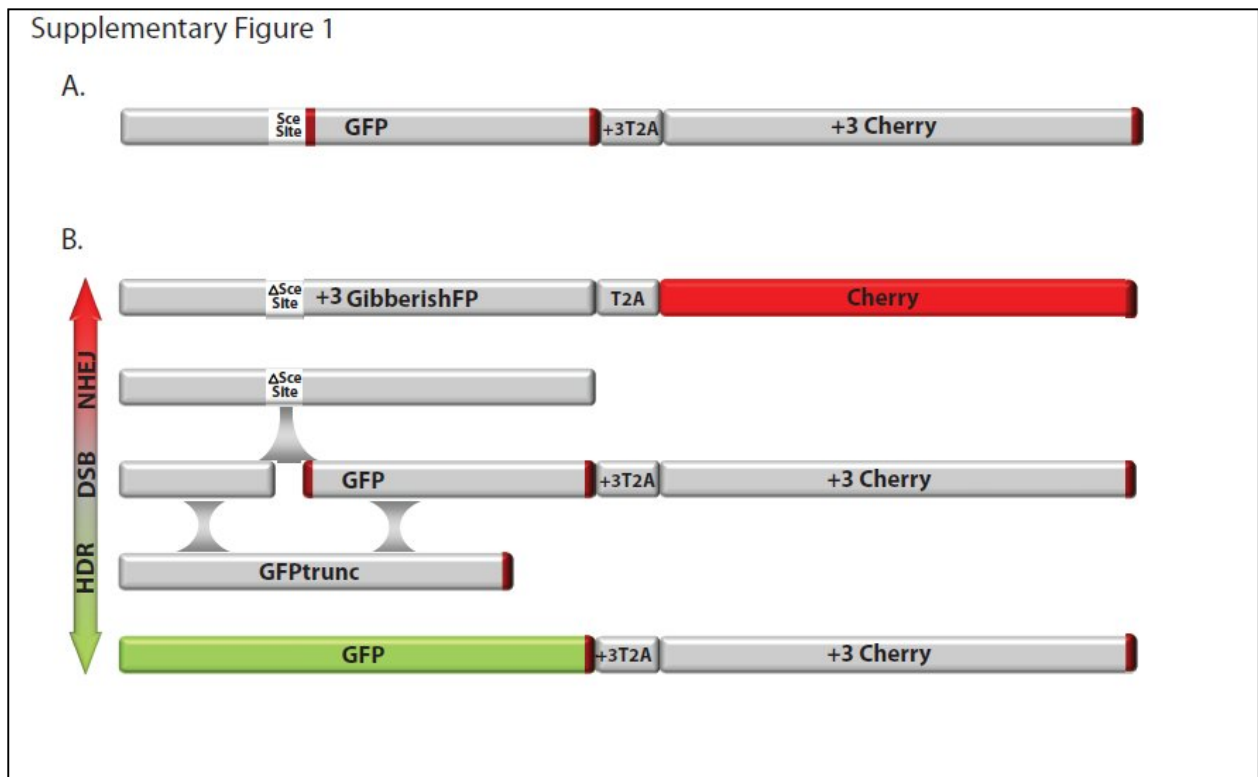


Supplementary Figures

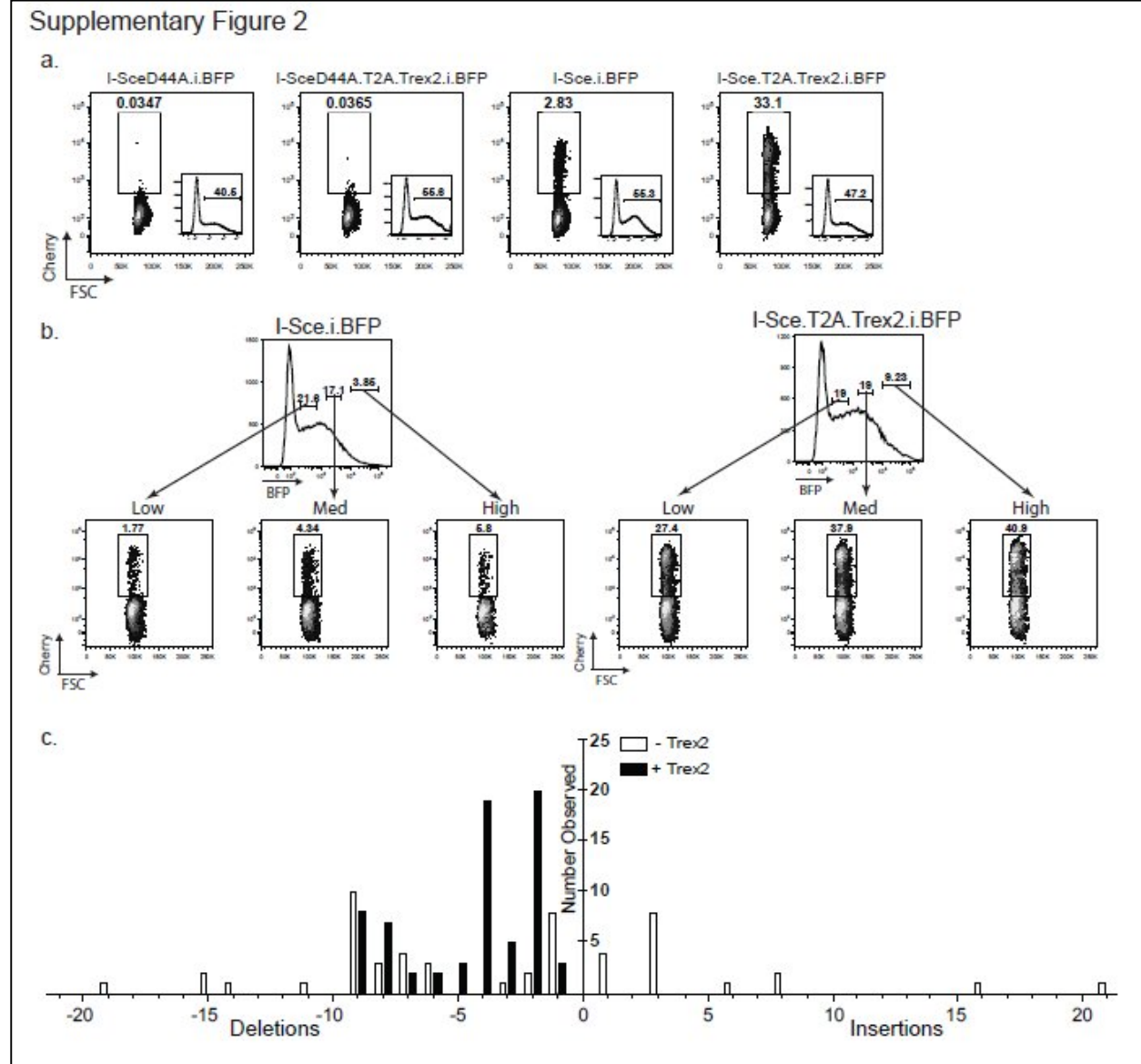
Supplementary Figure 1. Schematic of the Traffic Light Reporter (TLR).

(a). Schematic of the TLR locus harbouring the I-SceI target site embedded within the +1 GFP reading frame, followed by the T2A.mCherry ORFs in the +3 reading frame. (b). Diagram of the TLR outcomes following repair pathway choice. A fluorescent GFP protein will be translated if a homology-directed repair (HDR) event occurs, while a fluorescent mCherry protein will be expressed if a mutagenic NHEJ event occurs that results in a +3 frameshift.



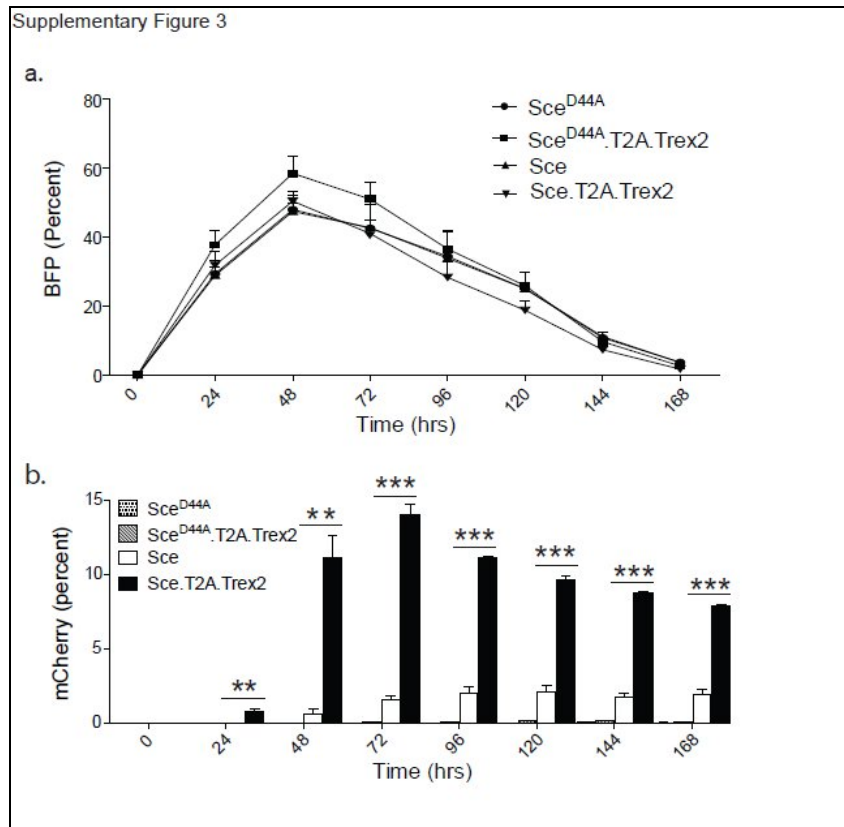
Supplementary Figure 2. Trex2 increases gene disruption frequency of I-SceI mediated breaks

(a). Representative flow plots 72 hours post transfection of HEK293T traffic light reporter cells with indicated vectors. Cherry indicates gene disruption rates observed in transfected cells, inset flow plots show gating for BFP positive cells to normalize for transfection efficiency. (b) Gating analysis of BFP fluorescence (analyzed as low, med, and high) of HEK293T TLR-Sce cells following transfection with the indicated vectors. (c) Sizes of insertions and deletions found in HEK293T TLR-Sce cells with or without Trex2.



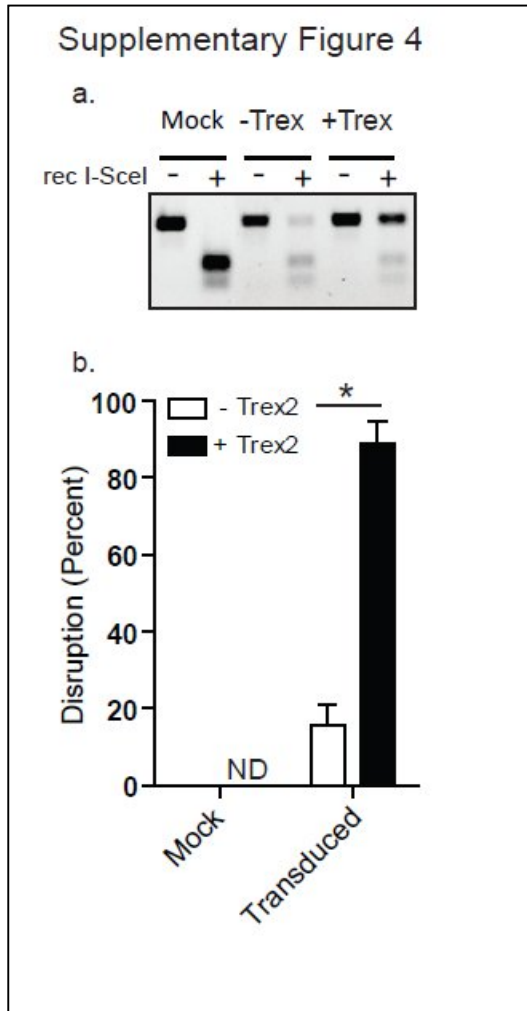
Supplementary Figure 3. Kinetic analysis of repair.

(a). Analysis of BFP expression at the time-points indicated following transfection with the indicated vectors. The constructs shown are tagged to BFP by an IRES sequence downstream of either I-SceI or Trex2. (b) Quantification of 3 experiments of HEK293T cells transfected with the indicated vectors, analyzed at the indicated time-points. Cherry indicates gene disruption rates observed in transfected cells.



