

SSR Primers

SUCCESSFUL
UNSUCCESSFUL

Scaffold	C.r. Start	C.r. End	Repeat	Primer 1	Primer 2	Approximate Annealing Temp. Primer 1	Approximate Annealing Temp. Primer 2	C.r. Product Size
1	35154	35227	GAG	GATAGGAATTGCAAGAGTGGGGC	AAGTGCAGCAGTCTGGTGATGTG	65	64	237
1	98231	98359	CA-AC	GACCCCTTCTCTTTGCAGTTTGAA	CCCTAAAACGCTTCTGTATGGCAC	64	64	256
1	113240	113301	GT	AGCTATGCACGGCATACTACTCCC	AAATGGAAATGGAAACGATGCAAG	64	65	215
1	170656	170715	GCT	GTAGCGCATGAGATCAAACACAGC	TGCCTTTCTACCGCACACTAAC	65	64	284
1	213015	213080	AC	TCACCCCTCTAACCCCTCTGTGTA	CAGCGTAGAACCTTCAGGAAGAGC	65	64	252
1	225547	225586	CAG	ATATTACGCCTCTCCGACAACAGC	CAGCTTCTTTGTGCGCTTGACTT	64	64	272
1	260619	260737	CA	GCTCTTATGACCACTCCCATCACA	TTGACTCCTAGCTCCTCGCCTATG	64	65	258
1	277728	277832	GT	AGATGCATCATTTGATGGGATGAA	ACTTCTCGTTGGAGAACCTTGACG	64	65	219
1	348007	348046	CAC	GACGCGAGATAAGATACAAACGCC	ATGAACATGCCATCAGTGAGAAC	65	64	244
1	518890	518953	GT	CTTGAGCTCATCTCCATCCCCTTA	CTCTCTATGTCCATCATTGCGACG	64	65	269
1	533361	533420	GT	AGAAGGTCTCAAACATCCGTGTGC	TCATAGCGACCATAGGTTCCAGGT	65	65	279
1	607573	607622	TG	CTGGGCGCTGTGTGTAGAAGTAA	CAAGCAACTGCTGCGAAGAAAGTA	64	65	231
1	633424	633521	TG	TCGTAGATAGGTAGGGGCTGCAAA	ACTGGCCAACCTCCATGAATCATT	65	64	281
1	645472	645526	CA	CAATCTTGGGACCACACTCG	AGCCCGTACTGTAAGCCCTTGTA	64	65	276
1	664909	664958	GGA	GACAAGGCATCTCACTCTGACTGG	GTAACAGTCTCCTGTCGTGCAGT	64	64	261
1	814477	814568	TG	GTCTCCTCGTGGTGGTGGTTAAAA	ACGCATCGCTACCTCTCACACATA	65	65	271
1	902655	902701	TG	ATGCCATGAACGTAAACAGCATC	TTCCTTTTACCCCTCGTTTGCTT	66	65	122
1	904203	904272	GT	GTGTAAGGCGGAAGTCTCAACCAC	CAATCTCGCATATAAACATGGCCC	65	65	292
1	971183	971259	GCT	TTACTGAGCAGGCATAACTCCCGT	CTCCGTCCGTCTCTGAACTTAACC	65	64	296
1	1098320	1098368	TG	AGTAGCACAGTAGGTCTCGACCA	CTTTCATGATGATGGGTGAACGC	64	64	294
1	1123309	1123358	GT	TCAACTAAATGACCATCACACCGC	CCCAATCGTCTACCATTTCATA	65	64	234
1	1269032	1269123	AC	GAACACAAACGTCAACGGAGGAT	ACAGCTGGCCGTGTTCAAGTGTGTA	64	65	267
1	1536883	1537038	GCCT	CTGTTCTGCAGTTCGTGGTGAG	AGAAAAGATCGCGATTCCAATGTC	66	64	265
1	1591289	1591343	TG	CGTGTGTGTGCAATATGTTGTGTG	GGTGTCAACGCTAACGCAAAGAT	64	64	159
1	1593923	1593974	CCTC	TGATAAACCGCTCCATAGCACAAAC	ACCCGCAGGACATCATATCCAC	64	65	290
1	1822001	1822136	CACG-CA	CAAATCAAGGGGGTACCCTAATCA	GTGAGGGATGAGGGTCTCGTATTG	64	65	243
1	2008936	2009067	TG-GT	AGTTAGGGATGTGCCACCATGAAT	CCCCTTTGTTCTGAGAGAGAGCAG	64	64	294
1	2017922	2018067	TG	CAAGTGGTTTTGACCCAACAGTGA	GTACCTCCTACGAGTTGTGCACGC	65	66	249
1	2105925	2106009	TG	CCTACCTGAAGGTGGGTGAAGCTA	GCTGCAAATCTACTTACAGTGCG	64	65	198
2	27753	27866	TG	TGCCATGAAGAACAGAAACCC	GCTTGGTAAGTTGGTAGCAGGCAT	65	64	281
2	101076	101183	CA	CACTGTGTCGACTGAAAGAGCCAT	TTGTTGGATGCACAGGTAAGGAAA	65	64	279
2	105195	105341	CA	GGTAGTTGGCGAGGCACTCAAAG	GCCACACGAGAGCAGAGTGACC	66	66	291
2	105969	106069	GT	ATCTGCATACGCCAAGACAGACAG	CGTACCGTGCCTGACTTGAGTAAA	64	65	232
2	169959	170040	TG	TGCACTACAATGACCATGAACTGG	ACGTGGTAAACAAGCGCTGCTCCT	64	68	298
2	186433	186487	AC	ATTCGTCAACTGTGCAGTTCGTGT	AGCGCGATTTTCTACGTGCATAGT	65	65	251
2	339488	339551	AC	CATCCAGCAATCCATCAATCTGAC	ACAACAAGCACGACGAGGAAGTC	64	65	150
2	367156	367201	CA	GTCTACCCCTAAACACGCACATT	GCGTCACAACAATCCCACATACTC	65	64	295
2	384923	385033	CA	GTGAGGTGTGAGGCCTGGTCTATT	CCAAATCGACTTCGAGGAATTCTG	64	65	279
2	434895	434948	TG	CCTCAGCCACGTTGTTACCCAG	ATCACAGTCTTTGCGCCTACTTCG	66	65	145
2	672175	672307	AC-AC	AGTTTCGTTAGCAGATTTGCCCAT	ACCACAAGCAAGGTTATCGCGT	65	65	300
2	704117	704174	GGC	CATGAACTCGATGAAATCCACGAA	ATCATTGCCGTTGTTGCTCTGTC	65	65	298
2	811230	811308	AC	CGCCAGAGATATTGTACCGAGACAC	TCTACGGTATGTGCATTCCCTCTG	65	64	291

2	863364	863431	TG	GAGTACGTTGGCGGGTTTTATGTC	CCGTGTGTGTA AACCACTGTGCTC	64	66	187
2	1088742	1088817	GGA	TCCTGATGTCGACACATGGCAG	CTGTGTGTGAACATGCCAAAAG	66	64	271
2	1187074	1187149	GT	GGATATGGCCTGAGACACCAGC	GCATGGGGGATGTCCTGATTCC	65	68	244
2	1197297	1197367	AC	GTATGGCACTGTACTCTCTGGCCC	GTGGAGTCGGTGTAGTGGACCAT	65	64	265
2	1205706	1205853	CA	GTGTGACCGTATGTCTTCCCTTCC	AGAAGCGAGAGCTGCGGGAGTT	65	68	284
2	1279924	1279991	TG	TCAATACCGCACTGGTAGGTATGC	ACAGGCTGTCTGAAGAATGTGCC	64	65	295
2	1467452	1467537	CA	GTTGGAACCTCAAGATGTCGTCCCT	AAGCTTATCGATACGGCTGACTGG	64	64	278
2	1657495	1657534	CA	CACTACCACTCTGCGGTAGCAT	GATTACACGAGATACGGGAAACGC	64	64	141
2	1809285	1809377	TGTG-GTGCCTGC-GTGTGTGC	GTTCCGGCAAGTCAATACCTGGAG	GTGCATGACGACTGAAGATGGAGT	64	64	237
2	1822279	1822325	AGG	GTTCTCATCCATGCTCGAGGAGTT	CCACAGCATCTGTAGCCACACC	65	65	266
2	1873356	1873485	TG	AACTACTGTGCCCTGCTGTCAAT	CAGCAATGCCTTAGCCTCAAGTTT	65	64	297
2	2016475	2016529	GT	CTACGCTATCAACCGGTGAGCAGT	TCAGTGAGTGCTAGCTGCCGTAGT	65	64	150
2	2036355	2036451	CA	AGCACGGTAAGAGATGTGTGGATG	CCTCATGAGCATCAACATCAGTGG	64	66	254
2	2061256	2061311	TG	TCTTCTGGTGTATCAATGGGC	GCTGGTACCGGCTTACTTGGGTA	65	65	247
3	42082	42256	GCAG	GTTTGCGCCGGTATGGTAATTTT	TGCTTTCATGTTCAAACAGTGGG	64	65	300
3	221912	221968	GT	GTGTGAATCGATACAGTGAGGCG	GGTGAGTGGAGCGCTGTACATAT	65	63	239
3	288245	288309	TG	CAGGCTACTCTGCTGTGGAGC	GTGACGGCTTAGCAACCACAG	65	66	127
3	303850	303889	CA	CTACGTTCTGCAAGAAATCTCCCG	TCCACTGACCGCAATGTATTGTTT	65	64	225
3	350192	350273	CA	TACGTCCAGTACGCCAGACCAAAC	CGGACACAGGCGTGAGAAGAGAT	66	67	272
3	430522	430581	GT	GATTGAAGGTTTGTAGAGCGCTAGG	GGGTGTGAGGTGTGTTAGCAGATG	64	65	198
3	460464	460522	CA	GTCAATTCTAGCCATTCTTGCCA	CCTCTGGATGGGGTCAACTTGTAG	65	65	138
3	479895	480015	GT-GT	TGTGTGTTAACA AAAATGCAGACGG	GTCTCAAAGCATCGCTGATCATT	65	64	206
3	606143	606185	TG	CAGTGACGGCAGCAATAGAACAAG	CCTAGGCATAAAAGCACGCTGAAG	65	65	258
3	725454	725530	GGCA	CAGGTACAGCGACACGTTGAGTG	GCTCTGTGCTACCTCTCTCCGCTA	65	65	219
3	765316	765395	CA	CCGGAGTATAATAGTTGCGGCTG	TCGGATCGAGCTGTGATCAATTAG	64	64	265
3	812172	812238	GGT	AGGAGCGTGGGAGGAACATGAG	TATGGCAATACCGACATACCCCA	67	65	155
3	836901	836993	GT	TGTACTACGCACAGTTCCAACGC	TACGTACGACTACGGCCAACGC	64	66	300
3	897765	897816	CAG	AGCAGTTTCCAGCCTGAAAGGAG	CAGCACCTCCACAGGTCAAGTC	65	64	211
3	908231	908283	GT	GTCGTTGTGTTTCTTGTGATCTG	GAAGCGGAGTTGTCTATCCCTGTG	65	65	297
3	984593	984685	AC	TACAATGACCTCAACCGACGCTTA	CGTTGTTCAAAGTGCTGTGGAGAG	64	65	246
3	1126226	1126284	GT	GGTATGTTGTTGATTCCCTCCACC	GGCTGGCAGATGACACGGTACT	64	65	291
3	1349819	1349883	GCA	CCTTGAACAAGGCTTCGACAGAG	AAGACACGCTATAGTCTCGGGCAC	64	64	189
4	51687	51752	GCAG	CCTGTCTCACTTACGGGATGTCT	CTTGCTAGCTCCAGATGAGTTCCC	66	64	220
4	104490	104544	CA	GATCCAGTGAGTAGCTCTGGGGAG	CTTTACCGGCTTACCGGCTATAC	64	65	294
4	190962	191068	CA	GGAGAATTGCATTCCACATAACCC	GGTCGTCGTCTGCATGTTATTTGA	64	65	229
4	269271	269340	CA	CCATGTCAGCCCTTTTTGAGG	AAAACAAGAAAAGCGAAGCTCACG	67	64	289
4	280540	280621	CA	ATGTGATGCCACTACTCTACCC	GATGAGCAAGTAGCCCATACGC	64	67	165
4	383284	383344	GCC	CCATGATGCCGTGCTACATAGAGT	ACCTGGATAACGTAACCGTGCTGT	64	64	288
4	430217	430272	AGC	GTGTTGTCAAAGGCAGAGAGCG	AAACATCCCAGCCAGTTTCATGC	64	66	300
4	493097	493158	ACCA	AGCTACTTAGAGCAGCCCCAATCC	TTTGGGTTCTTGCTTTTGGTTCTG	65	65	190
4	495963	496007	GT	GTTGCAAGGACTTAAACGGCTCTC	AAGAATGCGTTGGATGTTTTGGAC	64	65	285
4	516818	516907	AC	TGGTATTCGCGCTCTCTCGTTTAT	ATACCTAGCCCCAATCACCATTCC	65	65	234
4	734647	734722	AC	CAACGAGCATAAGCAACCGCTC	GTCGACATGTTTGGATTCTATCTGG	66	64	211
4	1008851	1008910	CTG	CTCCCAGTAGCACTGCTCGCCTT	GCAATAGAAGGGAATTCCTCAGCA	68	64	268
4	1147890	1147943	CA	CACTGATGCGCAGGTGTCATTG	AAAGGAGCAAGCAAGTGCTAGGG	67	65	227
4	1187632	1187690	CA-CACACATA	CTACTGCTCCCAGAGGTGGACAG	AGGAGCACTGAAGTAAGAGCACGG	64	65	161
4	1215424	1215465	TG	TCACTGAAATGAACACCGAACACA	GGCCTGCATCCTAATCCTAAATCC	64	64	296
4	1333360	1333532	TG	TCGTGATTGTGTATCCGAAGTGCT	TAACGCTTAGGCAGATGCTACCT	65	64	258

4	1356662	1356826	GT	ACATGTGCACAGAAGGAGGTCCA	GGATGCTGATGTGTACAATTCCTG	65	66	261
4	1470673	1470760	CA	TGAGTTTGAGAATTCAAGTCCAGCA	GTCCGTCTTACCTGCTACCACAT	64	65	279
4	1484670	1484750	GT	TGTGCATTTACACGAAATGAAGGG	GTGAACTCCGTCACTGACATCCAG	65	65	282
4	1486348	1486446	AC	TTGCTGATCACGCATCACCTATTT	GCTGAGCTGCAGGTAATGCGTA	64	65	233
4	1489472	1489537	AC	CGTGCCTGCCATACAAGTAAACAC	CTGCAGGCCAGTTCTTCATCCC	64	67	290
5	33846	33987	CA	AGGTATCCGTGATGTATTCCGACG	TGCATTACTGCATGGTTGTACGC	64	66	268
5	165819	165883	CA	TCTGGGTCTGTTTGTGGGATT	ACTAATGAATCGGGAACGAGAG	64	64	293
5	813732	813829	GT	CACGTCAITTGATCGATCAGCTT	CAGGTATTGGACAGGAATGCACAC	64	64	279
5	980224	980313	TG	CATGGCACAAATTTAAGAGGCTCG	CAACACACCTAAACATACCCCGT	65	65	167
5	1088984	1089023	AC	GCATACTGCTCTGTGCGTTTCTTG	CGAAGAGCGAGAGGTAGGTCATCA	65	66	190
5	1093281	1093335	TG	AGTGCTAGGGTGGACTGATCTTGG	CTCCGTCAACAACACCTGTTCAAG	64	65	260
5	1120088	1120168	AC	AGGGAAATTGAGCAGCGACAAG	TTGGGTTTGGAGTAGCTCTTCAGC	64	65	233
5	1259296	1259347	CA	TACTTGCTCCACAAAGGAAGGTCC	GGCACTGAACTGTATGGTGTGTCA	64	64	290
5	1337109	1337180	GT	TCTGTGATAGATCGGAAGTGGCCT	GCATCCCAATCAATAGTGTATGG	65	64	296
6	305282	305326	GT	CCCCAAATTTCCAAGATCCTCAG	ACTGCGAAGCAGAGGTACAGATGA	64	64	295
6	606003	606095	CA	GAGTGGGATAGGGCAAACCCTT	CGGTAGGATAGGTGTGTTCCGATG	64	65	233
6	764939	765096	AC	CCACAATTACCGAACAGACACAA	GACCCAGAAGTGGTGAGAGGTT	65	65	264
6	820459	820511	CA	CGCCTTTGATGGACCCAGACTC	CCCTTCGACCTGTCTTCAAGA	67	64	273
6	848128	848189	AC	TGCCATACTTCTACTGCTGCTG	TCTTTAAATTGACTGGCTTGGGGA	64	64	138
6	1072958	1073007	GT	GGTCTCCAGATGCTTAGTTGGTGC	TCGTTTCCGTACTCTGAACAAGA	65	65	283
6	1085562	1085616	CAC	CAGGGTGGGTGACTCGACAGTAG	GCGTGTGGTGGTGCAGTCAGTTAT	65	64	183
6	1209729	1209872	CA	CAACCCTGGATGATGCTTTTCTG	GTCTGTTCCGTATGTTGAGCTGG	65	64	271
6	1348798	1348889	TG	CACGTCCAGCATCAGGTCATCTAT	ATGCTTCAAGTCCCCAACCCAC	64	66	300
7	36528	36589	GT	TTTTGTATGGAATGTAGCGTGCTG	AGTGTGTCCAAGGGCTTACAGTCG	63	65	294
7	113987	114039	GT	AGCTGTGAACGCGCTTGTGTGTA	TAATGACGTCCAATGCACTACGG	67	65	203
7	361397	361441	AC	GAAGTCCACTGAGCCCTGGTTTT	CGAATGCGGAGAGCAGTATGTCTA	64	64	188
7	466916	466994	CA	CACGACATGCAAGTACGGTGTAGC	CACACAAAACATCTACCACACG	65	64	295
7	484511	484552	GCT	GCAAAACGTGAAGACAGGAGGAGT	AGCATATGTGGCTGCTCGAATG	65	64	241
7	519469	519529	TG	ATTACCAAATTCATGTGGCGATGC	GCAAGACGTCCGTGCTATATGTCG	65	66	300
7	522430	522525	CA	GGTTTTGCCAGATACCTTGCTCAC	GGGATACGGTTTTATCAGCGTCAG	65	64	285
7	554204	554286	CA	CCTGTACTTGTGGCACTCGTGAGA	GTTACATTCATGAGCGGGATGGTT	65	65	186
7	669159	669215	GT	CCTCCTACGTACCCCTCTCACATC	CATGGTCAACCAATCTCCATACA	64	65	281
7	974398	974447	GCT	GTTGGAGCTGATGAGTTCGACCA	TTGTTAAATTCAGCTCGCACGATG	65	65	299
7	980995	981050	CA	ATATCTGTGCCCTTTAACGGCTT	CTCTTCCATGACAGTCTCTTCC	64	64	196
7	1223251	1223337	GT	ACTGTGCTGTTGCTGACCTAGCC	ACAAACTCCGGGACTGCTCTCTCT	65	65	269
7	1269781	1269906	GT	AGCTCCGCGTGTGAAGCGTACT	GGTGGTATTGTGCTGCTTGGATTG	67	65	248
8	17554	17637	TG	AGCGGATGTTTCGTTACTTGCTGT	GACACACCCCTCACTAACCAGAC	65	65	286
8	80081	80148	GTG	TGTCTGACTTGCAAAGGAGTGGAG	ACAGCATGTATCTTCGCAATGACG	65	65	275
8	135341	135415	TG	GTTCCACTCAAACGCCACACTACA	GCATACAAGCGTGAATGAATGGTC	65	64	284
8	191618	191765	GT	ATGGCTGCTAAACACGTACACAG	CGGATGTACGGGTAATGTGATGTC	65	64	280
8	335574	335633	CCT	AGGCAGTGACCAGTCCCGATGAC	CTAGCGCACAGACAAGCATTGG	69	65	253
8	568169	568223	CCCT-CCTCCCT	AAGTGAGCAAATGAAAGCGAGAC	GACCAAGACGTTCTGTATCAAGGT	65	65	239
8	614730	614802	CA	TTTTGTCTGAGAGAGTGGTTTGCG	CACTGTGTCGGCGTTTGACATC	64	66	294
8	625983	626047	CA	ACGTACTGCTTGGCGTCTTGCT	GCATCCACAGGAAGGCATTCTAAA	65	65	178
8	801765	801835	GT	CCGAGTTCAGGGACACTACAAGT	AACCAAACACACGGTACATGTTGG	64	64	223
8	873750	873790	GT	ATGACGAAGTAAAACGCGGGACTA	CAGTGTGTGTGCTCATGTTGCAT	64	65	298
8	972012	972135	AC	AGGTATCCGTAATAAACCGGCG	TATCATGCAATATTTCTGGGGC	65	64	254
8	1088595	1088651	TG	CAAGCAGCTGATAATTTGACGTG	CGTTATCAGCGGACAGGGACTC	65	65	298
8	1152615	1152664	CA	TGGCTCTCAGAAGTAACACACGCT	TGCGTTAATCCATACCCCTGATCT	64	64	233

