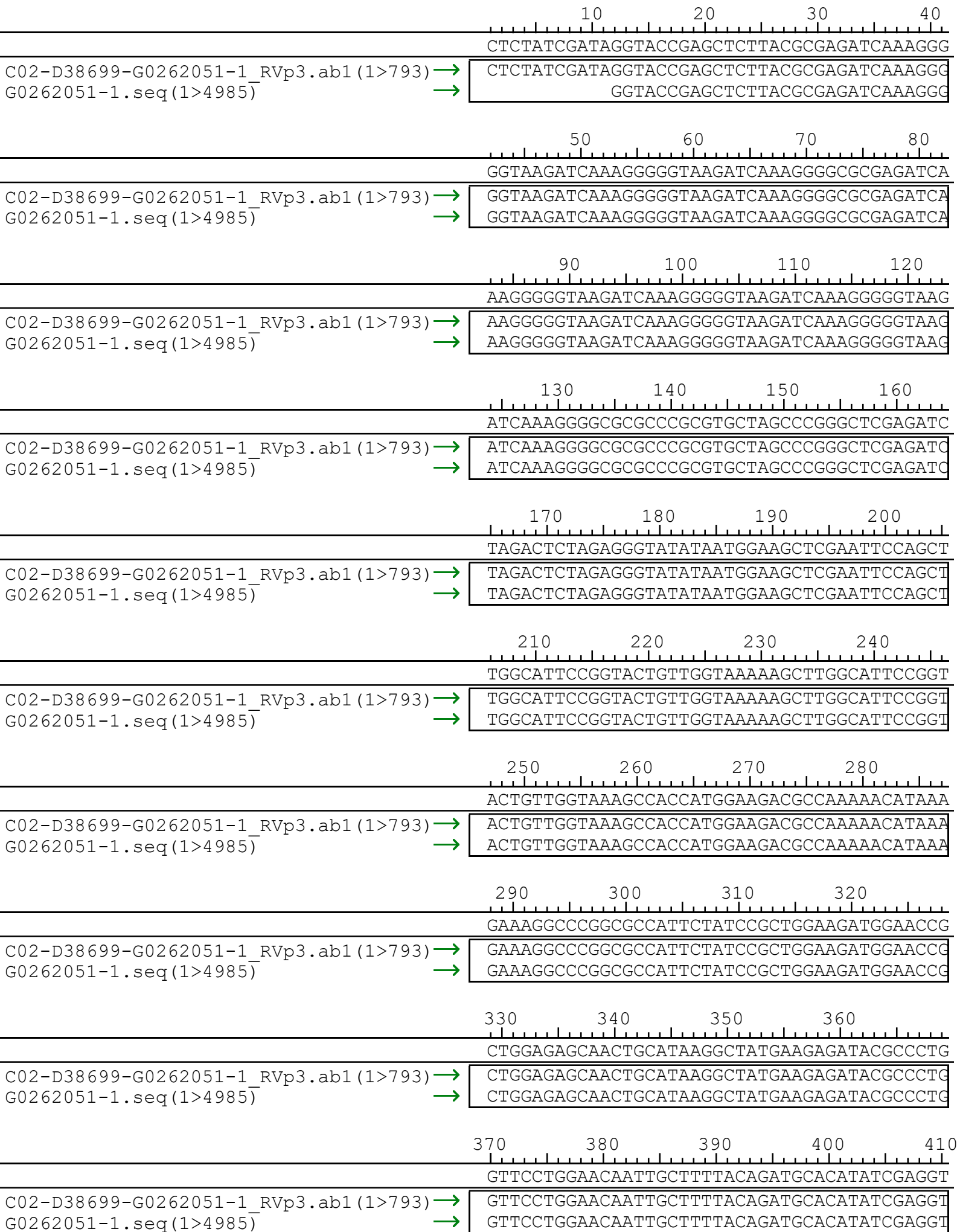


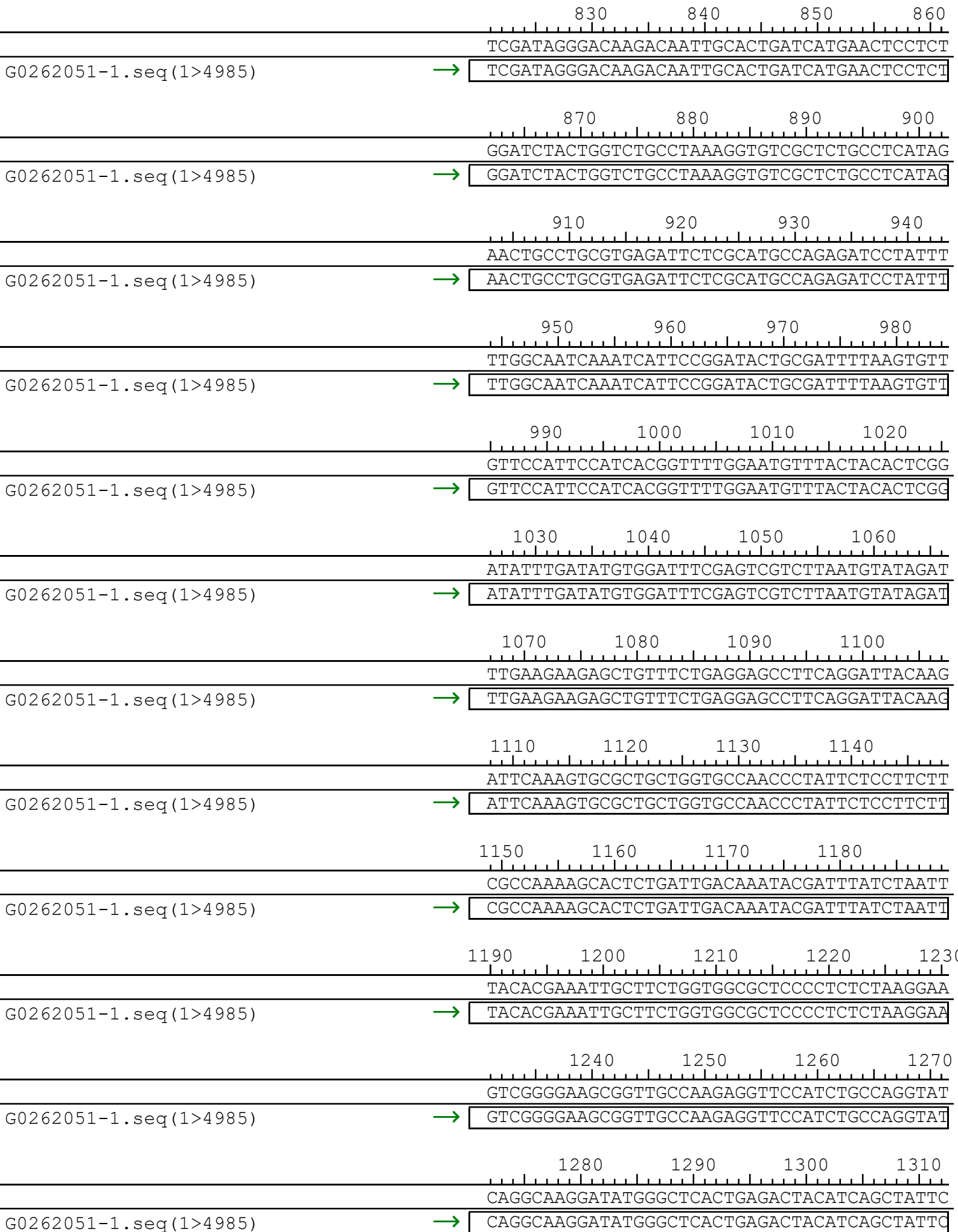
Project: Untitled.SQD Contig 1

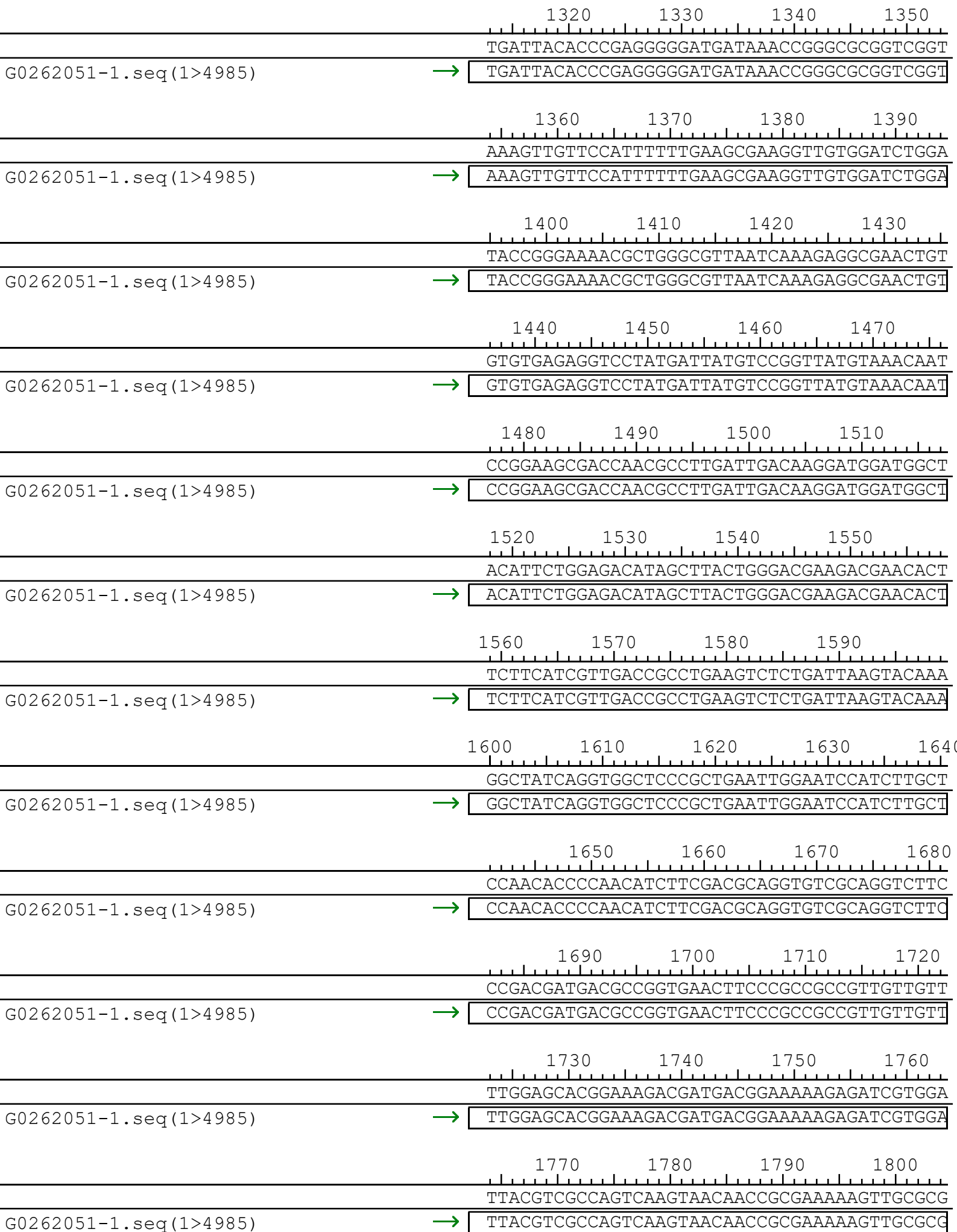


Project: Untitled.SQD Contig 1

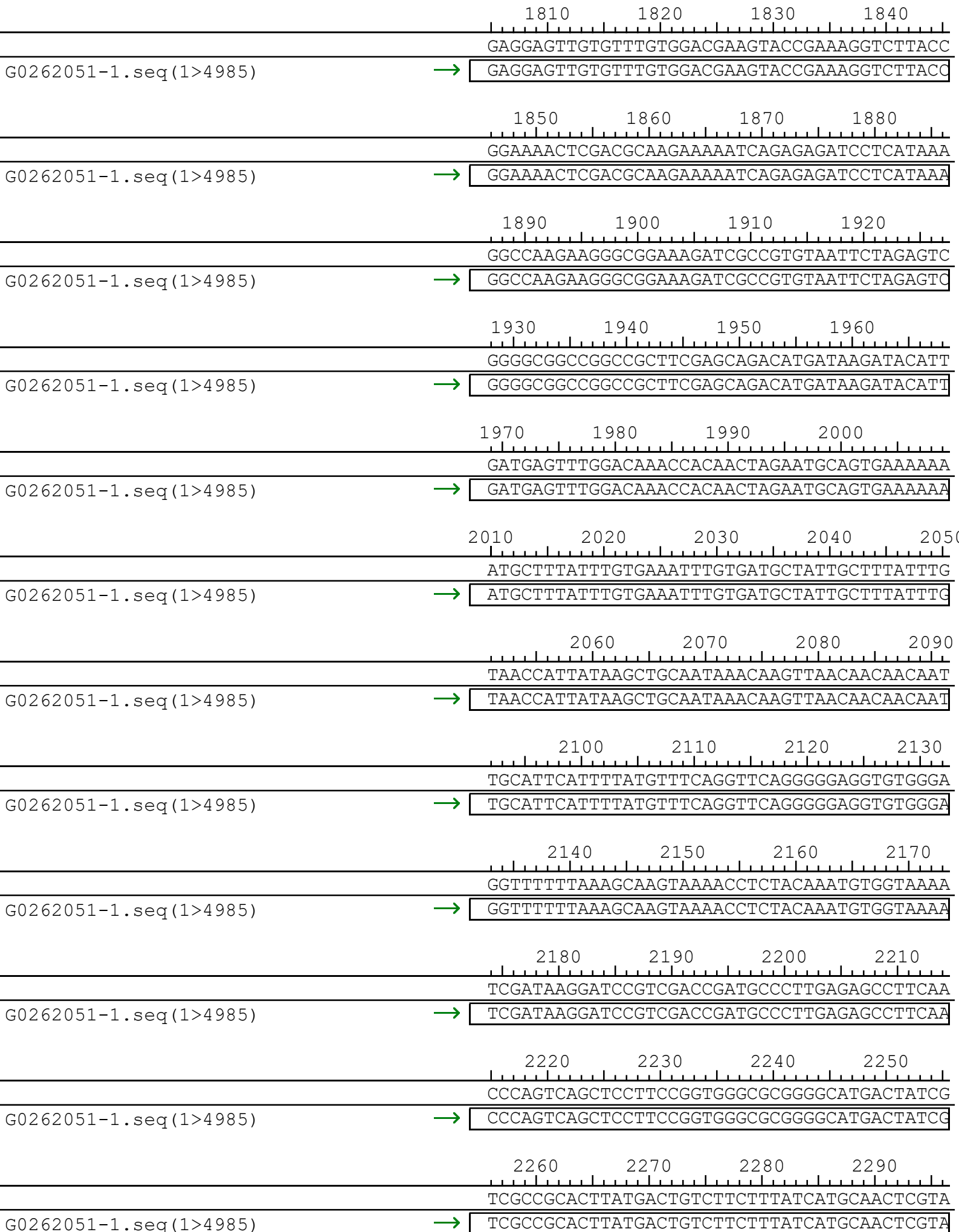
		420	430	440	450	
		GGACATCACTTACGCTGAGTACTTCGAAATGTCCGTTCCGGT				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	GGACATCACTTACGCTGAGTACTTCGAAATGTCCGTTCCGGT				
G0262051-1.seq (1>4985)	→	GGACATCACTTACGCTGAGTACTTCGAAATGTCCGTTCCGGT				
		460	470	480	490	
		TGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCAC				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	TGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCAC				