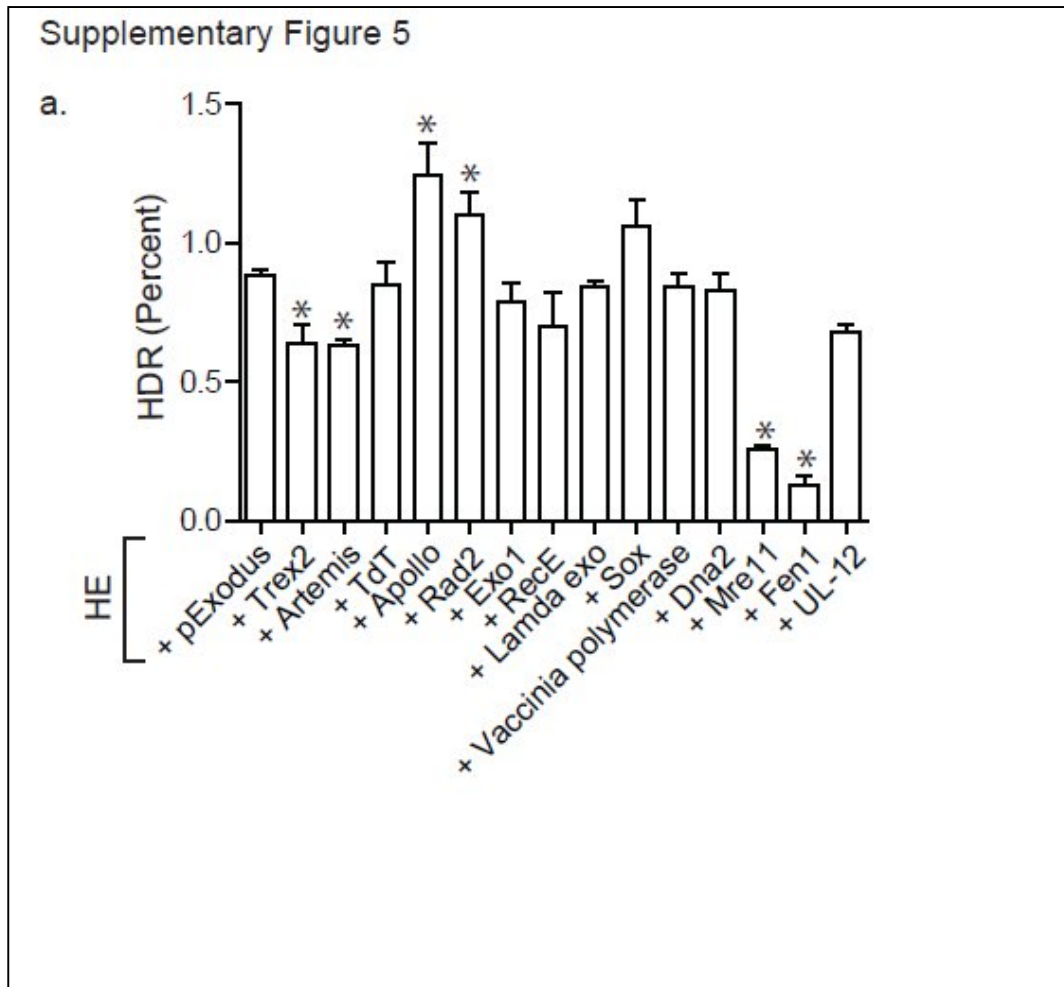
Supplementary Figure 4. Trex2 increases the gene disruption efficiency of I-SceI in primary MEFs.

(a) Digestion of PCR amplified I-SceI site in primary MEFs derived from the “Sce-SCID” mouse model 72hrs post transduction with Sce.i.BFP and Sce.T2A.Trex2.i.BFP LV at an MOI of 10. Recombinant (rec) I-SceI resistant bands indicate gene disruption. (b) Quantitation of 2 independent experiments as performed in a. ND, not determined.



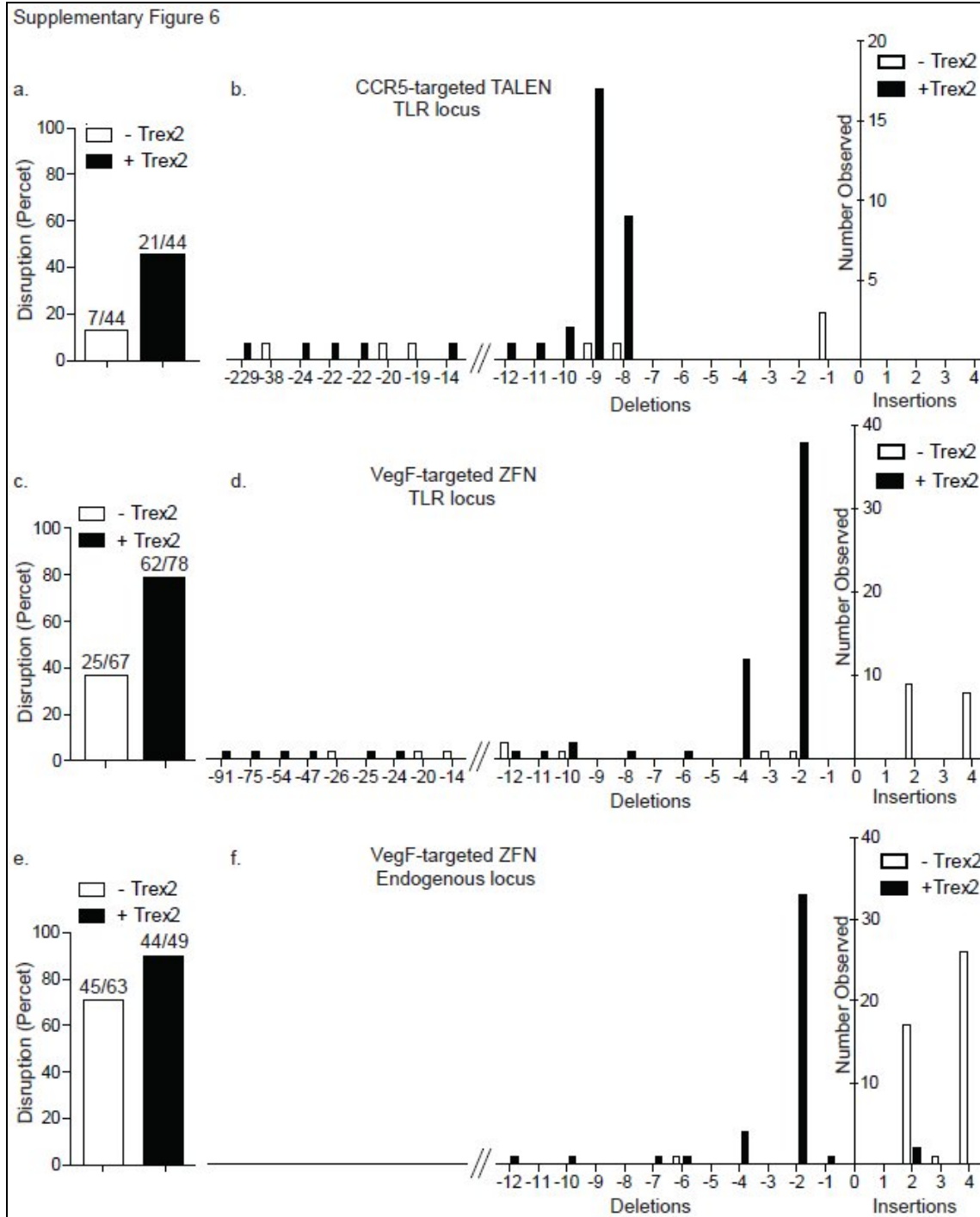
Supplementary Figure 5. Rates of homology-directed repair (HDR) in cells expressing I-SceI and an end-processing enzyme.

(a). Quantitation of homology-directed repair (HDR) of 3 independent experiments of HEK293T I-SceI TLR cells expressing I-SceI and either pExodus (control empty vector) or an end-processing enzyme. Measurement of HDR is based on GFP fluorescence from the Traffic Light reporter assay, 72 hours post-transfection. Error bars represent standard error of the mean (SEM), and *p*-values (with * representing $p < 0.05$) were calculated using the Student's two-tailed unpaired t-test. *p* values indicate a significant difference between samples expressing an enzyme from the library with designer endonuclease, compared to endonuclease with pExodus.



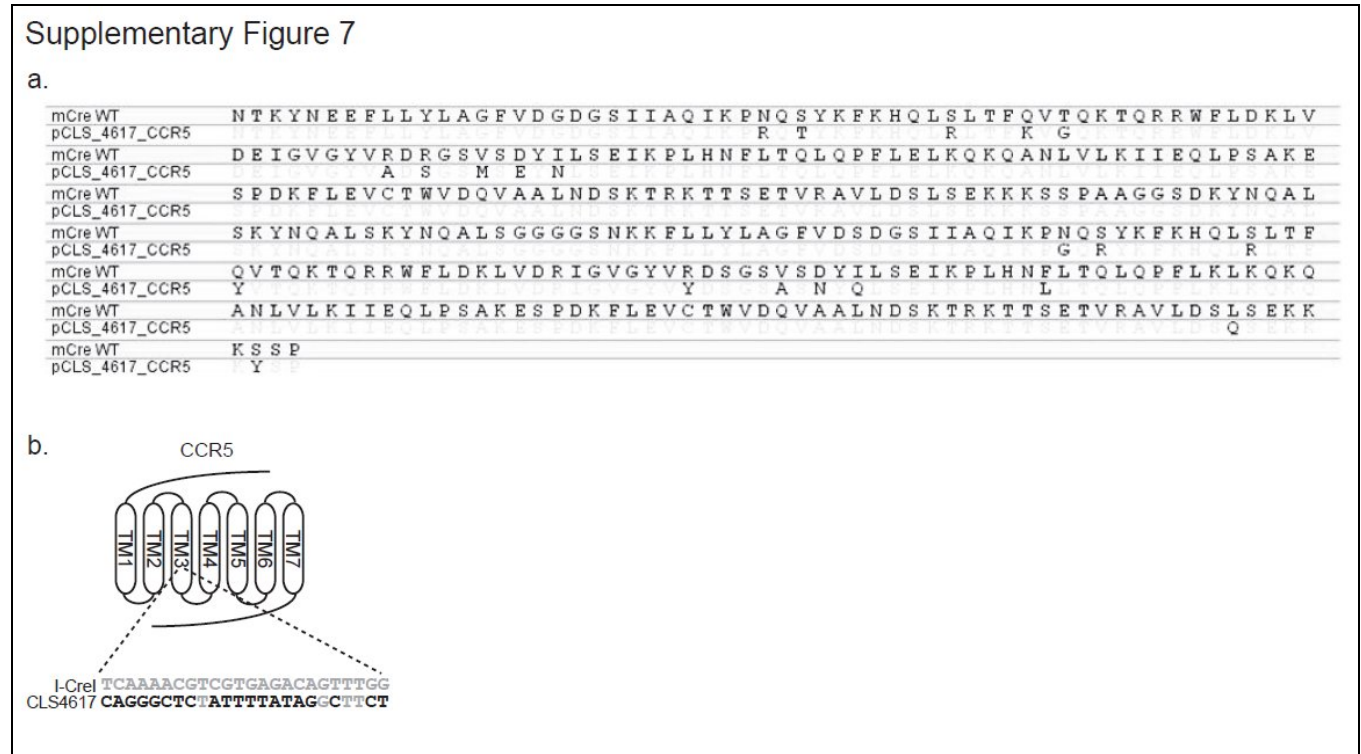
Supplementary Figure 6. Modification rates and mutation spectra of TALEN or ZFN with and without Trex2 by sequencing analysis.

(a, c, e). Quantification of overall disruption rates by CCR5 TALEN at TLR locus (a), VegF ZFN at TLR locus (c) or endogenous locus (e) with or without Trex2. Numbers above bars represent mutated sequences over total sequences analyzed. **(b, d, f).** Base pair modifications induced by CCR5 TALEN (b), or VegF ZFN (d, f) with or without Trex2.



