

# CLUSTAL 2.1 multiple sequence Alignment

MF288709.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCAGATCT
MF288708.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCAGATCT
MF288713.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288710.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288712.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATTT
MF288711.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATTT
MF288714.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288716.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288715.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288717.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288727.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288726.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288724.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288721.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288720.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288719.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288718.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288725.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288723.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
MF288722.1	ATGGCGCGCTTTGAGGATCCAACACGGCGACCCCTACAAGCTACCTGATCT
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MF288709.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288708.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288713.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288710.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288712.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288711.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288714.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288716.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288715.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288717.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288727.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288726.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288724.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288721.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288720.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288719.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288718.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288725.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288723.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
MF288722.1	GTGCACGGAAGTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
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MF288709.1	ATTGCAAGACAGTATTGGAACCTTACAGAGGTATTTGAATTTGCATTTAAA
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# CLUSTAL 2.1 multiple sequence Alignment

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MF288708.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288713.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288710.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288712.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288711.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288714.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288716.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288715.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288717.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288727.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288726.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288724.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288721.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288720.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288719.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288718.1      ATTGCAAGACAGTTTTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288725.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288723.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
MF288722.1      ATTGCAAGACAGTATTGGAACCTACAGAGGTATTTGAATTTGCATTTAAA
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MF288709.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288708.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288713.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288710.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288712.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288711.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288714.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288716.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288715.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288717.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288727.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288726.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288724.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288721.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288720.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288719.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288718.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288725.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288723.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
MF288722.1      GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
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MF288709.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288708.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288713.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288710.1      ATGTATAGATTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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# CLUSTAL 2.1 multiple sequence Alignment

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MF288712.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288711.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288714.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288716.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCGGACT
MF288715.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCGGACT
MF288717.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288727.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288726.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288724.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288721.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288720.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288719.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288718.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288725.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288723.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
