

# CLUSTAL 2.1 multiple sequence Alignment

MF288709.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288708.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288710.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288711.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288712.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288713.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288714.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288715.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288716.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288717.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288718.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288719.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288720.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288721.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288722.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288723.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288724.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288725.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288726.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
MF288727.1	ATGCATGGACCTAAGGCAACAGTGCAAGACATTGTATTGCATTTAGAGCC
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MF288709.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288708.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288710.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288711.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288712.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288713.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288714.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288715.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288716.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288717.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288718.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288719.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288720.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288721.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288722.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288723.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288724.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288725.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288726.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
MF288727.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
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MF288709.1	CAGAGGAAGAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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# CLUSTAL 2.1 multiple sequence Alignment

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MF288708.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288710.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288711.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288712.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288713.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288714.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288715.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288716.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288717.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288718.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288719.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288720.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288721.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288722.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288723.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288724.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288725.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288726.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
MF288727.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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MF288709.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288708.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288710.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288711.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288712.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288713.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288714.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288715.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288716.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288717.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288718.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288719.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288720.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288721.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288722.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288723.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288724.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288725.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288726.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
MF288727.1      GCCCGACGAGCCGAACCACAACGTCACACACTGTTGTGTATGTGTTGTAA
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MF288709.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
MF288708.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
MF288710.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
MF288711.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
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# CLUSTAL 2.1 multiple sequence Alignment

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MF288712.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288713.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288714.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288715.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288716.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288717.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288718.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288719.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288720.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288721.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288722.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288723.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288724.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288725.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288726.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
MF288727.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
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MF288709.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288708.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288710.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288711.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288712.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288713.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288714.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288715.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288716.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288717.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288718.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288719.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288720.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288721.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288722.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288723.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288724.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288725.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288726.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
MF288727.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
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MF288709.1      TGTGCATCCCAGCAGTAA
MF288708.1      TGTGCATCCCAGCAGTAA
MF288710.1      TGTGCATCCCAGCAGTAA
MF288711.1      TGTGCATCCCAGCAGTAA
MF288712.1      TGTGCATCCCAGCAGTAA
MF288713.1      TGTGCATCCCAGCAGTAA
MF288714.1      TGTGCATCCCAGCAGTAA
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**CLUSTAL 2.1 multiple sequence Alignment**

MF288715.1	TGTGCATCCCAGCAGTAA
MF288716.1	TGTGCATCCCAGCAGTAA
MF288717.1	TGTGCATCCCAGCAGTAA
MF288718.1	TGTGCATCCCAGCAGTAA
MF288719.1	TGTGCATCCCAGCAGTAA
MF288720.1	TGTGCATCCCAGCAGTAA
MF288721.1	TGTGCATCCCAGCAGTAA
MF288722.1	TGTGCATCCCAGCAGTAA
MF288723.1	TGTGCATCCCAGCAGTAA
MF288724.1	TGTGCATCCCAGCAGTAA
MF288725.1	TGTGCATCCCAGCAGTAA
MF288726.1	TGTGCATCCCAGCAGTAA
MF288727.1	TGTGCATCCCAGCAGTAA

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### Consensus sequence

>/chido/chido\_E7 Consensus threshold=0.7

ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCCCCAAAATGAA  
ATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACTCAGAGGAAGAAAACGATGAA  
ATAGATGGAGTTAATCATCAACATTTACCAGCCCGACGAGCCGAACCACAACGTCACACA  
ATGTTGTGTATGTGTTGTAAGTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCA  
GACGACCTTCGAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG  
TGTGCATCCCAGCAGTAA

## Primers data

### ACCEPTABLE LEFT PRIMERS

0-based	#	self	self	hair-	qual-						
#	sequence	start	ln	N	GC%	Tm	any_th	end_th	pin	lity	
0	TGCATGGACCTAAGGCAACA	1	20	0	50.00	59.596	0.34	0.00	41.41	2.404	
1	TGCATGGACCTAAGGCAACAT	1	21	0	47.62	59.994	0.34	0.00	41.41	3.006	
2	ATGCATGGACCTAAGGCAACA	0	21	0	47.62	59.994	1.29	0.00	41.41	3.006	
3	GCATGGACCTAAGGCAACA	2	19	0	52.63	57.735	0.00	0.00	41.41	3.265	
4	TGCATGGACCTAAGGCAAC	1	19	0	52.63	57.735	0.34	0.00	0.00	3.265	
5	GCATGGACCTAAGGCAACAT	2	20	0	50.00	58.232	0.00	0.00	41.41	3.768	
6	ATGCATGGACCTAAGGCAAC	0	20	0	50.00	58.232	1.29	0.00	0.00	3.768	
7	GCATGGACCTAAGGCAACATT	2	21	0	47.62	58.897	0.00	0.00	41.41	4.103	
8	CATGGACCTAAGGCAACATTG	3	21	0	47.62	57.212	0.00	0.00	41.41	5.788	

### ACCEPTABLE RIGHT PRIMERS

0-based	#	self	self	hair-	qual-					
#	sequence	start	ln	N	GC%	Tm	any_th	end_th	pin	lity
0	GGATGCACACCACGGACA	308	18	0	61.11	59.968	6.86	0.00	0.00	0.032
1	CTGCTGGGATGCACACCA	314	18	0	61.11	59.965	6.10	4.92	38.12	0.035
2	ACTGCTGGGATGCACACC	315	18	0	61.11	59.965	0.00	0.00	38.12	0.035
3	TGCTCGAAGGTCGTCTGC	254	18	0	61.11	59.741	6.26	6.26	43.45	0.259
4	GCTCGTCGGGCTGGTAAA	160	18	0	61.11	59.736	10.59	0.00	0.00	0.264
5	TGCTGGGATGCACACCAC	313	18	0	61.11	60.282	3.46	0.78	38.12	0.282
6	TTGTGGTTTCGGCTCGTCG	170	18	0	61.11	60.355	0.00	0.00	0.00	0.355
7	TGACGTTGTGGTTCGGCT	175	18	0	55.56	59.498	0.00	0.00	35.95	0.502
8	ATGCACACCACGGACACA	306	18	0	55.56	59.492	0.00	0.00	0.00	0.508
9	TGCACACCACGGACACAC	305	18	0	61.11	60.513	0.00	0.00	0.00	0.513
10	GCACACCACGGACACACA	304	18	0	61.11	60.513	0.00	0.00	0.00	0.513
11	GCTCGAAGGTCGTCTGCT	253	18	0	61.11	59.431	6.06	0.00	43.45	0.569
12	GTGACGTTGTGGTTCGGC	176	18	0	61.11	59.370	0.00	0.00	35.47	0.630
13	ACGTTGTGGTTTCGGCTCG	173	18	0	61.11	60.661	0.00	0.00	0.00	0.661
14	CGTTGTGGTTCGGCTCGT	172	18	0	61.11	60.661	0.00	0.00	0.00	0.661
15	GGGATGCACACCACGGAC	309	18	0	66.67	60.746	12.79	0.00	0.00	0.746
16	CTGGGATGCACACCACGG	311	18	0	66.67	60.747	2.08	0.00	0.00	0.747
17	AGCTGCTGGAATGCTCGA	265	18	0	55.56	59.015	0.00	0.00	30.41	0.985
18	CAGCTGCTGGAATGCTCG	266	18	0	61.11	58.901	21.71	0.00	34.51	1.099
19	GCTCGTCGGGCTGGTAAAT	160	19	0	57.89	60.153	10.59	0.00	0.00	1.153
20	ATGCTCGAAGGTCGTCTGC	255	19	0	57.89	60.154	6.26	6.26	43.45	1.154
21	GACGTTGTGGTTCGGCTC	174	18	0	61.11	58.759	0.00	0.00	31.86	1.241
22	GTTGTGGTTTCGGCTCGTC	171	18	0	61.11	58.759	0.00	0.00	0.00	1.241
23	TGGGATGCACACCACGGA	310	18	0	61.11	61.245	6.10	0.00	0.00	1.245
24	GATGCACACCACGGACAC	307	18	0	61.11	58.746	0.00	0.00	0.00	1.254
25	AGCTGCTGGAATGCTCGAA	265	19	0	52.63	59.702	0.00	0.00	30.41	1.298
26	TACTGCTGGGATGCACACC	316	19	0	57.89	59.700	0.00	0.00	38.12	1.300
27	TGTGGTTTCGGCTCGTCG	169	17	0	64.71	59.693	0.00	0.00	0.00	1.307
28	TGGGATGCACACCACGG	310	17	0	64.71	59.592	6.10	0.00	0.00	1.408
29	GCTGGGATGCACACCACG	312	18	0	66.67	61.434	3.27	0.42	0.00	1.434

