

Figure 1

ClustalW multiple sequence alignment

2 Sequences Aligned Processing time: 1.9 seconds
Gaps Inserted = 0 Conserved Identities = 3375
Score = 199998

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
Open Gap Penalty = 15.0 Extend Gap Penalty = 6.7

Multiple Alignment Parameters:
Open Gap Penalty = 15.0 Extend Gap Penalty = 6.7
Delay Divergent = 30% Transitions: Weighted

1. GagPol pGM297 vs. coGagPol pGM691

Aligned Length = 4391 Gapped Segments = 0 Total Mismatches (including gaps) = 1016
Identities = 3375 (76.9%)

GagPol pGM297	1	ATGGGGGCGGTACCTCAGCACTAAATAGGAGACAATTAGACCAATTTGAGAAAATACGA	60
coGagPol pGM691	1	ATGGGAGCTGCCACATCTGCCCTGAATAGACGGCAGCTGGACCAATTCGAGAAGATCAGA	60

GagPol pGM297	61	CTTCGCCCCAACGGAAAGAAAAAGTACCAAATTAACATTTAATATGGGCAGGCAAGGAG	120
coGagPol pGM691	61	CTGCGGCCCAACGGCAAGAAGTACCAGATCAAGCACCTGATCTGGGCCGGCAAGAG	120

GagPol pGM297	121	ATGGAGCGCTTCGGCCTCCATGAGAGGTTGTTGGAGACAGAGGAGGGGTGTAAAAGAAATC	180
coGagPol pGM691	121	ATGGAAAGATTTCGGCCTGCACGAGCGGCTGCTGGAAACCGAGGAAGGCTGCAAGAGAATT	180

GagPol pGM297	181	ATAGAAGTCCTCTACCCCTAGAACCAACAGGATCGGAGGGCTTAAAAAGTCTGTTCAT	240
coGagPol pGM691	181	ATCGAGGTGCTGTACCCCTCTGGAACCTACCGGCTCTGAGGGCTGAAGTCCCTGTTCAT	240
		**	
GagPol pGM297	241	CTTGTTGCGTACTATATTGCTTGACAAAGGAACAGAAAGTGAAGACACAGAGGAAGCA	300
coGagPol pGM691	241	CTCGTGTGCGTGTGTACTGCCTGCACAAAGAACAGAAAGTGAAGGACACCGAAGAGGCC	300

GagPol pGM297	301	GTAGCAACAGTAAGACAACACTGCCATCTAGTGGAAAAAGAAAAAGTGCAACAGAGACA	360
coGagPol pGM691	301	GTGGCCACAGTTAGACAGCACTGCCACCTGGTGGAAAAAGAGAAAGTCCGCCACAGAGACA	360
		**	
GagPol pGM297	361	TCTAGTGGACAAAAGAAAAATGACAAGGGAATAGCAGCGCCACCTGGTGGCAGTCAGAAT	420
coGagPol pGM691	361	AGCAGCGGCCAGAAGAGAACGACAAGGGAATTTGCTGCCCTTCTGGCGGCAGCCAGAAT	420
		**	
GagPol pGM297	421	TTTCCAGCGCAACAAGGAAATGCCGTTGACATGTACCCCTTGTACCGCGCACCTTA	480
coGagPol pGM691	421	TTTCCTGCTCAGCAGCAGGGAACGCCGTTGGTGCACGTTCCACTGAGCCCTAGAACACTG	480

GagPol pGM297	481	AATGCGTGGGTAAAAGCAGTAGAGGAGAAAAAATTTGGAGCAGAAATAGTACCCATGTTT	540
coGagPol pGM691	481	AATGCCCTGGGTCAAAGCCGTGGAAGAGAGAAGTTTGGCGCCGAGATCGTGCCCATGTTTC	540

GagPol pGM297	541	CAAGCCCTATCAGAAGGCTGCACACCTATGACATTAATCAGATGCTTAATGTGTAGGA	600
coGagPol pGM691	541	CAGGCTCTGTCTGAGGGCTGCACCCCTTACGACATCAACCAGATGCTGAACGTGCTGGGA	600
		**	
GagPol pGM297	601	GATCATCAAGGGGCATTACAAATAGTGAAAGAGATCATTAATGAAGAAGCAGCCCAGTGG	660
coGagPol pGM691	601	GATCACCAGGGCGCTCTGCAGATCGTGAAAGAGATCATCAACGAAGAGGCTGCCCAAGTGG	660

GagPol pGM297	661	GATGTAACACACCCACTACCCGAGGACCCCTACCAGCAGGACAGCTCAGGGACCCCTCGC	720
coGagPol pGM691	661	GACGTGACACATCCATTGCCTGTGGACCTCTGCCAGCCGGACAACCTGAGAGATCTTAGA	720
		**	
GagPol pGM297	721	GGCTCAGATATAGCAGGGACCACCAGCTCAGTACAAGAACAGTTAGAAATGGATCTATACT	780
coGagPol pGM691	721	GGCTCTGATATCGCCGGCACCACCAGCTCTGTGCAAGAGCAGCTGGAATGGATCTACACC	780

GagPol pGM297	781	GCTAACCCCGGGTAGATGTAGGTGCCATCTACCGGAGATGGATTATTTCTAGGACTTCAA	840
coGagPol pGM691	781	GCCAACTCTAGATGGACGTGGCGCCATCTACAGAAGATGGATCATCTTGGGCTGCAG	840

2/28

GagPol pGM297 1981 GTAGAGTAGGAGGAGAAAAATGCATACAATACCCCAATATTTTGCATAAAGAAGAAGGACA 2040
coGagPol pGM691 1981 GCAGAGTTGGCGGCAGAACGCCCTACAATACCCCTATCTTCTGCATCAAGAAAAAGGACA 2040
* * * * *

GagPol pGM297 2041 AATCCCAGTGGAGGATGCTAGTAGACTTTAGAGAGTTAAATAAGGCAACCAAGATTCT 2100
coGagPol pGM691 2041 AGAGCCAGTGGCGGATGCTGGTGGACTTTAGAGAGCTGAACAAGGCTACCCAGGACTTCT 2100
* * * * *

GagPol pGM297 2101 TTGAAGTGCAATTAGGGATACCCACCCAGCAGGATTAAGAAAGATGAGACAGATAACAG 2160
coGagPol pGM691 2101 TCGAGGTGCAGCTGGGAATTCTCATCTTCCCGGCTGCGGAAGATGAGACAGATCACAG 2160
* * * * *

GagPol pGM297 2161 TTTTAGATGTAGGAGACGCCATTATTCCATACCATTTGGATCCAAATTTAGGAAATATA 2220
coGagPol pGM691 2161 TGCTGGATGTGGGCGACGCCCTACTACAGCATCCCTCTGGACCCCAACTTCAGAAAGTACA 2220
* * * * *

GagPol pGM297 2221 CTGCTTTTACTATTCCCACAGTGAATAATCAGGGACCCGGGATTAGGTATCAATTCAACT 2280
coGagPol pGM691 2221 CCGCCTTCACAAATCCCCACCGTGAACAATCAAGGCCCTGGCATCAGATACAGTTCAACT 2280
* * * * *

GagPol pGM297 2281 GTCTCCCGCAAGGGTGGAAAGGATCTCCTACAATCTTCCAAAATACAGCAGCATCCATT 2340
coGagPol pGM691 2281 GCCTGCCTCAAGGCTGGAAGGGCAGCCCCACCATTTTTCAGAAATACCGCCGCGCAGCATCC 2340
* * * * *

GagPol pGM297 2341 TGGAGGAGATAAAAAGAACTTGCCAGCACTAACCATTTGTACAATACATGGATGATTTAT 2400
coGagPol pGM691 2341 TGGAAGAAATCAAGAGAAACCTGCCTGCTCTGACCATCGTGCAGTACATGGACGATCTGT 2400
* * * * *

GagPol pGM297 2401 GGGTAGGTTCTCAAGAAAATGAACACACCCATGACAAATTAGTAGAACAGTTAAGAACAA 2460
coGagPol pGM691 2401 GGGTCGGAAGCCAAGAGAATGAGCACACCCACGACAAGCTGGTGAACAGCTGAGAACAA 2460
* * * * *

GagPol pGM297 2461 AATTACAAGCCTGGGGCTTAGAAACCCAGAAAAGAAGGTGCAAAAAGAACCCCTTATG 2520
coGagPol pGM691 2461 AGCTGCAGGCCTGGGGCTCGAAACCCCTGAGAAGAAGGTGCAAAAAGAACCTCTTACG 2520
* * * * *

GagPol pGM297 2521 AGTGGATGGGATACAACTTTGGCCTCACAATGGGAATAAGCAGAAATACAACTGGAGG 2580
coGagPol pGM691 2521 AGTGGATGGGCTACAAGCTGTGGCCTCACAAGTGGGAGCTGAGCCGGATTCAAGTCGAAG 2580
* * * * *

