC	sf003589_01AC_CT_F	ACGTTGGATGGCAGGGACACGAGTTATTTG	sf003589_01AC_CT_R	ACGTTGGATGTTCACACTCACCACGTATGC	sf003589_01AC_CT_P	CCTAGTCACTTTAACCCTA
sequenom	SEQ011	sf003610_01AT	sf003610_01AT_AT_F	ACGTTGGATGTAGCTGGGCGTGCTTAACTG	sf003610_01AT_AT_R	ACGTTGGATGGACTCTGAGAACGTATACCG	sf003610_01AT_AT_P	GGGTATACCGTAAACCCATTCCCCCC
sequenom	SEQ011	sf003700_02GT	sf003700_02GT_TC_F	ACGTTGGATGGCGGTGACTATACTGTTGTG	sf003700_02GT_TC_R	ACGTTGGATGTACAATCGACCGAGAGCATC	sf003700_02GT_TC_Pa	AGACCGAGAGCATCTCATTTATAC
sequenom	SEQ011	sf003728_02AT	sf003728_02AT_TC_F	ACGTTGGATGAACCAGCCTATCAAGTGGTC	sf003728_02AT_TC_R	ACGTTGGATGACAACAGGAACAGCATCCAG	sf003728_02AT_TC02_Pa	ACAGCATCCAGACTGAACATAG
sequenom	SEQ011	sf003836_01CT	sf003836_01CT_TA_F	ACGTTGGATGGAGGTTTCTACTGTCACCTG	sf003836_01CT_TA_R	ACGTTGGATGCGACTGCAACTGAAAGCAAC	sf003836_01CT_TA_Pa	AAACTGAAAGCAACATGGGCATGC

sequenom	SEQ011	sf004064_01AT	sf004064_01AT_CA_F	ACGTTGGATGGAACACAGTGGTCTCCATAG	sf004064_01AT_CA_R	ACGTTGGATGCACATGCCACCCAATATGAG	sf004064_01AT_CA02_Pa	AGTATAATAAACTAGGACTAATAGACTA
sequenom	SEQ011	sf004112_01AC	sf004112_01AC_AG_F	ACGTTGGATGATATGGCCTGTTGAAGTGGG	sf004112_01AC_AG_R	ACGTTGGATGCAGACAGGATTAGGAACGAC	sf004112_01AC_AG_P	ACTCATCTAAACGCTCC
sequenom	SEQ011	sf004602_04AG	sf004602_04AG_GA_F	ACGTTGGATGAAAGAGACAGTTCTGCCTCC	sf004602_04AG_GA_R	ACGTTGGATGCTAGGAATGCTTACTGTGAC	sf004602_04AG_GA02_Pa	TGGCCTCCATTACCTCAAAG
sequenom	SEQ011	sf006081_01AT	sf006081_01AT_GT_F	ACGTTGGATGCGTGGCGGATAGAATTACTC	sf006081_01AT_GT_R	ACGTTGGATGGTCAGGGCATAGCACTTTTC	sf006081_01AT_GT_P	TTCCCGCCTTACATCAAAGTTACCTGAA
sequenom	SEQ012	sf000023_02AC	sf000023_02AC_TC_F	ACGTTGGATGCAAACGTGATATCTGTCCCC	sf000023_02AC_TC_R	ACGTTGGATGAGTCCCCAGTCAAAGTGAAG	sf000023_02AC_TC_Pa	TTCCAATAATGGTCAGAATCA
sequenom	SEQ012	sf000179_01AC	sf000179_01AC_TC_F	ACGTTGGATGACAGCGGAGGAGATTTGTTC	sf000179_01AC_TC_R	ACGTTGGATGACCTGCATTGACACAGATGG	sf000179_01AC_TC_Pa	GGGAGCTATAGTGACAGCAGTTAG
sequenom	SEQ012	sf000209_01AG	sf000209_01AG_CT_F	ACGTTGGATGTCTGTTCATTAGCCAGAGCC	sf000209_01AG_CT_R	ACGTTGGATGCGGTCCGATCAGTTTTTCTC	sf000209_01AG_CT_P	AGCCATTGTGACTTAAATGTCTC
sequenom	SEQ012	sf000230_01CG	sf000230_01CG_TA_F	ACGTTGGATGTGAAAGTAGCCTGGGTTGTG	sf000230_01CG_TA_R	ACGTTGGATGCATGAGCGTCACCAACCAAT	sf000230_01CG_TA02_Pa	TGCGTCACCAACCAATGAAAAG
sequenom	SEQ012	sf000633_01AT	sf000633_01AT_GT_F	ACGTTGGATGGAGATTTCCACTCCTTCACC	sf000633_01AT_GT_R	ACGTTGGATGGCCGTTGATAGAACGGTAAC	sf000633_01AT_GT02_Pa	CAGGTCGTGGTTTTTAAATTGTCTGG
sequenom	SEQ012	sf000706_01CT	sf000706_01CT_AG_F	ACGTTGGATGGGTCAATGAATGCATCCTCG	sf000706_01CT_AG_R	ACGTTGGATGTTGCTATGGGCTGGACAATG	sf000706_01CT_AG_P	GCTGGACAATGGCAGAGGTGTCCAATTGCA
sequenom	SEQ012	sf000719_01CT	sf000719_01CT_AT_F	ACGTTGGATGTCAGCCTTCAGCTAAAACCC	sf000719_01CT_AT_R	ACGTTGGATGAATGGGAATGTCACTCGAGG	sf000719_01CT_AT_P	ATGAATGTGAATGTCACTCGAGGGGAGAG
sequenom	SEQ012	sf000905_02CT	sf000905_02CT_AT_F	ACGTTGGATGCTTGTTATGGGCGTCTCTTC	sf000905_02CT_AT_R	ACGTTGGATGCTGCAATTGGTCAAGTTGGG	sf000905_02CT_AT_P	AAACAATACACTTTCGAGTTTGTACA
sequenom	SEQ012	sf000966_03CT	sf000966_03CT_AG_F	ACGTTGGATGTCTCCCTGATGTGAGGAAAG	sf000966_03CT_AG_R	ACGTTGGATGCTGCAGCAGAACACACATAC	sf000966_03CT_AG_P	CCCCTCTGGTTGGCTCAGTCTT
sequenom	SEQ012	sf001069_01AG	sf001069_01AG_GT_F	ACGTTGGATGCCTGGTTTTCTCCTCAGATG	sf001069_01AG_GT_R	ACGTTGGATGGGGACAAACCTGCATGTTTC	sf001069_01AG_GT02_P	GTTCTTCTCATGGGCTTT
sequenom	SEQ012	sf001437_01AT	sf001437_01AT_AG_F	ACGTTGGATGTGTCGACCAGGGTGAGGTTT	sf001437_01AT_AG_R	ACGTTGGATGTTTCTCTTGTTCCAGGCGAG	sf001437_01AT_AG_P	GGGAAGGGTGAGGTTTGTCACAACC
sequenom	SEQ012	sf001601_01AC	sf001601_01AC_CT_F	ACGTTGGATGTCCAAGACCATGGATGAGAG	sf001601_01AC_CT_R	ACGTTGGATGATTGCAGGGATGTGCAGTAG	sf001601_01AC_CT_P	ATGTCTGACCAATACTGTCCTAT
sequenom	SEQ012	sf001644_01AG	sf001644_01AG_GT_F	ACGTTGGATGCAAACAGACATGTCATCACG	sf001644_01AG_GT_R	ACGTTGGATGTTACATGCACCAGATGCTCC	sf001644_01AG_GT_Pa	TTTTGGGGACCGAGCAAAGAATTTC
sequenom	SEQ012	sf001686_01CT	sf001686_01CT_GA_F	ACGTTGGATGGAGTTGAGCCGTTCTGTATC	sf001686_01CT_GA_R	ACGTTGGATGTCTGTCAGACAGTCCAGGTG	sf001686_01CT_GA_Pa	GGCAACGTGGTGACAG
sequenom	SEQ012	sf001996_02CG	sf001996_02CG_AG_F	ACGTTGGATGACCATGGGCCAAAAAGCTTG	sf001996_02CG_AG_R	ACGTTGGATGTTCATTCTCCACAGTGCCTC	sf001996_02CG_AG_P	TGCCTCACAAGTGCTA
sequenom	SEQ012	sf002203_01CT	sf002203_01CT_AG_F	ACGTTGGATGGGTTCAATCCCTTTGCATCC	sf002203_01CT_AG_R	ACGTTGGATGGGTGGCAGAACACCAGTTTT	sf002203_01CT_AG_P	CCTTTCAATGCTTTTCAGC
sequenom	SEQ012	sf002250_01AG	sf002250_01AG_CA_F	ACGTTGGATGAAAGATGGCTGATCTCCCTC	sf002250_01AG_CA_R	ACGTTGGATGTTGTGCACTTTTCGTCCTTG	sf002250_01AG_CA_P	CCCCACTACAAATGGGCCAAAACAAT
sequenom	SEQ012	sf002353_02AT	sf002353_02AT_CT_F	ACGTTGGATGATTTCAACCAGCCATGGGAG	sf002353_02AT_CT_R	ACGTTGGATGAGTTGTTGCCACTCACCCTG	sf002353_02AT_CT_P	GGTGGTTGATGCCCTT
sequenom	SEQ012	sf002792_01AG	sf002792_01AG_AG_F	ACGTTGGATGGTTCATTGTGGTGAACGGAC	sf002792_01AG_AG_R	ACGTTGGATGAAGAGTTTCAGTAGCCCTGC	sf002792_01AG_AG02_P	GGCAAGCCTCTGTAGAACAATGG
sequenom	SEQ012	sf003076_01CT	sf003076_01CT_AG_F	ACGTTGGATGCAGTGGTTTAGATGGTACGC	sf003076_01CT_AG_R	ACGTTGGATGACACCGCTATTTCCTGGTTG	sf003076_01CT_AG_P	CCCTTTTGGTCACATAAACTGAAATTAGGC
sequenom	SEQ012	sf003092_01CT	sf003092_01CT_TC_F	ACGTTGGATGTTCCAAGCCCTAGATTTGCC	sf003092_01CT_TC_R	ACGTTGGATGATATCAACTGACTGGAGGGC	sf003092_01CT_TC_Pa	ATTCATAATTCTATATCATTACAGC
sequenom	SEQ012	sf003118_01GT	sf003118_01GT_GA_F	ACGTTGGATGCTATGAGGAGTGGTGTGTTC	sf003118_01GT_GA_R	ACGTTGGATGCCATACAAAACCCTCTGTAG	sf003118_01GT_GA_Pa	GGAAAAAACCCTCTGTAGTGTATGGCGG
sequenom	SEQ012	sf003334_01CT	sf003334_01CT_AG_F	ACGTTGGATGTTATAGCTTCAAATAGGCCC	sf003334_01CT_AG_R	ACGTTGGATGGGCCTATGTAACCTAGCCAG	sf003334_01CT_AG_P	CCATTTATTTGTGTTCTGGAAAATGTGAAC
sequenom	SEQ012	sf003500_02CT	sf003500_02CT_CT_F	ACGTTGGATGAGAGGCGCGATGAATTTAAG	sf003500_02CT_CT_R	ACGTTGGATGTGACAGCTGACAATGTGCTC	sf003500_02CT_CT02_P	CGTGCTCTTGGCTCGAGC