G0262051-1.seq (1>4985)	→	TGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCAC				
		500	510	520	530	
		AGAATCGTCGTATGCAGTGAAAACCTCTCTTCAATTCTTTAT				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	AGAATCGTCGTATGCAGTGAAAACCTCTCTTCAATTCTTTAT				
G0262051-1.seq (1>4985)	→	AGAATCGTCGTATGCAGTGAAAACCTCTCTTCAATTCTTTAT				
		540	550	560	570	
		GCCGGTGTTGGGCGCGTTATTTATCGGAGTTGCAGTTGCGC				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	GCCGGTGTTGGGCGCGTTATTTATCGGAGTTGCAGTTGCGC				
G0262051-1.seq (1>4985)	→	GCCGGTGTTGGGCGCGTTATTTATCGGAGTTGCAGTTGCGC				
		580	590	600	610	
		CCGCGAACGACATTTATAATGAACGTGAATTGCTCAACAGT				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	CCGCGAACGACATTTATAATGAACGTGAATTGCTCAACAGT				
G0262051-1.seq (1>4985)	→	CCGCGAACGACATTTATAATGAACGTGAATTGCTCAACAGT				
		620	630	640	650	
		ATGGGCATTTTCGCAGCCTACCGTGGTGTTTCGTTTCCAAAAA				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	ATGGGCATTTTCGCAGCCTACCGTGGTGTTTCGTTTCCAAAAA				
G0262051-1.seq (1>4985)	→	ATGGGCATTTTCGCAGCCTACCGTGGTGTTTCGTTTCCAAAAA				
		660	670	680	690	
		GGGGTTGCAAAAAATTTTGAACGTGCAAAAAAAGCTCCCAA				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	GGGGTTGCAAAAAATTTTGAACGTGCAAAAAAAGCTCCCAA				
G0262051-1.seq (1>4985)	→	GGGGTTGCAAAAAATTTTGAACGTGCAAAAAAAGCTCCCAA				
		700	710	720	730	
		TCATCCAAAAAATTATTATCATGGATTCTAAAACGGATTAC				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	TCATCCAAAAAATTATTATCATGGATTCTAAAACGGATTAC				
G0262051-1.seq (1>4985)	→	TCATCCAAAAAATTATTATCATGGATTCTAAAACGGATTAC				
		740	750	760	770	
		CAGGGATTTTCAGTCGATGTACACGTTTCGTACATCTCATCT				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	CAGGGATTTTCAGTCGATGTACACGTTTCGTACATCTCATCT				
G0262051-1.seq (1>4985)	→	CAGGGATTTTCAGTCGATGTACACGTTTCGTACATCTCATCT				
		780	790	800	810	820
		ACCTCCCGGTTTTTAATGAATACGATTTTGTGCCAGAGTCCT				
C02-D38699-G0262051-1_RVp3.ab1 (1>793)	→	ACCTCCCGGTTTTTA				
G0262051-1.seq (1>4985)	→	ACCTCCCGGTTTTTAATGAATACGATTTTGTGCCAGAGTCCT				