GagPol pGM297 2581 AAAAAGATGAATGGACTGTCAATGACATCCAGAAGTTAGTTGGGAACTAAATTTGGGCAG 2640
coGagPol pGM691 2581 AGAAGGACGAGTGGACCGTGAACGACATCCAGAACTCGTGGGCAAGCTGAATTTGGGCAG 2640
* * * * *

GagPol pGM297 2641 CACAATTGTATCCAGGTCTTAGGACCAAGAATATATGCAAGTTAATTAGAGGAAAGAAAA 2700
coGagPol pGM691 2641 CCCAGCTGTATCCCGGCCTGAGGACCAAGAACATCTGCAAGCTGATCCGGGGAAAGAA 2700
* * * * *

GagPol pGM297 2701 ATCTGTTAGAGCTAGTGACTTGGACACCTGAGGCAGAAGCTGAATATGCAGAAAATGCAG 2760
coGagPol pGM691 2701 ACCTGCTGGAAGTGGTCACTGGACACCTGAGGCCGAGGCCGAATATGCCGAGAAATGCCG 2760
* * * * *

GagPol pGM297 2761 AGATTCTTAAAACAGAACAGGAAGGAACCTATTACAAACCAGGAATACCTATTAGGGCAG 2820
coGagPol pGM691 2761 AAATCCTGAAAACCGAGCAAGAGGGGACCTACTACAAGCCTGGCATTTCCAATCAGAGCTG 2820
* * * * *

GagPol pGM297 2821 CAGTACAGAAATTTGAAGGAGACAGTGGAGTTACCAATTCAAACAAGAAGGACAAAGTCT 2880
coGagPol pGM691 2821 CCGTGCAGAAACTGGAAGGCGGCCAGTGGTCTTACCAGTTTAAAGCAAGAAGGCCAGGTCC 2880
* * * * *

GagPol pGM297 2881 TGAAAGTAGGAAAAATACACCAAGCAAAAGAACCCCATACAAATGAACCTTCGCACATTAG 2940
coGagPol pGM691 2881 TGAAAGTGGGCAAGTACACCAAGCAGAAGAACACCCACACCAACGAGCTGAGGACACTGG 2940
* * * * *

GagPol pGM297 2941 CTGGTTTAGTGCAGAAGATTGCAAGAAGCTCTAGTTATTTGGGGGATATTACCAGTTC 3000
coGagPol pGM691 2941 CTGGCTGGTCCAGAAAATCTGCAAGAGGCCCTGGTCATTTGGGGCATCCTGCCCTGTTTC 3000
* * * * *

GagPol pGM297 3001 TAGAACTCCCGATAGAAAAGAGAGGTATGGGAACAATGGTGGGCGGATTACTGGCAGGTAA 3060
coGagPol pGM691 3001 TGGAACCTGCCATTGAGCGGGAAGTGTGGGAACAGTGGTGGGCGGATTACTGGCAAGTGT 3060
* * * * *

GagPol pGM297 3061 GCTGGATTCCCGAATGGGATTTTGTGTCAGCACCCACCTTTGCTCAAACTATGGTACACAT 3120
coGagPol pGM691 3061 CTTGGATCCCGAGTGGGACTTCGTGTCTACCCCTCCTCTGCTGAAACTGTGGTACACCC 3120
* * * * *


