

5' t g g a a g g g c t a a t t c a c t c c c a a g a a g a c a a g a t a t c c t t g a t c t g t g g a t c t a 55
 3' a c c t t c c c g a t t a a g t g a g g g t t t c t t c t g t t c t a t a g g a a c t a g a c a c c t a g a t
 LTR
 HIV U3

c c a c a c a c a a g g c t a c t t c c c t g a t t a g c a g a a c t a c a c a c c a g g g c c a g g g g t c 110
 g g t g t g t g t t c c g a t g a a g g g a c t a a t c g t c t t g a t g t g t g g t c c c g g t c c c a g
 LTR
 HIV U3

a g a t a t c c a c t g a c c t t t g g a t g g t g c t a c a a g c t a g t a c c a g t t g a g c c a g a t a 165
 t c t a t a g g t g a c t g g a a a c c t a c c a c g a t g t t c g a t c a t g g t c a a c t c g g t c t a t
 LTR
 HIV U3

 pHAGE-A0050-8050

a g g t a g a a g a g g c c a a t a a a g g a g a g a a c a c c a g c t t g t t a c a c c c t g t g a g c c t 220
 t c c a t c t t c t c c g g t t a t t t c c t c t c t t g t g g t c g a a c a a t g t g g g a c a c t c g g a
 LTR
 HIV U3

<  pHAGE-A0050-8050

g c a t g g g a t g g a t g a c c c g g a g a g a g a a g t g t t a g a g t g g a g g t t g a c a g c c g c 275
 c g t a c c c t a c c t a c t g g g c c t c t c t t c a c a a t c t c a c c t c c a a a c t g t c g g c g
 LTR
 HIV U3

c t a g c a t t t c a t c a c g t g g c c c g a g a g c t g c a t c c g g a g t a c t t c a a g a a c t g c t 330
 g a t c g t a a a g t a g t g c a c c g g g c t c t c g a c g t a g g c c t c a t g a a g t t c t t g a c g a
 LTR
 HIV U3

gatatcgagccttgctacaagggactttccgctggggactttccagggaggcgtgg 385
 ctatagctcgaacgatgttcctgaaaggcgaccctgaaaggtcctccgcacc
 LTR
 HIV U3

cctgggaggggactggggagtggcgagccctcagatcctgcatataagcagctgct 440
 ggaccgcccctgaccctcacggctcgggagtctaggacgtatattcgtcgacga
 LTR
 HIV U3

pHAGE-S501-1000

ttttgctgtactgggtctctctggttagaccagatctgagcctgggagctctct 495
 aaaacggacatgaccagagagaccaatctggtctagactcggaccctcgagaga
 LTR
 HIV U3 HIV R

ggctaactagggaaaccactgcttaagcctcaataaagcttgcccttgagtgcttc 550
 ccgattgatcccttgggtgacgaattcggagttatttcgaacggaactcacgaag
 LTR
 HIV R

aagtagtggtgcccgtctgttggtgactctggtaactagagatccctcagacc 605
 ttcatcacacacgggcagacaacacactgagaccattgatctctagggagtctgg
 LTR
 HIV U5

HIV R

cttttagtcagtggtgaaaatctctagcagtgggcgcccgaacagggacttgaaag 660
 gaaaatcagtcacaccttttagagatcgtcaccgcgggcttgtccctgaactttc
 LTR PSI
 HIV U5
 PBS-K

cgaaagggaaaccagaggagctctctcgacgcaggactcggcttgc tgaagcgcg 715
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gctttccctttggtctcctcgagagagctgctgctcctgagccgaacgacttcgcg

PSI

pHAGE-A0550-0050

HIV-PSI

cacggcaagaggcgaggggaggcgactggtgagtacgccaaaattttgactagc 770
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gtgccgttctccgctccccgccgctgaccactcatgcggtttttaaaactgatcg

PSI

HIV-PSI

ggaggctagaaggagagagatgggtgagagagcgtcagtaattaagcgggggagaa 825
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 cctccgatcttctctctctaccacgctctcgcagtcataattcgccccctctt

PSI

HIV-PSI

HR-ePSI

ttagatcgcgatgggaaaaaattcggttaaggccagggggaaagaaaaatataa 880
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 aatctagcgtacccttttttaagccaattccggtcccccttcttttttatatt

PSI

HR-ePSI

atataaacatataagtagatgggcaagcaggagctagaacgattcgcagttaatcct 935
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 taattttgtatatcataccggttcgtccctcgatcttgctaagcgtcaattagga

PSI

HR-ePSI

pHAGE-S1001-1500

ggcctgttagaaacatcagaaggctgtagacaaataactgggacagctacaacat 990
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ccggacaatctttgtagtcttccgacatctgtttatgaccctgtc gatgttgta

PSI

HR-ePSI

cccttcagacaggatcagaagaacttagatcattatataatacagtagcaaccct 1045
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ggaagtctgtcctagctcttcttgaatctagtaatatattatgtcatcgttggga

PSI

HR-ePSI

ctattgtgtgcatcaaaggatagagataaaagacaccaaggaagctttagacaag 1100
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gataacacacgtagtcttctatctctattttctgtggttccttcgaaatctgttc
 PSI
 HR-ePSI

atagaggaagagcaaaacaaaagtaagaccaccgcacagcaagcggccggccgct 1155
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 tatctccttctcgttttggtttcattctgggtggcgtgtcgttcgccggccggcga
 PSI
 HR-ePSI

gatcttcagacctggaggaggagatatgagggacaattggagaagtgaattatat 1210
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ctagaagtctggacctcctcctctatactccctgttaacctcttcaacttaatata
 pHAGE-A1050-0550

aatataaagtagtaaaaattgaaccattaggagtagcaccaccaaggcaaga 1265
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ttatatttcatcatttttaacttggtaatcctcatcgtgggtggttcggtttct

