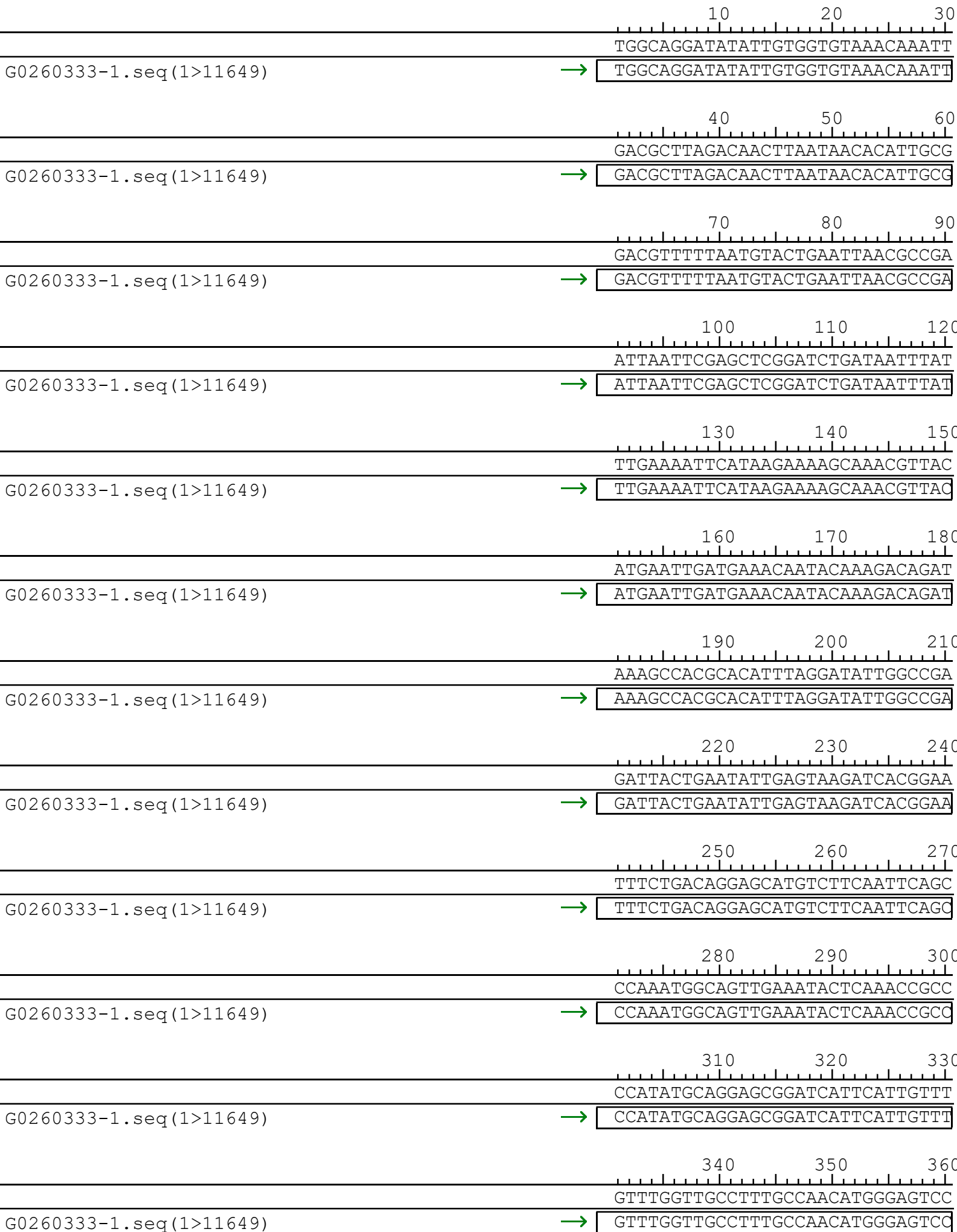


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		370 380 390	AAGATTCTGCAGTCAAATCTCGGTGACGGG
G0260333-1.seq (1>11649)	→		AAGATTCTGCAGTCAAATCTCGGTGACGGG
		400 410 420	CAGGACCGGACGGGGCGGTACCGGCAGGCT
G0260333-1.seq (1>11649)	→		CAGGACCGGACGGGGCGGTACCGGCAGGCT
		430 440 450	GAAGTCCAGCTGCCAGAAACCCACGTCATG
G0260333-1.seq (1>11649)	→		GAAGTCCAGCTGCCAGAAACCCACGTCATG
		460 470 480	CCAGTTCCCGTGCTTGAAGCCGGCCGCCCG
G0260333-1.seq (1>11649)	→		CCAGTTCCCGTGCTTGAAGCCGGCCGCCCG
		490 500 510	CAGCATGCCGCGGGGGGCATATCCGAGCGC
G0260333-1.seq (1>11649)	→		CAGCATGCCGCGGGGGGCATATCCGAGCGC
		520 530 540	CTCGTGCATGCGCACGCTCGGGTCGTTGGG
G0260333-1.seq (1>11649)	→		CTCGTGCATGCGCACGCTCGGGTCGTTGGG
		550 560 570	CAGCCCGATGACAGCGACCACGCTCTTGAA
G0260333-1.seq (1>11649)	→		CAGCCCGATGACAGCGACCACGCTCTTGAA
		580 590 600	GCCCTGTGCCTCCAGGGACTTCAGCAGGTG
G0260333-1.seq (1>11649)	→		GCCCTGTGCCTCCAGGGACTTCAGCAGGTG
		610 620 630	GGTGTAGAGCGTGGAGCCCAGTCCCGTCCG
G0260333-1.seq (1>11649)	→		GGTGTAGAGCGTGGAGCCCAGTCCCGTCCG
		640 650 660	CTGGTGGCGGGGGGAGACGTACACGGTCGA
G0260333-1.seq (1>11649)	→		CTGGTGGCGGGGGGAGACGTACACGGTCGA
		670 680 690	CTCGGCCGTCCAGTCGTAGGCGTTGCGTGC
G0260333-1.seq (1>11649)	→		CTCGGCCGTCCAGTCGTAGGCGTTGCGTGC
		700 710 720	CTTCCAGGGGCCCGCGTAGGCGATGCCGGC
G0260333-1.seq (1>11649)	→		CTTCCAGGGGCCCGCGTAGGCGATGCCGGC

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		GACCTCGCCGTCCACCTCGGCGACGAGCCA		
G0260333-1.seq(1>11649)	→	GACCTCGCCGTCCACCTCGGCGACGAGCCA		
		760	770	780
		GGGATAGCGCTCCC GCAGACGGACGAGGTC		
G0260333-1.seq(1>11649)	→	GGGATAGCGCTCCC GCAGACGGACGAGGTC		
		790	800	810
		GTCCGTCCACTCCTGCGGTTCTGCGGCTC		
G0260333-1.seq(1>11649)	→	GTCCGTCCACTCCTGCGGTTCTGCGGCTC		
		820	830	840
		GGTACGGAAGTTGACCGTGCTTGTCTCGAT		
G0260333-1.seq(1>11649)	→	GGTACGGAAGTTGACCGTGCTTGTCTCGAT		
		850	860	870
		GTAGTGGTTGACGATGGTGCAGACCGCCGG		
G0260333-1.seq(1>11649)	→	GTAGTGGTTGACGATGGTGCAGACCGCCGG		
		880	890	900
		CATGTCCGCCTCGGTGGCACGGCGGATGTC		
G0260333-1.seq(1>11649)	→	CATGTCCGCCTCGGTGGCACGGCGGATGTC		
		910	920	930
		GGCCGGGCGTCGTTCTGGGCTCATCGATTC		
G0260333-1.seq(1>11649)	→	GGCCGGGCGTCGTTCTGGGCTCATCGATTC		
		940	950	960
		GATTTGGTGTATCGAGATTGGTTATGAAAT		
G0260333-1.seq(1>11649)	→	GATTTGGTGTATCGAGATTGGTTATGAAAT		
		970	980	990
		TCAGATGCTAGTGTAATGTATTGGTAATTT		
G0260333-1.seq(1>11649)	→	TCAGATGCTAGTGTAATGTATTGGTAATTT		
		1000	1010	1020
		GGGAAGATATAATAGGAAGCAAGGCTATTT		
G0260333-1.seq(1>11649)	→	GGGAAGATATAATAGGAAGCAAGGCTATTT		
		1030	1040	1050
		ATCCATTTCTGAAAAGGCGAAATGGCGTCA		
G0260333-1.seq(1>11649)	→	ATCCATTTCTGAAAAGGCGAAATGGCGTCA		
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		CCGCGAGCGTCACGCGCATTCCGTTCTTGC		
G0260333-1.seq(1>11649)	→	CCGCGAGCGTCACGCGCATTCCGTTCTTGC		