# Primers data

30	CAGCTGCTGGAATGCTCGA	266	19	0	57.89	60.449	21.71	0.00	34.51	1.449
31	GTGGTTCGGCTCGTCGG	168	17	0	70.59	60.495	0.00	0.00	0.00	1.495
32	GAAGGTCGTCTGCTGAGCT	249	19	0	57.89	59.411	5.83	0.00	0.00	1.589
33	TGACGTTGTGGTTTCGGCTC	175	19	0	57.89	60.593	0.00	0.00	35.95	1.593
34	GATGCACACCACGGACACA	307	19	0	57.89	60.597	0.00	0.00	0.00	1.597
35	GTGTGACGTTGTGGTTCGG	178	19	0	57.89	59.360	0.00	0.00	0.00	1.640
36	TGCTGGAATGCTCGAAGGT	262	19	0	52.63	59.321	0.00	0.00	0.00	1.679
37	GCTGCTGGAATGCTCGAAG	264	19	0	57.89	59.280	0.00	0.00	0.00	1.720
38	GGGATGCACACCACGGA	309	17	0	64.71	59.258	12.79	0.00	0.00	1.742
39	ACAGCTGCTGGAATGCTCG	267	19	0	57.89	60.744	31.00	5.48	35.51	1.744
40	GGCTCGTCGGGCTGGTAA	161	18	0	66.67	61.767	8.47	0.00	0.00	1.767
41	AAGGTCGTCTGCTGAGCT	248	18	0	55.56	58.215	5.83	0.00	0.00	1.785
42	AGGTCGTCTGCTGAGCTT	247	18	0	55.56	58.215	5.83	0.00	0.00	1.785
43	GCTCGAAGGTCGTCTGCTG	253	19	0	63.16	60.804	6.06	0.00	43.45	1.804
44	CGAAGGTCGTCTGCTGAGC	250	19	0	63.16	60.804	0.00	0.00	37.02	1.804
45	CTCGAAGGTCGTCTGCTGA	252	19	0	57.89	59.123	0.00	0.00	43.45	1.877
46	TCGAAGGTCGTCTGCTGAG	251	19	0	57.89	59.123	0.00	0.00	43.45	1.877
47	GTGACGTTGTGGTTCGGCT	176	19	0	57.89	60.886	0.00	0.00	35.95	1.886
48	ATGCACACCACGGACACAC	306	19	0	57.89	60.892	0.00	0.00	0.00	1.892
49	GCTGCTGGAATGCTCGAA	264	18	0	55.56	58.105	0.00	0.00	0.00	1.895
50	ACCACGGACACACAAAGGA	300	19	0	52.63	59.091	0.00	0.00	0.00	1.909
51	TGGAATGCTCGAAGGTCGT	259	19	0	52.63	59.028	0.00	0.00	43.45	1.972
52	GCTCGTCGGGCTGGTAA	160	17	0	64.71	59.026	10.59	0.00	0.00	1.974
53	TCGTCGGGCTGGTAAATGT	158	19	0	52.63	59.023	0.00	0.00	0.00	1.977
54	TGCACACCACGGACACA	305	17	0	58.82	59.010	0.00	0.00	0.00	1.990
55	CACCACGGACACACAAAGG	301	19	0	57.89	58.978	0.00	0.00	0.00	2.022
56	GAAGGTCGTCTGCTGAGCTT	249	20	0	55.00	60.038	7.47	7.47	38.04	2.038
57	AGGTCGTCTGCTGAGCTTTC	247	20	0	55.00	60.038	0.00	0.00	0.00	2.038
58	GGTCGTCTGCTGAGCTTTCT	246	20	0	55.00	60.038	0.00	0.00	0.00	2.038
59	AAGGTCGTCTGCTGAGCTT	248	19	0	52.63	58.946	5.83	4.25	34.13	2.054
60	AGGTCGTCTGCTGAGCTTT	247	19	0	52.63	58.946	5.83	0.00	0.00	2.054
61	TCGAAGGTCGTCTGCTGA	251	18	0	55.56	57.925	0.00	0.00	43.45	2.075
62	CTCGTCGGGCTGGTAAATGT	159	20	0	55.00	60.108	0.00	0.00	0.00	2.108
63	CTGGAATGCTCGAAGGTCGT	260	20	0	55.00	60.109	0.00	0.00	43.45	2.109
64	TGGAATGCTCGAAGGTCGTC	259	20	0	55.00	60.109	0.00	0.00	43.45	2.109
65	GCACACCACGGACACACAA	304	19	0	57.89	61.110	0.00	0.00	0.00	2.110
66	TGTGACGTTGTGGTTCGG	177	18	0	55.56	57.888	0.00	0.00	0.00	2.112
67	GGCTCGTCGGGCTGGTA	161	17	0	70.59	61.167	8.47	0.00	0.00	2.167
68	GGAATGCTCGAAGGTCGTCT	258	20	0	55.00	59.826	0.00	0.00	43.45	2.174
69	TGTGACGTTGTGGTTCGGC	177	19	0	57.89	61.175	0.00	0.00	35.47	2.175
70	GAAGGTCGTCTGCTGAGC	249	18	0	61.11	57.823	0.00	0.00	0.00	2.177
71	ACGGACACACAAAGGACAGG	297	20	0	55.00	60.179	0.00	0.00	0.00	2.179
72	CTCGAAGGTCGTCTGCTGAG	252	20	0	60.00	60.179	0.00	0.00	43.45	2.179
73	GGACACACAAAGGACAGGGT	295	20	0	55.00	59.817	0.00	0.00	0.00	2.183
74	GGTTCGGCTCGTCGGG	166	16	0	75.00	59.806	0.00	0.00	0.00	2.194
75	CACACCACGGACACACAA	303	18	0	55.56	57.790	0.00	0.00	0.00	2.210
76	CGTTGTGGTTCGGCTCG	172	17	0	64.71	58.750	0.00	0.00	0.00	2.250

## Primers data

77	TGCTCGAAGGTCGTCTGCT	254	19	0	57.89	61.269	11.58	0.00	43.45	2.269
78	TGCTGGGATGCACACCA	313	17	0	58.82	58.729	6.10	4.92	38.12	2.271
79	ACAGCTGCTGGAATGCTC	267	18	0	55.56	57.684	31.00	0.00	35.51	2.316
80	CCACGGACACACAAAGGAC	299	19	0	57.89	58.683	0.00	0.00	0.00	2.317
81	TCGTCGGGCTGGTAAATGTT	158	20	0	50.00	59.678	0.00	0.00	0.00	2.322
82	TTACTGCTGGGATGCACACC	317	20	0	55.00	60.322	0.00	0.00	38.12	2.322
83	GGATGCACACCACGGACAC	308	19	0	63.16	61.325	6.86	0.00	0.00	2.325
84	CTGCTGGGATGCACACCAC	314	19	0	63.16	61.338	3.46	0.78	38.12	2.338
85	TGTGGTTTCGGCTCGTCGG	169	18	0	66.67	62.352	0.00	0.00	0.00	2.352
86	TGTGTGACGTTGTGGTTTCG	179	19	0	52.63	58.625	0.00	0.00	0.00	2.375
87	CACACCACGGACACACAAAG	303	20	0	55.00	59.623	0.00	0.00	0.00	2.377
88	GCTGGAATGCTCGAAGGTC	261	19	0	57.89	58.612	0.00	0.00	0.00	2.388
89	CTGCTGGAATGCTCGAAGG	263	19	0	57.89	58.609	0.00	0.00	0.00	2.391
90	TGCTGGAATGCTCGAAGGTC	262	20	0	55.00	60.392	0.00	0.00	0.00	2.392
91	CTGCTGGAATGCTCGAAGGT	263	20	0	55.00	60.392	0.00	0.00	0.00	2.392
92	AAGGTCGTCTGCTGAGCTTT	248	20	0	50.00	59.605	4.25	0.00	34.76	2.395
93	GCACACCACGGACACAC	304	17	0	64.71	58.565	0.00	0.00	0.00	2.435
94	CGTCGGGCTGGTAAATGTTG	157	20	0	55.00	59.554	0.00	0.00	0.00	2.446
95	GGTCGTCTGCTGAGCTTTC	246	19	0	57.89	58.549	0.00	0.00	0.00	2.451
96	CACCACGGACACACAAAGGA	301	20	0	55.00	60.463	0.00	0.00	0.00	2.463
97	CCACGGACACACAAAGGACA	299	20	0	55.00	60.463	0.00	0.00	0.00	2.463
98	ACCACGGACACACAAAGGAC	300	20	0	55.00	60.463	0.00	0.00	0.00	2.463
99	CTCGAAGGTCGTCTGCTG	252	18	0	61.11	57.533	0.00	0.00	43.45	2.467
100	CGAAGGTCGTCTGCTGAG	250	18	0	61.11	57.533	0.00	0.00	37.02	2.467
101	CACACCACGGACACACAAA	303	19	0	52.63	58.528	0.00	0.00	0.00	2.472
102	ACCACGGACACACAAAGG	300	18	0	55.56	57.448	0.00	0.00	0.00	2.552
103	AACAGCTGCTGGAATGCTC	268	19	0	52.63	58.436	31.00	0.00	35.51	2.564
104	GTTTCGGCTCGTCGGGC	165	16	0	75.00	60.567	2.73	2.73	0.00	2.567
105	CGTCGGGCTGGTAAATGT	157	18	0	55.56	57.390	0.00	0.00	0.00	2.610
106	CGGACACACAAAGGACAGG	296	19	0	57.89	58.383	0.00	0.00	0.00	2.617
107	ACACACAAAGGACAGGGTGT	293	20	0	50.00	59.376	0.00	0.00	44.69	2.624
108	TGCTGGAATGCTCGAAGG	262	18	0	55.56	57.376	0.00	0.00	0.00	2.624
109	GCTGGAATGCTCGAAGGT	261	18	0	55.56	57.374	0.00	0.00	0.00	2.626
110	GACGTTGTGGTTTCGGCTCG	174	19	0	63.16	61.655	0.00	0.00	31.86	2.655
111	CGTTGTGGTTTCGGCTCGTC	172	19	0	63.16	61.655	0.00	0.00	0.00	2.655
112	GTTGTGGTTTCGGCTCGTCG	171	19	0	63.16	61.655	0.00	0.00	0.00	2.655
113	GGAATGCTCGAAGGTCGTC	258	19	0	57.89	58.333	0.00	0.00	43.45	2.667
114	CTGGAATGCTCGAAGGTCG	260	19	0	57.89	58.329	0.00	0.00	44.56	2.671
115	CTCGTCGGGCTGGTAAATG	159	19	0	57.89	58.322	0.00	0.00	0.00	2.678
116	GGTCGTCTGCTGAGCTTT	246	18	0	55.56	57.317	5.83	0.00	0.00	2.683
117	GCTGGGATGCACACCAC	312	17	0	64.71	58.284	0.36	0.00	0.00	2.716
118	TTGTGTGACGTTGTGGTTTCG	180	20	0	50.00	59.278	0.00	0.00	0.00	2.722
119	AATGCTCGAAGGTCGTCTGC	256	20	0	55.00	60.738	6.26	6.26	43.45	2.738
120	AGCTGCTGGAATGCTCGAAG	265	20	0	55.00	60.744	0.00	0.00	30.41	2.744
121	ACACCACGGACACACAAAGG	302	20	0	55.00	60.747	0.00	0.00	0.00	2.747
122	TTCGGCTCGTCGGGCT	164	16	0	68.75	60.757	10.99	0.00	0.00	2.757
123	ACACCACGGACACACAAAG	302	19	0	52.63	58.225	0.00	0.00	0.00	2.775



