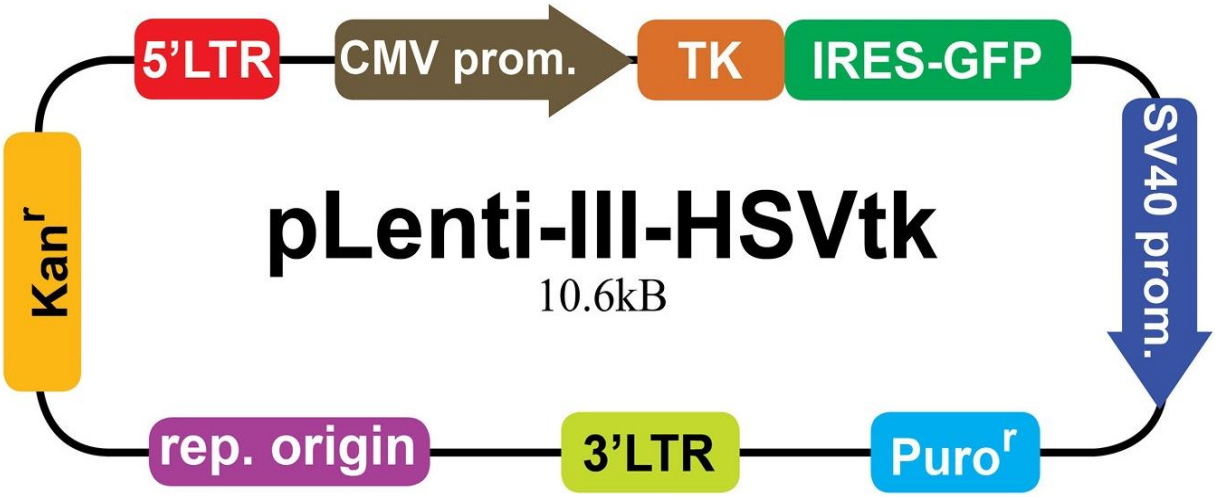
DATA SHEET

LV048

Vector Name	pLenti-III-HSVtk
VectorType	Lentivirus
Antibiotic Information	Puromycin
Sequencing Primers	CMV sequencing primer 5`---CGC AAA TGG GCG GATGGC GTG---3`



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541   caacatgccttacaaggagagaaaaagcaccgtgcatgccgattggtggaagtaaggtgg 600
        GTTGTACGGAATGTTCCTCTCTTTTTCGTGGCACGTACGGCTAACCACCTTCATTCCACC

601   tacgatcgtgccttattaggaaggcaacagacgggtctgacatggattggacgaaccact 660
        ATGCTAGCACGGAATAATCCTTCCGTTGTCTGCCCAGACTGTACCTAACCTGCTTGGTGA

                                                    HIV-1_5_LTR other(715,895)>>>
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661   gaattgccgcattgcagagatattgtatttaagtgcctagctcgatacataaacgggtct 720
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721   ctctggttagaccagatctgagcctgggagctctctggctaactagggaacccactgctt 780
        GAGACCAATCTGGTCTAGACTCGGACCCTCGAGAGACCGATTGATCCCTTGGGTGACGAA

781   aagcctcaataaagcttgccttgagtgcttcaagtagtgtgtgcccgtctgttgtgtgac 840
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841   tctggtaactagagatccctcagacccttttagtcagtgtggaaaatctctagcagtggc 900
        AGACCATTGATCTCTAGGGAGTCTGGGAAAATCAGTCACACCTTTTAGAGATCGTCACCG

901   gcccgaacagggacttgaaagcgaaagggaaaccagaggagctctctcgacgcaggactc 960
        CGGGCTTGTCCCTGAACTTTCGCTTTCCCTTTGGTCTCCTCGAGAGAGCTGCGTCCTGAG