sequenom	SEQ012	sf003595_01CT	sf003595_01CT_AT_F	ACGTTGGATGTGTACACTTTTCCAATGC	sf003595_01CT_AT_R	ACGTTGGATGGCCTAGTCACAGCATTTACG	sf003595_01CT_AT_P	CACAATAAAGTGTGTACAG
sequenom	SEQ012	sf003614_01CT	sf003614_01CT_GT_F	ACGTTGGATGGACCTGAAGTTCAGCAGTAG	sf003614_01CT_GT_R	ACGTTGGATGTCTGACTGACGGAACTGATG	sf003614_01CT_GT_Pa	CATCTTTAAACCTTACAGGT
sequenom	SEQ012	sf003813_11CT	sf003813_11CT_AG_F	ACGTTGGATGAAGACATGGTTACTGACGGC	sf003813_11CT_AG_R	ACGTTGGATGTTCTCTCTCTCCCAGCCAAC	sf003813_11CT_AG02_P	CCTGACCCCAACGAGGAGCT
sequenom	SEQ012	sf004055_02CT	sf004055_02CT_AT_F	ACGTTGGATGTAGCGCAGGATTTTACGACC	sf004055_02CT_AT_R	ACGTTGGATGCCAGTGTCAGTGTCCTAATG	sf004055_02CT_AT_P	CAGGGAGACTTGTAATTCAGC
sequenom	SEQ012	sf006073_01CT	sf006073_01CT_GA_F	ACGTTGGATGAGCCTGGAGTGTTTTTTCTG	sf006073_01CT_GA_R	ACGTTGGATGAGTGGCCGTCGTCAAGTTTG	sf006073_01CT_GA_Pa	TCTGTTTGCTGCTAGTG
sequenom	SEQ013	sf000002_01AG	sf000002_01AG_AG_F	ACGTTGGATGGCACAAGAGAGCTATATTAC	sf000002_01AG_AG_R	ACGTTGGATGGAGAGCCCTTCACAGTTTAG	sf000002_01AG_AG_P	CCTCCCTTTGCTACGTGGATA
sequenom	SEQ013	sf000017_01CT	sf000017_01CT_GC_F	ACGTTGGATGCACAATGCAGATCCCAGATG	sf000017_01CT_GC_R	ACGTTGGATGGGCCTCCAGCTTTAATTGTG	sf000017_01CT_GC02_Pa	ATAAGTACTCTCTGAATGGGAT
sequenom	SEQ013	sf000021_01AG	sf000021_01AG_CA_F	ACGTTGGATGTAATGACCTCTAGCCACCTC	sf000021_01AG_CA_R	ACGTTGGATGATAAACAGCTGTGTGGGACG	sf000021_01AG_CA_Pa	GGGATGGGTCTGCTGGAT
sequenom	SEQ013	sf000086_01CT	sf000086_01CT_CT_F	ACGTTGGATGTATCCATAGGGCAAGCGTAG	sf000086_01CT_CT_R	ACGTTGGATGGCGAAGTCGTGACACAAAAG	sf000086_01CT_CT_P	AAACGTGCTTATAGACAAC
sequenom	SEQ013	sf000088_01AC	sf000088_01AC_GA_F	ACGTTGGATGGGTTTGCGAGAACACAAAGC	sf000088_01AC_GA_R	ACGTTGGATGTCCACTGGTCTGGTGTATTC	sf000088_01AC_GA_Pa	CAACTATATTGTATTTAATAAACTTGGGAC
sequenom	SEQ013	sf000119_01AG	sf000119_01AG_AG_F	ACGTTGGATGCAGCAGCTATTGTTGCTATC	sf000119_01AG_AG_R	ACGTTGGATGACAAACAGTGTCCTAGGGAG	sf000119_01AG_AG_P	GAATTACTTACAGCAGACTGAATACAGT
sequenom	SEQ013	sf000139_01CG	sf000139_01CG_GT_F	ACGTTGGATGCCTAATGTTACGAAATACCC	sf000139_01CG_GT_R	ACGTTGGATGGCGGTCCTTTTGACTGCAAC	sf000139_01CG_GT_Pa	CAAGTATAAGCCTAATAGACACATTT
sequenom	SEQ013	sf000157_01AT	sf000157_01AT_CA_F	ACGTTGGATGAGATCAGCAGAGCAGACAAG	sf000157_01AT_CA_R	ACGTTGGATGCGATATTTTCCCATGGCCTG	sf000157_01AT_CA_P	TGGAGTTGTGTAGTCTAA
sequenom	SEQ013	sf000175_01CT	sf000175_01CT_GT_F	ACGTTGGATGTTGTCCCAACAGAAACACAG	sf000175_01CT_GT_R	ACGTTGGATGAGACGATTGGGCCAATTTCC	sf000175_01CT_GT02_P	CGGCCAATTTCCCAAAGCA
sequenom	SEQ013	sf000392_01AC	sf000392_01AC_CT_F	ACGTTGGATGAGCCGTTTTGAAGCTGGTCC	sf000392_01AC_CT_R	ACGTTGGATGGTGATGCACCTCATTTGAGC	sf000392_01AC_CT_P	TTGGAATGCAGTTGGT
sequenom	SEQ013	sf000583_02CT	sf000583_02CT_TC_F	ACGTTGGATGTTAGTGCTACCACTAGAGGG	sf000583_02CT_TC_R	ACGTTGGATGTTAGACTGGGCTTCTCTTCC	sf000583_02CT_TC_Pa	TCCACAGTTAGCTGCAGGCGTGC
sequenom	SEQ013	sf000717_02AG	sf000717_02AG_TC_F	ACGTTGGATGGTTTCTGTTTCTCATCTCAC	sf000717_02AG_TC_R	ACGTTGGATGGTCTTGTAGGAAGTCAGATG	sf000717_02AG_TC02_Pa	CTGTGGCTTTGAAATGTATCC
sequenom	SEQ013	sf000747_02CT	sf000747_02CT_CT_F	ACGTTGGATGATGTTGTATTCTGACACTGG	sf000747_02CT_CT_R	ACGTTGGATGAAAGTCACTCTTAAGGCCCC	sf000747_02CT_CT_P	AGTAAGGCCCCATGTAGGTT
sequenom	SEQ013	sf000978_02CT	sf000978_02CT_GA_F	ACGTTGGATGGCGAACCGTCTTGCATTAAC	sf000978_02CT_GA_R	ACGTTGGATGGAAACGTCTCTAGTTGCCAG	sf000978_02CT_GA_Pa	TTGCTAGAACATTGCCA
sequenom	SEQ013	sf001164_02GT	sf001164_02GT_TC_F	ACGTTGGATGAACTAGCTGGAAATGATCAC	sf001164_02GT_TC_R	ACGTTGGATGAAACCTCTGACGTCAGTAGC	sf001164_02GT_TC_Pa	GGAGATCACTGGACAAGTTTAAGG
sequenom	SEQ013	sf001692_03CG	sf001692_03CG_CT_F	ACGTTGGATGTTCCTGTGGCCTTCTGTTTC	sf001692_03CG_CT_R	ACGTTGGATGGTAGGAAGAACAAAGGACGC	sf001692_03CG_CT_P	CAAAGTACGCTAACAAAGAGAAACGCTGAT
sequenom	SEQ013	sf002333_01AC	sf002333_01AC_AG_F	ACGTTGGATGTGCCTTATCTGTATACGCTC	sf002333_01AC_AG_R	ACGTTGGATGTGCATCACACTACTGTACAC	sf002333_01AC_AG_P	GGGGAGGAACTGGAAATTGAAGTGC
sequenom	SEQ013	sf003018_09CT	sf003018_09CT_AG_F	ACGTTGGATGGTTCAGCACTGCCTCATTTC	sf003018_09CT_AG_R	ACGTTGGATGGGTATGACGTTCACTCTGAC	sf003018_09CT_AG_P	CCCTATCCACCAGGTGGCT
sequenom	SEQ013	sf003105_01CT	sf003105_01CT_TC_F	ACGTTGGATGCTAACTTTGCATCCGCACTG	sf003105_01CT_TC_R	ACGTTGGATGACAACTCCATGCACAAGGAC	sf003105_01CT_TC_Pa	GTCACGGAACATTTTACCAG
sequenom	SEQ013	sf003208_01CT	sf003208_01CT_TC_F	ACGTTGGATGTACACAAACCTTAGCTCCCC	sf003208_01CT_TC_R	ACGTTGGATGTGTACAAAGAGAGGATGCGG	sf003208_01CT_TC_Pa	CTCACAGGCGGCCATCTTAATTT
sequenom	SEQ013	sf003442_01CG	sf003442_01CG_AG_F	ACGTTGGATGAGCACAGCCAACCACTTTAC	sf003442_01CG_AG_R	ACGTTGGATGAAGCTGTCTCCTGGGCTTAA	sf003442_01CG_AG_P	GGTTACATTATGCAGGGCATC
sequenom	SEQ013	sf003538_01AG	sf003538_01AG_GT_F	ACGTTGGATGCAAATCAAGCACTTCAAATG	sf003538_01AG_GT_R	ACGTTGGATGTGGTGCTACTTCACATGGAG	sf003538_01AG_GT_Pa	CCTCCTAGAGGCTACATATGCAAGACAA
sequenom	SEQ013	sf003697_01CT	sf003697_01CT_CA_F	ACGTTGGATGCAAAAATGTGTGTCGTTGGG	sf003697_01CT_CA_R	ACGTTGGATGATGGGCAAAGAGGGCTATTC	sf003697_01CT_CA_Pa	CTGCAAAGAGGGCTATTCTAAAAT

sequenom	SEQ013	sf003715_01AT	sf003715_01AT_CT_F	ACGTTGGATGTAGATGTTCAGGCCAAGACC	sf003715_01AT_CT_R	ACGTTGGATGCTTACAAGTCTGGAAATGTG	sf003715_01AT_CT02_P	TGTGATAATGCATGGAATGC
sequenom	SEQ013	sf003726_01CT	sf003726_01CT_GT_F	ACGTTGGATGCCATCATTCAACACTCCTCC	sf003726_01CT_GT_R	ACGTTGGATGTGCTCATCTAGCAACTCAGG	sf003726_01CT_GT02_P	CCAAACTCAGGTGCTTTCATTA
sequenom	SEQ013	sf004016_01AT	sf004016_01AT_AG_F	ACGTTGGATGCCAGTCTGTCATAACCCATC	sf004016_01AT_AG_R	ACGTTGGATGGAACACAGAGACAATGGAGG	sf004016_01AT_AG_P	GGGGAATTTTGAGGTGTGTAATTACAACA
sequenom	SEQ013	sf004099_01CG	sf004099_01CG_TA_F	ACGTTGGATGGGAAACACATATCTGGTGAG	sf004099_01CG_TA_R	ACGTTGGATGGTGGAGAGTTCATCATTAGC	sf004099_01CG_TA_Pa	GGGCAGATCTGTTGCCAATTGG
sequenom	SEQ013	sf004299_15GT	sf004299_15GT_CT_F	ACGTTGGATGGGGACTCCACACATTACAAA	sf004299_15GT_CT_R	ACGTTGGATGAACTAACAGTTAGCATGGTG	sf004299_15GT_CT_P	GAAAAGCTGAACAAAGTAATTTTCTA
sequenom	SEQ013	sf005138_03AG	sf005138_03AG_CA_F	ACGTTGGATGGGAAGGCATCCTCAAAATTC	sf005138_03AG_CA_R	ACGTTGGATGCTCATCACTGTATCGTGTGC	sf005138_03AG_CA_Pa	GGGGTAGTGTGCATTTCTCCAGGGTCGC
sequenom	SEQ014	sf004149_01AG	sf004149_01AG_GC_F	ACGTTGGATGGGACTATGTACAACAAGTGG	sf004149_01AG_GC_R	ACGTTGGATGATGATGGCATGACTATGAGG	sf004149_01AG_GC_Pa	CCCTGTATTTTCATCCATATCGGAT
sequenom	SEQ014	sf004155_01AG	sf004155_01AG_GT_F	ACGTTGGATGGCTTTTGCTTTTACTACGGC	sf004155_01AG_GT_R	ACGTTGGATGGATGCTGGTAGCCTAGAATA	sf004155_01AG_GT_P	CAGCCTAGAATAAATGTTATGGAAG
sequenom	SEQ014	sf004209_01GT	sf004209_01GT_AT_F	ACGTTGGATGCCTCACGCTAACAATTACCC	sf004209_01GT_AT_R	ACGTTGGATGATCCCCAACACTCCTTTGTC	sf004209_01GT_AT_P	CACGCCTTTGTCGTACTATAGGC
sequenom	SEQ014	sf004240_01AG	sf004240_01AG_GA_F	ACGTTGGATGTAAACTCCCCCCTCATACTC	sf004240_01AG_GA_R	ACGTTGGATGTATGACACCTCCAATGTGGG	sf004240_01AG_GA_Pa	CAGACAAAAAACTGCTCGA
sequenom	SEQ014	sf004252_02GT	sf004252_02GT_GT_F	ACGTTGGATGGTTCATGTCTCAGACACTGG	sf004252_02GT_GT_R	ACGTTGGATGTGAGGAGGTATTAAGTCCAG	sf004252_02GT_GT_P	TGAAGGCTGCTGTGGCTCTGCT
sequenom	SEQ014	sf004257_02CG	sf004257_02CG_GA_F	ACGTTGGATGTTATGTTCCACAAGTGGCCC	sf004257_02CG_GA_R	ACGTTGGATGTTAACATGGCAAGACAGAAC	sf004257_02CG_GA_Pa	AGACAGAACAAATTCTTATTTACAA
sequenom	SEQ014	sf004260_01AT	sf004260_01AT_TC_F	ACGTTGGATGCAGAACTGGCAGATGGAAAG	sf004260_01AT_TC_R	ACGTTGGATGATTTGTCTTCTGCCGTTCCC	sf004260_01AT_TC_Pa	TCTTTCCCAATGCCCACAA
sequenom	SEQ014	sf004387_01AG	sf004387_01AG_TC_F	ACGTTGGATGTCATTAGTGCTGCATCTGCG	sf004387_01AG_TC_R	ACGTTGGATGCCTACGTGTTAGATACAGGC	sf004387_01AG_TC_Pa	CTGCAACATTCCCAGTACAC
sequenom	SEQ014	sf004426_01AG	sf004426_01AG_CT_F	ACGTTGGATGGAAGCACTGCTTTGTTACGG	sf004426_01AG_CT_R	ACGTTGGATGAGCAAAGCCCTACATCTCTG	sf004426_01AG_CT_P	CTGTTCCTGAATACAGGCAGCCTACA
sequenom	SEQ014	sf004438_02CT	sf004438_02CT_CT_F	ACGTTGGATGACTGGACCTGGAAAGATTGG	sf004438_02CT_CT_R	ACGTTGGATGGTTAGTAGCCTAATTCACAG	sf004438_02CT_CT_P	GGTAACAGTAAACAATAGAGCTAGA
sequenom	SEQ014	sf004529_01CT	sf004529_01CT_AT_F	ACGTTGGATGGATCTCATTTTAGCAGCGAC	sf004529_01CT_AT_R	ACGTTGGATGGGCCAGATATTGCAATTGCG	sf004529_01CT_AT_P	CTCCATCAGACAAGTGAC
sequenom	SEQ014	sf004545_01AC	sf004545_01AC_CA_F	ACGTTGGATGCCTTATATTAAACAAACCAG	sf004545_01AC_CA_R	ACGTTGGATGTGTCTTAGTGTTGGTGTGCC	sf004545_01AC_CA_Pa	TTTTATTGTAATTTATTTTGTTTACAATT
sequenom	SEQ014	sf004562_01AG	sf004562_01AG_CA_F	ACGTTGGATGTCAAAGTGCACAGTGAGGAG	sf004562_01AG_CA_R	ACGTTGGATGTAACCTATTGGCTAGCCCAG	sf004562_01AG_CA_Pa	GTTAGGAATGGTCAACACAG
sequenom	SEQ014	sf004632_01AG	sf004632_01AG_CT_F	ACGTTGGATGGAAAGACAAATGTTTCTTTCG	sf004632_01AG_CT_R	ACGTTGGATGAGAGTAGGTGTATAACGTGG	sf004632_01AG_CT_P	CAACGATAACTAAGAAGTAGAA
sequenom	SEQ014	sf004642_07AG	sf004642_07AG_AG_F	ACGTTGGATGCGTCCATAATGTCAACAGGG	sf004642_07AG_AG_R	ACGTTGGATGACCTCTGGTTTGGAGTTGTG	sf004642_07AG_AG_P	GGGAGGGGTGATTGAACTGCAC
sequenom	SEQ014	sf004684_01AG	sf004684_01AG_AT_F	ACGTTGGATGGTAGGTTGGTAAGACTGGAG	sf004684_01AG_AT_R	ACGTTGGATGAACTGACATGCCAAGGATCG	sf004684_01AG_AT_P	ACTCATATCGACCATATATTGTGTTCCC
sequenom	SEQ014	sf004732_01CG	sf004732_01CG_CT_F	ACGTTGGATGTTCAACAGACTTTTTCCCGC	sf004732_01CG_CT_R	ACGTTGGATGAGATTGCCTCTGACTGTTCC	sf004732_01CG_CT_P	TTCCCCACGTTCTTTG
sequenom	SEQ014	sf004762_01AT	sf004762_01AT_CT_F	ACGTTGGATGTCGCTTGCAGCAATGTTGAG	sf004762_01AT_CT_R	ACGTTGGATGATAACAGCAGCAGAGGAGTC	sf004762_01AT_CT_P	CCCCTCTCATCGGCAACTAATA
sequenom	SEQ014	sf004765_01CG	sf004765_01CG_CT_F	ACGTTGGATGGCACCTGTAATGAGTGAATG	sf004765_01CG_CT_R	ACGTTGGATGGTTGTGTGACTCACATGCTG	sf004765_01CG_CT_P	TTACCACAAGGGATGACAA
sequenom	SEQ014	sf004817_02GT	sf004817_02GT_CG_F	ACGTTGGATGTGGGTGTCATAAAGAAAGGG	sf004817_02GT_CG_R	ACGTTGGATGACTGTCCCTATTCCTGTTAG	sf004817_02GT_CG_P	GACATGACTTTACCATGTTG
sequenom	SEQ014	sf004818_06CT	sf004818_06CT_CA_F	ACGTTGGATGGGGATAGCCAATCCAGATTC	sf004818_06CT_CA_R	ACGTTGGATGCATTAAGGCCACATAGCACC	sf004818_06CT_CA_Pa	CGGAGTTGGTCATTTTGG
sequenom	SEQ014	sf004848_01CT	sf004848_01CT_AT_F	ACGTTGGATGCAAGACATGGCATAAGAGGG	sf004848_01CT_AT_R	ACGTTGGATGTAACGACGAACGATTGCTTG	sf004848_01CT_AT_P	TAAAGTATCGTCCAACCC