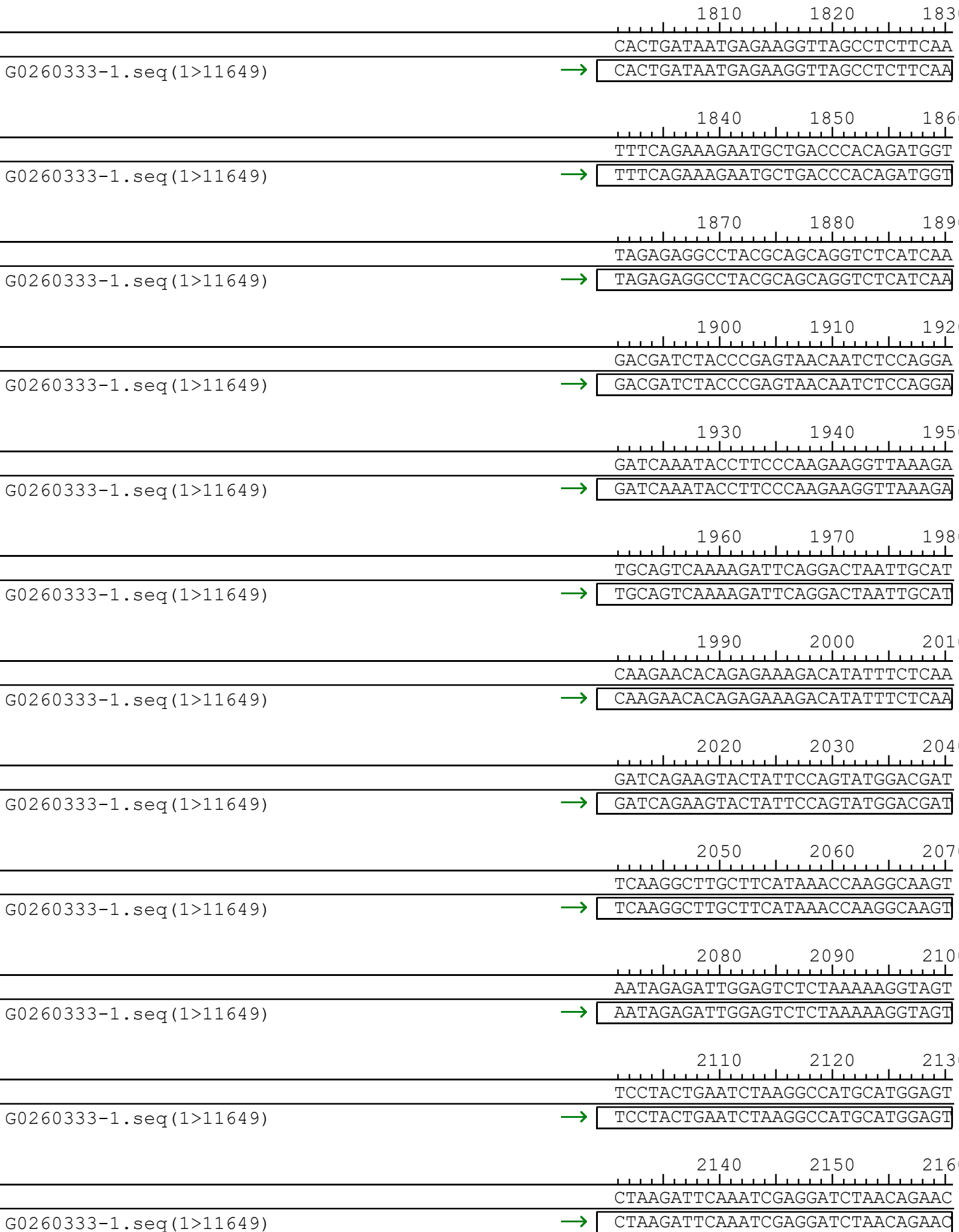
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		1090	1100	111
		TGTAAAGCGTTGTTTGGTACACTTTTGACT		
G0260333-1.seq(1>11649)	→	TGTAAAGCGTTGTTTGGTACACTTTTGACT		
		1120	1130	114
		AGCGAGGCTTGGCGTGTGACGCGTATCTATT		
G0260333-1.seq(1>11649)	→	AGCGAGGCTTGGCGTGTGACGCGTATCTATT		
		1150	1160	117
		CAAAGTCGTTAATGGCTGCGGATCAAGAA		
G0260333-1.seq(1>11649)	→	CAAAGTCGTTAATGGCTGCGGATCAAGAA		
		1180	1190	120
		AAAGTTGGAATAGAAACAGAATACCCGCGA		
G0260333-1.seq(1>11649)	→	AAAGTTGGAATAGAAACAGAATACCCGCGA		
		1210	1220	123
		AATTCAGGCCCGGTTGCCATGTCCTACACG		
G0260333-1.seq(1>11649)	→	AATTCAGGCCCGGTTGCCATGTCCTACACG		
		1240	1250	126
		CCGAAATAAACGACCAAATTAGTAGAAAAA		
G0260333-1.seq(1>11649)	→	CCGAAATAAACGACCAAATTAGTAGAAAAA		
		1270	1280	129
		TAAAACTGACTCGGATACTTACGTCACGT		
G0260333-1.seq(1>11649)	→	TAAAACTGACTCGGATACTTACGTCACGT		
		1300	1310	132
		CTTGCGCACTGATTTGAAAAATCTCAGAAT		
G0260333-1.seq(1>11649)	→	CTTGCGCACTGATTTGAAAAATCTCAGAAT		
		1330	1340	135
		TCCAATCCCACAAAAATCTGAGCTTAACAG		
G0260333-1.seq(1>11649)	→	TCCAATCCCACAAAAATCTGAGCTTAACAG		
		1360	1370	138
		CACAGTTGCTCCTCTCAGAGCAGAATCGGG		
G0260333-1.seq(1>11649)	→	CACAGTTGCTCCTCTCAGAGCAGAATCGGG		
		1390	1400	141
		TATTC AACACCCTCATATCAACTACTACGT		
G0260333-1.seq(1>11649)	→	TATTC AACACCCTCATATCAACTACTACGT		
		1420	1430	144
		TGTGTATAACGGTCCACATGCCGGTATATA		
G0260333-1.seq(1>11649)	→	TGTGTATAACGGTCCACATGCCGGTATATA		

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		1450 1460 147	CGATGACTGGGGTTGTACAAAGGCGGCAAC
G0260333-1.seq(1>11649)	→		CGATGACTGGGGTTGTACAAAGGCGGCAAC
		1480 1490 150	AAACGGCGTTCCCGGAGTTGCACACAAGAA
G0260333-1.seq(1>11649)	→		AAACGGCGTTCCCGGAGTTGCACACAAGAA
		1510 1520 153	ATTTGCCACTATTACAGAGGCAAGAGCAGC
G0260333-1.seq(1>11649)	→		ATTTGCCACTATTACAGAGGCAAGAGCAGC
		1540 1550 156	AGCTGACGCGTACACAACAAGTCAGCAAAC
G0260333-1.seq(1>11649)	→		AGCTGACGCGTACACAACAAGTCAGCAAAC
		1570 1580 159	AGACAGGTTGAACTTCATCCCCAAAGGAGA
G0260333-1.seq(1>11649)	→		AGACAGGTTGAACTTCATCCCCAAAGGAGA
		1600 1610 162	AGCTCAACTCAAGCCCAAGAGCTTTGCTAA
G0260333-1.seq(1>11649)	→		AGCTCAACTCAAGCCCAAGAGCTTTGCTAA
		1630 1640 165	GGCCCTAACAAGCCCACCAAAGCAAAAAGC
G0260333-1.seq(1>11649)	→		GGCCCTAACAAGCCCACCAAAGCAAAAAGC
		1660 1670 168	CCACTGGCTCACGCTAGGAACCAAAGGCC
G0260333-1.seq(1>11649)	→		CCACTGGCTCACGCTAGGAACCAAAGGCC
		1690 1700 171	CAGCAGTGATCCAGCCCCAAAAGAGATCTC
G0260333-1.seq(1>11649)	→		CAGCAGTGATCCAGCCCCAAAAGAGATCTC
		1720 1730 174	CTTTGCCCCGGAGATTACAATGGACGATTT
G0260333-1.seq(1>11649)	→		CTTTGCCCCGGAGATTACAATGGACGATTT
		1750 1760 177	CCTCTATCTTTACGATCTAGGAAGGAAGTT
G0260333-1.seq(1>11649)	→		CCTCTATCTTTACGATCTAGGAAGGAAGTT
		1780 1790 180	CGAAGGTGAAGGTGACGACACTATGTTTAC
G0260333-1.seq(1>11649)	→		CGAAGGTGAAGGTGACGACACTATGTTTAC

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		2170	2180	219
		TCGCCGTGAAGACTGGCGAACAGTTCATAC		
G0260333-1.seq (1>11649)	→	TCGCCGTGAAGACTGGCGAACAGTTCATAC		
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		AGAGTCTTTTACGACTCAATGACAAGAAGA		
G0260333-1.seq (1>11649)	→	AGAGTCTTTTACGACTCAATGACAAGAAGA		
		2230	2240	225
		AAATCTTCGTCAACATGGTGGAGCACGACA		
G0260333-1.seq (1>11649)	→	AAATCTTCGTCAACATGGTGGAGCACGACA		
		2260	2270	228
		CTCTGGTCTACTCCAAAAATGTCAAAGATA		
G0260333-1.seq (1>11649)	→	CTCTGGTCTACTCCAAAAATGTCAAAGATA		
		2290	2300	231
		CAGTCTCAGAAGACCAAAGGGCTATTGAGA		
G0260333-1.seq (1>11649)	→	CAGTCTCAGAAGACCAAAGGGCTATTGAGA		
		2320	2330	234
		CTTTTCAACAAAGGATAATTTCGGGAAACC		
G0260333-1.seq (1>11649)	→	CTTTTCAACAAAGGATAATTTCGGGAAACC		
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		TCCTCGGATTCCATTGCCCAGCTATCTGTC		
G0260333-1.seq (1>11649)	→	TCCTCGGATTCCATTGCCCAGCTATCTGTC		
		2380	2390	240
		ACTTCATCGAAAGGACAGTAGAAAAGGAAG		
G0260333-1.seq (1>11649)	→	ACTTCATCGAAAGGACAGTAGAAAAGGAAG		
		2410	2420	243
		GTGGCTCCTACAAATGCCATCATTGCGATA		
G0260333-1.seq (1>11649)	→	GTGGCTCCTACAAATGCCATCATTGCGATA		
		2440	2450	246
		AAGGAAAGGCTATCATTCAAGATCTCTCTG		
G0260333-1.seq (1>11649)	→	AAGGAAAGGCTATCATTCAAGATCTCTCTG		
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		CCGACAGTGGTCCCAAAGATGGACCCCCAC		
G0260333-1.seq (1>11649)	→	CCGACAGTGGTCCCAAAGATGGACCCCCAC		
		2500	2510	252
		CCACGAGGAGCATCGTGGAAAAAGAAGACG		
G0260333-1.seq (1>11649)	→	CCACGAGGAGCATCGTGGAAAAAGAAGACG		

