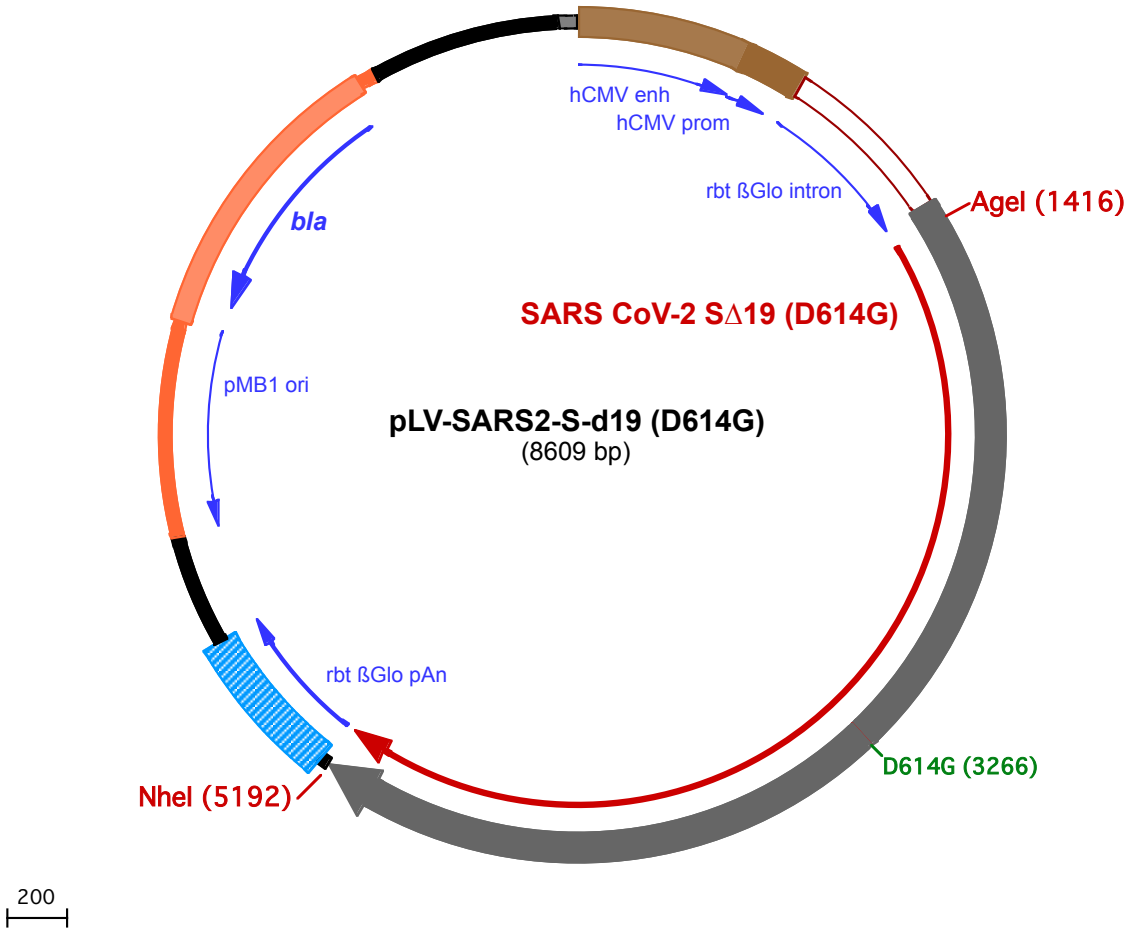
hCMV enh
hCMV prom
rbt ßGlo intron
AgeI (1416)
bla
SARS CoV-2 SΔ19 (D614G)
pMB1 ori
pLV-SARS2-S-d19 (D614G)
(8609 bp)
rbt ßGlo pAn
D614G (3266)
NheI (5192)
200


AgeI (1416)

D614G (3266)

