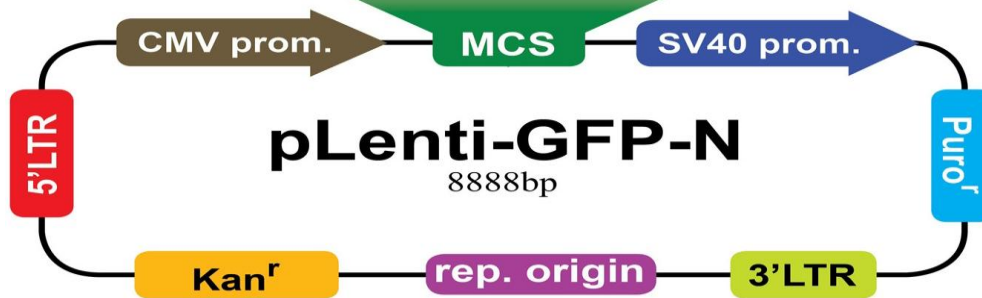


LV031

Vector Name	pLenti-III-GFP-N
VectorType	Lentiviral vector
Antibiotic Information	Puromycin
Sequencing Primers	CMV sequencing primer 5' ---CGC AAA TGG GCG GTA GGC GTG ---3'
	Reverse sequencing primer 5' ---TAG TCA GCC ATG GGG CGG AGA ---3'

5'-- ATG (In frame GFP Reporter) CAA TTG AGT ACT
MfeI *ScaI*
SnaBI *KpnI*
TAC GTA GGT ACC CCA GTG TGG TGG CCT GCA GGT
EcoRI *SpeI* *AgeI* *StuI* *Sall* *EcoRV*
GAA TTC ACT AGT ACC GGT AGG CCT GTC GAC GAT
ApaI *NotI* *BamHI* *XbaI*
ATC GGG CCC GCG GCC GCT GGA TCC TCT AGA CTG
XhoI *HA-Tag*
CAG CTC GAG TAC CCA TAC GAC GTC CCA GAC TAC
GCT TGA --3'



Sequence

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Genebank

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Text Map

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 HIV-1_psi_pack other (1006,1050)>>>
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 RRE reg (1557,1790)>>>
 |
 1501 gcacccaccaaggcaagagaagagtggtgcagagagaaaaagagcagtggaatagga 1560
 CGTGGGTGGTTCCGTTCTCTCTCACCACGCTCTCTTTTTTCTCGTCACCCCTTATCCT
 ORF_1 rf (1) (1600,2301)>>>
 |
 1561 gctttgttcttgggttcttgggagcagcaggaagcactatggcgagcgtcaatgacg 1620
 CGAAACAAGGAACCAAGAACCCTCGTCGTCCTTCGTGATACCCGCGTCGAGTTACTGC
 1621 ctgacggtacaggccagacaattatgtctgtatagtgacagcagacaacaattgtctg 1680
 GACTGCCATGTCCGGTCTGTTAATAACAGACCATATCACGTCGTCGCTTGTAAACGAC
 1681 agggctattgagcgcacagcatctgttgaactcacagctctggggcatcaagcagctc 1740
 TCCCGATAACTCCGCTTGTCTGAGACAACGTTGAGTGTGACACCCCGTAGTTCTGTCGAG

1741 caggcaagaatcctggctgtgaaagatacctaaggatcaacagctcctggggatttg 1800
GTCCGTTCTTAGGACCGACACCTTCTATGGATTTCCTAGTTGTCGAGGACCCCTAAAC

1801 ggttgctctgaaaaactcatttgaccactgctgtgccttggaatgctagttggagtaat 1860
CCAACGAGACCTTTTGAGTAAACGTGGTGACGACACGGAACTTACGATCAACCTCATTA

1861 aaatctctggaacagatttggaaatcacacgacctggatggagtgaggacagagaaattaac 1920
TTTAGAGACCTTGTCTAAACCTTAGTGTGCTGGACCTACCTCACCTGTCTCTTTAATTG