gaagagtgggtgcagagagaaaaagagcagtgggaataggagctttgttccttgg 1320
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ctctcaccacgtctctctttttctcgtcacccttatcctcgaacaaggaacc
 RRE

gttcttgggagcagcaggaagcactatgggvcgagcgtcaatgacgctgacggta 1375
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 caagaacctcgtcgtccttctgtgatacccgctcgcagttactgcgactgccaat
 RRE

caggccagacaattattgtctggtatagtgacagcagcagaacaatttgctgaggg 1430
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gtccggtctgttaataacagaccatatcacgtcgtcgtccttggttaaacgactccc
 RRE
 pHAGE-S1501-2000

ctattgaggcgaacagcatctgttgcaactcacagtctggggcatcaagcagct 1485
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gataactccgcgttgctcgtagacaacgttgagtgtcagaccccgtagttcgtcga
 RRE

ccaggcaagaatcctggctgtggaagatacctaaggatcaacagctcctgggg
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ggTccgttcttaggaccgacacctttctatggatttcctagttgtcgaaggaccc



atttgggggttgctctggaaaactcatttgcaccactgctgtgccttggaaatgcta
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 taaacccaacgagaccttttgagtaaactgtggtgacgacacggaaccttacgat

gttgagtaataaatcctctggaacagatttggaaatcacacgacctggatggagtg
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 caacctcattattagagaccttgtctaaaccttagtgtgctggacctacctcac



ggacagagaaattaacaattacacaagcttaatacactccttaattgaagaatcg
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 cctgtctctttaattgttaatgtgttcgaattatgtgaggaattaacttcttagc



caaacaccagcaagaaaagaatgaacaagaattattggaattagataaatgggcaa
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gttttggtcgttcttttcttacttgttcttaataaccttaatctatttaccggtt

gtttgtggaattggtttaacataacaaattggctgtggtatataaaattattcat
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 caaacaccttaaccaaattgtattgtttaaccgacaccatataattttaataagta

aatgatagtaggaggcttggtaggtttaagaatagtttttgctgtactttctata
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ttactatcatcctccgaacctccaaattcttatcaaaaacgacatgaaagatat

gtgaatagagttaggcagggatattcaccattatcgtttcagaccacctcccaa
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 cacttatctcaatccgtccctataagtggtaatagcaaagtctgggtggagggtt



ccccgaggggaccgacaggcccgaaaggaatagaagaagaagggtggagagagaga
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ggggctcccctgggctgtccgggcttccttatcttcttcttccacctctctctct

cagagacagatccattcgattagtgaaacggatctcgacggtatcgccgaattcac
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gtctctgtctaggtaaagctaatacacttgacctagagctgccatagcggcttaagtg



aaatggcagttatccatccacaatttttaaagaaaaggggggattggggggtacag 2090
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ttaccgtcataagtaggtgttaaaattttcttttccccctaacccccacatgtc

HIV cpPu (Trip)

pHAGE-A2050-1550

tgcaggggaaagaatagtagacataatagcaacagacatacaaaactaaagaatta 2145
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 acgtcccctttcttatcatctgtattatcgttgtctgtatgtttgatttcttaat

HIV cpPu (Trip)

< pHAGE-A2050-1550

caaaaacaaattacaaaattcaaaattttcgggtttattacaggacagcagag 2200
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gttttgtttaatgttttaagttttaaaagcccaataatgtccctgtcgtctc

HIV cpPu (Trip)

atccagtttggactagtAATGTAGTCTTATGCAATACTCTTGTAGTCTTGCAACA 2255
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 taggtcaaacctgatcaTTACATCAGAATACGTTATGAGAACATCAGAACGTTGT

HIV cpPu (Trip)

RSV promoter

TGGTAACGATGAGTTAGCAACATGCCTTACAAGGAGAGAAAAAGCACCGTGCATG 2310
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ACCATTGCTACTCAATCGTTGTACGGAATGTTCTCTCTTTTTCGTGGCACGTAC

RSV promoter

CCGATTGGTGGAAAGTAAGGTGGTACGATCGTGCCTTATTAGGAAGGCAACAGACG 2365
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 GGCTAACCACCTTCATTCCACCATGCTAGCACGGAATAATCCTTCCGTTGTCTGC