# Primers data

124	TGGTTCGGCTCGTCTGGG	167	17	0	70.59	61.808	0.00	0.00	0.00	2.808
125	ACTGCTGGGATGCACACCA	315	19	0	57.89	61.833	6.10	4.92	38.12	2.833
126	AACAGCTGCTGGAATGCT	268	18	0	50.00	57.163	31.00	8.45	35.51	2.837
127	CGTCGGGCTGGTAAATGTT	157	19	0	52.63	58.151	0.00	0.00	0.00	2.849
128	CCACGGACACACAAAGGA	299	18	0	55.56	57.132	0.00	0.00	0.00	2.868
129	CGGACACACAAAGGACAGGG	296	20	0	60.00	60.885	0.00	0.00	0.00	2.885
130	AGAAACAGCTGCTGGAATGC	271	20	0	50.00	59.113	11.85	0.18	35.51	2.887
131	GAAACAGCTGCTGGAATGCT	270	20	0	50.00	59.113	12.08	0.00	35.51	2.887
132	AAACAGCTGCTGGAATGCTC	269	20	0	50.00	59.113	31.00	0.00	35.51	2.887
133	TGGAATGCTCGAAGGTCTG	259	18	0	55.56	57.089	0.00	0.00	44.56	2.911
134	GGAATGCTCGAAGGTCTGT	258	18	0	55.56	57.087	0.00	0.00	43.45	2.913
135	TCGTCTGGGCTGGTAAATG	158	18	0	55.56	57.076	0.00	0.00	0.00	2.924
136	CACGGACACACAAAGGACAG	298	20	0	55.00	59.063	0.00	0.00	0.00	2.937
137	GTGTTCAGAAACAGCTGCTGG	277	21	0	52.38	60.002	31.00	14.58	45.78	3.002
138	ACACACAAAGGACAGGGTGTT	293	21	0	47.62	59.995	0.00	0.00	42.16	3.005
139	TCGGCTCGTCTGGGCT	163	15	0	73.33	60.018	10.99	0.00	0.00	3.018
140	GGACACACAAAGGACAGGG	295	19	0	57.89	57.979	0.00	0.00	0.00	3.021
141	CAGCTGCTGGAATGCTCGAA	266	20	0	55.00	61.023	21.71	0.00	34.51	3.023
142	GGATGCACACCACGGAC	308	17	0	64.71	57.975	6.86	0.00	0.00	3.025
143	CTGGGATGCACACCACG	311	17	0	64.71	57.970	0.00	0.00	0.00	3.030
144	AAACAGCTGCTGGAATGCT	269	19	0	47.37	57.953	31.00	8.45	35.51	3.047
145	CTGCTGGGATGCACACC	314	17	0	64.71	57.947	0.00	0.00	38.12	3.053
146	TGGTTCGGCTCGTCTGG	167	16	0	68.75	58.943	0.00	0.00	0.00	3.057
147	CACGGACACACAAAGGACA	298	19	0	52.63	57.927	0.00	0.00	0.00	3.073
148	TGTGTGACGTTGTGGTTCGG	179	20	0	55.00	61.085	0.00	0.00	0.00	3.085
149	TGTTTCAGAAACAGCTGCTGGA	276	21	0	47.62	60.134	31.00	16.80	40.45	3.134
150	GAAACAGCTGCTGGAATGCTC	270	21	0	52.38	60.135	12.08	0.00	35.51	3.135
151	CGGCTCGTCTGGGCTG	162	15	0	80.00	59.845	10.99	8.50	0.00	3.155
152	TGACGTTGTGGTTCGGC	175	17	0	58.82	57.822	0.00	0.00	35.47	3.178
153	TTCTGGCTCGTCTGGGCTG	164	17	0	70.59	62.201	6.26	6.26	0.00	3.201
154	GTTCTGGCTCGTCTGGGCT	165	17	0	70.59	62.203	10.99	0.00	0.00	3.203
155	GGTCGTCTGCTGAGCTTTCTA	246	21	0	52.38	59.797	0.00	0.00	0.00	3.203
156	GCTCGAAGGTCTGTCTGC	253	17	0	64.71	57.778	0.00	0.00	43.45	3.222
157	TTACTGCTGGGATGCACAC	317	19	0	52.63	57.752	0.00	0.00	38.12	3.248
158	CTGGGATGCACACCACGGA	311	19	0	63.16	62.253	2.08	0.00	0.00	3.253
159	GAATGCTCGAAGGTCTGTCTG	257	20	0	55.00	58.727	0.00	0.00	43.45	3.273
160	ACACAAAGGACAGGGTGTTCA	291	21	0	47.62	59.716	0.00	0.00	41.36	3.284
161	AACAGCTGCTGGAATGCTCG	268	20	0	55.00	61.304	31.00	5.48	35.51	3.304
162	GGCTCGTCTGGGCTGGTAAA	161	19	0	63.16	62.305	8.47	0.00	0.00	3.305
163	GACACACAAAGGACAGGGTG	294	20	0	55.00	58.691	0.00	0.00	37.29	3.309
164	TGTTTCAGAAACAGCTGCTGG	276	20	0	50.00	58.688	31.00	14.58	40.45	3.312
165	TGCACACCACGGACACACA	305	19	0	57.89	62.317	0.00	0.00	0.00	3.317
166	ATTGTGTGACGTTGTGGTTCG	181	21	0	47.62	59.671	0.00	0.00	0.00	3.329
167	ACGGACACACAAAGGACAG	297	19	0	52.63	57.620	0.00	0.00	0.00	3.380
168	CAGAAACAGCTGCTGGAATGC	272	21	0	52.38	60.402	12.65	0.18	35.51	3.402
169	GACACACAAAGGACAGGGTGT	294	21	0	52.38	60.408	0.00	0.00	44.69	3.408
170	GAAACAGCTGCTGGAATGC	270	19	0	52.63	57.586	9.13	0.00	35.51	3.414