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3201 TCGGCGGAGTGAGCGTGATTACGCCCGGAACCAATACCAGCAATCAGGTTGCCGTCCTGTATCAGGGCGTGAATTGCACCGAGGTACCTGTCGCCATCCA
 592 F  G  G  V  S  V  I  T  P  G  T  N  T  S  N  Q  V  A  V  L  Y  Q  G  V  N  C  T  E  V  P  V  A  I  H
3301 CGCTGACCAACTTACACCCACATGGCGAGTATATTCCACCGGCTCCAACGTCTTTCAGACACGTGCTGGATGTCTGATCGGTGCAGAACACGTTAATAAT
 625    A  D  Q  L  T  P  T  W  R  V  Y  S  T  G  S  N  V  F  Q  T  R  A  G  C  L  I  G  A  E  H  V  N  N
3401 AGCTACGAGTGTGATATCCCCATCGGTGCTGGAATATGCGCCTCTTATCAAACTCAAACCAACTCTCCTAGGCGGGCACGTAGTGTAGCATCCCAAAGTA
 659  S  Y  E  C  D  I  P  I  G  A  G  I  C  A  S  Y  Q  T  Q  T  N  S  P  R  R  A  R  S  V  A  S  Q  S
3501 TCATTGCCTACACAATGAGCCTCGGTGCTGAGAATTCTGTCGCCTACAGCAACAACTCCATTGCTATCCCTACTAACTTCACAATCAGTGTGACAACTGA
 692  I  I  A  Y  T  M  S  L  G  A  E  N  S  V  A  Y  S  N  N  S  I  A  I  P  T  N  F  T  I  S  V  T  T  E
3601 AATTCTGCCCGTATCTATGACCAAAACAAGCGTTGACTGCACCATGTACATCTGTGGCGATTCTACCGAATGTAGCAATCTCCTCCTGCAATACGGATCA
 725    I  L  P  V  S  M  T  K  T  S  V  D  C  T  M  Y  I  C  G  D  S  T  E  C  S  N  L  L  L  Q  Y  G  S
3701 TTCTGCACTCAGCTGAATCGTGCCCTCACAGGTATTGCAGTTGAGCAGGACAAGAATACGCAGGAAGTGTTTGCCCAGGTGAAGCAAATCTACAAAACTC
 759  F  C  T  Q  L  N  R  A  L  T  G  I  A  V  E  Q  D  K  N  T  Q  E  V  F  A  Q  V  K  Q  I  Y  K  T
3801 CACCCATAAAAGACTTTGGCGGATTCAATTTCTCACAGATCCTGCCCGATCCCTCAAAACCCTCCAAGCGTAGCTTTATCGAGGATCTGCTCTTCAACAA
 792  P  P  I  K  D  F  G  G  F  N  F  S  Q  I  L  P  D  P  S  K  P  S  K  R  S  F  I  E  D  L  L  F  N  K
3901 GGTAACCCTCGCAGATGCCGGTTTCATCAAGCAGTATGGCGATTGTCTGGGAGACATCGCCGCTCGGGACCTGATCTGTGCACAGAAGTTCAATGGACTG
 825    V  T  L  A  D  A  G  F  I  K  Q  Y  G  D  C  L  G  D  I  A  A  R  D  L  I  C  A  Q  K  F  N  G  L
4001 ACCGTGCTGCCTCCCTTGCTGACCGACGAGATGATAGCCCAATACACTAGCGCCCTGCTGGCCGGCACCATCACTTCTGGGTGGACATTCGGAGCTGGCG
 859  T  V  L  P  P  L  L  T  D  E  M  I  A  Q  Y  T  S  A  L  L  A  G  T  I  T  S  G  W  T  F  G  A  G
4101 CTGCCCTTCAGATTCCTTTTGCTATGCAGATGGCCTACCGCTTTAACGGCATCGGTGTGACACAAAACGTTCTGTATGAAAACCAGAAACTCATCGCCAA