8	1170205	1170276	GT	GCGCCGTGTTCAAAAGGTAGTAG	TACCCACAACACGTACCGTAATCC	66	63	290
8	1202383	1202451	CA	CTTTGCACACACTCACTGTTCCGG	GTACTIONCGCCCGCTTGTACTCC	65	66	299
8	1225302	1225436	GT	CCATCGGCGTTTCTTGTAACATC	CTGTGCGCGTGTAAGCTACAATTT	65	64	242
8	1244613	1244701	TG	ACAGCCAGCTTGGTGATCTCGTA	GTATATCAGGAGGACGTGCGGGTGT	65	65	252
8	1245049	1245101	CA	CTAACCGCTGCCTGTTCAATCATC	AGCTTCGTGCAAACAAGCTGAGT	66	64	267
8	1266453	1266569	TG	ACCAGCAAGTGGGTGCATTTTT	GTCACTGACATCATCACTCCCACA	64	64	212
8	1272320	1272378	TG	CCTCACCTAGATGCGCGTACAGT	TTCATCTCGCGTTCCTGTTAAAT	64	65	254
8	1304306	1304365	GT	GGCATAGCGACGGAGACTACC	ATGTAGAGGGATGTGACACGCAC	67	64	249
9	3778	3837	AC	GTAGCACCATATGGGTGGAGTGG	AGAACTGCGCCAAGATTTGCACG	64	69	278
9	9554	9657	CA	ACCACTCCTTCACTACCAAACCCA	TTGTTCTTTTCAAGACAACCTGCT	65	65	295
9	59801	59909	GT	CTGGAGGGCCAGGTAGCCACAGC	GATTCTATTTACGGTACCACCGC	69	64	267
9	319779	319826	GTG	CTACCTGTGCGACTTCCTTGAGC	TATAACGTCCCCTCATGGTCTTGG	64	65	261
9	320922	321001	CTGC	AACAAACGTGGTGTGTGCGATGG	AGGAGTTGCTGTTTGCTACGGTG	65	64	299
9	324592	324637	GT	ACCACAGCAGCCTCAAGGTAGGT	CAGGCACGGATAGGTGTAGGGTAG	65	65	218
9	438069	438117	CA	GCACCTTACCCAAAGCTCTCAAG	CGCAGACTTGTGAGGGGCTAGT	64	65	123
9	442180	442255	GT	TGTGACTACAGCATATCCACGGG	CCCATCCAGCCTAACCCATCTAGT	65	65	222
9	456640	456716	GT	GTTACCGTACGACAGGCAAGAGC	GATGAAGGACCAGGTCTAGTCTCA	64	65	198
9	468136	468240	GT-TGTGGTACA	TCCCACACCAGTGTGTTTGATG	TATTGTGTATTGCATGCGTTGGGA	65	66	297
9	545803	545851	AC	AAATACATGGCACGCACTACATGG	GTCCTGTTTGTTCATTGATGTCC	65	64	213
9	561561	561639	AC	TGCTTATGGGACAGGGATTACAGG	CCTAAGGGTGTGCCTAAGGTGTGT	65	64	247
9	612954	613042	GT	CTGATTCCTATCCGTTGCAAGCAC	GAGTACTTCCTGGGTGCCATTGTG	66	66	270
9	679014	679063	GT	GTGGTGCAGAACCTGTCGTACT	TACATCCGTGATGATGATTGAGCC	64	65	224
9	686515	686578	GT	TTCTGCAGGAAGTTGTAGTAGCCG	ATACACGCAATCATACTGCCCT	63	64	219
9	687919	687984	CA	GTGAAGAGCCAGATGCGTGACC	TTGAAACAGGATGAGCGTACGTGT	66	65	253
9	733472	733523	TG	GAGCAGTCAACCTTCCAATCATCC	ATGCTCCCTGATCACCCACCTC	65	66	285
9	798267	798350	CA	GCAGAAGCAGAGAAGCGTACACAA	CTCACTGGGGTTTGGGTGGTAG	65	64	244
9	830968	831067	AC	ATGGCAGTAGTGTGTTCCAAACCA	GGGACATGAGGGGAAGTAGAATGA	64	64	299
9	894915	895005	GT	CTTGCAATAGCAAGCCTAATGGGAC	CAGTCAACCATCACGTTTTTACC	65	64	270
9	957447	957629	CA-AC	CCTGAGATTTGCGTACGCTTAC	AGGCGAGGCCCATAGGTTGTATT	65	65	284
9	1009090	1009191	TG	CGACGGCCAATGTAATAAACACA	GATCCTCTGAACCCCAACTAGTGC	64	64	294
9	1028755	1028865	GT-GCGTGT	AGGAAAAGGAGAGTAGAGCGCGAG	ACCCGAGAGGGTGTGTAGTGTAGG	65	64	221
9	1248863	1248994	TG-GCGTGC	GACATGAGTGGAGCCGAGTTCA	CAAGGGAGGTGAGCAAACAGTTG	64	65	267
10	126830	126910	GT	CTTTGACAAGTCAAGAAGTCCCA	AGGCATCTACGGTAGGCATGTGAT	64	65	186
10	233442	233496	GT	TCTCAGACACCACGTCTGTGTTT	TCTAGATGCATACTGCGTTACGGG	66	64	182
10	258534	258611	GT	CGGGAGCACTACTTCACTCAGACC	ACCGCCACAGAAGTTAAGCATACT	65	64	229
10	305146	305199	CA	CTATCCCCTATCATCTTTGGCTG	GGAACACGTAAACAGACCCGGAT	64	66	228
10	398179	398292	TGCG-GT	CTGATCCTGAATAAGCAGGGGTTG	CACCAAATGACCTTCACTGACAG	65	64	300
10	506010	506076	CA	GGAAATACGCAAAATAGCGAGCAC	ATTGTTTTTGCAGGTCCTGTGTT	64	65	297
10	509735	509792	GT	TGAAGCTGAGTGAGGTATGCTGCT	CGTATCGTGAAGATCACACACGC	64	64	292
10	557310	557380	GT	AGCTGGTACCCCAAGAACCAC	CTTTCCAGTCGCCCAACCTCAT	65	66	269
10	589053	589094	CA	GCGAATGACACACCTTCCACATAC	CCTACCTCAACCCCAACATCAAT	64	64	288
10	600141	600187	GA	CGTAGTGACAGGGTTCAACGGAG	GAAGTAGAAACATGGAGGGCCTGA	65	64	280
10	646902	647004	GT	ATGCAGGTACCAACGAGAAGTC	GCTGAGTAGGTGTAGGGCAGCAAT	64	64	228
10	681317	681459	CACG-CA	CACTGGAATAACATGCGAGAATGG	AAGCGAGCGTCTCTTAGAGCTGAC	64	64	289
10	712308	712374	GT	CCTGGTAGAAGCCCTGACGTTG	CCACCTGGCAGCTCTGATTTAGTT	65	64	215
10	749574	749657	CA	AATACATAGGGGGACATCGGGAAT	GTACAGGTCTGATTTGGTTGGAGC	64	66	292
10	804884	804926	GT	TGAGTCTGCATAGGTTGCATTTCA	CCGTGGGTTGTAGGTTCTTGATA	66	65	278
10	807180	807225	GT	AGTGAGGCCATACATTACCATGA	TGTTGTACTCGTGATGCCGTAGGT	64	64	288
10	818100	818165	TG	TACCCATCTGAGCCAGCAGATAC	TCGCAGAAGACACATACTGCTCTG	65	64	131

10	820993	821051	AC	AGGTCGGACGCTTGACGTAAGTAG	GGGACTACCTGAAGAAGCGGTGTA	64	64	170
10	867680	867727	CAG	GAGCACAGATCGTTGCAGGAG	TGCTGCTGGCTTCGCAAACACT	66	69	283
11	543	583	GT	ACCTGGAACAGCTCATCTACACC	GTGCCCCAGGTCTGACTTAAACAT	64	64	274
11	61711	61833	AC	TCCTGATAACATAGGTGTTCCGGTT	ACTGTAGTCGCGATGCATGAAGTT	63	64	279
11	82626	82688	AC	TTCTCGACAAAGTGTCCCAAT	CATCACACGCACAATACCACAATG	65	65	216
11	384907	384971	CA	TGAAGTGCAAGTGGCTTCTCAGC	GACGCCATGATGTTCTGTCTGAGT	65	64	262
11	416891	416980	GT	CGTATGCACCTGCATCGTGTAT	ACACGCAAAACAGCCTATTCCAT	65	64	231
11	573022	573114	CA	AACAATGGTGTCCCAAACGTAGG	AGATGTCGCCCGATGTGTTGTC	65	66	215
11	710613	710670	CA	GGGTTATAAACGAAAGGTTTGCCG	GTCAAGGTGCTCATCCTGTGAGTC	65	64	158
11	806669	806715	TGC	ACGGAGGCCAGGATGTCCATGT	ATACCTTGTGGGACTGCGTGTCCA	69	68	289
11	825051	825095	CA	CTCACCAGCATTGACAGCACCAT	TTACGGGCACAGTATGACAGTTCG	66	65	116
11	826632	826704	CAG	AGGACGGCGTTTATGATGTTGAAG	GACCGACGTAGTCGCCACCATT	65	67	242
11	836815	836885	AC	CACGCTCTACAAGCCTCACACAAC	GGCACAGACAGACGACATGAGG	65	65	176
11	864087	864182	GT	AGGTCCTTGTGTTCCGAGTACAGC	GTGTGTACCATGACTCGGGCATT	65	65	245
11	895457	895543	CA	AGGAGCGTGTGTATTATCCAAGA	ACAGGACTTCAAGCTAATGCTGGG	64	64	275
11	898948	898998	CAG	TTTCTACAGGAAGTAAGGCCGAG	TGCACGTAACCCTAGCTACTCCGT	64	65	216
11	899335	899389	GT	CACCACAACAGCCAAGATGACAG	GACGCTGCCATCTATTCAATCA	65	65	225
11	1025841	1025929	AC	TCAAGGATGATTTGGGCCTTAGAA	TGGGTTTGTGGGTAAGTGTGAG	64	65	300
11	1061233	1061320	GT	AGCCCTCTAAGCTGTTCCCTCCCTA	GCTTCTCCAGCTTGTGTTTC	64	64	292
11	1109379	1109448	CAC	AGCATTACTACTCATCTGGCTTTCGAG	AGCGCTGATGGGTTGGAGCTTG	65	69	268
11	1172720	1172820	CA	CCCCTATGCCTCTTGCTCTGTTT	TCACCGTGAGTACATGATTGCGT	64	64	294
12	74012	74055	CA	CTCGCTTGGGTATGTAAGTGCCTC	CAAGTACCAGGCAATCAAGAGGGT	64	64	250
12	226190	226274	GT	AGTAGCCCGGGAGTAAGCCAATTA	GCGATGGATGATCACATTACATT	65	65	242
12	312385	312450	AC	GCAAATACGGTGGTCTACTTGGGA	GCAGGTGGGTACGTCTGTAGGG	65	65	157
12	379987	380033	TG	AAGAAGAACATCGACATCGTGCTG	ACAACACGGTTTGTGGGACAAAAT	64	65	201
12	475402	475454	GCA	CAATCTTCTTCGTTCCAGCT	TACTCACAGCGCAGGTTGAGAAGT	64	64	287
12	503636	503700	TG	AAATCCGCGGTGTAACCTCGTTG	AGCCTTAGACTGCTTTAGCGCT	65	64	292
12	534895	534953	TCC	CTCTTGACGCTAATTCCTCCATC	CTACTGTGCGGCTCTACAAGCGTT	64	65	204
12	595311	595389	TGC	AGCTCCATCCATTCCGTTAGTTCC	CATGTCAAGCATCTCTTCAGAGCC	65	64	216
12	654279	654405	GT-AGGTGG	TCCCGCCGACTAAGTACAGTAACA	ACAAGTACCGCTACATCGTGTCCA	64	64	281
12	706835	706954	GT-TG	CTCCGGTCCGTACACCTTCTCATA	GGGGCGTTCCTGGTATTCAACT	65	65	291
12	755708	755749	CA	GGGGACTAGGGAGTAAGCACAGGT	ATGAGCCTGCCTTGTGGTGTAGAT	64	65	264
12	823226	823277	TG	GGAAAACAGCCGTTCCCGTATATT	GAGCTGCTCAACCACAAACTCAAG	65	64	250
12	858006	858047	GCC	ACAGCTGTAGTTGCAGGCCAAAATG	ATATACGTTGACCCATTGACACCG	64	63	236
12	923086	923206	AC	GTGGCCATCCTTCAACACAAGTC	CGCCTAGCGAAAAGTCATATACCG	65	64	281
12	953936	953977	AC	GTGTGCGTGTACAGTATGAGCTGC	CGCAGGACAGTGTACCTACCGTTT	65	65	218
12	1046019	1046092	AC	CTTCCACTCAACGCTTACAGACTA	GACAGGTGAGCCTTCTTACACA	64	65	214
12	1071110	1071165	AC	CCGCCAATTCTGTACGAGTGA	TTGTGTATGCGAGCTTTGAAGAA	64	65	119
13	20173	20253	CA	CAACACACCAAGAAATTGGGTC	GGCCGAAGCTGCAGTACTTTACAA	64	65	247
13	69740	69842	CA	ACACGAATGGATACATGCCTTCAA	CAATCAGCACAGCCCACTTGTGTC	64	65	266
13	99680	99751	GT	TGCAGCAGAACCTGTTTAGAGTGC	CTGCTCTCCTCGTCTTCCAAAAC	65	64	190
13	335480	335572	TG	GAATGAGTGATACTGAGTGCAGCGT	TGCGCTTATTAATGAGTCTCTGCG	64	64	210
13	540981	541049	CCTG	AACAAGCTGCTCAGCCAACACTT	CTTGGACTGCAGGAAGTGGATGTA	64	64	282
13	637340	637432	GGT	CAGCTCGTACAGTAGATCTGTTTGG	AGCTTTAAACCCGCAACTAGGGAG	65	64	268
13	685497	685592	AC	GTATGTGTTACGCGTTATGGGTGC	CTCACAGGTACATGCACAGCAATG	64	64	288
13	717338	717380	AC	AGTGCTCATCTTACAGTAGCGGCTT	GTCCATCAGGTACGACAGGGTTTC	64	65	289
13	754274	754349	TG	AGTTTGAGAGGTGAGCTGGAATGG	GTAAGGCAGTAAAAGCAGCGGAGGA	65	65	192
13	818107	818161	GT	GGCGCTAGCAGCAAGTAAGACTA	CGCTGGTACACGTGAGTAATGGAC	65	64	172
13	982454	982548	GT	CGGTACAACCTGTACTCGCTCTTC	CGAGCATAAAGCACGACTGATGTG	63	66	187

13	1000378	1000493	AC	GGCAGAGTAAGAGCCAGGAGACAG	GTTCAAGTTTGACAATGTGCTCGC	65	65	280
13	1066230	1066298	AC	CACTCCCGTACCTGCTTCTTGAAT	TGGGTGCTGCAATCTCATTACTGT	64	65	217
13	1074742	1074808	AC	AGCAGCGGATAGAATATCTCGACG	GTGGTGTACCACTACATCCGGGAG	64	65	234
13	1086203	1086269	GT	CCCCATGTTACTGCACTGCTTAT	ACACATGGCACAACATTCACTCA	65	64	261
13	1089295	1089364	CA	TTAAGAAGTACGGCAGGGTGTTC	GTGTTCAAGTCGCGCTTTGATGA	64	65	296
13	1121039	1121144	GT	CGTGTTCGTGTTTCGTGTATCGT	CCTGCTCCTTACCCTCTTGCACT	65	65	199
14	204426	204473	GT	GACTCATATGGGACGAGCAGATG	CAGATGTGCCCAATAAGTCAGG	66	64	214
14	247251	247304	CA	AGCCACGAAATACAGAAGCCAAAA	TAGCAGGTTTAGTGCCCGAGGTAA	65	65	244
14	348357	348428	GT	TGAGAGTATTTGCGGCTTTGAACA	TCAGCTTATTCTCATTGGCATCA	65	65	217
14	438673	438798	TG	ACCTTGAGAGCGGTGAGGTAAGT	CCTTTGTCATTCTCAAACACACG	65	64	287
14	474123	474226	AC	TGGTACCAGCATGTAAGCAGCGAT	ATGTGCTCACACAGATGCCGACT	65	66	292
14	484975	485092	AC	AGGGTTTGGATATAGGTTGGGCTG	CGCTTTCCATCCATCTCAGTCTT	65	64	300
14	598006	598068	GCA	GTCATTACCGGAGCTGACCAGAAT	CAGCAGCGTGAAGCTGAACTCC	64	66	201
14	728626	728679	GT	GGAAACGCTGCATGAAGATGTG	GGTCCCCTTTGGAATCGGTATTT	65	65	183
14	731430	731497	TGA	GCCAAGATCTACGCCGAGTACCT	AATGGCACTAGCTTTAGCCTGCC	64	64	239
14	836762	836815	AC	CATCTCTTTTGCATCTCGTTCGTG	CTACCAACTACCATCAGCCCATCC	65	64	300
14	941895	942059	CAC-GGCACG	ACGACCACCACACAAAGGGAG	GTGTTGGATCCACGACATGAGG	67	64	296
14	1000493	1000538	GT	AGATGGACGACACGGATAGCTAGG	CACCTTAGGGTACTCCCTCACACG	64	65	287
14	1060665	1060747	AC	CTCAGCAATCCCTTCTCCCTTGT	GGATGTGTTGCTGGGGTTTATTGT	64	65	253
14	1166673	1166785	CA	CATCACTCCTAAGCCTTCTGCGAT	TGTACATGCGTGACTGGGTAGAGG	65	65	284
15	45599	45705	CA-GA	TGTCCCGAGTACTTGACCATGAGA	GAAGATCGCAGACCTCCTCAATGT	65	65	281
15	298178	298256	AC	CGTTGCATTATATGTTGGCGTCAC	AGTTGCTGACAATGGAGTTGTGGA	65	65	279
15	576555	576605	CA	CTTTCTGCCTGACGCTCTAACC	AGGATGTGCAAGTCGTACACCACA	65	65	180
15	577117	577178	TGCC	TGTACAATCCCTCCTTCTGTTGGC	GTGTGAGTGGCGGATTTGGAATAC	65	65	258
15	711410	711466	GCA	AGACACGCTTTCCAGTCGTAGAA	AGTGCAATTGATGTTGTCTGCGTT	65	65	281
15	842458	842539	AC	ACGGCTGTACTCACATACCAGC	CTGGAGCAGCCACTCGTACTGTT	64	65	267
15	882302	882404	CAC	GGCAGATGTTTCTCGTTTCTCGTT	GGAAAGCCTGGACATCAACCTATG	64	65	300
15	921411	921477	CA	GATACAAGGTCTTGAGTCAACCCG	CCTCTGTACCTTGATGCTGTGTGG	65	65	269
15	998242	998296	TG	TGTGTGAAGCCAAGCTAAGACTGC	CACACAAAAGGCTCACACTGCAT	65	64	131
16	32049	32092	CCT	ACATCCCTGGTGGGTGGTAATG	GCACCTCACTAAGCCACAGGTTG	65	65	263
16	60809	60856	AC	CAGAACTCAATTATGTTGACGCGG	TTCAAACAAGCGTCCGGGTAATAT	64	64	273
16	63751	63812	AC	TAGGGTAGTACATCCCAGCCAAA	ATCGACTCGCACCTGTCCAAC	64	65	255
16	314642	314704	TG	GAAAGAGCGCTGGGTGAGTTATTC	AGACTCCTGAGCCTCGCATTACAC	64	65	174
16	458557	458607	CAGC	AGTTGTGGCGTACTTCTCTCCCT	CCTAGCAGCCATTGCTTCCACT	65	64	213
16	467138	467223	GT	ACTCATGACCAGACGGGACACATA	TACTCGCGCTACAGGTCAGACAAA	65	65	295
16	581274	581324	TG	GCAGCAACGTGATCTACAACGTCT	CAATCTCCATACCCCTCAACGTA	64	65	295
16	586347	586515	GT	CTGCAGGCTCAGCCAAAGATTAT	GTGCCGCTGGCATAGGATAGATT	65	66	259
16	595819	595887	CA	CTTCTCTCTCGCATCGTACAACA	GTTGCTTGATGAACTGTGCTACC	64	65	290
16	730098	730174	GT	GGTTCAGGGCTGCTTTATGAACAC	CGGTCACTGAAAGTCTGCTGAG	65	64	230
16	1029866	1029927	GT	AGGAGACAGCAACTGAAGGCTGTG	CAAGCACTGGTTCGGTACGTCA	66	65	296
16	1132554	1132594	CA	AGTCAGGCACCAATAAGCAGGAAG	ACAGGCAGTGGCTTACCGTACAAT	64	65	288
17	214463	214535	TG	GAGGCGTGTATGGTACCGAAATTG	CATCCTGTCTTCTAAACCCATGCC	65	65	297
17	292188	292370	GT-TG	TTTGTGTGTGCGGTTAAACAGCTT	GGCAGGTGTGACTTTACACCAAT	64	65	260
17	453151	453190	GCT	GCGCCTCCTCCATTAAGATAACCT	TGGTTACCAACCAGTACGGCTACC	64	65	280
17	460446	460488	AC	ATGATGAATGTGGGAATCAACGTG	TCACACAAGTCATGCAATGCTACG	65	65	256
17	478168	478226	GT	ATGTGGGACGGCTTCAAACTAC	GTGACACGTACACGTGCCGTAAG	65	64	159
17	561025	561104	CA	CAGATTGTGAATTGCGGTCTCCT	TCTACCTTTCTGTGTTCCACGGT	64	65	250
17	596608	596726	GT	CTTCCCTTGCACACTGAGAGCCAAT	GTCCCTCCTGCAATGAACTGCC	65	67	261
17	818538	818602	TG	CGGTGCCCTTCGAGTCTTCTAC	CGTGCGTTTTATGTTTCGATACAGG	65	64	238