sequenom	SEQ014	sf004870_01CG	sf004870_01CG_GA_F	ACGTTGGATGCACGCCTTACAACAGAATAG	sf004870_01CG_GA_R	ACGTTGGATGGAAGTCTGCCCAGTCAAAAG	sf004870_01CG_GA_Pa	GAGGATTAATAATTATACTGTACAAG
sequenom	SEQ014	sf004904_09CT	sf004904_09CT_CG_F	ACGTTGGATGGGCATGCAGAGTTCAATTAG	sf004904_09CT_CG_R	ACGTTGGATGAAGACCGGGCATTCAACTTG	sf004904_09CT_CG_P	TTGAAGTTGATACTGTTTCCATGGTAA
sequenom	SEQ014	sf004909_01GT	sf004909_01GT_TA_F	ACGTTGGATGGCCCTGTTAACTCCTTAGTG	sf004909_01GT_TA_R	ACGTTGGATGATGGGACAATGATCACTGAG	sf004909_01GT_TA_Pa	GAGCACTGAGATCATATGCAAAT
sequenom	SEQ014	sf004913_01GT	sf004913_01GT_CA_F	ACGTTGGATGGAAGCCAGATGTTAAGATGAC	sf004913_01GT_CA_R	ACGTTGGATGCCCCAGATTTGAGTCTGTAG	sf004913_01GT_CA_P	TTTCAAATGACAAGGCAATCTCACAA
sequenom	SEQ014	sf004975_01CG	sf004975_01CG_TC_F	ACGTTGGATGGGAAGTTTGCTGCAAATGAG	sf004975_01CG_TC_R	ACGTTGGATGAACGGCCTCGTACTCTATTC	sf004975_01CG_TC_Pa	CAGCCTCGTACTCTATTCTAGATC
sequenom	SEQ014	sf004977_01AT	sf004977_01AT_CT_F	ACGTTGGATGGCCTTGATGTTCATCAGTCC	sf004977_01AT_CT_R	ACGTTGGATGAGTCATCTTTCCCTTCCAGC	sf004977_01AT_CT_P	CCTCTCCATTTATAGACAATTTGTC
sequenom	SEQ014	sf005000_09CT	sf005000_09CT_TC_F	ACGTTGGATGATGCCGTTCTGTACCATCAC	sf005000_09CT_TC_R	ACGTTGGATGCCTAACAATTCCACAACTAC	sf005000_09CT_TC_Pa	GTCCACAACTACTACCTTATACAC
sequenom	SEQ014	sf005054_02AC	sf005054_02AC_GA_F	ACGTTGGATGCCACCCAACTACTCAATTCC	sf005054_02AC_GA_R	ACGTTGGATGTGTTCTCAATTGAGGCGCAG	sf005054_02AC_GA_Pa	GAGGCGCAGATAAGCG
sequenom	SEQ014	sf005079_01AG	sf005079_01AG_CA_F	ACGTTGGATGACCCACCATCACAACTCGAC	sf005079_01AG_CA_R	ACGTTGGATGGAACATCTGAAATATTGTCTG	sf005079_01AG_CA_P	ATTCCGATCTGTGTCTTTCCATTGCTGTG
sequenom	SEQ014	sf005248_01AG	sf005248_01AG_CT_F	ACGTTGGATGTTGCTGGGATTTACCACCAC	sf005248_01AG_CT_R	ACGTTGGATGGGGTAGCCAATCCAGATTTC	sf005248_01AG_CT_P	TTACACACTCAGGTATAGCAC
sequenom	SEQ014	sf005272_01CG	sf005272_01CG_GC_F	ACGTTGGATGAGTATGAGGGAGTGTGAGAG	sf005272_01CG_GC_R	ACGTTGGATGTTAGCCATTTTTCCTCCCCG	sf005272_01CG_GC_Pa	CCGGTGTCATGTGACT
sequenom	SEQ014	sf005409_04AT	sf005409_04AT_CA_F	ACGTTGGATGAGATGTATTGGAGTAGTGCC	sf005409_04AT_CA_R	ACGTTGGATGTCAGGCATTTACAGCCTCAC	sf005409_04AT_CA_P	TGTGGTATGGCATCAGACAGAAAT
sequenom	SEQ014	sf005410_01AG	sf005410_01AG_CA_F	ACGTTGGATGGGATGAGCAATGTCAGAGCG	sf005410_01AG_CA_R	ACGTTGGATGTATCCATGCCCAATGGGAAC	sf005410_01AG_CA_Pa	ACTCCATTCCGGCTCCA
sequenom	SEQ014	sf005420_01CG	sf005420_01CG_GA_F	ACGTTGGATGTTGAAGATGGTGATGGTCTC	sf005420_01CG_GA_R	ACGTTGGATGGATGCCATCAAGGCCAAAAC	sf005420_01CG_GA_Pa	ACACTTTAGTGTTTTAAAGCA
sequenom	SEQ015	sf000020_CT	sf000020_CT_CT_F	ACGTTGGATGGGCGATCTCTGTTCCTAATG	sf000020_CT_CT_R	ACGTTGGATGGGTAAAGTGGTAGAGGTAGC	sf000020_CT_CT_P	AGATCAGATTATTCTTTGTGAGAG
sequenom	SEQ015	sf000382_AG	sf000382_AG_GA_F	ACGTTGGATGTGGCAAAATCAAAGCCAGAC	sf000382_AG_GA_R	ACGTTGGATGGTTTGTAGACTGGCTACATC	sf000382_AG_GA_Pa	GGCTACATCTTATATCATCATCT
sequenom	SEQ015	sf000508_CT	sf000508_CT_TC_F	ACGTTGGATGGTGTGTGACATATTCTCCCC	sf000508_CT_TC_R	ACGTTGGATGTTGCTCAGAGAGCCAGAGAG	sf000508_CT_TC_Pa	GAGTTACACAGAGACGTGTCATC
sequenom	SEQ015	sf000559_AG	sf000559_AG_GA_F	ACGTTGGATGGGTGATAGTGGGACTGATAG	sf000559_AG_GA_R	ACGTTGGATGAAGAAGAGCAGGTTGCCCAG	sf000559_AG_GA_Pa	GGGTGTCCTTCTCCTTCATAGGAC
sequenom	SEQ015	sf000681_AT	sf000681_AT_AT_F	ACGTTGGATGGATACTCCCACACAAAACCC	sf000681_AT_AT_R	ACGTTGGATGGAGGTATGAGGTATTGGAGG	sf000681_AT_AT_P	GCAAGGTAAAGTATGTAGTAT
sequenom	SEQ015	sf000684_CT	sf000684_CT_TC_F	ACGTTGGATGTGTATAATGAGTAGGCCCCC	sf000684_CT_TC_R	ACGTTGGATGGCATGCTCCACTTTTGAACC	sf000684_CT_TC_Pa	CCCCTCTTTGTATAACCTATGCATACAC
sequenom	SEQ015	sf000744_AT	sf000744_AT_AT_F	ACGTTGGATGCAGTGAAGGGAACTGACCAC	sf000744_AT_AT_R	ACGTTGGATGCACTCGGTATGTTCTTCCTC	sf000744_AT_AT_P	CTATGGTCTTCCTCTGTATCTTGAGAGCTG
sequenom	SEQ015	sf001105_AG	sf001105_AG_AG_F	ACGTTGGATGTGTCTCTGAAAGCACCAATC	sf001105_AG_AG_R	ACGTTGGATGTACCACACATGGCACATGAG	sf001105_AG_AG_P	CCTCCTTATATTAATAACTCCCCTGTAGT
sequenom	SEQ015	sf001667_AG	sf001667_AG_GA_F	ACGTTGGATGGCCTCTCACACAAACTGTAG	sf001667_AG_GA_R	ACGTTGGATGAGTCACTGCAATTCACAGCC	sf001667_AG_GA_Pa	TGGGCCGGGTTTAGATT
sequenom	SEQ015	sf001831_AC	sf001831_AC_CA_F	ACGTTGGATGCCAGTACATTTCCAGCTGTG	sf001831_AC_CA_R	ACGTTGGATGTCATTGGTATCAACTGATGC	sf001831_AC_CA_Pa	CTCCTCAACTGATGCCCTACT
sequenom	SEQ015	sf002145_CG	sf002145_CG_CG_F	ACGTTGGATGTCTGACAGGTACACACACAG	sf002145_CG_CG_R	ACGTTGGATGGTCATTCTGGACAGGAGTTC	sf002145_CG_CG_P	GCAGTCTGGACAGGAGTTCCTACAGTA
sequenom	SEQ015	sf003455_AG	sf003455_AG_AG_F	ACGTTGGATGATAACCAGTAGGGCAACGTC	sf003455_AG_AG_R	ACGTTGGATGTATACGAAGTCGCTGACAAC	sf003455_AG_AG_P	GGTCGTTGATATAAATGTTAATGAATTAGC
sequenom	SEQ015	sf003520_AG	sf003520_AG_GA_F	ACGTTGGATGGATGCAGGGAGACAGTATTG	sf003520_AG_GA_R	ACGTTGGATGATGAGAGAGGATAGAAAGGG	sf003520_AG_GA_Pa	GGCAGAATGAATATCATGTCAATTA
sequenom	SEQ015	sf003994_GT	sf003994_GT_GT_F	ACGTTGGATGCCCCATGTATGTTTCTCAAG	sf003994_GT_GT_R	ACGTTGGATGTCAAGCCCCAACAATATAGG	sf003994_GT_GT_P	ACCTCTTTAAGAGCTACACATTTGT