                                              HIV-1_psi_pack other(1006,1050)>>>
                                                                  |
961   ggcttgctgaagcgcgcacggcaagaggcgaggggcggcgactggtgagtacgccaaaaa 1020
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1081  ggagaattagatcgcgatgggaaaaaattcggttaaggccaggggggaaagaaaaaatata 1140
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1141  aattaaaacatatagtatgggcaagcagggagctagaacgattcgcagttaatcctggcc 1200
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1201  tgttagaaacatcagaaggctgtagacaaatactgggacagctacaaccatcccttcaga 1260
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1261  caggatcagaagaacttagatcattatataatacagtagcaaccctctattgtgtgcatc 1320
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1321  aaaggatagagataaaagacaccaaggaagctttagacaagatagaggaagagcaaaaca 1380
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1381  aaagtaagaccaccgcacagcaagcccgctgatcttcagacctggaggaggagatatgag 1440
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1441  ggacattggagaagtgaattatataaatataaagtagtaaaaattgaaccattaggagta 1500
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                                                        RRE reg(1557,1790)>>>
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1501  gcacccaccaaggcaaagagaagagtggtgcagagagaaaaaagagcagtgggaatagga 1560
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                                                  ORF_1 rf(1)(1600,2301)>>>
                                                                  |
1561  gctttgttccttgggttcttgggagcagcaggaagcactatgggcgcagcgtcaatgacg 1620
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1621  ctgacggtacaggccagacaattattgtctggtatagtgcagcagcagaacaatttgctg 1680
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1681  agggctattgaggcgcaacagcatctgttgcaactcacagtctggggcatcaagcagctc 1740
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1741  caggcaagaatcctggctgtggaaagatacctaaaggatcaacagctcctggggatttgg 1800
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1801  ggttgctctggaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaat 1860
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1861  aaatctctggaacagatttggaatcacacgacctggatggagtgggacagagaaattaac 1920
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1921  aattacacaagcttaatacactccttaattgaagaatcgcaaaaccagcaagaaaagaat 1980
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1981  gaacaagaattattggaattagataaatgggcaagtttgtggaattggtttaacataaca 2040
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2041  aattggctgtggtatataaaattattcataatgatagtaggaggcttggtaggtttaaga 2100
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2101  atagtttttgctgtactttctatagtgaatagagttaggcagggatattcaccattatcg 2160
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2221  ggtggagagagagacagagacagatccattcgattagtgaacggatctcgacggtatcga 2280
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2281  aagcttgggattcgaatttaaaagaaaaggggggattgggggtacagtgcaggggaaag 2340
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2341  aatagtagacataatagcaacagacatacaaactaaagaactacaaaaacaaattacaaa 2400
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2401  aattcaaaattttcgggtttttcgaacctagggttccgcgttacataacttacggtaaat 2460
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                                                     |
2581  actgcccacttggcagtacatcaagtgtatcatatgccaagtacgccccctattgacgtc 2640
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2641  aatgacggtaaatggcccgcctggcattatgcccagtacatgaccttatgggactttcct 2700
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2701  acttggcagtacatctacgtttagtcatcgctattaccatggtgatgcggttttggcagt 2760
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2761  acatcaatgggcgtggatagcggtttgactcacggggatttccaagtctccaccccattg 2820
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2821  acgtcaatgggagtttgttttggcaccaaaatcaacgggactttccaaaatgtcgtaaca 2880
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2941  gagctcgtttagtgaaccgtcagatcgcctggagacgccatccacgctgttttgacctcc 3000
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                                        tetO reg(3022,3061)>>>
                                                |
3001  atagaagaaccgagtttaaactccctatcagtgatagagatctccctatcagtgatagag 3060
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                                     ORF_5 rf(3)(3078,4298)>>>
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3061  actagacggtcgccaccatggcctcgtaccccggccatcaacacgcgtctgcgttcgacc 3120
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3121  aggctgcgcgttctcgcggccatagcaaccgacgtacggcgttgcgccctcgccggcagc 3180
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3241  acggtccccacgggatggggaaaaccaccaccacgcaactgctggtggccctgggttcgc 3300
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3361  agacaatcgcgaacatctacaccacacaacaccgcctcgaccagggtgagatatcggccg 3420
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3481  ccgacgccgttctggctcctcatatcgggggggaggctgggagctcacatgccccgcccc 3540
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3541  cggccctcaccctcatcttcgaccgccatcccatcgccgccctcctgtgctacccggccg 3600
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3601  cgcggtaccttatgggcagcatgacccccaggccgtgctggcgttcgtggccctcatcc 3660
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3661  cgccgaccttgcccggcaccaacatcgtgcttggggcccttccggaggacagacacatcg 3720
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3721  accgcctggccaaacgccagcgccccggcgagcggctggacctggctatgctggctgcga 3780
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3781  ttcgccgcgtttacgggctacttgccaatacggtgcggtatctgcagtgcggcgggtcgt 3840
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3841  ggcgggaggactggggacagctttcggggacggccgtgccgccccagggtgccgagcccc 3900