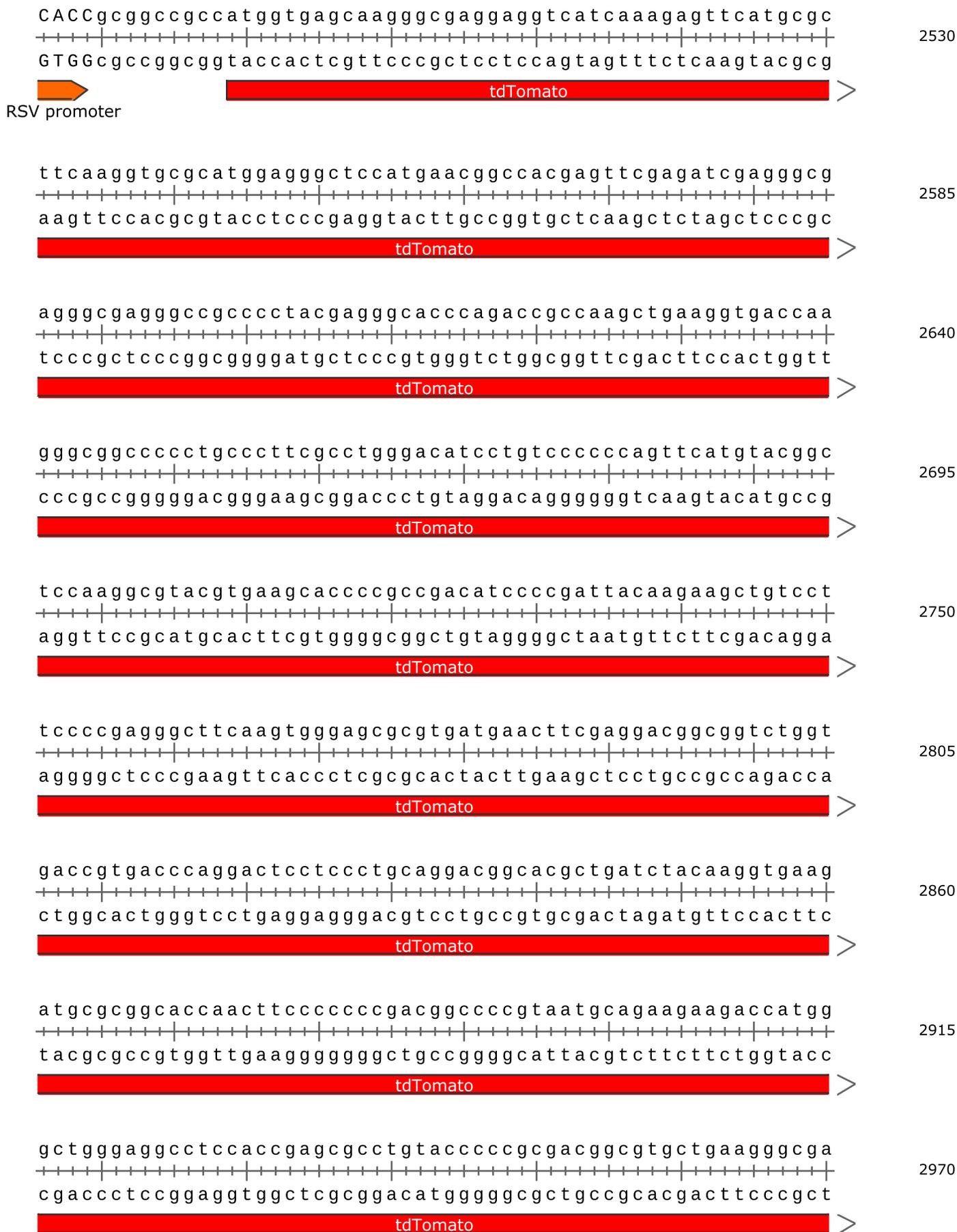
RSV promoter

GGTCTGACATGGATTGGACGAACCACTGAATTCCGCATTGCAGAGATATTGTATT 2420
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 CCAGACTGTACCTAACCTGCTTGGTGACTTAAGGCGTAACGTCTCTATAACATAA

RSV promoter

TAAGTGCCTAGCTCGATACAATAAACGCCATTTGACCATTACCACATTGGTGTG 2475
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ATTCACGGATCGAGCTATGTTATTTGCGGTAAACTGGTAAGTGGTGTAAACCACAC

RSV promoter



gatccaccaggccctgaagctgaaggacggcggccactacctggtggagttcaag 3025
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
ctaggtggtccgggacttgcacttccctgccgccggtgatggaccacctcaagttc
tdTomato >

accatctacatggccaagaagcccgtgcaactgcccggctactactacgtggaca 3080
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
tggtagatgtaccggttcttcgggcacgttgacgggccgatgatgatgcacctgt
tdTomato >

ccaagctggacatcacctcccacaacgaggactacaccatcgtggaacagtacga 3135
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
ggttcgacctgtagtgagggtgttgctcctgatgtggtagcaccttgtcatgct
tdTomato >

gcgctccgagggccgccaccacctgttcctggggcatggcacccggcagcacccggc 3190
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
cgcgaggctcccggcgggtggtggacaaggaccccgtaccgtggccgctcgtggccg
tdTomato >

agcggcagctccggcaccgcctcctccgaggacaacaacatggccgtcatcaag 3245
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
tcgccgtcgaggccgtggcggaggaggctcctgttgtgtaccggcagtagtttc
tdTomato >

agttcatgcgcttcaagggtgcgcatggagggtccatgaacggccacgagttcga 3300
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
tcaagtacgcgaagttccacgcgtacctcccgaggtaacttgccggtgctcaagct
tdTomato >

gatcgagggcgagggcgagggccgccctacgagggcacccagaccgccaagctg 3355
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
ctagctcccgctcccgctcccggcggggatgctcccgtgggtctggcggttcgac
tdTomato >

aaggtgaccaagggcggccccctgcccttcgcctgggacatcctgtccccccagt 3410
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
ttccactggttcccggcgggggacgggaagcggaccctgtaggacaggggggtca
tdTomato >

tcatgtacggctccaaggcgtacgtgaagcaccgccgacatccccgattacaa 3465
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
agtacatgccgaggttccgcacgacttcgtggggcggctgtaggggctaagtgt
tdTomato >

gaagctgtccttccccgagggcttcaagtgggagcgcgtgatgaacttcgaggac 3520
 cttcgacaggaaggggctcccgaagttcacctcgcgcaactacttgaagctcctg
 tdTomato >

ggcggctctggtgaccgtgaccaggactcctccctgcaggacggcacgctgatct 3575
 ccgccagaccactggcactgggtcctgaggaggagcgtcctgcccgtgcgactaga
 tdTomato >

acaaggtgaagatgcgcggcaccaacttccccccgacggccccgtaatgcagaa 3630
 tgttccacttctacgcgccgtggttgaaggggggctgccggggcattacgtctt
 tdTomato >

gaagaccatgggctgggaggcctccaccgagcgcctgtacccccgacggcgtg 3685
 cttctggtacccgaccctccggaggtggctcgcggacatgggggctgcccgcac
 tdTomato >

ctgaagggcgagatccaccaggccctgaagctgaaggacggcggccactacctgg 3740
 gacttcccgtcttaggtggtccgggacttcgacttcttgcgcgggtgatggacc
 tdTomato >

tggagttcaagaccatctacatggccaagaagcccgctgcaactgcccggctacta 3795
 acctcaagttctggtagatgtaccggttcttcgggcacgttgacgggccgatgat
 tdTomato >

ctacgtggacaccaagctggacatcacctcccacaacgaggactacaccatcgtg 3850
 gatgcacctgtggttcgacctgtagtgagggtgttgctcctgatgtggtagcac
 tdTomato >

gaacagtacgagcgtccgagggccgccaccacctgttccctgtacggcatggacg 3905
 cttgtcatgctcgcgaggctcccggcgggtggtggacaaggacatgccgtacctgc
 tdTomato >

