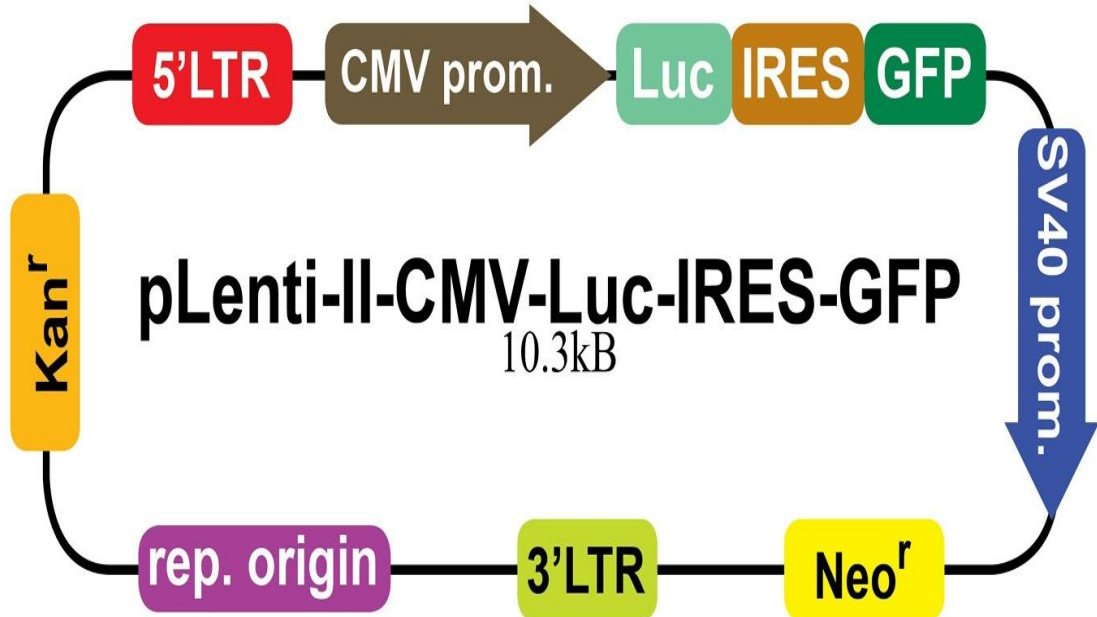


LV052

Vector Name	pLenti-II-CMV-Luc-IRES-GFP
VectorType	Lentivirus
Antibiotic Information	Neomycin
Sequencing Primers	CMV sequencing primer 5'---CGC AAA TGG GCG GATGGC GTG---3'



Sequence

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Genebank

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Gentaur Molecular Products
Voortstraat 49
1910 Kampenhout, Belgium

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 CACGCGCTCGTTTTAAATTCGATGTTGTTCCGTTCCGAACCTGGCTGTTAATTACATCAGA
 661 tatgcaatactctttagtcttgcacatggtaacgatgagttagcaacatgccttaaa 720
 ATACGTTATGAGAATCAGAACGTTGTACCATTTGCTACTCAATCGTTGTACGGAATGTT
 721 ggagagaaaaagcaocgtgcatgcccattggtggaagttaaggtgtagcagctgctgctta 780
 CCTCTCTTTTTTCGTGGCAGCTACGGCTAACACCTTCATTCACCATGCTAGCACGGAAAT
 781 ttaggaaggcaacagacgggtctgacatggattggacgaaccaatgcccattgc 840
 AATCCTTCGGTGTCTGCCCAGACTGTACTTAACCTGCTGGTGACTTAACGGCGTAACG

 HIV-1_5_LTR other(880,1060)>>>
 |
 841 agagatattgtatttaagtgcttagctcgatatacaaacgggtctctctggttagaccag 900
 TCTCTATAACATAAATTCACGGATCGAGCTATGTATTTGCCAGAGAGACCAATCTGGTC
 901 atctgagcctgggagctctctggtaactagggaaaccaactgcttaagcctcaataaagc 960
 TAGACTCGGACCTCGAGAGACCGATTGATCCCTTGGGTGACGAATTCGGAGTTATTTTCG
 961 ttgccttgagtgctcaagtagtgtgtgcccgtctgttgtgtagctctggtaactagaga 1020
 AACGGAATCAGCAAGTTCATCACACACGGGACGAACACACTGAGACCATTGATCTCT
 1021 tccctcagacccttttagtcagtggtgaaatctctagcagtgccgcccgaacagggact 1080
 AGGGAGTCTGGGAAATCAGTACACCTTTTAGAGATCGTCACCGCGGGCTTGTCCCTGA
 1081 tgaagcgaagggaaccagaggagctctctcgacgcaggactcggcttgctgaagcgc 1140
 ACTTTCGCTTTCCCTTTGGTCTCCTCGAGAGAGCTGCGTCTGAGCCGAACGACTTCGCG