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3901  agagcaacgcgggcccacgaccccatatcggggacacgttatttaccctgtttcgggccc 3960
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3961  ccgagttgctggcccccaacggcgacctgtataacgtgtttgcctgggccttggacgtct 4020
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4021  tggccaaacgcctccgttccatgcacgtctttatcctggattacgaccaatcgcccgccg 4080
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4081  gctgccgggacgccctgctgcaacttacctccgggatggtccagacccacgtcaccaccc 4140
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                                                        SmaI
                                                         |
                                                       XmaI
                                                        | |
4141  ccggctccataccgacgatatgcgacctggcgcgcacgtttgcccgggagatgggggagg 4200
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                        EcoRI                    StuI
                          |                       |
4201  ctaacgaattcaattcactagtaccggtaggcctgtcgacgatatcgggcccgcggccgc 4260
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4261  tggatccggatccgcccctctccctccccccccccctaacgttactggccgaagccgcttg 4320
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                                          ires_emcv reg(4350,4850)>>>
                                                          |
4321  gaataaggccggtgtgcgtttgtctatatgttattttccaccatattgccgtcttttggc 4380
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4381  aatgtgagggcccggaaacctggccctgtcttcttgacgagcattcctaggggtctttcc 4440
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4501  gcttcttgaagacaaacaacgtctgtagcgaccctttgcaggcagcggaacccccccacct 4560
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4621  caaccccagtgccacgttgtgagttggatagttgtggaaagagtcaaatggctctcctca 4680
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4681  agcgtattcaacaaggggctgaaggatgcccagaaggtaccccattgtatgggatctgat 4740
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                                    ORF_6 rf(5)(4763,5698)<<<
                                                          |
4741  ctggggcctcggtgcacatgctttacatgtgtttagtcgaggttaaaaaaacgtctaggc 4800
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                                                  ORF_3 rf(2)(4850,5581)>>>
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4801  cccccgaaccacggggacgtggttttcctttgaaaaacacgatgataatatggccacaac 4860
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                          EGFP reporter(4862,5578)>>>
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4861  catggtgagcaagggcgaggagctgttcaccggggtggtgcccatcctggtcgagctgga 4920
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4981  cggcaagctgaccctgaagttcatctgcaccaccggcaagctgcccgtgccctggcccac 5040
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5041  cctcgtgaccaccctgacctacggcgtgcagtgcttcagccgctaccccgaccacatgaa 5100
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5101  gcagcacgacttcttcaagtccgccatgcccgaaggctacgtccaggagcgcaccatctt 5160
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5581  aagcggccgcgacctgcagctcgagtacccatacgacgtcccagactacgcttgagttta 5640
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5701  atctcaattagtcagcaaccaggtgtggaaagtccccaggctccccagcaggcagaagta 5760
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                                                        SV40 origin(5817,5894)>>>
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5821  cgcccctaactccgcccagttccgcccattctccgccccatggctgactaatttttttta 5880
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                                            SfiI
                                             |
                          ORF_2 rf(1)(5884,6552)>>>
                            |                 |
5881  tttatgcagaggccgaggccgcctcggcctctgagctattccagaagtagtgaggaggct 5940
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                                puro marker(5953,6552)>>>
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6001  cctcgggccgtacgcaccctcgccgccgcgttcgccgactaccccgccacgcgccacacc 6060
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6061  gtggacccggaccgccacatcgagcgggtcaccgagctgcaagaactcttcctcacgcgc 6120
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6121  gtcgggctcgacatcggcaaggtgtgggtcgcggacgacggcgccgcggtggcggtctgg 6180
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6181  accacgccggagagcgtcgaagcgggggcggtgttcgccgagatcggcccgcgcatggcc 6240
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6241  gagttgagcggttcccggctggccgcgcagcaacagatggaagggctcctggcgccgcac 6300
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6301  cggcccaaggagcccgcgtggttcctggccaccgtcggcgtctcgcccgaccaccagggc 6360
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6361  aagggtctgggcagcgccgtcgtgctccccggagtggaggcggccgagcgcgccggggtg 6420
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6481  accgtcaccgccgacgtcgaggtgcccgaaggaccgcgcacctggtgcatgacccgcaag 6540
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6541  cccggtgcctgaacgcgttccggaaatcaacctctggattacaaaatttgtgaaagattg 6600
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6601  actggtattcttaactatgttgctccttttacgctatgtggatacgctgctttaatgcct 6660
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6661  ttgtatcatgctattgcttcccgtatggctttcattttctcctccttgtataaatcctgg 6720
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6901  cgctgctggacaggggctcggctgttgggcactgacaattccgtggtgttgtcggggaag 6960
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                                    HIV-1_5_LTR other(7215,7395)>>>
                                                  |
7201  tttttgcttgtactgggtctctctggttagaccagatctgagcctgggagctctctggct 7260
      AAAAACGAACATGACCCAGAGAGACCAATCTGGTCTAGACTCGGACCCTCGAGAGACCGA