 892 A  A  L  Q  I  P  F  A  M  Q  M  A  Y  R  F  N  G  I  G  V  T  Q  N  V  L  Y  E  N  Q  K  L  I  A  N
4201 CCAGTTCAACAGTGCTATCGGTAAGATACAGGATAGCCTGTCATCCACTGCCAGCGCATTGGGAAAGTTGCAGGATGTAGTGAACCAGAATGCCCAGGCA
 925    Q  F  N  S  A  I  G  K  I  Q  D  S  L  S  S  T  A  S  A  L  G  K  L  Q  D  V  V  N  Q  N  A  Q  A
4301 CTTAACACCCTGGTGAAACAGCTCTCTTCAAATTTTGGTGCCATTTCTAGCGTGCTGAATGACATACTGAGCCGGTTGGACAAGGTGGAGGCTGAAGTGC
 959  L  N  T  L  V  K  Q  L  S  S  N  F  G  A  I  S  S  V  L  N  D  I  L  S  R  L  D  K  V  E  A  E  V
4401 AGATTGATAGGCTGATAACTGGGCGCCTTCAGTCTCTTCAGACCTATGTGACCCAGCAGCTCATCCGCGCTGCTGAAATTCGCGCATCCGCTAACCTGGC
 992 Q  I  D  R  L  I  T  G  R  L  Q  S  L  Q  T  Y  V  T  Q  Q  L  I  R  A  A  E  I  R  A  S  A  N  L  A
4501 AGCAACCAAAATGTCCGAGTGTGTGCTGGGTCAGTCTAAGAGAGTGGACTTTTGCGGGAAGGGGTATCACCTGATGTCTTTTCCTCAGTCTGCACCCCAT
1025    A  T  K  M  S  E  C  V  L  G  Q  S  K  R  V  D  F  C  G  K  G  Y  H  L  M  S  F  P  Q  S  A  P  H
4601 GGTGTGGTCTTTCTGCACGTGACTTATGTCCCAGCTCAGGAAAAGAACTTCACTACAGCCCCAGCCATCTGCCACGATGGGAAAGCCCACTTTCCCAGGG
1059  G  V  V  F  L  H  V  T  Y  V  P  A  Q  E  K  N  F  T  T  A  P  A  I  C  H  D  G  K  A  H  F  P  R
4701 AAGGCGTATTCGTGTCCAATGGTACTCATTGGTTCGTCACTCAGAGAAATTTCTACGAGCCCCAGATTATAACCACTGACAATACATTTGTATCCGGCAA
1092 E  G  V  F  V  S  N  G  T  H  W  F  V  T  Q  R  N  F  Y  E  P  Q  I  I  T  T  D  N  T  F  V  S  G  N
4801 TTGTGATGTGGTTATCGGGATTGTGAATAATACTGTTTACGATCCTTTGCAGCCAGAGCTGGACTCCTTCAAGGAGGAGCTTGACAAATATTTTAAGAAT
1125    C  D  V  V  I  G  I  V  N  N  T  V  Y  D  P  L  Q  P  E  L  D  S  F  K  E  E  L  D  K  Y  F  K  N
4901 CACACATCACCTGACGTCGACCTCGGAGATATTTCAGGAATCAATGCTTCCGTGGTCAATATTCAGAAGGAGATAGACAGGCTGAATGAGGTTGCCAAGA
1159  H  T  S  P  D  V  D  L  G  D  I  S  G  I  N  A  S  V  V  N  I  Q  K  E  I  D  R  L  N  E  V  A  K
5001 ACCTCAACGAGTCTCTGATCGATCTGCAGGAGTTGGGCAAGTACGAACAGTATATCAAATGGCCATGGTACATTTGGCTTGGGTTCATTGCTGGGCTGAT
1192 N  L  N  E  S  L  I  D  L  Q  E  L  G  K  Y  E  Q  Y  I  K  W  P  W  Y  I  W  L  G  F  I  A  G  L  I
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NheI (5192)