# Primers data

171	GCTGGAATGCTCGAAGGTCG	261	20	0	60.00	61.424	0.00	0.00	44.56	3.424
172	AATGCTCGAAGGTCGTCTG	256	19	0	52.63	57.574	0.00	0.00	43.45	3.426
173	GCTCGTCGGGCTGGTAAATG	160	20	0	60.00	61.429	10.59	0.00	0.00	3.429
174	ACGTTGTGGTTTCGGCTCGT	173	19	0	57.89	62.435	0.00	0.00	0.00	3.435
175	TACTGCTGGGATGCACACCA	316	20	0	55.00	61.488	6.10	4.92	38.12	3.488
176	ACACACAAAGGACAGGGTG	293	19	0	52.63	57.505	0.00	0.00	37.29	3.495
177	CACACAAAGGACAGGGTGT	292	19	0	52.63	57.505	0.00	0.00	44.69	3.495
178	GTCGTCTGCTGAGCTTTCT	245	19	0	52.63	57.494	0.00	0.00	0.00	3.506
179	GACGTTGTGGTTTCGGCT	174	17	0	58.82	57.486	0.00	0.00	31.86	3.514
180	ACGTTGTGGTTTCGGCTC	173	17	0	58.82	57.486	0.00	0.00	0.00	3.514
181	GTTGTGGTTTCGGCTCGT	171	17	0	58.82	57.486	0.00	0.00	0.00	3.514
182	ATGCACACCACGGACAC	306	17	0	58.82	57.460	0.00	0.00	0.00	3.540
183	GGCTCGTCGGGCTGGT	161	16	0	75.00	61.543	8.47	0.00	0.00	3.543
184	TGGGATGCACACCACGGAC	310	19	0	63.16	62.545	6.10	0.00	0.00	3.545
185	GGGATGCACACCACGGACA	309	19	0	63.16	62.545	12.79	0.00	0.00	3.545
186	AGAAACAGCTGCTGGAATGCT	271	21	0	47.62	60.547	14.60	5.01	35.51	3.547
187	GTTTCAGAAACAGCTGCTGGA	275	20	0	50.00	58.402	31.00	16.80	35.51	3.598
188	ATGCTCGAAGGTCGTCTGCT	255	20	0	55.00	61.600	11.58	0.55	43.45	3.600
189	AGGTCGTCTGCTGAGCT	247	17	0	58.82	57.400	5.83	0.00	0.00	3.600
190	TCGGCTCGTCGGGCTG	163	16	0	75.00	61.604	6.26	6.26	0.00	3.604
191	GAAGGTCGTCTGCTGAGCTTT	249	21	0	52.38	60.607	8.40	2.28	36.71	3.607
192	AAGGTCGTCTGCTGAGCTTTC	248	21	0	52.38	60.607	4.25	0.00	34.76	3.607
193	GGCTCGTCGGGCTGG	161	15	0	80.00	59.383	8.47	0.00	0.00	3.617
194	GCACACCACGGACACACAAA	304	20	0	55.00	61.649	0.00	0.00	0.00	3.649
195	CTCGTCGGGCTGGTAAATGTT	159	21	0	52.38	60.675	0.00	0.00	0.00	3.675
196	CACACAAAGGACAGGGTGTTT	292	21	0	52.38	59.324	0.00	0.00	42.16	3.676
197	GCTGCTGGAATGCTCGA	264	17	0	58.82	57.303	0.00	0.00	0.00	3.697
198	AGCTGCTGGAATGCTCG	265	17	0	58.82	57.295	0.00	0.00	30.41	3.705
199	GCTGCTGGAATGCTCGAAGG	264	20	0	60.00	61.713	0.00	0.00	0.00	3.713
200	CGTTTTCTTCTCTGAGTCGC	114	21	0	52.38	59.278	0.00	0.00	0.00	3.722
201	GAATGCTCGAAGGTCGTCT	257	19	0	52.63	57.276	0.00	0.00	43.45	3.724
202	GTCGCTTAATTGCTCGTGACA	98	21	0	47.62	59.275	6.82	0.00	0.00	3.725
203	ACATTGTGTGACGTTGTGGT	183	20	0	45.00	58.255	0.00	0.00	0.00	3.745
204	CACACAAAGGACAGGGTGTT	292	20	0	50.00	58.237	0.00	0.00	42.16	3.763
205	GCTCGTCGGGCTGGTA	160	16	0	68.75	58.231	10.59	0.00	0.00	3.769
206	GACACACAAAGGACAGGGT	294	19	0	52.63	57.199	0.00	0.00	0.00	3.801
207	GTCGGGCTGGTAAATGTTGA	156	20	0	50.00	58.184	0.00	0.00	0.00	3.816
208	GTGACGTTGTGGTTTCGGCTC	176	20	0	60.00	61.828	0.00	0.00	35.95	3.828
209	GATGCACACCACGGACACAC	307	20	0	60.00	61.842	0.00	0.00	0.00	3.842
210	TTGTGGTTTCGGCTCGTC	170	17	0	58.82	57.158	0.00	0.00	0.00	3.842
211	ACAAAGGACAGGGTGTTTCAGA	289	21	0	47.62	59.156	0.00	0.00	0.00	3.844
212	AGGACAGGGTGTTTCAGAAACA	285	21	0	47.62	59.156	0.01	0.00	43.06	3.844
213	TTGTGGTTTCGGCTCGTCGG	170	19	0	63.16	62.852	0.00	0.00	0.00	3.852
214	GATGCACACCACGGACA	307	17	0	58.82	57.129	0.00	0.00	0.00	3.871
215	ACTGCTGGGATGCACAC	315	17	0	58.82	57.088	0.00	0.00	38.12	3.912
216	TCGTCGGGCTGGTAAATGTTG	158	21	0	52.38	60.942	0.00	0.00	0.00	3.942
217	CGTCGGGCTGGTAAATGTTGA	157	21	0	52.38	60.942	0.00	0.00	0.00	3.942

# Primers data

218	CACAAAGGACAGGGTGTTCAG	290	21	0	52.38	59.050	0.00	0.00	0.00	3.950
219	GTTTCAGAAACAGCTGCTGGAA	275	21	0	47.62	59.050	20.26	11.82	35.51	3.950
220	TGAGTCGCTTAATTGCTCGTG	101	21	0	47.62	59.007	0.00	0.00	0.00	3.993
221	AGTCGCTTAATTGCTCGTGAC	99	21	0	47.62	59.007	4.62	4.62	0.00	3.993
222	CACAAAGGACAGGGTGTTC	290	20	0	50.00	57.949	0.00	0.00	0.00	4.051
223	ACACAAAGGACAGGGTGTTC	291	20	0	50.00	57.947	0.00	0.00	41.36	4.053
224	CTGGAATGCTCGAAGGTCGTC	260	21	0	57.14	61.064	0.00	0.00	43.45	4.064
225	GGAATGCTCGAAGGTCGTC	258	21	0	57.14	61.064	0.00	0.00	43.45	4.064
226	TTCGGCTCGTCGGGC	164	15	0	73.33	58.930	2.73	2.73	0.00	4.070
227	TCGCTTAATTGCTCGTGACA	97	20	0	45.00	57.927	0.00	0.00	0.00	4.073
228	GGACACACAAAGGACAGGGTG	295	21	0	57.14	61.085	0.00	0.00	37.29	4.085
229	AACATTGTGTGACGTTGTGGT	184	21	0	42.86	58.912	0.00	0.00	0.00	4.088
230	ACATTGTGTGACGTTGTGGTT	183	21	0	42.86	58.912	0.00	0.00	0.00	4.088
231	TCAGAAACAGCTGCTGGAATG	273	21	0	47.62	58.843	22.36	15.68	35.51	4.157
232	AGCTCAATTCTGGCTTCACAC	220	21	0	47.62	58.842	0.00	0.00	0.00	4.158
233	GCTCAATTCTGGCTTCACACT	219	21	0	47.62	58.842	0.00	0.00	0.00	4.158
234	TCGTCTGCTGAGCTTTCTACT	244	21	0	47.62	58.836	0.18	0.00	0.00	4.164
235	TGCTCGTGACATAGAAGGTCA	88	21	0	47.62	58.832	0.00	0.00	42.62	4.168
236	ACAGCTGCTGGAATGCTCGA	267	20	0	55.00	62.176	31.00	0.00	35.51	4.176
237	GCTCGAAGGTCGTCTGCTGA	253	20	0	60.00	62.201	6.06	0.00	43.45	4.201
238	TCGAAGGTCGTCTGCTGAGC	251	20	0	60.00	62.201	0.00	0.00	43.45	4.201
239	CGAAGGTCGTCTGCTGAGCT	250	20	0	60.00	62.207	5.83	0.00	37.02	4.207
240	GGACAGGGTGTTCAGAAACAG	284	21	0	52.38	58.778	0.00	0.00	45.78	4.222
241	GTCGTCTGCTGAGCTTTCTAC	245	21	0	52.38	58.745	0.00	0.00	0.00	4.255
242	GAGTCGCTTAATTGCTCGTGA	100	21	0	47.62	58.740	0.00	0.00	0.00	4.260
243	CGTGACATAGAAGGTCAACCG	84	21	0	52.38	58.740	0.00	0.00	45.96	4.260
244	CTGAGTCGCTTAATTGCTCGT	102	21	0	47.62	58.737	0.00	0.00	0.00	4.263
245	CTGCTGGAATGCTCGAAGGTC	263	21	0	57.14	61.338	0.00	0.00	0.00	4.338
246	GGACAGGGTGTTCAGAAACA	284	20	0	50.00	57.658	0.01	0.00	43.06	4.342
247	TTCAGAAACAGCTGCTGGAA	274	20	0	45.00	57.653	20.95	12.30	35.51	4.347
248	ACAAAGGACAGGGTGTTCAG	289	20	0	50.00	57.652	0.00	0.00	0.00	4.348
249	TGAGTCGCTTAATTGCTCGT	101	20	0	45.00	57.636	0.00	0.00	0.00	4.364
250	AGTCGCTTAATTGCTCGTGA	99	20	0	45.00	57.636	0.00	0.00	0.00	4.364
251	TCGGGCTGGTAAATGTTGATG	155	21	0	47.62	58.635	0.00	0.00	0.00	4.365
252	CGGGCTGGTAAATGTTGATGA	154	21	0	47.62	58.635	0.00	0.00	0.00	4.365
253	GTCGGGCTGGTAAATGTTGAT	156	21	0	47.62	58.634	0.00	0.00	0.00	4.366
254	GTGTGACGTTGTGTTTCGGC	178	20	0	60.00	62.369	0.00	0.00	35.47	4.369
255	GTGGTTTCGGCTCGTCG	168	16	0	68.75	57.630	0.00	0.00	0.00	4.370
256	GTGTTTCAGAAACAGCTGCTG	277	20	0	50.00	57.604	27.02	27.02	45.78	4.396
257	CCACGGACACACAAAGGACAG	299	21	0	57.14	61.406	0.00	0.00	0.00	4.406
258	CACGGACACACAAAGGACAGG	298	21	0	57.14	61.406	0.00	0.00	0.00	4.406
259	GTCGCTTAATTGCTCGTGAC	98	20	0	50.00	57.579	0.00	0.00	0.00	4.421
260	AGGTCGTCTGCTGAGCTTTCT	247	21	0	52.38	61.436	0.00	0.00	0.00	4.436
261	CAACATTGTGTGACGTTGTGG	185	21	0	47.62	58.551	0.00	0.00	0.00	4.449
262	TGCTCGAAGGTCGTCTGCTG	254	20	0	60.00	62.478	11.58	0.00	43.45	4.478
263	TGGAATGCTCGAAGGTCGTCT	259	21	0	52.38	61.498	0.00	0.00	43.45	4.498
264	TCTGAGTCGCTTAATTGCTCG	103	21	0	47.62	58.470	0.00	0.00	0.00	4.530