7261  aactagggaacccactgcttaagcctcaataaagcttgccttgagtgcttcaagtagtgt 7320
      TTGATCCCTTGGGTGACGAATTCGGAGTTATTTCGAACGGAACTCACGAAGTTCATCACA

7321  gtgcccgtctgttgtgtgactctggtaactagagatccctcagacccttttagtcagtgt 7380
      CACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGTCTGGGAAAATCAGTCACA

7381  ggaaaatctctagcagtagtagttcatgtcatcttattattcagtatttataacttgcaa 7440
      CCTTTTAGAGATCGTCATCATCAAGTACAGTAGAATAATAAGTCATAAATATTGAACGTT

7441  agaaatgaatatcagagagtgagaggaacttgtttattgcagcttataatggttacaaat 7500
      TCTTTACTTATAGTCTCTCACTCTCCTTGAACAAATAACGTCGAATATTACCAATGTTTA

7501  aaagcaatagcatcacaaatttcacaaataaagcatttttttcactgcattctagttgtg 7560
      TTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACAC

7561  gtttgtccaaactcatcaatgtatcttatcatgtctggcatctatgtcgggtgcggagaa 7620
      CAAACAGGTTTGAGTAGTTACATAGAATAGTACAGACCGTAGATACAGCCCACGCCTCTT

7621  agaggtaatgaaatggcattatgggtattatgggtctgcattaatgaatcggccaacgat 7680
      TCTCCATTACTTTACCGTAATACCCATAATACCCAGACGTAATTACTTAGCCGGTTGCTA
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7681  cccggtgtgaaataccgcacagatgcgtaaggagaaaataccgcatcaggcgctcttccg 7740
      GGGCCACACTTTATGGCGTGTCTACGCATTCCTCTTTTATGGCGTAGTCCGCGAGAAGGC

7741  cttcctcgctcactgactcgctgcgctcggtcgttcggctgcggcgagcggtatcagctc 7800
      GAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCATAGTCGAG

7801  actcaaaggcggtaatacggttatccacagaatcaggggataacgcaggaaagaacatgt 7860
      TGAGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTCTTGTACA

                                                pBR322 origin(7901,8520)<<<
                                                                      |
7861  gagcaaaaggccagcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgtttttcc 7920
      CTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTTTCCGGCGCAACGACCGCAAAAAGG

7921  ataggctccgccccctgacgagcatcacaaaaatcgacgctcaagtcagaggtggcgaa 7980
      TATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTT

7981  acccgacaggactataaagataccaggcgtttcccccctggaagctccctcgtgcgctctc 8040
      TGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAG

