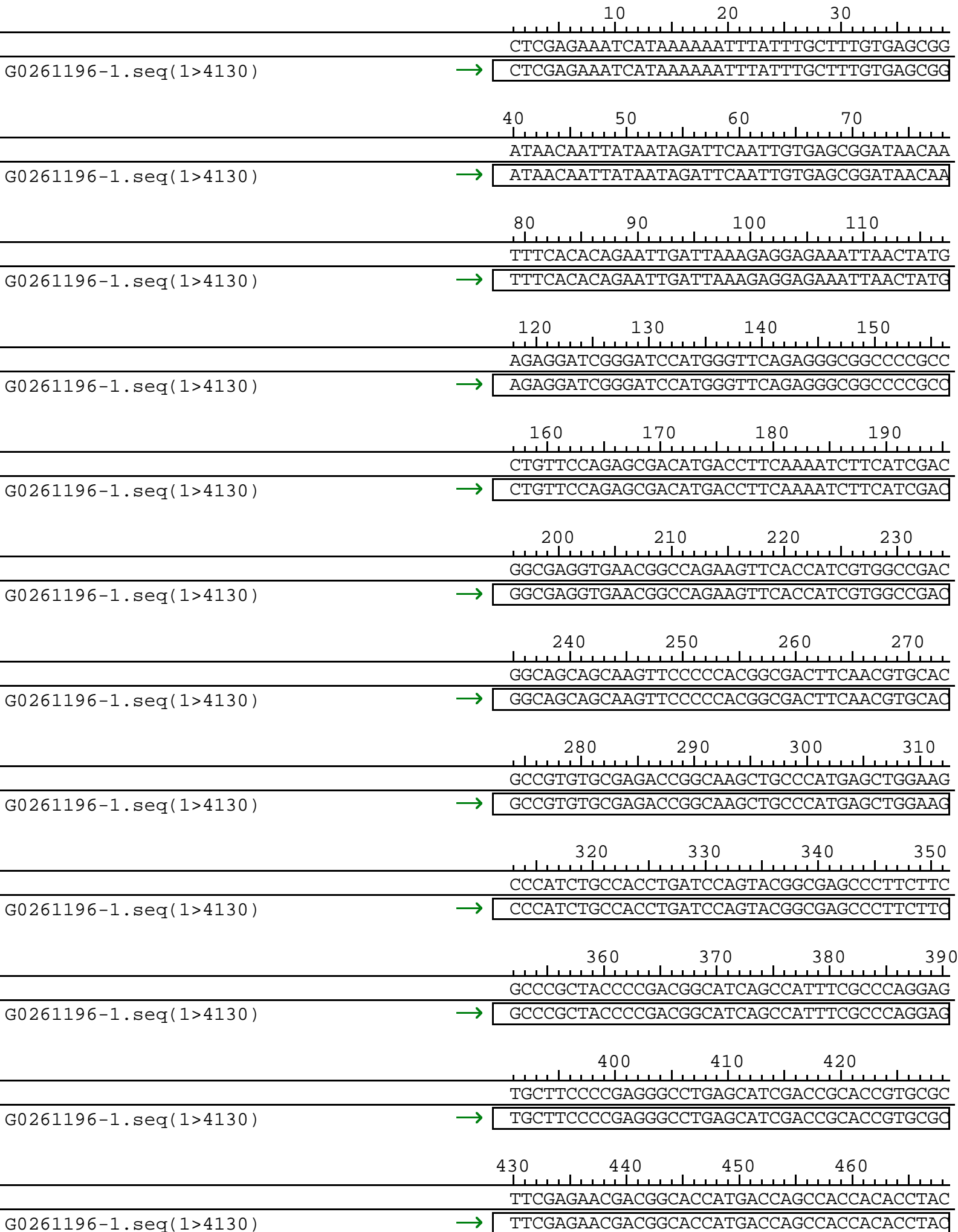


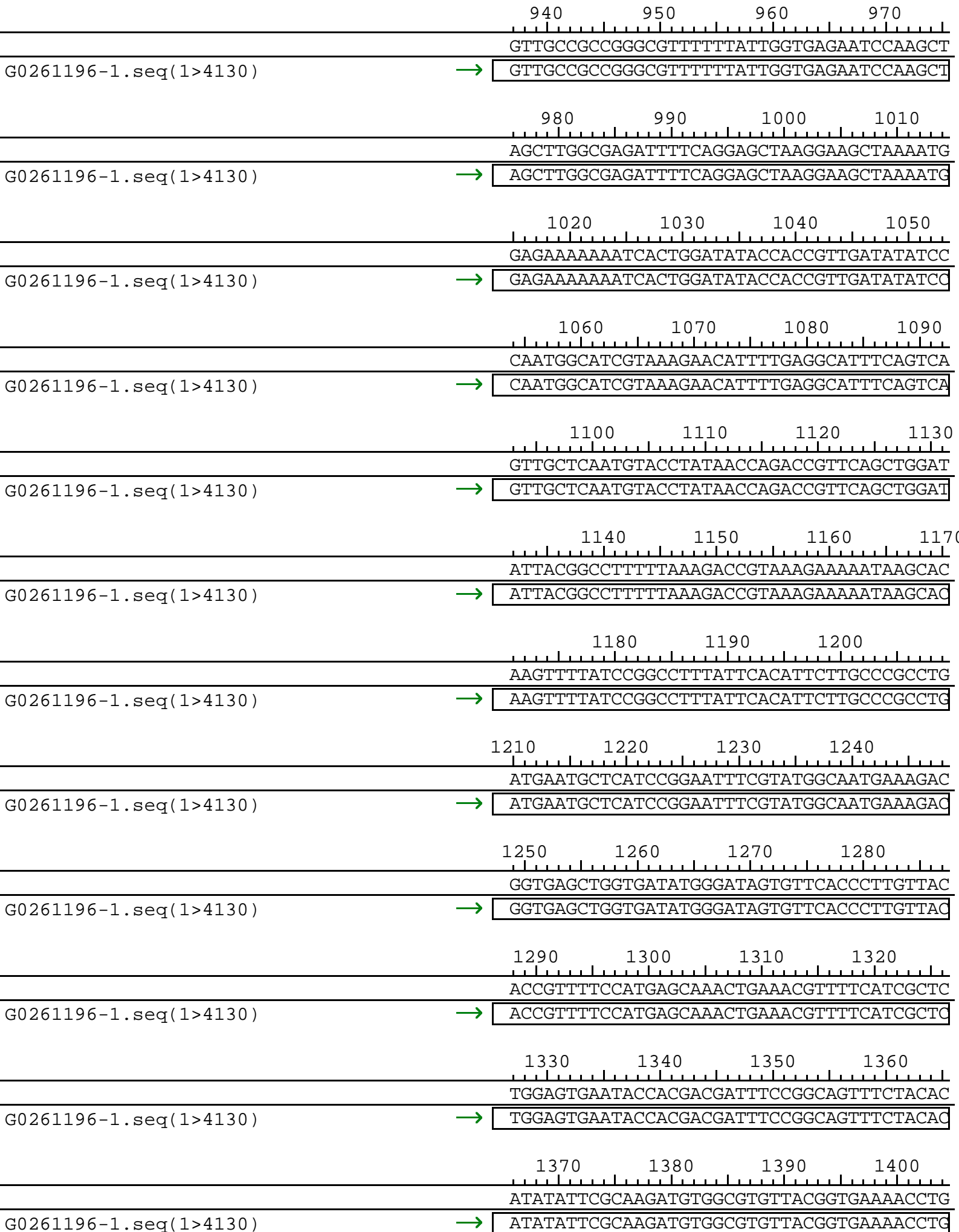
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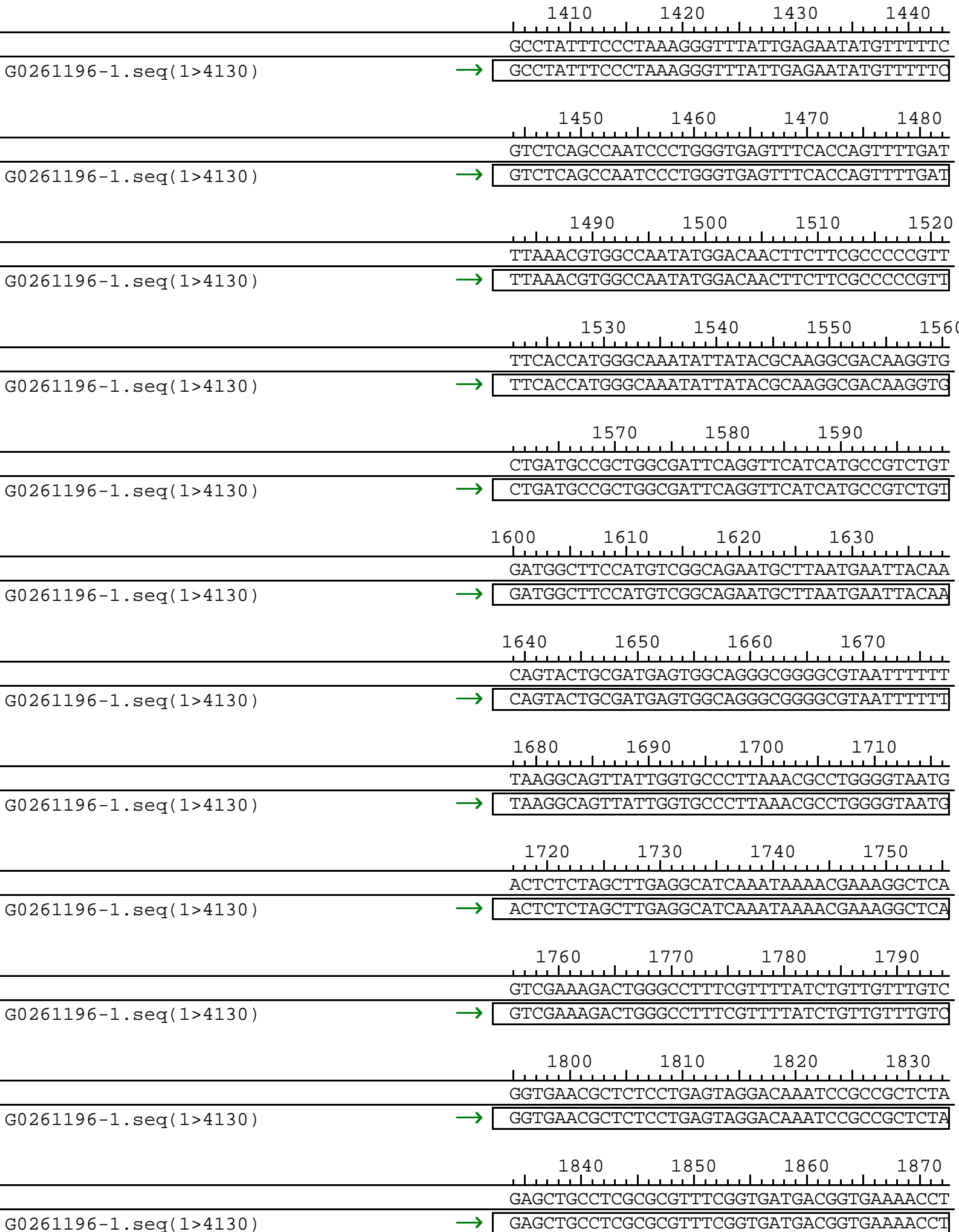
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	470	480	490	500
	GAGCTGGACGACACCTGCGTGGTGAGCCGCATCACCGTG			
G0261196-1.seq(1>4130)	→	GAGCTGGACGACACCTGCGTGGTGAGCCGCATCACCGTG		
	510	520	530	540
	AACTGCGACGGCTTCCAGCCCGACGGCCCCATCATGCGC			
G0261196-1.seq(1>4130)	→	AACTGCGACGGCTTCCAGCCCGACGGCCCCATCATGCGC		
	550	560	570	580
	GACCAGCTGGTGGACATCCTGCCCAACGAGACCCACATG			
G0261196-1.seq(1>4130)	→	GACCAGCTGGTGGACATCCTGCCCAACGAGACCCACATG		