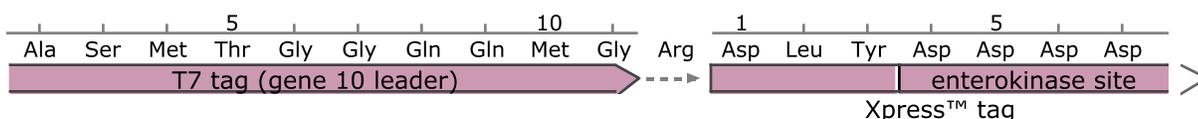
agctgtacaagtctggcagcggagagggcagaggaagtcttctaaccatgcggtga 3960
 tcgacatgttcagaccgtcgccttcccgctctccttcagaagattgtacgccact
 tdTomato GSG Bridge T2A

tdTomato (Stop Removed)

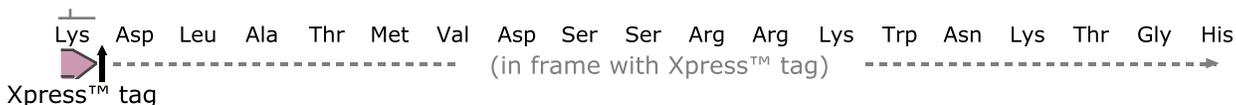
cgtggaggagaatcccggccctATGGGTTCTCATCATCATCATCATGGTATG 4015
 gcacctcctcttagggccgggaTACCCAAGAGTAGTAGTAGTAGTAGTACCATAC



GCTAGCATGACTGGTGGACAGCAAATGGGTCGGGATCTGTACGACGATGACGATA 4070
 CGATCGTACTGACCACCTGTCGTTTACCCAGCCCTAGACATGCTGCTACTGCTAT



AGGATCTCGCCACCATGGTCTGACTCATCACGTCGTAAGTGGGAATAAGACAGGTCA 4125
 TCCTAGAGCGGTGGTACCAGCTGAGTAGTGCAGCATTACCTTATTCTGTCCAGT



CGCAGTCAGAGCTATAGGTCGGCTGAGCTCACTCGAGAACGTCTATATCAAGGCC 4180
 GCGTCAGTCTCGATATCCAGCCGACTCGAGTGAGCTCTTGCAGATATAGTTCCGG
 Ala Val Arg Ala Ile Gly Arg Leu Ser Ser Leu Glu Asn Val Tyr Ile Lys Ala
 (in frame with Xpress™ tag)

GACAAGCAGAAGAACGGCATCAAGGCGAACTTCAAGATCCGCCACAACATCGAGG 4235
 CTGTTTCGTCTTCTTGCCGTAGTTCGCTTGAAGTTCTAGGCGGTGTTGTAGCTCC
 Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
 (in frame with Xpress™ tag)

ACGGCGGGCGTGACGCTCGCCTACCACTACCAGCAGAACACCCCATCGGGCGACGG 4290
 TGCCGCCGCACGTCGAGCGGATGGTGTATGGTCGTCTTGTGGGGGTAGCCGCTGCC
 Asp Gly Gly Val Gln Leu Ala Tyr His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 (in frame with Xpress™ tag)

CTGGCCACCCCTCGTGACCACCCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTAC 4675
 GACCGGGTGGGAGCACTGGTGGGACTGGATGCCGCACGTACGAAAGTCGGCGATG
 Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr
 (in frame with Xpress™ tag)

GCaMP6f

CCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACA 4730
 GGGCTGGTGTACTTCGTCTGTGCTGAAGAAGTTCAGGGCGGTACGGGCTTCCGATGT
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 (in frame with Xpress™ tag)

GCaMP6f

TCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGA 4785
 AGGTCCTCGCGTGGTAGAAGAAGTTCCTGCTGCCGTTGATGTTCTGGGCGCGGCT
 Ile Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 (in frame with Xpress™ tag)

GCaMP6f

GGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGAC 4840
 CCACTTCAAGCTCCCCTGTGGGACCACTTGGCGTAGCTCGACTTCCCCTAGCTG
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 (in frame with Xpress™ tag)

GCaMP6f

TTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTGCCGGACC 4895
 AAGTTCCTCCTGCCGTTGTAGGACCCCGTGTTTCGACCTCATGTTGGACGGCCTGG
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Leu Pro Asp
 (in frame with Xpress™ tag)

GCaMP6f

AACTGACTGAAGAGCAGATCGCAGAATTTAAAGAGGAATTCTCCCTATTTGACAA 4950
 TTGACTGACTTCTCGTCTAGCGTCTTAAATTTCTCCTTAAGAGGGATAAACTGTT
 Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Glu Phe Ser Leu Phe Asp Lys
 (in frame with Xpress™ tag)

GCaMP6f

GGACGGGGATGGGACAATAACAACCAAGGAGCTGGGGACGGTGATGCGGTCTCTG 5005
 CCTGCCCCCTACCCTGTTATTGTTGGTTCCTCGACCCCTGCCACTACGCCAGAGAC
 Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu
 (in frame with Xpress™ tag)

GCaMP6f

GGGCAGAACCCACAGAAGCAGAGCTGCAGGACATGATCAATGAAGTAGATGCCG 5060
 CCCGTCTTGGGGTGTCTTTCGTCTCGACGTCCTGTACTAGTTACTTCATCTACGGC
 Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
 (in frame with Xpress™ tag)

GCaMP6f

ACGGTGACGGCACAATCGACTTCCCTGAGTTCCTGACAATGATGGCAAGAAAAAT 5115
 TGCCACTGCCGTGTTAGCTGAAGGGACTCAAGGACTGTTACTACCGTTCTTTTAA
 Asp Gly Asp Gly Thr Ile Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met
 (in frame with Xpress™ tag)