8041  ctgttccgaccctgccgcttaccggatacctgtccgcctttctcccttcgggaagcgtgg 8100
      GACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCTTCGCACC

8101  cgctttctcatagctcacgctgtaggtatctcagttcggtgtaggtcgttcgctccaagc 8160
      GCGAAAGAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCG

8161  tgggctgtgtgcacgaacccccgttcagcccgaccgctgcgccttatccggtaactatc 8220
      ACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAG

8221  gtcttgagtccaacccggtaagacacgacttatcgccactggcagcagccactggtaaca 8280
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8281  ggattagcagagcgaggtatgtaggcggtgctacagagttcttgaagtggtggcctaact 8340
      CCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGA

8341  acggctacactagaaggacagtatttggtatctgcgctctgctgaagccagttaccttcg 8400
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8401  gaaaaagagttggtagctcttgatccggcaaacaaaccaccgctggtagcggtggttttt 8460
      CTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTTTGGTGGCGACCATCGCCACCAAAAA

8461  ttgtttgcaagcagcagattacgcgcagaaaaaaaggatctcaagaagatcctttgatct 8520
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8521  tttctacggggtctgacgctcagtggaacgaaaactcacgttaagggattttggtcatga 8580
      AAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCCTAAAACCAGTACT

8581  gattatcaaaaaggatcttcacctagatccttttaaattaaaaatgaagttttaaatcaa 8640
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8641  tctaaagtatatatgagtaaacttggtctgacagttaccaatgcttaatcagtgaggcac 8700
      AGATTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTG

8701  ctatctcagcgatctgtctatttcgttcatccatagttgcctgactccccgtcgtgtaga 8760
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8761  taactacgatacgggagggcttaccatctggccccagtgctgcaatgataccgcgagacc 8820
      ATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGG

8821  cacgctcaccggctccagatttatcagcaataaaccagccagccggaagggccgagcgca 8880
      GTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTCGCGT

8881  gaagtggtcctgcaactttatccgcctccatccagtctattaattgttgccgggaagcta 8940
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8941  gagtaagtagttcgccagttaatagtttgcgcaacgttgttgaaaaaggatcttcaccta 9000
      CTCATTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACTTTTTCCTAGAAGTGGAT

9001  gatccttttcacgtagaaagccagtccgcagaaacggtgctgaccccggatgaatgtcag 9060
      CTAGGAAAAGTGCATCTTTCGGTCAGGCGTCTTTGCCACGACTGGGGCCTACTTACAGTC

9061  ctactgggctatctggacaagggaaaacgcaagcgcaaagagaaagcaggtagcttgcag 9120
      GATGACCCGATAGACCTGTTCCCTTTTGCGTTCGCGTTTCTCTTTCGTCCATCGAACGTC

                                                NEOKAN prom(9173,9222)>>>
                                                                      |
9121  tgggcttacatggcgatagctagactgggcggttttatggacagcaagcgaaccggaatt 9180
      ACCCGAATGTACCGCTATCGATCTGACCCGCCAAAATACCTGTCGTTCGCTTGGCCTTAA

9181  gccagctgggggcgccctctggtaaggttgggaagccctgcaaagtaaactggatggcttt 9240
      CGGTCGACCCCGCGGGAGACCATTCCAACCCTTCGGGACGTTTCATTTGACCTACCGAAA