MF288722.1      ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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MF288709.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288708.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288713.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288710.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288712.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288711.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288714.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288716.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288715.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288717.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288727.1      CTGTGTATGGAGACACATTGGAGAACTAACTAACACTGGGTTATACAAT
MF288726.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288724.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288721.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288720.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288719.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288718.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288725.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288723.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
MF288722.1      CTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTTATACAAT
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MF288709.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288708.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288713.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288710.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288712.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288711.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
MF288714.1      TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
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# CLUSTAL 2.1 multiple sequence Alignment

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

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MF288709.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288708.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288713.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288710.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288712.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288711.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288714.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288716.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288715.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288717.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288727.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288726.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288724.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288721.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288720.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288719.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288718.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288725.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288723.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT  
MF288722.1 ACTTAGACACCTTAATGAAAAACGACGATTTTCAACATAGCTGGGCACT

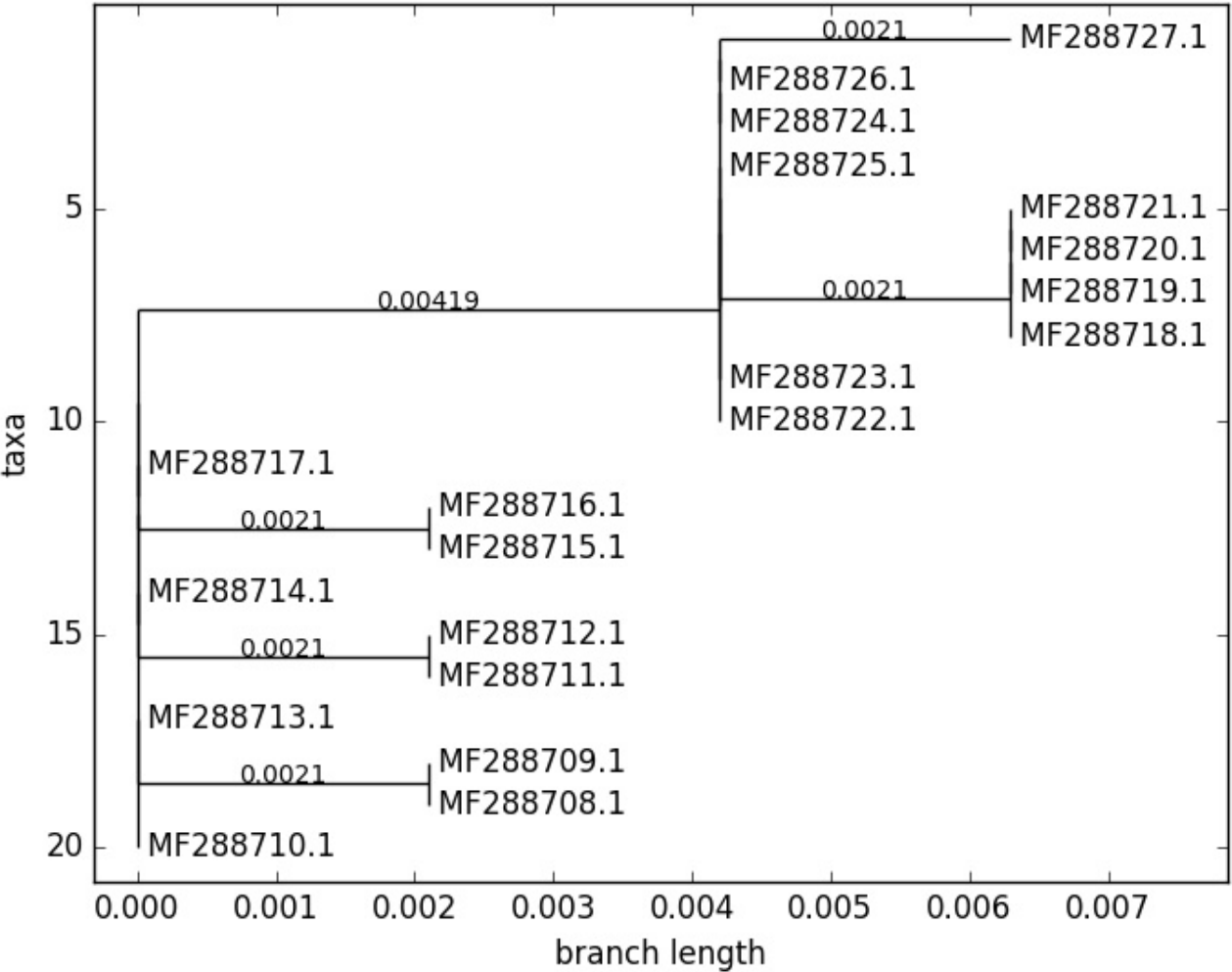
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MF288709.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288708.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288713.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288710.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288712.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288711.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288714.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288716.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288715.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC  
