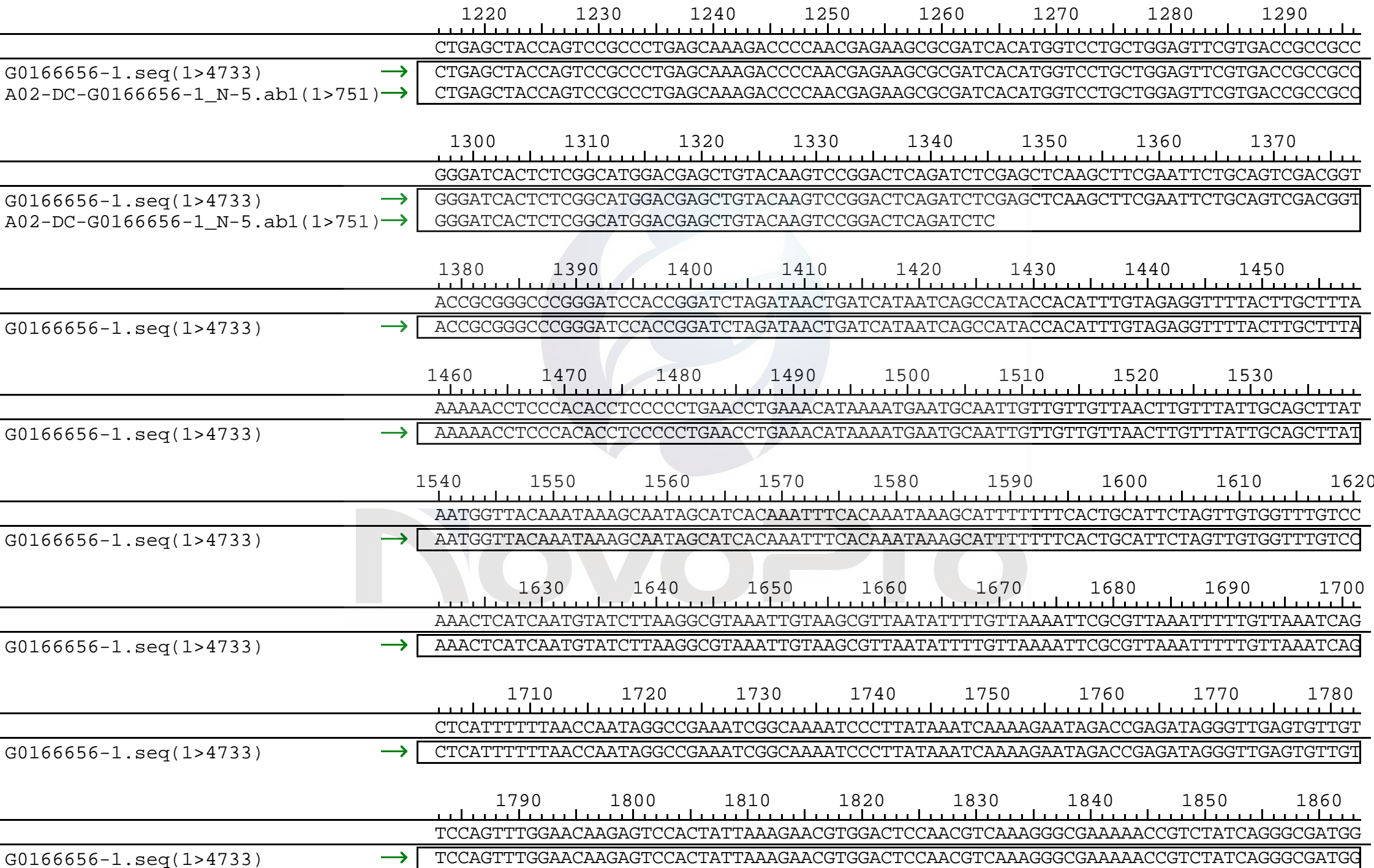


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	650	660	670	680	690	700	710	720	
	GTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACC								
G0166656-1.seq(1>4733)	→	GTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACC							
A02-DC-G0166656-1_N-5.ab1(1>751)	→	GTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACC							
	730	740	750	760	770	780	790	800	810
	TACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCTGGCCCACCCTCGTGACCACCTTCGGC								
G0166656-1.seq(1>4733)	→	TACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCTGGCCCACCCTCGTGACCACCTTCGGC							
A02-DC-G0166656-1_N-5.ab1(1>751)	→	TACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCTGGCCCACCCTCGTGACCACCTTCGGC							
	820	830	840	850	860	870	880	890	
	TACGGCCTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCTAC								
G0166656-1.seq(1>4733)	→	TACGGCCTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCTAC							
A02-DC-G0166656-1_N-5.ab1(1>751)	→	TACGGCCTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAAGGCTAC							
	900	910	920	930	940	950	960	970	
	GTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG								
G0166656-1.seq(1>4733)	→	GTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG							
A02-DC-G0166656-1_N-5.ab1(1>751)	→	GTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTG							
	980	990	1000	1010	1020	1030	1040	1050	
	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAAC								
G0166656-1.seq(1>4733)	→	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAAC							
A02-DC-G0166656-1_N-5.ab1(1>751)	→	GTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAAC							
	1060	1070	1080	1090	1100	1110	1120	1130	
	AGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGAC								
G0166656-1.seq(1>4733)	→	AGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGAC							
A02-DC-G0166656-1_N-5.ab1(1>751)	→	AGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGAC							
	1140	1150	1160	1170	1180	1190	1200	1210	
	GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC								
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A02-DC-G0166656-1_N-5.ab1(1>751)	→	GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC							