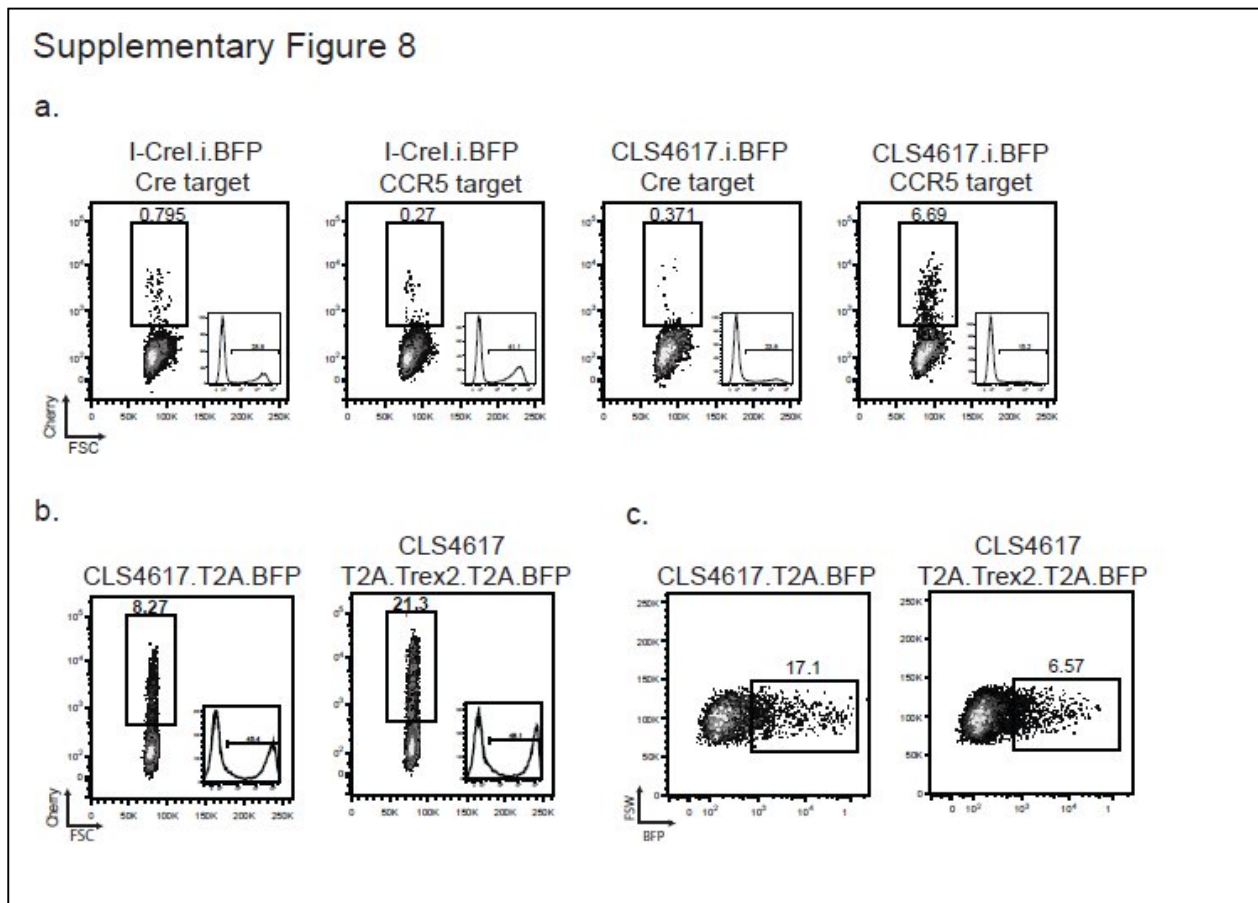
Supplementary Figure 7. Sequence alignment and schematic CLS4617 with mCreWT.

(a). mCreWT refers to the sequence of the wild-type monomerized Cre enzyme, while pCLS_4617_CCR5 refers to the amino acid residues changed in the re-designed enzyme, referred to as CLS4617. (b). Schematic of the CLS4617 target site, compared to the I-CreI target site, within the third transmembrane domain of the CCR5 gene.



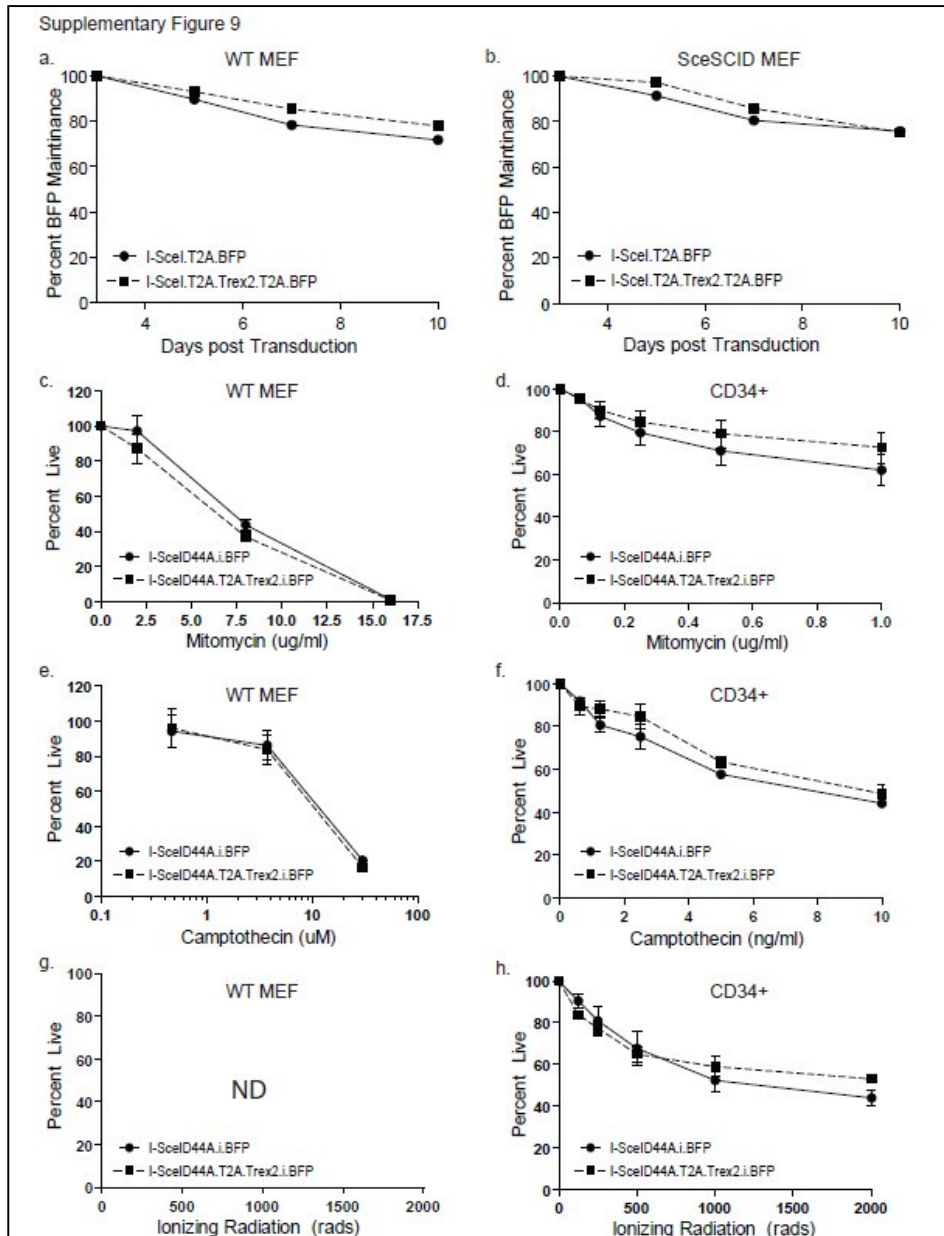
Supplementary Figure 8. Trex2 increases knockout of CCR5 with an engineered homing endonuclease.

(a) Representative flow plots from HEK293T cells containing traffic light reporters with the I-CreI cognate and CLS4617 targets following transfection with each enzyme. (b) Representative flow plot following transfection of HEK293T traffic light reporter cells with CLS4617 target with the indicated vectors. (c) Representative flow plot following transduction of CD34⁺ cells with lentiviral vectors at an MOI of 20.



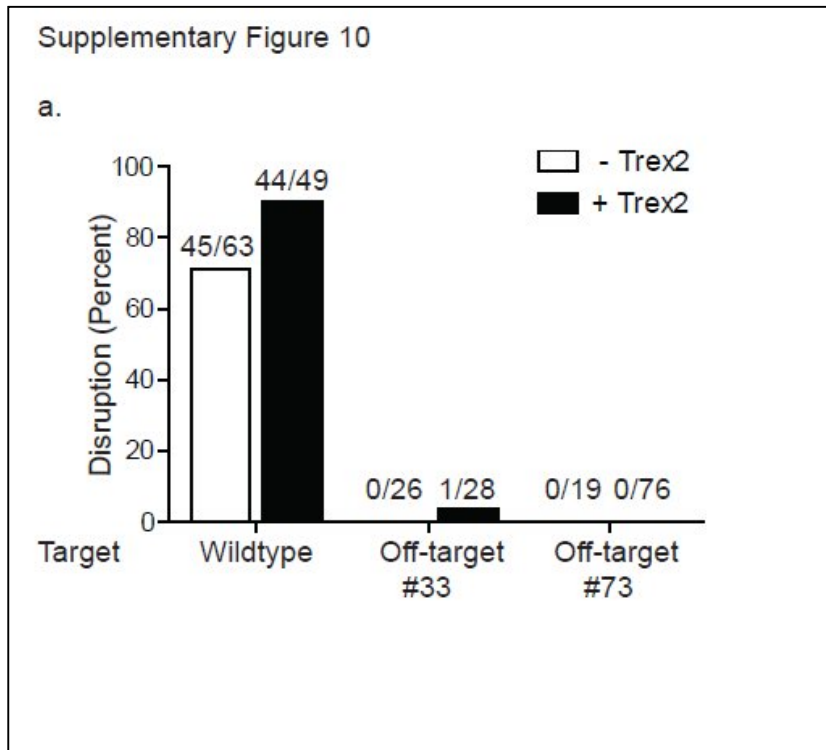
Supplementary Figure 9. Trex2 does not cause toxicity or sensitivity to DNA damaging agents.

(a,b). BFP maintenance in WT MEF (a) and SceSCID MEF (b) primary cells expressing I-SceI with or without co-expression of Trex2 over 10 day period. (c, d). Survival of WT MEFs (c) or CD34+ human primary cells (d) by quantification of propidium iodide negative cells following transduction with indicated recombinant LV, and treatment with mitomycin C at the indicated doses. (e, f) Survival of WT MEFs (e) or CD34+ human primary cells (f) by quantification of propidium iodide negative cells following transduction with indicated recombinant LV, and treatment with camptothecin at the indicated doses. (g). Survival of WT MEFs transduced with the indicated vectors and treated with ionizing radiation was not determined (ND), as no death was detectable with the indicated doses of radiation. (h) Survival of CD34+ human primary cells following transduction with indicated recombinant LV, and treatment with ionizing radiation at the indicated doses.



Supplementary Figure 10. Off-target effects of VegF ZFN with or without Trex2.

(a). Sequence analysis of mutations induced by VegF ZFN with or without Trex2 at the indicated genomic loci. Off-targets refer to published loci¹⁷. Numbers above bars represent mutated sequences over total sequences analyzed.



Supplementary Tables

Supplementary Table 1: Homing endonucleases used in this study and their target sites.

Homing Endonucleases	Target
I-SceI	TAGGGATAACAGGGTAAT
I-LtrI	AATGCTCCTATACGACGTTTAG
I-Gpil	TTTTCTGTATATGACTTAAAT
I-GzeI	GCCCCTCATAACCCGTATCAAG
I-xMpeMI (unpublished, A.R.L., A.M.S.)	TAGATAACCATAAGTGGCTAAT
I-PanMI	GCTCCTCATAATCCTTATCAAG
I-CreI	TCAAAACGTCGTGAGACAGTTTGG
I-OnuI	TTTCCAATTATTCAACCTTTTA
I-HjeMI	TTGAGGAGGTTTCTCTGTTAAT
I-Anil	TGAGGAGGTTTCTCTGTAAA
CLS4617	CAGGGCTCTATTTTATAGGCTTCT

Supplementary Table 2: Library of DNA end-processing enzymes.