MF288717.1 ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAACGACTC

# CLUSTAL 2.1 multiple sequence Alignment

```
MF288727.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288726.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288724.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288721.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288720.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288719.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288718.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288725.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288723.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
MF288722.1      ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
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MF288709.1      CAACGACGCAGAGAAACACAAGTATAA
MF288708.1      CAACGACGCAGAGAAACACAAGTATAA
MF288713.1      CAACGACGCAGAGAAACACAAGTATAA
MF288710.1      CAACGACGCAGAGAAACACAAGTATAA
MF288712.1      CAACGACGCAGAGAAACACAAGTATAA
MF288711.1      CAACGACGCAGAGAAACACAAGTATAA
MF288714.1      CAACGACGCAGAGAAACACAAGTATAA
MF288716.1      CAACGACGCAGAGAAACACAAGTATAA
MF288715.1      CAACGACGCAGAGAAACACAAGTATAA
MF288717.1      CAACGACGCAGAGAAACACAAGTATAA
MF288727.1      CAACGACGCAGAGAAACACAAGTATAA
MF288726.1      CAACGACGCAGAGAAACACAAGTATAA
MF288724.1      CAACGACGCAGAGAAACACAAGTATAA
MF288721.1      CAACGACGCAGAGAAACACAAGTATAA
MF288720.1      CAACGACGCAGAGAAACACAAGTATAA
MF288719.1      CAACGACGCAGAGAAACACAAGTATAA
MF288718.1      CAACGACGCAGAGAAACACAAGTATAA
MF288725.1      CAACGACGCAGAGAAACACAAGTATAA
MF288723.1      CAACGACGCAGAGAAACACAAGTATAA
MF288722.1      CAACGACGCAGAGAAACACAAGTATAA
*****
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### Consensus sequence

>/papilomita/papilomita\_E6 Consensus threshold=0.7

ATGGCGCGCTTTGAGGATCCAACACGGCGACCTACAAGCTACCTGATCTGTGCACGGAA  
CTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTATATTGCAAGACAGTATTGGAA  
CTTACAGAGGTATTTGAATTTGCATTTAAAGATTTATTTGTGGTGTATAGAGACAGTATA  
CCGCATGCTGCATGCCATAAATGTATAGATTTTTTATTCTAGAATTAGAGAATTAAGACAT  
TATTCAGACTCTGTGTATGGAGACACATTGGAAAACTAACTAACACTGGGTATACAAT  
TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAACTTAGACAC  
CTTAATGAAAAACGACGATTXCACAACATAGCTGGGCACTATAGAGGCCAGTGCCATTCG  
TGCTGCAACCGAGCACGACAGGAAXGACTCCAACGACGCAGAGAAACACAAGTATAA

# 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	TGACGTTGTGGTTTCGGCT	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	GTGACGTTGTGGTTTCGGC	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	CGTTGTGGTTTCGGCTCGT	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	GACGTTGTGGTTTCGGCTC	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	GTGGTTTCGGCTCGTCGG	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	GTGTGACGTTGTGGTTTCGG	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	GTGACGTTGTGGTTTCGGCT	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	TGTGACGTTGTGGTTTCGG	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	TGTGACGTTGTGGTTTCGGC	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	GGTTTCGGCTCGTCGGG	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	CGTTGTGGTTTCGGCTCG	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	GTTCGGCTCGTCGGGC	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	ACATTGTGTGACGTTGTGGT	183	20	0	45.00	58.255	0.00	0.00	0.00	3.745
203	CACACAAAGGACAGGGTGTT	292	20	0	50.00	58.237	0.00	0.00	42.16	3.763