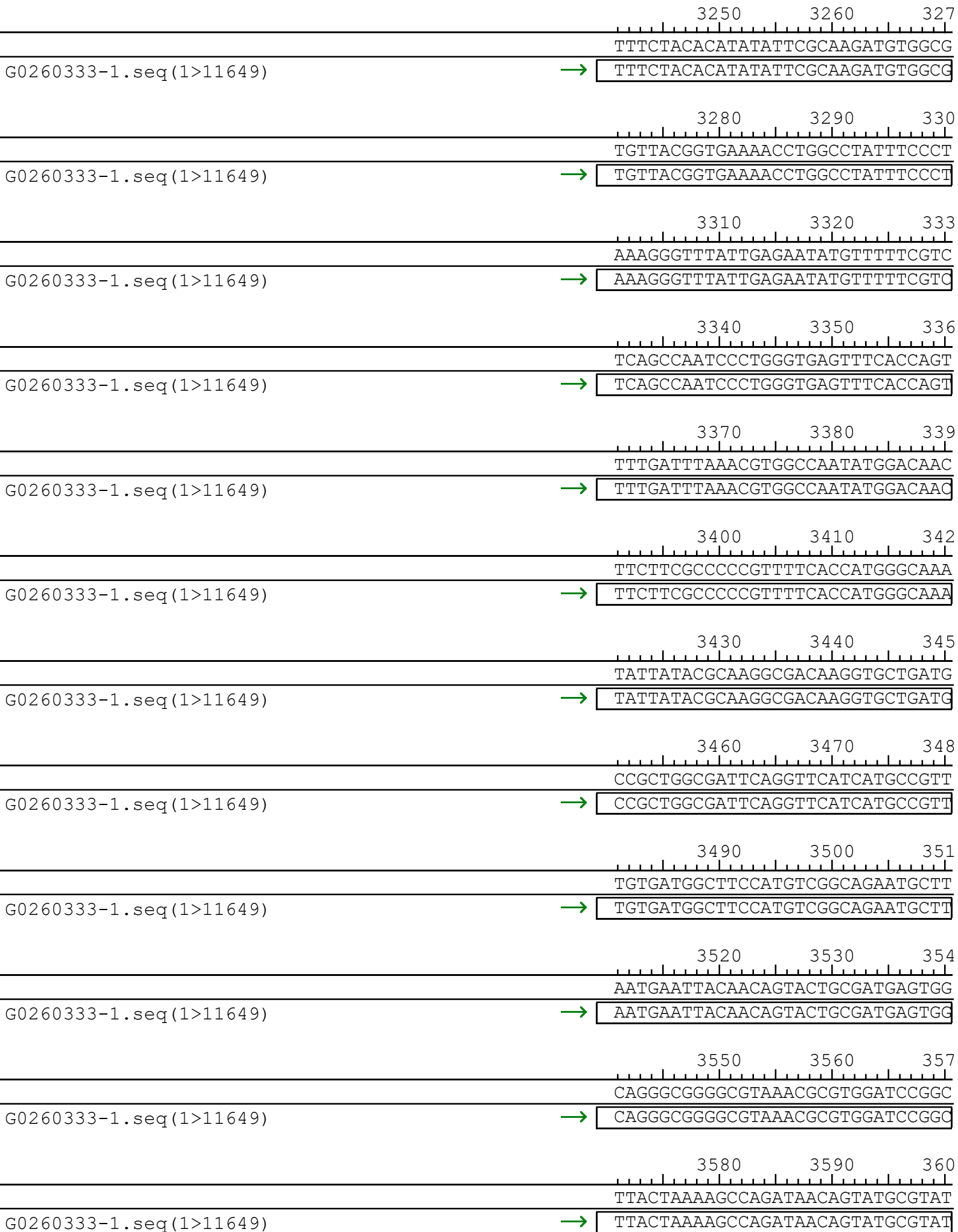
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G0260333-1.seq(1>11649)	→	TTCCAACCACGTCTTCAAAGCAAGTGGATT		
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		GATGTGACATCTCCACTGACGTAAGGGATG		
G0260333-1.seq(1>11649)	→	GATGTGACATCTCCACTGACGTAAGGGATG		
		2590	2600	261
		ACGCACAATCCCCTATCCTTCGCAAGACC		
G0260333-1.seq(1>11649)	→	ACGCACAATCCCCTATCCTTCGCAAGACC		
		2620	2630	264
		CTTCCTCTATATAAGGAAGTTCATTTTCATT		
G0260333-1.seq(1>11649)	→	CTTCCTCTATATAAGGAAGTTCATTTTCATT		
		2650	2660	267
		TGGAGAGGACACGCTCGAGATCACAAGTTT		
G0260333-1.seq(1>11649)	→	TGGAGAGGACACGCTCGAGATCACAAGTTT		
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		GTACAAAAAAGCTGAACGAGAAACGTAAAA		
G0260333-1.seq(1>11649)	→	GTACAAAAAAGCTGAACGAGAAACGTAAAA		
		2710	2720	273
		TGATATAAATATCAATATATTTAAATTAGAT		
G0260333-1.seq(1>11649)	→	TGATATAAATATCAATATATTTAAATTAGAT		
		2740	2750	276
		TTTGCATAAAAAACAGACTACATAAATACTG		
G0260333-1.seq(1>11649)	→	TTTGCATAAAAAACAGACTACATAAATACTG		
		2770	2780	279
		TAAACACAACATATCCAGTCACTATGGCG		
G0260333-1.seq(1>11649)	→	TAAACACAACATATCCAGTCACTATGGCG		
		2800	2810	282
		GCCGCATTAGGCACCCCAGGCTTTTACACTT		
G0260333-1.seq(1>11649)	→	GCCGCATTAGGCACCCCAGGCTTTTACACTT		
		2830	2840	285
		TATGCTTCCGGCTCGTATAATGTGTGGATT		
G0260333-1.seq(1>11649)	→	TATGCTTCCGGCTCGTATAATGTGTGGATT		
		2860	2870	288
		TTGAGTTAGGATCCGTCGAGATTTTCAGGA		
G0260333-1.seq(1>11649)	→	TTGAGTTAGGATCCGTCGAGATTTTCAGGA		

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		GCTAAGGAAGCTAAAATGGAGAAAAAATC		
G0260333-1.seq(1>11649)	→	GCTAAGGAAGCTAAAATGGAGAAAAAATC		
		2920	2930	294
		ACTGGATATACCACCGTTGATATATCCCAA		
G0260333-1.seq(1>11649)	→	ACTGGATATACCACCGTTGATATATCCCAA		
		2950	2960	297
		TGGCATCGTAAAGAACATTTTGAGGCATTT		
G0260333-1.seq(1>11649)	→	TGGCATCGTAAAGAACATTTTGAGGCATTT		
		2980	2990	300
		CAGTCAGTTGCTCAATGTACCTATAACCAG		
G0260333-1.seq(1>11649)	→	CAGTCAGTTGCTCAATGTACCTATAACCAG		
		3010	3020	303
		ACCGTTCAGCTGGATATTACGGCCTTTTTA		
G0260333-1.seq(1>11649)	→	ACCGTTCAGCTGGATATTACGGCCTTTTTA		
		3040	3050	306
		AAGACCGTAAAGAAAAATAAGCACAAAGTTT		
G0260333-1.seq(1>11649)	→	AAGACCGTAAAGAAAAATAAGCACAAAGTTT		
		3070	3080	309
		TATCCGGCCTTTATTCACATTCTTGCCCGC		
G0260333-1.seq(1>11649)	→	TATCCGGCCTTTATTCACATTCTTGCCCGC		
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		CTGATGAATGCTCATCCGGAATTCCGTATG		
G0260333-1.seq(1>11649)	→	CTGATGAATGCTCATCCGGAATTCCGTATG		
		3130	3140	315
		GCAATGAAAGACGGTGAGCTGGTGATATGG		
G0260333-1.seq(1>11649)	→	GCAATGAAAGACGGTGAGCTGGTGATATGG		
		3160	3170	318
		GATAGTG TTCACCCTTGTTACACCGTTTTTC		
G0260333-1.seq(1>11649)	→	GATAGTG TTCACCCTTGTTACACCGTTTTTC		
		3190	3200	321
		CATGAGCAA ACTGAAACGTTTTTCATCGCTC		
G0260333-1.seq(1>11649)	→	CATGAGCAA ACTGAAACGTTTTTCATCGCTC		
		3220	3230	324
		TGGAGTGAATACCACGACGATTTCCGGCAG		
G0260333-1.seq(1>11649)	→	TGGAGTGAATACCACGACGATTTCCGGCAG		

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G0260333-1.seq (1>11649)	→	TTGCGCGCTGATTTTTGCGGTATAAGAATA		
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		TATACTGATATGTATACCCGAAGTATGTCA		
G0260333-1.seq (1>11649)	→	TATACTGATATGTATACCCGAAGTATGTCA		
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		AAAAGAGGTATGCTATGAAGCAGCGTATTA		
G0260333-1.seq (1>11649)	→	AAAAGAGGTATGCTATGAAGCAGCGTATTA		
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		CAGTGACAGTTGACAGCGACAGCTATCAGT		
G0260333-1.seq (1>11649)	→	CAGTGACAGTTGACAGCGACAGCTATCAGT		
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		TGCTCAAGGCATATATGATGTCAATATCTC		
G0260333-1.seq (1>11649)	→	TGCTCAAGGCATATATGATGTCAATATCTC		
		3760	3770	378
		CGGTCTGGTAAGCACAACCATGCAGAATGA		
G0260333-1.seq (1>11649)	→	CGGTCTGGTAAGCACAACCATGCAGAATGA		
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G0260333-1.seq (1>11649)	→	AGCCCGTCGTCTGCGTGCCGAACGCTGGAA		
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G0260333-1.seq (1>11649)	→	AGCGGAAAATCAGGAAGGGATGGCTGAGGT		
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		CGCCCGGTTTATTGAAATGAACGGCTCTTT		
G0260333-1.seq (1>11649)	→	CGCCCGGTTTATTGAAATGAACGGCTCTTT		
		3880	3890	390
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G0260333-1.seq (1>11649)	→	TGCTGACGAGAACAGGGGCTGGTGAAATGC		
		3910	3920	393
		AGTTTAAGGTTTACACCTATAAAAGAGAGA		
G0260333-1.seq (1>11649)	→	AGTTTAAGGTTTACACCTATAAAAGAGAGA		
		3940	3950	396
		GCCGTTATCGTCTGTTTGTGGATGTACAGA		
G0260333-1.seq (1>11649)	→	GCCGTTATCGTCTGTTTGTGGATGTACAGA		