17	863580	863679	CA	CCAGATACACGATTTATTGCCAG	CATAACAGCCTCCACTTTCAGCCT	64	64	245
17	904620	904692	CA	GCAGAATCCATTCAACACCGATT	GCTCTCGTCTTCATGTGCGAAAAT	64	64	275
17	932040	932130	AC	AAGGAAAGCACCAGGTGGAACAT	TGTGTACCCATAGTGAAACACGGC	65	65	260
17	934552	934708	CA-CA	ACGCCACATGCCTTTGTTTTATTC	CAAGGTTTGAGCGGTAGCAAGTG	65	65	293
17	948509	948583	AC	AGGTGACCGAGACACAGACGAAG	TTTGTTCGAAACATGACATTGCCT	65	64	248
17	953384	953580	CA-CA	CACCTGGCAAAGCAACTTGTCTA	CCTGGACAACCACCTTCCTAAC	64	65	278
17	1113749	1113824	GT	CCCCGTAGATTACGAACACGC	ATACCATTCTCACCGCCCTTAT	65	66	278
18	62094	62142	GCC	CTGCAGACAAGGCTCCATCAG	GGACGGTAGTAGCAGTCAAGCTGT	66	65	234
18	87557	87650	AC	CACATGCATACACCCTGCCT	CCTCTCGCTCCAGGTAAGTCAAT	65	66	297
18	344350	344413	ACC	GCCACTACCCTTGTTGCTATTCA	CGGCTATGACAACTTTGCTTTCC	65	65	159
18	393316	393500	GCA	GGACAGGATGCCCAATCAATG	CTTCACCGACAACGAGGCCACT	67	67	295
18	588699	588755	GT	GTGGGGTGTAGCAGTGTGTTGA	CAAGCGCAGCTACATTCCACATA	65	64	179
18	626605	626644	GCAC	TGACAAAGCATCAATACCAGCACA	ATCATGTGGGATCATGTAACGCTG	64	65	247
18	694007	694163	GT	CACGGCATTACCACCTTCATTCTA	TAGAAATGGCAGCGTCAACCAGTA	64	65	295
18	892069	892182	AC	AAGTGCAAACCGCTCAATCCAAAC	TACTGCAGCAGGTATACGACCACG	67	65	284
18	960997	961157	GT	GGAGAGGCCTGGACTCAGCCAT	CTTTGTGAGGTATGGTGCGGTATG	68	64	248
18	1033972	1034062	CA	ACCTGCACGCATAGAGACACAC	AGCAAGCTGGTGTGATCGTATACCC	65	64	279
18	1038656	1038757	AC	CTTGATCAAATCCACTAGCAGGG	GGCGCAATGTGTTTATAAGTCTCC	65	66	277
19	26779	26858	GT	GTCACACGCCAAGGACTGTGTT	GAGTGGTTCAAGTGGGAGACCAAG	65	65	267
19	216232	216309	CTG	CTGCAGCGACTTTGACATTGTCTT	AGCTGCCTCTGCCCAAAGTTCT	64	65	296
19	312325	312373	GT	CATGAAAACAAAAGTGGAGGGTTT	GGGGCCATGTGTTTGTCTTGTA	64	65	206
19	323917	324088	GTGT	GAGGGCCGACTACGAGGAGTTCT	TAGGCATACCACCAAGAAACCAGG	66	65	245
19	559070	559110	AC	CAGTGTGTAGGTTGAGCACAGGA	GAGCCGGAGATGTTTACGTTTGAG	65	65	229
19	646813	646860	TG	GATGCAGGAGGTGGTTAGTTTCAT	TCTTGTGGGAAGGATACCTCCATT	64	64	294
19	768554	768609	CA	GCTTCTCCATATTTIACTCGCCC	GCAGGTCCAGGAAGGTAAGTATGT	65	64	147
19	850556	850612	CA	ACAGCAGGTACGAATGTCAGCAA	AGACCTACACTGTTTCTGGCGACC	65	65	259
19	887139	887228	GT	GAAGCAGTTGTGGCTCAGCTC	CTGTGTGTGTGATCTGGGTCCGT	66	66	229
19	934248	934320	GT	AGTCGGGGCTTTTGGAGTTGAG	AGGTCACTCTGCCCAGTAAATC	69	64	266
19	936219	936301	CTG	AATGTCAACGTTATCGAGTTCCGC	GTGGAGGTGGCTACATGGTTGGT	65	66	290
19	994765	994888	AC	TGTCAACCTAGGTGCTGGGAACAC	CTGCACGATTGATGGTCTCCTTAC	66	64	300
19	1050042	1050166	AC	AGGCAGGGGAGACATAGGTAGGAG	GACCCTATGACCACCATCTGTTCC	65	65	289
20	117076	117176	CA	CAGTACCTGTGACGGAACACAAGC	GCTGTGCTTCGGATGCTGTCTG	65	67	196
20	138960	139003	GT	AGCTCCTGGAAGGTGTCAGTCTTG	ACAGCTTATGCCTACAGCCCACTC	65	64	290
20	140649	140706	TG	GGAGGATGAAGGCAAAGGGATTAC	GTGTGGGTAGCAGGGAGCTTTGAT	65	66	280
20	174781	174909	GT	ATCTGATGCTGTCTCCCCGCGT	CTTCAATGCATCCATCCCCACAT	69	67	275
20	185543	185623	GT	GACTGCACCTCCGACAGCCCT	GCCAAACAGGTAGACCATGGGTAG	68	64	200
20	196711	196821	GT	CTGCCCTGCTGTATGTCTCAAT	CGTTTCAGGGTTGGCTGGTAAAT	65	66	298
20	220887	220959	TG	CAATCAACCACACAGGCTACGAAC	CATGGGGAGTCAGCAACATATCAG	64	64	240
20	308699	308761	GT	GTGCCGCTCTCAGGGTAATCACT	GGCAGTTCCACTTCACTGTCCAC	65	65	254
20	497858	497942	CA	TATACATGGTACCCTCGGGACTCG	CTGAAGGTGCTAGGCACGAAACAT	65	65	203
20	527924	527990	GT	CTCATACTAAACCCATGCAGCAA	TGAACAGGCATAGCGCTTACAAC	64	64	295
20	597424	597477	CAC	TATGTGTTTGTGGCTGGTTGCTTC	ATCATGGTCACCAGTCAATTTCC	65	65	256
20	624616	624671	TG	GGAGAGCCTGATTGCTCTGCAC	TTGAAGAGATACCCTGAGGGGTCA	65	65	300
20	782236	782308	CA	CCGAAACGCATGCTAACAGTACAT	GCTATTATTCCTGACTGGCCGCTA	64	64	256
20	864242	864317	CA	ATGTGTTGTGATCCAAGCCGTG	GAGAGTGCATCGATCGTATGTTGG	65	65	295
20	906085	906179	TG	CAGAACTGCGCTACCATTAGGCT	CGCATCCATCAGATACAAAGCAAG	64	65	205
20	989202	989242	CAG	CGTCACTCCAACGACAACAAGG	AGCCCGTACCCTCATGTCTTCTAC	65	64	261
21	7210	7319	CA	CTAAGCCGTGCTCGCTACTTTAC	GTGGCTGCAGGCAACAGTCTCATC	64	67	239
21	149556	149628	CA	GGTAGAGTAGAAGGGGGCAGTTCC	GCTCAGCTGTTCAATGTGGTCAAT	64	64	282

21	364798	364898	AC	TTTGGCCAACAACCTCTACCCAATC	CTCGCGGAGGTGACTTTGAACAG	65	67	300
21	466999	467043	TG	CCTACAAGCCCAGGTTCAAGGTAA	AGATGTGGGTGACAAACTCCACAC	64	64	161
21	932972	933018	CCTG	CCTACCCCAACAACCTACAACCAAC	ACTATCTGCCGTATTGCTGCCGTA	64	65	247
21	959277	959325	GT	TAGCACAGGTTGAGGCCTCCTTAC	CCTGTGCATTTAGGTTTAGAGCCA	64	63	187
21	1000407	1000516	GT	GAAGCTTGAGGGATGTGCGTGTAT	AGGTGTGGTTGTCCGATTTACTGC	65	65	250
21	1006147	1006220	AC	CCATGACGAGGTTAAGCGAGTCCT	CTTCAGCCTGCCAGCAGAAACAT	64	67	257
22	36937	37030	AGC	CTGGACCCAGACTTCCTTGTGATT	CTGCATGCAATTGCGAGTTTATTG	64	65	239
22	92961	93051	GT	TAATTCCTTGACTTGTGCCCCCT	CACCGAAACCAATCAATGCAAAC	63	65	263
22	102820	102920	CA	ATGTAGACTTGGGCTGCGGACTAC	TTTCCTAACACAGATCCTGCGGTC	64	65	297
22	215095	215135	CA	AGGGACTGCGAACTGTCACCTG	TTCGAGAGCTGAAGCAAAACATTG	66	64	165
22	215614	215656	CA	GTCGGGCAGAGTGCAGTTGTAGT	GTCAGTGACACAGATGAGCCAGG	65	64	130
22	262789	262884	CA	GGTGGACAGACTGATCAAACACCA	GTCACCAAGAAGTGAGTGCCATGT	65	64	267
22	444238	444287	CCG	CCCAGGGGGTGTAAAGGAACTG	GCTTGTGCCGTAGGAGCCAGAT	65	66	295
22	471026	471102	CA	CCTGCAGTGCCAACTCTATCTTCA	CCCACCTGCAAATAGTTCAACACC	64	65	252
22	474915	474972	TG	TGTCGTACGGTATGGTAGGTGTCG	CACTCTTGCTCAAATGAGAACCG	65	64	243
22	475774	475857	TG	CTAAGATCGATGTTGGTGCAACGC	CCGCACGTGAAGATATTCGGTACT	66	65	300
22	490267	490314	CTG	TGCCTCACTTTGGGCTAAACTGTC	AGCTCCAGCTGGAGTGATCG	65	66	261
22	546238	546280	CA	CACACTGGTACCAACTGATGCCGTC	GATCAACCCAGTAAGTGGAATGGC	64	64	117
22	636362	636403	AC	ACGCAGACGCACTTATAGTCTCCC	TTGGCAGTCAAACACCAGATTGTT	64	64	258
22	687843	687904	GT	GTCAGAAGAACAACGACCCCATCT	ACACAGGCAGACACAAGTTTGGAA	64	65	293
22	750685	750754	TG	TCCATCATTTCCACCAGGTTTACA	AGGAAATTGAAGTTGGAGTGGGG	64	64	300
22	839268	839320	GCA	CTCCTCCGTGTATCCTCCAAAAT	CTGCTCTACTAACGCAGTTGCTC	65	64	232
22	883484	883594	CA	AATAGCCTCTCGCGACCTACCTTC	CGACACTTATGGTACGTGCTCCAC	65	64	297
22	929508	929610	CA	AGACAGAGCACGTGAAGCTCCTTG	ATGGAGGTGTTTTTCGTGCTGAC	66	64	269
22	942501	942566	TG	CAAAGTGGAGACCTACACGCCATA	CATACCGTTGCTGTGAAAAACCTT	64	65	215
22	964608	964752	CA	AGTAACTCTGTTGACGCCGTCTGG	CTGCCCGCGCACCTATACAGT	65	68	287
22	983334	983417	AC	ACGTGTTGTTGTGCAGCCTACCTA	GAAGGGAGGATGGGAAGAGAGT	65	65	218
23	22404	22465	CA	AACGTACTGTCTTGTGCACGTGTA	GTTCTTGACCTCACCTTTTCAG	65	64	157
23	99293	99392	CA	ATATCCATGCAGCATTAGCCACAG	GTTTGTGTGTGCTCAAACCGTTCA	64	66	241
23	107687	107739	TG	TAGAGTTCGTGACCAACAAGTCGC	GTAAGTTTGCACGGCAGCCTTAG	64	65	274
23	332075	332270	TG	GTACCTTGTGACGCGGGAACAGC	CTCACCAGGTCTATTGCGTGCC	65	66	299
23	492383	492483	CA-CACACC	GGCAAGAGTGAGGTACGAAGAGGA	GGCACCTACGAAATGATCCAGAAG	65	65	296
23	593524	593575	CA	GTGTTAAGAGGCAAGGACTGGACC	CTATCTACCTGGGGTTGACGGACA	64	65	275
23	885943	886112	CAGG	TAGTGCACATTGGGTCTCAAGGAC	GTGGCTCATGGAAGTTTTGGTG	64	64	249
23	894531	894639	AC-ACACGC	GAGCTCTGATGGACAAGCAATCAA	GGTTATGTACGTGCGTGCTAATGC	64	64	265
23	923412	923475	CA	CCGAATGTCCCTCCACATAAG	GACCCCGTAAATCCATTCCAC	64	65	262
23	957715	957779	AC	AAACCAAGCTAACCTAGCAAGGGC	CAGGGTTAAGGTCTCGACACAGGT	64	64	207
23	963275	963369	GT	GATGCTGGACATTGACCTTACCA	CTCCATCCATCCCTCTAGAGTCCA	64	64	255
23	966927	966986	GAG	GATGAGGCCACGGCAGATACGTT	CTGCCAGAGACAGGGACCTTGG	68	67	208
23	1020253	1020374	CA	CGAGGTCTACTGCATCTTCCAACC	AAGTGCTGCATGCGGCTATTTATC	65	65	275
24	128493	128616	CA	CACAGGTGCTACAATGCTTCCG	AATAGGCCCAACAGATTCACTTGC	65	64	284
24	413252	413402	GT	ACACAGGCGTAAACAAACTCTGGG	GAGTACGCCAAGAGAATGGAGCAC	65	65	282
24	461420	461503	AC	ACGTATTGGTAAGTCTGGCGTCGT	GGGCAGCTCAGGACGTTGTCTC	65	67	203
24	542729	542786	AT	CTTGCATTAGTTGGCAACACCAAG	GAGCCGACAGGTTGGTAATACTGG	64	65	293
24	634877	634919	GCA	CCGTATTTCTTCATTTGCAGTGTGCG	CTCTTCTAGTTCGGGATGGTGTGCG	65	65	288
24	682216	682256	CGC	ACACTGCTGCCCTCTGGAATTG	ATATTTCCGGGACTCTGCCGTACA	65	64	283
24	724509	724566	GCA	AGAGAGCTTGTTCGTACGCCGTC	CGTTCAGTGCTGATGACACACG	66	65	278
24	853637	853713	AGC	GACGCCTTCTGGCTGCAAGTCT	CTTCTGCAGTCTCAGCACGCTCT	67	65	248
24	1017758	1017849	AC	CACACCTACATCCCCTGCTTACA	TTGCAGCATGAGGTGATACACAGA	65	65	291

25	50759	50808	TG	CACTCGTGGATGTTGGCATTAGAC	TCTGCGTTATGTTTTAGCACTCCG	64	64	179
25	71795	71870	TG	TGTACCTGTACGTTTGGTCGGAGA	CAGCACCTTGGTTTGAAGCTG	64	66	249
25	89181	89227	CCG	GCGTATTGTTGCGCATCCTTATTT	GGTAGAACACGTAAGTGCCTGTGGG	65	66	182
25	91645	91700	AC	TTGGAGCACACATCAACCAAAGTT	AACGGTGAAGCCAGTGCATTTTAG	64	65	286
25	100428	100476	CA	TTGGAGCACACATCAACCAAAGTT	ATTTAGCGCTGCGTGTTCAGACT	64	65	206
25	201129	201240	GT	ATTGAGCTTGTGGATCCGTGTTTT	GGAGTAGGTGGGTTTGTAGGACC	65	65	282
25	222702	222803	GT	GGAGTACTGGACTACCTCAGGGC	GGCTTCCAACATAAAGGGTAAGGC	65	64	265
25	381439	381495	AC	TATGTTGAGGCGTCTGTGGTGTA	GAGATGCGTGTATCCAACCTTTT	65	64	227
25	460992	461082	CA	AGCAGCCCCACCATGTAGATCAT	GTGCCGGTCTGCTGATACACCT	66	65	246
25	504535	504594	GT	TACCACCAGTTCAGCAGCTCTAC	CGTGAGGCAGGAGATAAGGTAAGC	64	64	267
25	727067	727112	AC	ACCTACACGGCCCTCTCTCCTT	ACCTGATGATGTGGTTGATGTGC	64	64	288
25	756135	756194	TG	CCTCTCAGTTTCCCTCTCTTGCTG	AGGCAGTGAAGGAATGGCATAACA	64	65	299
25	761185	761302	CA	AACCCTGCACGCAGACAAAATAG	CTGTGTGTACATCCAATGCGGG	64	66	299
25	798290	798460	CA-AC	CCTCACACTTTCACCTTCCCTCTC	ACCTTGTCCACAAAGGTGACCTCC	64	66	293
26	98705	98818	TG	GTCAAAGGCAGCAGATCACATCAC	ACACATCTATGTGGGAGCTGCAAG	65	64	297
26	135277	135341	AC	CACTCTTGTGGTCTCGTGATCCTG	ACTACTACACCACGTAGCCATGCG	65	64	299
26	238410	238464	GT	GGACTTCTACTCTCCAACACGGA	GAACAGCGTCTGAGCAGCAGTC	64	64	253
26	243832	243913	GT	CTCATGCTCATCTCTGGTGGTCAAC	AATAGGGAGTATGGGGTTGGTGCT	67	64	246
26	261462	261530	GT	TATGAGGAAAGCGGTCTGGTACTTC	AGGTCGCCGCAACACTTGTATAAC	64	65	281
26	315147	315249	CA	GGTTGGTAATGCGATCTCGGAC	CTGGTGTTCGGATTTGACAGGTG	64	65	194
26	361577	361637	CA	CACCTTCTCCTCTTTTCATTCTT	CCTCGATTACGGTATGCAGTGACA	64	65	258
26	396201	396245	CTG	AGCCGTACGTCATGCTCCGACA	GACGAAATGGAGGTCGACGGTG	69	68	263
26	426751	426802	TG	ACAAACTCAAGGTCTACATCCGCC	CCAATGGCACATCAATTTCATAACC	64	64	147
26	542688	542737	GAG	CTGGACCGACTGGTTTGTGTATG	CAATCGCAATTCAGTCTGCTG	64	66	263
26	557955	558116	CA	CCACAAAACCTCACGCTGTCTA	ACAGATACGTGTGGAGGGCAACG	65	67	300
26	582728	582785	GTG	ATACAGGTGACTCAGGGCGACAAG	GAACCATGCATAACAGCACTCACC	65	64	278
26	654196	654263	CA	GTGCTTTCTAACACGAATAGCGGG	CTGGACCGCTACCTCAAGGAGAAC	65	66	186
26	671127	671222	TG	CAGCTGGAAGAAGTTCATAACGCC	CGCAGCATCTATGTGAGTGAGTGA	65	64	268
26	747383	747436	AC	GTCCGTCATATGAGACTGGCACAC	CTGTTGCGTAGGAGGGAACATGAC	65	66	183
26	798173	798341	TG-GT	TTCATCTTGCTCTCCACAAAGTGC	CAGTCACGTGTATGCTCACCCC	64	65	263
26	843307	843355	GCT	CTGTCTGAGCAGCAGACCCTGATA	CTGTTACCACCAGACCTGTTGAC	65	65	158
26	875324	875397	TG	CGACGGAAGGTGGAGTGAGCAT	TTCGGGCATAAATACTGTGTGTCG	68	65	236
26	895020	895071	TG	CTGAAGCTGGTCTAGTCCAGTGC	CCACCGCTAACAACACGACACTTA	66	65	270
27	267398	267439	CA	TCGAGATACACAGGCACACAATGA	GTCAACATCGTGCCACTCTACAC	64	65	169
27	271343	271467	CA	CCGTCTTGTTGTTAAACCGTTTGG	TAATTCCTGAGGTGTACGGCAA	65	64	292
27	567324	567376	CA	GTCGTCTATCGCCTTTAGCCTTC	AGGCCATGGAGCTGTACATGGAG	65	66	276
27	629145	629194	CCTC	TCAGCATATGCTACTCATGCCA	AGTTTGTTCGTGAGTTCGGCAAG	64	64	285
27	672246	672351	GT	CTTCTCGGGACACAGCTACATCAA	CTCATACAATGCGCTCAGGGAGT	64	64	252
27	677891	677972	GT	GTAGTTGTTCACAATGGGCACGTC	ATAATCAAACCCACCCCTTCCGT	64	65	215
27	773877	773949	CA	TACAGCAACGACCGTAGCAGGTAG	CAGTGGGTAAGTGGAGCGGATGT	64	66	284
27	799834	799875	TG	GGCTGTAGCAACGGACAGGATG	GTCTGTGAGGAAAGTCCGAAGCG	66	66	280
27	812951	813015	TG	CTCAATTGTGGACCTTGTCTCCT	CAGCTGGTTGAGGCTGTAGCTAGG	64	65	291
27	859705	859762	CA	CTGTGGAGAGGGGATGAGGATATG	AAGAACTTGTCGTAAGTCTACGC	65	64	253
27	860182	860246	AC	AATGCTTGGGTGCAAGTCACTCAG	CGCGAGGGAGATAGAGTTAGGTGA	66	65	133
27	860982	861027	GT	GATGCGCTGCATTTACTTTGTGAC	ACACATCCTCCACAAAGCACTCC	65	64	196
28	64061	64116	GCCT	CAAGTCCGAGGGATGGACTGTG	TGCATGATCACCTACGCCAAGTAC	67	65	278
28	84695	84740	GCAG	AAGCACTGTGTGAGGTCTCCCC	CTCACCATGGGACTGATGACAATG	65	65	268
28	196263	196336	GCA	GCATGCCGGAAGTCACTGGAAG	ATGATCGCTGTGAGTGCCTCT	68	65	270
28	207624	207744	GGGA	AAGCATTTACGAAGGCTTGGGTG	CTCACCCATTGTCGGACATGTAAA	65	65	279