204	GCTCGTCGGGCTGGTA	160	16	0	68.75	58.231	10.59	0.00	0.00	3.769
205	GACACACAAAGGACAGGGT	294	19	0	52.63	57.199	0.00	0.00	0.00	3.801
206	GTCTGGGCTGGTAAATGTTGA	156	20	0	50.00	58.184	0.00	0.00	0.00	3.816
207	GTGACGTTGTGGTTTCGGCTC	176	20	0	60.00	61.828	0.00	0.00	35.95	3.828
208	GATGCACACCACGGACACAC	307	20	0	60.00	61.842	0.00	0.00	0.00	3.842
209	TTGTGGTTTCGGCTCGTC	170	17	0	58.82	57.158	0.00	0.00	0.00	3.842
210	ACAAAGGACAGGGTGTTTCAGA	289	21	0	47.62	59.156	0.00	0.00	0.00	3.844
211	AGGACAGGGTGTTTCAGAAACA	285	21	0	47.62	59.156	0.01	0.00	43.06	3.844
212	TTGTGGTTTCGGCTCGTCGG	170	19	0	63.16	62.852	0.00	0.00	0.00	3.852
213	GATGCACACCACGGACA	307	17	0	58.82	57.129	0.00	0.00	0.00	3.871
214	ACTGCTGGGATGCACAC	315	17	0	58.82	57.088	0.00	0.00	38.12	3.912
215	TCGTCGGGCTGGTAAATGTTG	158	21	0	52.38	60.942	0.00	0.00	0.00	3.942
216	CGTCGGGCTGGTAAATGTTGA	157	21	0	52.38	60.942	0.00	0.00	0.00	3.942
217	CACAAAGGACAGGGTGTTTCAG	290	21	0	52.38	59.050	0.00	0.00	0.00	3.950

# Primers data

218	GTTCAGAAACAGCTGCTGGAA	275	21	0	47.62	59.050	20.26	11.82	35.51	3.950
219	TGAGTCGCTTAATTGCTCGTG	101	21	0	47.62	59.007	0.00	0.00	0.00	3.993
220	AGTCGCTTAATTGCTCGTGAC	99	21	0	47.62	59.007	4.62	4.62	0.00	3.993
221	CACAAAGGACAGGGTGTTCA	290	20	0	50.00	57.949	0.00	0.00	0.00	4.051
222	ACACAAAGGACAGGGTGTTTC	291	20	0	50.00	57.947	0.00	0.00	41.36	4.053
223	CTGGAATGCTCGAAGGTCGTC	260	21	0	57.14	61.064	0.00	0.00	43.45	4.064
224	GGAATGCTCGAAGGTCGCTCTG	258	21	0	57.14	61.064	0.00	0.00	43.45	4.064
225	TTCGGCTCGTCGGGC	164	15	0	73.33	58.930	2.73	2.73	0.00	4.070
226	GGACACACAAAGGACAGGGTG	295	21	0	57.14	61.085	0.00	0.00	37.29	4.085
227	AACATTGTGTGACGTTGTGGT	184	21	0	42.86	58.912	0.00	0.00	0.00	4.088
228	ACATTGTGTGACGTTGTGGTT	183	21	0	42.86	58.912	0.00	0.00	0.00	4.088
229	TCAGAAACAGCTGCTGGAATG	273	21	0	47.62	58.843	22.36	15.68	35.51	4.157
230	AGCTCAATTCTGGCTTCACAC	220	21	0	47.62	58.842	0.00	0.00	0.00	4.158
231	GCTCAATTCTGGCTTCACACT	219	21	0	47.62	58.842	0.00	0.00	0.00	4.158
232	TCGTCTGCTGAGCTTTCTACT	244	21	0	47.62	58.836	0.18	0.00	0.00	4.164
233	ACAGCTGCTGGAATGCTCGA	267	20	0	55.00	62.176	31.00	0.00	35.51	4.176
234	GCTCGAAGGTCGTCTGCTGA	253	20	0	60.00	62.201	6.06	0.00	43.45	4.201
235	TCGAAGGTCGTCTGCTGAGC	251	20	0	60.00	62.201	0.00	0.00	43.45	4.201
236	CGAAGGTCGTCTGCTGAGCT	250	20	0	60.00	62.207	5.83	0.00	37.02	4.207
237	GGACAGGGTGTTTCAGAAACAG	284	21	0	52.38	58.778	0.00	0.00	45.78	4.222
238	GTCGTCTGCTGAGCTTTCTAC	245	21	0	52.38	58.745	0.00	0.00	0.00	4.255
239	GAGTCGCTTAATTGCTCGTGA	100	21	0	47.62	58.740	0.00	0.00	0.00	4.260
240	CTGAGTCGCTTAATTGCTCGT	102	21	0	47.62	58.737	0.00	0.00	0.00	4.263
241	CTGCTGGAATGCTCGAAGGTC	263	21	0	57.14	61.338	0.00	0.00	0.00	4.338
242	GGACAGGGTGTTTCAGAAACA	284	20	0	50.00	57.658	0.01	0.00	43.06	4.342
243	TTCAGAAACAGCTGCTGGAA	274	20	0	45.00	57.653	20.95	12.30	35.51	4.347
244	ACAAAGGACAGGGTGTTTCAG	289	20	0	50.00	57.652	0.00	0.00	0.00	4.348
245	TGAGTCGCTTAATTGCTCGT	101	20	0	45.00	57.636	0.00	0.00	0.00	4.364
246	AGTCGCTTAATTGCTCGTGA	99	20	0	45.00	57.636	0.00	0.00	0.00	4.364
247	TCGGGCTGGTAAATGTTGATG	155	21	0	47.62	58.635	0.00	0.00	0.00	4.365
248	CGGGCTGGTAAATGTTGATGA	154	21	0	47.62	58.635	0.00	0.00	0.00	4.365
249	GTCGGGCTGGTAAATGTTGAT	156	21	0	47.62	58.634	0.00	0.00	0.00	4.366
250	GTGTGACGTTGTGGTTCCGC	178	20	0	60.00	62.369	0.00	0.00	35.47	4.369
251	GTGGTTCCGGCTCGTCG	168	16	0	68.75	57.630	0.00	0.00	0.00	4.370
252	GTGTTTCAGAAACAGCTGCTG	277	20	0	50.00	57.604	27.02	27.02	45.78	4.396