GCaMP6f

GAAATACAGGGACACGGAAGAAGAAATTAGAGAAGCGTTCGGTGTGTTTGATAAG 5170
 CTTTATGTCCCTGTGCCTTCTTCTTTAATCTCTTCGCAAGCCACACAAACTATTC
 Lys Tyr Arg Asp Thr Glu Glu Glu Ile Arg Glu Ala Phe Gly Val Phe Asp Lys
 (in frame with Xpress™ tag)

GCaMP6f

GATGGCAATGGCTACATCAGTGCAGCAGAGCTTCGCCACGTGATGACAAACCTTG 5225
 CTACCGTTACCGATGTAGTCACGTCGTCTCGAAGCGGTGCACTACTGTTTGGAAC
 Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
 (in frame with Xpress™ tag)

GCaMP6f

GAGAGAAGTTAACAGATGAAGAGGTTGATGAAATGATCAGGGAAGCAGACATCGA 5280
 CTCTCTTCAATTGTCTACTTCTCCAACACTTTACTAGTCCCTTCGTCTGTAGCT
 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Ile Asp
 (in frame with Xpress™ tag)

GCaMP6f

TGGGGATGGTCAGGTAAACTACGAAGAGTTTGTACAAATGATGACAGCGAAGTGA
 ACCCCTACCAGTCCATTTGATGCTTCTCAAACATGTTTACTACTGTCGCTTCACT
 Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys *
 (in frame with Xpress™ tag)

5335

GCaMP6f

ggatcctaataaacctctggattacaaaatttgtgaaagattgactggatttctt
 cctaggattagttggagacctaattgttttaaacacttttctaactgaccataagaa

5390

WPRE

pHAGE 3' CDS

aactatgttgctccttttacgctatgtggatacgctgctttaatgcctttgtatc
 ttgatacaacgaggaaaatgcgatacacctatgcgacgaaattacggaaacatag

5445

WPRE

pHAGE 3' CDS

atgctattgcttcccgtatggcctttcattttctcctccttgtataaatcctgggt
 tacgataacgaagggcataccgaaagtaaaagaggaggaacatatttaggaccaa

5500

WPRE

pHAGE-A3550-3050

gctgtctctttatgaggagttgtggcccggtgtcaggcaacgctggcgtggtgtgc
 cgacagagaaatactcctcaacaccgggcaacagtcctgaccgcaccacacg

5555

WPRE

actgtgtttgctgacgcaacccccactggttggggcattgccaccacctgtcagc
 tgacacaaacgactgctgttgggggtgaccaaccccgtaacggtggtggacagtcg

5610

WPRE

pHAGE-S4001-4500

tcctttccgggactttcgctttccccctccctattgccacggcgggaactcatcgc
 aggaaaggccctgaaagcgaaagggggagggataacggtgccgccttgagtagcg

5665

WPRE

pHAGE-S4001-4500

cgctgccttgcccgtgctggacaggggctcggctggtgggcaactgacaattcc 5720
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gcggacggaacgggcgacgacctgtccccgagccgacaaccctgactgtaagg
 WPRE

gtggtggtgtcggggaaatcatcgtcctttccttggctgctcgcctgtggtgcca 5775
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 caccacaacagccccttagtagcaggaaggaaccgacgagcggacacaacggt
 WPRE

cctggattctgcgcgggacgtccttctgctacgtcccttcggccctcaatccagc 5830
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ggacctaaagacgcgccctgcaggaagacgatgcaggggaagccgggagttaggctc
 WPRE

ggaccttccttcccgcggcctgctgccggctctgcggccttctccgcgtcttcgc 5885
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 cctggaaggaagggcgccggacgacggccgagacgccggagaaggcgcagaagcg
 WPRE

cttcgccctcagacgagtcggatctcccttggggccgcctccccgcctgagatcc 5940
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gaagcgggagtctgctcagcctagagggaaaccggcggaggggcggactctagg
 WPRE

HIV nef

oligo #91 sequencing sense

pHAGE-A4050-3550

ttaagaccaatgacttacaaggcagctgtagatcttagccactttttaaaagaa 5995
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 aaattctggttactgaatgttccgctcgacatctagaatcggtgaaaaattttctt
 HIV nef

< pHAGE-A4050-3550

HIV PPT

aaggggggactggaagggctaattcactcccaacgaagacaagatctgctttttg 6050
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ttccccctgaccttcccgattaagtgagggttgcttctgttctagacgaaaaac
 HIV PPT dU3 LTR

HIV nef

HIV R

cttgtaactgggtctctctggtttagaccagatctgagcctgggagctctctggcta 6105
 |||
 gaacatgaccagagagaccaatctggtctagactcggaccctcgagagaccgat
 dU3 LTR
 HIV R

||
 Difference from 5' LTR

actaggaaccactgcttaagcctcaataaagcttgccttgagtgcttcaagta 6160
 |||
 tgatcccttgggtgacgaattcggagttatttcgaacggaactcacgaagtcat
 dU3 LTR
 HIV R HIV U5

gtgtgtgcccgtctgttgtgtgactctggtaactagagatccctcagaccctttt 6215
 |||
 cacacacgggcagacaacacactgagaccattgatctctagggagtctgggaaa
 dU3 LTR
 HIV U5

agtcagtgtggaaaatctctagcagtagtagttcatgtcatcttattattcagta 6270
 |||
 tcagtcacaccttttagagatcgtcatcatcaagtacagtagaataataagtcatt
 dU3 LTR 3' Flank
 HIV U5

pHAGE-S4501-5000

tttataacttgcaagaaatgaatatcagagagtgagaggcccgggttaattaag 6325
 |||
 aaatattgaacgtttctttacttatagtctctcactctccgggcccaattaattc
 3' Flank

gaaagggctagatcattcttgaagacgaaagggcctcgtgatacgcctatTTTTA 6380
 |||
 ctttcccgatctagtaagaacttctgctttcccggagcactatgCGGATAAAAAT
 pHAGE-S6001-6500

taggttaatgtcatgataataatggtttcttagacgtcaggtggcacttttCGGG 6435
 |||
 atccaattacagtactattattaccaagaatctgcagtcaccctgaaaagccc

gaaatgtgCGCGGAACCCctatttGTTTatttttctaaatacattcaaataTGTa 6490
 |||
 ctttacacgCGCCTTGGGGATAAACAAAAGatttatGTAAGTTTatacat