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5101 AGCTATCGTCATGGTGACAATTATGTTGTGTTGCATGACATCCTGCTGTAGTTGTCTGAAGGGCTGCTGCTCATGCGGCAGCTGTTGCTAAAGCTAGCCT
1225    A  I  V  M  V  T  I  M  L  C  C  M  T  S  C  C  S  C  L  K  G  C  C  S  C  G  S  C  C  •
5201 CGAGGGATCCGTCGAGGAATTCACTCCTCAGGTGCAGGCTGCCTATCAGAAGGTGGTGGCTGGTGTGGCCAATGCCCTGGCTCACAAATACCACTGAGAT

5301 CTTTTTCCCTCTGCCAAAAATTATGGGGACATCATGAAGCCCCTTGAGCATCTGACTTCTGGCTAATAAAGGAAATTTATTTTCATTGCAATAGTGTGTT

5401 GGAATTTTTTGTGTCTCTCACTCGGAAGGACATATGGGAGGGCAAATCATTTAAAACATCAGAATGAGTATTTGGTTTAGAGTTTGGCAACATATGCCCA

5501 TATGCTGGCTGCCATGAACAAAGGTTGGCTATAAAGAGGTCATCAGTATATGAAACAGCCCCCTGCTGTCCATTCCTTATTCCATAGAAAAGCCTTGACT

5601 TGAGGTTAGATTTTTTTTATATTTTGTTTTGTGTTATTTTTTTCTTTAACATCCCTAAAATTTTCCTTACATGTTTTACTAGCCAGATTTTTCCTCCTCT

5701 CCTGACTACTCCCAGTCATAGCTGTCCCTCTTCTCTTATGGAGATCCCTCGACGGATCGGCCGCAATTCGTAATCATGTCATAGCTGTTTCCTGTGTGAA

5801 ATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
5901 GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCT
6001 TCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAG
6101 GGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC

6201 TGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC

6301 TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT

6401 CGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC

6501 GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT
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6601 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA

6701 CCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA

6801 CGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAA

6901 TCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAG
                                    287  •  W  H  K  I  L  S  A  G  I  E  A  I  Q  R  N  R  E  D  M  T
7001 TTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCC
 266  A  Q  S  G  T  T  Y  I  V  V  I  R  S  P  K  G  D  P  G  L  A  A  I  I  G  R  S  G  R  E  G  A  G
7101 AGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAA
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7201 GCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCA
 199  A  L  T  L  L  E  G  T  L  L  K  R  L  T  T  A  M  A  V  P  M  T  T  D  R  E  D  N  P  I  A  E  N  L
7301 GCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTT
 166  E  P  E  W  R  D  L  R  T  V  H  D  G  M  N  H  L  F  A  T  L  E  K  P  G  G  I  T  T  L  L  L  N
7401 GGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACC
 133  A  A  T  N  D  S  M  T  I  A  A  S  C  L  E  R  V  T  M  G  D  T  L  H  K  E  T  V  P  S  Y  E  V
7501 AAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCA
  99  L  D  N  Q  S  Y  H  I  R  R  G  L  Q  E  Q  G  A  D  I  R  S  L  V  A  G  C  L  L  V  K  F  T  S  M
7601 TCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGC
  66  M  P  F  R  E  E  P  R  F  S  E  L  I  K  G  S  N  L  D  L  E  I  Y  G  V  R  A  G  L  Q  D  E  A
7701 ATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATA
  33  D  K  V  K  V  L  T  E  P  H  A  F  V  P  L  C  F  A  A  F  F  P  I  L  A  V  R  F  H  Q  I  S  M
7801 CTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTC
7901 CGCGCACATTTCCCCGAAAAGTGCCACCTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAA
8001 TAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACG
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8601 CGCTCTAGA
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