sequenom	SEQ015	sf004013_AC	sf004013_AC_CA_F	ACGTTGGATGTGTGTTGTGCGTGCATG	sf004013_AC_CA_R	ACGTTGGATGGGATTTGGGAAGTGAACTGC	sf004013_AC_CA_P	CCTCACACTGACACCA
sequenom	SEQ015	sf004038_AG	sf004038_AG_AG_F	ACGTTGGATGAACTAGAGCGGATAACCATC	sf004038_AG_AG_R	ACGTTGGATGCCGGGTGTAAGATAACAATG	sf004038_AG_AG_P	CCCCAGGGTTAAACCGTTCC
sequenom	SEQ015	sf004090_CG	sf004090_CG_GC_F	ACGTTGGATGAATAAACCAGGCCAGAGATG	sf004090_CG_GC_R	ACGTTGGATGCGGCCGTTTTATGGTTTTGC	sf004090_CG_GC_Pa	CCGCCTGTCAACCTCTATT
sequenom	SEQ015	sf004131_AG	sf004131_AG_AG_F	ACGTTGGATGGAAAACCCCAAACCAGGAAC	sf004131_AG_AG_R	ACGTTGGATGAGATTCTGCGTGTAAACGCC	sf004131_AG_AG_P	GGGGTACGTAGAATGATGTGATTAC
sequenom	SEQ015	sf004357_CT	sf004357_CT_CT_F	ACGTTGGATGAACTGCAAACATGGCAACCC	sf004357_CT_CT_R	ACGTTGGATGATGTCTAATTCCTCCGCTCC	sf004357_CT_CT_P	TGTTGCAGCAATGATAATGTGGA
sequenom	SEQ015	sf004379_CT	sf004379_CT_TC_F	ACGTTGGATGGTGAGGTCAACTCAGAGTTC	sf004379_CT_TC_R	ACGTTGGATGGTTTCCTAGGTGACCTGGAG	sf004379_CT_TC_Pa	GACCTGGAGGTGAGCC
sequenom	SEQ015	sf004475_CT	sf004475_CT_TC_F	ACGTTGGATGCCGATGTTGTACCTTTGAGC	sf004475_CT_TC_R	ACGTTGGATGTTTGTGTCCCAAATGGCACC	sf004475_CT_TC_Pa	ATGGCACCCTATGTATAATACACTATATA
sequenom	SEQ015	sf004521_CG	sf004521_CG_CG_F	ACGTTGGATGGATCCATGTGATTTCGTGCC	sf004521_CG_CG_R	ACGTTGGATGGTGTCAGGAGAAACGTTAC	sf004521_CG_CG_P	ACATATAGTGATATAAATGATTTTGTATA
sequenom	SEQ015	sf004541_AC	sf004541_AC_CA_F	ACGTTGGATGCCCCTCTTTTCTCATTCCTC	sf004541_AC_CA_R	ACGTTGGATGCGCATGACACCACAATTGAG	sf004541_AC_CA_Pa	CCCATCTAACTAAATCCCAGACGACA
sequenom	SEQ015	sf004614_AG	sf004614_AG_AG_F	ACGTTGGATGGGAACTAGCGCTATCAATGG	sf004614_AG_AG_R	ACGTTGGATGCAGGCCTGATTTCCCACATA	sf004614_AG_AG_P	CCCTTTCCCACATAATTCCCTTCACTC
sequenom	SEQ015	sf004897_AT	sf004897_AT_TA_F	ACGTTGGATGGTGGCTATGACGGTGATTTC	sf004897_AT_TA_R	ACGTTGGATGTTTTTGCGTCTGTTTCCCCC	sf004897_AT_TA_Pa	GGCATAGCTGCCTATTAAAG
sequenom	SEQ015	sf005186_CT	sf005186_CT_TC_F	ACGTTGGATGCCTTTCTTCCAACCTCCATC	sf005186_CT_TC_R	ACGTTGGATGGTTGACCAGGGCTTTGTTAG	sf005186_CT_TC_Pa	CTTGTTAGTAACACTCCTAGA
sequenom	SEQ015	sf005258_AC	sf005258_AC_CA_F	ACGTTGGATGTTGGCTTCCTGGCTTGTAAC	sf005258_AC_CA_R	ACGTTGGATGAGAGCTCCCCCATCTGATAG	sf005258_AC_CA_Pa	CGATAGCAGAGTCGAAGTA
sequenom	SEQ015	sf005286_CT	sf005286_CT_CT_F	ACGTTGGATGAAAAAGTTGACGCGCGTCTG	sf005286_CT_CT_R	ACGTTGGATGCCACTCTTTCCCGATTTACC	sf005286_CT_CT_P	ACTTGCACGATCTACAC
sequenom	SEQ015	sf005443_CG	sf005443_CG_GC_F	ACGTTGGATGGCAATCACAACCAATTGAGC	sf005443_CG_GC_R	ACGTTGGATGTCCATCTTGGCCATCCATTC	sf005443_CG_GC_Pa	TCAAGCGTTGAAGTCAATATCT
sequenom	SEQ015	sf005501_AG	sf005501_AG_GA_F	ACGTTGGATGAGACACATCCTGCCATTTGC	sf005501_AG_GA_R	ACGTTGGATGTTTTCCAAGTACCAAAGCTG	sf005501_AG_GA_Pa	ATGTTCCTTACTCTGTGG
sequenom	SEQ015	sf005540_CT	sf005540_CT_TC_F	ACGTTGGATGCAGAGCATTTATCCCACAAC	sf005540_CT_TC_R	ACGTTGGATGTGGACATCTCAATTTCTCCC	sf005540_CT_TC_Pa	ACTTATGCAAACACTTGCAACATGACCT
sequenom	SEQ015	sf005590_CT	sf005590_CT_TC_F	ACGTTGGATGTGCAGTGTGTGACTGAAAGC	sf005590_CT_TC_R	ACGTTGGATGATGTGACATGTGACGGTGAG	sf005590_CT_TC_Pa	AGGGGAGACAGTGATAGTGGTAT
sequenom	SEQ015	sf005652_AG	sf005652_AG_GA_F	ACGTTGGATGGAGCGAGCATGAATATGA	sf005652_AG_GA_R	ACGTTGGATGTGCATTTTAGGCTGTCGCTG	sf005652_AG_GA_Pa	GACACCATTTCACTGTTGT
sequenom	SEQ015	sf005654_CT	sf005654_CT_CT_F	ACGTTGGATGATCTACCGGCACAATCTCAC	sf005654_CT_CT_R	ACGTTGGATGTAAATGACGTTTCTGGCGGG	sf005654_CT_CT_P	CTCACTATAGCCTTTGCATCACACTGTTGT
sequenom	SEQ015	sf005769_CTb	sf005769_CTb_CT_F	ACGTTGGATGGCCGCTGAAAAGAATCCTTG	sf005769_CTb_CT_R	ACGTTGGATGTGTGTATCTGGACCACACTG	sf005769_CTb_CT_P	TTTCCTCCTGAGAGCA
sequenom	SEQ015	sf006000_AG	sf006000_AG_GA_F	ACGTTGGATGATTGACACACCATAAGTAGC	sf006000_AG_GA_R	ACGTTGGATGACGTTGGCAGATGCAGTGGA	sf006000_AG_GA_Pa	GATGCAGTGGATTGAGA
sequenom	SEQ015	sf006410_AG	sf006410_AG_GA_F	ACGTTGGATGCTGTTGAAAAGGCAGTCATC	sf006410_AG_GA_R	ACGTTGGATGACTCAAGACCCTCACATAAG	sf006410_AG_GA_Pa	AACCATGTTCTATGATTTCTAATATTT
sequenom	SEQ016	sf000518_GT	sf000518_GT_GT_F	ACGTTGGATGCCACTTCACTGTTATGCTGG	sf000518_GT_GT_R	ACGTTGGATGGGCTAGTGGAAGAAGACATC	sf000518_GT_GT_P	GCTGAGAAACCATTGAGCTCAGAAATAT
sequenom	SEQ016	sf000554_CT	sf000554_CT_TC_F	ACGTTGGATGCAGGTTGACTGTGTCTCTAC	sf000554_CT_TC_R	ACGTTGGATGCTAGCCAGGTCTCTAGACAG	sf000554_CT_TC_Pa	GAGGGGAGAGACAGCATGCATGTA
sequenom	SEQ016	sf000656_AG	sf000656_AG_GA_F	ACGTTGGATGCCGACTGCATATGAATAGAG	sf000656_AG_GA_R	ACGTTGGATGTACGCGTGATTGGATTCCTG	sf000656_AG_GA_Pa	ATCCCAATAAATTATTTCTCCCAATCA
sequenom	SEQ016	sf001196_AG	sf001196_AG_GA_F	ACGTTGGATGAATGGGATACGCTGTCTGAG	sf001196_AG_GA_R	ACGTTGGATGTACAGTCACCTTTGCCATCC	sf001196_AG_GA_Pa	GCTTGCGTTAATGACCT
sequenom	SEQ016	sf001288_CT	sf001288_CT_CT_F	ACGTTGGATGAGACCAGACACAAACATGAG	sf001288_CT_CT_R	ACGTTGGATGTCCAGTCACCAGATGGATTG	sf001288_CT_CT_P	AGCTTATTCATCTGCCACA