		3970	3980	399	GTGATATTATTGACACGCCCGGGCGACGGA
G0260333-1.seq (1>11649)	→				GTGATATTATTGACACGCCCGGGCGACGGA
		4000	4010	402	TGGTGATCCCCCTGGCCAGTGCACGTCTGC
G0260333-1.seq (1>11649)	→				TGGTGATCCCCCTGGCCAGTGCACGTCTGC
		4030	4040	405	TGTCAGATAAAGTCTCCCGTGAAC TTTACC
G0260333-1.seq (1>11649)	→				TGTCAGATAAAGTCTCCCGTGAAC TTTACC
		4060	4070	408	CGGTGGTGCATATCGGGGATGAAAGCTGGC
G0260333-1.seq (1>11649)	→				CGGTGGTGCATATCGGGGATGAAAGCTGGC
		4090	4100	411	GCATGATGACCACCGATATGGCCAGTGTGC
G0260333-1.seq (1>11649)	→				GCATGATGACCACCGATATGGCCAGTGTGC
		4120	4130	414	CGGTCTCCGTTATCGGGGAAGAAGTGGCTG
G0260333-1.seq (1>11649)	→				CGGTCTCCGTTATCGGGGAAGAAGTGGCTG
		4150	4160	417	ATCTCAGCCACCGCGAAAATGACATCAAAA
G0260333-1.seq (1>11649)	→				ATCTCAGCCACCGCGAAAATGACATCAAAA
		4180	4190	420	ACGCCATTAACCTGATGTTCTGGGGAATAT
G0260333-1.seq (1>11649)	→				ACGCCATTAACCTGATGTTCTGGGGAATAT
		4210	4220	423	AAATGTCAGGCTCCCTTATACACAGCCAGT
G0260333-1.seq (1>11649)	→				AAATGTCAGGCTCCCTTATACACAGCCAGT
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		4240	4250	426	CTGCAGGTCGACCATAGTGACTGGATATGT
G0260333-1.seq (1>11649)	→				CTGCAGGTCGACCATAGTGACTGGATATGT
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→				CTGCAGGTCGACCATAGTGACTGGATATGT
		4270	4280	429	TGTGTTTTACAGTATTATGTAGTCTGTTTT
G0260333-1.seq (1>11649)	→				TGTGTTTTACAGTATTATGTAGTCTGTTTT
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→				TGTGTTTTACAGTATTATGTAGTCTGtTTT

		4300	4310	432	TTATGCAAAATCTAATTTAATATATTGATA
G0260333-1.seq(1>11649)	→				TTATGCAAAATCTAATTTAATATATTGATA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				TTATGCAAAATCTAATTTAATATATTGATA
		4330	4340	435	TTTATATCATTTTACGTTTCTCGTTCAGCT
G0260333-1.seq(1>11649)	→				TTTATATCATTTTACGTTTCTCGTTCAGCT
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				TTTATATCATTTTACGTTTCTCGTTCAGCT
		4360	4370	438	TTCTTGTACAAAGTGGTGCCTAGGTGAGTC
G0260333-1.seq(1>11649)	→				TTCTTGTACAAAGTGGTGCCTAGGTGAGTC
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				TTCTTGTACAAAGTGGTGCCTAGGTGAGTC
		4390	4400	441	TAGAGAGTTAATTAAGACCCGGGACTAGTC
G0260333-1.seq(1>11649)	→				TAGAGAGTTAATTAAGACCCGGGACTAGTC
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				TAGAGAGTTAATTAAGACCCGGGACTAGTC
		4420	4430	444	CCTAGAGTCCTGCTTTAATGAGATATGCCGA
G0260333-1.seq(1>11649)	→				CCTAGAGTCCTGCTTTAATGAGATATGCCGA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				CCTAGAGTCCTGCTTTAATGAGATATGCCGA
		4450	4460	447	GACGCCTATGATCGCATGATATTTGCTTTC
G0260333-1.seq(1>11649)	→				GACGCCTATGATCGCATGATATTTGCTTTC
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				GACGCCTATGATCGCATGATATTTGCTTTC
		4480	4490	450	AATTCTGTTGTGCACGTTGTAAAAACCTG
G0260333-1.seq(1>11649)	→				AATTCTGTTGTGCACGTTGTAAAAACCTG
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				AATTCTGTTGTGCACGTTGTAAAAACCTG
		4510	4520	453	AGCATGTGTAGCTCAGATCCTTACCGCCGG
G0260333-1.seq(1>11649)	→				AGCATGTGTAGCTCAGATCCTTACCGCCGG
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				AGCATGTGTAGCTCAGATCCTTACCGCCGG
		4540	4550	456	TTTCGGTTCATTCTAATGAATATATCACCC
G0260333-1.seq(1>11649)	→				TTTCGGTTCATTCTAATGAATATATCACCC
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				TTTCGGTTCATTCTAATGAATATATCACCC
		4570	4580	459	GTTACTATCGTATTTTTATGAATAATATTC
G0260333-1.seq(1>11649)	→				GTTACTATCGTATTTTTATGAATAATATTC
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1(1>793)	→				GTTACTATCGTATTTTTATGAATAATATTC