253	CCACGGACACACAAAGGACAG	299	21	0	57.14	61.406	0.00	0.00	0.00	4.406
254	CACGGACACACAAAGGACAGG	298	21	0	57.14	61.406	0.00	0.00	0.00	4.406
255	AGGTCGTCTGCTGAGCTTTCT	247	21	0	52.38	61.436	0.00	0.00	0.00	4.436
256	CAACATTGTGTGACGTTGTGG	185	21	0	47.62	58.551	0.00	0.00	0.00	4.449
257	TGCTCGAAGGTCGTCTGCTG	254	20	0	60.00	62.478	11.58	0.00	43.45	4.478
258	TGGAATGCTCGAAGGTCGTCT	259	21	0	52.38	61.498	0.00	0.00	43.45	4.498
259	TCTGAGTCGCTTAATTGCTCG	103	21	0	47.62	58.470	0.00	0.00	0.00	4.530
260	GGGATGCACACCACGG	309	16	0	68.75	57.451	12.79	0.00	0.00	4.549
261	GCTCGTCGGGCTGGT	160	15	0	73.33	58.449	10.59	0.00	0.00	4.551
262	TCAGAAACAGCTGCTGGAAT	273	20	0	45.00	57.426	31.00	17.58	35.51	4.574
263	AGCTCAATTCTGGCTTCACA	220	20	0	45.00	57.426	0.00	0.00	0.00	4.574
264	TGTGACGTTGTGGTTCGGCT	177	20	0	55.00	62.581	0.00	0.00	35.95	4.581

# Primers data

265	GGCTCGTCGGGCTGGTAAAT	161	20	0	60.00	62.589	8.47	0.00	0.00	4.589
266	TTGTGTGACGTTGTGGTTCGG	180	21	0	52.38	61.599	0.00	0.00	0.00	4.599
267	ATGCACACCACGGACACACA	306	20	0	55.00	62.601	0.00	0.00	0.00	4.601
268	GCTCAATTCTGGCTTCACAC	219	20	0	50.00	57.374	0.00	0.00	0.00	4.626
269	CAGAAACAGCTGCTGGAATG	272	20	0	50.00	57.369	19.76	10.50	35.51	4.631
270	CAAAGGACAGGGTGTTTCAGA	288	20	0	50.00	57.362	0.00	0.00	0.00	4.638
271	GTCGTCTGCTGAGCTTTCTA	245	20	0	50.00	57.361	0.00	0.00	0.00	4.639
272	TCGTCTGCTGAGCTTTCTAC	244	20	0	50.00	57.361	0.00	0.00	0.00	4.639
273	AGGACAGGGTGTTTCAGAAAC	285	20	0	50.00	57.360	0.00	0.00	35.85	4.640
274	CGTCTGCTGAGCTTTCTACT	243	20	0	50.00	57.354	0.18	0.00	0.00	4.646
275	GAATGCTCGAAGGTCGTCTGC	257	21	0	57.14	61.648	6.26	6.26	43.45	4.648
276	CACCACGGACACACAAAGGAC	301	21	0	57.14	61.670	0.00	0.00	0.00	4.670
277	GAGTCGCTTAATTGCTCGTG	100	20	0	50.00	57.297	0.00	0.00	0.00	4.703
278	CATTGTGTGACGTTGTGGTTC	182	21	0	47.62	58.285	0.00	0.00	0.00	4.715
279	TCGGGCTGGTAAATGTTGAT	155	20	0	45.00	57.201	0.00	0.00	0.00	4.799
280	TGCACACCACGGACACACAA	305	20	0	55.00	62.805	0.00	0.00	0.00	4.805
281	AAACAGCTGCTGGAATGCTCG	269	21	0	52.38	61.812	31.00	5.48	35.51	4.812
282	AACATTGTGTGACGTTGTGG	184	20	0	45.00	57.158	0.00	0.00	0.00	4.842
283	CATTGTGTGACGTTGTGGTT	182	20	0	45.00	57.158	0.00	0.00	0.00	4.842
284	CGGGCTGGTAAATGTTGATG	154	20	0	50.00	57.150	0.00	0.00	0.00	4.850
285	TTCAGAAACAGCTGCTGGAAT	274	21	0	42.86	58.132	21.26	9.35	35.51	4.868
286	TCCTCTGAGTCGCTTAATTGC	106	21	0	47.62	58.106	3.66	0.00	0.00	4.894
287	CCTCTGAGTCGCTTAATTGCT	105	21	0	47.62	58.101	3.66	0.00	0.00	4.899
288	CAGCTGCTGGAATGCTCGAAG	266	21	0	57.14	61.927	21.71	0.00	34.51	4.927
289	CAAAGGACAGGGTGTTTCAGAA	288	21	0	47.62	58.069	0.00	0.00	0.00	4.931
290	AAGGACAGGGTGTTTCAGAAAC	286	21	0	47.62	58.068	0.00	0.00	35.85	4.932
291	CACACCACGGACACACAAAGG	303	21	0	57.14	61.935	0.00	0.00	0.00	4.935
292	CTGAGTCGCTTAATTGCTCG	102	20	0	50.00	57.013	0.00	0.00	0.00	4.987
293	TGGCTTCACACTTACAACACA	210	21	0	42.86	58.007	0.00	0.00	0.00	4.993
294	TTACTGCTGGGATGCACACCA	317	21	0	52.38	62.004	6.10	4.92	38.12	5.004
295	GTTTTCTTCCTCTGAGTCGCT	113	21	0	47.62	57.967	0.00	0.00	0.00	5.033
296	AATGCTCGAAGGTCGTCTGCT	256	21	0	52.38	62.099	11.58	0.55	43.45	5.099
297	ACACCACGGACACACAAAGGA	302	21	0	52.38	62.124	0.00	0.00	0.00	5.124
298	ACCACGGACACACAAAGGACA	300	21	0	52.38	62.124	0.00	0.00	0.00	5.124
299	ACAACATTGTGTGACGTTGTG	186	21	0	42.86	57.870	5.36	0.00	41.89	5.130
300	TCGTTTTCTTCCTCTGAGTCG	115	21	0	47.62	57.716	0.00	0.00	0.00	5.284
301	GCACACCACGGACACACAAAG	304	21	0	57.14	62.514	0.00	0.00	0.00	5.514
302	ACGGACACACAAAGGACAGGG	297	21	0	57.14	62.522	0.00	0.00	0.00	5.522