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coGagPol pGM691 4261 TGGTGCTGAAGGATGGCTCTGATCTGAAGGTGGTGCCCAGACGGAAGGCCAAGATTATCA 4320
      **** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
GagPol pGM297 4321 AGGATTATGAACCCAAACAAAGAGTGGGTAATGAGGGTGACGTGGAAGGTACCAGGGGAT 4380
coGagPol pGM691 4321 AGGATTACGAGCCCAACAGCGCTGGGCAATGAAGGCGACGTTGAGGGCACAAGAGGCA 4380
      ***** * * * * * * * * * * * * * * * * * * * * * * * * * * *
GagPol pGM297 4381 CTGATAACTAA 4391
coGagPol pGM691 4381 GCGACAATTGA 4391
      ** * * * *
```

Figure 2A

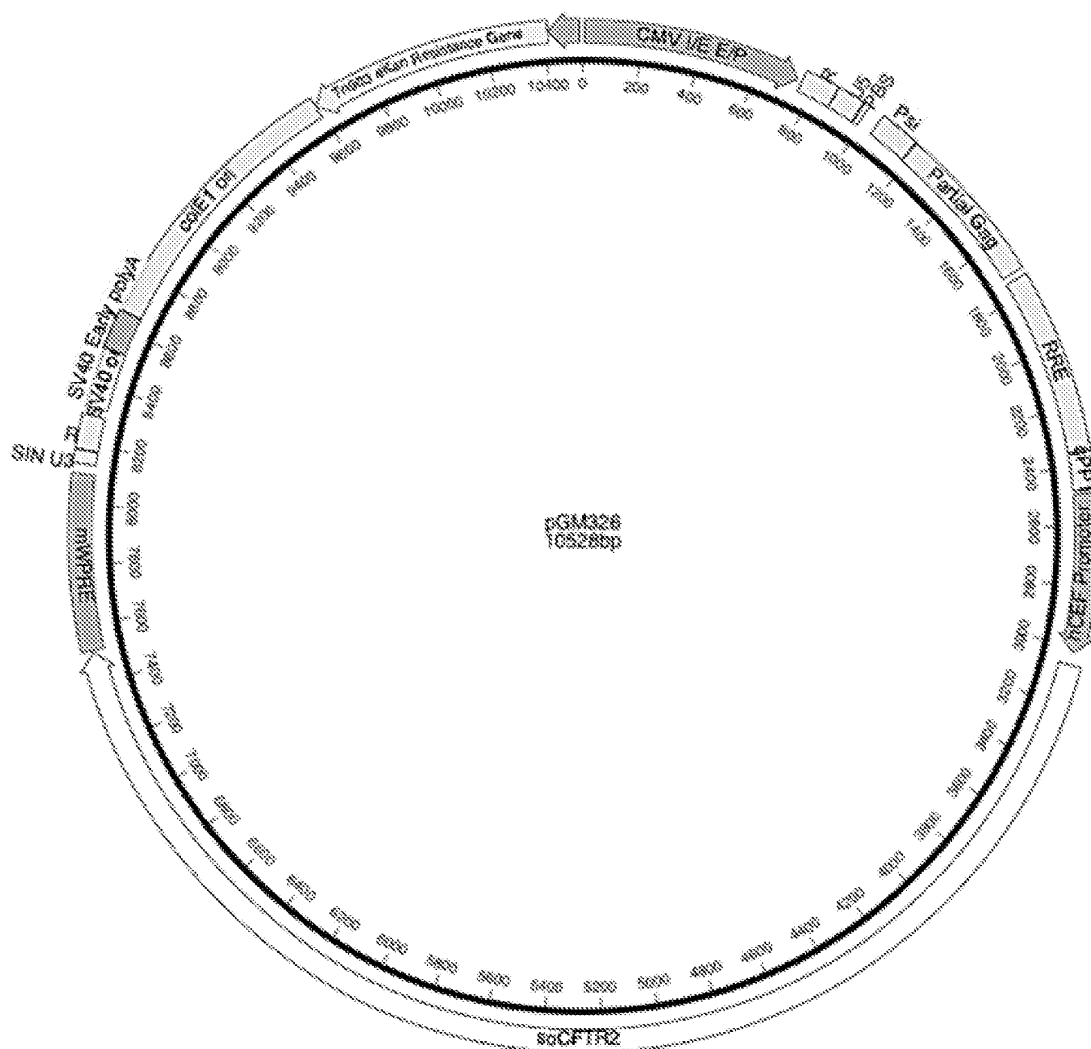