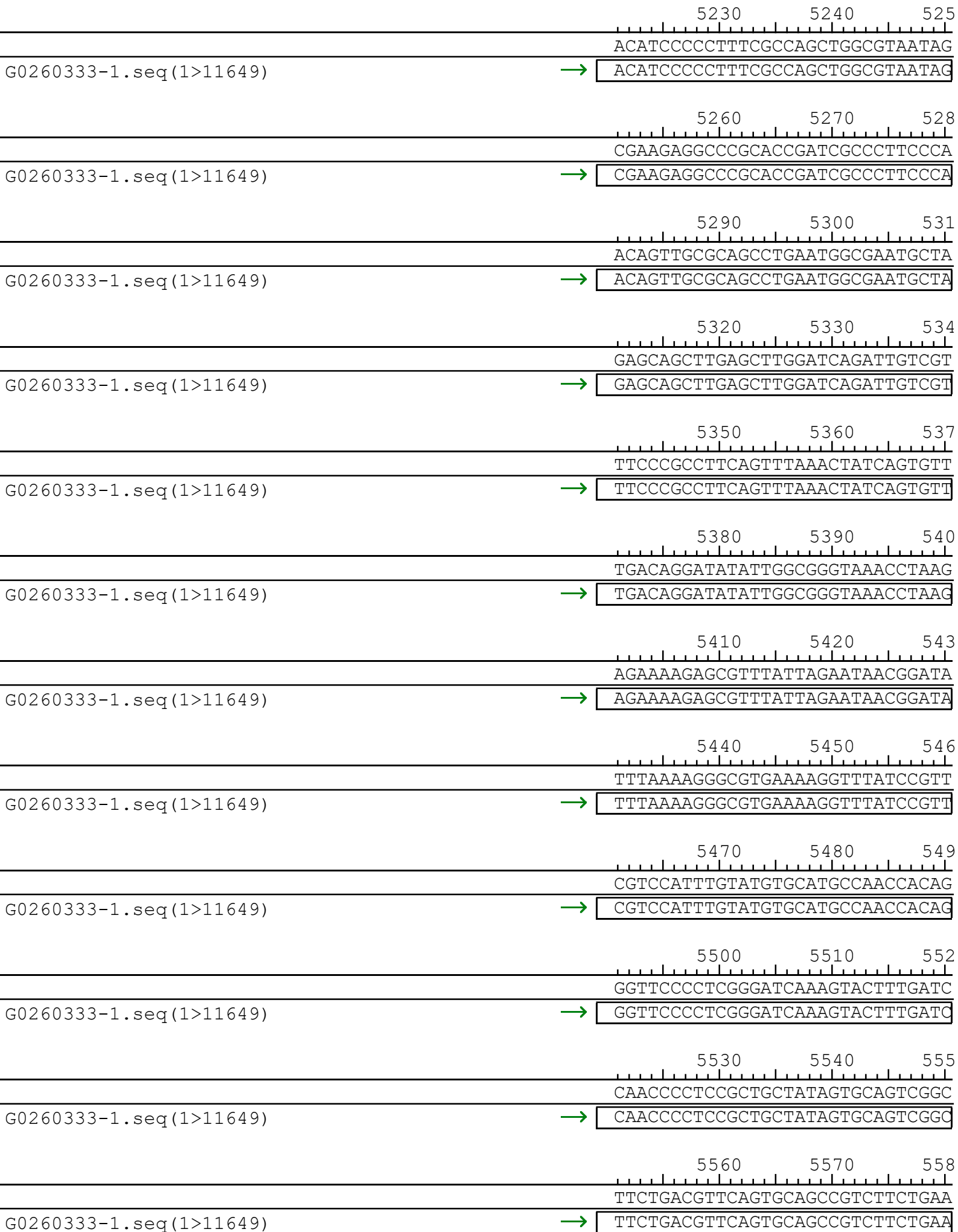
Project: Untitled.SQD Contig 1

		4600 4610 462	TCCGTTCAATTTACTGATTGTACCCTACTA
G0260333-1.seq (1>11649)	→		TCCGTTCAATTTACTGATTGTACCCTACTA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		TCCGTTCAATTTACTGATTGTACCCTACTA
		4630 4640 465	CTTATATGTACAATATTTAAAATGAAAACAA
G0260333-1.seq (1>11649)	→		CTTATATGTACAATATTTAAAATGAAAACAA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		CTTATATGTACAATATTTAAAATGAAAACAA
		4660 4670 468	TATATTGTGCTGAATAGGTTTATAGCGACA
G0260333-1.seq (1>11649)	→		TATATTGTGCTGAATAGGTTTATAGCGACA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		TATATTGTGCTGAATAGGTTTATAGCGACA
		4690 4700 471	TCTATGATAGAGCGCCACAATAACAAACAA
G0260333-1.seq (1>11649)	→		TCTATGATAGAGCGCCACAATAACAAACAA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		TCTATGATAGAGCGCCACAATAACAAACAA
		4720 4730 474	TTGCGTTTTATTATTACAAATCCAATTTTA
G0260333-1.seq (1>11649)	→		TTGCGTTTTATTATTACAAATCCAATTTTA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		TTGCGTTTTATTATTACAAATCCAATTTTA
		4750 4760 477	AAAAAAGCGGCAGAACCGGTCAAACCTAAA
G0260333-1.seq (1>11649)	→		AAAAAAGCGGCAGAACCGGTCAAACCTAAA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		AAAAAAGCGGCAGAACCGGTCAAACCTAAA
		4780 4790 480	AGACTGATTACATAAATCTTATTCAAATTT
G0260333-1.seq (1>11649)	→		AGACTGATTACATAAATCTTATTCAAATTT
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		AGACTGATTACATAAATCTTATTCAAATTT
		4810 4820 483	CAAAGTGCCCCAGGGGCTAGTATCTACGA
G0260333-1.seq (1>11649)	→		CAAAGTGCCCCAGGGGCTAGTATCTACGA
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		CAAAGTGCCCCAGGGGCTAGTATCTACGA
		4840 4850 486	CACACCGAGCGGCGAATAATAACGCTCAC
G0260333-1.seq (1>11649)	→		CACACCGAGCGGCGAATAATAACGCTCAC
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		CACACCGAGCGGCGAATAATAACGCTCAC
		4870 4880 489	TGAAGGGAActCCGTTCCCCGCCGCGCG
G0260333-1.seq (1>11649)	→		TGAAGGGAActCCGTTCCCCGCCGCGCG
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→		TGAAGGGAActCCGTTCCCCGCCGCGCG

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G0260333-1.seq (1>11649)	→	CATGGGTGAGATTCCTTGAAGTTGAGTATT		
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→	CATGGGTGAGATTCCTTGAAGTTGAGTATT		
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		GGCCGTCCGCTCTACCGAAAGTTACGGGCA		
G0260333-1.seq (1>11649)	→	GGCCGTCCGCTCTACCGAAAGTTACGGGCA		
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→	GGCCGTCCGCTCTACCGAAAGTTACGGGCA		
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G0260333-1.seq (1>11649)	→	CCATTCAACCCGGTCCAGCACGGCGGCCGG		
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→	CCATTCAACCCGGTCCAGCACGGCGGCCGG		
		4990	5000	501
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G0260333-1.seq (1>11649)	→	GTAACCGACTTGCTGCCCCGAGAATTATGC		
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→	GTAACCGACTTGCTGCCCCGAGAATTATGC		
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G0260333-1.seq (1>11649)	→	AGCATTTTTTTGGTGTATGTGGGCCCCAAA		
B12-D37476-G0260333-1_G0176846-V-SEQF.ab1 (1>793)	→	AGCATTTTTTT		
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G0260333-1.seq (1>11649)	→	TGAAGTGCAGGTCAAACCTTGACAGTGACC		
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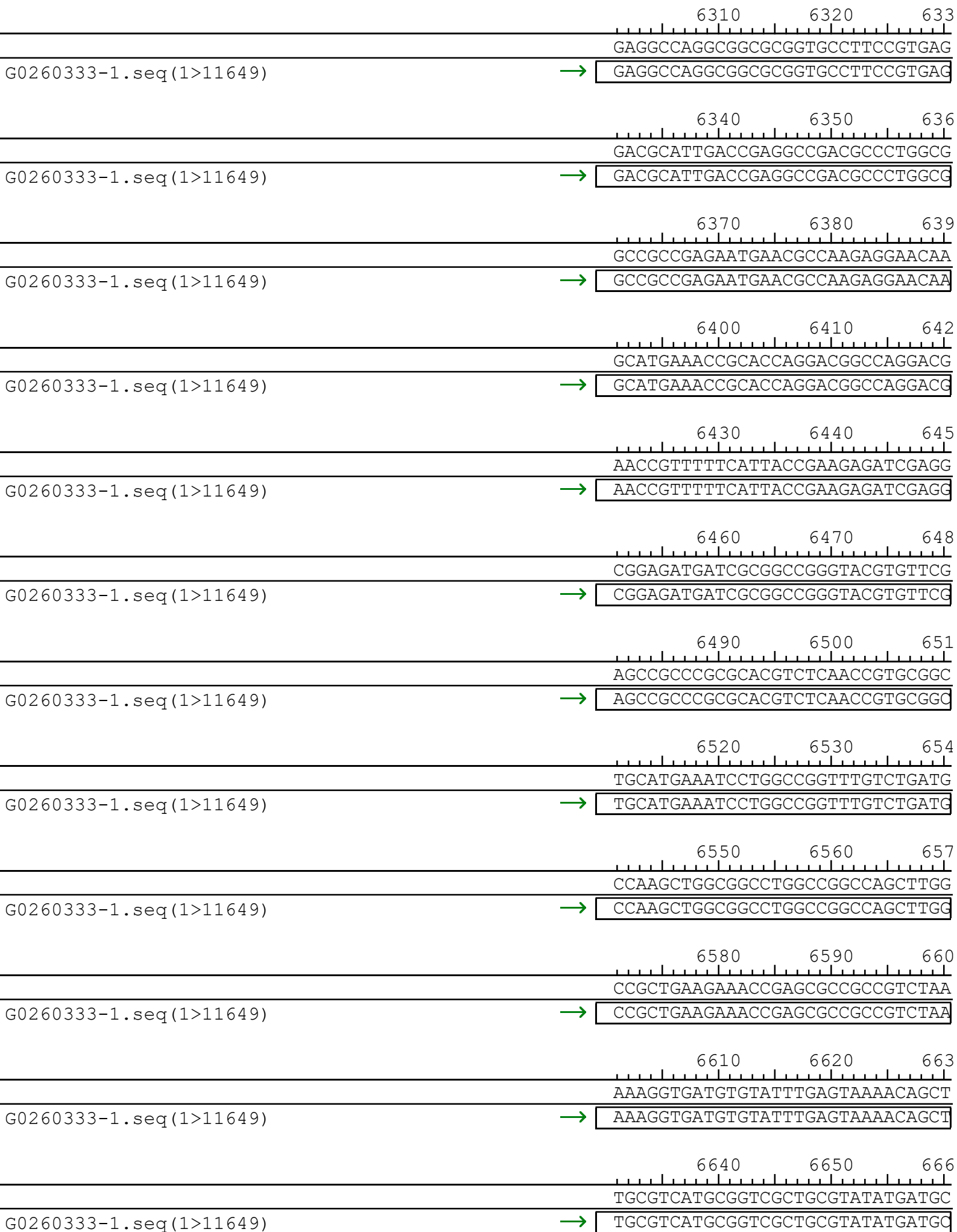


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G0260333-1.seq(1>11649)	→	CGACAGGCTGCCGCCCTGCCCTTTTCCTGG		
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		CGTTTTCTTGTGCGGTGTTTTAGTCGCATA		
G0260333-1.seq(1>11649)	→	CGTTTTCTTGTGCGGTGTTTTAGTCGCATA		
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G0260333-1.seq(1>11649)	→	CATTACGCCATGAACAAGAGCGCCGCCGCT		
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		GGCCTGCTGGGCTATGCCCGCGTCAGCACC		
G0260333-1.seq(1>11649)	→	GGCCTGCTGGGCTATGCCCGCGTCAGCACC		
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G0260333-1.seq(1>11649)	→	GACGACCAGGACTTGACCAACCAACGGGCC		
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		GAACTGCACGCGGCCGGCTGCACCAAGCTG		
G0260333-1.seq(1>11649)	→	GAACTGCACGCGGCCGGCTGCACCAAGCTG		
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		TTTTCGAGAAGATCACCGGCACCAGGCGC		
G0260333-1.seq(1>11649)	→	TTTTCGAGAAGATCACCGGCACCAGGCGC		
		5860	5870	588
		GACCGCCCGGAGCTGGCCAGGATGCTTGAC		
G0260333-1.seq(1>11649)	→	GACCGCCCGGAGCTGGCCAGGATGCTTGAC		
		5890	5900	591
		CACCTACGCCCTGGCGACGTTGTGACAGTG		
G0260333-1.seq(1>11649)	→	CACCTACGCCCTGGCGACGTTGTGACAGTG		
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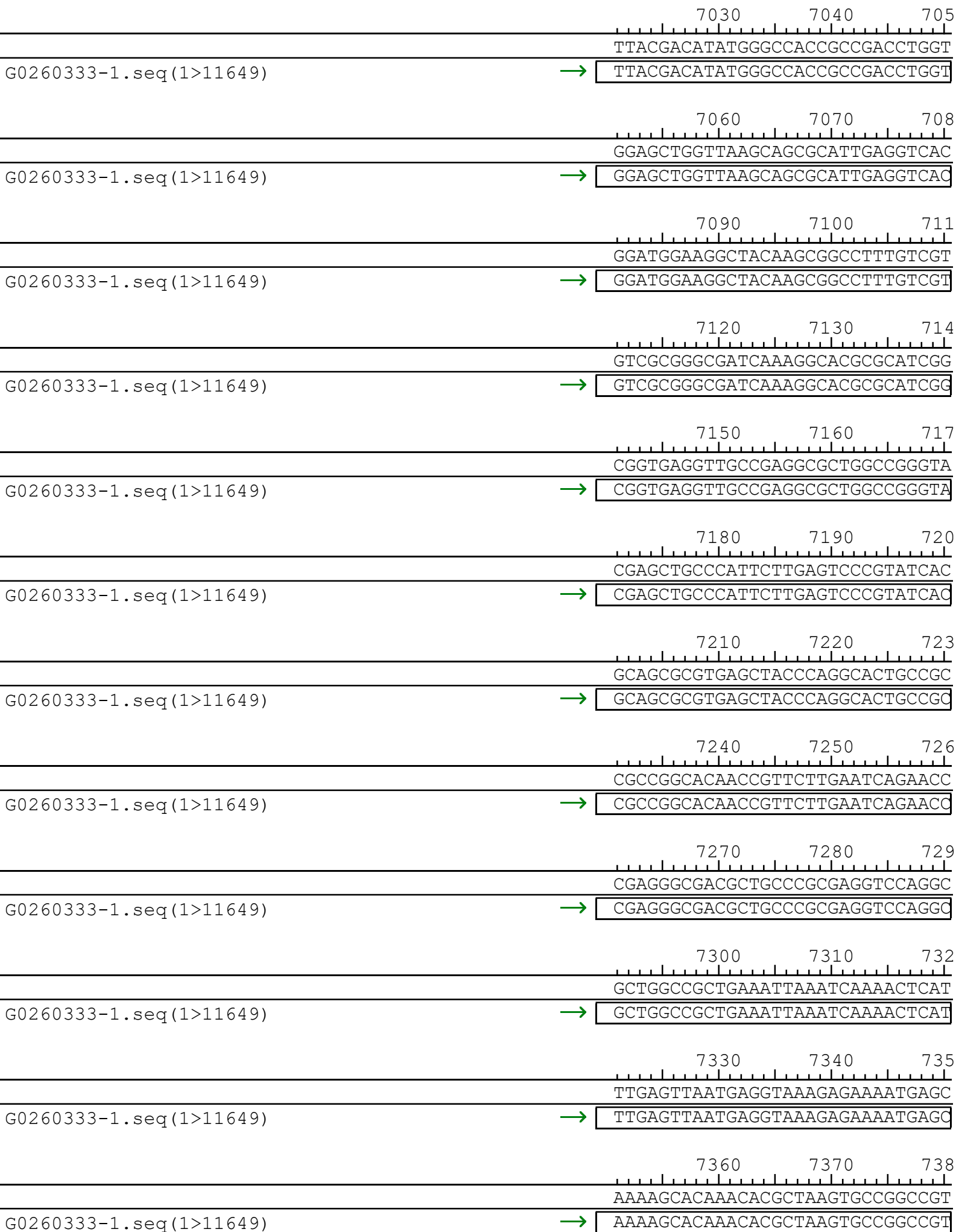
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G0260333-1.seq (1>11649)	→	GGCATTGCCGAGTTCGAGCGTTCCTAATC
G0260333-1.seq (1>11649)	→	ATCGACCGCACCCGGAGCGGGCGCGAGGCC
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G0260333-1.seq (1>11649)	→	CTTGAGCGCAGCGAGGAAGTGACGCCACC