 HIV-1_psi_pack other(1171,1215)>>>
 |
 1141 gcacggcaagaggcgagggggcgogactggtgagtagcgcacaaaattttgactagcggag 1200
 CGTGCCGTTCTCCGCTCCCGCCGCTGACCACCTCATGCGGTTTTTAAACTGATCGCCTC
 1201 gctagaaggagagatgggtgagagcgtcagttatgaagcgggggagaattagatcgc 1260
 CGATCTTCTCTCTTACCACGCTCTCGCAGTCATAATTCGCCCTCTTAATCTAGCG

 NruI
 |
 1261 gatgggaaaaaattcggttaagccaggggaaagaaaaataaaattaaaacatataag 1320
 CTACCTTTTTTAAGCCAATTCGGTCCCTTTCTTTTTTATATTTAATTTGTATATC
 1321 tatgggcaagcagggagctagaacgattcgcagttaatcctggcctgttagaacaatcag 1380
 ATACCGTTCGTCCTCGATCTGCTAAGCGTCAATTAGGACCGGACAATCTTTGTAGTC
 1381 aaggctgtagacaaaactgggacagctacaaccatccccttcagacaggatcagaagaac 1440
 TTCCGACATCTGTTATGACCCCTGTCGATGTTGGTAGGGAAGTCTGTCTTAGTCTTCTTG
 1441 ttagatcattatataatacagtagcaaccctctattgtgtgcatcaaggatagagataa 1500
 AATCTAGTAATATATATGTCATCGTTGGGAGATAACACACGTAGTTTCTATCTCTAT
 1501 aagacaccaaggaagcttttagacaagatagaggaagagcaaaaagaaagtaagaccaccg 1560
 TTCTGTGGTTCCTTCGAAATCTGTTCTATCTCCTTCTCGTTTTGTTTTTCAATCTGGTGGC
 1561 cacagcaagcgcgctgattctcagacctggaggagagatagagggacaattgagaag 1620
 GTGTCGTTCCGCGGACTAGAAAGTCTGGACCTCCTCCTCTATACTCCCTGTTAACTCTTC
 1621 tgaattatataataaaagtagtaaaaattgaaccattaggagtagcaccaccaagc 1680
 ACTTAATATATTTATATTTCAATTTTTAACTTGGTAATCCTCATCGTGGGTGGTTCCG

 RRE reg(1723,1956)>>>
 |
 1681 aaagagaagagtggtgagagagaaaaagagcagtgaggaaataggagctttgttccttg 1740
 TTTCTCTTCTCACCACGCTCTCTTTTTTCTCGTCACCTTATCCTCGAAACAAGGAACC

 ORF_3 rf(2)(1766,2569)>>>
 |
 1741 gttcttgggagcagcaggaagcactatgggagcagcgtcaatgacgctgacggtacaggc 1800
 CAAGAACCCTCGTCGTCCTTCGTGATACCGCGTCGCAGTTACTGCGACTGCCATGTCCG
 1801 cagacaattattgtctggtatagtgagcagcagacaatttctgagggtattgagc 1860
 GTCTGTTAATAACAGACCATATCACGTCGTCGTTGTTAAACGACTCCCGATAACTCCG
 1861 gcaacagcatctgttcaactcacagtctgggcatcaagcagctccaggcaagaatcct 1920
 CGTTGTCGTAGACAACGTTGAGTGTGACACCCGTTAGTTCGTCGAGGTCCGTTCTTAGGA
 1921 ggctgtggaagatacctaaggaatcaacagctcctgggatttggggttctctggaag 1980
 CCGACACCTTTCTATGGATTCTAGTTGTCGAGGACCCCTAAACCCCAACGAGACCTTT