Figure 2B

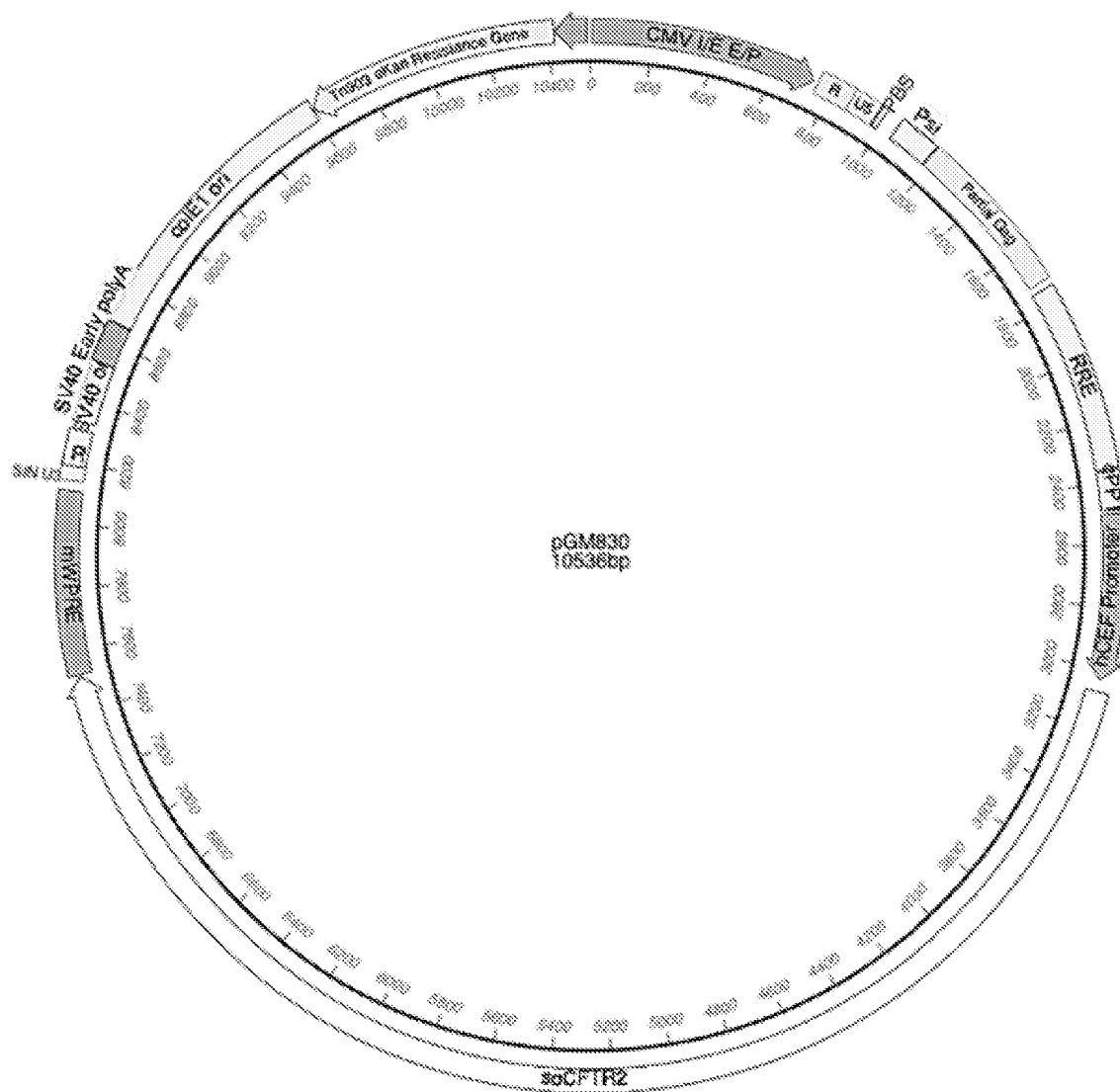


Figure 2C

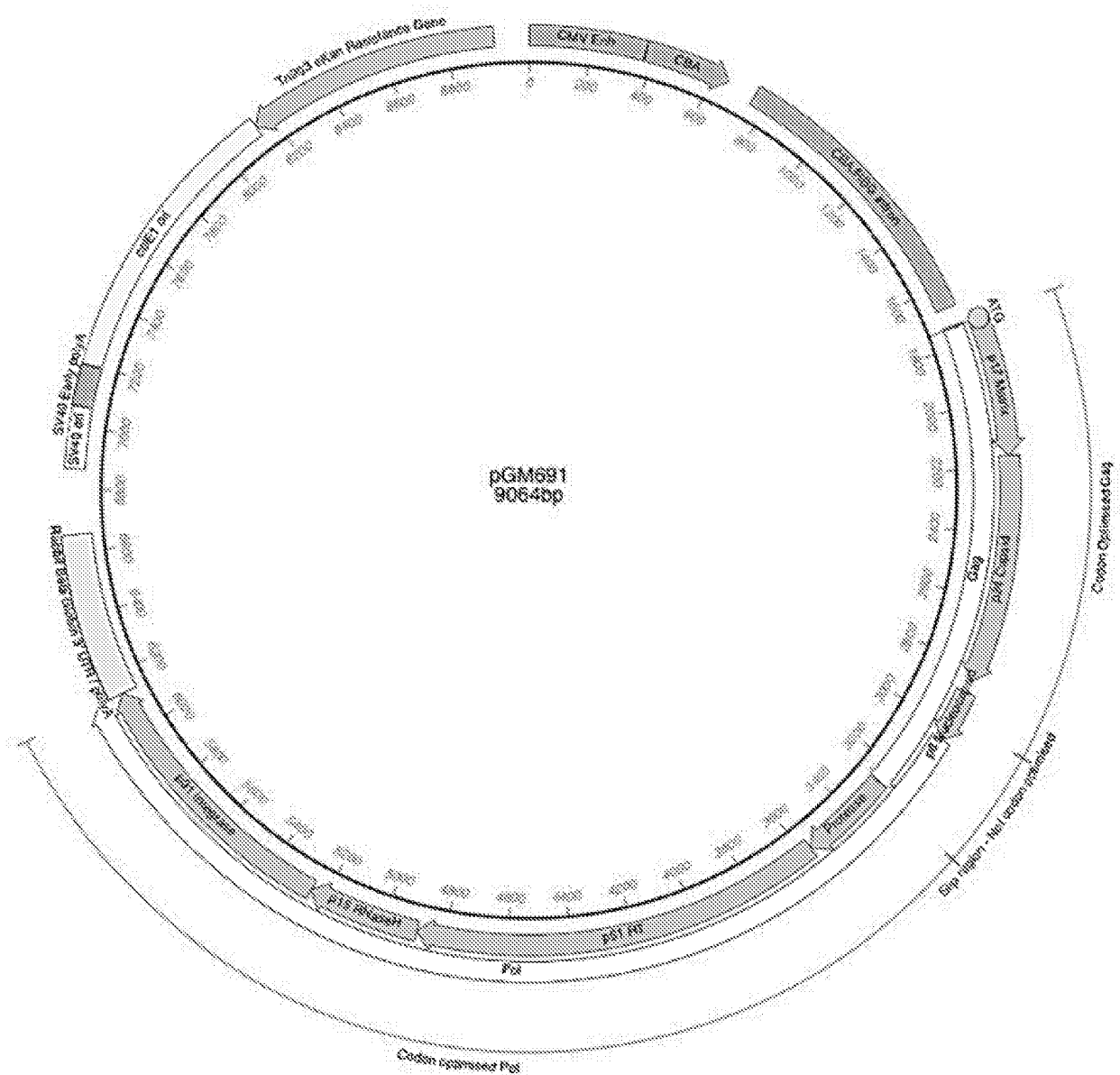


Figure 2D

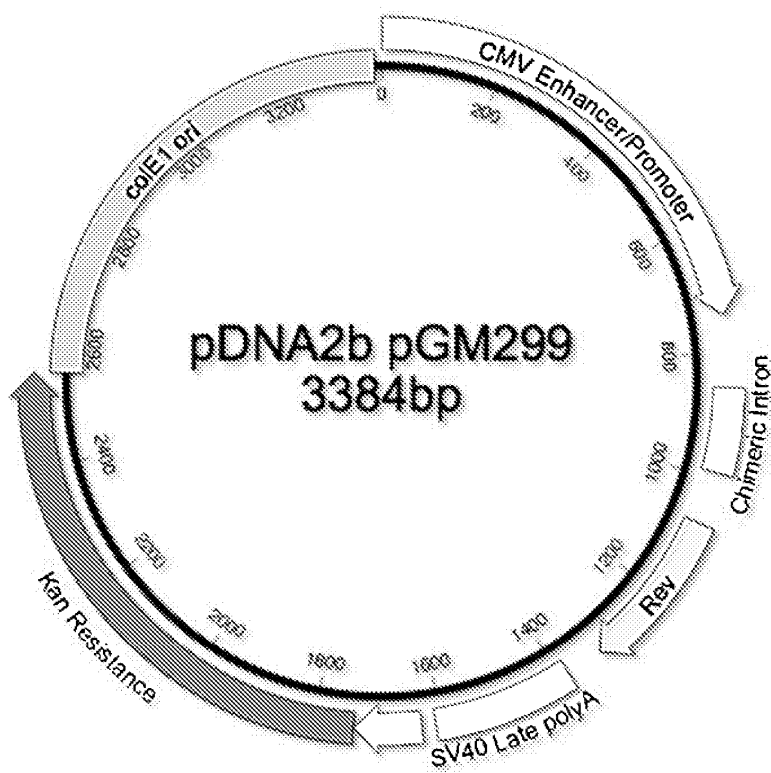


Figure 2E

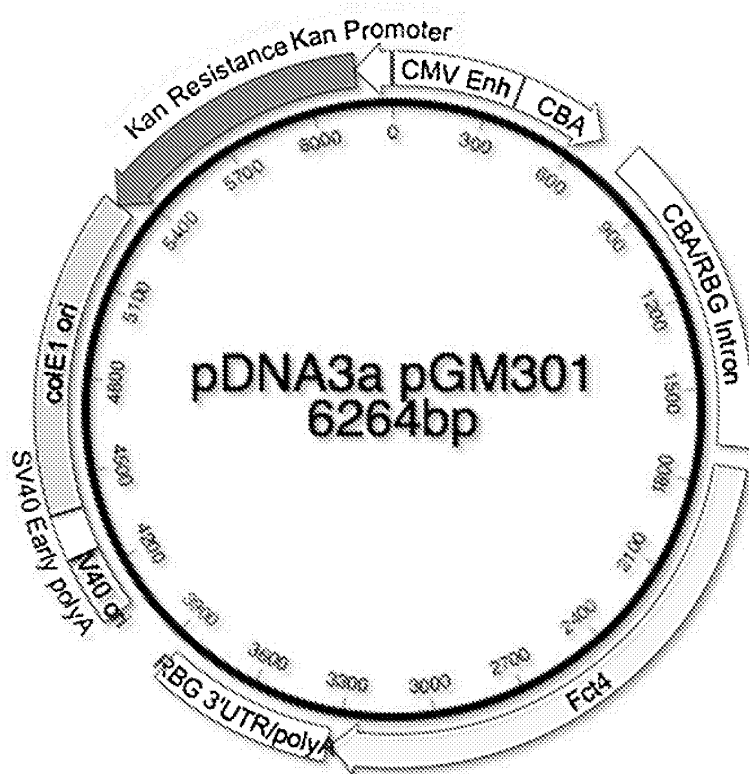
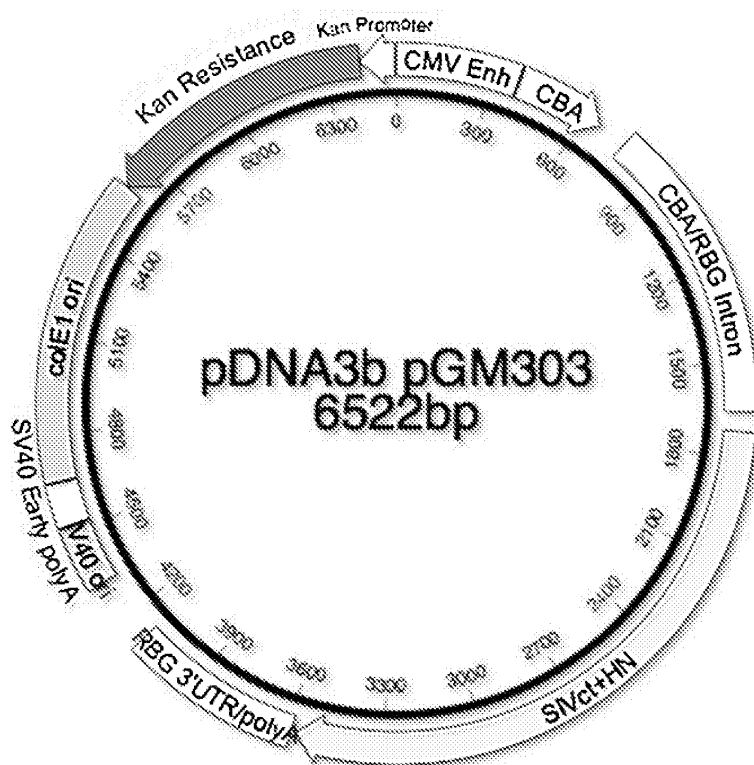


Figure 2F



[illegible]