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		GAAAGGCGGGTCAGGCAAGACGACCATCGC		
G0260333-1.seq(1>11649)	→	GAAAGGCGGGTCAGGCAAGACGACCATCGC		
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		AACCCATCTAGCCCGCGCCCTGCAACTCGC		
G0260333-1.seq(1>11649)	→	AACCCATCTAGCCCGCGCCCTGCAACTCGC		
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G0260333-1.seq(1>11649)	→	CGGGGCCGATGTTCTGTTAGTCGATTCCGA		
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G0260333-1.seq(1>11649)	→	TCCCCAGGGCAGTGCCCGCGATTGGGCGGC		
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G0260333-1.seq(1>11649)	→	CGTGCGGGAAGATCAACCGCTAACCGTTGT		
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G0260333-1.seq(1>11649)	→	CGGCATCGACCGCCCGACGATTGACCGCGA		
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G0260333-1.seq(1>11649)	→	CGTGAAGGCCATCGGCCGGCGGCGACTTCGT		
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G0260333-1.seq(1>11649)	→	CTTGGCTGTGTCCGCGATCAAGGCAGCCGA		
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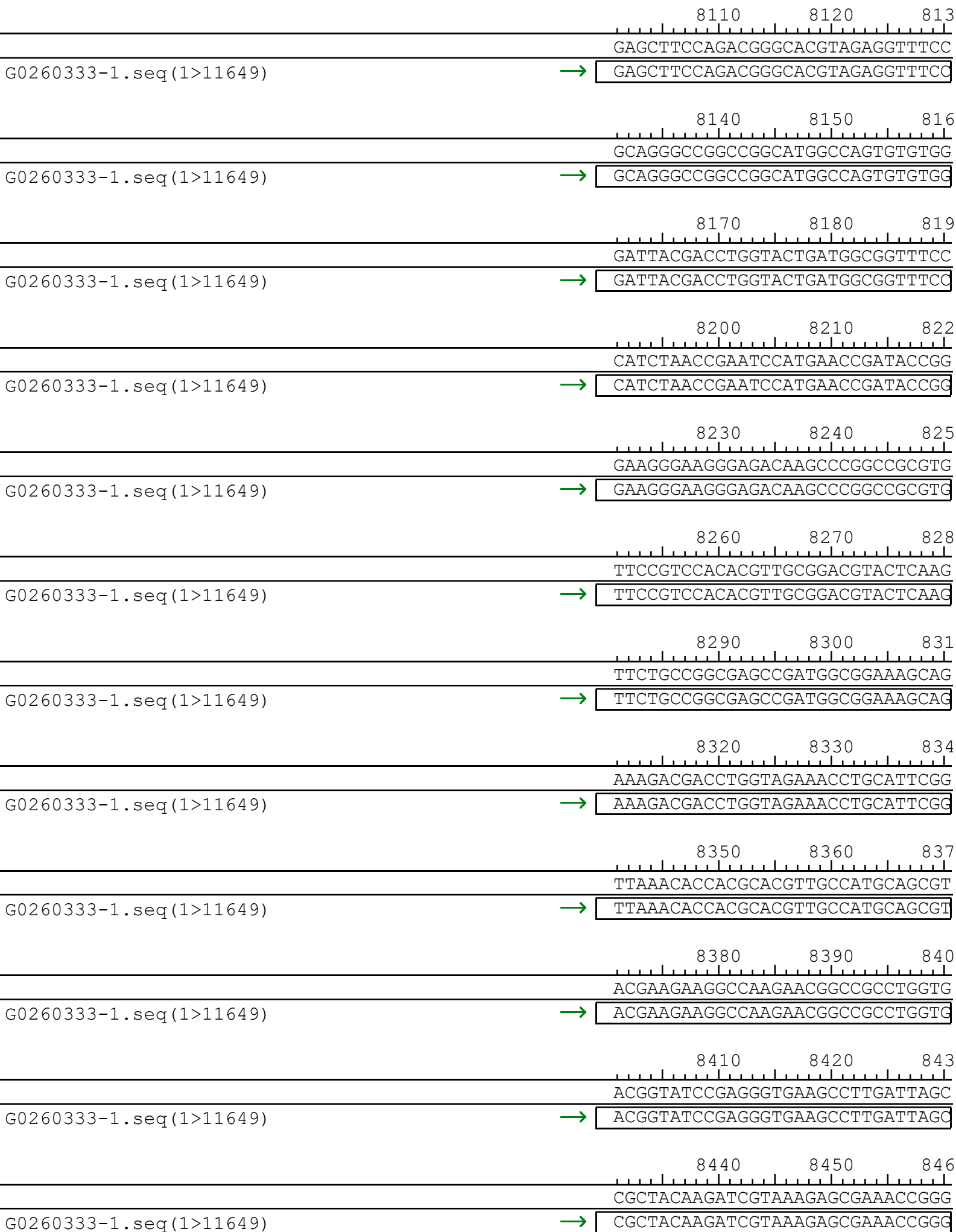
Project: Untitled.SQD Contig 1