1981 actcatttgaccactgctgtgccttggaatgctagttggagtaataaatctctggaaca 2040
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2041 gatttggaaatcacacgacctggatggagtgaggacagagaaattaacaattacacaagctt 2100
CTAAACCTTAGTGTGCTGGACCTACCTCACCCTGTCTCTTAATTGTTAATGTGTTTCGAA

2101 aatacactccttaattgaagaatcgcaaaaccagcaagaaagaatgaacaagaattatt 2160
TTATGTGAGGAATTAACCTCTTAGCGTTTGGTCTCTTTTCTTACTTGTCTTAATAA

2161 ggaattagataaaatgggcaagtttgggaattggtttaacatacaaaattggctgtggta 2220
CCTTAATCTATTTACCCGTTCAAACACCTTAACCAAAATTGATGTGTTAACCACACCAT

2221 tataaaattattcataatgatagtaggaggcttggtaggtttaagaatagtttttctgtg 2280
ATATTTAATAAGTATTAATCATCTCCGAACCATCCAATCTTATCAAAAACGACA

2281 actttctatagtagaataagtagtaggaggtatccaccattatcgtttcagaccacct 2340
TGAAGATATCACTTATCAATCCGTCCTATAAGTGGTAATAGCAAGTCTGGTGGGA

2341 cccaaccccgaggggaccgctagggttccgcgttacataacttaacggtaaatggcccg 2400
GGGTGGGGCTCCCTGGGCGATCCAAGGCGCAATGTATTGAATGCCATTTACCGGGCG

2401 ctggctgaccgccaacgacccccgccattgacgtcaataatgacgtatggtcccatag 2460
GACCGACTGGCGGGTGTCTGGGGCGGGTAACTGCAGTTATTACTGCATFACAAGGTATC

2461 taacgcaatagggactttccattgacgtcaatgggtggagatattacggtaaactgccc 2520
ATTGGGTTATCCCTGAAAGGTAACCTGCAGTTACCCACCTCAATAATGCCATTTGACGGG

NdeI
|

2521 acttggcagtagacaaagtgtatcatalgccaagtacgccccctattgacgtcaatgacg 2580
TGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGGGATAACTGCAGTTACTGC

2581 gtaaatggcccgctggcattatgccagtagacacttatggacttctactctggc 2640
CATTACCAGGGCGGACCGTAATACGGGTGATGACTGGAATACCTGAAAGGATGAACCG

2641 agtacatctacgtattagtcacgctattaccatgggtgacggttttggcagtagacca 2700
TCATGTAGATGCATAATCAGTAGCGATAATGGTACCACACTACGCCAAAACCGTCATGGT

2701 atggcggtggatagcggtttgactcaaggggatttccaagtctccacccattgacgtca 2760
TACCCGCACCTATCGCAAACAGTGCCTTAAAGGTTACAGAGTGGGGTAACCTGCAGT

CMV prom(2819,2900)>>>

2761 atgggagttgttttggcaccaaaatcaacgggacttttccaaaatgctgtaataaccccc 2820
TACCTCAAACAAAACCGTGGTTTAGTTCCTGAAAGGTTTACAGCATTATTGGGGC

2821 ccccgtagcgaatgggaggtgagcgtgacggtgggaggtctatataagcagagctc 2880
GGGGCAACTGCCTTACCAGCATCCGCACATGCCACCTCCAGATATATTCGTCTCGAG

2881 gtttagtgaacgtagcagtagcactagaagctttattgaggtgattatcacagttaaattg 2940
CAAACTCACTTGGCAGTCTAGTATCTCGAATAACGCCATCAAAATAGTGTCAATTTAAC

2941 ctaacgtagcagtagcttctgacacaacagctctcgaacttaagctgcagaagttggtcgt 3000
GATTGCGTCAGTACGAGACTGTGTTGTGTCAGAGCTGAATTCGACGCTTCAACCAGCA

chim_int other(3015,3147)>>>

3001 gaggaactgggaggttaagtagtcaaggttacaagacaggtttaaggagaccaatagaaac 3060
CTCCGTGACCCGTCCATTATAGTTCATAGTTCATAGTTCATAGTTCATAGTTCATAGTTC

3061 tgggctgtgagacagagaagactcttgcgttctgataggcactattggtcttactg 3120
ACCCGAACAGCTCTGTCTCTTCTGAGAACGCAAGACTATCCGTGGATAACCAAGATGAC