303	CGGACACACAAAGGACAGGGT	296	21	0	57.14	62.522	0.00	0.00	0.00	5.522
304	TCTGGCTTCACACTTACAACA	212	21	0	42.86	57.448	0.00	0.00	0.00	5.552
305	CTGGCTTCACACTTACAACAC	211	21	0	47.62	57.391	0.00	0.00	0.00	5.609
306	AACAGCTGCTGGAATGCTCGA	268	21	0	52.38	62.651	31.00	0.00	35.51	5.651
307	ACAGCTGCTGGAATGCTCGAA	267	21	0	52.38	62.651	31.00	0.00	35.51	5.651
308	TACTGCTGGGATGCACACCAC	316	21	0	57.14	62.660	3.46	0.78	38.12	5.660
309	AAAGGACAGGGTGTTTCAGAAA	287	21	0	42.86	57.337	0.00	0.00	0.00	5.663
310	CGAAGGTCGTCTGCTGAGCTT	250	21	0	57.14	62.671	7.47	7.47	38.04	5.671
311	TAGCTCAATTCTGGCTTCACA	221	21	0	42.86	57.299	2.49	0.00	33.07	5.701

Primers data

312	ATGCTCGAAGGTCGTCTGCTG	255	21	0	57.14	62.738	11.58	0.00	43.45	5.738
313	TTTTCTTCCTCTGAGTCGCTT	112	21	0	42.86	57.247	0.00	0.00	0.00	5.753
314	CGTCTGCTGAGCTTTCTACTA	243	21	0	47.62	57.233	0.18	0.00	0.00	5.767
315	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: 094ZHN7B015

Database: Nucleotide collection (nt)

45,172,210 sequences; 162,240,808,426 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 3, 2017 6:38 PM  
Number of letters in database: 162,240,808,426  
Number of sequences in database: 45,172,210

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: 45172210  
Number of Hits to DB: 218553  
Number of extensions: 108  
Number of successful extensions: 108  
Number of sequences better than 10: 0  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 108  
Number of HSP's successfully gapped: 0  
Length of query: 20  
Length of database: 162240808426  
Length adjustment: 17  
Effective length of query: 3  
Effective length of database: 161472880856  
Effective search space: 484418642568  
Effective search space used: 484418642568  
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: 094ZXP4014

Database: Nucleotide collection (nt)

45,172,210 sequences; 162,240,808,426 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	0.79
MF288725.1	Human papillomavirus type 18 isolate C451606_R3_19...	39.2	0.79
MF288724.1	Human papillomavirus type 18 isolate C451606_R2_15...	39.2	0.79
MF288723.1	Human papillomavirus type 18 isolate C451606_R1_12...	39.2	0.79
MF288722.1	Human papillomavirus type 18 isolate C387957_R1_11...	39.2	0.79
MF288721.1	Human papillomavirus type 18 isolate 1209155_R1_P_...	39.2	0.79
MF288720.1	Human papillomavirus type 18 isolate 1174820_N-P, ...	39.2	0.79
MF288719.1	Human papillomavirus type 18 isolate C487627_R2_15...	39.2	0.79
MF288718.1	Human papillomavirus type 18 isolate C487627_R1_11...	39.2	0.79
MF288717.1	Human papillomavirus type 18 isolate 1533526_N-P, ...	39.2	0.79
MF288716.1	Human papillomavirus type 18 isolate C458963_R2_15...	39.2	0.79
MF288715.1	Human papillomavirus type 18 isolate C458963_R1_12...	39.2	0.79
MF288714.1	Human papillomavirus type 18 isolate C533713_R3_17...	39.2	0.79
MF288713.1	Human papillomavirus type 18 isolate C533713_R2_14...	39.2	0.79
MF288712.1	Human papillomavirus type 18 isolate C578032_R3_17...	39.2	0.79
MF288711.1	Human papillomavirus type 18 isolate C578032_R2_14...	39.2	0.79
MF288710.1	Human papillomavirus type 18 isolate C335048_R3_19...	39.2	0.79
MF288709.1	Human papillomavirus type 18 isolate C412607_R2_15...	39.2	0.79
MF288708.1	Human papillomavirus type 18 isolate C412607_R1_12...	39.2	0.79
MF288707.1	Human papillomavirus type 18 isolate C440384_R1_13...	39.2	0.79
MF288706.1	Human papillomavirus type 18 isolate C425046_R2_16...	39.2	0.79
MF288705.1	Human papillomavirus type 18 isolate C425046_R1_13...	39.2	0.79