1921 aattacacaagcttaatacactccttaattgaagaatcgaaaaccagcaagaaaagaat 1980
TTAATGTGTTCGAATTATGTGAGGAATTAACCTTCTTAGCGTTTTGGTCGTTCTTTTCTTA

1981 gaacaagaattattggaattagataaaatgggcaagtttgggaattggtttaacataaca 2040
CTTGTCTTAATAACCTTAATCTATTTACCCGTTCAAACACCTTAACCAATTGTATTGT

2041 aattggctgtggtatataaaaattattcataatgatagtaggaggcttgtaggtttaaga 2100
TTAACCGACACCATATATTTAATAAGTATTACTATCATCTCCGAACCATCCAAATTC

2101 atagttttgctgtactttctatagtaatagagtaggagggatattcaccattatcg 2160
TATCAAAAACGACATGAAAGATATCACTTATCTCAATCCGTCCTATAAGTGGTAATAGC

2161 tttcagaccacacctcccaaccccgaggggacccgacaggcccgaaggaatagaagaagaa 2220
AAAGTCTGGGTGGAGGTTGGGGCTCCCTGGGCTGTCCGGGCTTCTTATCTTCTTCTT

2221 ggtggagagagagacagagacagatccattcgattagtgaacggatctcgacggtatcga 2280
CCACCTCTCTCTGTCTCTGTCTAGGTAAGCTAATCACTTGCCTAGAGTGCATAGCT

2281 aagcttgggattcgaatttaaaagaaaagggggattgggggtacagtcaggggaaag 2340
TTCGAACCTAAGCTTAAATTTCTTTTCCCCCTAACCCCATGTCACGTCCTCCCTTC

2341 aatagtagacataatagcaacagacatacaaaactaagaactacaaaaacaaattacaaa 2400
TTATCATCTGTATTATCGTTGTCTGTATGTTTGATTCTTGATGTTTTTGTTAATGTTT

2401 aattcaaaatthttgggtttttcgaacctagggttcccggttacataacttacggtaaat 2460
TTAAGTTTTAAAAGCCAAAAAGCTTGGATCCAAGGCGCAATGTATTGAATGCCATTTA

2461 ggccccctggctgaccgccccacgccccgcccattgacgtcaataatgacgtatggt 2520
CCGGGCGGACCGACTGGCGGGTTGCTGGGGCGGGTAACTGCAGTTATTACTGCATACAA

2521 cccatagtaacgccaatagggaactttccattgacgtcaatgggtggagtatttacggtaa 2580
GGGTATCATTTGCGTTATCCCTGAAAGGTAACGTCAGTTACCCACCTCATAAATGCCATT

NdeI
|

2581 actgccccacttggcagtacatcaagtgtatcatatgccaagtacgccccctattgacgtc 2640
TGACGGGTGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGGGATAACTGCAG

2641 aatgacggtaaatggccccctggcattatgcccagtacatgacctatgggactttcct 2700
TTACTGCCATTTACCGGGCGGACCGTAATACGGGTCATGTACTGGAATACCCCTGAAAGGA

2701 acttggcagtacatctacgttttagtcacgctattaccatgggtgatgcggttttggcagt 2760
TGAACCGTCATGTAGATGCAATCAGTAGCGATAATGGTACCCTACGCCAAAACCGTCA

2761 acatcaatggcggtgatagcggtttgactcaeggggatttccaagtctccaccccattg 2820
TGTAGTTACCCGCACCTATCGCCAAACTGAGTGCCCTAAAGGTTACAGGTTGGGGTAAC

2821 acgtcaatgggagtttgttttggcaccaaaatcaacgggactttccaaaatgtcgtaaca 2880
TGCAGTTACCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCATTGT

CMV prom (2885, 2966) >>>
|

2881 actccgccccattgacgcaaatggcggttagcggtgacggtgggaggtctatataagca 2940
TGAGGCGGGGTAACGCGTTTACCCGCCATCCGCACATGCCACCTCCAGATATATTCGT