	590	600	610	620
	TTCCCCACGGCCCCAACGCCGTGCGCCAGCTGGCCTTC			
G0261196-1.seq(1>4130)	→	TTCCCCACGGCCCCAACGCCGTGCGCCAGCTGGCCTTC		
	630	640	650	660
	ATCGGCTTCACCACCGCCGACGGCGGCCTGATGATGGGC			
G0261196-1.seq(1>4130)	→	ATCGGCTTCACCACCGCCGACGGCGGCCTGATGATGGGC		
	670	680	690	700
	CACTTCGACAGCAAGATGACCTTCAACGGCAGCCGCGCC			
G0261196-1.seq(1>4130)	→	CACTTCGACAGCAAGATGACCTTCAACGGCAGCCGCGCC		
	710	720	730	740
	ATCGAGATCCCCGGCCACACTTCGTGACCATCATCACC			
G0261196-1.seq(1>4130)	→	ATCGAGATCCCCGGCCACACTTCGTGACCATCATCACC		
	750	760	770	780
	AAGCAGATGAGGGACACCAGCGACAAGCGCGACCACGTG			
G0261196-1.seq(1>4130)	→	AAGCAGATGAGGGACACCAGCGACAAGCGCGACCACGTG		
	790	800	810	
	TGCCAGCGCGAGGTGGCCTACGCCACAGCGTGCCCCGC			
G0261196-1.seq(1>4130)	→	TGCCAGCGCGAGGTGGCCTACGCCACAGCGTGCCCCGC		
	820	830	840	850
	ATCACCAGCGCCATCGGTAGCGACGAGGATTGAAAGCTT			
G0261196-1.seq(1>4130)	→	ATCACCAGCGCCATCGGTAGCGACGAGGATTGAAAGCTT		
	860	870	880	890
	AATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAA			
G0261196-1.seq(1>4130)	→	AATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAA		
	900	910	920	930
	TGACCTCAGAACTCCATCTGGATTTGTTTCAGAACGCTCG			
G0261196-1.seq(1>4130)	→	TGACCTCAGAACTCCATCTGGATTTGTTTCAGAACGCTCG		