MF288704.1	Human papillomavirus type 18 isolate C627893_R2_16...	39.2	0.79
MF288703.1	Human papillomavirus type 18 isolate C627893_R1_13...	39.2	0.79
MF288702.1	Human papillomavirus type 18 isolate C644657_R4_21...	39.2	0.79
MF288701.1	Human papillomavirus type 18 isolate C644657_R3_18...	39.2	0.79
MF288700.1	Human papillomavirus type 18 isolate C644657_R2_14...	39.2	0.79



## BLAST INFORMATION

MF288699.1	Human papillomavirus type 18 isolate C644657_R1_11...	39.2	0.79
MF288698.1	Human papillomavirus type 18 isolate C335048_R2_15...	39.2	0.79
MF288697.1	Human papillomavirus type 18 isolate 1445230_R2_P...	39.2	0.79
MF288696.1	Human papillomavirus type 18 isolate 1581449_N-P, ...	39.2	0.79
MF288695.1	Human papillomavirus type 18 isolate C440737_R1_11...	39.2	0.79
MF288694.1	Human papillomavirus type 18 isolate C439921_R1_11...	39.2	0.79
MF288693.1	Human papillomavirus type 18 isolate C430899_R1_11...	39.2	0.79
MF288692.1	Human papillomavirus type 18 isolate C353934_R1_11...	39.2	0.79
MF288691.1	Human papillomavirus type 18 isolate 1390622_R1_P...	39.2	0.79
MF288690.1	Human papillomavirus type 18 isolate C532476_R1_11...	39.2	0.79
MF288689.1	Human papillomavirus type 18 isolate 1508690_N-P, ...	39.2	0.79
MF288688.1	Human papillomavirus type 18 isolate 1115002_N-P, ...	39.2	0.79
MF288687.1	Human papillomavirus type 18 isolate C406921_R1_11...	39.2	0.79
MF288686.1	Human papillomavirus type 18 isolate C575918_R2_14...	39.2	0.79
MF288685.1	Human papillomavirus type 18 isolate C575918_R1_10...	39.2	0.79
MF288684.1	Human papillomavirus type 18 isolate 1389481_N-P, ...	39.2	0.79
MF288683.1	Human papillomavirus type 18 isolate 1310091_R1_P...	39.2	0.79
MF288682.1	Human papillomavirus type 18 isolate C385149_R2_15...	39.2	0.79
MF288681.1	Human papillomavirus type 18 isolate C385149_R1_11...	39.2	0.79
MF288680.1	Human papillomavirus type 18 isolate C340709_R1_12...	39.2	0.79
MF288679.1	Human papillomavirus type 18 isolate C310065_R1_13...	39.2	0.79
MF288678.1	Human papillomavirus type 18 isolate C498643_R2_15...	39.2	0.79
MF288677.1	Human papillomavirus type 18 isolate C498643_R1_11...	39.2	0.79

## ALIGNMENTS

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

Score = 39.2 bits (42), Expect = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79

# 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 = 0.79

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 = 0.79

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 = 0.79

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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79

# 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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 = 0.79  
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 3, 2017 6:38 PM  
Number of letters in database: 162,240,808,426  
Number of sequences in database: 45,172,210

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: 45172210  
Number of Hits to DB: 304465  
Number of extensions: 124  
Number of successful extensions: 124  
Number of sequences better than 10: 0  
Number of HSP's better than 10 without gapping: 0  
Number of HSP's gapped: 124  
Number of HSP's successfully gapped: 0  
Length of query: 21  
Length of database: 162240808426  
Length adjustment: 18  
Effective length of query: 3  
Effective length of database: 161427708646  
Effective search space: 484283125938  
Effective search space used: 484283125938  
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)