ORF_5 rf (5) (2960, 3997) <<<
|

2941 gagctcgttttagtgaaccgtcagatcgctggagacgcatccacgctgttttgacctcc 3000

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CTGAGCAAATCACTTGGCAGTCTAGCGGACCTCTGCGGTAGGTGCGACAAAACCTGGAGG

tetO reg(3022,3061)>>>
|
3001 atagaagaaccgagtttaaacctccctatcagtgatagagatccctatcagtgatagag 3060
TATCTTCTTGGCTCAAATTTGAGGGATAGTCACTATCTCTAGAGGGATAGTCACTATCTC

EGFP reporter(3068,3784)>>>
|
ORF_3 rf(2)(3068,3934)>>>
|
3061 agctagcatggtgagcaagggcgaggagctgttcaccgggggtggtgcccacctcctggtoga 3120
TCGATCGTACCCTCGTTCCCGCTCCTCGACAGTGGCCCCACCACGGGTAGGACCAGCT

3121 gctggaaggcgacgtaaacggccacaagttcagcgtgtccggcgagggcgagggcgatgc 3180
CGACCTGCCGCTGCATTTGCCGGTGTTCAGTGCACAGGCCGCTCCCGCTCCCGCTACG

3181 cacctacggcaagctgaccctgaagttcactctgcaccaccggcaagctgcccgtgcccctg 3240
GTGGATGCCGTTTCGACTGGGACTTCAAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGAC

3241 gcccaccctcgtgaccaccctgaactacggcgtgacgtgctcagccgctacccccgaacca 3300
CGGGTGGGAGCACTGGTGGGACTGGATGCCGCACGTCACGAAGTCGGCGATGGGGCTGGT

3301 catgaagcagcagcactcttcaagtcgccaatgcccgaaggctacgtccaggagcgcac 3360
GTACTTCGTCGTGCTGAAGAGTTCAGGCGGTACGGGCTTCCGATGCAGGTCTCCGCTG

3361 catcttttcaaggacgacggcaactacaagaccgcgcccaggtgaagttcaggggoga 3420
GTAGAAGAAGTTCCTGCTGCCGTTGATGTCTGGGCGCGGCTCCACTTCAAGCTCCCGCT

3421 caccctggtgaaccgcatcgagctgaaggcctcgaactcaaggaggacggcaacatcct 3480
GTGGGACCACTTGGCGTAGCTCGACTTCCCGTAGCTGAAGTTCCTCCTGCCGTTGTAGGA

3481 ggggcacaagctggagtacaactacaacagccacaacgtctatcatggccgacaagca 3540
CCCCGTGTCGACCTCATGTTGATGTTGTTCGGTGTTCGAGATATAGTACCGGCTGTTTCGT

3541 gaagaacggcatcaaggtgaactcaagatccgccacaacatcgaggacggcagcgtgca 3600
CTCTTGCCGTAGTTCACCTTGAAGTTCAGGCGGTGTTGTAGCTCCTGCCGTCGACGCT

3601 gctcgcgaccactaccagcagaaccccccatggcgacggccccgtgctgctgcccga 3660
CGAGCGGCTGGTGTGATGGTCTGTTGGGGTAGCCGCTGCCGGGGCACGACGACGGGCT

3661 caaccactacctgagcaccagtcgcccctgagcaaaagccccaacgagaagcgcgatca 3720
GTTGGTGTGACTCGTGGGTGAGGCGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGT

3721 catggtcctgctggagttcgtgacgcgcccgggatcactctcgccatggacgagctgta 3780
GTACCAGGACGACCTCAAGCACTGGCGGGCGCCCTAGTGAGAGCCGTACTGTCTCGACAT

KpnI EcoRI
| |
3781 caagcaattgagtaacttacgtaggtacccagtggtggtgcccctgaggtgaattcactag 3840
GTTTCGTTAACTCATGAATGCATCCATGGGGTACACCACCGGACGTCACCTTAAGTGATC