Project: Untitled.SQD Contig 1

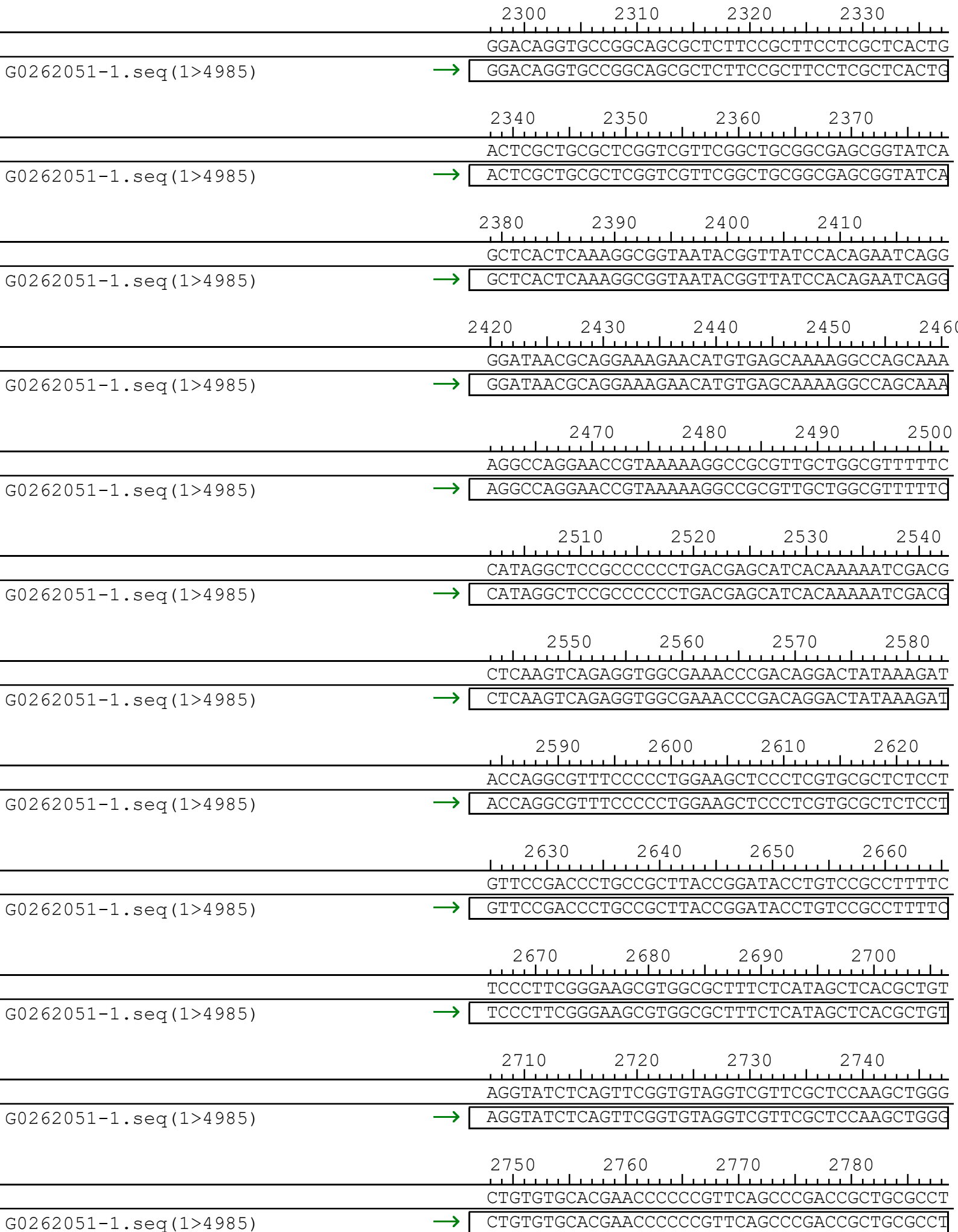




Project: Untitled.SQD Contig 1



Project: Untitled.SQD Contig 1



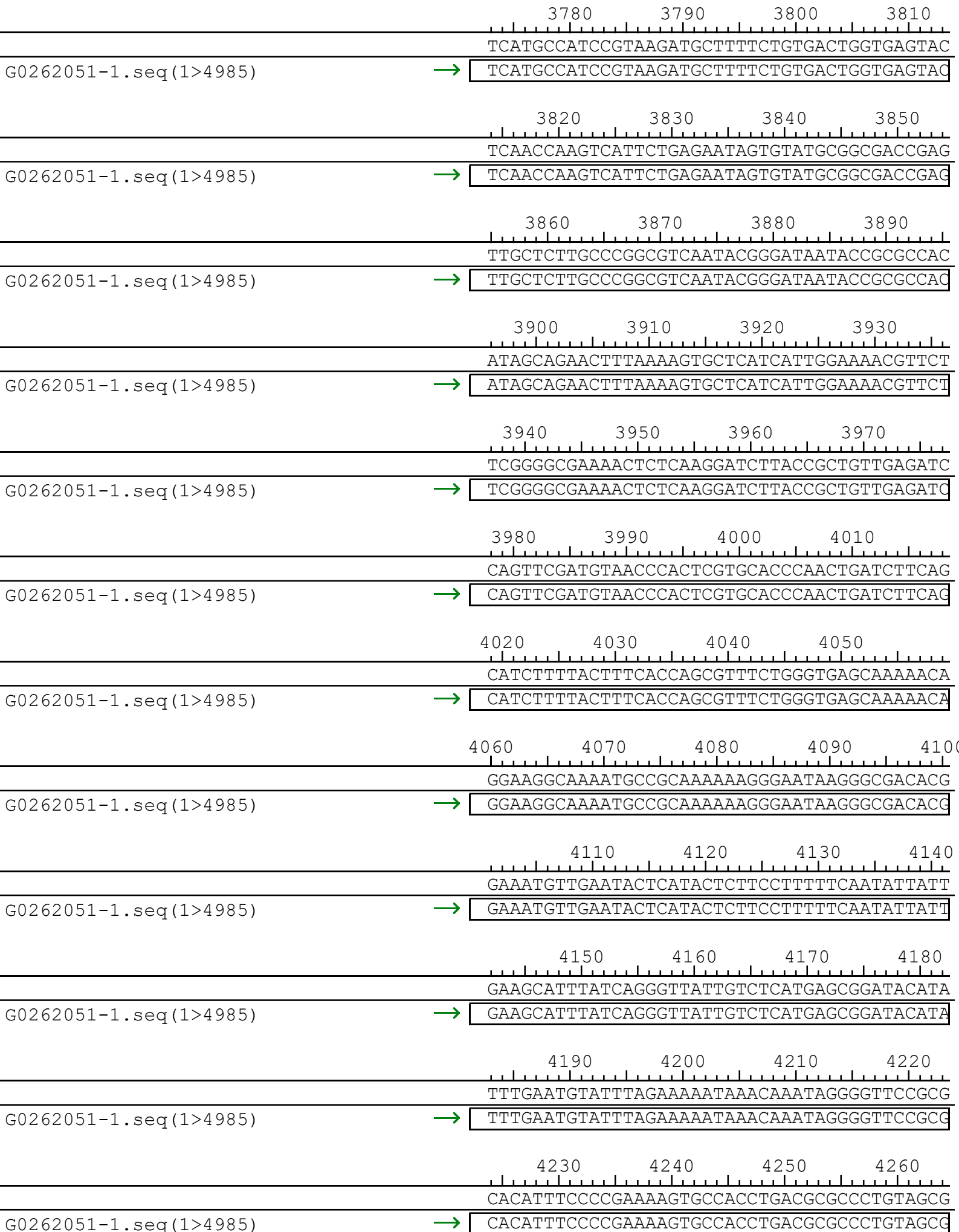
Project: Untitled.SQD Contig 1

	2790	2800	2810	2820	
	TATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC				
G0262051-1.seq (1>4985)	→	TATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC			
	2830	2840	2850	2860	2870
	GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG				
G0262051-1.seq (1>4985)	→	GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG			
	2880	2890	2900	2910	
	CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGT				
G0262051-1.seq (1>4985)	→	CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGT			
	2920	2930	2940	2950	
	GGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGT				
G0262051-1.seq (1>4985)	→	GGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGT			
	2960	2970	2980	2990	
	ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT				
G0262051-1.seq (1>4985)	→	ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT			
	3000	3010	3020	3030	
	TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCG				
G0262051-1.seq (1>4985)	→	TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCG			
	3040	3050	3060	3070	
	GTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAA				
G0262051-1.seq (1>4985)	→	GTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAA			
	3080	3090	3100	3110	
	AAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC				