28	216326	216367	AC	GGTTCGGTCTCTTATCTCTTGCCA	CAGCGATTGGAATTAAGGGTTGAA	64	65	147
28	218707	218746	TG	GCACCTTCAAAGCAGTCTGTCTA	CTACTACCCATTGCATGTCCCCTC	64	64	294
28	220024	220090	AC	CAGGTTGACTGGGAGCTGTGTCTA	ACCTTTGACGGTGAGCGAAAGG	64	66	274
28	228060	228105	GGC	GGTGACGACGATAGACAGGCGTA	GGAGGTCAGACGCACGGTGAGA	65	69	216
28	311135	311177	CACG	GTGAGTCCTTGCCCTACCAGGTGT	GCTGAAACGAGTGAAGCTAGAGGC	64	64	206
28	346358	346404	CA	TGGGTGCTGCTCATCCACATAAA	GTCAGGATCTGAGGGGAAAAGAT	64	64	272
28	622794	622839	GT	GTCATCCCATAACACAGTGTCCA	TTGCCAAATAACCTTCTTCCTCA	65	64	252
28	829049	829101	TG	CCTGAGCGGAAGATACGTAAATCCA	GAACACGTGTGTTTCTCGCATGTC	65	66	163
29	30861	30912	GT	TTAGCGTCACCTCCGCTATTCTA	TCTGTGTGCAAGCCCTTTAGTGA	65	65	259
29	38118	38245	CACA	TACCTAAGCCTGAGGGCCATGATA	GATGTAGAACGTCTGCGTCAGCAT	64	64	231
29	69156	69282	TG	CTTATTGATGCGGTGCGACTTGTA	TGCATGGGAATAATGAAACGTGAG	65	65	203
29	95119	95169	CA	CCCATTATTGCACTTCGGTACACA	CAAAGAAAGAACGCTTTGGCATT	64	64	288
29	161188	161343	TG-TG	AGTAGAGCTGGTGATGGGGATAGC	CTGTCAAGTTGCTCTGGCACCTAT	64	64	297
29	343698	343824	CA	CCTGCTCAAACCTTGACCATGACG	GTGAACATGTGGCGTGTGATGAT	66	65	286
29	402392	402441	AC	CAACATCGCACTCAACTCACAATG	TTATTATATTCAAACCGCGGCGG	64	64	261
29	483277	483365	CA	GCACTCAGACAAATCACTGCACAA	GGAAAACAGTAACATAACGGAGCCC	64	64	297
29	727550	727648	GT	AACTGATCGAGGTAGGACTTTTCG	TGTAGTAGCCGGAGCCTGCTGTAA	65	66	295
29	838418	838476	AC	GCCTATCAAATCGGATATGCCAC	ACGTGAGAGCAGCGGGTATTCTTA	64	65	266
29	843318	843371	TG	TAGTACTCCTTCAGGTTGGGCGAG	ACACGTGTCAGTATCGTGACCCAA	64	65	192
29	847006	847081	AC	CTCCTTTGGGATCGGAACAGACTA	AGGTGCGAGACAGGATATTTCGC	64	64	168
29	847282	847325	AC	CGAATATCCTGTCTCGCACCTG	TGGTGATGGTAGTTGTGTTTTGGG	64	65	291
30	6347	6412	GT	CCTGCATGATGTGGTGATTGATG	TTGTTCCAGTTGAGATACCTTGCG	65	64	200
30	67641	67810	AC	GTGCACCGCACGTGTAATAGG	ATCCACGTGAATTTACCGTACAGC	64	63	294
30	81141	81256	CA-AC	GTCTTGAGTACATGCGGCTCTTGA	ACCTGGGAGACTTCATCTACGGTG	64	64	222
30	268058	268110	CA	CTTCTACCGGCCGACACTCTAGC	AACTCCAAGGCGATACCTCCAC	65	66	256
30	274035	274142	CA	GCGCGTCAACAACAAGATATCAC	CAACATCCAACCTCCAACCTGCATC	64	64	257
30	383782	383847	TG	ACAAGGAAAAGATAAGCGCAAGGCT	ACTGCACGTGTTTCATGTGGTGTAG	65	64	284
30	403168	403255	GT	ACTGATGTACCGATGTAGGACGGC	TCCTTGATAGCGGCATCACTAACA	65	65	296
30	489537	489726	GCGT-GT-TG	TCAGACTTGAACCAGGCTTGAC	AGTAACTCCATTGGGTGGCTAACG	65	64	281
30	563674	563745	CA	CAACACAGGCTGGCAATACGAG	TCAAACATGGTGTGAAATTGGTCC	65	65	184
30	573319	573370	GCA	TGAAATTGCAAGAAGTCCGCAG	TGATCAGTAGTAGTGCTGGCCTCG	64	64	300
30	604551	604605	TG	GGCTTCTTGTGCTCAGCAATACAC	ACCTCTGCCTCACAACCTGAGACCT	64	64	280
31	11890	11963	AC	CAGCACTCATCTGAAGACACCCAT	TCTTGTCATCCTATGGGCAGTCAC	64	64	296
31	47357	47399	GCA	GCACAGCTGATGGAGATTCTTTGA	GCTGTCACTGCTGTAGCCAACACT	64	65	264
31	130250	130368	GT	TGCAGACTTGCATTCTGACAGAGG	CGTTGGAGCTGACAGCAGTCCC	65	68	282
31	255833	255872	GGT	TCAGTCACAGTCACACTGAACTGC	AACGGATATGGTTTCAGGACTGCAT	64	64	262
31	409327	409409	CA	CAAGCAGTGACGGGACAATGC	GTCATGACATGTCCAATCCCCC	65	65	283
31	514732	514772	CCAC	CCAACCCACGTCGTAGCGTACC	ATCTTCAGGACGGCAGATGAGC	67	65	268
31	549455	549505	CA	ACTCGCACATGTTCTACTTGACG	TATCACTCCGTCCCTCACACGAAT	64	66	288
31	658633	658716	CA	CGTCTGGCCTACAACGTACCCTTA	CTACATGAGCGTCGACCCCTGAC	65	67	284
32	191105	191190	GT	ATTGCTTACCATACTCACTGGGC	CGCACTTGATAAGGACTGAGCTA	64	64	284
32	224139	224179	CA	AACCTCTTTCAGCTAAACTGGGGC	TCTGGATCGAGATGGAGGGTTAAG	65	64	214
32	233971	234051	GT	GACCTGGCTGGTGAGAGAAGAGAG	GTGAGATGAGCTCGTTGGACACAC	65	65	211
32	240885	240958	GT	CATCCTCATGTGGTGAGGCTCG	ACACAAGAAGATTGACGGCCTAGC	67	64	288
32	283190	283273	CA	GTAAGCACATCCAGCCAAAGACAA	TTGAGCGCCCACGTAAGAGTAAAT	64	65	274
32	438225	438290	AGCC	AATGGATCGAGGTAATGGCTGTG	CGTTGGGGCTGTGCTATCTATTGT	64	65	266
32	519902	520018	CA-TCACGCCCCG	CACGCGCATACATTCAAACATACA	CTTGACTTGCAGAGTCTGGAGCTG	64	65	249
32	552287	552357	TG	GGGTAGTCTTCCAGTCCGAACAA	AGAGCATCAGACATCACCCAACG	64	65	287
32	565831	565915	CA	TTGCCTTTACCTCAGCCTTATGC	GGATGGTGGTAGGTGTGTGGGTAG	64	65	196
32	636420	636480	CA	CATGAGGGGCTACAGGGCTAGG	AGGTGGTGACTAGCACCTTGGG	66	64	246

32	649655	649732	TGC	GTCAAAGGTTGTGCTCCTCGTGATG	CTCCATGCATCTCGTTTTTGTCTC	65	64	275
33	83621	83691	GT	GTTGTTTCGTCGTGTGCATGAGAG	ACTGCAGCGGACTTTAGCAGCAC	65	67	138
33	212104	212216	CA	CCTGGAAAGATTCCATGCATCAC	AGCTGGGCACTGAGTTCATGT	64	65	275
33	356846	356890	AC	ACCGGGGATGTGAAGATTAAACAC	CAGTGGCAAGATACTCAGTGCTGG	64	65	278
33	358592	358654	TG	AAACCCACAAGATAGACAAAGCCC	ACCCAAATTCATCCATGCTCTA	63	64	221
33	468700	468783	AC	TCGAGGTGGGGCTAAGAAGTACAC	GAGAGAACAAGAGGAAAGGGGTTGG	64	65	278
33	650550	650637	AC	CAGAGTTGCGGAGATCACCAGTTA	GGGCATGCTAGCTTGTTCAGTA	64	64	299
33	684399	684462	GT	TGACAGCAAACCATAAACACTTGGG	GAAGATGGAGCATCCACAGAGTGA	65	65	163
33	701323	701397	ACC	CGAAAGGTCTGTCTGTACAGCATGT	TCCGTAGTTGTGCATCACCTGTTT	65	64	271
33	704074	704196	TG	GTATGCGACCGATGCTCTGTGTAG	GGTACCATTACCGGACTGCTGAGT	65	64	292
33	753089	753212	TG	AAATGTTTGTCTGCAACCCACG	CAATACATGAAGCACTGCCTTTGC	66	65	291
34	91086	91136	TG	TGGAAATCGTTGTTGTGATCCTGT	GTATCTACGGCCATAGGCCACT	64	64	289
34	91456	91530	GT	GACTGGGGCTCTGTATCCACCTAC	GACAGGTACCCAGGCCATAACCAT	64	65	266
34	118622	118716	CA	CATCACAGTGACCACACCTAGCG	CTCAATCTCCTCATTGCGTGTGAG	65	65	282
34	131467	131528	TG	ATACACACGGTGGTGTGACGATG	AGTCCGTCACCTGTGGAACACAC	65	65	271
34	343401	343479	AC	ATGCCTAGACAACGTCCCTACACG	GTGCACGTGTGTTACAATGCACA	65	65	200
34	345438	345502	GT	ACATGCTGATGAAGATCAGCTGC	CTGTGCAAGTAAACCCACTTTCCG	65	65	172
34	489577	489624	AC	CTGTCTACGCGAATGTTTTCTT	CCTGTATGTGTTGCCACTTGCCT	64	65	284
34	539334	539416	TGG	GTGTGGTCCGATGACTAAGCAACA	ACACGCAACATAACGGCATGAG	65	65	274
34	606702	606748	GTGC	GCCCTTTGCCTTACCGGTATACAT	ACATAACGGACAGAAAAATTCGC	65	64	280
34	688567	688653	GGT-TGGTGGTTG	GTTGATGAGGAAGATGATGGGGTC	GAACGGTGTACGGCATGTCATC	65	64	270
35	35442	35487	AC	TGTGGATGTCACACAAAGTGAAGG	CATGTCCGTTAGTCTGGTGCGTAG	64	65	216
35	40472	40518	TGT	CTTGGAGCTCTGCAGTACCCTGA	CCATGCCCTTAACGGACTTTTACA	65	65	287
35	106235	106281	GTG	CACAGCGATGACCTTTATGAGCAC	GCTCCCCAGCTCTTACAACTGAA	65	65	294
35	277020	277097	TG-TGGC	CAGGAGCCTGAGTTCAACGTGAT	ATCCACTCACTCCCACCACTATCC	65	64	218
35	460336	460403	CA	CCTTTGCTTGTGCCTCTTATCACC	CCTGGTAGGTGAGGTCTTCTTCA	65	64	176
35	637327	637367	GCA	CGTCTACCGAGACACCACAGTCAC	GGAGGAGCGTGAAGTTTGAGGATA	65	64	206
35	667484	667551	TG	GGAGGAGGTGCTAGAGAGGCTGTA	GTTGGTTCCACAGCGAGATTACCT	64	64	212
35	684892	684938	AC	GGAGCAGAAGGAGTAGAAGCAGGA	GGTGGCTGGTAGGACATGAGTTG	64	65	271
35	686207	686311	AC	CGCACATACACACGGTCTTCTTTC	GCTGCACCTTCTTAGCCCCATC	65	66	295
35	710583	710630	GTGG	ACAACGAGCTCCTGGACAGCCT	GCACCTACTCACTGATGCGTGAT	66	64	164
36	52428	52493	GCT	AAAGGCTCCAAAGGGATGTGAAG	AGCAGGAGTCGCCCTTAAAAAG	64	66	164
36	62017	62103	GCC-GCCGCCGCT	CCTTGAGGGAATCCTTGCTATCCT	GGCTACAGCGGCAATATTGGAA	64	65	286
36	143389	143468	GT-GTGTGC	CTCAGTCACGAGCATGTAGTCCGT	GGTCGTGAGTGCAAGTAGACGAGA	65	65	255
36	345097	345158	AC	CCAGACATGATGTAGCTTGCATT	CAGTAAGCCACGTAGCGGATAAGG	64	65	216
36	479546	479600	GT	GCACACGCAACGGAACAAGTATAA	CTGTTGCGATTCTGTCTTGAATGG	65	65	257
36	481845	482020	AC	GGTTATGAGGGACTGGGGTTAT	AGGTGGTGCCTGTAGGATAGCTC	64	66	292
36	544742	544796	GT	CCTTTGGTGTGTTACTTGACCCAG	GAGGGCTTTTGTTCGCTCTGTAA	63	64	286
37	65280	65350	GT	GGCGGAGAGCTCCAAGTCTACAT	GTGCGTGTGTAACCTCACGGTAG	65	65	265
37	70149	70305	GT	ATAGTGTGAGCTGGTCTCTGGCG	TAAATGTCAAATTTATGCCAGCCG	66	64	299
37	158367	158418	CA	GAGCCATGCACTTACGGTACAACA	AGCCTTGAGCCCCTGTAACCTCAC	65	65	275
37	178685	178741	GGCT	GATGGGACAGTGGTGGTAAAGTCC	ATGGGCTCCTCCCACTATGTGTAG	64	64	235
37	494139	494219	CAGG	ATGCACAGTATTTCAAGCATCGT	ATAAATAGTCGGCCGCGACCTTAG	64	65	264
37	530408	530458	GT	TGTGGAGACCTCCAAGTTGAACAG	ACCACCACAGTACTCCCTTACCCA	64	64	185
37	534181	534305	CCTG	AATGAAGAGCTGGACACTCACACC	AGGTCACTGAGTTGTTTGACGCTG	64	65	298
37	556937	556996	AC	CAGTCCCTCGCTTACGCTTC	CCTACTACGCGGGCATCCACAG	66	68	192
37	558268	558362	GT	TCACACGTCACACTCCACAGACTC	CGTATGAGCGCTTCAAGACAACAA	64	65	285
38	13263	13365	AC	TGGTTGGCAGTTTTATTGCATGAC	CTGCCACTCCATCAATAGGTCAGA	65	64	252
38	141892	141988	GGA	GAAGTACCGCTTTGCGTACGAGTC	ATCTTGCGGGCTTAACCATAGACA	65	64	296

38	379232	379281	CCTG	ATCCTTCCTGTGTGCCATACCAAC	AGCAGCTCCTTGAGGCTGATGTA	65	64	185
38	428785	428848	GT	GACGCTTGTCTGCATCTACCGTACT	CATTGCAGCGCTCATGGATGTC	64	68	268
39	482013	482097	AC	ACCTCCCGAGTTGAGTTACCCAG	GCTCTTGGATCTGTCGTACCTCGT	64	65	269
40	388985	389123	GCT-CAGGAGCAG-CAG	CGCAGGCTCACTGCTGCAAATA	CGAGGCGCTTGTGAGAATGTGT	67	66	253
40	421637	421720		CA	TGACCTTAGCAGCGACCTAAACC	TGCTGGAGGTTGTCGAAATGTCTT	65	66
40	549192	549323	GT	ATGTTGACAAATACGCTCGACCAA	TTCCCGGCTTTTTGCAAGTTAGTA	64	64	288
40	572798	572893	TG	GCTCCAGTGTTTACTGCTGCCAC	ACAGCAGTACTTGCGCTACGGTC	65	64	277
40	605845	605984	TG	CTGGACATGCTCGCAACTACAGAG	CAATCCTGGGGTGTAAAGTAACCGA	65	65	253
42	56170	56211	GGC	ACACCACGACCCTAACCTTCATGT	CACATGGTGTAGTTGCAGGTGGT	65	64	237
42	60598	60666	CA	TACGTGAAGTGGTCAGTGAGTCCC	GTGCTCTCAGCGCATACGAGTAAT	64	64	289
42	65028	65116	TG	CACCGTGTACCTCATCCGTCAG	GTA AACACCCGCTGTTTCTACCA	65	65	272
42	106991	107077	GT	GTGTATGCTGTTTGTGGGGTTTA	ACAGAAAGCCTGTCAGTCCTCCC	64	65	295
42	249167	249275	CA	GTGAGCAGTGTTTCGCTCACTTGAC	CGTTGAGGAATAGTACAACGCACG	65	64	299
42	396018	396196	GT-GT	CGGATTGCGAATTGTTGCGTAGTA	AATCACGCAATGGCACACATAATC	66	65	269
42	470413	470482	GGT	GATGTACATGAGGTTGTCGATGCC	ACAAATCTCGGTTGGCTTCTGAG	64	66	284
43	117491	117567	CA	CTCAACCTGTACTACACCCCGC	CTTCGCTCTCACGTGGTTGGTC	65	66	272
43	164911	164986	GCT	GCAACATCCCACCTACACGACG	GAGCTGGCTCAGGCTATGGTGG	66	67	211
43	184267	184347	GT	CTTGTTGATGGTGTGCTAGGAGGG	AAGTTGGGCTTGAAGCTCTTACCA	66	64	210
43	186343	186411	GCAG	CGTTCATAGTGCTCTTCAGGTCA	GCTGCTGGAGCTACTTGACACAAC	64	64	142
43	193519	193587	AC	GTGCCTGCTGCTCATAGCAGGTT	AAGACTTCATCTTGGAGGCAAACG	67	64	180
43	219325	219371	TG	ATATGGCAATGGTGCAAGTTTCAG	GGCTACCTGTACACCCGTGTTCTT	64	64	138
43	243481	243574	CTG-CTGCTGTTG	TCCTCAGACTCCATGTCCTCATTC	ACTTCGACGACAACAGCAGCGGAG	63	68	211
43	263832	263878	AC	ACCTCACCTCATAGAAGGCGTCC	GGA ACTGATTTAGGGCGCAGAGTA	65	64	228
43	311690	311793	AC	ATGCGTATCTACCCGTTTCCCT	AAGATCTTTGGCGAGACCTCCAAG	65	66	267
43	392225	392265	GT	TCAGGTTGGTGTAGTTGGTTTGGGA	AGTGACGCTTTAAGAGAACCCTG	64	65	177
43	535638	535739	GT-GTGC	GTCCACTGGACGCCAGGTGTTT	CAGAGGTTCCGGGGTAAACTGCTAA	68	64	240
44	57045	57139	CA	GCTTCTCTCCTCATCAGCTCCAG	CGCAATACTGATGTGCGTTCTCAT	64	65	228
44	85261	85307	AC	GACCTGCTATCTCGTCTGCCTCTC	AAAGGTAGAGAACCGGAAGTGCGTG	65	64	135
44	136165	136230	CA	AGTGTGTCTGTGGCGTCGATGA	CGAGTGTTGTTTGGAAATGAGAGGA	66	64	275
44	354672	354735	AC	ACCACTTCCACAAGCCTCAATCAT	ATGTGAATGCATGTGTCTATCGCC	65	65	254
44	385264	385359	TG-TGCG	TCCTGCCGTGTGAACTACTACTG	TACTGTTACGGCACACGTTCCAA	64	65	295
44	432703	432771	CTGC	GTCATCTACGACGCACGACAGGTT	AGGTCGAAGTTGACCATGTGGC	66	65	298
44	606646	606739	CA	TACCAGTCCAGTGCCCTCAACAC	GGTGACGGTATGGGAGGGAGAG	64	65	153
45	234814	234964	CA	CAAACCTTTCCCACCCAGTATG	ACCTGGCCCAGTTTTGCTCTGA	65	67	288
45	282823	282934	CA	TGAGTAAGACAAGCACCCCTGCT	AACCTGCTGCCTTGTGTATCCT	64	65	293
45	454128	454207	CA	CTACTCCCTCCTGTTTCCGTGACT	GCTACCGCTCTACTCTATCCCTGG	65	64	249
45	495691	495745	GT	AAGATAGGAAAGGCCAACACACCA	CACCCAGAGCAACATACAGGCATA	65	65	285
45	497786	497827	AC	CCTTATTTGTTTTGGAGGGAGGG	AATAGATGTTTGGTATGGGCGTGC	64	65	298
45	536106	536160	GTGC	GTGATTTTGTGTGCGGTAGTTCG	AATGAGTCCCACCGTGTACAGCTT	64	65	237
46	10611	10737	CCA	GCAGGTATCGAATGTGTGTGGTGT	GTTGAGGTTGATGAACACGTCGC	65	66	264
46	172618	172688	TG	CTACCTCTTCAACGGTTTTGCTC	AACACTCTCACGTTTTGCGTAGG	64	65	297
46	229682	229726	GT	CTGGTGGATCTGTATGTGGCATGT	GTTCTGGACTGGCAGGACTTAGGA	65	65	120
46	243201	243286	GT	TAAGAGCTTGACAGCAAATCCAGG	AGCTGCCCCCTGGCACTGTATGAG	63	68	297
46	380804	380880	CA	TGATCCCCAGGAGTCTACCTAGCA	TGCAATCACCTTGCTGTTGGTATT	65	64	272
46	398662	398710	AC	GCTAACACTGGGCTGTACGACCTT	GCCTTCTTGTGCTTGTCTTGTGTC	64	64	233
46	414676	414751	CA	CAAGTCCAGTGTGCGAGTGAACCAC	TCATGACCACCGTACATGACCC	65	65	298
46	587300	587341	TG	GATTGTGGATCCGGAGAGAAAGA	CTCACTCCAGTCAGTGCAGGTAGC	65	64	300
46	607170	607273	GT	ACACACAAGCCACCCAGTCAATC	CTGTTGCTGTTGATCATGGCTTG	65	64	255