sequenom	SEQ016	sf001359_AG	sf001359_AG_GA_F	ACGTTGGATGCCGGAGTGCTTATAGTACAG	sf001359_AG_GA_R	ACGTTGGATGCATCCCTTTCCTTTGAATAC	sf001359_AG_GA_Pa	GGCGTTGAATACACATTGTCATTTATATCA
sequenom	SEQ016	sf001812_AG	sf001812_AG_AG_F	ACGTTGGATGTGTGCAACTGCAGCTTTACG	sf001812_AG_AG_R	ACGTTGGATGCCCATCTGCTGGAACCAAC	sf001812_AG_AG_P	TGGAACCAACCCTTTC
sequenom	SEQ016	sf001916_AG	sf001916_AG_GA_F	ACGTTGGATGAAGAACAGTGTACCGGAAAG	sf001916_AG_GA_R	ACGTTGGATGCGGCAAGTTAGCTAATGTTC	sf001916_AG_GA_Pa	GTTCCGAATATGAGGCAATC
sequenom	SEQ016	sf002018_AC	sf002018_AC_CA_F	ACGTTGGATGGATTGAGGTGGAGCTGATTG	sf002018_AC_CA_R	ACGTTGGATGCCCAGGAAGGTTTTATAACTG	sf002018_AC_CA_P	ACAGGAAGGTTTTATAACTGTAATAA
sequenom	SEQ016	sf002131_AG	sf002131_AG_GA_F	ACGTTGGATGGTCATCAGTATCACATTGGC	sf002131_AG_GA_R	ACGTTGGATGCTGACACTGCTATCTTTGCC	sf002131_AG_GA_Pa	GGGGAGTCTATTAAACATGGAGTCATGTA
sequenom	SEQ016	sf002439_CT	sf002439_CT_CT_F	ACGTTGGATGTTCCACGGCCTGTAAGTAAC	sf002439_CT_CT_R	ACGTTGGATGGATAACACGCTGAGTCAACC	sf002439_CT_CT_P	CGCTGAGTCAACCTAAAGAT
sequenom	SEQ016	sf002640_AG	sf002640_AG_AG_F	ACGTTGGATGCCCTTACACAATCAGTTTGC	sf002640_AG_AG_R	ACGTTGGATGCTTGAGATGATTCCCACAGG	sf002640_AG_AG_P	TGTCAACTCTCCCTCC
sequenom	SEQ016	sf003633_AG	sf003633_AG_GA_F	ACGTTGGATGGAAGGTATTGTGAGAGACGC	sf003633_AG_GA_R	ACGTTGGATGTACACACCTCCACATGGAAC	sf003633_AG_GA_Pa	CACATGGAACATTAAAGAACAAG
sequenom	SEQ016	sf003647_CG	sf003647_CG_GC_F	ACGTTGGATGGCAATCACAACCAATTGAGC	sf003647_CG_GC_R	ACGTTGGATGTCCATCTTGGCCATCCATTC	sf003647_CG_GC_Pa	CTCTGTCAAGCGTTGAAGTCAATATCT
sequenom	SEQ016	sf003788_GT	sf003788_GT_GT_F	ACGTTGGATGTTATTGCAGTCCATTTGTG	sf003788_GT_GT_R	ACGTTGGATGCTCCATCAAGAAGTCATGGG	sf003788_GT_GT_Pa	GAATCTTGAGCTATCAGTTATCCTGTAT
sequenom	SEQ016	sf004056_CT	sf004056_CT_TC_F	ACGTTGGATGGAAGGATGTCATTGGACCAG	sf004056_CT_TC_R	ACGTTGGATGAACCTCTGGATTGTCAAGGG	sf004056_CT_TC_Pa	CTTAATCAAATCTCCCCTTGAATCTATC
sequenom	SEQ016	sf004192_AG	sf004192_AG_GA_F	ACGTTGGATGGTGTGAGAATAGCCTAGATG	sf004192_AG_GA_R	ACGTTGGATGTGGGAGTCTGCTGAATAGTC	sf004192_AG_GA_Pa	AGAAAATCTTAGGATTTTGATACCATTATA
sequenom	SEQ016	sf004214_AG	sf004214_AG_GA_F	ACGTTGGATGAACTACCTGTACCCTTTGTC	sf004214_AG_GA_R	ACGTTGGATGGGGTGTGATTTATCAGTATG	sf004214_AG_GA_Pa	CCCTTTACTCTTTCAAATTCTACTGTATGA
sequenom	SEQ016	sf004288_AG	sf004288_AG_GA_F	ACGTTGGATGGAAGCATAGTGAATTAAAC	sf004288_AG_GA_R	ACGTTGGATGCCTAACCCACTCACAATATG	sf004288_AG_GA_Pa	TTCACCCAAAAGGCATT
sequenom	SEQ016	sf004416_AC	sf004416_AC_CA_F	ACGTTGGATGTCCCGTTGTTTGATGCTTGG	sf004416_AC_CA_R	ACGTTGGATGTCCTCCATATGTATCAGCAG	sf004416_AC_CA_P	GGGGAGCAGAAATAAGACCGAT
sequenom	SEQ016	sf004423_AG	sf004423_AG_AG_F	ACGTTGGATGACACAGCAGTGAATCTTTCC	sf004423_AG_AG_R	ACGTTGGATGGGCCACCTAATCAACATTTC	sf004423_AG_AG_P	TTCCACAAGGTCTTTCCCTG
sequenom	SEQ016	sf004714_CT	sf004714_CT_CT_F	ACGTTGGATGCAGATGCAGACTCAGATTTT	sf004714_CT_CT_R	ACGTTGGATGACACATTGGCTGTGTACAGG	sf004714_CT_CT_P	ATACTGGTGCATAGAGTTGTA
sequenom	SEQ016	sf004795_CT	sf004795_CT_CT_F	ACGTTGGATGGGGATCTTTCAAGAAGCTTAG	sf004795_CT_CT_R	ACGTTGGATGCCAGCAGTTATGTCATGCAG	sf004795_CT_CT_P	AGAAATAAGGCATAACTGTTAAGAA
sequenom	SEQ016	sf004811_AT	sf004811_AT_TA_F	ACGTTGGATGCATGAAGAAAATCAAGGTCTC	sf004811_AT_TA_R	ACGTTGGATGCTCTTCAAAACAACTGTGTC	sf004811_AT_TA_Pa	AATACCCGTTATAGCATAATCGTTA
sequenom	SEQ016	sf004890_AC	sf004890_AC_CA_F	ACGTTGGATGGAACAGAGCAATACTCAGTC	sf004890_AC_CA_R	ACGTTGGATGAGGTTTCTACCCTACATTCC	sf004890_AC_CA_P	TCTATAGAATTTCTTAATATTATGTAGTT
sequenom	SEQ016	sf004917_CT	sf004917_CT_TC_F	ACGTTGGATGAGCAATAAGATATGTTGGGG	sf004917_CT_TC_R	ACGTTGGATGAATCTGTTTCCTGCCGTCTG	sf004917_CT_TC_Pa	AGGGGTAGGGGACTTGCCTGAAC
sequenom	SEQ016	sf004984_AG	sf004984_AG_GA_F	ACGTTGGATGGGGATGTGCAGACATTATTC	sf004984_AG_GA_R	ACGTTGGATGTGCACCCATAGTTATGTCAC	sf004984_AG_GA_Pa	CATAGTTATGTCACATGCTTTC
sequenom	SEQ016	sf005052_AG	sf005052_AG_GA_F	ACGTTGGATGTAGAACCGATCTGGGACTC	sf005052_AG_GA_R	ACGTTGGATGATTACACATACCCGAGACCC	sf005052_AG_GA_Pa	TACCCGTGACAATCAGATCAGA
sequenom	SEQ016	sf005168_AC	sf005168_AC_CA_F	ACGTTGGATGGGCCCAGTGGAAATGAATAG	sf005168_AC_CA_R	ACGTTGGATGTGAGTGTTACTTCTCCCGTG	sf005168_AC_CA_Pa	AATGTGGTGGATTATTGAAG
sequenom	SEQ016	sf005344_AT	sf005344_AT_TA_F	ACGTTGGATGCACAAGCGTCACATGTCTTC	sf005344_AT_TA_R	ACGTTGGATGATTAACCCCTTTTTGGGTAG	sf005344_AT_TA_Pa	TTTGGGTAGGCACAAA
sequenom	SEQ016	sf005440_CT	sf005440_CT_TC_F	ACGTTGGATGGATACAAGGAAAAAGATTGG	sf005440_CT_TC_R	ACGTTGGATGTCCACAACATGAACAGACAC	sf005440_CT_TC_Pa	CCAAATGAACAGACACAATATCAC
sequenom	SEQ016	sf005459_AC	sf005459_AC_CA_F	ACGTTGGATGAAGCATAATGGAGTCCCCTG	sf005459_AC_CA_R	ACGTTGGATGGTCTGATTTACCTCATGCAG	sf005459_AC_CA_Pa	TAACAGACACATGTTTAAAAAATG
sequenom	SEQ016	sf005663_CT	sf005663_CT_TC_F	ACGTTGGATGACAACCTGTTGATCGAGGAC	sf005663_CT_TC_R	ACGTTGGATGTCACAGAGCTGACTGATCAC	sf005663_CT_TC_Pa	TGGGTGTATGTGTGCGCGA

sequenom	SEQ016	sf005769_Cta	sf005769_CTa_CT_F	ACGTTGGATGGAGAGCTATCATCCAGATCG	sf005769_CTa_CT_R	ACGTTGGATGGCAAAACGTCTTCTAGTTGG	sf005769_CTa_CT_P	AAAGTTGGGCTTCCATAG
sequenom	SEQ016	sf006000_CT	sf006000_CT_CT_F	ACGTTGGATGTTGGCAGATGCAGTGGATTG	sf006000_CT_CT_R	ACGTTGGATGATTGACACACCATAAGTAGC	sf006000_CT_CT_P	AGAGATTTTTGCATGGGC
sequenom	SEQ017	sf000132_AG	sf000132_AG_GA_F	ACGTTGGATGAGTAACACAGATCCGCCTTG	sf000132_AG_GA_R	ACGTTGGATGATGCTTTATACACCCCGTGC	sf000132_AG_GA_Pa	GGGAAATTGGGGATTGTGTTTACTTTG
sequenom	SEQ017	sf000364_AG	sf000364_AG_GA_F	ACGTTGGATGCTTGCTCTTGTGATGAGATG	sf000364_AG_GA_R	ACGTTGGATGTCTGCTTCTAGCTCCTATGC	sf000364_AG_GA_Pa	CCATTACTAGCTCTTTCCTA
sequenom	SEQ017	sf000505_CT	sf000505_CT_CT_F	ACGTTGGATGAACCGGACGATTCCATTCAG	sf000505_CT_CT_R	ACGTTGGATGTGTTTCACTCCACGCTGTTG	sf000505_CT_CT_P	CTTTCAGGATTGTCGTCTA
sequenom	SEQ017	sf000612_AT	sf000612_AT_AT_F	ACGTTGGATGCCGACAGAGACTTCTCAAAC	sf000612_AT_AT_R	ACGTTGGATGGCAAAATGTCTAGTTGTAATG	sf000612_AT_AT_P	AAAATGTCTAGTTGTAATGACGTCA
sequenom	SEQ017	sf000754_AC	sf000754_AC_CA_F	ACGTTGGATGCAGGTTTGTGTGTTTCACCG	sf000754_AC_CA_R	ACGTTGGATGGAGGGAATAACTCTCATTCTG	sf000754_AC_CA_Pa	AACTCTCATTCTGACATTTTAC
sequenom	SEQ017	sf000899_CT	sf000899_CT_CT_F	ACGTTGGATGACCCTGATGTGCCTTATTGC	sf000899_CT_CT_R	ACGTTGGATGTGGCTGTGTCTTGAATGCTG	sf000899_CT_CT_P	ACATGATATACCACGGGTA
sequenom	SEQ017	sf000991_AT	sf000991_AT_TA_F	ACGTTGGATGGGGAATAGTCTCATAATAGGC	sf000991_AT_TA_R	ACGTTGGATGGACTCTTACACGAATAGAAC	sf000991_AT_TA_Pa	TGGATATTACATGACTATTACATGACTATT
sequenom	SEQ017	sf001353_GT	sf001353_GT_GT_F	ACGTTGGATGGAGAGTCTGAGGAAGTGTTG	sf001353_GT_GT_R	ACGTTGGATGATGGACCATAGAGCATGGAG	sf001353_GT_GT_Pa	GGCATGGAGACTCTCCTC
sequenom	SEQ017	sf003142_AG	sf003142_AG_GA_F	ACGTTGGATGTCTCTGATCAAATCTTCTC	sf003142_AG_GA_R	ACGTTGGATGCGAACTTCCATTTAGCATAG	sf003142_AG_GA_Pa	CAATTTTATATGTACATACTATCTGAT
sequenom	SEQ017	sf003899_CT	sf003899_CT_TC_F	ACGTTGGATGGCACAATGTCCAACAATTCC	sf003899_CT_TC_R	ACGTTGGATGATGTCACCCTATGACTTTGG	sf003899_CT_TC_Pa	ACCCTATGACTTTGGAAACAT
sequenom	SEQ017	sf004211_GT	sf004211_GT_GT_F	ACGTTGGATGGCCACTAGCACCAATTATAC	sf004211_GT_GT_R	ACGTTGGATGCTGGTTCAGAATGCTAAGCC	sf004211_GT_GT_Pa	CCTAAAATGCTAATATACGCTAACA
sequenom	SEQ017	sf004254_CT	sf004254_CT_CT_F	ACGTTGGATGCGTTTCTCACTTGGAAACAG	sf004254_CT_CT_R	ACGTTGGATGAGCTCAAGGTTGCTCAACTG	sf004254_CT_CT_P	TAGGGAAGAGAGATGTACT
sequenom	SEQ017	sf004319_GT	sf004319_GT_GT_F	ACGTTGGATGTATGGGACAGGAAGTCACAG	sf004319_GT_GT_R	ACGTTGGATGGGCTTGCAAATCCTAAGTGG	sf004319_GT_GT_Pa	AAGTTTGGTTAAATGGAAATAAACAT
sequenom	SEQ017	sf004353_AG	sf004353_AG_GA_F	ACGTTGGATGGGCTCAATAGCAACACACAG	sf004353_AG_GA_R	ACGTTGGATGCCTGATTAATGCCAGATCTT	sf004353_AG_GA_Pa	ACAAAACATGAGCAGC
sequenom	SEQ017	sf004373_AG	sf004373_AG_GA_F	ACGTTGGATGACGCTTAGATAAGTCCCCTG	sf004373_AG_GA_R	ACGTTGGATGTGAGGTGACAAGGGATACAG	sf004373_AG_GA_Pa	CCTATTGATTTTTATGGGTGACCTAAC
sequenom	SEQ017	sf004560_GT	sf004560_GT_GT_F	ACGTTGGATGGTGCTGAATTCCTGAAGAAC	sf004560_GT_GT_R	ACGTTGGATGAGATGGGTGAGGGATATTTG	sf004560_GT_GT_P	GAATTGAGCATGGCAGC
sequenom	SEQ017	sf004583_AC	sf004583_AC_CA_F	ACGTTGGATGAGCAGTGGGCTAATCCAAAG	sf004583_AC_CA_R	ACGTTGGATGGAGTAAGGAAACCCATAGCC	sf004583_AC_CA_Pa	GCTAACGTTACTTACTTTTAAAT
sequenom	SEQ017	sf004624_CT	sf004624_CT_CT_F	ACGTTGGATGGAACCAGTTTGCTACAGCAC	sf004624_CT_CT_R	ACGTTGGATGCACTAAGGTCACTTGCAAAC	sf004624_CT_CT_P	TCCTGTTGTTGCATGAT
sequenom	SEQ017	sf004651_AG	sf004651_AG_AG_F	ACGTTGGATGAAAGGGTCTCTGTGATGGTG	sf004651_AG_AG_R	ACGTTGGATGCGAGAGAGAGAAACAACACG	sf004651_AG_AG_P	CGTTATACAAGAAAACAACAGATC
sequenom	SEQ017	sf004685_AGa	sf004685_AGa_AG_F	ACGTTGGATGCTCAGACAGATCCACTGAAC	sf004685_AGa_AG_R	ACGTTGGATGCACTAACAAAGCCAGTGTGC	sf004685_AGa_AG_P	GTGTGCAGTAGGGCGG
sequenom	SEQ017	sf004685_CG	sf004685_CG_GC_F	ACGTTGGATGCACTAACAAAGCCAGTGTGC	sf004685_CG_GC_R	ACGTTGGATGCTCAGACAGATCCACTGAAC	sf004685_CG_GC_Pa	GGGGTACTAGGCGATGATGCAT
sequenom	SEQ017	sf004839_CT	sf004839_CT_CT_F	ACGTTGGATGCGTGCTTTTTCTCCAAACCC	sf004839_CT_CT_R	ACGTTGGATGTGTCCAAAAGTGCTTGGCAG	sf004839_CT_CT_P	GGCTTGGCAGGTCATATTTGATAA
sequenom	SEQ017	sf004938_CT	sf004938_CT_TC_F	ACGTTGGATGCCAATTATGCTTTGCTTTTG	sf004938_CT_TC_R	ACGTTGGATGCTCAACTGTGAATGGTCCTG	sf004938_CT_TC_Pa	AGTTTGGATTTGGCTTCACGTTAATCGT
sequenom	SEQ017	sf005311_CG	sf005311_CG_CG_F	ACGTTGGATGGTTACTTGTGTAGTGGAGTC	sf005311_CG_CG_R	ACGTTGGATGTGGTTAGCTTCACCTACCTG	sf005311_CG_CG_P	GCATGGTAGTAACATGAGTTG
sequenom	SEQ017	sf005440_AG	sf005440_AG_GA_F	ACGTTGGATGTGTGTCTGTTCATGTTGTGG	sf005440_AG_GA_R	ACGTTGGATGAGCTGTAACTTCTCAGCTAC	sf005440_AG_GA_Pa	TCTGTAACTTCTCAGCTACATATTG
sequenom	SEQ018	sf000020_CT	sf000020_CT_TC_F	ACGTTGGATGGAGAAGGCCCTAATGCAATG	sf000020_CT_TC_R	ACGTTGGATGGCGATCTCTGTTCCTAATGC	sf000020_CT_TC_Pa	AGGATGCAACTGACCTGGC