# Primers data

265	TGACATAGAAGGTCAACCGGA	82	21	0	47.62	58.468	9.46	0.00	41.96	4.532
266	GGGATGCACACCACGG	309	16	0	68.75	57.451	12.79	0.00	0.00	4.549
267	GCTCGTCGGGCTGGT	160	15	0	73.33	58.449	10.59	0.00	0.00	4.551
268	TCAGAAACAGCTGCTGGAAT	273	20	0	45.00	57.426	31.00	17.58	35.51	4.574
269	AGCTCAATTCTGGCTTCACA	220	20	0	45.00	57.426	0.00	0.00	0.00	4.574
270	TGTGACGTTGTGGTTCGGCT	177	20	0	55.00	62.581	0.00	0.00	35.95	4.581
271	GGCTCGTCGGGCTGGTAAAT	161	20	0	60.00	62.589	8.47	0.00	0.00	4.589
272	TTGTGTGACGTTGTGGTTCGG	180	21	0	52.38	61.599	0.00	0.00	0.00	4.599
273	ATGCACACCACGGACACACA	306	20	0	55.00	62.601	0.00	0.00	0.00	4.601
274	TCGCTTAATTGCTCGTGACAT	97	21	0	42.86	58.383	0.00	0.00	0.00	4.617
275	GTGACATAGAAGGTCAACCGG	83	21	0	52.38	58.382	0.00	0.00	45.96	4.618
276	GCTCAATTCTGGCTTCACAC	219	20	0	50.00	57.374	0.00	0.00	0.00	4.626
277	CAGAAACAGCTGCTGGAATG	272	20	0	50.00	57.369	19.76	10.50	35.51	4.631
278	CAAAGGACAGGGTGTTTCAGA	288	20	0	50.00	57.362	0.00	0.00	0.00	4.638
279	GTCGTCTGCTGAGCTTTCTA	245	20	0	50.00	57.361	0.00	0.00	0.00	4.639
280	TCGTCTGCTGAGCTTTCTAC	244	20	0	50.00	57.361	0.00	0.00	0.00	4.639
281	AGGACAGGGTGTTTCAGAAAC	285	20	0	50.00	57.360	0.00	0.00	35.85	4.640
282	CGTCTGCTGAGCTTTCTACT	243	20	0	50.00	57.354	0.18	0.00	0.00	4.646
283	GAATGCTCGAAGGTGCTCTGC	257	21	0	57.14	61.648	6.26	6.26	43.45	4.648
284	CACCACGGACACACAAAGGAC	301	21	0	57.14	61.670	0.00	0.00	0.00	4.670
285	GAGTCGCTTAATTGCTCGTG	100	20	0	50.00	57.297	0.00	0.00	0.00	4.703
286	CATTGTGTGACGTTGTGGTTC	182	21	0	47.62	58.285	0.00	0.00	0.00	4.715
287	TCGGGCTGGTAAATGTTGAT	155	20	0	45.00	57.201	0.00	0.00	0.00	4.799
288	TGCACACCACGGACACACAA	305	20	0	55.00	62.805	0.00	0.00	0.00	4.805
289	AAACAGCTGCTGGAATGCTCG	269	21	0	52.38	61.812	31.00	5.48	35.51	4.812
290	AACATTGTGTGACGTTGTGG	184	20	0	45.00	57.158	0.00	0.00	0.00	4.842
291	CATTGTGTGACGTTGTGGTT	182	20	0	45.00	57.158	0.00	0.00	0.00	4.842
292	CGGGCTGGTAAATGTTGATG	154	20	0	50.00	57.150	0.00	0.00	0.00	4.850
293	TTCAGAAACAGCTGCTGGAAT	274	21	0	42.86	58.132	21.26	9.35	35.51	4.868
294	TCCTCTGAGTCGCTTAATTGC	106	21	0	47.62	58.106	3.66	0.00	0.00	4.894
295	CCTCTGAGTCGCTTAATTGCT	105	21	0	47.62	58.101	3.66	0.00	0.00	4.899
296	CAGCTGCTGGAATGCTCGAAG	266	21	0	57.14	61.927	21.71	0.00	34.51	4.927
297	CAAAGGACAGGGTGTTTCAGAA	288	21	0	47.62	58.069	0.00	0.00	0.00	4.931
298	AAGGACAGGGTGTTTCAGAAAC	286	21	0	47.62	58.068	0.00	0.00	35.85	4.932
299	CACACCACGGACACACAAAGG	303	21	0	57.14	61.935	0.00	0.00	0.00	4.935
300	TGCTCGTGACATAGAAGGTC	88	20	0	50.00	57.059	0.00	0.00	35.83	4.941
301	GCTCGTGACATAGAAGGTCA	87	20	0	50.00	57.059	0.00	0.00	42.62	4.941
302	CTGAGTCGCTTAATTGCTCG	102	20	0	50.00	57.013	0.00	0.00	0.00	4.987
303	TGGCTTCACACTTACAACACA	210	21	0	42.86	58.007	0.00	0.00	0.00	4.993
304	TTACTGCTGGGATGCACACCA	317	21	0	52.38	62.004	6.10	4.92	38.12	5.004
305	GTTTTCTTCTCTGAGTCGCT	113	21	0	47.62	57.967	0.00	0.00	0.00	5.033
306	AATGCTCGAAGGTGCTCTGCT	256	21	0	52.38	62.099	11.58	0.55	43.45	5.099
307	ACACCACGGACACACAAAGGA	302	21	0	52.38	62.124	0.00	0.00	0.00	5.124
308	ACCACGGACACACAAAGGACA	300	21	0	52.38	62.124	0.00	0.00	0.00	5.124
309	ACAACATTGTGTGACGTTGTG	186	21	0	42.86	57.870	5.36	0.00	41.89	5.130
310	TTGCTCGTGACATAGAAGGTC	89	21	0	47.62	57.768	0.00	0.00	35.83	5.232
311	GCTCGTGACATAGAAGGTCAA	87	21	0	47.62	57.768	0.00	0.00	45.96	5.232