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		1880 1890 1900 1910	CTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCT
G0261196-1.seq(1>4130)	→		CTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCT
		1920 1930 1940 1950	GTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGC
G0261196-1.seq(1>4130)	→		GTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGC
		1960 1970 1980	GTCAGCGGGTGTGTCGGGGCGCAGCCATGAC
G0261196-1.seq(1>4130)	→		GTCAGCGGGTGTGTCGGGGCGCAGCCATGAC
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		GTGTCCGGGGCGCAGCCATGAC
		1990 2000 2010 2020	CCAGTCACGTAGCGATAGCGGAGTGATACTGGCTTAAC
G0261196-1.seq(1>4130)	→		CCAGTCACGTAGCGATAGCGGAGTGATACTGGCTTAAC
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		CCAGTCACGTAGCGATAGCGGAGTGATACTGGCTTAAC
		2030 2040 2050 2060	TATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCAT
G0261196-1.seq(1>4130)	→		TATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCAT
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		TATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCAT
		2070 2080 2090 2100	ATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAA
G0261196-1.seq(1>4130)	→		ATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAA
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		ATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAA
		2110 2120 2130 2140	TACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGAC
G0261196-1.seq(1>4130)	→		TACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGAC
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		TACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGAC
		2150 2160 2170 2180	TCGCTGCGCTCGGTCGTTCCGGCTGCGGCGAGCGGTATCA
G0261196-1.seq(1>4130)	→		TCGCTGCGCTCGGTCGTTCCGGCTGCGGCGAGCGGTATCA
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		TCGCTGCGCTCGGTCGTTCCGGCTGCGGCGAGCGGTATCA
		2190 2200 2210 2220	GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCA
G0261196-1.seq(1>4130)	→		GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCA
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCA
		2230 2240 2250 2260	GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAG
G0261196-1.seq(1>4130)	→		GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAG
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAG

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		2270 2280 2290 2300	CAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCC
G0261196-1.seq(1>4130)	→		CAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCC
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		CAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCC
		2310 2320 2330 2340	TTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAA
G0261196-1.seq(1>4130)	→		TTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAA
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		TTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAA
		2350 2360 2370	AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
G0261196-1.seq(1>4130)	→		AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
		2380 2390 2400 2410	CTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTC
G0261196-1.seq(1>4130)	→		CTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTC
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		CTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTC
		2420 2430 2440 2450	GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC
G0261196-1.seq(1>4130)	→		GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC
		2460 2470 2480 2490	CTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCT
G0261196-1.seq(1>4130)	→		CTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCT
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		CTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCT
		2500 2510 2520 2530	CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
G0261196-1.seq(1>4130)	→		CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
		2540 2550 2560 2570	GTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT
G0261196-1.seq(1>4130)	→		GTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		GTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT
		2580 2590 2600 2610	CAGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTT
G0261196-1.seq(1>4130)	→		CAGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTT
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		CAGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTT
		2620 2630 2640 2650	GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA
G0261196-1.seq(1>4130)	→		GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→		GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA

		2660	2670	2680	2690
		GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA			
G0261196-1.seq(1>4130)	→	GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA			
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→	GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA			
		2700	2710	2720	2730
		GGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTAC			
G0261196-1.seq(1>4130)	→	GGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTAC			
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→	GGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTAC			
		2740	2750	2760	
		GGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTG			
G0261196-1.seq(1>4130)	→	GGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTG			
D01-D38121-G0261196-1_M13-75.ab1(1>793)	→	GGCTACACTAGAAGGACAGTATTTGGTATCT			
		2770	2780	2790	2800
		CTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT			
G0261196-1.seq(1>4130)	→	CTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT			
		2810	2820	2830	2840
		TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT			
G0261196-1.seq(1>4130)	→	TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT			
		2850	2860	2870	2880
		TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGA			
G0261196-1.seq(1>4130)	→	TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGA			
		2890	2900	2910	2920
		TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGAC			
G0261196-1.seq(1>4130)	→	TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGAC			
		2930	2940	2950	2960
		GCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTC			
G0261196-1.seq(1>4130)	→	GCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTC			
		2970	2980	2990	3000
		ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTA			
G0261196-1.seq(1>4130)	→	ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTA			
		3010	3020	3030	3040
		AATTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATAT			
G0261196-1.seq(1>4130)	→	AATTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATAT			
		3050	3060	3070	3080
		GAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGT			
G0261196-1.seq(1>4130)	→	GAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGT			