sequenom	SEQ018	sf000062_CG	sf000062_CG_CG_F	ACGTTGGATGGGGTAGTAGTCTGGGTAAAG	sf000062_CG_CG_R	ACGTTGGATGCCTTGGAACAAGGATGGAAC	sf000062_CG_CG_P	ACGCCACTGAAACACACA
sequenom	SEQ018	sf000151_AT	sf000151_AT_TA_F	ACGTTGGATGTTATCATGTGAGGCTCAGGG	sf000151_AT_TA_R	ACGTTGGATGGACCTAATAGTCAACGGGAG	sf000151_AT_TA_Pa	GACGGGAGTACTCATGATGGCACA
sequenom	SEQ018	sf000310_AC	sf000310_AC_CA_F	ACGTTGGATGCTGTGGCTAAACATGTTAAGT	sf000310_AC_CA_R	ACGTTGGATGGGGAAGAGTACAAACAGAGC	sf000310_AC_CA_P	CCTGAAGAGTACAAACAGAGCTGGGAC
sequenom	SEQ018	sf000364_GT	sf000364_GT_GT_F	ACGTTGGATGTTGTAAAATGGCGTCGACAG	sf000364_GT_GT_R	ACGTTGGATGGGAAAGATCTGTTCTTGCTC	sf000364_GT_GT_P	AGGAAAGAGCTAGTAATGG
sequenom	SEQ018	sf001287_CT	sf001287_CT_TC_F	ACGTTGGATGCTGTCTATATATCGACCAGG	sf001287_CT_TC_R	ACGTTGGATGGAGACTTTAAAATCTCAAG	sf001287_CT_TC_Pa	GCTCGATATTCAATTAAGAAGCG
sequenom	SEQ018	sf001394_AT	sf001394_AT_TA_F	ACGTTGGATGAATGGGATGGGCTCTTAGTG	sf001394_AT_TA_R	ACGTTGGATGGCTATGACCTTCATGCAATG	sf001394_AT_TA_Pa	AGAGTAAATGAGGTGAGAGATTA
sequenom	SEQ018	sf001546_AC	sf001546_AC_CA_F	ACGTTGGATGTACGAGGTGTAGCTGTGATG	sf001546_AC_CA_R	ACGTTGGATGGGCTGTCAACAGACAAGTAG	sf001546_AC_CA_P	AAGTAGTCACAAACGCAACCACACACA
sequenom	SEQ018	sf001846_AG	sf001846_AG_AG_F	ACGTTGGATGCACACTAGATATGGATCACG	sf001846_AG_AG_R	ACGTTGGATGATGCTTATCGTTCCACCACC	sf001846_AG_AG_P	CCGTCGGCTTTAATATTTGACTT
sequenom	SEQ018	sf002055_AG	sf002055_AG_GA_F	ACGTTGGATGGACTGATGCATTGTCACCTG	sf002055_AG_GA_R	ACGTTGGATGTAAACCCCAGTTTGCTGTCG	sf002055_AG_GA_Pa	CCACCACTGAATCAGACAGTG
sequenom	SEQ018	sf002721_GT	sf002721_GT_GT_F	ACGTTGGATGATTAGTGATGATGGGACTGC	sf002721_GT_GT_R	ACGTTGGATGGCCTCTGGAAAAACACACTG	sf002721_GT_GT_Pa	ACTCTGGAAAAACACACTGACTATATGAA
sequenom	SEQ018	sf003016_AG	sf003016_AG_GA_F	ACGTTGGATGCCTCTATTTACAGAGGGAAG	sf003016_AG_GA_R	ACGTTGGATGGACCAAAGTCCCACAAACAC	sf003016_AG_GA_Pa	CCCCCAGCACATAACTACAGATCTTTGTC
sequenom	SEQ018	sf003382_AG	sf003382_AG_GA_F	ACGTTGGATGGCACTACTTTTGACCAGAGC	sf003382_AG_GA_R	ACGTTGGATGTCTAGCACAACGTCATAAGC	sf003382_AG_GA_Pa	AACCCTAATCCCTGTATAGTG
sequenom	SEQ018	sf003611_AC	sf003611_AC_CA_F	ACGTTGGATGGACATAGCTCAACATGTCTG	sf003611_AC_CA_R	ACGTTGGATGGCTGCAGGAGAATCTAAATG	sf003611_AC_CA_P	TGTCGATGTACCTTTATCCAGATAA
sequenom	SEQ018	sf003639_CT	sf003639_CT_CT_F	ACGTTGGATGCCGTTGTTATTTCGAGCGTG	sf003639_CT_CT_R	ACGTTGGATGAACAAACCTTTAATCCACC	sf003639_CT_CT_P	ACAAACCTTTAATCCACCATGTAACC
sequenom	SEQ018	sf003755_CT	sf003755_CT_TC_F	ACGTTGGATGGCAGGAGTACTTTAAATTGTG	sf003755_CT_TC_R	ACGTTGGATGCTGCAGCAACAGAACATGTG	sf003755_CT_TC_Pa	TGTGAATTAAGTGGATTATAATTAAATAAC
sequenom	SEQ018	sf003922_GT	sf003922_GT_GT_F	ACGTTGGATGCCACAATGTAAGACATGCAC	sf003922_GT_GT_R	ACGTTGGATGCCTTTCCTGGGTAGCTTATC	sf003922_GT_GT_P	CAAGGATTTGTGATCACATTCTCA
sequenom	SEQ018	sf003974_GT	sf003974_GT_GT_F	ACGTTGGATGTCTTTGTTCCCTACCCTTGC	sf003974_GT_GT_R	ACGTTGGATGGGTAGTCACTCTGCTCTTTC	sf003974_GT_GT_Pa	ATCTTTCCTGAAGTCCATGATC
sequenom	SEQ018	sf004008_AG	sf004008_AG_AG_F	ACGTTGGATGTCTTCAGTTCCCAGTTTAGC	sf004008_AG_AG_R	ACGTTGGATGCTAGCTGGATAAAACATGGC	sf004008_AG_AG_P	AGGATTGAATTCCATGAGACTTCTT
sequenom	SEQ018	sf004045_CT	sf004045_CT_CT_F	ACGTTGGATGTGTCTCTGTGTGATGCTGTG	sf004045_CT_CT_R	ACGTTGGATGCGGATGACATTTTCCACCTG	sf004045_CT_CT_P	GAGGAAAAACACCAACAGAAAAACAC
sequenom	SEQ018	sf004434_AT	sf004434_AT_CG_F	ACGTTGGATGTGCAAGATATGGGCTACTAC	sf004434_AT_CG_R	ACGTTGGATGCGAGTGGAAATCCAATAGCC	sf004434_AT_CG_P	GGTCTTTGCTTTTTAGACC
sequenom	SEQ018	sf004471_AG	sf004471_AG_GA_F	ACGTTGGATGGATTGCCCAGTGACATTGTG	sf004471_AG_GA_R	ACGTTGGATGGACTCCATCTTCTGGTTGGC	sf004471_AG_GA_Pa	TGGTTGGCTCTCTCCGC
sequenom	SEQ018	sf004521_CG	sf004521_CG_CG02_F	ACGTTGGATGTCACTTAATGGACTCCAGGC	sf004521_CG_CG02_R	ACGTTGGATGGTGTCAGGAGAAACGTTAC	sf004521_CG_CG02_P	ACATATAGTGATATAAATGATTTTGTATA
sequenom	SEQ018	sf004656_AC	sf004656_AC_CA_F	ACGTTGGATGATGTTTCGAAAGCAGGCTCC	sf004656_AC_CA_R	ACGTTGGATGTATCTACTGCCCGAGAAGTG	sf004656_AC_CA_Pa	GGGTTTGCTTATTAAAAGAGACATAAA
sequenom	SEQ018	sf004668_AC	sf004668_AC_CA_F	ACGTTGGATGTCACTGAGATAGCCAAGGAG	sf004668_AC_CA_R	ACGTTGGATGTCCCAGAAGTGGTTAGATTC	sf004668_AC_CA_P	AGTTAGCTGGTTTCTGACGT
sequenom	SEQ018	sf004712_CT	sf004712_CT_CT_F	ACGTTGGATGTCCACCTTGGCTTATTGCAC	sf004712_CT_CT_R	ACGTTGGATGTGCAGTTATCTTAGCCAGCC	sf004712_CT_CT_P	TTGCAGCTAACAATTAGCTAAATGACAT
sequenom	SEQ018	sf004715_AC	sf004715_AC_CA_F	ACGTTGGATGACTGTACTAGTGCACGTGAC	sf004715_AC_CA_R	ACGTTGGATGGGGTTTGGTAATGTCCCAC	sf004715_AC_CA_Pa	TGTCCCACACCCAACC
sequenom	SEQ018	sf004741_CG	sf004741_CG_CG_F	ACGTTGGATGAGATGACAGGAAATGGAGCG	sf004741_CG_CG_R	ACGTTGGATGCAGTCAATTTGCAGAGCAGG	sf004741_CG_CG_P	GTTGTTCTAGATGAAGGC
sequenom	SEQ018	sf004774_AG	sf004774_AG_AG_F	ACGTTGGATGAACCTGCAGCCTGATCAAAG	sf004774_AG_AG_R	ACGTTGGATGTGGCAATGGTATGGCACATC	sf004774_AG_AG_P	TTGGGTACGTAGCACAAGCATCTAGA

sequenom	SEQ018	sf005157_CT	sf005157_CT_CT_F	ACGTTGGATGGAACATCATTGTTGGAGCAG	sf005157_CT_CT_R	ACGTTGGATGCTTTTAAAATGGGCCTTTGC	sf005157_CT_CT_P	GATTAGAGAAACTCATGAAACA
sequenom	SEQ018	sf005160_AC	sf005160_AC_CA_F	ACGTTGGATGCTTGAAGGCTCTTACGTTGG	sf005160_AC_CA_R	ACGTTGGATGGTTGAGGTCAGAAGTAGAAG	sf005160_AC_CA_Pa	ATCAGATGGAGTTGAAGACGA
sequenom	SEQ018	sf006410_AG	sf006410_AG_GA02_F	ACGTTGGATGGCTTCAATTGGCTCCATATC	sf006410_AG_GA02_R	ACGTTGGATGTGTAAACTCAAGACCCTCAC	sf006410_AG_GA02_Pa	AAACCATGTTCTATGATTTCTAATATTT

Table S3 Description and annotation of the 281 SNP (single nucleotide-polymorphism) markers used to build the linkage map in the Brook charr, *Salvelinus fontinalis*.