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G0260333-1.seq(1>11649)	→	TTGGCCAGCCTGGCAGACACGCCAGCCATG		
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		AAGCGGGTCAACTTTCAGTTGCCGGCGGAG		
G0260333-1.seq(1>11649)	→	AAGCGGGTCAACTTTCAGTTGCCGGCGGAG		
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		GATCACACCAAGCTGAAGATGTACGCGGTA		
G0260333-1.seq(1>11649)	→	GATCACACCAAGCTGAAGATGTACGCGGTA		
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		CGCCAAGGCAAGACCATTACCGAGCTGCTA		
G0260333-1.seq(1>11649)	→	CGCCAAGGCAAGACCATTACCGAGCTGCTA		
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G0260333-1.seq(1>11649)	→	TCTGAATACATCGCGCAGCTACCAGAGTAA		
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		ATGAGCAAATGAATAAATGAGTAGATGAAT		
G0260333-1.seq(1>11649)	→	ATGAGCAAATGAATAAATGAGTAGATGAAT		
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G0260333-1.seq(1>11649)	→	TTTAGCGGCTAAAGGAGGCGGCATGGAAAA		
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		TCAAGAACAACCAGGCACCGACGCCGTGGA		
G0260333-1.seq(1>11649)	→	TCAAGAACAACCAGGCACCGACGCCGTGGA		
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G0260333-1.seq(1>11649)	→	ATGCCCCATGTGTGGAGGAACGGGCGGTTG		
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		GCCAGGCGTAAGCGGCTGGGTTGTCTGCCG		
G0260333-1.seq(1>11649)	→	GCCAGGCGTAAGCGGCTGGGTTGTCTGCCG		
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G0260333-1.seq(1>11649)	→	CGAGGAATCGGCGTGAGCGGTCGCAAACCA		
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G0260333-1.seq(1>11649)	→	TCCGGCCCGGTACAAATCGGCGCGGCGCTG		
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		GGTGATGACCTGGTGGAGAAGTTGAAGGCC		
G0260333-1.seq(1>11649)	→	GGTGATGACCTGGTGGAGAAGTTGAAGGCC		
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G0260333-1.seq(1>11649)	→	GCGCAGGCCGCCAGCGGCAACGCATCGAG		
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		GCAGAAGCACGCCCCGGTGAATCGTGGCAA		
G0260333-1.seq(1>11649)	→	GCAGAAGCACGCCCCGGTGAATCGTGGCAA		
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		GCGGCCGCTGATCGAATCCGCAAAGAATCC		
G0260333-1.seq(1>11649)	→	GCGGCCGCTGATCGAATCCGCAAAGAATCC		
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G0260333-1.seq(1>11649)	→	CGGCAACCGCCGGCAGCCGGTGCGCCGTCG		
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G0260333-1.seq(1>11649)	→	ATTAGGAAGCCGCCAAGGGCGACGAGCAA		
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G0260333-1.seq(1>11649)	→	CCAGATTTTTTCGTTCGGATGCTCTATGAC		
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G0260333-1.seq(1>11649)	→	GTGGGCACCCGCGATAGTCGCAGCATCATG		
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		GACGTGGCCGTTTTCCGTCTGTCTGAAGCGT		
G0260333-1.seq(1>11649)	→	GACGTGGCCGTTTTCCGTCTGTCTGAAGCGT		
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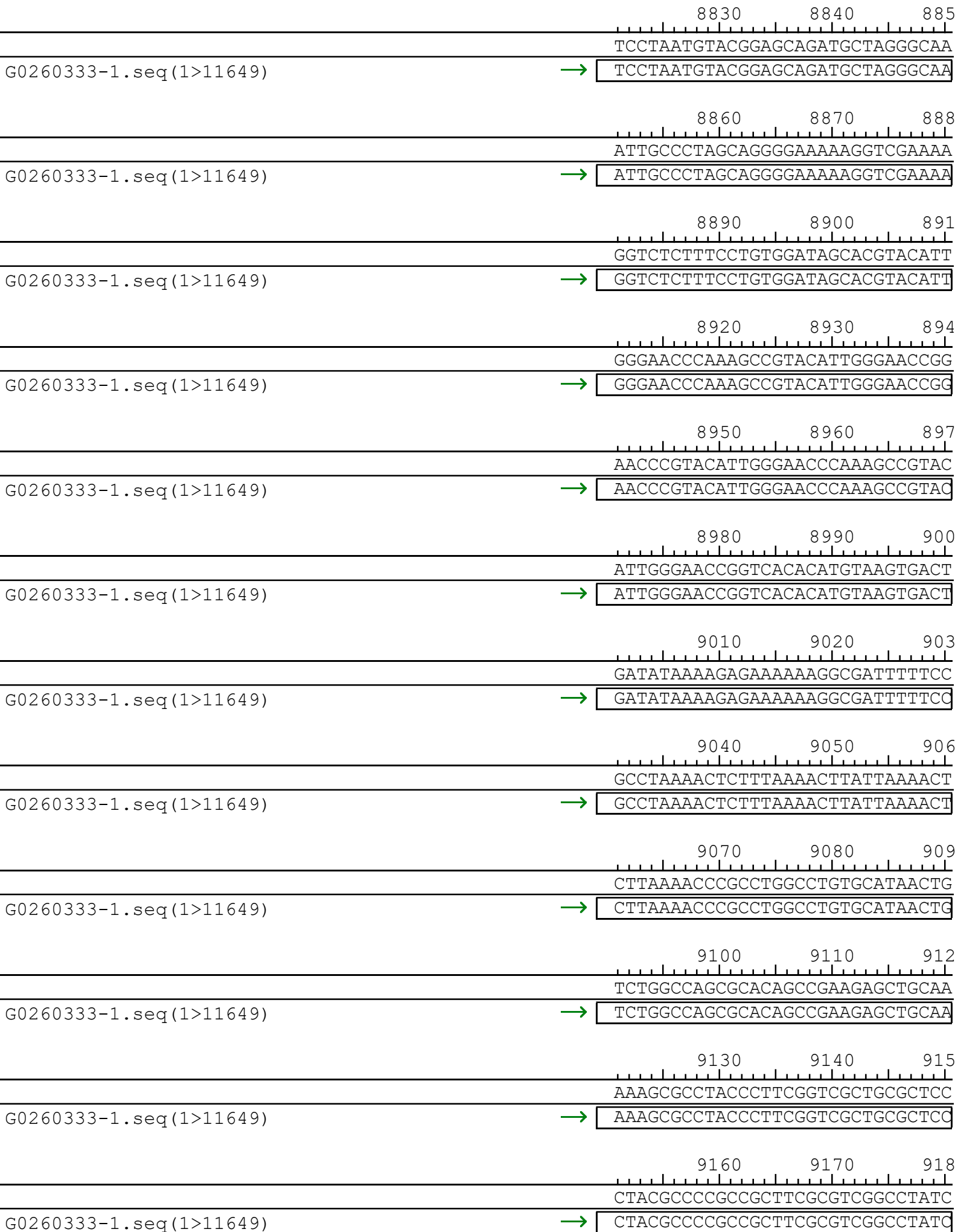
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G0260333-1.seq (1>11649)	→	GATTGGATGTACCGCGAGATCACAGAAGGC		
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		AAGAACCCGGACGTGCTGACGGTTCACCCC		
G0260333-1.seq (1>11649)	→	AAGAACCCGGACGTGCTGACGGTTCACCCC		
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G0260333-1.seq (1>11649)	→	GATTACTTTTTGATCGATCCCGGCATCGGC		
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G0260333-1.seq (1>11649)	→	CGTTTTCTCTACCGCCTGGCACGCCGCGCC		
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G0260333-1.seq (1>11649)	→	GCAGGCAAGGCAGAAGCCAGATGGTTGTTTC		
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G0260333-1.seq (1>11649)	→	AAGACGATCTACGAACGCAGTGGCAGCGCC		
		8680	8690	870
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G0260333-1.seq (1>11649)	→	GGAGAGTTCAAGAAGTTCTGTTTCACCGTG		
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		CGCAAGCTGATCGGGTCAAATGACCTGCCG		
G0260333-1.seq (1>11649)	→	CGCAAGCTGATCGGGTCAAATGACCTGCCG		
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G0260333-1.seq (1>11649)	→	GAGTACGATTTGAAGGAGGAGGCGGGGCAG		
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G0260333-1.seq (1>11649)	→	GCTGGCCCGATCCTAGTCATGCGCTACCGC		
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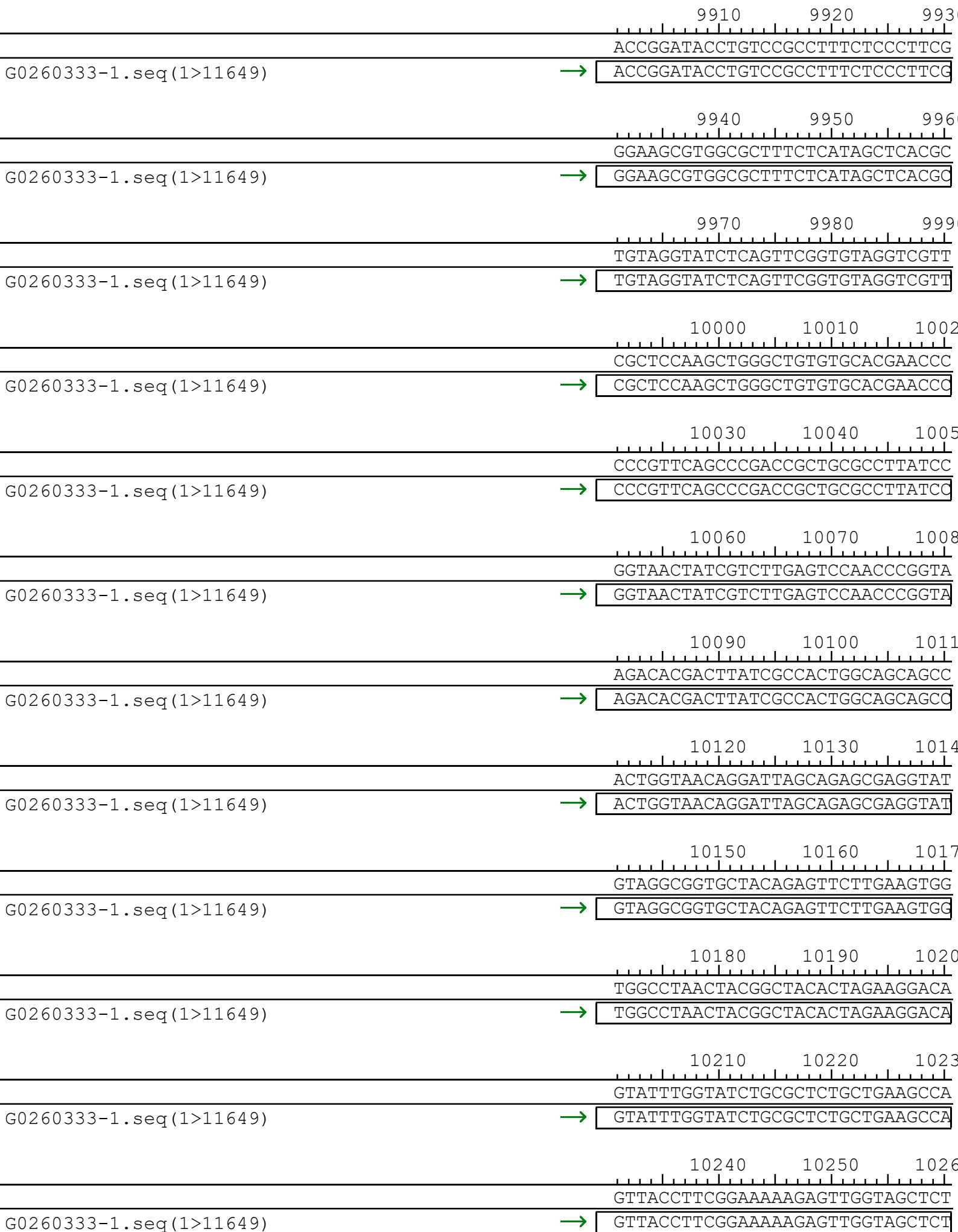
Project: Untitled.SQD Contig 1