46	633919	633985	AC	CCTCTTGCCCTCCCTTTAAACACG	ACATCACACCACCCACCGACTG	66	67	295
47	217210	217275	TG	TACAGAACCACCTCCTCACCCTGT	AAATGCTTTAATATGCCCCCATCC	65	64	259
47	218085	218125	CA	CACGGCTTGCTCTATGTTGATTG	AGCTGCATCAGGGTGAGGGTACTA	65	65	279
47	234857	234927	GT	AGCAGGAAGGCGTGTTACATCAGT	CCTTTTTCCCTTTGCCATCCTTAC	65	64	184
47	243133	243175	GT	TTTGTGTCCTGGTCTGAACCTCCA	GATAATTGCATTAGCGTCAGGGCT	65	64	288
47	267725	267781	GT	GATGTACCAGTTCATCGTGGGCTC	CAGTGAAGGTGTTGCGTGACAGAT	66	65	271
47	282358	282442	GT	AACGGCGGTTATGTGCTCGTACT	AAGCTAGGTCCAGGCGTTAGCC	65	65	224
47	322484	322549	TGC	CGTACACTTCGTACAGCACGTTCC	AGCCTACTCGTGCATTGGCTG	65	68	236
47	349075	349129	GT	TGGACGTGTTGTTTTTCGACATTC	GTTGTGTGTTCCATCCCTTAGGCT	65	64	242
47	351024	351064	AC	GTGACTTGCAGGTACGTGGTCAAC	AACGCGCACATTCTAACATAGCAA	65	64	205
47	373065	373122	AC	CAGGCCTGAGTAAATAGGCAACG	GCAAGGGTTGTGTGAAACATTGAG	65	64	286
47	453450	453532	AC	AAAATAGGCTGCAACGACAGCATT	ACTGCACCTCTCAATGACGGATTT	65	65	226
47	566153	566199	TG	CACACACGAGTATCCACCCACCT	AGCGCCTTCTGCTCTTCCCCTCT	65	69	234
48	60770	60858	CGTG-GT	AGCCCTTGACCGCATACTCAAG	ATGCATTGACAAGTCACGCACATA	64	64	180
48	64564	64637	CA	CCCCCTTCTACCTGTATTCTGCT	GTGCGTTAAGAAACACGGGATAGG	64	64	227
48	64816	64885	GT	CAAGGTATGTAGGGGCTGGTGAAG	TCCACCTCCAGGCAGAGAATAAC	65	65	219
48	361910	361955	TG	GTGGACGAGGTGGGTTGAATGTAT	ATTTGCTGTTAGCAGGCGTATGGT	65	65	255
48	464244	464316	AC	CTCGCATAACAGTGGCCTACAG	AGGTCCATAAAGACCGGCACATAC	65	64	271
49	53289	53377	AC	GCCTGCACGTTAGGACACCTCTAT	AGTGTGCTGCGCGTATACATTAGG	64	64	265
49	72134	72235	AC	CTTAAACATCTCCGCGTCAGTGC	CCCATGAACATCGTGAAGTACCAG	65	64	270
49	147077	147174	AGC	CTCAGCGTGTGGAAAGTAAGGGG	GCTGACACAGTCATTACGATTGCC	66	65	273
49	164655	164729	GT	ATGTCCTTACCTCGAGCTCTCCT	TGTAACAGCAAGCCACCATGATT	66	64	282
49	289958	290008	GT	CAGAGGTGTGAGCAGCTGGTAGTC	GTGAGTCCAGTACCCTTGATGCG	64	65	230
49	406162	406285	CA-AG	GCGGTAGTGGTATGTTTGACAGATG	CTTTATGTGCAGCCTGGTTGGTTC	64	65	283
49	445279	445357	GCAG	TTGGTCTCCACTCCGCTCTATAC	CGTCTATCATCCGTTCTGCAGGTA	64	64	243
49	528601	528680	CCA-CCG	TGAGCTATGAATGCAGTCTCCAG	AGCATGCTGATGAAGCTCACCG	64	67	203
49	546532	546658	CA-AC	CTGCTGTGCTCACTTGTITGCTC	CAACTGCAATTCAGCCGAGTG	64	65	290
50	15765	15825	AC	ATCAGGTGCGCCAGGTACACTTGA	GCACGTGGAGGTGTTGTTGGAC	65	67	253
50	41980	42024	TGC	CTCGAGGGAGATCACACCCTG	CGATGATAACGTCATTGACCTGGA	67	65	184
50	124250	124298	GT	CTGCCTGAGTTCACCTTGCTGG	GCAGTCGTTACAAACAATGAACC	66	64	212
50	214227	214291	GT	AGATTGCGGTTGGGACTAACACAC	ACGTTGTAACACCTACAGCCGTA	65	64	171
50	226094	226141	TG	GGCCTAGCGTTAGCAACTAGGGTT	CACCTGCTACTGCCTCTGATGTC	64	64	270
50	233107	233187	CA	GCACGTACGCACGATTGTTAATGT	CTTTGGGTGTTCAATTTGGGGTTT	65	65	206
50	349529	349643	GT	TACCATTCACTCCAGGGCTTTGTT	AGGAGGAGGGCATCTATCTATCCG	65	64	300
50	456263	456324	TG	AGCGACTGAAGGTGAGTGTGACTG	CCGTATGTTCCCTTCCCCTAAGAT	65	65	149
50	456734	456807	AC	CCTACCTGCTGAAATAGCGACAC	TGACTGTGTCATTACAGCTTTTGGG	65	64	264
50	458213	458265	TG	AGGTCTGTGTGTTGAAACCTCAACG	TGTGTAAGGAGGGGAAACATTCGT	64	64	177
50	482439	482518	TG	CGAATTGGTGCCTTGATATGCT	CACCTTGCATACGCTCACCACTAGC	65	65	270
50	483198	483283	GT	ATAAGTACAGCATGGCTGTGCGAC	TATTGGGAAACGATTACCACGGTC	64	64	232
50	571189	571243	AC	CAGGTTGTAGGCATTGCTAACACG	GTCGTGCAGGATGTTTCATGGTAAA	64	65	294
51	16044	16111	TG	AGGGAACGTTACCAACAGCCAGTA	CGACAACAACCGATAACGACCTCT	65	65	228
51	390431	390471	CAG	GAGCGAAGTATCCATCGAGACGAG	GTGCCTTTCCTCAAATGCACTG	65	65	286
51	557679	557751	CA	AAGCAATCAAAGCATTCTGTACG	AATCAGCGTATCCACCGGTTAAG	64	66	225
51	596348	596423	GT	AAAGCTCTTCAACCACCATCTCAC	GAGGAGGAAGTAGCCGAGCACC	65	65	284
52	116277	116383	CA	CTGACTCACCACGGCAACACTTAT	GACTCTGGCGTCTACGTGTGCTT	64	66	261
52	121627	121775	CA	AGAAACGAAGAACGAAGCGATACC	GGGTGTACGACAGACCAGACGAG	64	65	298
52	186039	186120	CA	TAGCAGTAGAGGCGAGGTGTGATTA	GACCCACGACGAAGTATCAAGTT	65	64	225
52	196568	196666	GT	GAGGGCTACAAGATCTTCTGGG	ACTTGCTGTACTTGGAGAGGTGC	64	65	289
52	272259	272357	AC	CAAATACACGCATCACATATCGGC	ACACACAGACCATGACGGAAAAGA	65	65	274

52	293604	293657	GT	CTCCCCAGTAGAACATGCCAG	CCTCTGCTCTTCCACTGCTCTAGG	65	65	289
52	353320	353372	CA-ACGCAC	TCTATTTGCTAGCGCTTCTGGTGA	GGATGTTTACGGATGATGGGTGAT	64	65	285
52	361985	362096	CA	CCACTTGCCAATAGTAGGACTGGG	GTGACCCGCTTTGAGAAAGACAC	65	65	246
52	372974	373089	CA	GGCCTCGTCAACAAAACCCAC	ATGATTGTCCACACGAAGCAAAGA	68	65	231
52	389751	389840	GT	TTCTAAATCCTGTGTTTCGGTGG	CATAACCAGACGACCCCAAATCTT	65	64	298
52	535998	536041	GT	ACTCATCAGACCCACCCCGTACT	AACGTGTTGTGAAACCAGGTGAAA	65	64	300
53	81864	81959	CA	TTCAGGAGAAGGTCATTGACACCA	AGGCAGTCGTGTAATGGGAGTAGC	65	64	227
53	87485	87525	CA	AGGACAGGGTCAGTGCAGGTATGT	CCACTGCACACAAGCTAGCCAAC	65	66	288
53	256693	256774	AC	GTGCTAACATCACCAAGATGCCGT	TGGACGTGTTAAGTCATTATGCCG	66	65	193
53	308480	308520	GGGA	ATTTCTTCCAGCCTACCCCAACAT	CACACTGATCTCGCGCCTTTTAT	65	65	297
53	326818	326884	GT	CATGGATTGTTGTCGGCGCTTA	TGCTTCCAGAACGAACGCATATC	67	66	299
53	345468	345508	CTG	ACCACTGTCGAGCGTTCCTCCT	AGCGGCAGTTATTTGGCAGGTA	66	65	282
53	496806	496867	AC	CCGAGGACAGTCAAAGTGTGAAAA	GGTGGAGGACTACAGCATCTCCAG	64	65	223
53	543235	543306	GGC	CTCCTACTGGCAAGGTGCCTTTT	CAGCCATGGTGGTTTTCTCAGA	64	66	264
54	246012	246149	GGCA	CGGCAGTGTCTCCAGTGTGTAGTT	GTTTGCAGTGTATCCCCGTCTC	64	67	287
54	319850	319922	GT	AACGCGTTACAGAGTCGAGAAG	CATGTGGGTGCGGAATGCTACAC	65	64	224
54	339416	339530	AC	GTATCCGGCTTGGTACTGTTTGA	AGGTGGACCCCTCCGACAAGGT	65	69	287
54	445546	445640	CA	ACACAGCACTTAGGGTTTTCTCGC	AGACCCGCTATCATATGTGTCCGA	64	66	249
55	9843	9906	GT	ACACGCAAAAACACAAAGTGTCTG	ATGCTGACATGCACATTCTTTGCT	64	65	295
55	98681	98775	CA	CAACCATCGCCGCTTACTACTTA	ACTGCACCAGGCTGACCAACAC	65	66	282
55	130017	130069	CGC	CACCTCGTCTCTATCATTACCGCC	CTTTGGTGGTCCGTGACAGGAA	65	66	116
55	418999	419088	TG	GTGCAGGCTTGTAGGACTTGAGGT	CCTGGACTTCATCATCGCCTTTAT	65	64	216
55	426211	426268	GT	AAAACGGGAACATATCAAGTGCCT	CCATGATCGTTATCCTGCTGATTG	64	64	269
55	530198	530338	AC	GGCGATACTGCGTAACTGCGATAG	GTGTTACGGTTACCCAGGCAC	66	64	263
55	535228	535299	AC	GTCTTCAGAACTCTCTCCCGCAAC	ACACACGCACCGTATGCATATCTC	64	65	271
56	76316	76491	GT	CAGTGCCTGTATGAGACGTGTGC	CTTGATGTCATCCCACAGCCAG	65	65	292
56	114133	114182	GT	TTGGCGGGCATGACTAGTTTAGAT	GTCAGGTGGAGCCTATCGTTGCT	64	65	174
56	226563	226673	CA	GCAAAATTGTAACCCCTCCTGCAC	ACACAGTCATCCTGGGACACAATG	64	65	190
56	250756	250810	TG	CTTGGCAGTGGGCACTAAATGAAT	CGTACTGCATGGTATCGTACAGCG	65	65	164
56	265680	265756	GT	TCCAGAGGGTTCGTTGATCTTC	GCACACCGGTGAGACATCGATAC	65	66	283
56	304169	304242	TCC	CTCTCCTCTCAAATCCCATCCTT	CATGTAACGCCACTGCACCTCT	65	64	299
56	335782	335844	CA	CCATCATCAGTACCCAGAAAGTGC	GCCTTGCCCTCAGCATTCTTTTT	64	65	298
56	351329	351394	CA	CACAACACTCGAGAAGGCAATCAT	ACGACGTACAAAAGTGGGTTTTGG	64	65	284
56	430982	431057	AC	TCCCTGCAGTTTCTGATACTCGT	ACGTTAGGAAAGGCGTGATTGTGT	65	65	289
56	445900	446036	GT	CACAGAGTGTAAAAGGGGTTTCGG	AGCGTAACTGGGAGAAGACAGGTG	65	65	232
56	479313	479361	AC	CCTCTTCCAGTGCTTCTGTCTA	TCTTTGGCATACTCCACAACCAGA	65	65	207
56	515812	515895	CA	CAAGATGTGATGGCCGTGAGAC	AACGTGAGCACTTGCAGATACAG	65	64	267
56	523602	523763	GT	AACAGATGTTGAAGCGCAGTTGTC	CAAGTTCTCATACTCCCTCGGCAC	64	65	289
56	536285	536429	CTC	GCCTCAGCATGACTAGGTCCAGA	CTGCCGTACACACTCGGCTACAG	65	66	295
56	545063	545135	CA	GTGTTTTAGGTGAAGCCGCAAACT	CCACTCTTGCAAGCAAGGCCTAC	64	66	237
56	546691	546810	CA	CAGCTAGTGCACGCTCGAGATAGA	CAGCAGCAGCATTCTGTACCTGAT	65	64	294
57	53861	53927	GT	AACAGGGAAGCTCCAACATCAATC	GGTTTTCTAGCTACCCGTTCTG	64	65	291
57	108889	108971	CA	CCTCGTCATACGATACTCGTGCTC	GAGAACGTGCAGTGCTTTGTGGT	64	65	221
57	240231	240331	GAG	CGTGAAGTAGCCACTTACCCAGA	ACAGGTGAGCCTCAGGTTCTTGAC	63	65	256
57	413121	413185	AC	CACGATGGGTGTGTGAGTTTTAC	TTGGAAAAGGCGCACAGTAGGTAT	64	64	140
57	434131	434188	AC	CTTCTGGGAATGGTGGGAACTAC	GAGGAGTGACAGCTGGGAAAAGC	65	64	291
58	43351	43396	AC	TTCCAGTCTTTTTCTGCCGTAG	GCACCGGTAAATTTCTGTTTCGTA	65	65	135
58	76859	76910	GT	GCGTGTCCGTTATGTCAACAATTT	TATGGCTTGGCTTGGTCAAGTAGG	65	65	246
58	104474	104572	GT	CAATACCAACTCCACATCCGTGTC	TGCGCAAGGCACATACTAAATCTG	64	65	237