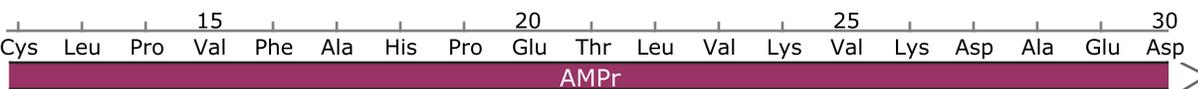
tccgctcatgagacaataaccctgataaatgcttcaataatattgaaaaaggaag 6545
 aggcgagtactctgttattgggactatttacgaagttattataactttttccttc



agtatgagtattcaacattttccgtgtcgccttattcccttttttgccgcatttt 6600
 tcatactcataagttgtaaaggcacagcgggaataagggaaaaaacgccgtaaaa



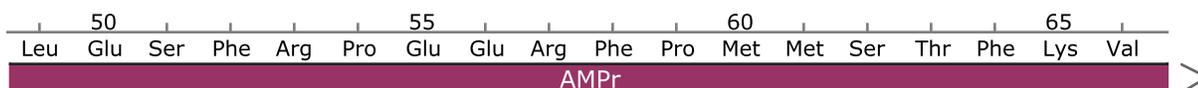
gccttctgtttttgctcaccagaaacgctggtgaaagtaaaagatgctgaaga 6655
 cgggaaggacaaaaacgagtggttctttgcgaccactttcattttctacgacttct



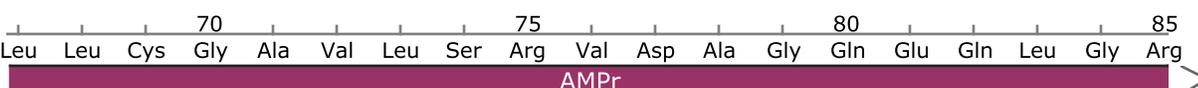
tcagttgggtgcacgagtggttacatcgaactggatctcaacagcggtaagatc 6710
 agtcaaccacgtgctcacccaatgtagcttgacctagagttgtcgccattctag



cttgagagttttcgccccgaagaacgttttccaatgatgagcacttttaagttc 6765
 gaactctcaaaagcggggcttcttgcaaaaggttactactcgtgaaaatttcaag



tgctatgtggcgcggtattatcccgtgttgacgccgggcaagagcaactcggtcg 6820
 acgatacaccgcgccataatagggcacaaactgcggcccggttctcgttgagccagc



ccgcatacactatttctcagaatgacttgggttgagtactcaccagtcacagaaaag
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ggcgatggtgataagagcttactgaaccaactcatgagtggtcagtgctcttttc

6875

90 95 100
 Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys

AMPr

pHAGE-S6501-7000

catcttacggatggcatgacagtaagagaattatgcagtgctgccataaccatga
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gtagaatgcctaccgtactgtcatttctcttaatacgtcacgacgggtattgggtact

6930

105 110 115 120
 His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met

AMPr

gtgataaactgcggccaaacttacttctgacaacgatcggaggaccgaaggagct
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 cactattgtgacgccggttgatgaagactggtgctagcctcctggcttcctcga

6985

125 130 135 140
 Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu

AMPr

aaccgcttttttgcacaacatgggggatcatgtaactcgccttgatcgttgggaa
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ttggcgaaaaaacgtggtgtacccctagtagcattgagcgggaactagcaaccctt

7040

145 150 155
 Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu

AMPr

ccggagctgaatgaagccatacceaacgacgagcgtgacaccacgatgcctgtag
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ggctcgaacttacttcgggtatggtttgctgctcgcactgtggtgctacggacatc

7095

160 165 170 175
 Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val

AMPr

pHAGE-A6550-6050

caatggcaacaacgttgcgcaaactattaactggcgaactacttactctagcttc
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gttaccgttggtgcaacgcggttgataattgaccgcttgatgaatgagatcgaag

7150

180 185 190 195
 Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser

AMPr

pHAGE-A6550-6050

ccggcaacaattaatagactggatggaggcggataaagttgcaggaccacttctg 7205
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ggccgttgttaattatctgacctacctccgcctatttcaacgtcctggtgaagac
 200 205 210
 Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu
 AMPr >

cgctcggcccttccggctggctggtttattgctgataaatctggagccggtgagc 7260
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gcgagccgggaaggccgaccgaccaataacgactatntagacctcggccactcg
 215 220 225 230
 Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu
 AMPr >

gtgggtctcgcggtatcattgcagcactggggccagatggtaagccctcccgtat 7315
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 caccagagcgcctatagtaacgtcgtgaccccggtctaccattcgggagggcata
 235 240 245 250
 Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 AMPr >

cgtagttatctacacgacggggagtcaggcaactatggatgaacgaaatagacag 7370
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 gcatcaatagatgtgctgcccctcagtccttgatacctacttgctttatctgtc
 255 260 265
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln
 AMPr >

pHAGE-S7001-7500

atcgctgagataggtgcctcactgattaagcattggtaactgtcagaccaagttt 7425
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 tagcgactctatccacggagtgactaattcgtaacattgacagtctggttcaaa
 270 275 280
 Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp *
 AMPr >

actcatatataacttttagattgatttaaaacttcatttttaatttaaaggatcta 7480
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 tgagtatataatgaaatctaactaaatttgaagtaaaaattaaattttcctagat