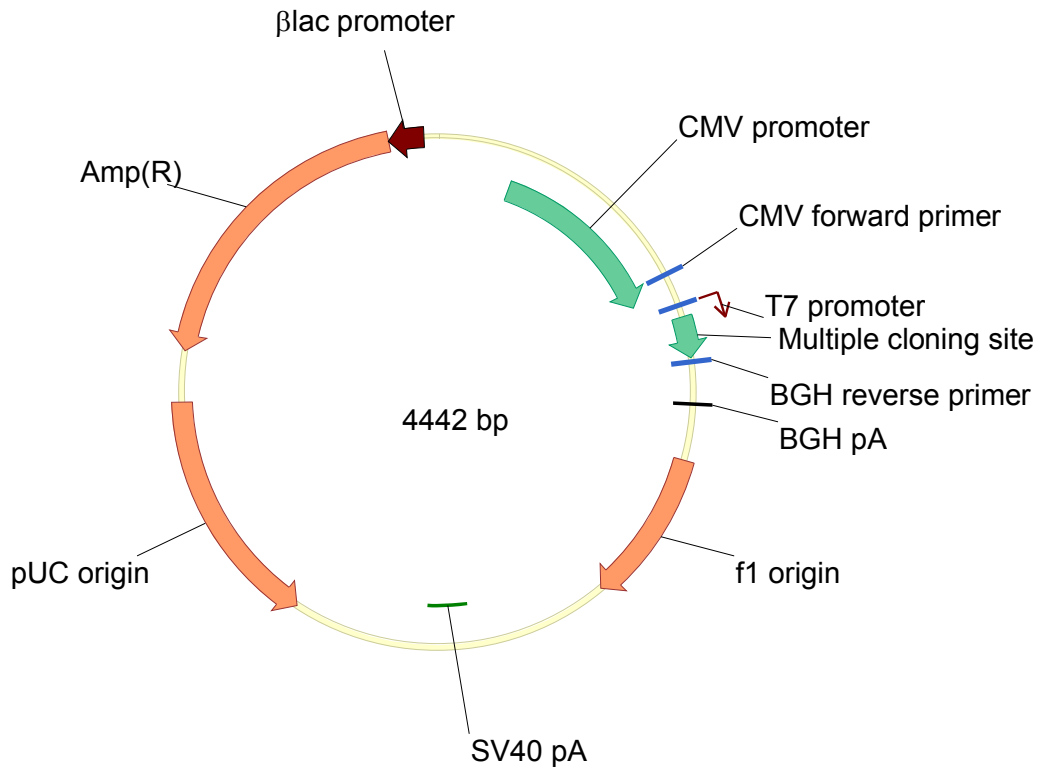
Enzyme	Gene name	Activity	Species of origin	NLS added	Reference
Apollo	SNM1B	5-3' exonuclease	Human	No	Lenain <i>et al</i> ¹
Artemis	Artemis	5-3' exonuclease	Human	No	Kurosawa <i>et al</i> ²
Dna2	DNA2	5-3' exonuclease, helicase	Human	No	Nimonkar <i>et al</i> ³
Exo1	EXO1	5-3' exonuclease	Human	No	Nimonkar <i>et al</i> ³ , Orans <i>et al</i> ⁴
Fen1	FEN1	5' flap endonuclease	Human	No	Jagannathan <i>et al</i> ⁵ , Tsutakawa <i>et al</i> ⁶
Mre11	MRE11	5-3' and 3-5' exonuclease	Human	No	Garcia <i>et al</i> ⁷
Rad2	n/a (catalytic domain of Exo1)	5-3' exonuclease (Exo1 catalytic domain)	Human	No	Lee and Wilson ⁸
TdT (terminal deoxynucleotidyl transferase)	TdT	Single-stranded template-independent DNA polymerase	Human	No	Mahajan <i>et al</i> ⁹
RecE	RecE	5-3' exonuclease	<i>E. coli</i>	Yes	Zhang <i>et al</i> ¹⁰
Lambda exonuclease	λ exonuclease	5-3' exonuclease	Bacteriophage λ	Yes	Zhang <i>et al</i> ¹¹
Sox (T24I mutation)	SOX	5-3' alkaline exonuclease	Kaposi's sarcoma-associated herpesvirus	Yes	Glaunsinger <i>et al</i> ¹² ; Daltroth <i>et al</i> ¹³
Vaccinia DNA polymerase	E9L	3-5' exonuclease	Vaccinia poxvirus	Yes	Gammon and Evans ¹⁴
UL-12	UL12	5-3' alkaline exonuclease	Herpes simplex virus (HSV)-1	Yes	Reuven <i>et al</i> ¹⁵ ; Balasubramanian <i>et al</i> ¹⁶

Supplemental References

1. Lenain, C. et al. The Apollo 5' exonuclease functions together with TRF2 to protect telomeres from DNA repair. *Curr Biol* 16, 1303-1310 (2006).
2. Kurosawa, A. & Adachi, N. Functions and regulation of Artemis: a goddess in the maintenance of genome integrity. *J Radiat Res (Tokyo)* 51, 503-509 (2010).
3. Nimonkar, A.V. et al. BLM-DNA2-RPA-MRN and EXO1-BLM-RPA-MRN constitute two DNA end resection machineries for human DNA break repair. *Genes Dev* 25, 350-362 (2011).
4. Orans, J. et al. Structures of human exonuclease 1 DNA complexes suggest a unified mechanism for nuclease family. *Cell* 145, 212-223 (2011).
5. Jagannathan, I., Peppenella, S. & Hayes, J.J. Activity of FEN1 endonuclease on nucleosome substrates is dependent upon DNA sequence but not flap orientation. *J Biol Chem* 286, 17521-17529 (2011).
6. Tsutakawa, S.E. et al. Human flap endonuclease structures, DNA double-base flipping, and a unified understanding of the FEN1 superfamily. *Cell* 145, 198-211 (2011).
7. Garcia, V., Phelps, S.E., Gray, S. & Neale, M.J. Bidirectional resection of DNA double-strand breaks by Mre11 and Exo1. *Nature* 479, 241-244 (2011).
8. Lee, B.I. & Wilson, D.M., 3rd The RAD2 domain of human exonuclease 1 exhibits 5' to 3' exonuclease and flap structure-specific endonuclease activities. *J Biol Chem* 274, 37763-37769 (1999).
9. Mahajan, K.N. et al. Association of terminal deoxynucleotidyl transferase with Ku. *Proc Natl Acad Sci U S A* 96, 13926-13931 (1999).
10. Zhang, J., Xing, X., Herr, A.B. & Bell, C.E. Crystal structure of E. coli RecE protein reveals a toroidal tetramer for processing double-stranded DNA breaks. *Structure* 17, 690-702 (2009).
11. Zhang, J., McCabe, K.A. & Bell, C.E. Crystal structures of lambda exonuclease in complex with DNA suggest an electrostatic ratchet mechanism for processivity. *Proc Natl Acad Sci U S A* 108, 11872-11877 (2011).
12. Glaunsinger, B., Chavez, L. & Ganem, D. The exonuclease and host shutoff functions of the SOX protein of Kaposi's sarcoma-associated herpesvirus are genetically separable. *J Virol* 79, 7396-7401 (2005).
13. Dahlroth, S.L. et al. Crystal structure of the shutoff and exonuclease protein from the oncogenic Kaposi's sarcoma-associated herpesvirus. *FEBS J* 276, 6636-6645 (2009).
14. Gammon, D.B. & Evans, D.H. The 3'-to-5' exonuclease activity of vaccinia virus DNA polymerase is essential and plays a role in promoting virus genetic recombination. *J Virol* 83, 4236-4250 (2009).
15. Reuven, N.B., Staire, A.E., Myers, R.S. & Weller, S.K. The herpes simplex virus type 1 alkaline nuclease and single-stranded DNA binding protein mediate strand exchange in vitro. *J Virol* 77, 7425-7433 (2003).
16. Balasubramanian, N., Bai, P., Buchek, G., Korza, G. & Weller, S.K. Physical interaction between the herpes simplex virus type 1 exonuclease, UL12, and the DNA double-strand break-sensing MRN complex. *J Virol* 84, 12504-12514 (2010).
17. Pattanayak, V., Ramirez, C.L., Joung, J.K., Liu, D.R. Revealing off-target cleavage specificities of zinc-finger nucleases by *in vitro* selection. *Nat Meth* 8, 765-770 (2011).

Supplementary Note 1: Vector Maps

pExodus



General Description

DNA Exodus MCS

Entire molecule length: 4442 bp

Feature Map

CDS (1 total)

Amp(R)

Start: 3446 End: 4306 (Complementary)

Original Location Description:

complement(3446..4306)

Qualifiers:

/in vitro="1020000"

Misc. Feature (1 total)

MCS

Start: 895 End: 1010

Original Location Description:

895..1010

Qualifiers:

/invtrogen="1630000"

PolyA Signal (1 total)

SV40 pA

Start: 2118 End: 2248

Original Location Description:

2118..2248

Qualifiers:

/invtrogen="1840000"

PolyA Site (1 total)

BGH pA

Start: 1028 End: 1252

Original Location Description:

1028..1252

Qualifiers:

/invtrogen="1870000"

Promoter Eukaryotic (1 total)

CMV promoter

Start: 232 End: 819

Original Location Description:

232..819

Qualifiers:

/invtrogen="2180000"

Promoter Prokaryotic (2 total)

T7 promoter

Start: 863 End: 879

Original Location Description:

863..879

Qualifiers:

/invitrogen="2370000"

bla promoter

Start: 4307 End: 4405 (Complementary)

Original Location Description:

complement(4307..4405)

Qualifiers:

/invitrogen="2330000"

Replication Origin (2 total)

f1 origin

Start: 1298 End: 1726

Original Location Description:

1298..1726

Qualifiers:

/invitrogen="2500000"

pUC origin

Start: 2631 End: 3301 (Complementary)

Original Location Description:

complement(2631..3301)

Qualifiers:

/invitrogen="2540000"

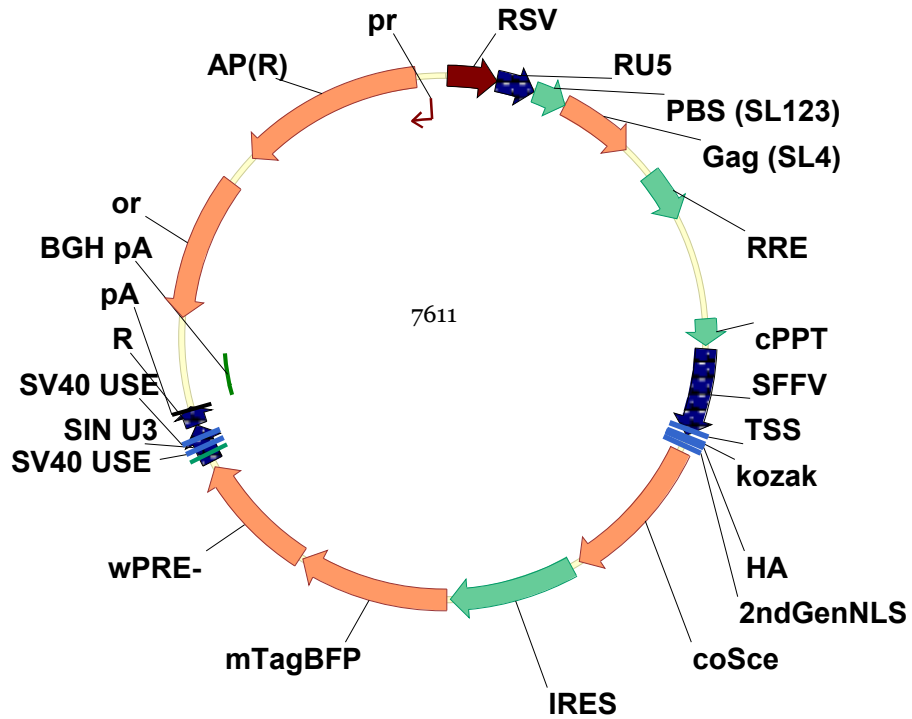
Sequence

```
1 gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg ccgcatagtt aagccagtat ctgctccctg cttgtgttt
101 ggaggtcgcct gagtagtgcg cgagcaaaat ttaagtaca acaaggcaag gcttgaccga caattgcatg aagaatctgc ttagggtag gcgttttgcg
201 ctgcttcgcg atgtacgggc cagatatacg cgttgacatt gattattgac tagttattaa tagtaatcaa ttacggggtc attagtcat agcccatata
301 tggagttccg cgttacataa cttacggtaa atggcccgc tggctgaccg cccaacgacc ccccccatt gacgtcaata atgacgtatg ttcccatagt
401 aacccaata gggacttcc attgacgtca atgggtggag tatttacggt aaactgccca ctggcagta catcaagtgt atcatatgcc aagtacgcc
501 cctattgacg tcaatgacgg taaatggccc gcctggcatt atgccagta catgacctta tgggacttct ctactggca gtacatctac gtattagtca
601 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggttg actcacgggg atttccaagt ctccaccca ttgacgtcaa
```