Primers data

312	TCGTTTTCTTCCTCTGAGTCG	115	21	0	47.62	57.716	0.00	0.00	0.00	5.284
313	GCACACCACGGACACACAAAG	304	21	0	57.14	62.514	0.00	0.00	0.00	5.514
314	ACGGACACACAAAGGACAGGG	297	21	0	57.14	62.522	0.00	0.00	0.00	5.522
315	CGGACACACAAAGGACAGGGT	296	21	0	57.14	62.522	0.00	0.00	0.00	5.522
316	TCTGGCTTCACACTTACAACA	212	21	0	42.86	57.448	0.00	0.00	0.00	5.552
317	TCGTGACATAGAAGGTCAACC	85	21	0	47.62	57.412	0.00	0.00	45.96	5.588
318	GACATAGAAGGTCAACCGGAA	81	21	0	47.62	57.395	0.00	0.00	42.08	5.605
319	CTGGCTTCACACTTACAACAC	211	21	0	47.62	57.391	0.00	0.00	0.00	5.609
320	AACAGCTGCTGGAATGCTCGA	268	21	0	52.38	62.651	31.00	0.00	35.51	5.651
321	ACAGCTGCTGGAATGCTCGAA	267	21	0	52.38	62.651	31.00	0.00	35.51	5.651
322	TACTGCTGGGATGCACACCAC	316	21	0	57.14	62.660	3.46	0.78	38.12	5.660
323	AAAGGACAGGGTGTTTCAGAAA	287	21	0	42.86	57.337	0.00	0.00	0.00	5.663
324	CGAAGGTCGTCTGCTGAGCTT	250	21	0	57.14	62.671	7.47	7.47	38.04	5.671
325	TAGCTCAATTCTGGCTTCACA	221	21	0	42.86	57.299	2.49	0.00	33.07	5.701
326	ATGCTCGAAGGTCGTCTGCTG	255	21	0	57.14	62.738	11.58	0.00	43.45	5.738
327	TTTTCTTCCTCTGAGTCGCTT	112	21	0	42.86	57.247	0.00	0.00	0.00	5.753
328	CGTCTGCTGAGCTTTCTACTA	243	21	0	47.62	57.233	0.18	0.00	0.00	5.767
329	ATTGCTCGTGACATAGAAGGT	90	21	0	42.86	57.105	0.00	0.00	0.00	5.895
330	ACTAGCTCAATTCTGGCTTCA	223	21	0	42.86	57.011	0.00	0.00	33.07	5.989

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## BLAST INFORMATION

BLASTN 2.7.1+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 20DX59DB015

Database: Nucleotide collection (nt)

45,448,023 sequences; 163,513,399,372 total letters

Query=

Length=20

Score E

Sequences producing significant alignments:

(Bits) Value

MF288727.1	Human papillomavirus type 18 isolate 1494573_N-P, ...	37.4	2.8
MF288726.1	Human papillomavirus type 18 isolate 1314304_N-P, ...	37.4	2.8
MF288725.1	Human papillomavirus type 18 isolate C451606_R3_19...	37.4	2.8
MF288724.1	Human papillomavirus type 18 isolate C451606_R2_15...	37.4	2.8
MF288723.1	Human papillomavirus type 18 isolate C451606_R1_12...	37.4	2.8
MF288722.1	Human papillomavirus type 18 isolate C387957_R1_11...	37.4	2.8
MF288721.1	Human papillomavirus type 18 isolate 1209155_R1_P_...	37.4	2.8
MF288720.1	Human papillomavirus type 18 isolate 1174820_N-P, ...	37.4	2.8
MF288719.1	Human papillomavirus type 18 isolate C487627_R2_15...	37.4	2.8
MF288718.1	Human papillomavirus type 18 isolate C487627_R1_11...	37.4	2.8
MF288717.1	Human papillomavirus type 18 isolate 1533526_N-P, ...	37.4	2.8
MF288716.1	Human papillomavirus type 18 isolate C458963_R2_15...	37.4	2.8
MF288715.1	Human papillomavirus type 18 isolate C458963_R1_12...	37.4	2.8
MF288714.1	Human papillomavirus type 18 isolate C533713_R3_17...	37.4	2.8
MF288713.1	Human papillomavirus type 18 isolate C533713_R2_14...	37.4	2.8
MF288712.1	Human papillomavirus type 18 isolate C578032_R3_17...	37.4	2.8
MF288711.1	Human papillomavirus type 18 isolate C578032_R2_14...	37.4	2.8
MF288710.1	Human papillomavirus type 18 isolate C335048_R3_19...	37.4	2.8
MF288709.1	Human papillomavirus type 18 isolate C412607_R2_15...	37.4	2.8
MF288708.1	Human papillomavirus type 18 isolate C412607_R1_12...	37.4	2.8
MF288707.1	Human papillomavirus type 18 isolate C440384_R1_13...	37.4	2.8
MF288706.1	Human papillomavirus type 18 isolate C425046_R2_16...	37.4	2.8
MF288705.1	Human papillomavirus type 18 isolate C425046_R1_13...	37.4	2.8
MF288704.1	Human papillomavirus type 18 isolate C627893_R2_16...	37.4	2.8
MF288703.1	Human papillomavirus type 18 isolate C627893_R1_13...	37.4	2.8
MF288702.1	Human papillomavirus type 18 isolate C644657_R4_21...	37.4	2.8
MF288701.1	Human papillomavirus type 18 isolate C644657_R3_18...	37.4	2.8

# BLAST INFORMATION

MF288700.1	Human papillomavirus type 18 isolate C644657_R2_14...	37.4	2.8
MF288699.1	Human papillomavirus type 18 isolate C644657_R1_11...	37.4	2.8
MF288698.1	Human papillomavirus type 18 isolate C335048_R2_15...	37.4	2.8
MF288697.1	Human papillomavirus type 18 isolate 1445230_R2_P_...	37.4	2.8
MF288696.1	Human papillomavirus type 18 isolate 1581449_N-P, ...	37.4	2.8
MF288695.1	Human papillomavirus type 18 isolate C440737_R1_11...	37.4	2.8
MF288694.1	Human papillomavirus type 18 isolate C439921_R1_11...	37.4	2.8
MF288693.1	Human papillomavirus type 18 isolate C430899_R1_11...	37.4	2.8
MF288692.1	Human papillomavirus type 18 isolate C353934_R1_11...	37.4	2.8
MF288691.1	Human papillomavirus type 18 isolate 1390622_R1_P_...	37.4	2.8
MF288690.1	Human papillomavirus type 18 isolate C532476_R1_11...	37.4	2.8
MF288689.1	Human papillomavirus type 18 isolate 1508690_N-P, ...	37.4	2.8
MF288688.1	Human papillomavirus type 18 isolate 1115002_N-P, ...	37.4	2.8
MF288687.1	Human papillomavirus type 18 isolate C406921_R1_11...	37.4	2.8
MF288686.1	Human papillomavirus type 18 isolate C575918_R2_14...	37.4	2.8
MF288685.1	Human papillomavirus type 18 isolate C575918_R1_10...	37.4	2.8
MF288684.1	Human papillomavirus type 18 isolate 1389481_N-P, ...	37.4	2.8
MF288683.1	Human papillomavirus type 18 isolate 1310091_R1_P_...	37.4	2.8
MF288682.1	Human papillomavirus type 18 isolate C385149_R2_15...	37.4	2.8
MF288681.1	Human papillomavirus type 18 isolate C385149_R1_11...	37.4	2.8
MF288680.1	Human papillomavirus type 18 isolate C340709_R1_12...	37.4	2.8
MF288679.1	Human papillomavirus type 18 isolate C310065_R1_13...	37.4	2.8
MF288678.1	Human papillomavirus type 18 isolate C498643_R2_15...	37.4	2.8

## ALIGNMENTS

>MF288727.1 Human papillomavirus type 18 isolate 1494573\_N-P, complete genome  
Length=7844

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288726.1 Human papillomavirus type 18 isolate 1314304\_N-P, complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

## BLAST INFORMATION

>MF288725.1 Human papillomavirus type 18 isolate C451606\_R3\_1915584\_(100w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288724.1 Human papillomavirus type 18 isolate C451606\_R2\_1584906\_(52w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288723.1 Human papillomavirus type 18 isolate C451606\_R1\_1201181\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288722.1 Human papillomavirus type 18 isolate C387957\_R1\_1124102\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)



# BLAST INFORMATION

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288721.1 Human papillomavirus type 18 isolate 1209155\_R1\_P\_R2\_FAIL, complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288720.1 Human papillomavirus type 18 isolate 1174820\_N-P, complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288719.1 Human papillomavirus type 18 isolate C487627\_R2\_1553725\_(52w), complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288718.1 Human papillomavirus type 18 isolate C487627\_R1\_1178751\_(0w), complete genome

# BLAST INFORMATION

Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288717.1 Human papillomavirus type 18 isolate 1533526\_N-P, complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288716.1 Human papillomavirus type 18 isolate C458963\_R2\_1584969\_(48w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288715.1 Human papillomavirus type 18 isolate C458963\_R1\_1201270\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