58	119469	119564	GTG	TACACCGTGAGTCTTGCCTAGCAG	GTGCTTTGAGCACACAGTCCGC	64	66	291
58	237783	237831	AC	TTCAGCTCCAGAGAATAGTTGGGC	ATGACGCGCTAAGACACAGTTCAT	65	64	127
58	285782	285832	AC	AAGTTCATCTGGTACATGTCGGGC	TAGCAGCTCGCTCCTTAGTCCCTA	65	64	219
58	360502	360565	GT	GGTGTGGTCATGTACGAAGTCTT	TGCCAACGGGTTTTAACTTCATCT	64	64	297
58	491970	492009	CAG	ATGCTGTTGATGAGATTACGCCCT	ATCATGATCAAGGTTGTCTGGTG	65	65	275
59	218187	218250	AC	TTGTTCTATCTGCAAGGAACGCTG	ACTGTCAAGGCTGCAGAACAAC	64	65	249
59	260608	260697	TG	GATGGACAGGATGAAGCCAACTT	TGAAATAGGGTATGGGTACGCAGC	64	65	280
59	312590	312649	TG	AGTGCTGTGGTGTGACCTCTGT	CTGACAAGCACAGCAAACCTCGAT	66	64	230
59	349060	349139	CA	ACGAAAAGATAGTGGGAAGGGGAG	GAATCTACCGACGGGAAGGGAG	64	65	227
59	486237	486336	CAGG	TCCAAGTACGGCCTGTCTTCTAC	GGGTTGGGGAACATGTTAAAGTCA	64	65	255
60	65163	65233	TG	CCGACCTGTGTGATAGAGAGAGGG	GGACGCAATTACCTGGCTGAATAG	65	64	229
60	127571	127633	AC	GCAGTCTCCTTCATCCATCCATTC	CTTTGTGGAGAATACCTCGCTCGT	65	64	250
60	129047	129090	CGTG	GATAGGGGTAGAGAAGCAATGGGC	GTGCAACATTCCAATCATCCTCC	65	64	207
60	274640	274714	GT	GCTGAACAAGCTGATGGACCTGTA	AGTCCGGTACATCAACATCCCCTC	64	66	300
61	198435	198491	TG	GACCGTAAAGTTGCGTTCATTCTG	GTGTCTGCTGCGGTATTAGCCTTT	65	64	287
61	248831	248912	CA	CAGAGGCTGGCTGTAGGTACG	TGCCAGTGAAGAATTCAGGAAGG	65	65	260
61	338594	338670	CA	GGTTGGCTATGGTTGAGGTTTG	GCGCACTCTTCTGTAATGTGTG	65	65	237
61	352967	353007	GGT	AAGAAGGAGAGCAAAGCCGTGAAG	GATGGCATCATGGATGTTGTGTTT	66	65	207
61	510268	510332	GT	CAGGGCTTTGACCTGGACTATGAC	CATCCCTTCTGCCCCTTAAGTT	65	64	246
61	517497	517542	GT	CGCTCCTGAACCGTTGTGATAAGT	AAGCACGACTAAGCTGGCGGTG	65	67	219
62	173143	173207	GT	TGCTTGAGGACATCAGTAAGTGCC	CTGGTAATATTAAGGGCGGGGCTA	64	65	270
62	180199	180317	CA-CACG	GGAACAAAATGTCGTAGGTCGCTC	GCAGTGTTACGTACGCCTCGACTA	65	64	244
62	399659	399732	GT	GTGCCTGTGGGCTTGAGAATAAGT	GTCAGTTTGCAGCTGCGTCAGTAT	64	65	292
62	463533	463607	TG	CTCGTGGCTATCACTGTTACACA	CAGCGCATAACAGTCTCGCTCT	64	64	269
62	476879	476974	GT	GTGATGCTGGATGAGTACGACTGG	GTGCTAGGCCTCAATTTGTTGTGA	65	64	217
62	494850	494909	GCA	CTATGCTGCGAGTTTGAAGTGGGAC	TTCCACATGCTCGCATAACAGTAC	66	65	221
62	505139	505191	TG	GAAGGACAAAAGCGGAACAAGGTA	CAGGTCACTACTCATGTCGGTACG	64	64	176
63	53539	53599	AC	TCACCTGACCCACAGGATGAG	CATGTGTACATTTCCGTGCCTGAC	66	65	186
63	159620	159672	CGCA	CGGAACCCACGTGTAAGTTGAAAT	GACTTCCTACTGGTACGTGGCGAG	65	65	295
63	280271	280335	CA	ATCTGTGCTCTCCTGTTCACTCCC	GAGAGGGTGGAAATTAGGCGGT	65	64	300
63	333835	333897	CTG	GATGCATGCGTAGGCTGGTGGT	TGAACCGCCTTCATACTACTGCTG	68	64	264
63	425432	425480	GCT	TGAGAGGGGCAGGAGTAAGACATC	AGTGGAGCGCAGATGATGAGGAT	65	66	241
63	497095	497136	GCA	ATACCGAACTGCCCTAACTGCTTC	CGAAACCACTGCCTGTGCCACT	63	68	298
63	500806	500861	AGC	GCTGTCCAGTTTGACCCACC	ATCACCAGCGCTCATGTCTATGG	69	65	292
63	507554	507640	GT	GTTGTCGTACACGATCAAGACGGT	TTCATGCTATGAAACACGCTCACA	64	64	268
64	123036	123075	AC	TGTACCCTCTGTGCATTTATCCG	GAAGGCAGATAGTGGGCTGTT	65	64	249
64	333402	333463	CAG	GGAGCGGGCTCTTCTTTACTA	GATCAACACGCTGTCAAACAGACC	65	65	171
64	401526	401665	GGT	GACACTGTGTATGGAGGTGCTGGT	GACTATAGGCCTTGACCCTCAAG	64	64	300
64	420593	420706	AC	GAGCACTGATGAAAGACAACCTCG	GACTCAGCATATTGAGTGTGGCGT	64	64	300
65	46103	46148	GAG	CGATTAGTCTGATGCTACCCAGG	GCTCCAAGTCTATTGCTCCGTCTC	65	64	263
65	126089	126187	GT	CTAGGATTTGGAACGCGCACAAAG	CTGATTCACGTGTTCCCTAGCCC	66	66	297
65	170100	170149	GCT	CTTTTCGAACTCAGCACCTCATC	ACCACGATGAAGGCAAGGCTAA	65	65	161
65	350947	350995	CAG	GCTGATACTGCTTCGCAGTCATTG	AAACGACGCCGTAGTATCGGAAC	65	65	213
66	238844	238919	TG	GAGGACGGCGAGAAGTACTGGAT	GTCAGCTAACAAGCGACGAAAACC	65	65	289
66	319219	319320	CA	CAAAAGAAAATAAACCCGCAGCAC	CTGCGAGTTCACACTCAACGTGAC	64	66	188
66	482024	482096	GT	GTGGTTGAATTTGATGCACAGAGC	TAGAGCTGTCCGCACCTCTCAACT	65	65	173
67	178047	178149	AC	AGTAAAGGGCACAGATTAGGGGC	TGGGTGAAAGCTACTACTGGCGA	64	64	296
67	266559	266608	AC	CATAGCGTACTGGACACGCACATA	ACTGACACCCGCCGTAGGAAC	64	68	149
67	346295	346386	GCCT	AGGGGCTATGAAGAAAAGGGACTG	CTGGAGGTAGTTTGGTTGATTGGG	64	64	260
67	355063	355112	GT	AGCCAGTCTCCATGTAGGCCA	CTACACGGTGCTTGGGTGTGCAAG	65	69	186

68	7194	7273	AGC	CTCGTCAGTCAGTTGGACGAGATG	CCTCAGCCATGCTTCGGAGTGT	65	68	256
68	78611	78661	AC	ATAGAATGCCTCCCTGTCTCGTTG	CACCTCAGTCAGCATGTCGAAGAT	64	65	210
68	88902	89021	AC	GCTGTGTATTTTGGACACGCAGGT	CACGTTACGTACTTTGACGACG	66	64	281
68	465811	465880	AC	CACAAACACACATCTGGTATCGCA	AGATCCGTCCTCGAAGGTGATG	65	64	234
69	253572	253676	TG	CTGTTTGCCTTTTCAACACAGATG	AGTGAGTCTTCGGTTTTGGTCAGC	65	65	296
69	363386	363450	AC	AATACCAACACGGTAGCGAGGTG	CTTTAACGCATCTGCCTCATCCC	65	66	256
69	370842	370936	GT	CTTGACTCCGGGAGGAATAGAGC	CTGCTCGTGAAGTCCATGACC	65	67	279
69	418066	418117	GCC	CTGTGTTATGAAGCGGTGGAACAG	CTGTCAGAGAGCGTCGGTACAGG	65	65	241
70	3010	3069	TG	CACACATCGACTATCACCCAGGAC	ACTCCTTCGCTGTTCTGTCTTGT	65	64	262
70	6021	6085	TG	GACTCAGTCCATCGTGTGAGCG	CCTTGTGCATTTCAATACACGCAT	65	65	180
70	50406	50458	AC	CACACCTACATTGGGATCACCGTA	CCACTGACATCAAGGTGTGCTTGT	65	65	161
70	122012	122064	GT	TAGATACGGGTTATGGAACAGCG	GACGTCAGACCAGTCTCAGGTG	65	65	240
70	129419	129482	GT	GATCCAAACCGTCCACCAAGTC	CACGCACACCTTGTTGTTTCTTTC	65	65	257
70	233017	233159	GT-TG	GTGTGTGTTGGCGATGCACAAG	GTTTCCATTGAGCCAGGTCCCTA	67	65	294
70	440901	440958	TG	GTGAACACGTCCGGGTACATGAAG	CTTACCCTCGTTGCTCCTCTCCTT	66	65	157
71	98065	98217	CA	AACAGTTTTATGCCTTGCGCATTT	GTCCCTCAAAGCATTGAGATTG	64	65	267
71	410197	410288	TG	CTGCGCAAAATCAGAAAGACAGAA	CGGCATCTTAGACGGGATGTTTT	64	64	265
72	170221	170268	CA	GACACACTTAACCTGACCCACACG	ACGGTACTATCGTTAGCCTGGAC	65	64	287
72	402405	402460	AC	GAGACCGAACACAACATTACACC	GCCTCCTCTTCTAGCTCAGCGATT	65	65	165
73	21257	21353	CA	TATTGGCTGCAACTAAGAGGGAGG	TGTTTGGCGTATCAGGTCAAATG	64	65	275
73	29575	29730	TG-GT	GTCCACCTCGTATGCGTACATGC	GGCTACAACCTGCGCTTTTCTAAA	65	64	273
73	329656	329704	CA	GTTGACCAAAGACCCAAATGACC	CCCCTTTGCTATCTATCCACATGC	64	64	297
73	370915	370962	CCGC	TTACTCCTGATGCGCATAATTCCA	GCGGTTAACGTATCTATGCGGTCT	64	64	287
74	76337	76405	GT	AGGCTCATGTCTTCTTCTGGTTG	GACTCCTCTCACGCTCCCTTGT	65	65	289
74	322486	322553	CA	CGAACGAACGAACCCTATCAAGTT	CAGGAGGTGTACCAGATGATCACG	64	65	216
74	364601	364656	TG	AAGCGTCTTGGATATGCTCTCCTG	GAACATGACCATTGGTGACCAGAC	65	64	226
74	368273	368413	CA-AC	TATGTGCCTTCCCCTGTGGTAATC	CGTCTCGGAACACGGGTGTAAG	65	65	270
75	62403	62499	CA	CCCGCTTACCTACCCACTATGCTT	CGACAGTGGATGTGTCCAGTAGGA	65	65	236
75	195087	195161	TG	GAATCACGCCAACTTCAGGTTCTC	GCCATTGCTGTCAAAGTATTGCTG	65	65	235
75	265109	265160	TG	CATGGTGGAGATCAACTTCTGTG	TGTCTAAACGCAGATCGAATGGAA	65	65	276
75	318230	318291	GCA	AGGAGAGCAAGGACACATGGTAGG	CAGAGGAGGAAAGGAAGTGGCTC	64	64	245
75	349628	349731	GT	ACGGTAGGGACGGTAGGGTGAG	CCCATCGCACATCATCTCTATCAG	65	65	239
75	390905	390948	GCCT	CAGAGGGGTTCACTATAACGGAG	ACCGTGAACCTTCTGACTGCTGATG	65	65	298
75	418015	418091	CA	CCGTACACGCACAGCCTAACTAGA	AATTCCTCCATCTGTGTACCCTG	64	65	249
76	59120	59201	AC	CACGAAACAATAGGACTGACGGTG	TCAAATTGTTTGTGGCCGTATCA	64	63	251
76	132952	133036	CA	ATCTGCCAGTTTGCAGACGAGT	ACCTGGTCCAGTTGGATGCGCT	66	69	290
76	136309	136374	GCA	ATGGTTTCGACATCGCAAATGG	ATGCTTTCATCTCCGAGTCCAGC	66	65	299
76	147270	147328	CA	GTAGCACAGATAACCCAAAACGC	GCTGTTCTTCAACTGGGTACCAT	64	65	246
76	148074	148136	TG	GTGGGTGAAGACGTAGATGGTGG	GAATCGTGTGGTCACTTACTCACG	65	64	226
76	150204	150244	TG	GATGCCGTTCTGATAAAGAGGGTG	GCTGGTGAAGTAGCAGGTGGAAGTT	65	65	254
76	158771	158878	AC	AATTGCAGCAAGCAGGTAATGGTT	AACCCCTGTGAGGCGGTAAGAT	65	65	211
76	160079	160131	GCT	GTGTTGCCTGAAAAGTCTGGGAG	AGCAGTCAGCTTGCACAATACCCT	66	65	240
76	166510	166557	GT	AACTAGGCCTGCTAAAGCGCCTC	CCTCCCCCGTCAATGTTTCATCA	66	68	245
76	435785	435892	AC	GTAGACATGGACGGTGTGTAGGCA	CTATGTGGTCCGTCGGGTGAAG	65	66	210
77	59648	59696	CTG-TGCTGCTGG	ATGTGCACGTTCTGGTCTGACAC	GAGTGGACCTCCACCTTACGTAGC	64	64	242
77	126577	126655	GT	CGCAAGCCACGTAGCAACAACC	GCCGCTCTCACTCCTCTTTATTT	68	65	286
77	164381	164447	GT	CTGATTTTGCACCTCAAGCTCC	CTAACCACCCCTGAAAACGCAC	64	64	296
77	177624	177674	GCA	GCGCAAATCGCAGTAACATAGTA	GAGCAGTGTATGACTTGTGGGTC	64	64	299
77	186274	186318	CA	GTCCTACGATCTCAATTTGCAGGC	TGTATCTGACCCGACTTTGGCGAC	65	65	300

77	256390	256509	CA	GCCCTAGTGGCTGATCCCAAAC	CAAGAGGTGAGGTCACATGCAAAG	66	65	269
77	399304	399381	TG	TGCATGCGTAAGTGTCCATTAGG	CTCTCTCCACAAGCTCATCGGT	65	65	189
77	447931	447980	GT	ACATCCACGAGAAACTGTGAGCAG	ACTCCAATGCTGTGACCTTGACAC	65	64	200
77	477962	478078	ACC	AATGGCACAAGCCTATCCCGTAT	AAGGGAAAAGAGGAACACAGGCTC	65	65	226
78	177208	177281	ACGC	CCCTGGCTCTCCCAATAATCTT	CCACGAGAATGAGGTCAAGTGTGT	64	64	263
78	301291	301340	AGC	ATGACATGGCAGTAACAGCTGACG	GTCAAAGAAGACCAGAAGCGGG	65	65	164
78	375685	375750	AC	GAATACGCGTCCAACCTTACCAC	AAGGTCAGTGTGAAAGGGAAAACG	65	64	137
79	42127	42235	GT	AGGCGCGTATGGATGGTACTATTT	AACTCTTGGCCGTACGTCTGTTC	63	64	300
79	114815	114890	CA	CATCCCATCTTTGCTTATCCCAA	CGTACCTACCTTCATGGGCAATCT	65	64	230
79	201032	201128	CA	ATGACGGAATAACAAGATCGACACG	AAGGGACTCCCCTGACCTTTAGC	64	65	294
79	228317	228364	AC	CTGCCTGTAICTGGCTGGTTTAGT	AGGGGCATACTACATGACAATCGG	64	65	299
79	428748	428790	CA	TGACCTTGAAGTGGTGGACTGAAG	AGACGCTGGTTAGCGGCAAAG	64	66	227
80	19691	19743	TG	CCGGTAGCAAGTAAGTGAGAGCGT	CATGCATTTAGGCACAAGTCAAGC	65	65	263
80	47860	47991	GT-TG	ACAGGCTACTCCTACTTCGCCTTG	ACACACGGTTCGTGATCCCTTTAT	64	64	299
80	49039	49125	AC	TTATTCTACCGGGACCTACCTCCG	CACCACCAGGCTACGTACAGGC	65	66	296
80	296037	296140	CA	TATGCCGCTTTGTCAACAGTTAGC	CCCCTGACTCCTGGATACTTCGTA	64	64	284
80	332729	332777	GTG	GTGTTGTCGAACAGTGGGATGACT	CATCGATTTCTGCACTTGCAT	64	64	276
80	350198	350298	TG	AGGTGCGTTTTGTGGAGTTCGTATT	GCACTAACACACAGTGGCAGACAA	65	64	287
80	377075	377157	GT	CATGCACTACTACCCGGACAGATG	CGAGGTTCGCATGGAGTAGATTGTA	64	64	201
80	434769	434898	CA-AC	CTTTCCTATTTCGTGCGTTCTCGAC	GAGTCGGAGTATCGGGAGCTGG	65	66	269
81	132788	132904	AC-CG	GCCCATCCATAACCATCTATCCAGA	TCGACTACCTGTCCAAGTTCGGTT	65	65	235
81	183238	183324	CA	CTGACAAGGGTCAGATGGAGGAGT	TGTACGGCTGTTTTGAGTACACGG	65	65	245
81	244856	244995	TGC	CCGTGCGTGTGCAAGTAACATTAT	ACTCGCTTGCATGCCGCTCTCT	65	69	294
81	289963	290038	CA	CCATGCTCCCTAACTCATACCCAC	CCACACCAATCACGTAGTCCACAT	64	65	173
81	293925	293964	GCT	ACACTTCCTGCTCCACTGCATGTC	GACCACGCGGAGCTGTTTGAAG	67	68	252
81	373979	374060	GT	AGTCCACGCTGCAGGCATACAT	ATGAATAAGTGTGCGCATGGTCAA	66	64	287
81	422019	422070	GT	CTAGTCACTCCCCCTCTCATCTGC	CAGTGCCTTTAGTGTTCGCATCC	64	65	295
82	29688	29777	TG	GTTGTGCTCCAGCTTCTCACGAC	AATGACCTGGAATAACCTGCGCT	65	65	229
82	392658	392746	AC	TTACTAATATGCCCGAGGACCCAT	GCGTCGTTCTGTTTGCCTCTTTT	64	64	224
82	418160	418275	TG	GTGAGAAGCTGATGCCGTTCTGTA	TACTCCTCTCCCCTGATGCTACCC	64	65	293
82	443489	443574	AC	TACCCTCACCATGGGAGATTGG	CGACTGCCTTGCAGTGTGTTAAAG	65	65	261
83	391664	391779	TG	TGTACGAGAGCACCATTGACCTGT	CGGGCTTCGTTTTCTTTTCTTA	65	65	275
83	407104	407187	TG	AACCACACCGTAATTGGATGGT	GTTGTTGCTACCGACTGTTGTTGC	65	65	262
83	447134	447202	TG	CACCATCGGTGACTTTTCCTTTTC	ACCCACACAGCGTCTCTTATCTCC	65	65	232
84	106701	106768	TG	GAAACATAAGATGAAAGGGCACGG	CACTAGCCCTGAATGTGAGAACCC	64	65	171
84	413568	413648	CA	GTAACCTGCCTGCGTGTCTCCCTT	GCAAAGCCCACCACACTCTTG	65	66	282
85	61088	61243	GT	GGATCCTCATCACCAGGTATCGTA	GGTACCTCACGACCAACCCACTAC	63	65	224
85	210991	211037	TG	CAGTAGCATGACCATTTGGAGCAG	AGTCCAGTACAGTAGGTGGTTGGT	65	64	242
85	279122	279200	TG	TACAGTGAGGACATGAGGCAGAGC	GCTCGACCGTGTATGGTGTATGTT	65	64	266
85	367980	368033	ACC	TGCAGCTGCTCTCTGTAAAACCAG	ACTCACACTGGCACGAACCTCTTT	65	65	244
86	97812	97891	CA	ATGCGGTTTTAGGTTAAGGGAAG	AACAAGCACTGGTTCGGGTTTG	64	65	292
86	99948	99998	CA	CCTGCATGTTTGTCTTTTGTCT	GCACCTCGCAGTAGTAGTCGCAT	65	65	258
86	123635	123679	CA	TTCTGTCCACACTGTACCTCCTGC	GTATAGGGCCTGGATGATGTGAGG	64	64	162
86	309100	309167	GGCA	ATCCTACAACCCCTAGGAGCGAAA	CAACTGCTTATCTGCGCACCTCT	65	65	148
87	108776	108882	TGG	CAACTCCGGCTATGAAGATACGCT	GTTGCTGGAAGCTGAGTCACAGAC	64	64	220
87	125628	125706	CA	TACATGGGGTAATGGGGTAAGCTG	GCTCTTCTCTTTCCGCTCACTTG	64	64	295
87	148168	148238	TG	CGGAAGTAGTGGTGGTGGCTTACT	CAAACATGGCTGCCTGCTCTATC	64	65	285
87	248350	248436	CA-CACGCAGT	TACCAGCCAGTGGTGTGACACTT	GACCAGCACTGAGGACGAGTACG	65	65	281
87	254073	254135	GT	TGCGAGGAGGTATCGAAGAAAGAG	CCGTCTACCGGCACTACGAGTC	65	65	219