3121 acatccactttgcttctctccacaggtgtccactcccagttcaattacagctcttaag 3180
TGTAGGTGAAACGGAAGAGAGGTGCCACAGGTGAGGGTCAAGTTAATGTCGAGAATTC

BamHI
|

T7 prom(3192,3210)>>> ORF_1 rf(1)(3220,4155)>>>

3181 gctagagtagttaaatacagactcactatagggatccaccatgacttcgaaagtttatgat 3240
CGATCTCATGAATTATGCTGAGTGATATCCCTAGGGTGGTACTGAAGCTTTCAAATACTA

3241 ccagaacaaaggaacggaatgataactggtccgcagtggtggccagatgtaaacaaatg 3300
GGTCTTGTCTTCTTCCCTACTATTGACCAGGCGTACCACCCGGTCTACATTTGTTTAC

3301 aatggtctgtgattcatttataattattatgattcagaaaaaacatgcagaaaaatgctgtt 3360
TTACAAGAACTAAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

3361 attttttaccatggttaacggcctctcttatttattgagcagatggtgtgcccacatatt 3420
TAAAAAATGTACCATTGCGCCGGAGAAGAAATAAATAAATAAATAAATAAATAAATAAATAA

3421 gagccagtagcgggtgattataccagacctattggtatgggcaaatcaggcaaatct 3480
CTCGGTCACTCGGCCACATAATATGGTCTGGAATAACCATACCCGTTTAGTCCGTTTAGA

3481 ggtaatgggtctcttataggttacttgatcattacaaaatcttactgcatggttgaaactt 3540
 CCATTACCAAGAATATCCAATGAAGTAGTAATGTTTATAGAATGACGTACCAAACTTGAA

3541 cttatatttaccagaagaatcatttttgtcggccatgatgtgggtgctgttttggcattt 3600
 GAATTAATGGTTCCTTAGTAAAACAGCCGGTACTAACCCACGAAACAAACCTGAAA

3601 cattatagctatgagcatcaagataagatcaaaagcaatagttcaccgtgaaagtgtagta 3660
 GTAATATCGATACTCGTAGTCTATTCTAGTTCGTTATCAAGTGGCACTTTCACATCAT

3661 gatgtgattgaatcatgggatgaatggcctgatattgaagaagatattgcgttgatcaaa 3720
 CTACACTAECTTAGTACCCTACTTACCGGACTATAACTTCTTCTATAACGCAACTAGTTF

3721 tctgaagaaggagaaaaatggttttggagaataaacttctctggtgaaaccatgttgcca 3780
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3781 tcaaaaatcatgagaagttagaaccagaagaatttgcagcatatcttgaaccattcaaa 3840
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3841 gagaaaggtagaagttcgtcgtccaacattatcatggcctcgtgaaatcccgttagtaaaa 3900
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3901 ggtggtaaacctgacgtgttacaattgttaggaattataatgcttatctacgtgcaagt 3960
 CCACCAATTGGACTGCAACATGTTTAAACAATCCTTAATATTACGAATAGATGCACCTCA

3961 gatgatttaccaaaaatgtttattgaaatcggaaccaggattcttttccaatgctattgtt 4020
 CTACTAAATGGTTTTTACAAATAACTTAGCCTGGGTCTAAGAAAAGGTTACGATAACAA

4021 gaaggtgccaagaagtttccctaactgaatttgcagaaagtaaaaggtcttcatTTTTcg 4080
 CTTCCACGGTCTTCAAGGATTAAGACTTAAACAGTTTCATTTTCCAGAAGTAAAAGC

4081 caagaagatgcacctgatgaaatgggaaaaatatacaaatcgttctgttgagcgagttctc 4140
 GTTCTTCTACGTGGACTACTTTACCCTTTTATATAGTTTACGAAAGCAACTCGCTCAAGAG

XbaI IRES reg(4163,4747)>>>

4141 aaaaatgaacaataattcttagagccctctccctccccccccctaacgttactggccga 4200
 TTTTACTTGTATTAAGATCTCGGGGAGAGGGAGGGGGGGGATTGCAATGACCCGGCT

ires_emcv reg(4239,4739)>>>

4201 agccgcttggaataagggcgggtgctgtttgtctatatgttattttccaccatattgccg 4260
 TCGGCGAACCTTATTCGGCCACACGCAACAGATATACAATAAAAGGTGGTATAACGGC