Figure 3

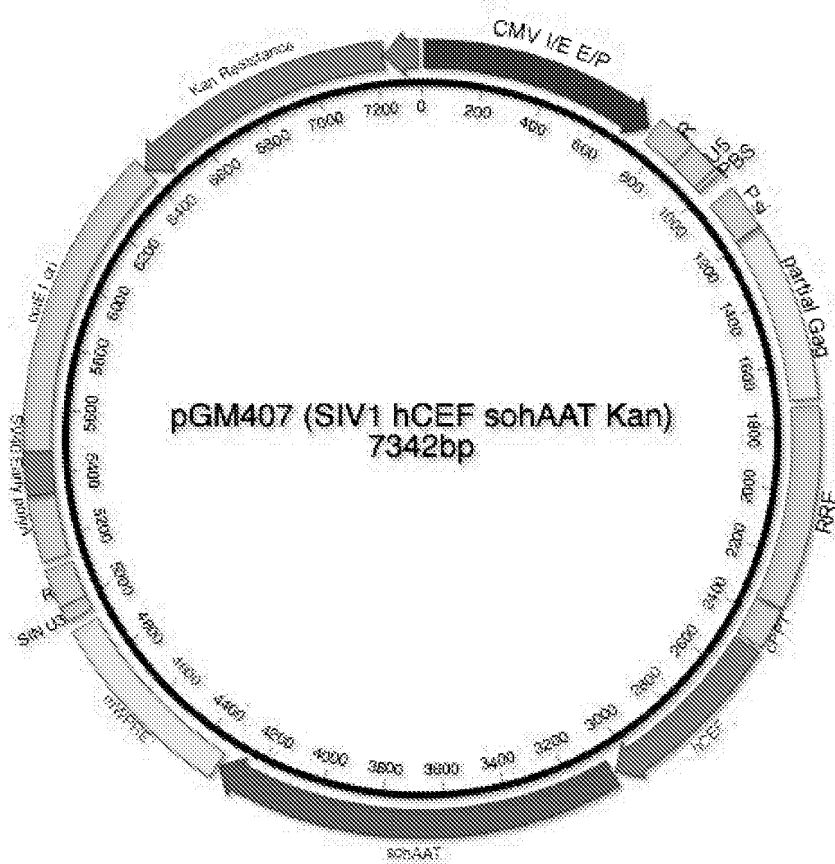


Figure 4A

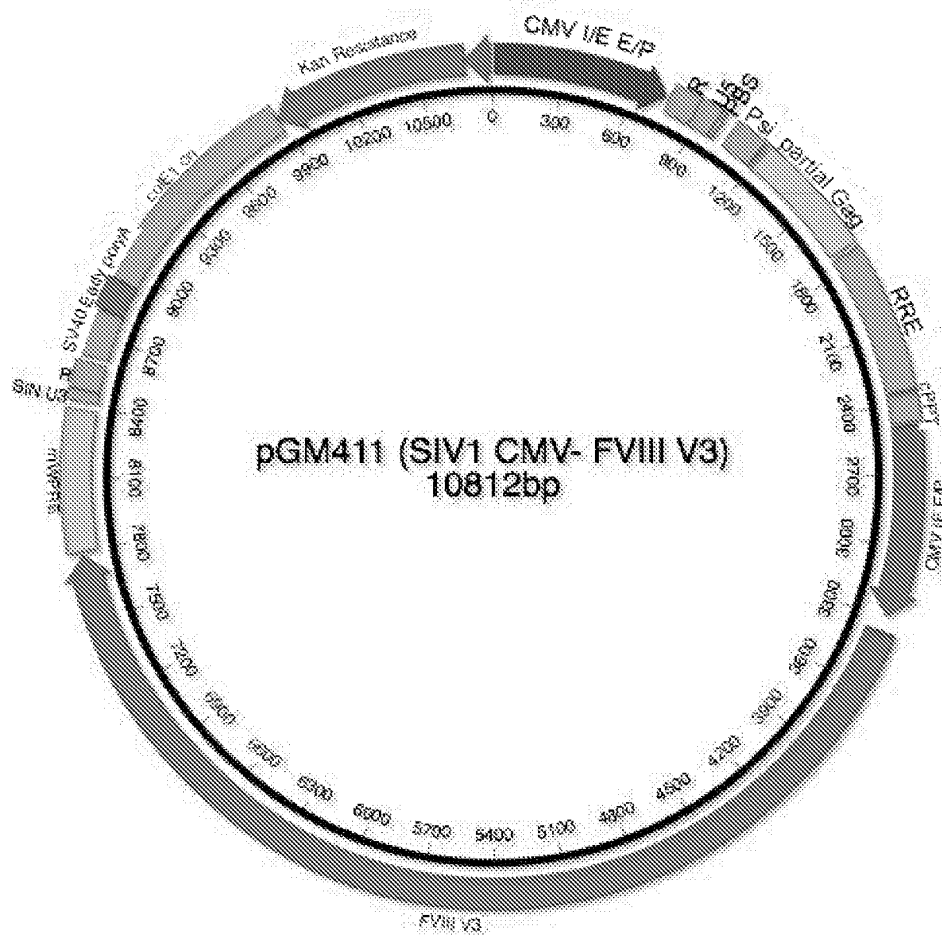


Figure 4B

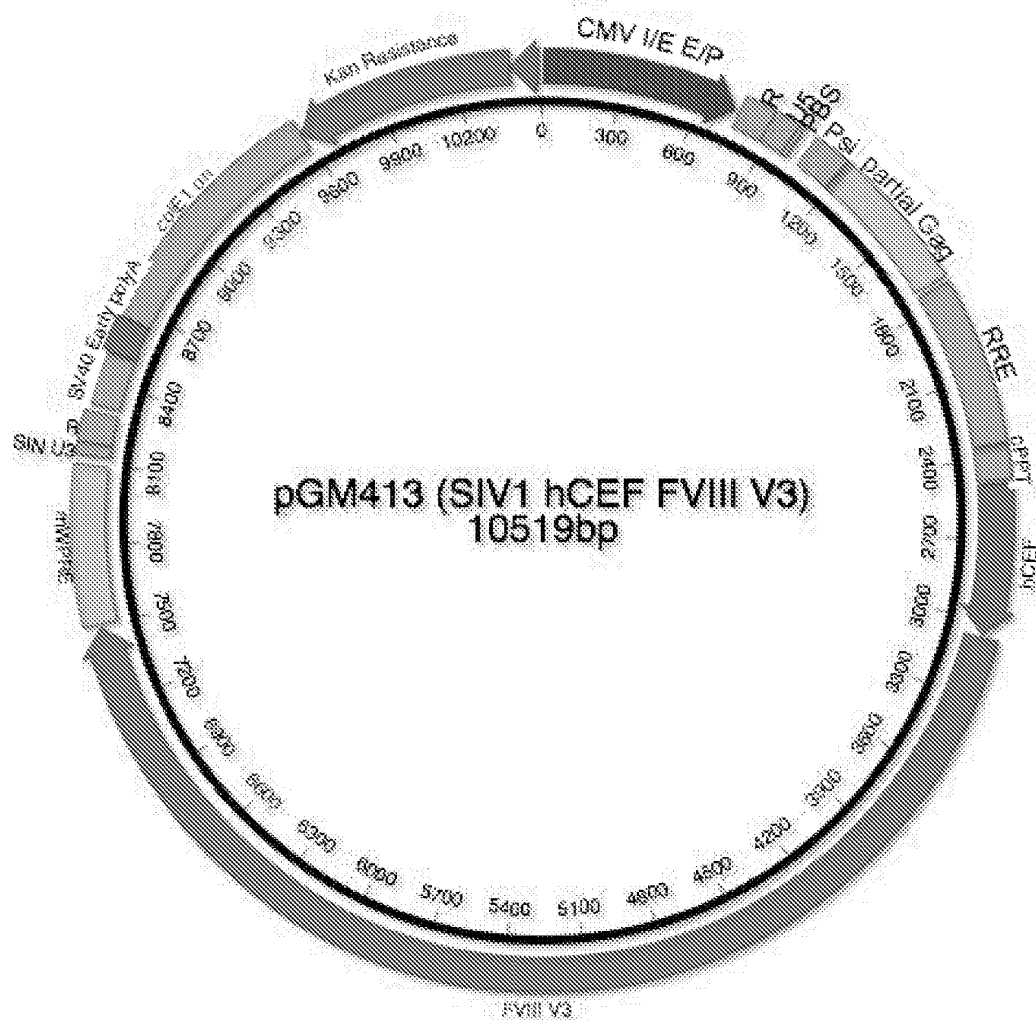


Figure 4C

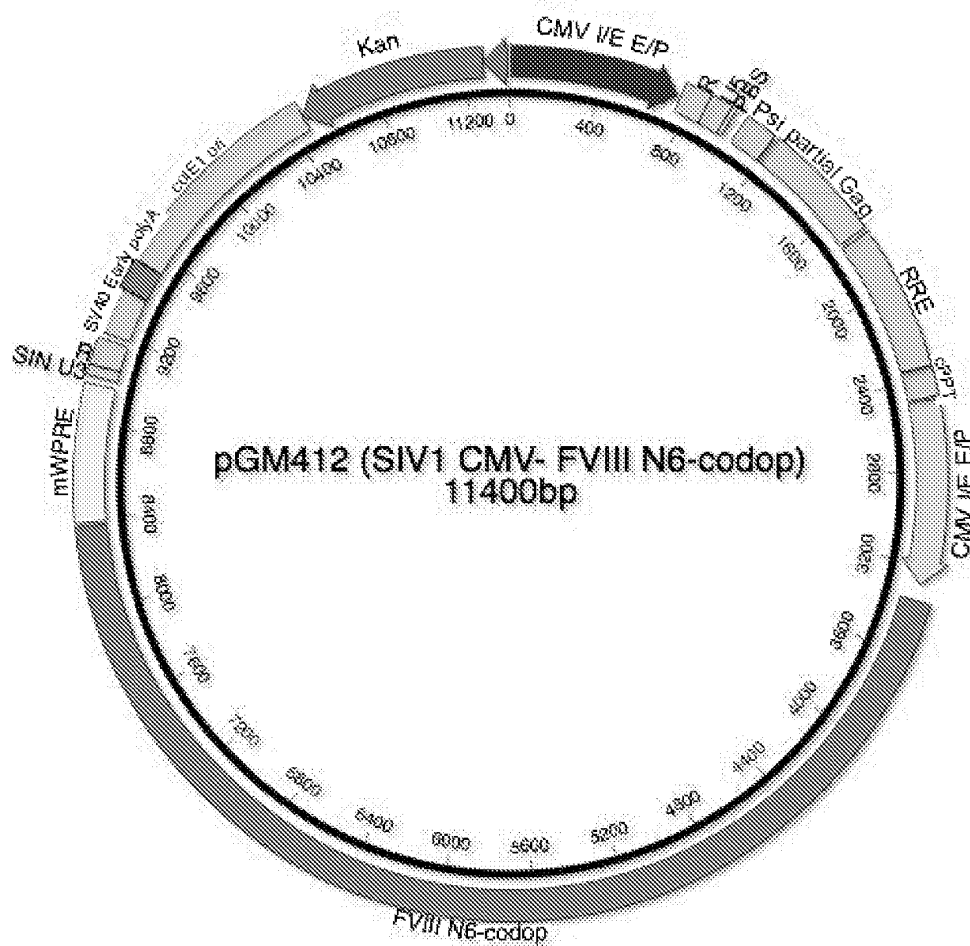


Figure 4D

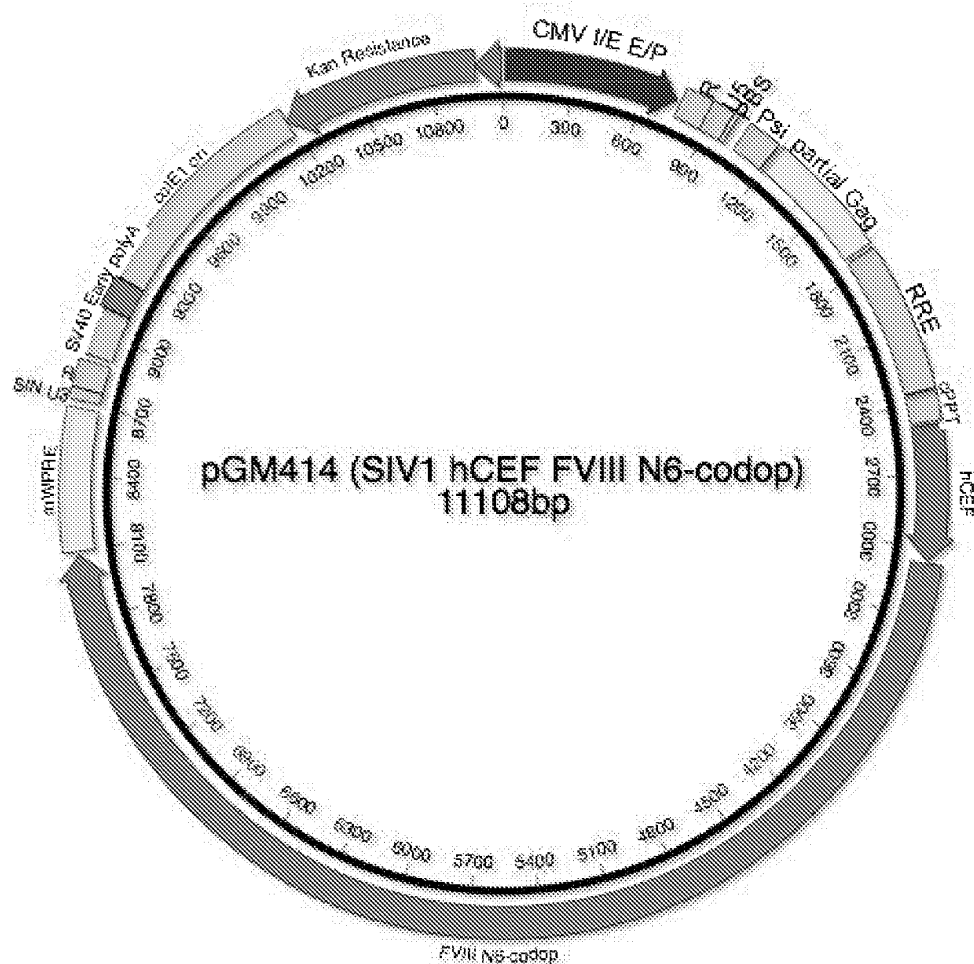


Figure 5A