701 tgggagtttg ttttgcacc aaaatcaacg ggactttcca aaatgtcgt acaactccgc cccattgacg caaatgggcg gtaggcgtgt acggtgggag
801 gtctataata cgagagctct ctggtaact agagaacca ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccaa gctggctagc
901 gtttaaactt aagcttgga cagctcgg atccactagt ccagtgtggt ggaattctgc agatatccag cacagtggcg gccgctcag tctagaggc
1001 ccgtttaaac ccgctgatca gcctcactg tgccttctag ttgcagcca tctgttgtt gccctcccc cgtgcctcc ttgacctgg aaggtgccac
1101 tcccactgtc ctttctaata aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg gggggggggg tggggcagga cagcaagggg
1201 gaggattggg aagacaatag caggcatgct ggggatgctg tgggtctat ggcttctgag gcgaaagaa ccagctgggg ctctaggggg tatccccag
1301 gcacctgtag cggcgcatta agcgcggcgg gtgtgggtg tacgcgcagc gtaccgcta cacttgcca gcacctagc cccgctcct tcgcttctt
1401 ccttcttt ctcgccagt tcggcgctt tccccgtaa gctctaaat gggggctccc ttagggctc cgatttagt cttacggca cctcagcccc
1501 aaaaaacttg attagggtga tggttcacgt agtgggcat gcacctgata gacggtttt gcctttga cgttggagtc cacgtttt aatagtgga
1601 tctgttcca aactggaaca acactcaacc ctatctcgtt ctattcttt gattataag ggattttgcc gatttcggc tattggttaa aaaatgagct
1701 gatttaacaa aaattaacg cgaattaatt ctgtggaatg tgtgtcagt aggggtgtgga aagccccag gctcccagc aggcagaagt atgcaaagcc
1801 tatcaggaca tagcgttggc taccctgat attgctaag agcttggcgg cgaatgggct gaccttcc tcgtcttta cggtatcgc gctcccatt
1901 cgcagcgcac gccttctat gccttctg acgagtctt ctgagcggga ctctggggtt cgaatgacc gaccaagcga gcccaacct gccatcaga
2001 gatttcgatt ccaccggc cttctatgaa aggttggct tcggaatct tttcgggac gccgctgga tgatctcca gcgagggat ctatctggt
2101 agttcttgc ccacccaac ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa ttcacaaat aaagcattt tttactgca
2201 ttctagtgt gtttgtcca aactcatca tgatcttat catgtctgta taccgtcag ctctagctag agcttggcgt aatcatggtc atagctgtt
2301 cctgtgtgaa attgtatcc gctcacaatt ccacacaaca tacgagccgg aagcataaag tgtaaaacct ggggtgccta atgagtgagc taactcacat
2401 taattcggt gcgctcactg cccgtttcc agtgggaaa cctgtctgc cagctcatt aatgaatcgg ccaacgcgc gggagaggcg gtttgcgat
2501 tggcgctct tccgttct cgctcactga ctgctcgc tcggtcttc ggctcggcg agcggatca gctcactca aggcggtaat acggtatcc
2601 acagaatcag gggataacg aggaagaac atgtgagca aaggccagca aaaggccagg aaccgtaaaa agcccgctt gctggcgtt ttccataggg
2701 tccgcccc tgacagcat cacaaaaatc gacgtcaag tcagaggtgg gaaaccga caggactata aagataccag gcgtttccc ctggaagtc
2801 cctgtgctc tctctgtc cgacctgcc gcttaccga tacgtctcc ctttctccc ttcgggaagc gtggcgctt ctcatagctc acgcttagg
2901 tatctcagt cgggtaggt cgttctcc aagctggct gtgtcacga accccctt cagccgacc gctgcctt atccgtaac tatctcttg
3001 agtcaacc ggtaagacac gacttatgc cactggcagc agccactgtt aacaggata gcagagcag gatgtaggc ggtgctacag agttctgaa
3101 gtgtggcct aactacgct acactagaag aacagtattt ggtatctgc ctctctgaa gccagttacc ttcgaaaa gagttgtag ctctgatcc
3201 ggcaaaaa ccaccgtg tagcggttt tttttgca agcagcagat tacgcgaga aaaaaaggat ctcaagaaga tctttgatc ttttctacgg
3301 ggtctgacg tcagtgaac gaaaactcac gtaaggat tttgtcatg agattatca aaaggatctt cacctagatc ttttaaat aaaaatgaag
3401 ttttaata atctaaagta tatatgagta aacttggct gacagttacc aatgctaat cagttaggca cctatctcag cgatctgtct atttctca
3501 tccatagtg cctgactccc cgtctgtag ataactacga tacggagggt cttaccatct ggccccagt ctgcaatgat accgcgagac ccacgtcac
3601 cggctcaga tttatcaga ataaaccagc cagccggaag ggccgagcga agaagtgtc ctgcaactt atccgctcc atccagtcta ttaattgtg
3701 ccgggaagct agagtaagta gttccagat taatagttg cgcaactgt ttgccattgc tacaggcatc gtgtgtcac gctcgtgtt tggtaggct

3801 tcattcagct ccggttcca acgatcaagg cgagttacat gatcccccatt gttgtcaaa aaagcggta gctcctcgg tctccgac gttgcagaa
 3901 gtaagtggc gcagtgta tcaatcatgg ttatggcagc actgcataat tcttctactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta
 4001 ctcaaccaag tcattctgag aatagtgtat gcggcgaccg agttgctct gccggcgtc aatacgggat aataccgcgc cacatagcag aactttaaa
 4101 gtgctcatca ttgaaaacg ttttcgggg cgaaaactct caagatctt accgctgtg agatccagtt c gatgtaacc cactcgtgca cccaactgat
 4201 cttcagcatc ttttacttc accagcgtt ctgggtgagc aaaaacagga aggcataatg ccgcaaaaaa gggaataagg gcgacacgga aatgttgaat
 4301 actcatactc tttcttttc aatattatg aagcattat cagggttatt gtctcatgag cggatacata ttgtaagtga tttagaaaaa taaacaaata
 4401 ggggttccgc gcacatttcc ccgaaaagt ccacctgacg tc

pCVL.SFFV.HA.NLS.Sce(Opt).IRES.mTagBFP



General Description

DNA Plasmid pCVL.SFFV.HA.NLS.SceOpt.IRES.mTagBFP

Entire molecule length: 7611 bp

Feature Map

CDS (5 total)

Gag (SL4)

Start: 572 End: 924

Original Location Description:

572..924

coSce

Start: 2438 End: 3139

Original Location Description:

2438..3139

mTagBFP

Start: 3784 End: 4485

Original Location Description:

3784..4485

wPRE-O

Start: 4500 End: 5080

Original Location Description:

4500..5080

AP(R)

Start: 6621 End: 7481 (Complementary)

bla gene- Ap(r) determinant

Original Location Description:

complement(6621..7481)

LTR (4 total)

RU5

Start: 236 End: 417

Original Location Description:

236..417

SFFV

Start: 1946 End: 2355

Original Location Description:

1946..2355

Qualifiers:

/gene="MESV"

/product="#AJ224005"

/SECDrawAs="Gene"

SIN U3

Start: 5112 End: 5293

Original Location Description:

5112..5293

R

Start: 5294 End: 5383

Original Location Description:

5294..5383

PBS (SL123)

Start: 418 End: 571

Original Location Description:

418..571

RRE

Start: 1081 End: 1322

Original Location Description:

1081..1322

cPPT

Start: 1806 End: 1929

Original Location Description:

1806..1929

kozak

Start: 2366 End: 2374

Original Location Description:

2366..2374

ATG

Start: 2375 End: 2377

Original Location Description:

2375..2377

HA

Start: 2381 End: 2407

Original Location Description:

2381..2407

2ndGenNLS

Start: 2408 End: 2431

Original Location Description:

2408..2431

IRES

Start: 3183 End: 3768

Original Location Description:

3183..3768

SV40 USE

Start: 5186 End: 5229

Original Location Description:

5186..5229

SV40 USE

Start: 5233 End: 5276

Original Location Description:

5233..5276

PolyA Signal (1 total)

BGH pA

Start: 5385 End: 5618

Original Location Description:

5385..5618

PolyA Site (1 total)

pA

Start: 5367 End: 5372

Original Location Description:

5367..5372

Primer (1 total)

Promoter Prokaryotic (2 total)

RSV

Start: 7 End: 235

Original Location Description:

7..235

pr

Start: 7546 End: 7551 (Complementary)

Original Location Description:

complement(7546..7551)

Replication Origin (1 total)

ori

Start: 5800 End: 6473 (Complementary)

Original Location Description:

complement(5800..6473)

mRNA (1 total)

TSS

Start: 2330 End: 2355

Original Location Description:

2330..2355

Sequence

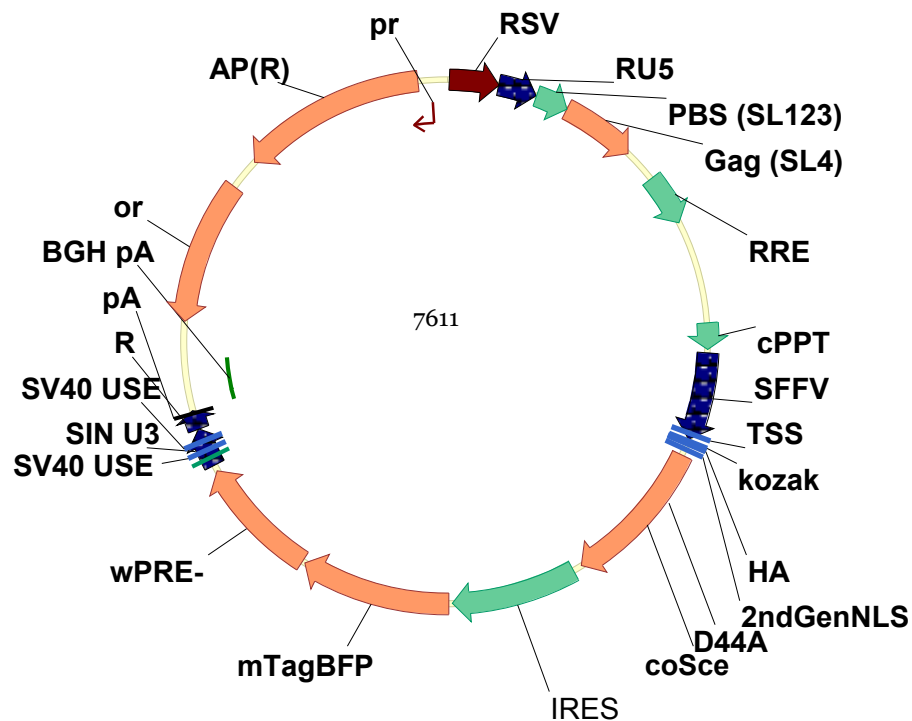
```
1  gacgtcaatg tagtcttatg caatactctt gtagtcttgc aacatggtaa cgatgagtta gcaacatgcc ttacaaggag agaaaaagca ccgtgcatgc
101 cgattggtgg aagtaagggt gtacgatcgt gccttattag gaaggcaaca gacgggtctg acatggattg gacgaaccac tgaattgccg cattgcagag
201 atattgtatt taagtgccta gctcgatata taaacgggtc tctctggta gaccagatct gagcctggga gctctctggc taactagga acccactgct
301 taagcctcaa taaagcttgc cttgagtct tcaagtagtg tgtcccgtc tgttgtgta ccttgtaac tagatatccc tcagaccctt ttagtcagtg
401 tggaaaatct cttagcagtg gcgccgaaca gggactgaa agcgaaggg aaaccagagg agctctctcg acgcaggact cggcttgctg aagcgcgcac
501 ggcaagaggc gaggggcggc gactggtgag tacgcaaaa attttgacta gcggaggcta gaaggagaga gatgggtgcg agagcgtcag tattaagcgg
```

601 gggagaatta gatcgcgatg ggaaaaaatt cggttaagcg cagggggaaa gaaaaaatat aaattaaac atatagtatg ggcaagcagg gagctagaac
701 gattcgcagt taatcctggc ctgtagaaa catcagaagg ctgtagacaa atactgggac agctacaacc atccctcag acaggatcag aagaacttag
801 atcattatat aatacagtag caaccctcta ttgtgtgcat caaaggatag agataaaga caccaaggaa gcttagaca agatagagga agagcaaac
901 aaaagtaaga ccaccgcaca gcaagcggcc ctgatctta gacctggagg aggagatag agggacaatt ggagaagtga attatataa tataaagtag
1001 taaaattga accattagga gtagcacca ccaaggcaaa gagaagagtg gtgcagagag aaaaagagc agtgggaata ggagcttgt tcctggggt
1101 cttgggagca gcaggaagca ctatggcgcg agcgtcaatg acgctgacgg tacaggccag acaattattg tctggtatag tgcagcagca gaacaattg
1201 ctgagggcta ttgaggcgca acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa gaatcctgag tctggaaaga tacctaaagg
1301 atcaacagct cctggggatt tgggggtgct ctgaaaaact catttgacc actgctgtgc ctggaatgc tagttggagt aatgaatctc tggaacagat
1401 ttggaatcac acgacctgga tggagtggga cagagaaatt aacaattaca caagctaat acactccta attgaagaat cgcaaaacca gcaagaaaag
1501 aatgaacaag aattattgga attagataa tgggcaagtt tgtggaattg gtttaacata acaattggc tgtgtatat aaaattatc ataagtag
1601 taggaggctt ggtaggttta agaatagttt ttgctgact ttctatagt aatagagta ggaggagata ttcaccata tcgttcaga cccacctcc
1701 aaccccagg ggaccgcaca ggcccgaagg aatagaaga gaaggtggag agagagacag agacagatcc atcgattag tgaacggatc tcgacggat
1801 cggttaactt taaaagaaa aggggggatt ggggggtaca gtgcagggga aagaatagta gacataatag caacagatc acaactaaa gaattacaaa
1901 aacaattac aaaaattca aattttatcg attacgctc acgtgctagc tgcagtaacg ccaatttgca aggcattgaa aaatacaaa ccaagaatg
2001 agaagttcag atcaaggcg ggtacatgaa aatagctaac gttggccaa acaggatctc tgcggtgagc agtttcggcc ccgcccggg gccaagaaca
2101 gatggtcacc gcagtttcgg ccccgcccg aggccaagaa cagatggtcc ccagataggg cccaacctc agcagttct taagacctc cagatgttc
2201 caggctccc caaggacctg aatgacctc gcgcttatt tgaattaacc aatcagcctg cttctgctt ctgttcgag gcttctgctt cccgagctc
2301 ataaaagagc tcacaacccc tcaactggcg cgccagtct ccgacagact gactgcccc ctcgagccc caccatggga tatccatagc atgtccaga
2401 ttatgcgcca cctaagaaga aacgcaaagt cgaattcaag aacatcaaga agaaccaggt catgaacctg ggcccaca gcaagctgct gaagagtagc
2501 aagaccagc tgatcgagct gaacatcgag cagttcgagg ccggcatcgg cctgactctg ggccagcct acatcaggag caggagcag ggcaagacct
2601 actgcatgca gttcagtgag aagaacaagg cctacatgga ccactgtgct ctgctgtacg accagtgggt gctgagcccc ccccaaga aggagagggt
2701 gaaccacctg ggcaacctgg tcatcactg gggcggccag acctcaagc accaggcctt caacaagctg gccaacctgt tcatctgaa caacaaga
2801 accatccca acaacctgtg ggagaactac ctgacccca tgagcctgct ctactgttc atggacgagc gcggcaagt ggactacaac aagaacagca
2901 ccaacaagag catctgtgct aacaccaga gttcacctt cgaggagggt gagtacctg tgaaggcct gaggacaag ttccagctga actgctactg
3001 gaagatcaac aagaacaagc ccatcatcta catcgacagc atgagctacc tgatcttcta caactgatc aagccctacc tgatccca gatgatgac
3101 aagctgcca acaccatcag cagcgagacc ttctgaagt gacctgagg tcgagcatgc atctaggcg gccaattccg cccctctcc tccccccc
3201 ctaactgtac tggccgaagc cgcttgaat aaggccggtg tgcgttctc tatatgtgat ttccacct attgccctt tttgcaatg tgaggcccg
3301 gaaacctgag cctgtcttct tgacagcat tcttaggggt cttccctc tcgcaaaagg aatgcaaggt ctgttgaatg tctgaagga agcagttct
3401 ctggaagctt ctgaagaca aacaactct gtagcagcc ttgaggca cggaacccc caactggcg acaggtgct ctgcccga aagccagtg
3501 tataagatac acctgcaaag gcgacacaac cccagtgcca cgttgtgagt tggatagttg tggaaagagt caaatggctc tcctcaagc tattcaaca
3601 ggggctgaag gatgccaga aggtaccca ttgatggga tctgatctgg ggcctgggt cacatgctt acatgttt agtcaggtt aaaaaact