87	310463	310546	CA	GGTCTAGCAGGTCTGAGCACCAGT	GTGATGGTTCTACAGGGTTTGCC	65	63	300
87	353396	353452	CA	AACCTCTTCCGCTAAGCACTCCTC	CCTTGGCTGTGTAGGGGTAGGTG	65	66	262
87	406635	406699	GCT	CGTACTGTACATTGACACCCGCAT	ACCACAGCCCACGTCTCGACAAC	65	69	282
87	408515	408565	GT	GTCTGAATTGTGCCGGAGAGGTAT	GAGACATAACGAATGTGTGCGAGG	64	65	256
87	423127	423256	ACAC	GTACGGCGCAGTAGGATGGTGT	AGTTACCAAGAAATACCAACGCCG	65	64	297
88	87385	87518	GT	AAACGTACCCATGTCATGTTACC	GTCAGGCAAGAGCATTGATAAGCA	64	64	253
88	100025	100079	TG	ACAATGCACGACGAGATCATT	CGCAGTGCAGATTACCCGTTACTAAT	65	65	186
88	121770	121815	TCCC	CTCCAGTCCACGAGAGTTAGGAA	GGTGGACATCTCGTTCTTCCAGAT	65	64	271
88	129107	129182	AC	GTACGAGAGGAGAGATTCGGCAAG	ACGTTGGTGTGAAACCGAAGGC	64	68	173
88	145985	146061	GT	AACAGGTGCTGCGACACATACTTC	CCTGACGTAGCAGAGGCCCTTAGAG	64	64	284
88	251347	251395	AC	AGGTCCTACTTCTCGCTCTTCGT	AATTGCTTCCACCACAAGTTGAT	64	64	205
88	291765	291931	TGTG	CTTGGGTGCAGTGTTCCTCCTTT	AGGGACTGCTTGCTTGCAAAGAC	65	66	235
88	327470	327519	TG	GCGTGTTCGACATATGTGTGTTA	ATCCGACTCCATGGGATCCACTAC	65	66	239
88	388018	388106	TG	CATCTTTGGAGATACGGCCAACAC	GCGGTACCTTCAGGTAACATTCGT	65	64	244
89	38621	38697	CA	GAGGAAGACGTCGTACACTGACCA	GATACTAAGGCAGGAAACTGCGT	64	63	296
90	68383	68509	GT	CCGGAACCGATTAGATGTGTGATT	GTTTAAACGGACGTACACTTCGCC	65	64	298
90	139473	139521	CAC	GTAAGCAATGAGCTTGTGCGATG	CAGAACCGACTGTACACAAGGGG	65	65	278
90	155285	155329	GT	CTGGAGTTCAAGATGGACGACTGG	CGGCATGTATTAATGTGGCTCACT	66	64	255
90	292879	292921	CA	GCGATGATCGTATCATAGTGTGCC	CACACATGCTGAATGAAGCTGAGA	64	64	200
90	295871	296041	TG-GT	CTGAGTCGGACGATAAAGGGTATGG	TTACTGCGTTATGGTGCTGTTGG	65	65	249
90	308058	308127	GT	GGGAAAGTAAGAGCCGAGGGACTA	GGTGGGATCAATGGTGTATAGTG	65	64	259
91	94016	94068	GGCA-GGCAGGCG	AGCCCCATCTTGGTCTCGTACTC	ATTCTGACCGTCGTCCAGAAC	65	64	238
91	176754	176842	TG	AAGTGCGCCAGACATCAAAACTA	ACTTTGATGTTGTACCCAACCCC	65	64	206
91	247595	247698	TG-GA	ACTAGAGGGCCGAGACGGAATGTA	CTGCTGGGCGTACCTGTAAATGTT	66	65	251
91	279954	280036	GT	CGTAAACAGGAAGGACACGCATTC	GTTGGTCTGGGAATGGTATACGGG	65	66	297
91	337002	337067	CA	AGTTACGCAAGAAACAAAGCAGCC	GACATCGCCACTATCAAGGTAGGC	64	65	234
91	405562	405650	CA	TCACAGGCTCCTCTTCATGCATAC	CTACTGGGACACCAGCCTTGACAC	64	66	181
92	1019	1102	AC	CCACCAACACACATAACGTGGAT	AATGTGATCTTGGGCGAAATCT	64	64	279
92	54264	54320	CA	GCAGCTTGAAGATTTTCATTGCAGA	GCTCAGCATCCCTATGCAGGATTA	64	65	260
92	192851	192897	GT	CTGCACAGGAACGAGTGCGGTA	GCACATCTCAACTTGCCTCTGT	67	65	151
92	214259	214385	GTGC	CTTCAACACATCCACCGAAACCTT	ACACTCCTTCCGTTACTGCTCTCG	65	65	229
92	218389	218477	TG	CAGCCCAAGCAAATAAAAGGAGGT	ATGGGACTGTAAGAGCGTGAGAGG	65	65	254
92	221195	221247	CTG	GAGTGATACCCCTCGGCTTCCTT	CCCTCGTCAACAAGCATCAACAAT	65	65	296
93	313757	313882	CA	GTCAACACATGTCCATTTCTGTC	AAGGCTGTGCCTGTCTGTGTAAGA	66	64	299
93	332147	332201	AC	CATGACGGTATCAATGGCCAAC	ATGTTGAAGTAGTCAAGCTGCGCC	65	65	299
93	333031	333115	CA	TGCAAGAGTTTTGTGTGACCATTT	GTGTCTTGCCCCCTTACCGTATC	65	66	296
93	334740	334841	GT	CGTGCCTCAGGGAATCTATTTCT	GCATGTATGGAACCATCTCAGG	64	64	241
94	6565	6643	CA	ATCGCCAACATTGAGTCATGTGAA	GACTGGGTCTGTGCTTTGTGG	65	66	288
94	272318	272369	AC	AGTGTACCCTGCAACACTGTGCTC	AGAGTTGATTTCCGGCTGTGAGGAG	64	65	272
95	51436	51516	GT	CCGCATTATCAACAGTCACCTGAT	CACTGGGGTAAGCAAGTATCACGA	64	64	251
95	59529	59570	CA	AACATACTGACGGACGACGAAA	CGCTGCAAGTATCAAAGTACCC	64	64	290
95	92865	92928	AT	GGATATATGCGTTTGACCACCACA	ACGGAACCTTACCACATTGACCGTT	64	64	296
95	116098	116161	GT	GCTGTACCTTTTCGTGTGCTTGC	AGCAAGTAAATCACGTGCGAGCAC	65	65	300
95	162591	162634	GCC	GATGAGGTTTTGCAGGATCAGGAC	GCCGCTATAGTGGTCCAGCATT	65	64	207
95	270677	270752	GT	GCATTGTGGTCTTCATTGAGCTTG	GGCGAGATATAGATGTTGGGCAG	65	64	293
95	330754	330850	AC	CCATACACGGTCAGCCATTTACAG	GCTCTCTCCACAAGGATCAGCTC	64	66	207
97	139881	139947	TG	GTACAGAGATTGGCAGCTTCAACG	GCCACTTGACGACATTGCTGAGTA	64	65	262
98	233205	233246	TG	TGCCACACATCTACTCATGCCTTT	CACATAGCTCATACGGCAAACCTCG	65	65	270
98	305165	305225	CTGC	CAGAATCCAGACCTTAATCAGGCG	GTCTCTGTCCAGGCCAGCTTGT	65	66	245

99	110905	110963	GT	GTTTGGGCCCTACTGGGTGGTC	GCCTCTTAGGCTCTTAGGCTCG	67	64	164
99	116528	116576	TG	GACGCTCGCTTGCTGTTGTAAC	AACGAGGACATGAGGTGCTGTCAC	65	66	287
99	217763	217881	AC	CAGGTCTGCAGCCAGACATCAG	GCCAAGAATAATGCCAACGGTTTA	65	65	263
100	37921	37982	AGC	GCCTCAGCACTCAACCTACTAGCG	CTCTTGAGCCCAGGCTGTTACT	65	65	124
100	150197	150248	GT	ACTCAGGTTACTGCATTTCAAGGC	GCCCACTCCCACATCATAACAATC	64	64	284
101	80572	80622	TG	GGAATGCAGTGTCTACGCTTTGT	CACCCCTGACGATCAACCACTAGG	64	65	246
101	142228	142292	GCA-CAGCAGCA	GCCGTACGTGCTCTCCAAATC	GTGGAGGGTAGGGACACAGGGTAG	66	66	237
101	283030	283096	TG	AGGAAAGCACAAATAGGAAGGGTC	AGAAGGACATCAAGTGGTTCCAGG	64	64	273
101	312203	312264	CA	CAGGAACTTGTGCTACCTGATGGA	AGCCTCAAGAACAAGTGGTAAGCG	64	65	277
102	179129	179178	GT	ACACGCATGATGGGTCAACGAAG	TACTTCGCAGATGACGACAAGGTG	68	65	263
102	197872	197931	CA	CTGGACCCCTACAGGTCACAGTC	ACCAAACCTGGACTCAAGCACCAC	64	65	199
102	241287	241332	TG	CAGCGGGGTCTTCTTTGTGTAT	ATCACGCATACCACAATTACCCG	65	64	159
102	243400	243485	AC	CTACAGTGCTAATACCCACGCGCT	CGAAAAGAACTCCGTCCCATAACA	65	65	281
103	123253	123329	CA	CCAATTCCAACAAGCAGGTCCC	CTTGGTCAACTGTGGAGGGGTTAG	66	65	169
103	229551	229591	GT	CTGTTGAGGAGCGCCGAGACACT	TGTTATGGTGGTGTGTGTTGGGAT	69	65	179
104	69735	69807	CA	GAACGGGTTGGCCTTCAAACT	GGCTGTTGAAACAAGTGTGGGTTT	65	66	252
104	92657	92780	CA	GTAGACACAATCCCGCTCTCT	CTTCTCAGCTTTGCCAGCACAT	65	65	298
104	143884	143935	GT	GATACCTACACGGATGGAGACCG	AACACCTGCAAGGATGGAGAGTC	64	65	294
104	144818	144932	CA	TTGAACCCGTTGCCTTTTATTG	TGTGTGTATCATATGCGCGAGAGA	65	64	270
105	60060	60190	CA	GTAACACTCTTCCCACCGCTCATC	CGACCCATCTCGACACTAGGAGAA	65	65	294
106	61768	61830	CA	GTAAGGTACATAGCGTGGGCCGTA	CTGACTTGTCCCACAACCTCCAACA	65	65	297
106	89744	89788	GT	CTCCCGACGTTTTTAGACAAGTG	CGCCACCAACTTAAGAGAACATC	65	65	180
106	109490	109538	AC	CAGTCCGTTCTGTGCAAAACATC	CGAGTACGGCAAAGACTTCAAGGT	65	64	152
106	144329	144372	GT	ACCAGTCCAAGCTACCGTAACCAA	CATGACTCCCCGCATGATACTTTT	65	65	242
106	184577	184623	AC	GTTGAGGAGGAAAGAGCCGTTTG	GTGTGGAGCGAAGTTGCTGATG	65	65	235
106	262420	262514	TG	GGTATGAGAATCAACGGTGTGTGC	ATGACCCTATGGACCTGACACCTC	64	64	276
106	319976	320089	CA	CCATTCTTTGCGGTACCTTCCAC	AGCCTAGGATTGTACTGTGCGGAG	65	64	294
106	326111	326175	CA	AGCAGTAACAAACGCAATGACGAG	GGCGGTGAAGATCATAAAGGACAC	64	65	222
107	169377	169439	TG	ACATTGCTGAAATTGTGTGCCTGT	CCTCATCACATTTCTTGTGCCATC	64	64	245
107	189489	189567	AC	CTCGCACACACTTGATACACCTGA	GTTCCAAGGAGTTGGATGTGGGT	64	65	241
107	250309	250355	GCA	AGCGGAGGACGTTGAGGAAGAC	ACTCAGGTAGTGAAGGCTCCAGA	66	64	197
108	44511	44594	CA	CATAGCCAACCACCGAAAACCTC	TTGAAATACCGTACCGCAGGTG	65	64	300
108	184739	184798	TG	GTGGTGAGTACGTGAGCGGATATG	AAGCCAAACAAGATAAACAGGCCA	64	64	224
108	228944	229017	GT	AGAAAGTGTATTTCCGGGAGGGAG	CAATACCCCTCCTGAATCACAAGC	64	65	258
109	78174	78245	GCT	ACACTGATGCCACAGGTCTACAGC	GCCTTTGATCAGCTGCTTTGAGTT	64	65	229
109	110426	110496	GT	TGTTTCTATGAGTATGTGCGTGCG	GACAAGCCCTGTACCCATGTCATA	64	64	192
109	213595	213654	GT	TACGATTGGATGGGGTAGAGTGT	CATGCAGGCATCTATCTGGGAATC	64	66	286
109	275451	275514	AC	GCTCCGTCCCCTACTACAACCTCT	GTGAGGGGTGAGACACGAAATGTA	65	64	256
109	354267	354322	GT	GTCTGATGTGGCTGGGTGTTT	CTCACATGCAGCTTGCCCTCTAT	65	64	264
109	355393	355457	CA	GTTTCCTAATCGGCATTTCCATCC	GAGACTCTCGAGGCTTTTGGTGTG	65	65	293
110	38836	38883	CA	CTGCCTGTCTGGACTCCTGAACCT	TCGTGTAGGTGTACTCCGCTTTT	65	65	201
110	139620	139674	CA	GGCCCTGAATCTCATAACAAACC	CTTCAGCTGGCTCAGGTGTTCA	64	65	280
110	145938	145983	CA	TCTATGGATGCTGGGTTTCGCTAT	CGTGGAGTGATTAGCGTCAGGTTA	65	64	150
111	125204	125317	GT	GGTGATTATGGTGCTCAGGGAGAC	CGCATATGGGACGACATCTATTG	65	64	300
112	210574	210637	CA	AGTATCCCCCTATCTTGTCCCACC	GTAGCAGGAGTCGATGGTGACG	64	64	218
112	248922	249050	AC	ATCTGGTCCCTTGGCATTGACAC	GGGTGTGGTGAACCTGTGGCGAG	67	69	294
112	249551	249594	TG	GCTGTTGTGCTTGTGAGTTGGTG	AACCTGGAGGAACAAGGATAGGGA	65	65	242
112	256648	256808	GT	GGTGGGTGATTTACGTATCGCATT	CCCGTCGCTCTGTAACCTCTTGT	65	65	269
113	108634	108719	AC	ACCTGCCTCCTTGGCATCAAGC	GCGACAAATTGATGGTGGCTATAA	68	65	300

113	221863	221903	CA	GGTTGTTGGACGCTCTAATGCTCT	GCTCTTCTCATCTGTCGCAATCAA	64	65	288
114	31025	31223	CACG-CA	TAGCTAGGTACGGGTTTGGTGCAA	TATGCATTGTTGTGTGTGACGCTT	65	64	286
114	128749	128790	GT	GCATGTACCGTATGGGTAACGCTC	CCTCTACAAGCACGCACTTAAGCA	65	64	289
114	135616	135672	GT	GCCTTCCCTCGTTCCTCGTCT	AATTATACGGCAGAGGACCAGCAG	65	64	251
114	138442	138486	GGC	GTTGGTAGGTCAGTCGCCCTACAG	AGACACCTGAGATGCCACGCAC	65	67	295
114	193747	193837	TG	GTCACCTAGTCCCATTCTCAAGGG	CCATTCCCATTTCGAAGTGAAGTC	65	65	229
115	130276	130440	AC-CA	ATGGGGTTGGGATTTAAGCTGC	GGTGACAGGTGGAGGACTGGTAAG	66	65	300
116	16868	16915	CAG	CTCGGGTGAGTGC AATCAGTAG	CCTGTAAGCCCAGACAGGTC AAAC	65	65	258
116	166418	166485	CA	CGCTTGTACTAGTAGGCCTGTGGC	CAAGGGAGTATGTCCCCGACACG	65	66	279
116	192406	192483	CA	TGCTGTACCGTATTGAGACATCGC	CTCAACTCTTCGTGAGCCCAGAC	65	64	275
117	165634	165728	CA	AGACGCCAAGACAAACACATGAAC	ATAAGCTGGGCTTCTGCATCTACG	64	64	215
118	188139	188197	TG	TCATCAGAACGGTCTCATAGTCG	CTGTTCCAAGCCTTCGTGGTAGG	64	66	239
118	222959	223037	AC	GTGTGCTGTAATTGGAAGGTGCTG	ACATCGCACTCAGCGAAGTCAAAG	65	67	219
119	95194	95292	TG	ACACTTACGCTTCCCTACCCCATCA	ACTCCTTTTATTAGGCTGGGCCTG	65	64	273
119	196208	196261	GT	CTAGGCTGATGGTCTATGGGATG	CAGGACGGGTGGATGATGATTG	65	66	286
119	222180	222270	GT	GACTTCAGCGCAGTCGAAAAGTG	CGGGTCTTAGTTTAGCCATGATCG	65	64	223
120	272322	272449	GT-GT	TGTTGAACCGATCACCCTGCTG	GAACCCCTACTTCTGCCACCAG	65	65	300
120	296951	297038	GT	TTCATCTCCGCAATGGACATACAC	GCTTCTCCAGCAAAAAGACAAACAT	65	64	183
120	310551	310603	GT	GTGAGCCGCCCTAATTGATTG	GACATCGGTGTGTTCTGAGAGGAG	65	64	177
120	323767	323815	GT	AACTTCGACGTCCGACAGGACC	GCATACTCAACCGAAACCCCTTAC	66	65	295
121	229577	229650	AC	CAGTTCTACGCGTAATGTGCCCTTG	GATTTGAGGCAGGACGATATGAGG	65	65	185
122	174736	174832	TG	AGCAGTCTCTACATCACACCGTGC	AGGATCCATGTACCCTTATGGC	65	64	187
123	64535	64584	AGGC	CACTTTTTGGAGTAGTCCCCCAGC	CGACGCTTGAGTGTCTGTTCAATAC	66	65	290
123	143885	143924	TG	GTAAGCAACATGCGTGGAGGTGT	AAACAGGCGGTGGTAAGCAGATAA	65	64	196
123	181410	181507	AC	GGGAATAAGGATCGAGGGGAGTCAC	ACAGTAGCGCTATGACCACCGCT	65	66	276
123	197278	197337	CAG	ACAGTACACGGTCCCGCAT	GCTCATCGCAGCTCTGTTGTAAC	68	66	290
125	10743	10835	TG	ATGGCGGTTGGTTCAACGTTTTT	CTGTCTCAAACCCATTAGGCCAAC	68	65	300
125	85861	85906	GT	ACAATGCTACGATACCGTGCTCCT	GGTAGGTCGTGGGGCACAATAAAA	65	64	200
125	99142	99196	GTGC	AGGGCCTACTTCTACCTGGTGAGC	CCTGACCTTCCCTTGTACTGGA	65	64	173
125	159580	159626	AC	GCTTCTGCTGCTGACCTATGCTC	ACCTGTACTTCTCTCTGGTGCG	64	65	267
126	20838	20900	GT	GCGTGTTCGATGGTTAGGTGTTA	GGGGAAGAGGGACAAAGGTAGAGA	65	65	247
126	27008	27093	AC	GCGCTCACAGTTAGCAGTGTGTT	GCCGTA CTGCCTGATGTACGAAGT	64	65	209
127	64906	64982	CAA	CAAAGGCATACACGGGAATCTAGC	CCGCGTTGTGTATGCAACATTTAT	64	64	148
127	100934	100978	AC	CGCATCAACCTTACCCACCTACTC	GTACACCAGGTGCGATGACACCGT	65	65	169
127	101832	101914	GT	ACCTGGGCTACAGCTATGAAGTGG	GCTAGCTCAGCAATCGACAGATCG	64	66	254
127	106053	106104	GT	AGACAGCGAGAGGATCGCTAATTT	CTTGAGAGATGTGCAAAAAGCGTGA	64	65	127
128	113660	113738	ACGC	TTTGTAAACCCGAGCAATAGTCAA	GGGTTTTTGCCTCCACTGAGACTA	64	64	290
128	174907	174984	AC	TGAGGGGTTTTACTTCTGTATGAT	GTGGTGGAGAACCCTGACAAGAT	64	64	218
128	183102	183156	CA	AAACACCCACCTAAGCACACG	CCACTACCTCCACCCTACCAAACA	65	65	293
128	258792	258845	GGCT-TGGCTGGT	GTACGACCGCCACATTTTCTAAC	GGAACGAAAAGTTAACTCCCCACC	64	65	279
128	260434	260481	AC	CACCCAAAGTAACCAGTAGCCAG	TAAGTGTAGGGCCTGTTTGGCTGT	65	65	296
129	104447	104515	GT	AAGGTCAAGGCGGCAGAGTACAT	GTAGGTACGTGTTTGCCTGTACGG	65	64	241
130	46880	46966	AC	AGAATAGCCACTTGGGAACGGAAC	ATCCGTCCTTGAGGGGAGGTTTTAC	65	66	295
130	72233	72343	GT	CATTGAATCAAACACTACCTCCCG	AACCTGCTCGCTACACACAGAG	63	65	297
130	109035	109090	CA	GTGTGCTGGTACTGGTAAAGTGG	CTAGTCCCCGTTTCTTGAATG	65	64	233
130	134497	134591	CA	TCAGCAACCAGCCAGATTATTACG	GTTGATCGCTCGTACACCTGAGT	64	65	263
130	147753	147796	CA	ACCAACTACCCACGCAGAGTC	CAGGTGATGTAGATGGCGGAGG	64	64	136
131	44213	44272	GGA	GTTGTTCTGGAGCTCTTCTTTGC	CATATGTCCTGGGTTTCCAGATGC	64	65	292
131	90028	90070	TG	CCTATGCATGTCCCTAGCTCTGCT	GAGGATGTGGGCAAAGGAACATAC	65	64	245