Ts: transition; Tv: transversion; C: coding region; NC: non coding region; S: synonymous; NS: non synonymous; LG: linkage group.

	SNP Name	Accession number	GenInfo Identifiers (GI)	Variation	Ts/Tv	C/NC	S/NS	LG
1	sf000002	BT050259	GI:209738381	A/G	Ts	NC	-	22
2	sf000017	XP_691985.3	GI:189515371	C/G	Tv	C	-	31
3	sf000020			C/T	Ts	C	NS	35
4	sf000021	BT044685.1	GI:209148638	A/C	Tv	C	-	14
5	sf000023			C/T	Ts	NC	-	-
6	sf000032			A/G	Ts	C	-	15
7	sf000062			C/G	Tv	NC	-	-
8	sf000071			A/C	Tv	NC	-	3
9	sf000078			A/T	Tv	NC	-	27
10	sf000086	XM_001921499.1	GI:189516301	C/T	Ts	NC	-	-
11	sf000088	XP_002609992.1	GI:260830085	A/G	Ts	NC	-	-
12	sf000119			A/G	Ts	NC	-	12
13	sf000124			A/G	Ts	C	-	17
14	sf000132			A/G	Ts	NC	-	13
15	sf000137	NM_200955	GI:41055673	A/T	Tv	C	NS	-
16	sf000139			G/T	Tv	NC	-	4
17	sf000151			A/T	Tv	NC	-	15
18	sf000157	NP_775368	GI:27545272	A/C	Tv	C	NS	25
19	sf000175	XP_001054847	GI:109498064	G/T	Tv	NC	-	-
20	sf000178			A/G	Ts	C	-	19
21	sf000179			C/T	Ts	NC	-	3
22	sf000191			C/G	Tv	NC	-	-

23	sf000209			C/T	Ts	NC	-	-
24	sf000228			A/T	Tv	NC	-	-
25	sf000310			A/T	Tv	NC	-	10
26	sf000324			A/C	Tv	NC	-	8
27	sf000327			A/G	Ts	NC	-	-
28	sf000364			A/G	Ts	C	NS	31
29	sf000364			G/T	Tv	C	NS	31
30	sf000382			A/G	Ts	NC	-	-
31	sf000390	BT057320	GI:221221062	C/T	Ts	NC	-	-
32	sf000392	CAAE01015004.1	GI:47226310	C/T	Ts	C	-	23
33	sf000397			C/G	Tv	NC	-	20
34	sf000428			A/T	Tv	NC	-	3
35	sf000505			C/T	Ts	C	-	1
36	sf000508			C/T	Ts	NC	-	4
37	sf000518			G/T	Tv	NC	-	-
38	sf000554	BT059059.1	GI:223648027	C/T	Ts	C	NS	2
39	sf000559	XM_001502487	GI:149728067	A/G	Ts	NC	-	-
40	sf000583	EF467299.1	GI:154795566	C/T	Ts	NC	-	8
41	sf000584	EU025714	GI:158702319	A/G	Ts	C	-	10
42	sf000612	NM_001020538	GI:66472671	A/T	Tv	NC	-	37
43	sf000633			G/T	Tv	C	-	-
44	sf000656			A/G	Ts	NC	-	20
45	sf000657			C/T	Ts	NC	-	2
46	sf000679	BT060419	GI:223673194	C/T	Ts	NC	-	-
47	sf000684	GU129140	GI:213512874	C/T	Ts	C	-	34
48	sf000706	NP_001117688	GI:185135493	A/G	Ts	NC	-	6
49	sf000717			C/T	Ts	NC	-	18
50	sf000719			A/T	Tv	NC	-	16

51	sf000744			A/T	Tv	C	NS	5
52	sf000747			C/T	Ts	NC	-	-
53	sf000754			A/C	Tv	NC	-	8
54	sf000810	BT045174	GI:209154407	C/T	Ts	NC	-	2
55	sf000854			G/T	Tv	NC	-	-
56	sf000878			C/T	Ts	NC	-	-
57	sf000891			A/C	Tv	C	NS	6
58	sf000899	EU025705	GI:158702261	C/T	Ts	NC	-	12
59	sf000905			A/T	Tv	C	-	31
60	sf000961			C/T	Ts	NC	-	5
61	sf000966			A/G	Ts	NC	-	13
62	sf000970			A/G	Ts	C	-	9
63	sf000978			A/G	Ts	NC	-	1
64	sf000991			A/T	Tv	C	-	-
65	sf001069			G/T	Tv	NC	-	-
66	sf001086	NM_001141083	GI:213513628	C/T	Ts	NC	-	-
67	sf001105			A/G	Ts	NC	-	17
68	sf001164			C/T	Ts	NC	-	-
69	sf001181			A/G	Ts	C	-	-
70	sf001184	CR391965	GI:167908776	C/T	Ts	NC	-	1
71	sf001196			A/G	Ts	NC	-	-
72	sf001284			G/T	Tv	NC	-	33
73	sf001287			C/T	Ts	C	-	-
74	sf001288			C/T	Ts	C	NS	2
75	sf001353			G/T	Tv	C	-	5
76	sf001359	GQ505860	GI:260182183	A/G	Ts	NC	-	-
77	sf001394			A/T	Tv	NC	-	6
78	sf001437			A/G	Ts	NC	-	-

79	sf001546			A/C	Tv	C	NS	28
80	sf001601			C/T	Ts	NC	-	8
81	sf001644			G/T	Tv	C	-	2
82	sf001661			G/T	Tv	C	-	-
83	sf001667			A/G	Ts	C	NS	17
84	sf001686			A/G	Ts	NC	-	-
85	sf001692			C/T	Ts	NC	-	12
86	sf001740			A/G	Ts	NC	-	7
87	sf001770			A/G	Ts	NC	-	21
88	sf001812	AC203446	GI:163955243	A/G	Ts	NC	-	9
89	sf001831			A/C	Tv	NC	-	40
90	sf001846			A/G	Ts	NC	-	30
91	sf001880	EF467300	GI:154795567	C/T	Ts	NC	-	-
92	sf001996	DQ246664	GI:80971723	A/G	Ts	NC	-	28
93	sf002018			A/C	Tv	NC	-	25
94	sf002024			A/G	Ts	NC	-	3
95	sf002033	AJ311906	GI:20873289	A/T	Tv	C	-	2
96	sf002055			A/G	Ts	C	NS	31
97	sf002131			A/G	Ts	C	-	1
98	sf002145	XM_683887	GI:292622326	C/G	Tv	C	NS	31
99	sf002155			A/G	Ts	NC	-	-
100	sf002175			C/T	Ts	NC	-	34
101	sf002203			A/G	Ts	C	-	7
102	sf002250	XM_001920907	GI:189520811	A/C	Tv	C	-	28
103	sf002333			A/G	Ts	NC	-	-
104	sf002353	NM_001141843	GI:213513502	C/T	Ts	NC	-	20
105	sf002439			C/T	Ts	NC	-	31
106	sf002633	BT072804	GI:224587929	A/C	Tv	C	-	-

107	sf002640			A/G	Ts	NC	-	21
109	sf002721			A/G	Ts	C	-	32
110	sf002948	CAAE01015039	GI:47222189	G/T	Tv	C	S	7
111	sf003018			A/G	Ts	NC	-	26
112	sf003063			A/C	Tv	NC	-	1
113	sf003076	EU025709	GI:158702304	A/G	Ts	NC	-	23
114	sf003084			A/G	Ts	C	-	4
115	sf003092			C/T	Ts	C	-	9
116	sf003105			C/T	Ts	NC	-	3
117	sf003118			A/G	Ts	NC	-	6
118	sf003141	BT056462	GI:221219345	A/T	Tv	NC	-	11
119	sf003142	CU062627	GI:150171078	A/G	Ts	NC	-	-
120	sf003197			A/G	Ts	NC	-	-
121	sf003208			C/T	Ts	NC	-	-
122	sf003334			A/G	Ts	NC	-	24
123	sf003382			A/G	Ts	C	NS	14
124	sf003407			C/T	Ts	NC	-	10
125	sf003442			A/G	Ts	C	-	24
126	sf003455			A/G	Ts	NC	-	11
127	sf003500	BT049606.1	GI:209737075	C/T	Ts	NC	-	1
128	sf003520			A/G	Ts	C	S	2
129	sf003538	AL840630	GI:41322894	G/T	Tv	NC	-	9
130	sf003560			C/T	Ts	C	S	-
131	sf003589			C/T	Ts	C	-	-
132	sf003595			A/T	Tv	NC	-	-
133	sf003601			C/T	Ts	NC	-	-
134	sf003610			A/T	Tv	C	-	1
135	sf003611			A/C	Tv	NC	-	-

136	sf003614	CAAE01014563	GI:47223303	G/T	Tv	NC	-	8
137	sf003621	BT059052	GI:223648013	C/T	Ts	NC	-	-
138	sf003633			A/G	Ts	C	S	21
139	sf003639	EF427381	GI:148362130	C/T	Ts	NC	-	30
140	sf003647			C/G	Tv	NC	-	40
141	sf003697			A/C	Tv	NC	-	37
142	sf003698			G/T	Tv	C	-	-
143	sf003700			C/T	Ts	NC	-	9
144	sf003713	XM_686639.3	GI:189530935	A/T	Tv	NC	-	25
145	sf003715	EU816603	GI:209962458	C/T	Ts	NC	-	11
146	sf003724			C/T	Ts	NC	-	-
147	sf003728			C/T	Ts	C	-	31
148	sf003755			G/T	Tv	NC	-	7
149	sf003788	XM_002660927	GI:292611089	G/T	Tv	NC	-	-
150	sf003813	EU621898	GI:187936476	A/G	Ts	NC	-	8
151	sf003836			A/T	Tv	NC	-	15
152	sf003897			A/G	Ts	NC	-	10
153	sf003899			C/T	Ts	NC	-	11
154	sf003919	GQ505860	GI:260182183	C/T	Ts	NC	-	1
155	sf003977	EU481821	GI:171474994	C/G	Tv	NC	-	-
156	sf003994			G/T	Tv	NC	-	-
157	sf004008			A/G	Ts	C	NS	-
158	sf004013	EU221180	GI:159033051	A/C	Tv	C	NS	38
159	sf004016			A/G	Ts	NC	-	2
160	sf004030	XM_689729	GI:189528958	A/T	Tv	NC	-	19
161	sf004038	NM_001165151	GI:259089170	A/G	Ts	NC	-	34
162	sf004055	XP_001921123	GI:189530039	A/T	Tv	C	NS	22
163	sf004056	EF467297	GI:154795564	C/T	Ts	C	NS	-

164	sf004064			A/C	Tv	NC	-	28
165	sf004070			A/G	Ts	NC	-	24
166	sf004090			C/G	Tv	C	NS	-
167	sf004099			A/T	Tv	NC	-	-
168	sf004112			A/G	Ts	NC	-	-
169	sf004131	NM_001173900	GI:291190431	A/G	Ts	NC	-	40
170	sf004149	FJ969490	GI:262189352	C/G	Tv	NC	-	6
171	sf004155	EU025709	GI:158702304	G/T	Tv	NC	-	-
172	sf004192			A/G	Ts	C	-	-
173	sf004209			A/T	Tv	NC	-	-
174	sf004211			G/T	Tv	NC	-	3
175	sf004214			A/G	Ts	NC	-	6
176	sf004240	EU621900	GI:187936480	A/G	Ts	NC	-	6
177	sf004252	NM_001140784	GI:213515209	G/T	Tv	NC	-	5
178	sf004254	BT071904	GI:224613219	C/T	Ts	C	-	13
179	sf004257	AB294121	GI:149773365	A/G	Ts	NC	-	3
180	sf004260			C/T	Ts	C	-	-
181	sf004288			A/G	Ts	C	-	-
182	sf004299	XM_001922165	GI:189531595	C/T	Ts	NC	-	10
183	sf004319	BT058994	GI:223647897	G/T	Tv	C	-	23
184	sf004353	NM_001124574	GI:185135642	A/G	Ts	C	S	40
185	sf004357	EU025708	GI:158702285	C/T	Ts	C	NS	4
186	sf004373			A/G	Ts	C	-	5
187	sf004379			C/T	Ts	NC	-	15
188	sf004387			C/T	Ts	C	-	-
189	sf004416	GU129140	GI:290760588	A/C	Tv	NC	-	31
190	sf004423			A/G	Ts	C	-	-
191	sf004426			C/T	Ts	NC	-	24