3701 ctaggccccc cgaaccacgg ggcagtgggt ttccttgaa aaacacgatg ataagcttg cacaacctt accggtcgcc accatgagcg agctgattaa
3801 ggagaacatg cacatgaagc tgtacatgga gggcaccgtg gacaaccatc acttcaagtg cacatccgag ggcaaggca agcctacga gggcaccag
3901 accatgagaa tcaagtggt cgaggcggc cctctccct tgccttca catctggct actagcttcc tctacggcag caagacctc atcaaccaca
4001 cccaggcat cccgacttc ttaagcagt ccttccctga gggcttaca tgggagagag tcaccacata cgaagacggg ggcgtgctga cggctacca
4101 ggacaccagc ctccaggagc gctgctcat ctacaacgtc aagatcagag ggggaactt cacatcaac ggccttga tgcagaagaa aacctcggc
4201 tgggagcct tcaccgagc gctgtacccc gctgacggcg gcctggaagg cagaaacgac atggcctga agctcgtggg cgggagccat ctgatcгаа
4301 acatcaagac cacatataga tccaagaac ccgtaagaa cctcaagatg cctggcgtct actatgtgga ctacagactg gaaagaatca aggaggcaa
4401 caacagacc tacgtcagc agcacgaggt ggcagtggcc agatactcg acctccctag caaactgggg cacaagctta attgattcta gagtcgacc
4501 agcatctac cgccattat acctatatt gttctgttt tcttgattg ggtatacatt taaatgtaa tagaacaana tgggtgggca atcattaca
4601 tttttagga tatgtaatta ctagtccag gtattgcca caagacaaa atgttaagaa acttcccgt tatttacgt ctgttctgt taatcaact
4701 ctggattaca aaatttga aagattgact gatattcta actatgttc tcttttacg ctgtgtggat atgtcttt atagcctctg tatctagcta
4801 ttgctcccg tacgcttct gtttctct cttgtataa atcctggtg ctgtcttt tagaggagt gtggcccgt gtccgtcaac gtggcgtgt
4901 gtgctctgtg tttctgac caacccac tggctggggc atggccaca cctgtcaact ctttctggg acttctgct tcccctccc gatcggcag
5001 gcagaactca tcgccctg cttgcccg tgctggacag gggctaggtt gctggcact gataatccg tgggtgtgc atcgctacct ttttaaaaga
5101 aaagggggga ctggaaggc taattcact ccaacgaaga caagatatca taactcgt tagcatacat tacaagaat tataattat ttgtaaatt
5201 tgtgatgcta ttgcttatt tgtaaccata tgtttattg tgaattgt gatgctatt cttattgt aaccattgt tttgctgt actggctct
5301 tctggtaga ccagatcga gcctgggagc tcttggtca actagggaac ccaactgcta agcctcaata aagcttgcct cgaccagct cgactgtgc
5401 ttctagtgc cagcatctg ttgtttccc ctcccctg ccttctga cctggaagg tgccactccc actgtcctt ctaataaaa tgaggaaatt
5501 gcatgcatt gtctagtag gtgtattct attctgggg gtgggtggg gcaggacagc aaggggagg attggaaga caatagcagg catgctgggg
5601 atcggtggg ctctatggc tgcagctga ttaatgaat ggccaacgcg cggggagagg cggtttgcgt attggcgtct cttccgttc ctgctcact
5701 gactcgtgc gctcgtctg tcggctcgg cgagcgtat cagctcact aaaggcgtata atcggttat ccacagaatc aggggataac gcaggaaaga
5801 acatgtgagc aaaaggccag caaaaggcca ggaaccgtaa aaaggccgcg ttgctggcgt ttttcatag gctccgccc cctgacgagc atcaaaaa
5901 tcgactca agtcagaggt ggcgaaacc gacaggacta taaagatacc aggcgttcc cctggaagc tccctgtgc gctctctgt tccacctg
6001 ccgctaccg gatactgtc gcctttct cctcgggaa gcgtggcgt tttcatagc tcacgctga ggtatctcag ttcggttag gtcgtctg
6101 ccaagctggg ctgtgtcac gaaccccc ttaccccga cgctcgcct tttccgta actatctct tgagtccaac ccgtaagac acgactatc
6201 gccactgca gcagccactg gtaaccagat tagcagagcg aggtatgtag cgggtgctac agatttctg aagtggtggc ctaactcgg ctactaga
6301 aggacagat ttggtatctg cgctctgctg aagccagta cttcggaaa aagattggt agctcttgat cggcaaaaca aaccaccgt ggtagcggg
6401 gttttttgt ttcaagcag cagattacgc gcagaaaaa aggatctca gaagatcct tgatctttc tacgggtct gacgctcagt ggaacaaaa
6501 ctcagttaa gggatttgg tcatgagatt atcaaaaagg atcttacct agatctttt aaataaaaa tgaagttta aatcaatca aagtatat
6601 gagtaactt ggtctgacag ttaccaatgc ttaacagtg aggcacatc ctacgcatc tcttatttc gttcatcat agttgcctga ctcccctg
6701 ttagataac tacgatacgg gaggcttac catctggccc cagtctgca atgataccg gagaccacg ctaccggct ccagattat cagcaataa

6801 ccagccagcc ggaagggccg agcgcagaag tggctctgca actttatccg cctccatcca gtctattaat tgttgccggg aagctagagt aagtagttcg
6901 ccagttaata gtttgcgcaa cgttggtgcc attgctacag gcatcgtggt gtcacgctcg tcgtttggta tggcttcatt cagctccggt tccaacgat
7001 caagggcagt tacatgatcc cccatgttgt gcaaaaaagc ggttagctcc ttcggtctc cgatcgttgt cagaagtaag ttggccgcag tgttatcact
7101 catggttatg gcagcactgc ataattctct tactgtcatg ccatccgtaa gatgctttc tgtgactggt gagtactcaa ccaagtcatt ctgagaatag
7201 tgtatcgggc gaccgagttg ctcttgcccg gcgtcaatac gggataatac cgccacat agcagaactt taaaagtct catcattgga aaacgttct
7301 cggggcgaaa actctcaagg atcttaccgc tgttgagatc cagttcagtg taaccactc gtgcaccaa ctgatcttca gcatcttita ctttcaccag
7401 cgtttctggg tgagcaaaaa caggaaggca aaatgccga aaaaaggaa taagggcgac acggaaatgt tgaatactca tactcttct ttttcaat
7501 tattgaagca tttatcaggg ttattgtctc atgagcggat acatattga atgtattag aaaaataaac aaataggggt tccgcgcaca tttcccga
7601 aagtccacc t

pCVL.SFFV.HA.NLS.Sce(Opt)D44A.IRES.mTagB



General Description

DNA Plasmid pCVL.SFFV.HA.NLS.SceOptD44A.IRES.mTagBFP

Entire molecule length: 7611 bp

Feature Map

CDS (5 total)

Gag (SL4)

Start: 572 End: 924

Original Location Description:

572..924

coSce

Start: 2438 End: 3139

Original Location Description:

2438..3139

mTagBFP

Start: 3784 End: 4485

Original Location Description:

3784..4485

wPRE-O

Start: 4500 End: 5080

Original Location Description:

4500..5080

AP(R)

Start: 6621 End: 7481 (Complementary)

bla gene- Ap(r) determinant

Original Location Description:

complement(6621..7481)

LTR (4 total)

RU5

Start: 236 End: 417

Original Location Description:

236..417

SFFV

Start: 1946 End: 2355

Original Location Description:

1946..2355

Qualifiers:

/gene=""MESV"

/product=""#AJ224005"

/SECDrawAs=""Gene"

SIN U3

Start: 5112 End: 5293

Original Location Description:

5112..5293

R

Start: 5294 End: 5383

Original Location Description:

5294..5383

PBS (SL123)

Start: 418 End: 571

Original Location Description:

418..571

RRE

Start: 1081 End: 1322

Original Location Description:

1081..1322

cPPT

Start: 1806 End: 1929

Original Location Description:

1806..1929

kozak

Start: 2366 End: 2374

Original Location Description:

2366..2374

ATG

Start: 2375 End: 2377

Original Location Description:

2375..2377

HA

Start: 2381 End: 2407

Original Location Description:

2381..2407

2ndGenNLS

Start: 2408 End: 2431

Original Location Description:

2408..2431

IRES

Start: 3183 End: 3768

Original Location Description:

3183..3768

SV40 USE

Start: 5186 End: 5229

Original Location Description:

5186..5229

SV40 USE

Start: 5233 End: 5276

Original Location Description:

5233..5276

PolyA Signal (1 total)

BGH pA

Start: 5385 End: 5618

Original Location Description:

5385..5618

PolyA Site (1 total)

pA

Start: 5367 End: 5372

Original Location Description:

5367..5372

Primer (1 total)

Promoter Prokaryotic (2 total)

RSV

Start: 7 End: 235

Original Location Description:

7..235

pr

Start: 7546 End: 7551 (Complementary)

Original Location Description:

complement(7546..7551)

Replication Origin (1 total)

ori

Start: 5800 End: 6473 (Complementary)

Original Location Description:

complement(5800..6473)

mRNA (1 total)

TSS

Start: 2330 End: 2355

Original Location Description:

2330..2355

Sequence

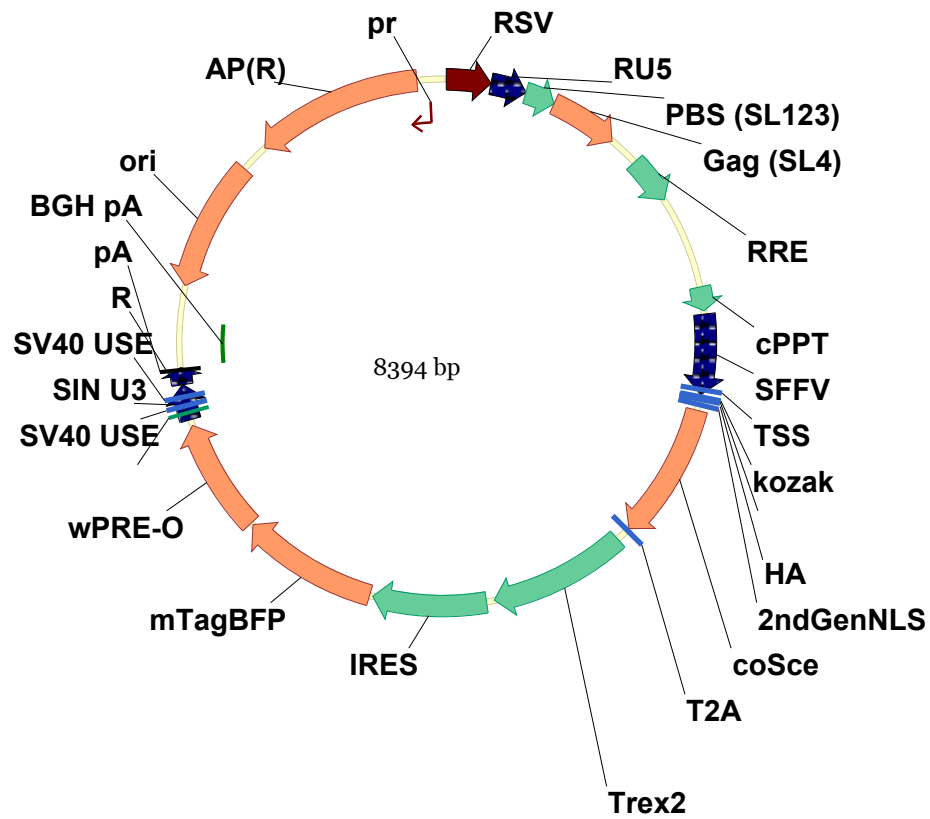
```
1 gacgtcaatg tagtcttatg caatactctt gtagtcttgc aacatggtaa cgatgagtta gcaacatgcc ttacaaggag agaaaaagca cogtgcacgc
101 cgattggtgg aagtaagggtg gtacgatcgt gccttattag gaaggcaaca gacgggtctg acatggattg gacgaaccac tgaattgccg cattgcagag
201 atattgtatt taagtgccta gctcgataca taaacgggtc tctctggtta gaccagatct gagcctggga gctctctggc taactagga acccactgct
301 taagcctcaa taaagcttgc cttgagtgtc tcaagtagtg tgtgccctgc tgttgtgtga ctctggtaac tagagatccc tcagaccctt ttagtcagtg
401 tggaaaatct ctagcagtg gccccgaaca gggactgaa agcgaaggagg aaaccagagg agctctctcg acgcaggact cggcttgctg aagcgcgcac
501 ggcaagaggc gaggggaggc gactggtgag tacgcaaaa atttgacta gcggaggcta gaaggagaga gatgggtgag agagcgtcag tattaagcgg
601 gggagaatta gatgcgatg ggaaaaaatt cggttaaggc cagggggaaa gaaaaaatat aaattaaac atatagtatg ggcaagcagg gagctagaac
```