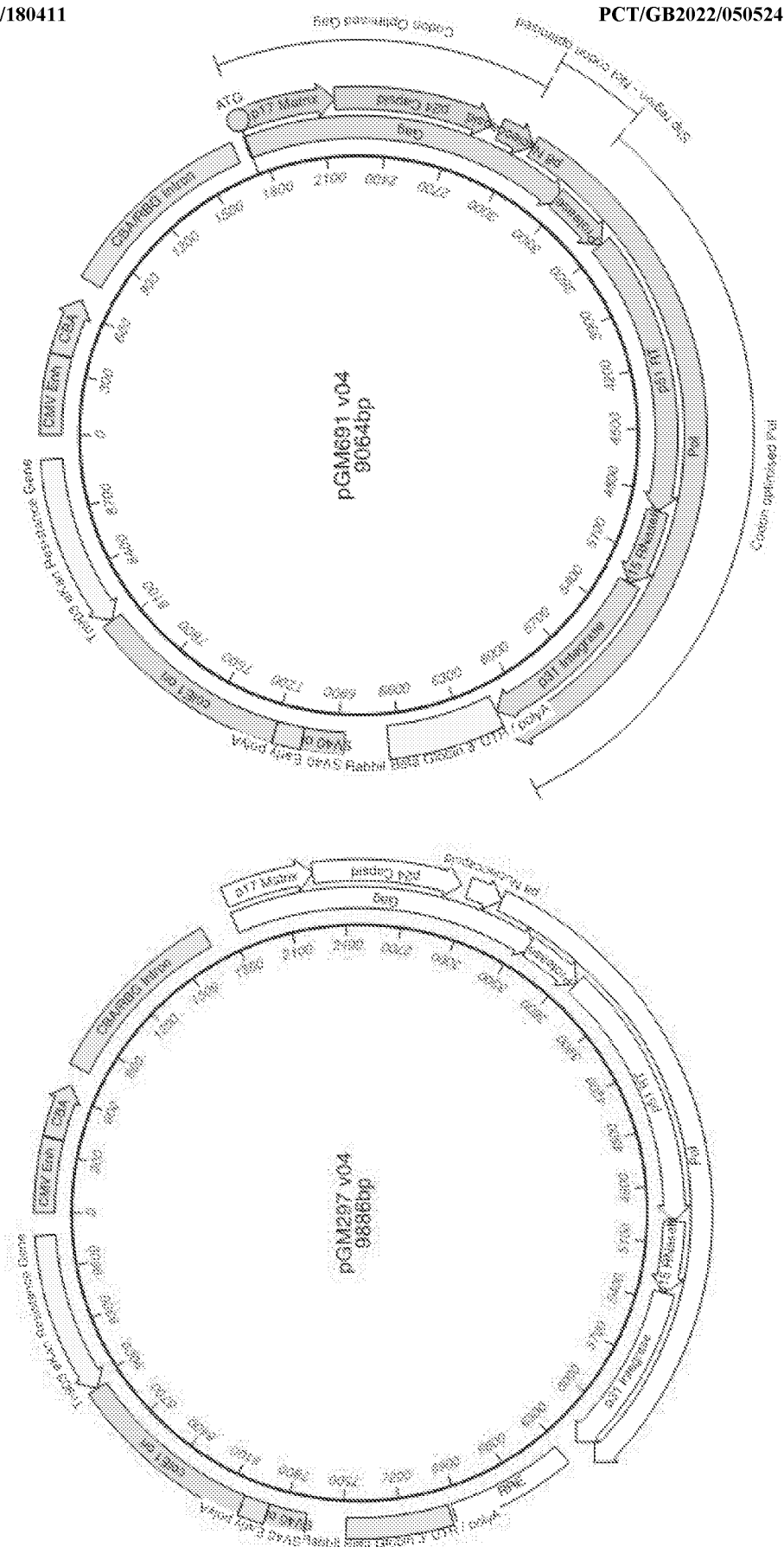
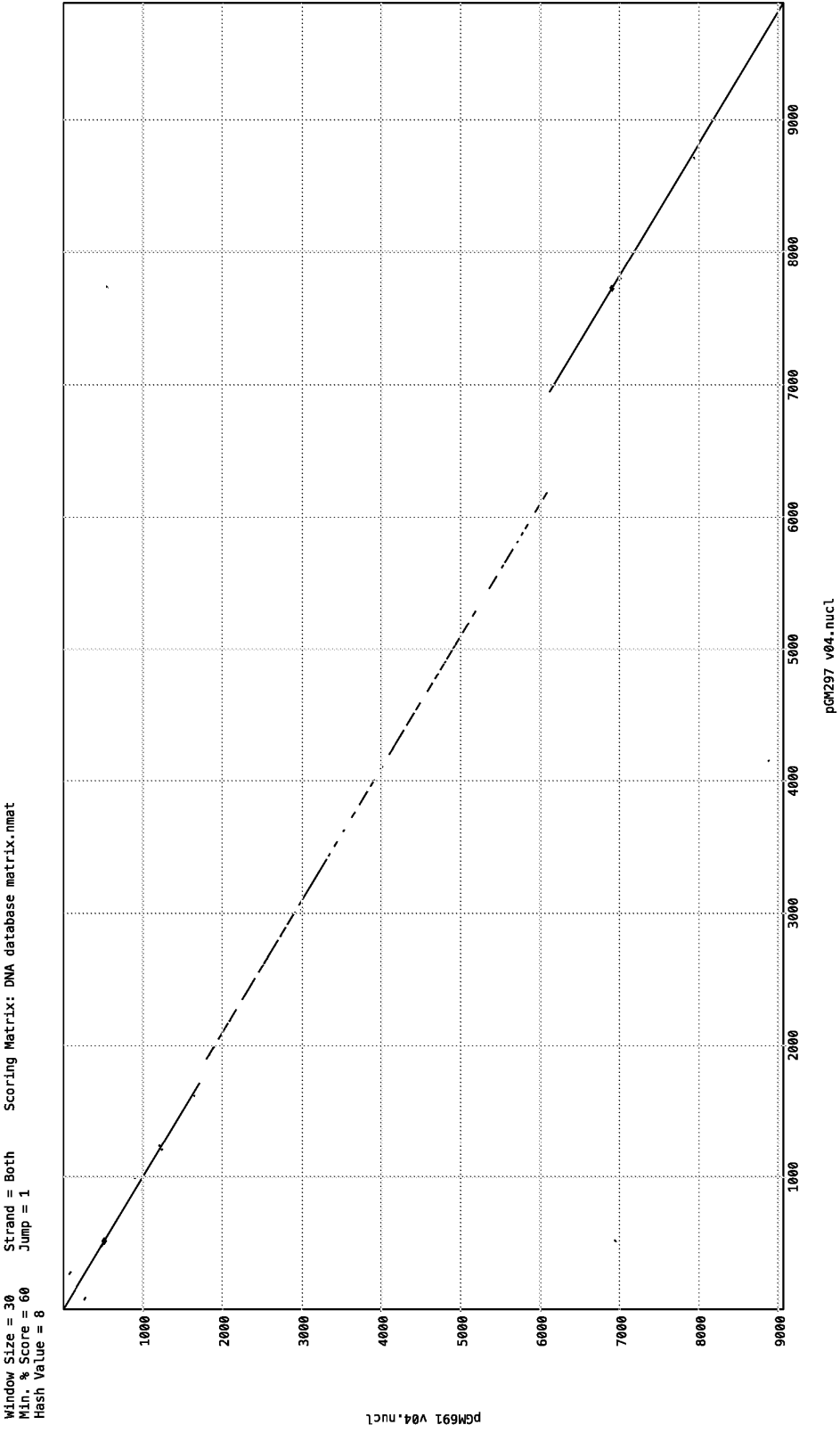


Figure 5B

Figure 5C



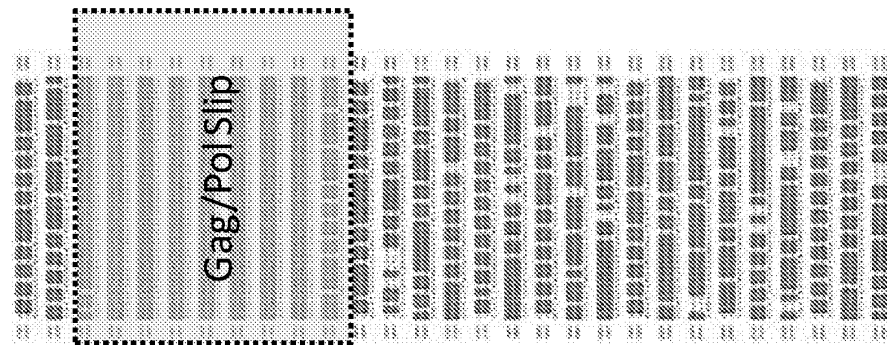
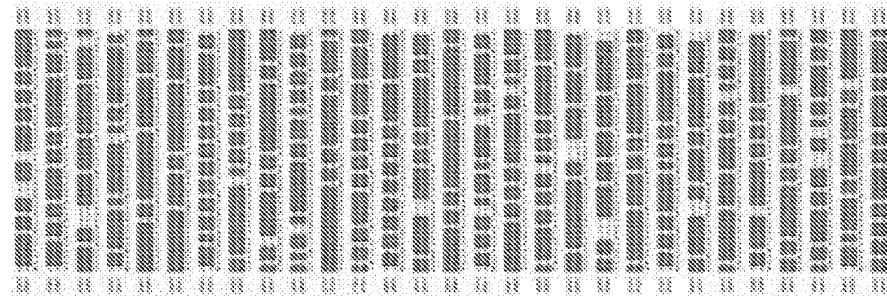
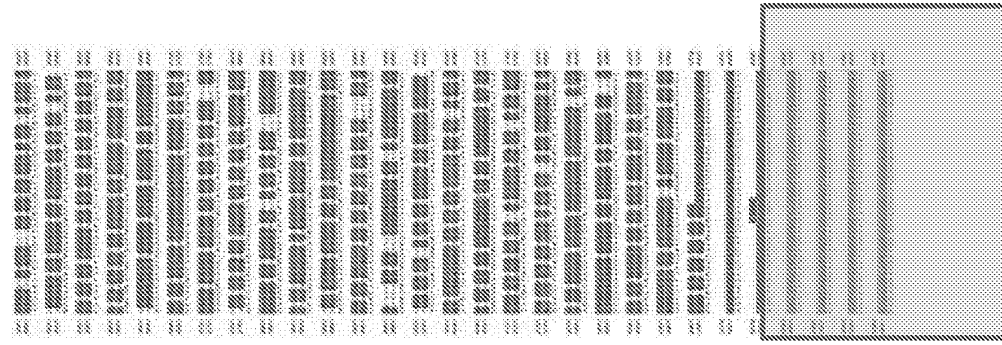
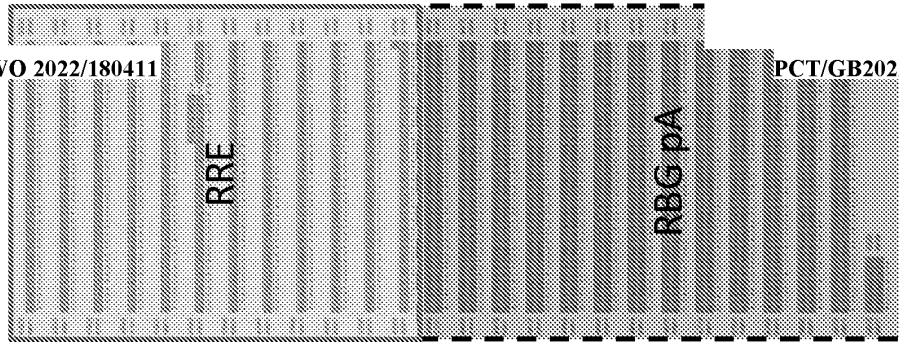


Figure 5D

Figure 5E