192	sf004438	BT045405	GI:209154869	C/T	Ts	C	NS	31
193	sf004475	EU621899	GI:187936478	C/T	Ts	C	S	25
194	sf004521			C/G	Tv	NC	-	1
195	sf004529			A/T	Tv	NC	-	38
196	sf004541			A/C	Tv	NC	-	2
197	sf004545	EF427379	GI:148362119	A/C	Tv	NC	-	-
198	sf004560			G/T	Tv	NC	-	3
199	sf004562			A/C	Tv	NC	-	7
200	sf004583	NM_001013274	GI:61651703	A/C	Tv	NC	-	-
201	sf004602	XM_001922165	GI:189531595	A/G	Ts	NC	-	-
202	sf004614			A/G	Ts	C	-	13
203	sf004624	EU816603	GI:209962458	C/T	Ts	NC	-	10
204	sf004632	EU025707	GI:158702273	C/T	Ts	NC	-	-
205	sf004642			A/G	Ts	NC	-	6
206	sf004651			A/G	Ts	C	NS	6
207	sf004656			A/C	Tv	NC	-	21
208	sf004668	FJ969489	GI:262189345	A/C	Tv	C	-	38
209	sf004684			A/T	Tv	NC	-	-
210	sf004685			A/G	Ts	NC	-	39
211	sf004685			A/G	Ts	C	NS	39
212	sf004685			C/G	Tv	C	NS	-
213	sf004714	EU025714	GI:158702319	C/T	Ts	C	-	27
214	sf004715			C/T	Ts	C	-	10
215	sf004732	AB258536	GI:118596560	C/T	Ts	NC	-	29
216	sf004741			C/G	Tv	NC	-	31
217	sf004762			C/T	Ts	NC	-	18
218	sf004765			C/T	Ts	C	NS	4
219	sf004774			A/G	Ts	C	-	3

220	sf004795	BT057087	GI:221220595	C/T	Ts	NC	-	10
221	sf004811	EU025709	GI:158702304	A/T	Tv	C	NS	15
222	sf004817	EU025714	GI:158702319	C/G	Tv	NC	-	-
223	sf004818	EU481821	GI:171474994	A/C	Tv	NC	-	2
224	sf004828	AJ716203	GI:52673235	A/T	Tv	NC	-	-
225	sf004839			C/T	Ts	C	-	39
226	sf004848	BT058155.1	GI:223646219	A/T	Tv	NC	-	17
227	sf004870			A/G	Ts	NC	-	7
228	sf004890	FJ969489	GI:262189345	A/C	Tv	NC	-	-
229	sf004897			A/T	Tv	NC	-	-
230	sf004904			C/G	Tv	NC	-	-
231	sf004909	EU481821	GI:171474994	A/T	Tv	C	NS	13
232	sf004913	BT059404	GI:223648717	A/C	Tv	NC	-	4
233	sf004917	BT072749	GI:224587877	C/T	Ts	NC	-	12
234	sf004938	EU025708	GI:158702285	C/T	Ts	NC	-	9
235	sf004975	EU221176	GI:159147122	C/T	Ts	NC	-	31
236	sf004977	EU025707	GI:158702273	C/T	Ts	NC	-	-
237	sf004984	NM_001140391	GI:213511551	A/G	Ts	C	NS	5
238	sf005000	DQ246664	GI:80971723	C/T	Ts	C	NS	-
239	sf005052	BT058930	GI:223647769	A/G	Ts	C	-	-
240	sf005054	BT059612	GI:223649133	A/G	Ts	NC	-	3
241	sf005079			A/C	Tv	NC	-	-
242	sf005104	EU025714	GI:158702319	A/C	Tv	NC	-	-
243	sf005138	NM_001145584	GI:224496041	A/C	Tv	NC	-	-
244	sf005160			A/C	Tv	C	-	31
245	sf005168	BX537340	GI:51592271	A/C	Tv	C	-	2
246	sf005182	SSSAT48S1	GI:501083	A/G	Ts	NC	-	-
247	sf005182	SSSAT48S1	GI:501083	A/G	Ts	NC	-	-

248	sf005186			C/T	Ts	NC	-	39
249	sf005248	EU481821	GI:171474994	C/T	Ts	NC	-	9
250	sf005258	EU221180	GI:159033051	A/C	Tv	NC	-	-
251	sf005272	EF467298	GI:154795565	C/G	Tv	NC	-	-
252	sf005286			C/T	Ts	NC	-	-
253	sf005311	GQ505859	GI:260182171	C/G	Tv	NC	-	-
254	sf005344	GU129140	GI:290760588	A/T	Tv	C	NS	32
255	sf005399	AM748538	GI:242098051	A/T	Tv	C	NS	-
256	sf005409	CR847272	GI:55058237	A/C	Tv	C	NS	8
257	sf005410	FJ969489	GI:262189345	A/C	Tv	NC	-	-
258	sf005420			A/G	Ts	NC	-	38
259	sf005440			C/T	Ts	NC	-	21
260	sf005440			A/G	Ts	C	S	-
261	sf005443			C/G	Tv	C	-	37
262	sf005459			A/C	Tv	NC	-	1
263	sf005501	BT072704	GI:224587835	A/G	Ts	NC	-	9
264	sf005540	EU816603	GI:209962458	C/T	Ts	C	-	19
265	sf005590			C/T	Ts	C	NS	35
266	sf005652			A/G	Ts	NC	-	8
267	sf005654	NM_001165392	GI:259155245	C/T	Ts	C	-	-
268	sf005663			A/G	Ts	NC	-	1
269	sf005695			C/T	Ts	C	-	-
270	sf005769	NM_001140223	GI:213511597	A/G	Ts	NC	-	14
271	sf005769	NM_001140223	GI:213511597	C/T	Ts	NC	-	14
272	sf005917	EU221180	GI:159033051	C/T	Ts	NC	-	-
273	sf006000	EU621898	GI:187936476	C/T	Ts	C	-	35
274	sf006000	EU621898	GI:187936476	A/G	Ts	NC	-	-
275	sf006057	XM_001919059	GI:189519277	A/G	Ts	C	S	-

276	sf006073	BX927363	GI:112183280	A/G	Ts	C	NS	39
277	sf006078	BT059612	GI:223649133	A/T	Tv	NC	-	-
278	sf006081	FJ969488	GI:262189341	G/T	Tv	NC	-	33
279	sf006102	GU129139	GI:290760560	A/C	Tv	C	NS	-
280	sf006197	NM_001140134	GI:213511349	A/T	Tv	NC	-	-
281	sf006410	XM_002663717	GI:292618742	A/G	Ts	NC	-	9

Table S4 Sequences of the contig build from the assembly of the 454 raw data

Table S4 is available for download at http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.111.001867/-/DC1.

Table S5 Description of the consenssus and sex-specific linkage maps build using Crimap in brook charr, *Salvelinus fontinalis.* **SNP: single nucleotide polymorphism; Msats: microsatellites**

Map	Consensus			Female			Male		
Linkage group	Number of markers (SNP/Msats)	Total length (cM)	Average marker spacing (cM)	Number of markers (SNP/Msats)	Total length (cM)	Average marker spacing (cM)	Number of markers (SNP/Msats)	Total length (cM)	Average marker spacing (cM)
1	16 (11/5)	132.2	8.26	16 (11/5)	187	11.6	16 (11/5)	77.8	4.23
2	16 (11/5)	130.2	8.14	16 (11/5)	169.3	10.5	16 (11/5)	65.4	4.08
3	15 (10/5)	95.7	6.38	15 (10/5)	101.1	6.74	15 (10/5)	33.3	2.22
4	8 (6/2)	73.2	9.15	8 (6/2)	65.4	8.2	8 (6/2)	24.1	3.01
5	11 (6/5)	95.2	8.65	11 (6/5)	70.3	6.39	11 (6/5)	28.3	2.57
6	11 (9/2)	77.5	7.04	11 (9/2)	67.8	6.2	11 (9/2)	25.9	2.35
7	9 (6/3)	46.6	5.17	9 (6/3)	34.5	3.8	9 (6/3)	12.3	1.36
8	11 (8/3)	81.2	7.38	10 (7/3)	129.3	12.9	10 (7/3)	44.2	4.42
9	10 (9/1)	82.3	8.23	10 (9/1)	45.4	4.5	10 (9/1)	26.5	2.65
10	9 (8/1)	63.6	7.06	9 (8/1)	43.6	4.8	8 (7/1)	17.8	2.22
11	8 (4/4)	70.1	8.76	8 (4/4)	64.4	8.1	8 (4/4)	25.9	3.23
12	6 (4/2)	78.4	13.06	6 (4/2)	58.1	9.7	6 (4/2)	24.8	4.13
13	7 (5/2)	74	10.57	7 (5/2)	67.9	9.7	7 (5/2)	26.9	3.84
14	6 (4/2)	68.5	11.41	6 (4/2)	52.1	8.7	6 (4/2)	21.3	3.55
15	6 (5/1)	52.6	8.76	6 (5/1)	42.6	7.1	6 (5/1)	17.4	2.9
16	4 (1/3)	42.8	10.7	4 (1/3)	29.9	7.4	4 (1/3)	11.9	2.97
17	6 (4/2)	30.3	5.05	6 (4/2)	27.5	4.6	6 (4/2)	21.3	1.83
18	5 (2/3)	24.9	4.98	5 (2/3)	34.5	6.9	5 (2/3)	6.9	1.38
19	4 (3/1)	61.1	15.27	4 (3/1)	66.8	16.7	4 (3/1)	22.4	5.6
20	5 (3/2)	67.2	13.44	5 (3/2)	71.2	14.2	5 (3/2)	21.9	4.38
21	6 (5/1)	60.7	10.11	6 (5/1)	61.2	10.2	6 (5/1)	20.4	3.4

22	5 (2/3)	45.8	9.16	5 (2/3)	77.8	15.6	5 (2/3)	27.1	5.42
23	4 (3/1)	29.2	7.3	4 (3/1)	33.9	8.5	4 (3/1)	11.4	2.85
24	5 (4/1)	49.3	9.86	5 (4/1)	66.1	13.2	5 (4/1)	20.3	4.06
25	4 (4/0)	29.8	7.45	4 (4/0)	35.6	8.9	4 (4/0)	11.2	2.8
26	3 (2/1)	11.5	3.83	3 (2/1)	34.1	11.4	3 (2/1)	4.5	1.5
27	3 (2/1)	27.8	9.26	3 (2/1)	43.5	14.5	3 (2/1)	11.5	3.83
28	4 (4/0)	3.9	0.975	4 (4/0)	23.1	5.7	4 (4/0)	2.8	0.7
29	2 (1/1)	42.3	21.15	2 (1/1)	44.4	22.2	2 (1/1)	24.5	12.25
30	3 (2/1)	63.9	21.3	3 (2/1)	22.4	7.5	3 (2/1)	32.3	10.76
31	17 (13/4)	72.3	4.25	16 (12/4)	121.2	7.5	15 (11/4)	41.9	2.79
32	3 (2/1)	59.1	19.7	3 (2/1)	78.5	26.2	3 (2/1)	32.5	10.83
33	2 (2/0)	1.4	0.7	2 (2/0)	3.6	1.8	2 (2/0)	1.1	0.55
34	3 (3/0)	41.8	13.93	3 (3/0)	66.1	22.1	3 (3/0)	24.5	8.16
35	3 (3/0)	2.4	0.8	3 (3/0)	11.5	3.8	3 (3/0)	3.8	1.26
36	3 (2/1)	29.1	9.7	2 (1/1)	48.7	24.3	3 (2/1)	20.3	6.76
37	3 (3/0)	6.5	2.16	3 (3/0)	12.7	4.2	3 (3/0)	4.5	1.5
38	11 (5/6)	12.9	1.17	11 (5/6)	24.1	2.2	10 (4/6)	5.9	0.59
39	5 (5/0)	4.5	0.9	5 (5/0)	5.2	1.1	5 (5/0)	2.1	0.42
40	4 (4/0)	5.6	1.4	4 (4/0)	5.9	1.4	4 (4/0)	2.4	0.6
Total	**266**	**2047.4**	**8.31**	**263**	**2248.3**	**9.53**	**261**	**861.3**	**3.6**