131	191156	191244	TG	CAGTCATCAGCTTCACTGCTACGC	ACCGTCATGCAGTGTGAAATTGTT	65	64	247
131	220203	220249	CAG	CAGCTTACAAGGGCCTCAACAGG	AACTCCTCATTACACCCCCGTA	66	64	268
131	257658	257709	GT	ACATCGTCAGCGACAGACACAAGT	TCCCCACACAGGTGAACACACTTA	65	65	250
132	84954	84995	CTG	CATCAGCGTTTATTACCCGTCAC	GTGTCAGATGCACTCATGTCCGA	65	65	288
132	130602	130720	CA	CAAAGCACATTGAGTCTCACCACA	TTGAGTCATGGGGTAACTGAAGCA	64	65	256
132	155566	155627	AC	CACTAAAACCCGCAATCACACAAA	CTACTCCCACCCCTCTATCCACCT	65	64	290
133	83668	83712	AC	CGATGAAGCACITTTAAATGCCC	CTTATGACGACGGCGATGTGAC	64	64	258
133	107738	107777	CA	AAGCTGACCGAGTCCATCAACAC	GGGGATATGTGCAGGGAGTGTATC	64	64	292
135	65421	65491	CA	TTTGATTTTACCCTGGGTATGGC	CAGCATCACGCTGAGTGACACG	65	67	300
135	125913	125956	CA	CGTCTTGATGCACCAACGTTATTC	GCACAGGCGGTAGAGAAGTAGCAT	64	65	273
135	143117	143159	GCG	ATTTTGCTGTGCGTCTCACTTGTC	ACACAGGCTACCCACGCTACTACC	64	64	260
136	61118	61163	GT	GCGTGTTAGGATTCCACACGTTTA	AACACACACGACGCCCTTTAC	64	65	111
136	74827	74869	CTG	GCAGCCGTCCTAATGTCCAAGATA	ATCCTGTCCGACTTCTGCGATG	65	65	270
136	90556	90625	CA	AACCTTTCTGTATCCGCTTTGT	CTGCAGGTTGTAAGGCAGCGAG	65	66	166
136	186324	186373	AC	GGATAGATGGTGGAAGCGGCTA	GTCACGTGCATCTCACCTCCTACA	64	65	298
137	3675	3760	CA	CTGGGGATGGTGAGAGGCCAAAC	GTGTATACGGTATCGTGTGCTG	67	65	232
137	68816	68871	CA	GGGCTTAACGGCTTAACGTAGACC	CGTCCATAACGGCCTGCTTAC	65	67	268
137	82222	82280	TG	GCGTACGGTGCATACTTTGTGAAC	GTGGTACACAACCTGGCTTCTTCCC	64	65	271
137	152872	152912	GCA	CAGGCACTGGCATCAAAGAAGAG	GTCGAGCACAGTCATTGCCGGTAG	65	69	287
137	217227	217308	GT	ATATGGACACACGGAAGGAAGGAC	ATACACATACGTGGCGGCTCAAAG	64	66	264
138	70703	70763	AC	TTGTTGCTTTGTCTGTTTTAGCGG	GTGCAATCAACCGCATCAAGTATT	64	64	258
139	201936	202048	CAG	TCATCCATGAAGCACCTACAGACG	AGCGTACTCCTGTCTGTGCGACT	65	64	294
139	225474	225586	CAC	AGAGCGCAGCTAAACACACAACAA	AGGGGAAGCGTGTGTACTGAAAAG	65	64	221
140	97510	97565	CAG	TGTTCAACACCTTTGAACTGGAGC	AGCCAGTGACGGCCTAGAGGAG	64	66	185
141	4259	4301	CAG	ATGATGACTGATGAAACACCTGGC	CTCCTGAAGCCCCAAGCTAGAAAC	64	65	289
141	111506	111589	AC	GTGATGACATACAGTGCTCCACA	AGCAGCGGGATGGGTCTAACCT	64	67	245
141	129166	129264	CCA	GTCTGATTGCTTGCCCTGTGTTGT	GCTCCCTACCTGTGTGGAGTGAAT	66	64	266
142	96427	96483	GT	TTGAAGAACACACGAAACATTGGC	ACGTGCTCCATGGGAACAAAAT	65	64	146
142	227280	227379	CCA	TGCGGCCAATAAAGTTTCGTAAATC	CAGCGTGAGCATGAGGATAGTGAT	65	64	219
143	131879	131923	TG	TTCAGGTGCTGATCGAAAGGTATG	GCAGCAGTCACAATGTTGATGAGA	64	64	291
143	178667	178742	CA	GTCGGATGGAGCAAGACAGGTTAC	AGATGGGTTTCAGGCAGTTAGACG	65	64	282
143	186550	186605	GT	CTGCAGCCAATCCACAGGTACTC	TCACAGACCAACACCTTCTCAAGC	65	65	290
144	35311	35413	CA	AAGCCAGCTTTAGCAGTCACACAA	CATGAGAGTGCGGTTACCGAAAG	64	65	183
144	190937	190984	TCC	GCACAAGTACGCGTCTCCTAACCT	ACCTATTCCGCAGACAGCAAGAAC	64	64	279
145	109816	109879	CGC	CTCCTGATTTTGTCACTGTCACGG	GTACCCTTACCTGGCTGCTGTGTT	65	64	187
145	216542	216582	TG	ATGCCTCATCTCCCACCTTGAC	CACACTAACCGCTCTACTTGCACC	64	65	299
145	219911	219975	TG	ACTATGCTACCACGGAACGGTCAT	GTCCTTCAAACAGCTATGCCGAGT	64	64	243
146	95260	95300	AGC	CTAGAGATATGGACGTTGGCGACC	GTTGGACAACCTGCCACGGAGTA	65	64	222
146	161505	161599	CA	GGGCTTGTACTGGTCCACAGTGTC	CGGCATACGGAACCTGAAGTTAGT	66	64	277
146	209358	209467	AGG	CCGCCAGGAGACAAGGTCAAAG	CCTTTCCTCCCTCAACAATTCTCA	67	64	204
147	39392	39451	TG	GTAGGCCGGATCCAGTTTGAAG	TAACGTACCACGCCACAACATACG	65	65	258
147	54176	54275	AG	TGAGTCGGTGGTGAAGTGTGTGA	CTAAGCCACAGCAGCATGACAGAT	65	64	272
147	124134	124186	GT	GCGCTGCCAGTTAGTTAGTTGGTG	ATTGCACGCGTACTGCACAAAG	66	65	297
147	161181	161236	GT	GGAATGCCGTGCTAATAGGGTG	ACTCATCTTAAATGCCCTTTTCG	64	65	300
148	113974	114050	CA	GACCTTGTCCTAGGTCACGCTT	GTAAGACGCGTATGGTGGGGAATA	65	65	192
148	124652	124718	CA	TAAGGAAACGGTGAAGGATGTGT	TAGAAGGAGGCGATGACTCTGGG	64	64	256
148	141832	141952	GT	CGTGGAGTCTTATAGCCCTTGT	CCCATTCAAATATTTACAGGGGTT	65	64	287
149	81195	81260	TG	CTGGCCGTAGAAGTAATACCTGCG	CTGCTCCTGTGTTCCACCTATCCT	65	64	195
150	81079	81269	CA-AC	AAACTGACTCTCGCCCTTTGAC	AACTCCACATCGTCAATGAATGTC	65	64	250

150	112491	112673	AC-AC	CTATCGGTTTTTGACTCGTGAGGG	AAGGCGCTGGAGTTGAAGAACTG	65	66	296
150	146633	146691	AC	CACAAAACCACAGCCTATCTGCAC	CTCTCGCTCCACCAGGTCTTGGAT	65	69	224
150	153060	153108	GT	GTGCAGATCTACTGCACCAACGAG	GGCCAGCAGCGATAGACGTAGTAG	65	65	225
150	197808	197910	TG	GCTCCGTGTCACTGGTGAGAA	GTACCCTTGGCCAGTTGCATGTT	67	66	239
151	14023	14105	GT	ACGTTGGGCTGGTCCACGTACA	TTCAAACCCACCAGTATCACGGTA	69	64	168
151	67457	67524	CA-ACACACACAT	CTCCTGTCTGATGCCATCTTATCC	GTTGTCTGCTTGTGAACACGACGTA	64	66	236
151	67977	68025	CA	AAATAGTTATGGCGAGCCGCTCTT	CTCCTCGTACGCGGTGGTCTTG	64	68	271
151	132940	132986	CA	GACCAGGTGTGGCGATCAAATAC	CACTGTTCTATTTGCGTTTGCCTG	64	64	257
152	30941	31014	AC	GTCTCTGTCAACACAGGAGAGCG	GAAGAGCCAGTGCCTGAAGCTCTA	64	65	283
154	60229	60374	GT-GT	GACTACGACCCCTCCGGTAGGTA	GGAGGTAGGACGAGTGGAGGTTCT	64	65	284
155	147328	147373	CA	ACACAGGCAGTTTCTCTAGCCTGC	AGGAGGCATGTCTGTTTGTGAGTG	65	64	212
155	170596	170653	CA	ACACACACCATTCTTTTTGAGCA	AGTCAGGGCAGTCAGAACCAGG	64	65	238
155	176551	176608	CA	GTGATCCCAGCGTCAGGCACAG	GAATGACGGTTAAGTGGTGTCCG	69	64	280
155	178472	178519	TCC	CTGAAAGCTATCGTAAGGCCGTTG	GGCAGCGATTACAGCTGGAGAATA	65	65	272
156	3448	3543	TG	AGCTCGCCAAAGATGGTGTAGTG	TCTCATCACCACACTGTTAGCTGC	64	63	270
156	8941	9014	GT	ACAGTACCCATGCAACAAGAAGCA	TCCCTTTCGCTTTCCTACTCACAC	65	64	265
156	14351	14454	GT	GTGGAAGGCAGTTCTGGTGTGTT	CATGACCACAGCAGACTACAGC	64	65	201
156	79002	79117	AC	TAACGGGTTACGGCCTGAAATTGT	GCAGCACCTGCGTAGATGGGTC	66	68	287
157	44903	44998	CA	ACTGGGTTGTACATACATGGTGG	ACCTCAACCTTGGGGACGTAAAAT	65	64	193
157	85960	86064	GA	GGCCTGCAGTTGTGTACAATCCTA	CAATCAGCACATCACACAATCCTG	64	64	296
157	172201	172334	AGC	CCTGGCATAGTTCTCGTTACAGGG	ATGAATTGATGATTGACAGCGCAT	65	64	288
157	183302	183358	AGGC	AGGTAACTTTGTGTGCTGGGGTCT	CATGACCTCAGGTACCCTGCATC	64	65	234
158	105854	105917	CA	CAGTGACAGGCTGAAGCGGTACTC	ACCAGCTACCGAGCGTTATAGCAA	66	65	176
159	19078	19147	AC	AATCTTGCCAGCGTGAACATTCA	TGTGGAGTCTGCCGATAGATGAAG	64	64	291
159	177254	177364	AC	GTATTGCGTACTGGGTCCAAGCAT	AAGTACACGTTGTCTGGGATGTGC	65	64	296
159	193544	193613	GT	TGGGTGTAAGTGTGCTTAGAAGGGA	AACATCATGAATGACCATGAAGCG	65	65	173
160	89004	89059	GT	ATAAAGCCCATGTCAACCATGCCT	TAGAAAATCCGGTTGAAGGACCC	66	65	298
160	155301	155419	CACG	CGCTCCTTTTCTTTTGCCTATC	CTACGTCAACTGGGCACCAACA	64	66	290
160	158473	158555	CAGG	TGTCACTTTGTGGGGTGTCTGGTA	CTGACACTGTGACGACATTGCAC	65	64	282
161	129743	129825	AC	GTGGGGAACCTAAGGAAGCTGGTC	GGTGTACATGTAAGTGTGGCTGGC	65	64	292
162	23206	23277	CA	CTTAACCCAAATCCTGCGCACTAC	GTCCACGTCGACAGGTTGGTTC	64	66	277
162	32582	32627	GGTT	CGCTATGTCGGAGTAGAAGATGGG	GATTTGAACTGGGTGCCCTTAACC	65	65	280
162	67552	67600	CTG	GTATCGCTGGCGGAGTCCAAGT	CCAGAGGAAGAGGCTAGGCACAA	66	66	158
162	78501	78573	CA	AAAGCATTGCGGAAGTCACCAG	GAAAAGCGCTTACTAGTTGCTCGC	65	64	248
162	81088	81170	GT	ACAGCACAATGGGAGAAGACACTG	TGTTGATCTGGATGAGAGTCTGACG	64	65	289
162	96529	96605	TGC	TAGTGCTGCATGAACCCACACT	GTTGCTTCCAAGCCGCATTGTCTT	66	69	300
164	12318	12406	AC	CAAGCATGTCACCATCGTAAAAT	GACAATGCCAGCTAGGACATGC	65	66	193
164	46571	46665	CA	GCGTTAGTACGGTGCATGTGATCT	GTCTACGCAGTTACACCAAGGCTG	64	64	267
164	67238	67296	GT	ATAGCATTTTGGGGGTAAGACACG	GCAATCCAAGCTAGCCAAGTAAGC	64	64	253
164	161269	161363	GT	GTCCCTCATCTCCTTCTGCATCC	CGCACGAGTTTACGAACAATAACG	65	64	284
167	137827	137876	GGA	CGCTGTTGTGGACATCTCATCTCT	GTA CTGCTGGCAACCTCCTCCA	65	65	257
167	145518	145601	CA	ACGCAGTAATCTACAAGCGCAACA	CCAGTAGAAAAGACCACGGCCTATG	65	65	221
168	98883	98924	TGC	TCCTGGAGAAGGAAATAGCTGTCTG	AGCTGCTGTTTACCTGGCACT	65	65	257
168	108586	108680	GCA	CTACCGTGCCTAATGATGATGC	GCTGAGAAAAGATGTCAACCACCG	66	65	265
169	42072	42238	AC	CAGCGTCAATCATAAATGCAGACC	ATCTCCAAGCTGCAGATCGACAC	64	65	296
169	146224	146291	GT	CCTTTGTCTGCAAGAGAACAGCAG	CACACCACCAATCGCCTATACTT	64	65	281
170	83478	83587	CAG	CAGGGGTACATCCAGCACTGCTAC	AGTATCAGCAGCGTCCGAAACAGG	66	64	297
170	129270	129319	GCA	TTGCTCCAGCTGAATACTACACGC	GTAGCCGTAAGATGCGCGGTGAG	64	69	242
171	71600	71661	GT	GGAGGAGGTGCAGAGCTACAAGAA	CCTTCCGACTTGCCACCCAACCTAC	65	66	269

171	97518	97569	TG	TCGAAAGCAAAACGCCCATATTAG	TGCATGCAGCTGTTGCTACACTTA	65	65	296
171	225630	225745	GCA-AGG	GTCACCATTACCACACTGATCCGA	AACTGCGCCCATATCCATTACAAG	65	65	240
173	72506	72571	CTGG	CCACATATGAGGAGTGTCTGTCACG	CAGGTGTCAGCCATTGAGAGAA	66	65	295
174	6765	6858	CA	ATGAGTTGACTTCTGGACACCACG	GAGACCGCAGGCATAACATACACA	64	65	187
174	41701	41767	TG	GACACGGCTGTACGACTTGGTAGG	TGGAAGTCGGTGTGCAATGATTAG	66	65	279
174	106235	106305	GT-GTGTGC	AGCTTCGTATCCAGATCAGCAC	GTTGCGTGAGGGTGGAAACTTGTA	65	66	174
174	140819	140859	TG	GATCATGAAAGGATCGGACTGGAC	TAACAGGACCCGTGCTAAACTG	65	64	297
177	115917	115978	CA	AATAACTCCCATGCCCCATTAC	AAGGAGTTCTACGTGGTGCACTCC	64	65	280
177	117026	117138	AC	GTCCACACACTTGCCGTACCATAG	GATGGATTGATAGGCAGGGGCT	64	65	231
177	120997	121083	CA	ACTTAGTAGCCAAGCCAAAATCGC	TATTCGCAACAGGTTTTCAACCAA	63	64	288
177	123145	123206	TG	GACCAGAGCCAGGAAGATCTGAAG	TAAGTAGCGCGGGGAAAGACAATA	64	64	292
177	125119	125172	GT	CTTCTCCTTAATCCGCTCCTGTGA	TAGCAGTACAAGCCCAATGCACAC	65	65	164
177	129323	129378	TG	ATGGAGGAGGATTCAGGTGGGTA	GCTAGCTGATCCGTCTCCTGACA	65	65	269
177	133703	133765	AC	GCTGATCCCATACGAAAGATACCG	TGTCCGAGTACAAGAACTACCGCC	64	65	291
178	39917	40007	CA	TACTGCTCACACGACAACCACTCA	TGGTGTATAGGCCGGGACAGTAAG	65	65	269
178	49869	49955	GGT	ACACGGTGAGAACAGGTGTTGAGA	CCGTGATTGTTGTAACCCAAACC	65	65	206
178	110986	111058	GT	GCACCGGTAGCGTTTGCAATTAC	CTATGGTGGCGTAAGTCTTCCTT	65	64	293
179	25919	26005	TCC	CTAAATGAACGCACCCGTATAGCC	ACATAGGCACGGATGTCGAACCTTG	64	66	269
180	94298	94375	TG	CCAGGAGAACCTGGAGAGAGAGTG	GCTCTGCAAGTCTGGGAGTGTAGC	65	65	148
180	128462	128594	AC-AC	CACAAGTCAGTAAGAACCCGAGCA	GTGTTGGAACAGGAAACGGAAAGA	64	65	288
181	71496	71552	CAG	GTTTCGATGTTTGGCACTTTTGTCC	CAATCTTAAAGCTCTTTCGGCCCT	65	64	300
182	136790	136837	TG	TTGTTAGAGTTTGTGTGATGGCG	GGGATGCAACCAAAGAGAGAAGG	65	65	285
183	58205	58285	TG	GAAGTGGATGTTGGTTGGTACTG	CAAGAGGAAAGGCTGATTAAGGGG	65	65	266
184	34560	34644	TGCC	TCCAAGCTGGTGAGAGGTGATATG	GGAGGTGCAGGGTAGTTAGATGGG	64	66	296
184	108769	108864	CAG	CTCCAGCCTTGAGAGACTCTGCTG	ATCCCTGGGGCACTGTGAGAAG	66	66	264
185	58981	59025	CCAA	GTCTCATGCTTCGCTGCGCTAGT	ACCTTGATTGGATTGAGGCAGAAC	67	64	192
185	69304	69383	AC	GCCCTGTCAATTTGGAGAATGAAT	GAAGATGTTGGTCTGCAGGGTTCT	64	65	225
186	58344	58402	CA	TTTTCTACAATGGTCTGTCCCCC	GAAACCATGCGGTAATGCCAAT	64	65	298
187	109150	109200	GT	CTGCTGTGGGCCAGTAAGACCTAT	CAATCACATGTTGGCTGCTTGTC	64	64	272
188	85780	85837	CAG	ATCACAAGAATGTAGAGGAGGCCG	TACCCCCAGTGTCTTAGCCAATTC	64	64	263
188	130370	130417	TGC	CCCTTGACTATTCGCTCTTGTTG	CCATCAGACACATTACGTGGACCT	65	64	288
189	52043	52090	CGC	CATGGTTACACAAGGATCGGGTTT	CCTCGCTGATCCTGTTGAAGCTAT	65	65	290
191	26757	26807	CA	GCGAGTGCCCTAAAGAAAAGGAAA	GTTTGTCAACACCGTCAAGGCTTC	65	66	281
191	79651	79699	CA	GTGACAAGGATGAGGGCAAACGAG	AGCACCCATTCAACAAAAGCATGT	65	65	127
191	93551	93647	TG	ACAAAGGAAAGCATGGTGCAAAGT	GAGTGGGCGAGACAAGATGGTACT	65	65	227
194	60658	60725	AC	CAAACGTGATGCCAATGAAATCC	GATGGTCCAGTTCGATGCAGTG	65	65	223
195	56945	56993	GCC	GGACAAGTGGGCACTCTGCTGTT	GAGGTCTGGTGGGCGCATTAG	66	69	290
196	33883	33949	CA	GGGTGTCGGTGTAGGTAATCTGG	CAGGTTGGTGTGTTACCTTTGAC	64	64	294
197	95850	95947	AC	GCGTCTCGTCTGTCTAGTTCCCTC	TGCAATCTCCTAACCAACTTGACAG	64	64	265
198	52647	52687	TGA	GTAAGTCTGAGTTTCTTCGGGGGCT	CACGCTTTGCTCATGGTTACTACG	65	65	235
199	97686	97727	GCC	GCCATCTGTCCCTCTAGCACGTA	TGAGTCCACCTTCTGGACCTCTG	64	65	246
200	38892	38960	AC	TCAATCTATCCGCTTGTCAATGGA	CAGCAGGTAGGTGTTTACTACGCC	64	65	137
201	43611	43666	CA	GGCACGTGTTACTTGAGAGCGATA	GAGGCTACAGGGGTAAGCGGAT	64	65	120
202	115429	115469	CA	ATCTCTTCGCTATGCACGGTAAA	CATGCTTCTTCCACCTCCGCTAT	65	64	295
207	12380	12472	CTG	CCCTTCTCCTCGATGGCTTACG	CGACAGCCAGGTGACGTCTGTG	66	68	246
207	62016	62082	CAG	GTGTAACGCACAATCGATCCACAC	ATGTGCGTCAACATGCTACAATGA	65	64	208
207	91537	91577	CA	ACAAGTTCGAGTGTGAGTTGGGA	TGAGTGTGTTGCTAGCGTCTGTG	64	64	264
214	38196	38248	GCT	CTCCGCTTCTGCTTCTTCAATTAT	CAACTGAGATCCCCTTTCGAGCTA	65	65	295
215	73192	73338	CA	AACGTGCATGAATGCTCTGTAACC	GGAAACATATGGGCAAAGGACTTG	64	65	289

216	48687	48860	CA	TCCCACGCATCTGAGAATGATAGA	CAAAGACAAGGCCACAGATGTACG	65	65	282
221	82002	82073	TG	CTTTGATGATAGAACGCGTCATGC	ACGTTGTGCTCTTACAAAAGCCGT	65	65	293
231	123185	123230	TG	ATGAGCCGTTTCATTGATGTGTGT	GTTTTGAGAGGAGAGATGGCGAGA	64	65	179