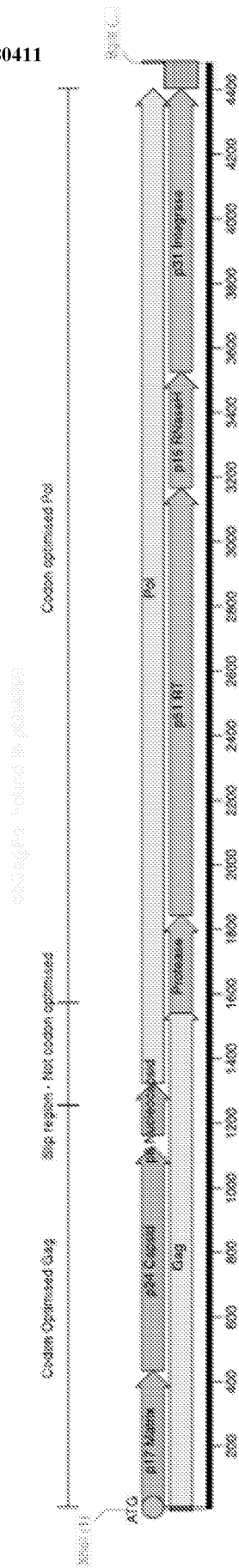


Figure 6

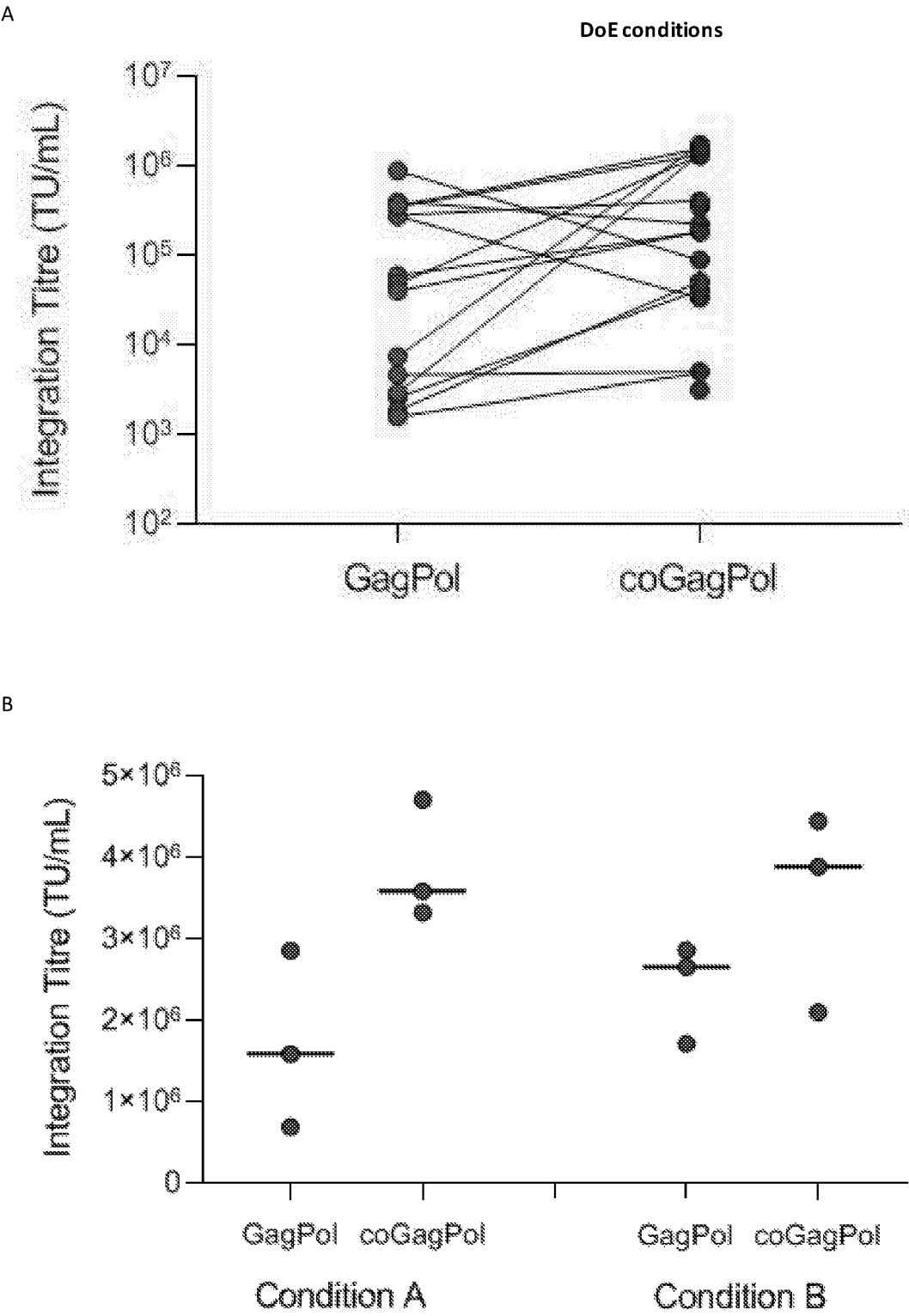
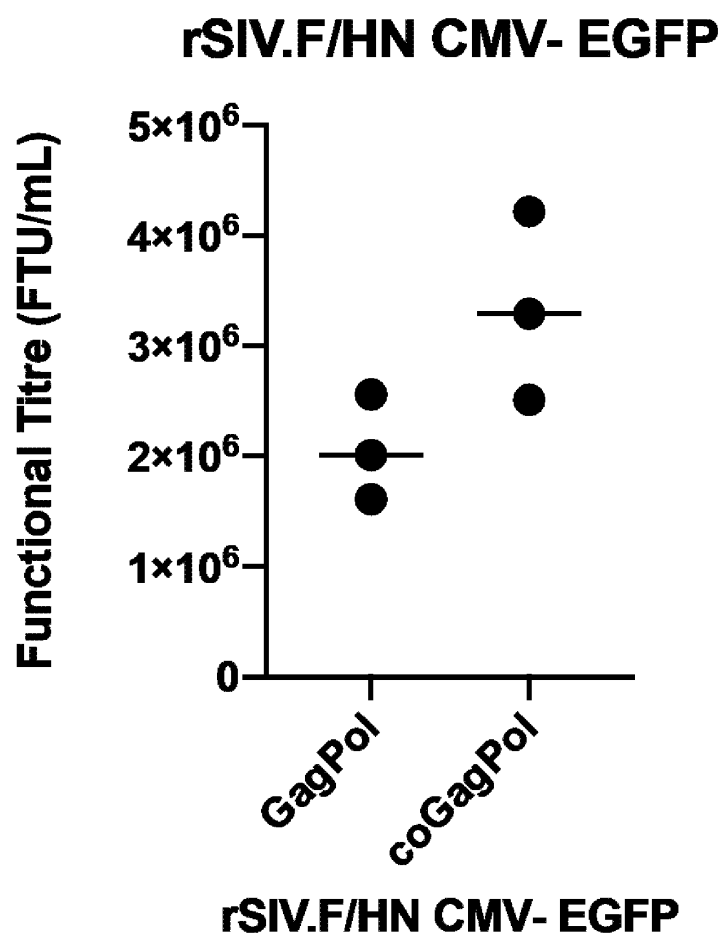
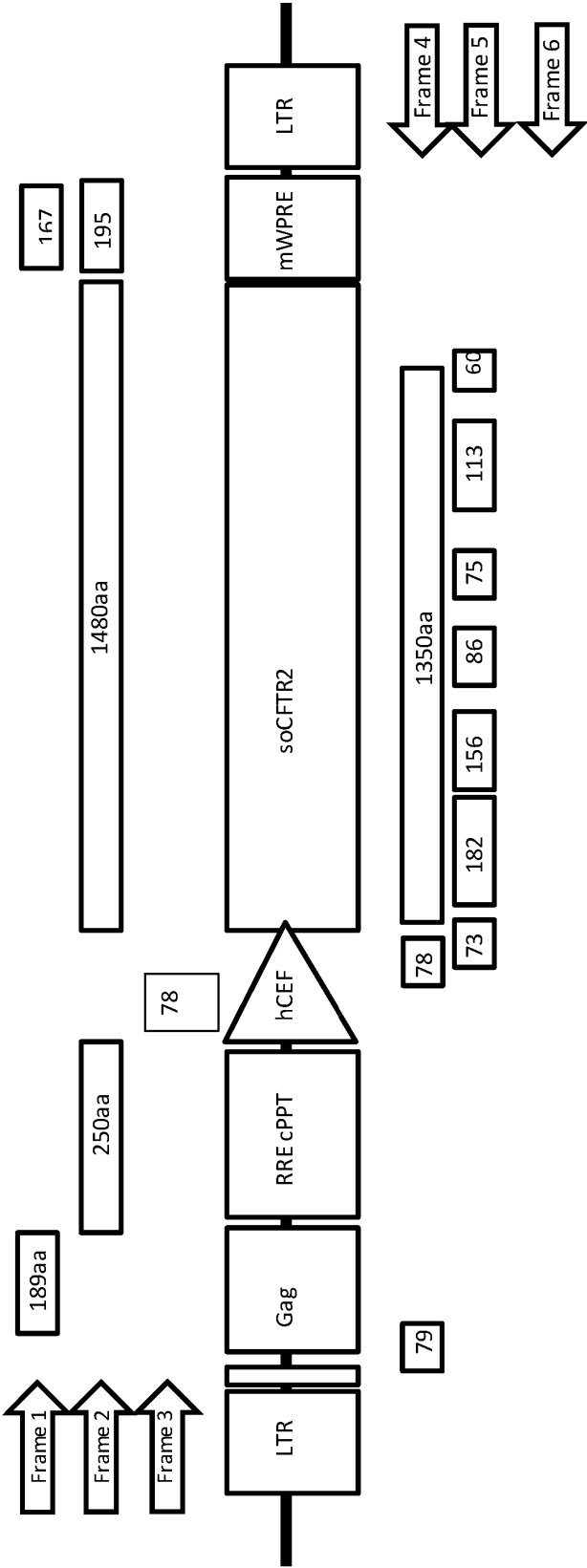


Figure 7



VGIM058 Genome (pGMS26 v04)

Figure 9



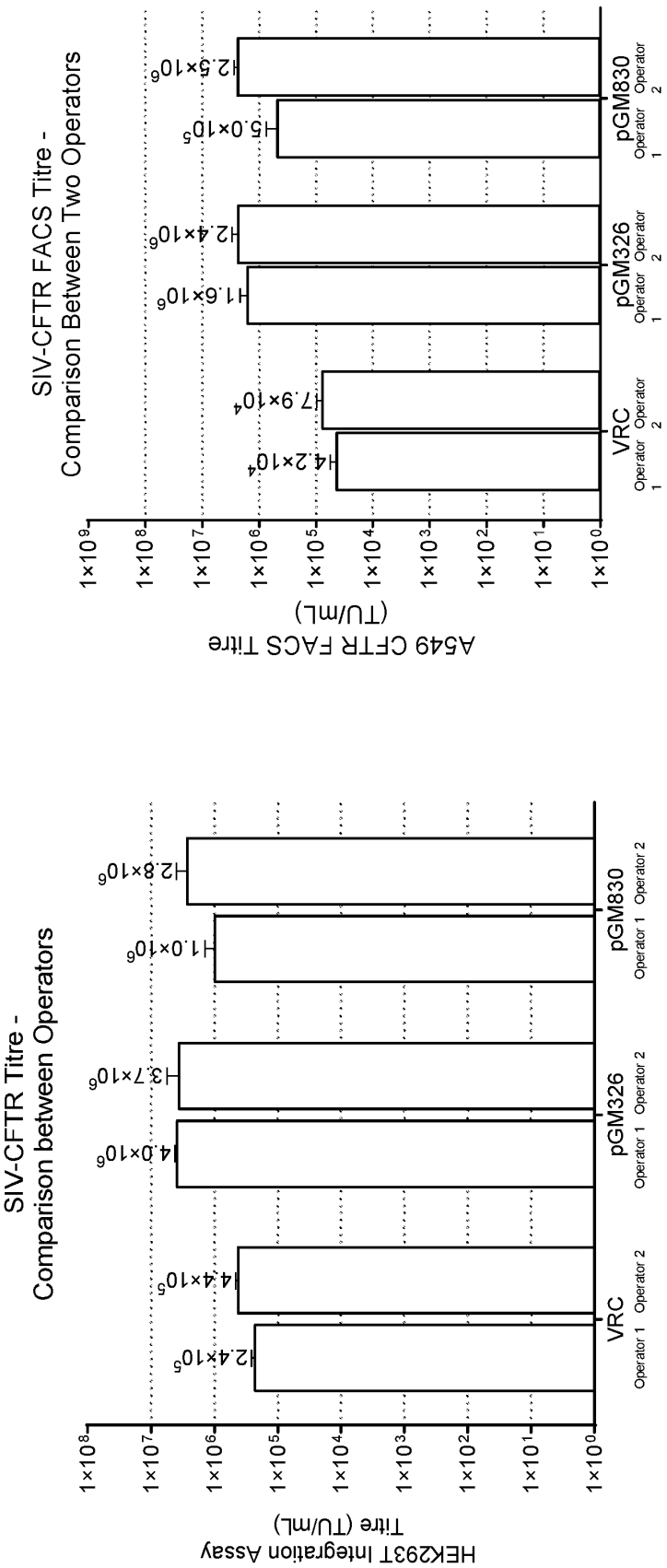


Figure 10

Figure 11