4261 tcttttggcaatgtgagggcccggaaacctggcctgtctcttgcagagcattcctag 4320
 AGAAAACCGTTACACTCCCGGGCCTTTGGACCGGGACAGAAGAACTGCTCGTAAGGATCC

4321 ggtctttccctctcgcacaaggaatgcaaggtctgttgatgtcgtgaaggaagcagtt 4380
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4381 cctctggaagcttcttgaagacaacaactctgtagcagacctttgcagggcaggggaac 4440
 GGAGACCTTCGAAGAACTTCTGTTTGTTCAGACATCGCTGGGAAACGTCCTCGCCTTG

4441 cccccactggcgacaggtgcctctcggcacaagccacgtgtataagatacacctgca 4500
 GGGGTGGACCGCTTCCACGGAGACGCCGTTTTCGGTGCACATATTCATGTGGACGT

4501 aaggcggcacaacccagtgccaogttgtgagttggatagttgtggaagagtcacaatgg 4560
 TTCCGCCGTGTTGGGTACGGTGCACACTCAACCTATCAACACCTTTCTCAGTTTACC

KpnI

4561 ctctctcaagcgtattcaacaaggggctgaaggatgccagaaggtacccattgtatg 4620
 GAGAGGAGTTCGATAGTTGTTCCCGACTTCTACGGGCTTCCATGGGGTAACATAC

ORF_6 rf(6)(4652,5527)<<<

4621 ggatctgatctgggctcgggtgcacatgctttacatgtgttttagtcaggttaaaaaa 4680
 CCTAGACTAGACCCCGGAGCCACGTGTACGAAATGTACACAAATCAGCTCCAATTTTTT

ORF_4 rf(2)(4739,5470)>>>

4681 cgtctaggccccccaaccaggggacgtggttttcttgaaaaacacgatgataatat 4740
 GCAGATCCGGGGGCTTGGTGCCCTGCACAAAAGGAACTTTTGTGCTACTATTATA

EGFP reporter(4751,5467)>>>

4741 ggccacaaccatggtgagcaagggcgaggagctgttccacgggggtggtgccatcctggt 4800
 CCGGTGTTGGTACCCTCGTTCCTCGACAAAGTGCCCCACACGGGTAGGACCA

4801 cgagctggacggcgacgtaaacggccacaagttcagcgtgtccggcgagggcgagggcga 4860
 GCTCGACCTGCCGCTGCAATTTGCCGTTTCAAGTCGCACAGGCCGCTCCCGTCCCGCT

4861 tgccacctacggcaagctgacctgaagttcatctgcaccaccggcaagctgcccgtgcc 4920
 ACGGTGGATGCCGTTTCGACTGGGACTTCAAGTAGACGTGGTGGCCGTTTCGACGGGACGG

4921 ctggcccacctcgtgaccacctgacctcggcgtgcagtgcttccagccgtaccocga 4980
 GACCGGGTGGGAGCACTGGTGGGACTGGATGCCGCACGTCACGAAGTCGGCGATGGGGCT

4981 ccacatgaagcagcagcagcttcttcaagtccgccaatgcccgaaggetacgtccaggagcg 5040
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5041 caccatcttcttcaaggacgacggcaactacaagaccgcccggaggtgaagtccgaggg 5100
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5101 cgacaccctgggtaaccgcatcgagctgaaggccatcgacttcaaggaggacggcaacat 5160
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5161 cctggggcacaagctggagtacaactacaacagccacaacgtctatatcatggccgacaa 5220
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5221 gcagaagaacggcatcaagggtgaactcaagatcccaccacaacatcgaggacggcagcgt 5280
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5281 gcagctcgccgaccactaccagcagaacacccccatcgccgacggccccgtgctgctgcc 5340
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5341 cgacaaccactacctgagcaccagtcgcccctgagcaaaagaccccaacgagaagcgcgga 5400
GCTGTGGTGTAGGACTCGTGGTTCAGGCGGGACTCGTTCCTGGGTTGCTCTCCGCT

5401 tcacatggctcctgctggagtctgtagccgcccgggatcaactctcgccatggacgagct 5460
AGTGTACCAGGACGACCTCAAGCACTGGCGGGGCCCTAGTGAGAGCCGTACCTGTGTCGA

NotI | XhoI 6xHis tag(5510,5527)>>>

5461 gtacaagtaagcggccgacccgaggtagtgggccccctaggctcgagcatcatcaacca 5520
CATGTTTCAATTCGCGCGTGGCGCCTCATGACCCGGGGATCCGAGCTCGTAGTAGTGGT