G0262051-1.seq (1>4985)	→	AAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC			
	3120	3130	3140	3150	
	TGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGG				
G0262051-1.seq (1>4985)	→	TGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGG			
	3160	3170	3180	3190	
	TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTA				
G0262051-1.seq (1>4985)	→	TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTA			
	3200	3210	3220	3230	
	AATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGA				
G0262051-1.seq (1>4985)	→	AATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGA			
	3240	3250	3260	3270	3280
	GTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGG				
G0262051-1.seq (1>4985)	→	GTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGG			

Project: Untitled.SQD Contig 1

		3290	3300	3310	3320	
		CACCTATCTCAGCGATCTGTCTATTTTCGTTCCATAGTT				
G0262051-1.seq (1>4985)	→	CACCTATCTCAGCGATCTGTCTATTTTCGTTCCATAGTT				
		3330	3340	3350	3360	
		GCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG				
G0262051-1.seq (1>4985)	→	GCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG				
		3370	3380	3390	3400	
		CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACC				
G0262051-1.seq (1>4985)	→	CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACC				
		3410	3420	3430	3440	
		CACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA				
G0262051-1.seq (1>4985)	→	CACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA				
		3450	3460	3470	3480	
		GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATC				
G0262051-1.seq (1>4985)	→	GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATC				
		3490	3500	3510	3520	
		CGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAG				
G0262051-1.seq (1>4985)	→	CGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAG				
		3530	3540	3550	3560	
		TAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCC				
G0262051-1.seq (1>4985)	→	TAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCC				
		3570	3580	3590	3600	
		ATTGCTACAGGCATCGTGGTGTACGCTCGTCTTGGTAT				
G0262051-1.seq (1>4985)	→	ATTGCTACAGGCATCGTGGTGTACGCTCGTCTTGGTAT				
		3610	3620	3630	3640	
		GGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTA				
G0262051-1.seq (1>4985)	→	GGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTA				
		3650	3660	3670	3680	3690
		CATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTC				
G0262051-1.seq (1>4985)	→	CATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTC				
		3700	3710	3720	3730	
		GGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTT				
G0262051-1.seq (1>4985)	→	GGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTT				
		3740	3750	3760	3770	
		ATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTG				
G0262051-1.seq (1>4985)	→	ATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTG				

Project: Untitled.SQD Contig 1



Project: Untitled.SQD Contig 1