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		3090	3100	3110	3120
		GAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC			
G0261196-1.seq(1>4130)	→	GAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC			
		3130	3140	3150	
		ATAGCTGCCTGACTCCCCGTCGTGTAGATAACTACGATA			
G0261196-1.seq(1>4130)	→	ATAGCTGCCTGACTCCCCGTCGTGTAGATAACTACGATA			
		3160	3170	3180	3190
		CGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA			
G0261196-1.seq(1>4130)	→	CGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA			
		3200	3210	3220	3230
		CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCA			
G0261196-1.seq(1>4130)	→	CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCA			
		3240	3250	3260	3270
		ATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGT			
G0261196-1.seq(1>4130)	→	ATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGT			
		3280	3290	3300	3310
		CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGT			
G0261196-1.seq(1>4130)	→	CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGT			
		3320	3330	3340	3350
		TGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGT			
G0261196-1.seq(1>4130)	→	TGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGT			
		3360	3370	3380	3390
		TTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTG			
G0261196-1.seq(1>4130)	→	TTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTG			
		3400	3410	3420	3430
		TCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGT			
G0261196-1.seq(1>4130)	→	TCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGT			
		3440	3450	3460	3470
		TCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG			
G0261196-1.seq(1>4130)	→	TCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG			
		3480	3490	3500	3510
		TGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTT			
G0261196-1.seq(1>4130)	→	TGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTT			
		3520	3530	3540	
		GTCAGAAGTAAGTTGGCCGAGTGTATCACTCATGGTT			
G0261196-1.seq(1>4130)	→	GTCAGAAGTAAGTTGGCCGAGTGTATCACTCATGGTT			

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	3550	3560	3570	3580
	ATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCC			
G0261196-1.seq(1>4130)	→	ATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCC		
	3590	3600	3610	3620
	GTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAG			
G0261196-1.seq(1>4130)	→	GTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAG		
	3630	3640	3650	3660
	TCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCT			
G0261196-1.seq(1>4130)	→	TCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCT		
	3670	3680	3690	3700
	TGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGC			
G0261196-1.seq(1>4130)	→	TGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGC		
	3710	3720	3730	3740
	AGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCG			
G0261196-1.seq(1>4130)	→	AGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCG		
	3750	3760	3770	3780
	GGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCC			
G0261196-1.seq(1>4130)	→	GGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCC		
	3790	3800	3810	3820
	AGTTCGATGTAACCCACTCGTGCACCCAACCTGATCTTCA			
G0261196-1.seq(1>4130)	→	AGTTCGATGTAACCCACTCGTGCACCCAACCTGATCTTCA		
	3830	3840	3850	3860
	GCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAA			
G0261196-1.seq(1>4130)	→	GCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAA		
	3870	3880	3890	3900
	ACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCG			
G0261196-1.seq(1>4130)	→	ACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCG		
	3910	3920	3930	
	ACACGGAAATGTTGAATACTCATACTCTTCTTTTTTCAA			
G0261196-1.seq(1>4130)	→	ACACGGAAATGTTGAATACTCATACTCTTCTTTTTTCAA		
	3940	3950	3960	3970
	TATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGC			
G0261196-1.seq(1>4130)	→	TATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGC		
	3980	3990	4000	4010
	GGATACATATTTGAATGTATTTAGAAAAATAAACAAATA			
G0261196-1.seq(1>4130)	→	GGATACATATTTGAATGTATTTAGAAAAATAAACAAATA		

4020 4030 4040 4050
GGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC
G0261196-1.seq(1>4130) → GGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC

4060 4070 4080 4090
GTCTAAGAAACCATTATTATCATGACATTAACCTATAAA
G0261196-1.seq(1>4130) → GTCTAAGAAACCATTATTATCATGACATTAACCTATAAA

4100 4110 4120
AATAGGCGTATCACGAGGCCCTTTCGTCTTCAC
G0261196-1.seq(1>4130) → AATAGGCGTATCACGAGGCCCTTTCGTCTTCAC