ggtgaagatcctttttgataatctcatgaccaaataccttaacgtgagttttcg 7535
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ccacttctaggaaaaactattagagtactggtttttagggaattgcaactcaaaagc

ttccactgagcgtcagaccccgtagaaaagatcaaaggatcttcttgagatcctt 7590
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 aaggtgactcgcagctctggggcatcttttctagtttccctagaagaactctaggaa

tttatagtcctgtcgggtttcgccacctctgacttgagcgtcgatTTTTGTGATG 8140
 aaatatcaggacagcccaaagcgggtggagactgaactcgcagctaaaaacactac



ctcgtcagggggcgagacctatggaaaaacgccagcaacgcggcctTTTTACGG 8195
 gagcagtcCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCC



ttcctggcctTTTTGCTGGCCTTTTTGCTCACATGTTCTTTCTGCGTTATCCCTG 8250
 aaggaccggaaaacgaccggaaaacgagtggtacaagaaggacgcaataggggac

attctgtggataaccgtattaccgcctTTGAGTGAGCTGATACCGCTCGCCGCGAG 8305
 taagacacctattggcataatggcggaaactcactcgcactatggcgagcggcgctc

ccgaacgaccgagcgcagcgcagtcagtgagcgcaggaagcgggaagagcgcCCAATA 8360
 ggcttgctggctcgcgtcgcctcagtcactcgccttctcgcggttatt



cgcaaaccgcctctccccgcgcgttggccgattcattaatgcagcaagctcatgg 8415
 gcgcttggcggagaggggCGCGCAACCggctaagtaattacgtcgttcgagtacc



ctgactaattTTTTTATTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTA 8470
 gactgattaaaaaaaaataaatacgtctccggctccggcggagccggagactcgat



ttccagaagtagtgaggaggctTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCC 8525
 aaggcttctcatcactcctccgaaaaaacctccggatccgaaaacgTTTTTCGAGG



ccgtggcacgacaggtttcccgactggaaagcgggcagtgagcgcAACGCAATTA 8580
 ggaccgtgctgtccaaagggtgaccttccgccgctcactcgcggttgcgTTAAT



SV40 ori

atgtgagttagctcactcattagggcaccaccaggcctttacactttatgcttcggc 8635
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 tacactcaatcgagtgagtaatccgtgggggtccgaaatgtgaaatacgaaggccg
 ← pHAGE-A8050-7550

tcgatatgttggtggtggaattgtgagcggataacaatttcacacaggaaacagctat 8690
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 agcatacaaacacaccttaacactcgcctattgttaaagtgtgtcctttgtcgata

gacatgattacgaatttcacaaataaagcattttttcactgcattctagttgtg 8745
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ctgtactaatgcttaaagtgtttatttcgtaaaaaaagtgacgtaagatcaacac

gtttgtccaaactcatcaatgtatccttatcatgtctggatcaactggataactca 8800
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 caaacagggtttgagtagttacatagaatagtacagacctagttgacctattgagt

agctaaccaaaatcatcccaaacttcccaccccataccctattaccactgccaat 8855
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 tcgattgggttttagtaggggttgaagggtgggggatgggataatggtgacggtta
 pHAGE-S1-500 >

tacctgtggtttcatttactctaaacctgtgattcctctgaattattttcatttt 8910
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 atggacaccaaagtaaattgagatttggacactaaggagacttaataaaagtaaaa
 pHAGE-S1-500

aaagaaattgtatttgttaaataatgtactacaaacttagtagt 3'
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ ... 8953
 ttctttaacataaacaatttatacatgatgtttgaatcatca 5'

Enzymes	Sites	
Acc65I	1	4436
AflIII	1	8224
AvrII	1	8503
BamHI	1	5336
BbvCI	1	1424
BfuAI	1	4893
BlpI	1	4148
BmtI	1	4020
BspDI	1	5277
BspEI	1	308
BspMI	1	4893
BssHII	1	711
BstAPI	1	1453
BstBI	1	4340
ClaI	1	5277
DraIII	1	212
DrdI	1	8122
EcoNI	1	1170
FseI	1	1150
HpaI	1	5235
KasI	1	637
KpnI	1	4440
MfeI	1	1189
NarI	1	638
NheI	1	4016
NotI	1	2481
NruI	1*	833*
PacI	1	6321
PaeR7I	1	4157
PciI	1	8224
PluTI	1	641
PpuMI	1	1934
PsiI	1	6274
SalI	1	4088
SfiI	1	8456
SfoI	1	639
SmaI	1	6313
SpeI	1	2212
SphI	1	2310
SspI	1	6531
TliI	1	4157
TspMI	1	6311
XhoI	1	4157
XmaI	1	6311

Feature	Location	Size (bp)			Type
✓ LTR	1 .. 636	636			misc_feature
/gene	= LTR				
/note	= Long Terminal Repeat				
✓ HIV U3	1 .. 453	453			misc_feature
/note	= Full Length HIV U3				
✓ pHAGE-A0050-8050	158 .. 179	22			primer_bind
✓ pHAGE-S501-1000	401 .. 421	21			primer_bind
✓ HIV R	454 .. 551	98			misc_feature
/note	= HIV Repeat Region				
✓ HIV U5	552 .. 636	85			misc_feature
/note	= HIV U5				
✓ PBS-K	636 .. 658	23			misc_feature
/note	= tRNA binding site for Lysine tRNA				
✓ PSI	637 .. 1155	519			misc_feature
/gene	= psi				
/product	= pbs-gag				
/note	= PSI Packaging Sequence				
✓ pHAGE-A0550-0050	667 .. 690	24			primer_bind
✓ HIV-PSI	697 .. 806	110			misc_feature
✓ HR-ePSI	807 .. 1144	338			misc_feature
✓ pHAGE-S1001-1500	898 .. 919	22			primer_bind
✓ pHAGE-A1050-0550	1166 .. 1189	24			primer_bind
✓ RRE	1303 .. 1536	234			misc_feature
/gene	= rre				
/product	= minimal RRE				
/note	= Rev Responsive Element				
✓ pHAGE-S1501-2000	1391 .. 1417	27			primer_bind
✓ pHAGE-A1550-1050	1650 .. 1678	29			primer_bind
✓ pHAGE-S2001-2500	1898 .. 1922	25			primer_bind