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2520 2530 2540 2550 2560 2570 2580 2590
GCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAA
G0166656-1.seq(1>4733) → GCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAA

2600 2610 2620 2630 2640 2650 2660 2670
GATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGTTCTCCGGCCGCTTGGGT
G0166656-1.seq(1>4733) → GATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGTTCTCCGGCCGCTTGGGT

2680 2690 2700 2710 2720 2730 2740 2750
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2760 2770 2780 2790 2800 2810 2820 2830
GCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCT
G0166656-1.seq(1>4733) → GCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCT

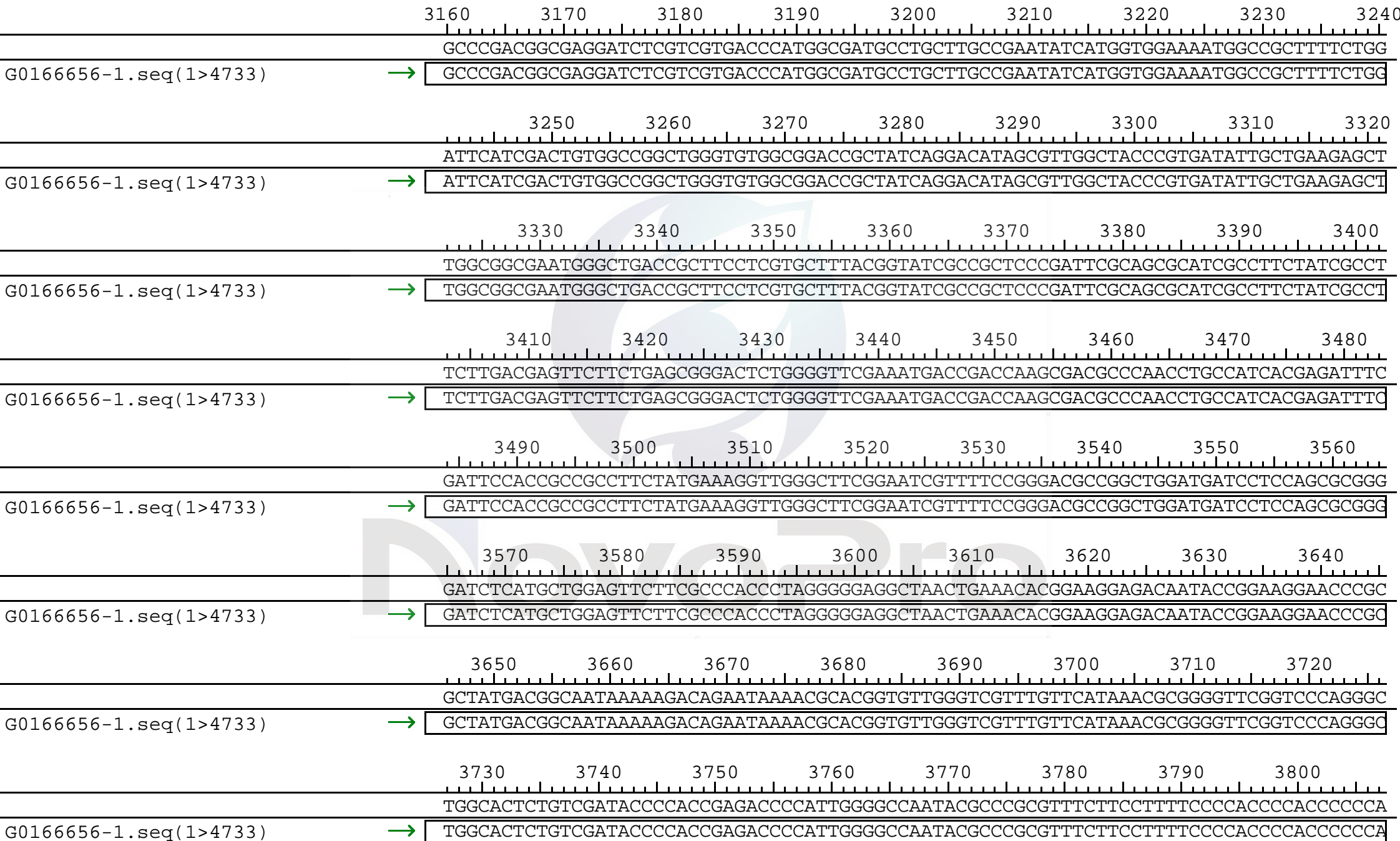
2840 2850 2860 2870 2880 2890 2900 2910
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2920 2930 2940 2950 2960 2970 2980 2990
GCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCA
G0166656-1.seq(1>4733) → GCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCCGGCGGCTGCA

3000 3010 3020 3030 3040 3050 3060 3070
TACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG
G0166656-1.seq(1>4733) → TACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG

3080 3090 3100 3110 3120 3130 3140 3150
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G0166656-1.seq(1>4733) → TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGAGCAT

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4460 4470 4480 4490 4500 4510 4520 4530
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G0166656-1.seq(1>4733) → GCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTT

4540 4550 4560 4570 4580 4590 4600 4610
TATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA
G0166656-1.seq(1>4733) → TATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA

4620 4630 4640 4650 4660 4670 4680 4690
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4700 4710 4720 4730
GATTCTGTGGATAACCGTATTACCGCCATGCAT
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