NotI
|
StuI EcoRV ApaI BamHI XbaI
| | | | |
3841 taccggtaggcctgtcgacgatatcgggcccgcggccgctggatcctctagactgcagct 3900
ATGGCCATCCGGACAGCTGCTATAGCCCGGGCGCCGGCGACCTAGGAGATCTGACGTCGA

XhoI SV40 prom(3949,4217)>>>
| |
3901 cgagtaaccatacgacgtcccagactacgcttgagtttaaacacgcgtggtgtggaagt 3960
GCTCATGGGTATGCTGCAGGGTCTGATGCGAACTCAAATTTGTGCGCACCCACCTTTCA

3961 ccccaggctcccagcaggcagaagtatgcaaagcatgcatctcaattagtcagcaacca 4020
GGGGTCCGAGGGGCTCCGCTTCATACGTTTCGTACGTAGAGTTAATCAGTCTGTTGGT

4021 ggtgtggaagtcccaggctcccagcaggcagaagtatgcaaagcatgcatctcaatt 4080

```

CCACACCTTTCAGGGTCCGAGGGTCCGTCCTTCATACGTTTCGTACGTAGATTAA

SV40 origin (4116,4193)>>>

4081 agtcagcaaccatagtagcccccactccgcccacccgcccactccgcccagtt 4140
TCAGTCGTTGGTATCAGGGCGGGATGAGGCGGGTAGGGCGGGATTGAGGCGGGTCAA

ORF_2 rf(1) (4183,4851)>>>

4141 ccgcccattctccgcccattggtgactaattttttttttatgagagccgagccg 4200
GGCGGTAAGAGGCGGGTACCGACTGATTAATAAATAAATACGTCCTCCGGTCCGGC

SfiI puro marker (4252,4851)>>>

4201 cctcggcctctgagctattccagaagtagtgaggagcttttttggaggccatgaccgag 4260
GGAGCCGGAGACTCGATAAGGCTTTCATCACTCCTCCGAAAAACCTCCGGTACTGGCTC

4261 tacaagcccacggtgcgctcgcaccgagcagcgtccctcgggcccgtacgcaecctc 4320
ATGTTTCGGGTGCCACGCGAGCGGTGGGCGCTGCTGCAGGGAGCCCGGCATGCGTGGGAG

4321 gccgcgcgcttcgcccactaccgcccacgcccacacccgtggaccggaccgcccacatc 4380
CGGCGCGCAAGCGGCTGATGGGGCGGTGCGCGGTGTGCACCTGGGCTGGCGGTGTAG

4381 gagggggtcaccgagctgcaagaactcttctcagcgcgctcgggctcgacatcggaag 4440
CTCGCCAGTGGCTCGACGTTCTTGAGAAGGAGTGCAGCGAGCCGAGCTGTAGCCGTTT

4441 gtgtgggtcgcggaacgagcgcgcccgggtggcgttgaccacgcccggagagcgtcga 4500
CACACCCAGCGCTGCTGCGCGGCCACCGCCAGACCTGGTGCAGGCTTCTCGCAGCTT

4501 gcggggggcgtgttcgcccagatcggcccgcgcatggccgagttgagcggttccggctg 4560
CGCCCCCGCCACAAGCGGCTCTAGCCGGGCGGTACCGGCTCAACTCGCCAAAGGGCCGAC

4561 gccgcgcagcaacagatggaaggctcctggcgcgcaaccggcccaggagcccgcgctgg 4620
CGGCGCGTCTGTTGCTACCTTCCCGAGGACCGCGCGTGGCCGGGTTCCTCGGGCCGACC

4621 ttcttgccaccgtcgggctctcgcggcaccaccagggaagggtctgggcagcgcgctc 4680
AAGGACCGGTGGCAGCCGAGAGCGGGCTGGTGGTCCCGTTCAGACCCGTCGCGGCAG

4681 gtgctccccgagtgaggcggccgagcgcgcccgggtgcccgccttctggagacctcc 4740
CACGAGGGGCTTACCTCCGCGGCTCGCGCGGCCACGGGCGGAAGGACCTCTGGAGG

4741 gcgcccgcgaacctcccccttctagagcggctcggcttaccgtaaccgcccagctcgag 4800
CGCGGGGCTTGGAGGGGAAGATGCTCGCCGAGCCGAAGTGGCAGTGGCGGCTGCAGCTC

4801 gtgcccgaaggaccgcaacctggtgcatgaccgcaagcccgggtgcctgaacgcttcc 4860
CACGGGCTTCTGGCGCGTGGACCACTACTGGGCGTTCGGGCCAGGACTTGCAGCAAGG

4861 ggaatcaacctctggattacaaaattgtgaaagattgactggtattcttaactatggt 4920