                                                          BclI
                                                            |
9241  ctcgccgccaaggatctgatggcgcaggggatcaagctctgatcaagagacaggatgagg 9300
      GAGCGGCGGTTCCTAGACTACCGCGTCCCCTAGTTCGAGACTAGTTCTCTGTCCTACTCC
```

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                                NTP_II marker(9314,10102)>>>
                                                     |
                                ORF_4 rf(2)(9311,10105)>>>
                                                   |  |
9301  atcgtttcgcatgattgaacaagatggattgcacgcaggttctccggccgcttgggtgga 9360
        TAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCT

9361  gaggctattcggctatgactgggcacaacagacaatcggctgctctgatgccgccgtgtt 9420
        CTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAA

9421  ccggctgtcagcgcaggggcgcccggttctttttgtcaagaccgacctgtccggtgccct 9480
        GGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGA

9481  gaatgaactgcaagacgaggcagcgcggctatcgtggctggccacgacgggcgttccttg 9540
        CTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAAC

9541  cgcagctgtgctcgacgttgtcactgaagcgggaagggactggctgctattgggcgaagt 9600
        GCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCA

9601  gccggggcaggatctcctgtcatctcaccttgctcctgccgagaaagtatccatcatggc 9660
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9661  tgatgcaatgcggcggctgcatacgcttgatccggctacctgcccattcgaccaccaagc 9720
        ACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCG

9721  gaaacatcgcatcgagcgagcacgtactcggatggaagccggtcttgtcgatcaggatga 9780
        CTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACT

9781  tctggacgaagagcatcaggggctcgcgccagccgaactgttcgccaggctcaaggcgag 9840
        AGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTC

9841  catgcccgacggcgaggatctcgtcgtgacccatggcgatgcctgcttgccgaatatcat 9900
        GTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTA

9901  ggtggaaaatggccgcttttctggattcatcgactgtggccggctgggtgtggcggaccg 9960
        CCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGC

9961  ctatcaggacatagcgttggctacccgtgatattgctgaagagcttggcggcgaatgggc 10020
        GATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCG

10021 tgaccgcttcctcgtgctttacggtatcgccgctcccgattcgcagcgcatcgccttcta 10080
        ACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGAT

10081 tcgccttcttgacgagttcttctgaattttgttaaaatttttgttaaatcagctcatttt 10140
        AGCGGAAGAACTGCTCAAGAAGACTTAAAACAATTTTAAAAACAATTTAGTCGAGTAAAA

10141 ttaaccaataggccgaaatcggcaacatcccttataaatcaaaagaatagaccgcgatag 10200
        AATTGGTTATCCGGCTTTAGCCGTTGTAGGGAATATTTAGTTTTCTTATCTGGCGCTATC

                                f1 origin(10210,10515)<<<
                                                     |
10201 ggttgagtgttgttccagtttggaacaagagtccactattaaagaacgtggactccaacg 10260
        CCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGC

10261 tcaaagggcgaaaaaccgtctatcagggcgatggcccactacgtgaaccatcacccaaat 10320
        AGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGTTTA

10321 caagtttttgcggtcgaggtgccgtaaagctctaaatcggaaccctaaagggagccccc 10380
        GTTCAAAAAACGCCAGCTCCACGGCATTTCGAGATTTAGCCTTGGGATTTCCCTCGGGGG

10381 gatttagagcttgacggggaaagccggcgaacgtggcgagaaaggaagggaagaaagcga 10440
        CTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCT

10441 aaggagcgggcgctagggcgctggcaagtgtagcggtcacgctgcgcgtaaccaccacac 10500
        TTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTG

10501 ccgcgcgcttaatgcgccgctacagggcgcgtccattcgccattcaggatcgaattaatt 10560
        GGCGCGCGAATTACGCGGCGATGTCCCGCGCAGGTAAGCGGTAAGTCCTAGCTTAATTAA

        10561 cttaattaacatcatcaataatatacctt 10589
                GAATTAATTGTAGTAGTTATTATATGGAA
```

Features

5'-LTR

Start: 486 End: 2177

Original Location Description:

486..2177

CMV Promoter

Start: 2433 End: 3061

Original Location Description:

2433..3061

TK

Gentaur Molecular Products
Voortstraat 49
1910 Kampenhout, Belgium

Start: 3062 End: 4211
Original Location Description:
3062..4211
IRES-GFP
Start: 4269 End: 5591
Original Location Description:
4269..5591
SV40 Promoter
Start: 5650 End: 5952
Original Location Description:
5650..5952
Puro
Start: 5953 End: 6552
Original Location Description:
5953..6552
3'-LTR
Start: 7638 End: 6553 (Complementary)
Original Location Description:
complement(7638..6553)
Kana
Start: 9311 End: 10102
Original Location Description:
9311..10102

Gentaur Molecular Products
Voortstraat 49
1910 Kampenhout, Belgium