SV40 prom(5562,5830)>>>

SV40ER reg(5539,5775)<<<

5521 tcaccattgagtatccggctggtgaatgtgtcagttagggtgtgaaagtccccagc 5580
AGTGGTAACCTACTAGGCCGACACCTTACACACAGTCAATCCACACCTTTCAGGGGTCC

5581 ctccccagcaggcagaagtatgcaaagcatgcatctcaattagtcagcaaccaggtgtgg 5640
GAGGGGTCGTCGCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACC

SV40 prom(5682,5884)>>>

5641 aaagtccccaggtccccagcaggcagaagtatgcaaagcatgcatctcaattagtcagc 5700
TTTCAGGGTCCGAGGGGTCGTCGCTTCATACGTTTCGTACGTAGAGTTAATCAGTCCG

SV40 origin(5729,5806)>>>

5701 aaaccatagtcgccccctaaactccgccccatccccccccctaaactccgccccattccgcca 5760
TTGGTATCAGGGCGGGATTGAGGCGGGTAGGGCGGGATTGAGGCGGGTCAAGGCGGGT

SfiI

5761 ttctccgccccatggctgactaattttttttatgagagggccgagggccgctccgccc 5820
AAGAGGCGGGTACCAGCTGATTAATAAATAAATACGTCTCCGGCTCCGGCGGAGCCG

StuI

5821 ctctgagctattccagaagtagtgaggagccttttttgaggcctaggcttttgcaaaaa 5880
GAGACTCGATAAGGTCTTCATCACTCTCCGAAAAAACCTCCGGATCCGAAAAAGCTTTT

ORF_2 rf(1)(5938,6732)>>>

5881 gcttgggctgcaggtcgagggcagctgatcaagagacaggatgaggatcgtttcgcatg 5940
CGAACCCGACGTCCGCTCCGCTAGACTAGTTCCTGTCCTACTCTAGCAAGCGTAC

NTP_II marker(5941,6729)>>>

5941 attgaacaagatggattgcacgaggttctccggccgcttgggtggagagctattcggc 6000
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6001 tatgactgggcacaacagacaatcggtgctctgatgccgcccgtttccggctgtcagcg 6060
ATACTGACCCGTGTTGCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCCG

6061 caggggcccggcttctttttgtaagaccgacctgtccgggtgcccgtgaatgaactgca 6120
GTCCCGCGGGCAAGAAAAACAGTTCCTGGCTGGACAGGCCACGGACTTACTTTGACGTC

6121 gacgaggcagcggctatcgtggctggccacgacggcgcttccctgcccagctgtgctc 6180
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6181 gacgttgactgaagcgggaagggtgctgctattggggcaagtgccggggcaggat 6240
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6241 ctctgtcatctcaactgtctcctgcccagaaagtatccatcatggctgatgcaatggc 6300
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6301 cggtgcatacgttgatccggctacctgcccattcgaccaccaagcgaacatcgcatc 6360

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 6721 gaggttctctgagcgggactctggggttcgatattagacaaggcagctgtagatcttagc 6780
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 delta_U3 other (6806,6858)>>>
 |
 6781 cactttttaaagaaaagggggactggaagggtcaattcactcccaacaaagacaagat 6840
 GTGAAAATTTTCTTTTCCCCCTGACCTTCGCGATTAGTGAGGGTTGTTTCTGTCTTA
 HIV-1_5_LTR other (6859,7039)>>>
 |
 6841 ctgcttttctgactggtctctctggttagaccagatctgagcctgggagctctctc 6900
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 |
 XmaI
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 7321 cagcaagggggaggattggaaagacaatagcaggcatgctggggatgctgggtgggtctat 7380
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 ClaI
 |
 7381 ggcttctgagggcgaagaaccagcagatcgatctgcatctatgtcgggtgaggagaaag 7440
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 7441 aggtaataaatggcattatgggtattatgggtctgcattaatgaaatcgcccaacgatcc 7500
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 7501 cgggtgaaataaccgcacagatgctgaaggagaaaaataccgcatcaggcgtcttccgct 7560
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 pBR322 origin (7719,8338)<<<
 |
 7681 gcaaaagccagcaaaagccaggaaccgtaaaaagccoggttgcgtggcgttttttcoat 7740
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