Feature	Location	Size (bp)			Type
✓ HIV cpPu (Trip)	2034 .. 2211	178			misc_feature
/gene	= cppt				
/note	= Central Poly Purine Track				
✓ pHAGE-A2050-1550	2084 .. 2112	29			primer_bind
✓ RSV promoter	2218 .. 2479	262			promoter
/note	= Rous sarcoma virus enhancer/promoter				
✓ tdTomato	2489 .. 3916	1428			misc_feature
/label	= tomato				
✓ tdTomato (Stop Removed)	3909 .. 3916	8			misc_feature
Pair 1	3917 .. 3982	66			misc_feature
Pair 02	3917 .. 3982	66			misc_feature
Pair 2	3917 .. 3982	66			misc_feature
Pair 03	3917 .. 3982	66			misc_feature
Pair 05	3917 .. 3982	66			misc_feature
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				

Feature	Location	Size (bp)			Type
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Reading Frame	3917 .. 3982	66			misc_feature
/note	= Reading Frame				
Seq #64	3917 .. 3982	66			misc_feature
/note	= Seq #64				
Seq eGFP_F	3917 .. 3982	66			misc_feature
/note	= Seq eGFP_F				
✓ GSG Bridge	3917 .. 3928	12			misc_feature
✓ T2A	3929 .. 3982	54			misc_feature
✓ GCaMP6f	3983 .. 5335	1353			misc_feature
✓ 6xHis	3992 .. 4009	18			CDS
/product	= 6xHis affinity tag				
/translation	= HHHHHH 6 amino acids = 840.9 Da				
✓ T7 tag (gene 10 leader)	4013 .. 4045	33			CDS
/product	= leader peptide from bacteriophage T7 gene 10				
/note	= promotes efficient translation in <i>E. coli</i>				
/translation	= MASMTGGQQMG 11 amino acids = 1.1 kDa				
✓ Xpress™ tag	4049 .. 4072	24			CDS
▶ 2 segments					
/product	= Xpress™ epitope tag, including an enterokinase recognition and cleavage site				
/translation	= DLY,DDDDK 8 amino acids = 998.0 Da				
✓ WPRE	5342 .. 5933	592			misc_feature
/gene	= WPRE				
/note	= Woodchuck Hepatitis Virus Posttranscriptional Regulatory Element				
✓ pHAGE 3' CDS	5370 .. 5404	35			primer_bind

Feature	Location	Size (bp)			Type
✓ pHAGE-A3550-3050	5448 .. 5471	24			primer_bind
✓ pHAGE-S4001-4500	5601 .. 5621	21			primer_bind
✓ oligo #91 sequencing sense	5894 .. 5917	24			primer_bind
✓ pHAGE-A4050-3550	5929 .. 5951	23			primer_bind
✓ HIV nef	5939 .. 6027	89			misc_feature
/note	= HIV nef				
✓ HIV PPT	5989 .. 6003	15			misc_feature
/note	= Polypurene Tract (Not degraded by RNaseH so it can serve as a primer for + strand DNA synthesis during viral life cycle)				
✓ dU3 LTR	6004 .. 6239	236			misc_feature
/gene	= dU3 LTR				
/note	= Deleted U3 Long-Terminal Repeat				
✓ HIV R	6041 .. 6156	116			misc_feature
/note	= HIV Repeat Region				
✓ Difference from 5' LTR	6052 .. 6052	1			modified_base
/note	= This T is a C in the 5' LTR				
✓ HIV U5	6157 .. 6239	83			misc_feature
/note	= HIV U5				
✓ pHAGE-S4501-5000	6237 .. 6268	32			primer_bind
✓ 3' Flank	6240 .. 6310	71			misc_feature
/note	= Chromosomal 3' Flanking Sequence carried over from original HIV integration site				
✓ pHAGE-S6001-6500	6343 .. 6365	23			primer_bind
✓ P-Bla	6514 .. 6548	35			promoter
/note	= Beta Lactamase Promoter				

Feature	Location	Size (bp)			Type
✓ AMP^r	6567 .. 7406	840			CDS
/gene	= AMP ^r				
/product	= beta-lactamase (mature form)				
/note	= Ampicillin Resistance Gene				
/translation	= RVALIPFFAAAFCLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRRPEERFPMMSDFKVLCCGAVLSRVDACRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAFLHNMGDHDVTRLDRWEPELDERDTTTPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPIIVVIYTTGSQATMDERNRQIAEIGASLIKHW				
	280 amino acids = 30.8 kDa				
✓ pHAGE-A6050-5550	6616 .. 6639	24			primer_bind
✓ pHAGE-S6501-7000	6816 .. 6840	25			primer_bind
✓ pHAGE-A6550-6050	7085 .. 7108	24			primer_bind
✓ pHAGE-S7001-7500	7336 .. 7360	25			primer_bind
✓ pHAGE-A7050-6550	7596 .. 7617	22			primer_bind
✓ ORI	7635 .. 8168	534			rep_origin
/gene	= ORI				
/note	= Bacterial Origin of Replication				
✓ pHAGE-S7501-8000	7840 .. 7864	25			primer_bind
✓ pHAGE-A7550-7050	8107 .. 8128	22			primer_bind
✓ pHAGE-S8001-8500	8343 .. 8362	20			primer_bind
✓ SV40 ori	8405 .. 8528	124			misc_feature
/gene	= SV40 ori				
✓ pHAGE-A8050-7550	8583 .. 8609	27			primer_bind
✓ pHAGE-S1-500	8848 .. 8876	29			primer_bind