701 gattcgagc taactctggc ctgtagaaa catcagaagg ctgtagacaa atactgggac agctacaacc atcccttcag acaggatcag aagaacttag
801 atcattatat aatacagtag caaccctcta ttgtgtgcat caaaggatag agataaaaga caccaaggaa gctttagaca agatagagga agagcaaaac
901 aaaaagtaaga ccaccgcaca gcaagcggcc ctgatctca gacctggagg aggagatatg agggacaatt ggagaagtga attatataaa tataaagtag
1001 taaaattga accattagga gtagcaccca ccaaggcaaa gagaagagt gtgcagagag aaaaaagagc agtgggaata ggagctttgt tccttgggtt
1101 ctggggagca gcaggaagca ctatgggcgc agcgtcaatg acgctgacgg tacaggccag acaattattg tctggtatag tgcagcagca gaacaattg
1201 ctgagggcta ttgaggcgca acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa gaatctggc tgtggaaaga tacctaagg
1301 atcaacagct cctggggatt tggggttct ctgaaaact catttgacc actgctgtgc ctggaatgc tagttggagt aatgaatct tgaacagat
1401 ttggaatcac acgacctgga tggagtggga cagagaaatt aacaattaca caagcttaac acactcctta attgaagaat cgcaaaacca gcaagaaaag
1501 aatgaacaag aattattgga attagataaa tgggcaagt tgtggaattg gtttaacata acaaatggc tgtgtatata aaaattatc ataatgatag
1601 taggaggctt gtaggttta agaatagtt ttgctgtact ttctatagt aatagagta ggcaggata ttaccatta tctttcaga cccactccc
1701 aaccccgagg ggaccgcaca ggcccgaagg aatagaaga gaaggtggag agagagacag agacagatcc attcgattag tgaacggatc tgcagcgtat
1801 cggtaactt taaaagaaa aggggggatt ggggggtaca gtgcagggga aagaatagta gacataatag caacagacat acaactaaa gaattacaaa
1901 aacaaattac aaaaattcaa aattttatc attacgctc acgtgctagc tgcagtaacg ccattttgca aggcattgga aataccaaa ccaagaatag
2001 agaagttcag atcaaggcgc ggtacatgaa aatagctaac gttggccaa acaggatct tgcggtgagc agtttcggcc ccgcccggg gccaagaaca
2101 gatggctacc gcagtttccg ccccgcccg aggccaagaa cagatggcc ccagatattg ccaaccctc agcagtttct taagacccat cagatgttct
2201 caggctcccc caaggacctg aatgacctc gcgcttatt tgaattaacc aatcagcctg ctctcgtt ctgttcgctc gcttctgct cccgagctc
2301 ataaaagagc tcacaacccc tactcggcg cgccagctct cgcagacact gactcggcg ctgagccgc cacatggga tatccatag atgtcccaga
2401 ttatcgcca cctaagaaga aacgcaagt cgaattcaag aatcaaga agaaccaggt catgaacctg ggcccaaca gcaagctgct gaaggagtag
2501 aagagccagc tgcagagct gaacatcag cagttcagg ccgcatcgg cctgatcctg ggcgctgct acatcaggag caggagcag ggcaagact
2601 actgatgca gttcagtg aagaacaagg cctacatgga ccagtgctc ctgctgacg accagtggt gctgagcccc cccacaaga agggaggggt
2701 gaaccacctg ggcaacctg tcatcactg gggcgccag acctcaagc accagcctt caacaagctg gccaacctg tcatcgtgaa caacaagaag
2801 accatcccc acaacctggt ggagaactac ctgaccccc tagcctggc ctactggtc atggagcagc gcgcaagtg ggactacaac aagaacagca
2901 ccaacaagag catcgtgctg aacaccaga gttcacctt caggagggtg gactacctg tgaaggcct gaggaacaag ttccagctga actgctact
3001 gaagatcaac aagaacaagc ccacatccta catcagacg atgagctacc tgcatttcta caacctgac aagccctacc tgatcccca gatgatgac
3101 aagctgcca acacatcag cagcagacc ttctgaagt gactgcagg tgcagctgc atctagggcg gccaattccg cccctctcc tccccccc
3201 ctaacgttac tggccgaagc cgcttgaat aaggccggtg tgcgtttgc tatatgtgat ttccacct attgccgtc ttggcaatg tgaggcccg
3301 gaaacctggc cgttcttct tgacagcat tctagggtt cttccctc tcgcaaaagg aatgcaaggt ctgtgaaat tctgaaaga agcagttct
3401 ctggaagctt ctgaaagaca aacaactct gtgacgacc ttgcaggca gcggaacccc ccactggcg acaggtgctc ctgcccga aagccactg
3501 tataagatac acctgcaaag gcggcacaac cccagtgcca cgttgtagt tggatagttg tggaaagagt caaatggctc tcctcaagc tattcaaca
3601 ggggctgaag gatgccaga aggtaccca ttgatggga tctgatctgg ggcctcgggt cacatgctt acatgttt agtcagggtt aaaaaaacg
3701 ctaggcccc cgaaccacgg ggacgtggtt ttctttgaa aaacacgatg ataagcttc cacaacctt accgctgccc accatgagc agctgataa

3801 ggagaacatg cacatgaagc tgtacatgga gggcaccgtg gacaaccatc acttcaagtg cacatccgag ggcgaaggca agccctacga gggcaccag
3901 accatgagaa tcaaggtggg cgagggcggc cctctcccct tgccttcca catcctggct actagcttcc tctacggcag caagacctc atcaaccaca
4001 cccagggcat ccccgacttc ttaagcagt ccttccctga gggcttaca tgggagagag tcaccacata cgaagacggg ggcgtgctga ccgctacca
4101 ggacaccagc ctccaggagc gctgctcat ctacaacgtc aagatcagag gggggaactt cacatccaac ggccctgtga tgcagaagaa aacctcggc
4201 tgggaggcct tcaccgagac gctgtacccc cgtgacggcg gcctggaagg cagaaaacac atggccctga agctcgtggg cgggagccat ctgatcga
4301 acatcaagc cacatataga tccaagaac ccgtaagaa cctcaagatg cctggcgtct actatgtgga ctacagactg gaaagaatca aggaggccaa
4401 caacgagacc tacgtcagc agcacgaggt ggcagtgccc agatactcgc acctccctag caaactgggg cacaagctta attgattcta gactgacccg
4501 agcatcttac cgccatttat accatattt gttctgttt tcttgatttg ggtatacatt taaatgtaa tagaacaana tgggtgggca atcattaca
4601 tttttaggga tatgtaata ctagtccagc tctgtgcca caagacaac atgttaagaa actttcccgt tatttacgt ctgttctgt taatcaact
4701 ctggattaca aaatttgta aagattgact gatatttta actatgttc tcttttacg ctgtgtggat atgtgcttt atagcctctg tatctagcta
4801 ttgctcccg tacggcttc gtttctcct cctgtataa atcctgggtg ctgtctctt tagaggagtt gtggcccgtt gtccgtaac gtggcgtgtg
4901 gtgctctgtg tttgctgac caacccccac tggctggggc attgccacca cctgtcaact ctttctggg actttcgtt tccccctcc gatcggcag
5001 gcagaactca tcgccctg cctgcccgc tctggagac gggctaggtt gctggcact gataattccg tgggtgtgc atcggtacct ttttaaaga
5101 aaagggggga ctggaaggc taattcact ccaacgaaga caagatata taactccta tagcacaat tacaagaat tataattat ttgtaaat
5201 tgtgatgcta ttgcttatt tgaaccata tgtttattg tgaattgt gatgctattg ctttattgt aaccattgct ttttctgt actgggtctc
5301 tctggtaga ccagatcga gcctgggagc tcttggtc actaggaac ccactccta agcctaata aagcttgcct cgaccagcct cgactgtcc
5401 ttctagtgc cagccatctg tttttgcc cccccctg ctttctga cctggaagg tgccactccc actgtcctt ctaataaaa tgggaaatt
5501 gcatcgcat ctctgagtag gtgtcattct attctggggg gtgggtggg gcagacagc aagggggagg attggaaga caatagcagg catgctgggg
5601 atcggtggg ctctatggc tgcagctca ttaatgaatc ggccaacgcg cggggagagg cggtttgcgt attggcgct cttcccttc ctgctcact
5701 gactcgtgc gctcgtcgt tcggctcgg cgagcggat cagctcactc aaaggcgta atacggtat ccacagaatc aggggataac gcaggaaga
5801 acatgtgagc aaaaggccag caaaaggcca ggaaccgtaa aaaggccgcg ttgctggcgt tttccatag gctccccc cctgacgagc atcaaaaa
5901 tcgacgcta agtcagaggt ggcgaaacc gacaggacta taaagatacc aggcgttcc ccctggaagc tcctcgtgc gctcctgt tccgacctg
6001 ccgctaccg gatactgtc cgccttttc cctcgggaa gcgtggcgt tctcatagc tcacgtgta ggtatctag ttcggttag gtcgttctg
6101 ccaagctggg ctgtgtcac gaacccccg ttcagcccga ccgctcgc tttatccgta actatctt tgagtccaac ccgtaagac acgacttat
6201 gccactgga gcagccactg gtaacaggat tagcagagcg aggtatgtag gcggtctac agagttctt aagtggtggc ctaactacg ctactaga
6301 aggacagat ttggtatctg cgctctcctg aagccagta cctcggaaa aagagttggt agctcttcat ccggcaaca aaccaccgt ggtagcgtg
6401 gttttttg ttcaagcag cagattacg gcagaaaaa aggatctca gaagatcctt tgatctttc tacgggtct gacgctcagt ggaacgaaa
6501 ctacgtaa gggatttgg tcatgagatt atcaaaaagg atctcact agatccttt aaataaaaa tgaagtta atcaatca aagtataat
6601 gagtaactt ggtctgacg ttaccaatgc ttaatcagt aggcacctat ctacgcatc tcttattc gttcatcat agttgctga cttccctg
6701 ttagataac tacgatacgg gagggcttac catctggccc cagtctgca atgataccg gagaccacg ctaccggct ccagattat cagcaataa
6801 ccagccagcc ggaagggccc agcgcagaag tggctctgca actttaccg cctcatca gtctatta tgttccggg aagctagat aagtagtctg

6901 ccagttaata gtttgcgcaa cgttggtgcc attgctacag gcatcgtggt gtcacgctcg tcgtttgga tggcttcatt cagctccggt tccaacgat
7001 caaggcgagt tacatgatcc cccatgtgt gcaaaaaagc ggtagctcc ttcggtcctc cgatcgttgt cagaagtaag ttggccgcag tgttatcact
7101 catggttatg gcagcactgc ataattctct tactgtcatg ccatccgtaa gatgcttttc tgtgactggt gactactcaa ccaagtcatt ctgagaatag
7201 tgotatcggc gaccgagttg ctcttgcccg gcgtcaatac gggataatac cgcgccacat agcagaactt taaaagtgtc catcattgga aaacgtttc
7301 cggggcgaaa actctcaagg atcttaccgc tgttgagatc cagttcgatg taaccactc gtgcaccaa ctgatctca gcatcttta tttccaccg
7401 cgtttctggg tgagcaaaaa caggaaggca aaatgccga aaaaaggaa taaggcgac acggaaatgt tgaatactca tactcttct tttcaatat
7501 tattgaagca tttatcaggg ttattgtctc atgagcggat acatattga atgtatttag aaaaataaac aaatagggt tccgcgcaca tttcccggaa
7601 aagtccacc t

pCVL.SFFV.HA.NLS.Sce(Opt).T2A.Trex2.IRES.mTagBFP



General Description

DNA Plasmid pCVL.SFFV.HA.NLS.SceOpt.T2A.Trex2.IRES.mTagBFP

Entire molecule length: 8394 bp

Feature Map

CDS (5 total)