CCTTTAGTTGGAGACCTAATGTTTAAACACTTCTTAAGTACCATAGTACGATAACGATAA

4921 gctcctttacgctatgtggatacgtgctttaaagcctttgtatcatgctattgcttcc 4980
CGAGGAAATGCGATACCTATGCGACGAAATTACGAAACATAGTACGATAACGAAAGG

4981 cgtatggctttcattttctcctcctgtataaatcctggtgctgtctctttatgaggag 5040
GCATACCGAAAGTAAAGAGGAGGAACATATTTAGGACCAACGACAGAGAAATACCTCCT

5041 ttgtggcccgttgtaggcaacgtggcgtggtgactggtttgctgacgcaaccccc 5100
AACACCGGGCAACAGTCCGTTGCACCGCACACACGTTGACACAACGACTGCGTTGGGGG

5101 actggttgggcatgcccaccctgtcagctccttccgggactttcgtttccccctc 5160
TGACCAACCCGTAACGGTGGTGGACAGTCGAGGAAAGGCCCTGAAAGCGAAAGGGGGAG

5161 cctattgcaagcgggaactcatgcccctgcttgcgctgctggacaggggctcgg 5220
GGATAACGGTGCCGCTTGGTAGCGGGCGGACGGAACGGGCGACGACCTGTCCCGAGCC

5221 ctgttgggcaactgacaattccgtggtgttgcggggaagctgagctcctttccatgctg 5280
GACAACCCGTGACTGTTAAGGCACCACAACAGCCCCCTTCGACTGCAGGAAAGGTACCGAC

5281 ctgcctgtgttgccacctggattctgcgcgaggacgtccttctgctacgtcccttcggcc 5340
GAGCGGACACAACGGTGGACCTAAGACGCGCCCTGCAGGAAGACGATGCAGGGAAGCCGG

5341 ctcaatccagcggaccttccctcccgcgctgctgcggtctgctgcgctcttcccggt 5400
GAGTTAGGTCGCCTGGGAAGGGCGCCGACGACGCGCCGAGACGCGGAGAAGCGCA

5401 ctgccttcgcccagacagatoggatctccctttgggocgctccccgctgtccgga 5460
GAGCGGAAGCGGGAGTCTGCTCAGCCTAGAGGGAACCCGGCGGAGGGCGGACAGCCCT

delta_U3 other (5461,5513)>>> HIV-1_5_LTR other (5514,5694)>>>

5461 tggagggttaattcactcccaacgaatacaagatctgctttttgctgtactgggtctc 5520
ACCTTCCCATTAAAGTGAGGGTTCCTTATGTTCTTAGACGAAAACGAACATGACCCAGAG

5521 tctggttagaccagatctgagcctgggagctctctggctaactaggaaccactgetta 5580
AGACCAATCTGGTCTAGACTCGGACCCTCGAGAGACCGATTGATCCCTTGGGTGACGAAT

5581 agcctcaataaagcttgcttgagtgcttcaagtagtggtgcccgtctgttggtgact 5640
TCGGAGTTATTTGCAACGGAACCTCACGAAGTTCATCACACACGGGAGACAAACACTGA

5641 ctggttaactagagatccctcagacccttttagtcagtggtgaaaatctctagcagtagta 5700
GACCATTGATCTCTAGGGAGTCTGGGAAAATCAGTCACACCTTTTAGAGATCGTCTCAT

5701 gttcatgtcatcttattattcagttattataaacttgcaagaaatgaatacagagagtg 5760
CAAGTACAGTAGAATAATAAGTCATAAAATTTGAACGTTTCTTTACTTATAGTCTCTCAC

5761 agaggaacttgtttattgcagcttataatggttcaataaagcaatagcatcacaatt 5820
TCTCCTTGAAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAA

5821 tcacaaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatg 5880
AGTGTTTATTTTCGTAATAAAGTGACGTAAGATCAACACCAACAGGTTTGTAGTAGTTAC

5881 tatcttatcatgtctggcatctatgtcgggtgctggagaaagaggtaatgaaatggcatta 5940
ATAGAAATAGTACAGACCCGTAGATACAGCCACGCTCTTTCTCCATTACTTTACCGTAAT

5941 tgggtattatgggtctgcattaatgaatcgcccaacgatcccgggtgaaataccgcaca 6000