## BLAST INFORMATION

>MF288714.1 Human papillomavirus type 18 isolate C533713\_R3\_1794175\_(52w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288713.1 Human papillomavirus type 18 isolate C533713\_R2\_1453915\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288712.1 Human papillomavirus type 18 isolate C578032\_R3\_1777990\_(53w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288711.1 Human papillomavirus type 18 isolate C578032\_R2\_1441689\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)

# BLAST INFORMATION

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288710.1 Human papillomavirus type 18 isolate C335048\_R3\_1978895\_(63w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288709.1 Human papillomavirus type 18 isolate C412607\_R2\_1595957\_(56w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288708.1 Human papillomavirus type 18 isolate C412607\_R1\_1241497\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288707.1 Human papillomavirus type 18 isolate C440384\_R1\_1310123\_N-P,

# BLAST INFORMATION

complete genome

Length=7842

Score = 37.4 bits (40), Expect = 2.8

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288706.1 Human papillomavirus type 18 isolate C425046\_R2\_1678154\_(54w),

complete genome

Length=7857

Score = 37.4 bits (40), Expect = 2.8

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288705.1 Human papillomavirus type 18 isolate C425046\_R1\_1388626\_(0w),

complete genome

Length=7857

Score = 37.4 bits (40), Expect = 2.8

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288704.1 Human papillomavirus type 18 isolate C627893\_R2\_1657900\_(46w),

complete genome

Length=7857

Score = 37.4 bits (40), Expect = 2.8

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
```

# BLAST INFORMATION

||||||||||||||||

Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288703.1 Human papillomavirus type 18 isolate C627893\_R1\_1382535\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288702.1 Human papillomavirus type 18 isolate C644657\_R4\_2179348\_(154w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288701.1 Human papillomavirus type 18 isolate C644657\_R3\_1822640\_(103w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288700.1 Human papillomavirus type 18 isolate C644657\_R2\_1488163\_(55w),  
complete genome  
Length=7857

# BLAST INFORMATION

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288699.1 Human papillomavirus type 18 isolate C644657\_R1\_1107720\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288698.1 Human papillomavirus type 18 isolate C335048\_R2\_1591561\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288697.1 Human papillomavirus type 18 isolate 1445230\_R2\_P\_R1\_FAIL, complete  
genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

## BLAST INFORMATION

>MF288696.1 Human papillomavirus type 18 isolate 1581449\_N-P, complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288695.1 Human papillomavirus type 18 isolate C440737\_R1\_1103988\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288694.1 Human papillomavirus type 18 isolate C439921\_R1\_1139309\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACA  20
|||||
Sbjct 591    TGCATGGACCTAAGGCAACA  610
```

>MF288693.1 Human papillomavirus type 18 isolate C430899\_R1\_1153841\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus



# BLAST INFORMATION

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288692.1 Human papillomavirus type 18 isolate C353934\_R1\_1193001\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288691.1 Human papillomavirus type 18 isolate 1390622\_R1\_P\_R2\_FAIL, complete  
genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288690.1 Human papillomavirus type 18 isolate C532476\_R1\_1127082\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288689.1 Human papillomavirus type 18 isolate 1508690\_N-P, complete genome  
Length=7857

# BLAST INFORMATION

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288688.1 Human papillomavirus type 18 isolate 1115002\_N-P, complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288687.1 Human papillomavirus type 18 isolate C406921\_R1\_1177005\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288686.1 Human papillomavirus type 18 isolate C575918\_R2\_1429982\_(50w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

# BLAST INFORMATION

>MF288685.1 Human papillomavirus type 18 isolate C575918\_R1\_1071512\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288684.1 Human papillomavirus type 18 isolate 1389481\_N-P, complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288683.1 Human papillomavirus type 18 isolate 1310091\_R1\_P\_R2\_FAIL, complete  
genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288682.1 Human papillomavirus type 18 isolate C385149\_R2\_1569977\_(54w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20

# BLAST INFORMATION

|||||

Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288681.1 Human papillomavirus type 18 isolate C385149\_R1\_1186655\_(0w),  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288680.1 Human papillomavirus type 18 isolate C340709\_R1\_1279365\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288679.1 Human papillomavirus type 18 isolate C310065\_R1\_1389573\_N-P,  
complete genome  
Length=7857

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

>MF288678.1 Human papillomavirus type 18 isolate C498643\_R2\_1564219\_(54w),  
complete genome  
Length=7857

# BLAST INFORMATION

Score = 37.4 bits (40), Expect = 2.8  
Identities = 20/20 (100%), Gaps = 0/20 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACA 20  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACA 610

Database: Nucleotide collection (nt)  
Posted date: Nov 28, 2017 10:38 AM  
Number of letters in database: 163,513,399,372  
Number of sequences in database: 45,448,023

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.625	0.410	0.780

Matrix: blastn matrix:2 -3  
Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 45448023  
Number of Hits to DB: 241145  
Number of extensions: 82  
Number of successful extensions: 82  
Number of sequences better than 10: 10  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 82  
Number of HSP's successfully gapped: 10  
Length of query: 20  
Length of database: 163513399372  
Length adjustment: 17  
Effective length of query: 3  
Effective length of database: 162740782981  
Effective search space: 488222348943  
Effective search space used: 488222348943  
A: 0  
X1: 22 (20.1 bits)  
X2: 33 (29.8 bits)  
X3: 110 (99.2 bits)  
S1: 28 (26.5 bits)  
S2: 38 (35.6 bits)

## BLAST INFORMATION

BLASTN 2.7.1+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 20DXPAR6014

Database: Nucleotide collection (nt)

45,448,023 sequences; 163,513,399,372 total letters

Query=

Length=21

Score	E						
Sequences producing significant alignments:						(Bits)	Value
MF288726.1	Human papillomavirus type 18 isolate 1314304_N-P, ...	39.2	0.80				
MF288725.1	Human papillomavirus type 18 isolate C451606_R3_19...	39.2	0.80				
MF288724.1	Human papillomavirus type 18 isolate C451606_R2_15...	39.2	0.80				
MF288723.1	Human papillomavirus type 18 isolate C451606_R1_12...	39.2	0.80				
MF288722.1	Human papillomavirus type 18 isolate C387957_R1_11...	39.2	0.80				
MF288721.1	Human papillomavirus type 18 isolate 1209155_R1_P_...	39.2	0.80				
MF288720.1	Human papillomavirus type 18 isolate 1174820_N-P, ...	39.2	0.80				
MF288719.1	Human papillomavirus type 18 isolate C487627_R2_15...	39.2	0.80				
MF288718.1	Human papillomavirus type 18 isolate C487627_R1_11...	39.2	0.80				
MF288717.1	Human papillomavirus type 18 isolate 1533526_N-P, ...	39.2	0.80				
MF288716.1	Human papillomavirus type 18 isolate C458963_R2_15...	39.2	0.80				
MF288715.1	Human papillomavirus type 18 isolate C458963_R1_12...	39.2	0.80				
MF288714.1	Human papillomavirus type 18 isolate C533713_R3_17...	39.2	0.80				
MF288713.1	Human papillomavirus type 18 isolate C533713_R2_14...	39.2	0.80				
MF288712.1	Human papillomavirus type 18 isolate C578032_R3_17...	39.2	0.80				
MF288711.1	Human papillomavirus type 18 isolate C578032_R2_14...	39.2	0.80				
MF288710.1	Human papillomavirus type 18 isolate C335048_R3_19...	39.2	0.80				
MF288709.1	Human papillomavirus type 18 isolate C412607_R2_15...	39.2	0.80				
MF288708.1	Human papillomavirus type 18 isolate C412607_R1_12...	39.2	0.80				
MF288707.1	Human papillomavirus type 18 isolate C440384_R1_13...	39.2	0.80				
MF288706.1	Human papillomavirus type 18 isolate C425046_R2_16...	39.2	0.80				
MF288705.1	Human papillomavirus type 18 isolate C425046_R1_13...	39.2	0.80				
MF288704.1	Human papillomavirus type 18 isolate C627893_R2_16...	39.2	0.80				
MF288703.1	Human papillomavirus type 18 isolate C627893_R1_13...	39.2	0.80				
MF288702.1	Human papillomavirus type 18 isolate C644657_R4_21...	39.2	0.80				
MF288701.1	Human papillomavirus type 18 isolate C644657_R3_18...	39.2	0.80				
MF288700.1	Human papillomavirus type 18 isolate C644657_R2_14...	39.2	0.80				