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G0260333-1.seq (1>11649)	→	CTACGGCCAGGCAATCTACCAGGGCGCGGA		
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G0260333-1.seq (1>11649)	→	CAAGCCGCGCCGTCGCCACTCGACCGCCGG		
		9280	9290	930
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G0260333-1.seq (1>11649)	→	CGCCACATCAAGGCACCCTGCCTCGCGCG		
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G0260333-1.seq (1>11649)	→	CATGCAGCTCCCGGAGACGGTCACAGCTTG		
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G0260333-1.seq(1>11649)	→	CGCTCTTCCGCTTCCTCGCTCACTGACTCG		
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		CTGCGCTCGGTTCGTTTCGGCTGCGGCGAGCG		
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G0260333-1.seq(1>11649)	→	TTATCCACAGAATCAGGGGATAACGCAGGA		
		9700	9710	972
		AAGAACATGTGAGCAAAAGGCCAGCAAAAG		
G0260333-1.seq(1>11649)	→	AAGAACATGTGAGCAAAAGGCCAGCAAAAG		
		9730	9740	975
		GCCAGGAACCGTAAAAAGGCCGCGTTGCTG		
G0260333-1.seq(1>11649)	→	GCCAGGAACCGTAAAAAGGCCGCGTTGCTG		
		9760	9770	978
		GCGTTTTTCCATAGGCTCCGCCCCCTGAC		
G0260333-1.seq(1>11649)	→	GCGTTTTTCCATAGGCTCCGCCCCCTGAC		
		9790	9800	981
		GAGCATCACAAAATCGACGCTCAAGTCAG		
G0260333-1.seq(1>11649)	→	GAGCATCACAAAATCGACGCTCAAGTCAG		
		9820	9830	984
		AGGTGGCGAAACCCGACAGGACTATAAAGA		
G0260333-1.seq(1>11649)	→	AGGTGGCGAAACCCGACAGGACTATAAAGA		
		9850	9860	987
		TACCAGGCGTTTCCCCCTGGAAGCTCCCTC		
G0260333-1.seq(1>11649)	→	TACCAGGCGTTTCCCCCTGGAAGCTCCCTC		
		9880	9890	990
		GTGCGCTCTCCTGTTCCGACCCTGCCGCTT		
G0260333-1.seq(1>11649)	→	GTGCGCTCTCCTGTTCCGACCCTGCCGCTT		

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		10270	10280	10290
		TGATCCGGCAAACAAACCACCGCTGGTAGC		
G0260333-1.seq(1>11649)	→	TGATCCGGCAAACAAACCACCGCTGGTAGC		
		10300	10310	10320
		GGTGGTTTTTTTTGTTTGCAAGCAGCAGATT		
G0260333-1.seq(1>11649)	→	GGTGGTTTTTTTTGTTTGCAAGCAGCAGATT		
		10330	10340	10350
		ACGCGCAGAAAAAAGGATCTCAAGAAGAT		
G0260333-1.seq(1>11649)	→	ACGCGCAGAAAAAAGGATCTCAAGAAGAT		
		10360	10370	10380
		CCTTTGATCTTTTCTACGGGGTCTGACGCT		
G0260333-1.seq(1>11649)	→	CCTTTGATCTTTTCTACGGGGTCTGACGCT		
		10390	10400	10410
		CAGTGAACGAAAACACGTTAAGGGATT		
G0260333-1.seq(1>11649)	→	CAGTGAACGAAAACACGTTAAGGGATT		
		10420	10430	10440
		TTGGTCATGCATTCTAGGTACTAAAACAAT		
G0260333-1.seq(1>11649)	→	TTGGTCATGCATTCTAGGTACTAAAACAAT		
		10450	10460	10470
		TCATCCAGTAAAATATAATATTTTATTTTC		
G0260333-1.seq(1>11649)	→	TCATCCAGTAAAATATAATATTTTATTTTC		
		10480	10490	10500
		TCCAATCAGGCTTGATCCCCAGTAAGTCA		
G0260333-1.seq(1>11649)	→	TCCAATCAGGCTTGATCCCCAGTAAGTCA		
		10510	10520	10530
		AAAAATAGCTCGACATACTGTTCTTCCCCG		
G0260333-1.seq(1>11649)	→	AAAAATAGCTCGACATACTGTTCTTCCCCG		
		10540	10550	10560
		ATATCCTCCCTGATCGACCGGACGCAGAAG		
G0260333-1.seq(1>11649)	→	ATATCCTCCCTGATCGACCGGACGCAGAAG		
		10570	10580	10590
		GCAATGTCATAACCACTTGTCCGCCCTGCCG		
G0260333-1.seq(1>11649)	→	GCAATGTCATAACCACTTGTCCGCCCTGCCG		
		10600	10610	10620
		CTTCTCCAAGATCAATAAAGCCACTTACT		
G0260333-1.seq(1>11649)	→	CTTCTCCAAGATCAATAAAGCCACTTACT		

		10630	10640	10650
		TTGCCATCTTTCACAAAGATGTTGCTGTCT		
G0260333-1.seq(1>11649)	→	TTGCCATCTTTCACAAAGATGTTGCTGTCT		
		10660	10670	10680
		CCCAGGTCGCCGTGGGAAAAGACAAGTTCC		
G0260333-1.seq(1>11649)	→	CCCAGGTCGCCGTGGGAAAAGACAAGTTCC		
		10690	10700	10710
		TCTTCGGGCTTTTCCGTCTTTAAAAAATCA		
G0260333-1.seq(1>11649)	→	TCTTCGGGCTTTTCCGTCTTTAAAAAATCA		
		10720	10730	10740
		TACAGCTCGCGCGGATCTTTAAATGGAGTG		
G0260333-1.seq(1>11649)	→	TACAGCTCGCGCGGATCTTTAAATGGAGTG		
		10750	10760	10770
		TCTTCTTCCAGTTTTTCGCAATCCACATCG		
G0260333-1.seq(1>11649)	→	TCTTCTTCCAGTTTTTCGCAATCCACATCG		
		10780	10790	10800
		GCCAGATCGTTATTCAGTAAGTAATCCAAT		
G0260333-1.seq(1>11649)	→	GCCAGATCGTTATTCAGTAAGTAATCCAAT		
		10810	10820	10830
		TCGGCTAAGCGGCTGTCTAAGCTATTCGTA		
G0260333-1.seq(1>11649)	→	TCGGCTAAGCGGCTGTCTAAGCTATTCGTA		
		10840	10850	10860
		TAGGGACAATCCGATATGTCGATGGAGTGA		
G0260333-1.seq(1>11649)	→	TAGGGACAATCCGATATGTCGATGGAGTGA		
		10870	10880	10890
		AAGAGCCTGATGCACTCCGCATACAGCTCG		
G0260333-1.seq(1>11649)	→	AAGAGCCTGATGCACTCCGCATACAGCTCG		
		10900	10910	10920
		ATAATCTTTTCAGGGCTTTGTTTCATCTTCA		
G0260333-1.seq(1>11649)	→	ATAATCTTTTCAGGGCTTTGTTTCATCTTCA		
		10930	10940	10950
		TACTCTTCCGAGCAAAGGACGCCATCGGCC		
G0260333-1.seq(1>11649)	→	TACTCTTCCGAGCAAAGGACGCCATCGGCC		
		10960	10970	10980
		TCACTCATGAGCAGATTGCTCCAGCCATCA		
G0260333-1.seq(1>11649)	→	TCACTCATGAGCAGATTGCTCCAGCCATCA		

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		10990	11000	11010
		TGCCGTTCAAAGTGCAGGACCTTTGGAACA		
G0260333-1.seq(1>11649)	→	TGCCGTTCAAAGTGCAGGACCTTTGGAACA		
		11020	11030	11040
		GGCAGCTTTCCTTCCAGCCATAGCATCATG		
G0260333-1.seq(1>11649)	→	GGCAGCTTTCCTTCCAGCCATAGCATCATG		
		11050	11060	11070
		TCCTTTTCCCGTTCCACATCATAGGTGGTC		
G0260333-1.seq(1>11649)	→	TCCTTTTCCCGTTCCACATCATAGGTGGTC		
		11080	11090	11100
		CCTTTATACCGGCTGTCCGTCATTTTTAA		
G0260333-1.seq(1>11649)	→	CCTTTATACCGGCTGTCCGTCATTTTTAA		
		11110	11120	11130
		TATAGGTTTTTCATTTTCTCCCACCAGCTTA		
G0260333-1.seq(1>11649)	→	TATAGGTTTTTCATTTTCTCCCACCAGCTTA		
		11140	11150	11160
		TATACCTTAGCAGGAGACATTCCTTCCGTA		
G0260333-1.seq(1>11649)	→	TATACCTTAGCAGGAGACATTCCTTCCGTA		
		11170	11180	11190
		TCTTTTACGCAGCGGTATTTTTCGATCAGT		
G0260333-1.seq(1>11649)	→	TCTTTTACGCAGCGGTATTTTTCGATCAGT		
		11200	11210	11220
		TTTTTCAATTCCGGTGATATTCTCATTTTA		
G0260333-1.seq(1>11649)	→	TTTTTCAATTCCGGTGATATTCTCATTTTA		
		11230	11240	11250
		GCCATTTATTATTTCTTCCCTCTTTTCTAC		
G0260333-1.seq(1>11649)	→	GCCATTTATTATTTCTTCCCTCTTTTCTAC		
		11260	11270	11280
		AGTATTTAAAGATACCCCAAGAAGCTAATT		
G0260333-1.seq(1>11649)	→	AGTATTTAAAGATACCCCAAGAAGCTAATT		
		11290	11300	11310
		ATAACAAGACGAACTCCAATTCCTGTTCC		
G0260333-1.seq(1>11649)	→	ATAACAAGACGAACTCCAATTCCTGTTCC		
		11320	11330	11340
		TTGCATTCTAAAACCTTAAATACCAGAAAA		
G0260333-1.seq(1>11649)	→	TTGCATTCTAAAACCTTAAATACCAGAAAA		