ACCCATAATACCCAGACGTAATTACTTAGCCGGTTGCTAGGGCCACACTTTATGGCGTGT

6001 gatgctgaaggagaaataaccgcatcaggcgtcttccgcttctcctcactgactgcgc 6060
CTACGCATTCCTCTTTATGGCGTAGTCCGCGAGAAGGCGAAGGAGCGAGTACTGAGCG

6061 tgcgctcgtgcttccgctcggcgagcgggtatcagctcactcaaaggcggtaatacgg 6120
ACGCGAGCCAGCAAGCCGACGCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCA

6121 tatccacagaatcaggggataacgcaggaagaacatgtgagcaaaaggccagcaaaagg 6180
ATAGGTGTCTTAGTCCCTATTGCGTCTTTCTTTGTACTCGTTTCCGGTCTGTTTCC

pBR322 origin (6200,6819)<<<

6181 ccaggaaccgtaaaaaggcgcggtgctggcggttttccataggctccgccccctgacg 6240
GGTCTTGGCATTTTTCCGGCGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGC

6241 agcatcaaaaaatcgacgctcaagtcagaggtggcgaaccggacaggactataaagat 6300
TCGTAGTGTTTTAGTGCAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATATTTCTA

6301 accaggcgtttccccctggaagctccctcgtgcgctctctggttccgacctgcccgetta 6360
TGGTCCGCAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAAT

6361 ccggatacctgtccgcctttctccctcgggaagcgtggcgctttctcatagctcagcgt 6420
GGCCTATGGACAGGCGGAAGAGGGGAAGCCCTTCGCACCGGAAAGAGTATCGAGTGGCA

6421 gtaggtatctcagttcgggtgtaggtcgttcgctccaagctgggctgtgtgcacgaacccc 6480
CATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTTCGACCCGACACCGTCTTGGGG

6481 ccggtcagcccagcgtgcgccttaccggtaactatcgtcttgagtcacacccggtaa 6540
GGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATT

6541 gacacgacttatcgccactggcagcagccactggtaacaggatttagcagagcgaggtatg 6600

CTGTGCTGAATAGCGGTGACCGTTCGTCGGTGACCATTGTCTAATCGTCTCGCTCCATAC

6601 taggcgggtgctacagagttcttgaagtggcctaactacggctacactagaaggacag 6660
ATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTGTCT

6661 tatttggtaactgctctgctgaagccagttaccttcggaaaaagagttggtagctctt 6720
ATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTCTCAACCATCGAGAA

6721 gatccggcaaaaaccaccgctggtagcgggtggttttttggttgcaagcagcagatta 6780
CTAGGCCGTTTGTGGTGGCGACCATCGCCACCAAAAAACAACGTTTCGTCTGCTAAT

6781 cgcgcagaaaaaaggatctcaagaagatcctttgatcttttctacggggtctgacgctc 6840
GCGCTCTTTTCTTAGAGTCTTCTTAGGAACTAGAAAAGATGCCCCAGACTCGCGAG

6841 agtggaaacgaaaactcagcttaagggattttggatcagattatcaaaaaggatcttca 6900
TCACCTTGCTTTTGGTGCATTCCTAAAACAGTACTCTAATAGTTTCTCTAGAAAGT

6901 cctagatccttttaataaaatgaagttttaaatacaatctaaagtataatagagtaaa 6960
GGATCTAGGAAAATTTAATTTTACTTCAAAATTTAGTTAGATTTTCAATATACTACTATT

6961 cttggtctgacagttaccaatgcttaacagtgaggcaccatctcagcagctgtctat 7020
GAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCCGTAGACAGATA

7021 ttctgtcctcagtagttgcctgactccccgtctgttagataactacgatacgggagggct 7080
AAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGA

7081 taccatctggccccagtgctgcaatgataccgagagaccacgctcaccggctccagatt 7140
ATGGTAGACCCGGGTACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGCTAA

7141 tatcagcaataaaccagccagccggaagggccgagcgcagaagtggctcctgcaactttat 7200
ATAGTCGTTATTTGGTCGTCGGCCTTCCCGCTCGCGTCTTACCAGGACGTTGAAATA

7201 ccgctccatccagctctatattgttgcgggaagctagagtaagtagttccagctta 7260
GGCGGAGGTAGGTACGATAATTAACAACGGCCCTTCGATCTCATTCAATCAAGCGGTCAAT

7261 atagtttgcgcaactgttgaaaaaggaactcctacctagatccttttccagtagaaagc 7320
TATCAAACGCGTTGCAACAACCTTTTCCTAGAAGTGGATCTAGGAAAAGTGCATCTTTCG

7321 cagtcgcgagaaacgggtgctgaccccgatgaatgtcagctactgggctatctggacaag 7380
GTCAGGCGTCTTTGCCACGACTGGGGCTACTTACAGTCGATGACCCGATAGACCTGTTC

7381 ggaaaaacgcaagcgcaagagaaagcaggtagcttgcagtggttacctatggcgatagct 7440
CCTTTGCGTTTCGCTTCTCTTTCGTCCTCGAACGTCACCCGAATGTACCCTATCGA

NEOKAN prom (7472, 7521) >>>

|

7441 agactggcggttttatggacagcaagcgaaccggaattgccagctggggcgccctctgg 7500
TCTGACCCGCCAAAATACCTGTCTGCTTGGCCTTAACGGTCGACCCCGGGGAGACC

7501 taaggttgggaagccctgcaaagtaaaactggatggctttctcggcccaaggatctgatg 7560
ATTCCAACCCTTCGGGACGTTTCATTGACCTACCGAAAAGAGCGGGGTTCTTAGACTAC

NTP_II marker (7613, 8401) >>>

|

BeII ORF_4 rf (2) (7610, 8404) >>>

| |

7561 ggcaggggatcaagctctgatcaagagacagatgaggatcgtttcgcattgattgaaca 7620
CGCGTCCCCTAGTTCGAGACTAGTTCTCTGCTTACTCCTAGCAAAGCGTACTAAGTGT

7621 agatggattgacgcaggttctcggccgcttgggtggagaggctattcggctatgactg 7680
TCTACCTAACGTGCGTCCAAGAGGCCGGCAACCCACCTCTCCGATAAGCCGATACGAC

7681 ggcacaacagacaatcggtgctctgatgcccogtgttcoggtgtcagcgcaggggagc 7740
CCGTGTTGCTGTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCCG

7741 cccggttcttttgcagaccgacctgtccgggtgcctgaatgaactgcaagacgagggc 7800
GGCCAAGAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGTCTCC

7801 agcgcggctatcgtggctggccacgacggggttccttgccagctgtgctcgacgtgt 7860
TCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACCGCTCGACACGAGCTGCAACA

7861 cactgaagcgggaaggactggctgtattggcggaagtgcggggcaggatctcctgtc 7920
GTGACTTCGCCCTTCCTGACCGACGATAAACCCTTCACGGCCCCGCTTAGAGGACAG

7921 atctcaacctgctcctgcccagaaagtatccatcatggctgatgcaatgcccggctgca 7980
TAGAGTGGAAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGT

7981 tacgcttgatccggctacctgcccattcgaccaccaagcgaacatcgcatcgagcgagc 8040
ATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTGTAGCGTAGCTCGCTCG

8041 acgtactcggatggaagccggtcttctgcatcaggatgatctggacgaagagcatcagg 8100
TGCATGAGCCTACCTTCGCCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCCC

8101 gctcgcgccagccgaactgttcgccaggctcaaggcgagcatgcccgaaggcaggatct 8160
CGAGCGCGGTCCGCTTGACAAGCGGTCCGAGTTCGCTCGTACGGGTGCCGCTCCTAGA

8161 cgtcgtgacctatggcgatgctgcttgcgcaatatcatggtggaatggcgcttttc 8220
GCAGCACTGGGTACCCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAG

8221 tggattcatcgactgtggcggctgggtgtggcggaaccgctatcaggacatagcgttggc 8280
ACCTAAGTAGCTGACACCGCCGACCCACACCGCTGGCGATAGTCTGTATCGCAACCG

8281 taccctgatattgctgaagagcttggcggcgaatgggtgacccgcttctcctgcttta 8340
ATGGGCACATAAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAAT

8341 cggatcgcgcgtcccagcttcgcagcgcacgcttctatcgcttcttgacgagttctt 8400
GCCATAGCGCGGAGGCTAAGCGTCCGCTAGCGGAAGATAGCGGAAGAACTGCTCAAGAA

8401 ctgaattttgttaaaatTTTTGTTAAATCAGTCAATTTTTTAAACCAATAGCCGAAATCG 8460
GACTTAAACAATTTTTAAACAATTTAGTTCGAGTAAAAAATGGTTATCCGGCTTTAGC

f1 origin(8509,8814)<<<

|

8461 gcaacatcccctataaatcaaaagaatagaccggataggggtgagtggttccagttt 8520
CGTTGTAGGGAATATTTAGTTTTCTTATCTGGCGCTATCCCACTCACACAAGGTCAAA

8521 ggaacaagagtccactattaagaacgtggactccaacgtcaaaaggcgaacaaacgctct 8580
CCTTGTCTCAGGTGATAATTTCTTGCACCTGAGGTGCGAGTTTCCCGCTTTTTGGCAGA

8581 atcaggcgatggcccactacgtgaaccatcacccaaatcaagtttttgcggctcaggt 8640
TAGTCCCCTACCGGTGATGCACTTGGTAGTGGGTTTAGTTCAAAAAACGCCAGTCCA

8641 gccgtaagctctaaatcggaaccctaaaggagccccgatttagagcttgacggggaa 8700
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8701 agccgggaaacgtggcgagaaaggaaggaagaagcgaaggagcggcgctagggcgc 8760
TCGGCCGCTTGACCGCTCTTCTCCTCCCTTCTTTCGCTTTCCTCGCCCGCATCCCGC

8761 tggcaagtgtagcggctacgctgocgtaaccaccacaccogcgcgcttaatgcccgc 8820
ACCGTTCACATCGCCAGTGCACCGGCATTGGTGGTGTGGGCGCGCAATTACGCGGCGA

8821 acagggcgcgtccattcgccattcaggatcgaattaattcttaattaacatcatcaata 8880
TGTCCCGCGCAGGTAAGCGGTAAGTCTAGCTTAATTAAGAATTAATTGTAGTAGTTATT

8881 tatacct 8888
ATATGGAA

Features

5'-LTR
Start: 486 End: 2177
Original Location Description:
486..2177
CMV Pro
Start: 2433 End: 3061
Original Location Description:
2433..3061
GFP

Start: 3068 End: 3784
Original Location Description:
3068..3784
SV40
Start: 3949 End: 4251
Original Location Description:
3949..4251
Pur
Start: 4252 End: 4851
Original Location Description:
4252..4851
3'-LTR
Start: 5937 End: 4852 (Complementary)
Original Location Description:
complement(5937..4852)
Kan
Start: 7610 End: 8401
Original Location Description:
7610..8401

GENTAUR