## BLAST INFORMATION

MF288699.1	Human papillomavirus type 18 isolate C644657_R1_11...	39.2	0.80
MF288698.1	Human papillomavirus type 18 isolate C335048_R2_15...	39.2	0.80
MF288697.1	Human papillomavirus type 18 isolate 1445230_R2_P...	39.2	0.80
MF288696.1	Human papillomavirus type 18 isolate 1581449_N-P, ...	39.2	0.80
MF288695.1	Human papillomavirus type 18 isolate C440737_R1_11...	39.2	0.80
MF288694.1	Human papillomavirus type 18 isolate C439921_R1_11...	39.2	0.80
MF288693.1	Human papillomavirus type 18 isolate C430899_R1_11...	39.2	0.80
MF288692.1	Human papillomavirus type 18 isolate C353934_R1_11...	39.2	0.80
MF288691.1	Human papillomavirus type 18 isolate 1390622_R1_P...	39.2	0.80
MF288690.1	Human papillomavirus type 18 isolate C532476_R1_11...	39.2	0.80
MF288689.1	Human papillomavirus type 18 isolate 1508690_N-P, ...	39.2	0.80
MF288688.1	Human papillomavirus type 18 isolate 1115002_N-P, ...	39.2	0.80
MF288687.1	Human papillomavirus type 18 isolate C406921_R1_11...	39.2	0.80
MF288686.1	Human papillomavirus type 18 isolate C575918_R2_14...	39.2	0.80
MF288685.1	Human papillomavirus type 18 isolate C575918_R1_10...	39.2	0.80
MF288684.1	Human papillomavirus type 18 isolate 1389481_N-P, ...	39.2	0.80
MF288683.1	Human papillomavirus type 18 isolate 1310091_R1_P...	39.2	0.80
MF288682.1	Human papillomavirus type 18 isolate C385149_R2_15...	39.2	0.80
MF288681.1	Human papillomavirus type 18 isolate C385149_R1_11...	39.2	0.80
MF288680.1	Human papillomavirus type 18 isolate C340709_R1_12...	39.2	0.80
MF288679.1	Human papillomavirus type 18 isolate C310065_R1_13...	39.2	0.80
MF288678.1	Human papillomavirus type 18 isolate C498643_R2_15...	39.2	0.80
MF288677.1	Human papillomavirus type 18 isolate C498643_R1_11...	39.2	0.80

## ALIGNMENTS

>MF288726.1 Human papillomavirus type 18 isolate 1314304\_N-P, complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288725.1 Human papillomavirus type 18 isolate C451606\_R3\_1915584\_(100w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
```

# BLAST INFORMATION

Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288724.1 Human papillomavirus type 18 isolate C451606\_R2\_1584906\_(52w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288723.1 Human papillomavirus type 18 isolate C451606\_R1\_1201181\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288722.1 Human papillomavirus type 18 isolate C387957\_R1\_1124102\_N-P,  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288721.1 Human papillomavirus type 18 isolate 1209155\_R1\_P\_R2\_FAIL, complete  
genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80



# BLAST INFORMATION

Identities = 21/21 (100%), Gaps = 0/21 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288720.1 Human papillomavirus type 18 isolate 1174820\_N-P, complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80

Identities = 21/21 (100%), Gaps = 0/21 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288719.1 Human papillomavirus type 18 isolate C487627\_R2\_1553725\_(52w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80

Identities = 21/21 (100%), Gaps = 0/21 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288718.1 Human papillomavirus type 18 isolate C487627\_R1\_1178751\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80

Identities = 21/21 (100%), Gaps = 0/21 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288717.1 Human papillomavirus type 18 isolate 1533526\_N-P, complete genome

# BLAST INFORMATION

Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288716.1 Human papillomavirus type 18 isolate C458963\_R2\_1584969\_(48w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288715.1 Human papillomavirus type 18 isolate C458963\_R1\_1201270\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288714.1 Human papillomavirus type 18 isolate C533713\_R3\_1794175\_(52w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||

# BLAST INFORMATION

Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288713.1 Human papillomavirus type 18 isolate C533713\_R2\_1453915\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288712.1 Human papillomavirus type 18 isolate C578032\_R3\_1777990\_(53w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288711.1 Human papillomavirus type 18 isolate C578032\_R2\_1441689\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288710.1 Human papillomavirus type 18 isolate C335048\_R3\_1978895\_(63w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80

# BLAST INFORMATION

Identities = 21/21 (100%), Gaps = 0/21 (0%)

Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288709.1 Human papillomavirus type 18 isolate C412607\_R2\_1595957\_(56w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288708.1 Human papillomavirus type 18 isolate C412607\_R1\_1241497\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288707.1 Human papillomavirus type 18 isolate C440384\_R1\_1310123\_N-P,  
complete genome  
Length=7842

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

# BLAST INFORMATION

>MF288706.1 Human papillomavirus type 18 isolate C425046\_R2\_1678154\_(54w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
||||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288705.1 Human papillomavirus type 18 isolate C425046\_R1\_1388626\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
||||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288704.1 Human papillomavirus type 18 isolate C627893\_R2\_1657900\_(46w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
||||||||||||||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288703.1 Human papillomavirus type 18 isolate C627893\_R1\_1382535\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

# BLAST INFORMATION

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288702.1 Human papillomavirus type 18 isolate C644657\_R4\_2179348\_(154w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288701.1 Human papillomavirus type 18 isolate C644657\_R3\_1822640\_(103w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288700.1 Human papillomavirus type 18 isolate C644657\_R2\_1488163\_(55w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288699.1 Human papillomavirus type 18 isolate C644657\_R1\_1107720\_(0w),  
complete genome  
Length=7857

## BLAST INFORMATION

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288698.1 Human papillomavirus type 18 isolate C335048\_R2\_1591561\_(0w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288697.1 Human papillomavirus type 18 isolate 1445230\_R2\_P\_R1\_FAIL, complete  
genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288696.1 Human papillomavirus type 18 isolate 1581449\_N-P, complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||||||||||||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

## BLAST INFORMATION

>MF288695.1 Human papillomavirus type 18 isolate C440737\_R1\_1103988\_N-P,  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288694.1 Human papillomavirus type 18 isolate C439921\_R1\_1139309\_N-P,  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288693.1 Human papillomavirus type 18 isolate C430899\_R1\_1153841\_N-P,  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288692.1 Human papillomavirus type 18 isolate C353934\_R1\_1193001\_N-P,  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus



## BLAST INFORMATION

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288691.1 Human papillomavirus type 18 isolate 1390622\_R1\_P\_R2\_FAIL, complete genome

Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288690.1 Human papillomavirus type 18 isolate C532476\_R1\_1127082\_N-P, complete genome

Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288689.1 Human papillomavirus type 18 isolate 1508690\_N-P, complete genome

Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288688.1 Human papillomavirus type 18 isolate 1115002\_N-P, complete genome

Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
>MF288687.1 Human papillomavirus type 18 isolate C406921_R1_1177005_N-P,
complete genome
Length=7857
```

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
>MF288686.1 Human papillomavirus type 18 isolate C575918_R2_1429982_(50w),
complete genome
Length=7857
```

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
>MF288685.1 Human papillomavirus type 18 isolate C575918_R1_1071512_(0w),
complete genome
Length=7857
```

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```

Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611

```

## BLAST INFORMATION

>MF288684.1 Human papillomavirus type 18 isolate 1389481\_N-P, complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288683.1 Human papillomavirus type 18 isolate 1310091\_R1\_P\_R2\_FAIL, complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288682.1 Human papillomavirus type 18 isolate C385149\_R2\_1569977\_(54w), complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

>MF288681.1 Human papillomavirus type 18 isolate C385149\_R1\_1186655\_(0w), complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

# BLAST INFORMATION

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288680.1 Human papillomavirus type 18 isolate C340709\_R1\_1279365\_N-P,  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288679.1 Human papillomavirus type 18 isolate C310065\_R1\_1389573\_N-P,  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288678.1 Human papillomavirus type 18 isolate C498643\_R2\_1564219\_(54w),  
complete genome  
Length=7857

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

Query 1 TGCATGGACCTAAGGCAACAT 21  
|||||  
Sbjct 591 TGCATGGACCTAAGGCAACAT 611

>MF288677.1 Human papillomavirus type 18 isolate C498643\_R1\_1192121\_(0w),  
complete genome  
Length=7857

## BLAST INFORMATION

Score = 39.2 bits (42), Expect = 0.80  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 1      TGCATGGACCTAAGGCAACAT  21
|||||||
Sbjct 591    TGCATGGACCTAAGGCAACAT  611
```

Database: Nucleotide collection (nt)  
Posted date: Nov 28, 2017 10:38 AM  
Number of letters in database: 163,513,399,372  
Number of sequences in database: 45,448,023

Lambda	K	H
0.634	0.408	0.912

Gapped

Lambda	K	H
0.625	0.410	0.780

Matrix: blastn matrix:2 -3  
Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 45448023  
Number of Hits to DB: 248852  
Number of extensions: 70  
Number of successful extensions: 70  
Number of sequences better than 10: 4  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 70  
Number of HSP's successfully gapped: 4  
Length of query: 21  
Length of database: 163513399372  
Length adjustment: 18  
Effective length of query: 3  
Effective length of database: 162695334958  
Effective search space: 488086004874  
Effective search space used: 488086004874  
A: 0  
X1: 22 (20.1 bits)  
X2: 33 (29.8 bits)  
X3: 110 (99.2 bits)  
S1: 28 (26.5 bits)  
S2: 38 (35.6 bits)