Gag (SL4)

Start: 572 End: 924

Original Location Description:

572..924

coSce

Start: 2438 End: 3139

Original Location Description:

2438..3139

mTagBFP

Start: 4567 End: 5268

Original Location Description:

4567..5268

wPRE-O

Start: 5283 End: 5863

Original Location Description:

5283..5863

AP(R)

Start: 7404 End: 8264 (Complementary)

bla gene- Ap(r) determinant

Original Location Description:

complement(7404..8264)

LTR (4 total)

RU5

Start: 236 End: 417

Original Location Description:

236..417

SFFV

Start: 1946 End: 2355

Original Location Description:

1946..2355

Qualifiers:

/gene=""MESV"

/product="#AJ224005"

/SECDrawAs="Gene"

SIN U3

Start: 5895 End: 6076

Original Location Description:

5895..6076

R

Start: 6077 End: 6166

Original Location Description:

6077..6166

Misc. Feature (11 total)

PBS (SL123)

Start: 418 End: 571

Original Location Description:

418..571

RRE

Start: 1081 End: 1322

Original Location Description:

1081..1322

cPPT

Start: 1806 End: 1929

Original Location Description:

1806..1929

kozak

Start: 2366 End: 2374

Original Location Description:

2366..2374

ATG

Start: 2375 End: 2377

Original Location Description:

2375..2377

HA

Start: 2381 End: 2407

Original Location Description:

2381..2407

2ndGenNLS

Start: 2408 End: 2431

Original Location Description:

2408..2431

Trex2

Start: 3218 End: 3925

Original Location Description:

3218..3925

IRES

Start: 3966 End: 4551

Original Location Description:

3966..4551

PolyA Signal (1 total)

BGH pA

Start: 6168 End: 6401

Original Location Description:

6168..6401

PolyA Site (1 total)

pA

Start: 6150 End: 6155

Original Location Description:

6150..6155

Primer (1 total)

CVL-34

Start: 1671 End: 1692

Original Location Description:

1671..1692

Promoter Prokaryotic (2 total)

RSV

Start: 7 End: 235

Original Location Description:

7..235

pr

Start: 8329 End: 8334 (Complementary)

Original Location Description:

complement(8329..8334)

Replication Origin (1 total)

ori

Start: 6583 End: 7256 (Complementary)

Original Location Description:

complement(6583..7256)

mRNA (1 total)

TSS

Start: 2330 End: 2355

Original Location Description:

2330..2355

Sequence

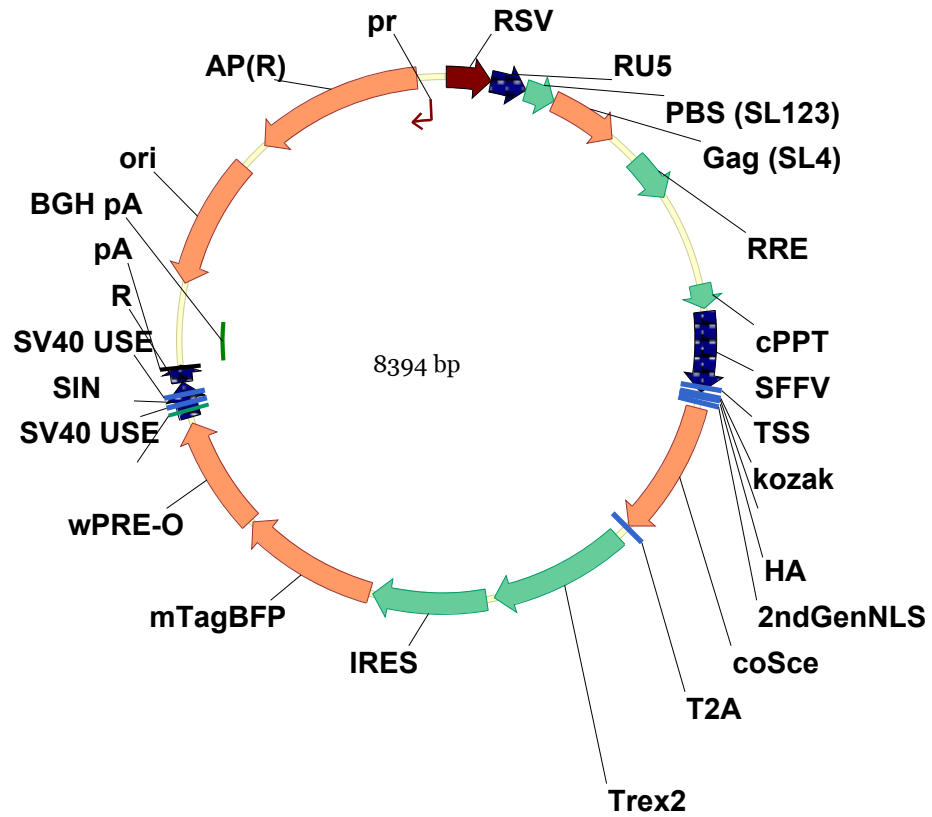
```
1 gacgtcaatg tagtcttatg caatactctt gtagtcttgc aacatggtaa cgatgagtta gcaacatgcc ttacaaggag agaaaaagca ccgtgcatgc
101 cgattggtgg aagtaagggtg gtacgatcgt gccttattag gaaggcaaca gacgggtctg acatggattg gacgaaccac tgaattgccattgcagag
201 atattgtatt taagtgccta gctcgataca taaacgggtc tctctggtta gaccagatct gagcctggga gctctctggc taactagggga acccactgct
301 taagcctcaa taaagcttgc cttagtgct tcaagtagtg tgtcccgtc tgttgtgta ctctgtaac tagagatccc tcagaccctt ttagtcagtg
401 tggaaaaatct ctagcagtgg cgcccgaaca gggacttgaa agcgaaggga aaaccagagg agctctctcg acgcaggact cggttctgtaagcgcgcac
501 ggcaagaggc gagggcgccg gactggtgag tacccaataa attttgacta gcggaggcta gaaggagaga gatgggtgcg agagcgtcag tattaagcgg
601 gggagaatta gatcgcatg ggaaaaaatt cggttaaggc cagggggaaa gaaaaaatat aaataaaac atatagtagt ggcaagcagg gagctagaac
701 gattcgcagt taatcctggc ctgttagaaa catcagaagg ctgtagacaa atactgggac agctacaacc atcccttcag acaggatcag aagaacttag
```

801 atcattatat aatacagtag caacctcta ttgtgtcat caaaggatag agataaaga caccaaggaa gcttagaca agatagga agagcaaac
901 aaaagtaaga ccaccgaca gcaagcgcc ctgatctca gacctggagg aggagatag agggacaatt ggagaagtga attatataaa tataaagtag
1001 taaaattga accattagga gtgacccca ccaaggcaaa gagaagagt gtgcagagag aaaaagagc agtgggaata ggagcttgt tccttgggt
1101 cttgggaca gcaggaaga ctatggcgc agcgtcaatg acgctgacgg tacaggccag acaattatg tctggtatag tgcagcagca gaacaattg
1201 ctgagggcta ttgaggcga acagcatctg ttgcaacta cagtctggg catcaagcag ctccaggcaa gaatctggc tgtgaaaga tacctaaagg
1301 atcaacagct cctggggatt tggggttct ctgaaaact cattgcacc actgctgtg cttggaatg tagttggagt aatgaatct tgaacagat
1401 ttggaatcac acgacctgga tggagtggga cagagaaatt aacaattaca caagctaat acactccta attgaagaat cgcaaacca gcaagaaaag
1501 aatgaacaag aattattgga attagataaa tgggcaagt tgtggaattg tttaacata acaattggc tgtgtatat aaaattatc ataatgatg
1601 taggaggctt gtaggttta agaatagtt ttgtgtact ttctatagt aatagagta ggcaggata ttcaccata tctttcaga cccactccc
1701 aaccccgagg ggaccgaca ggcccgaagg aatagaaga gaaggtggag agagagacag agacagatcc attcgattg tgaacggatc tgcagcgtat
1801 cgttaactt taaaagaaa aggggggatt ggggggtaca gtgcaggga aagaatagta gacataatag caacagacat acaactaaa gaattacaa
1901 aaaaattac aaaaattca aatttatcg attacgctc acgtgctagc tgcagtaacg ccattttgca agcatggaa aatacaaaa ccaagaatg
2001 agaagttcag atcaaggcgc ggtacatgaa aatagctaac gttggccaa acaggatc tgcggtgagc agtttcggcc ccggccggg gccaagaaca
2101 gatgtcacc gcagtttcg ccccgcccaggccaagaa cagatgttcc ccagatag cccaacctc agcagttct taagacccat cagatgtttc
2201 caggctccc caaggacctg aatgacctc gcgccttatt tgaattaacc aatcagcctg cttctgctt ctgttcgac gcttctgctt cccgagctt
2301 ataaaagagc tcacaaccc tcaactggcg cgccagtct ccgacagact gactgcccc ctcgagccc caccatggga tatccatag atgtcccaga
2401 ttatcgcca cctaagaaga aacgcaagt cgaattcaag aacatcaaga agaaccaggt catgaacctg ggcccaaca gcaagctgct gaaggagtac
2501 aagagccagc tgcagcagc gaacatcag cagttcagg ccggatcgg cctgatcct ggagcgcct acatcaggag caggagcag ggcaagact
2601 actgatcga gttcagtg aagaacaagg cctacatgga ccacgtgct ctgctgacg accagtggt gctgagccc ccccaaga agggagggg
2701 gaaccactg ggcaactgg tcatcactg gggcggcag acctcaagc accagcctt caacaagctg gccaacctg tcatcgtgaa caacaagaag
2801 accatccca acaactggt ggagaactac tgacccca tgagcctgct cactgttc atggacgac gcggcaagt ggactaac aagaacagca
2901 ccaacaagag catcgtgct aacaccaga gcttacctt cgaggaggtg gactacgg tgaaggcct gaggaaag ttccagctga actgctagc
3001 gaagatcaac aagaacaagc ccacatccta catcagacg atgactacc tgcatttcta caactgatc aagccctacc tgatccca gatgatgac
3101 aagctccca acaccatcag cagcagacc ttctgaagg gcggcggcg atccggtgag ggcagaggaa gtcttcaac atgcggtgac gtgaggaga
3201 atccggccc ctcggatct gagccactc gggctgagc cttgtattc ctgacatag aagcactg gctcccaac atggacctg agattcaga
3301 gatatcctt ttgtcttc accgtctc cctggagaac ccagaacgg atgattctg ttcttggg ctgccccg tctggaca gctcactg
3401 tgcattgccc cggagcccc cttactgccc aaggcagtg agtactggt ttgagcagc gaaagcctga tgcactgccc gaagctggt tcaatggcg
3501 ctgtgtaag gacactcag ggcttctaa gccccagga gggcccatc tgcctgtgg ccacaatg cttcattat gactccac tgcgtgac
3601 ggagctaca cgtctgggt cccatctcc ccaagacact gctgctgg acacactg tgcattcgg gcctggacc gtgctcacag ccagccacc
3701 agggctcaag gccgcaaaag ctacagcctg gccagtctt tccaccgcta cttcaggct gaaccagtg ctgccattc agcagaaggt gatgtcaca
3801 cctgctct gatctctc catcgtctc ctgagctct cgctggga gatgagcagg ccgcagctg ggctcatatt gagccatgt acgtgccac

3901 tgatgtcca agcctgaag cctgacctg aggtcgagca tgcatttagg gcggccaatt ccgccctct cctcccccc ccctaactg tactggccga
4001 agccgcttgg aataaggccg gtgtgcgttt gtctatatgt gattttccac catattgccg tcttttggca atgtgagggc ccggaaacct ggcctgtct
4101 tcttgacgag cattcctagg ggtctttccc ctctgccaa aggaatgcaa ggtctgttga atgtcgtgaa ggaagcagtt cctctggaag ctcttgaag
4201 acaacaacg tctgtagcga cctttgcag gcagcggaa cccccactg gcgacagggt cctctcggc caaaagccac gtgtataaga tacacctgca
4301 aaggcggcac aacccagtg ccacgttgg agttggatag ttgtgaaag agtcaaatg ctctctcaa gcgtattcaa caaggggctg aaggatgcc
4401 agaaggtacc ccattgatg ggatctgat tggggcctcg gtgcacatgc ttacatgtg tttagtcgag gtaaaaaaa cgtctaggcc ccccgaacca
4501 cggggcagtg gtttctttt gaaaaacag atgataagct tgccacaacc cttaccggtc gccacatga gcgagctgat taaggagaac atgcacatga
4601 agctgtacat ggagggcacc gtggacaacc atcactcaa gtgcacatcc gagggcgaag gcaagcccta cgagggcacc cagacatga gaatcaaggt
4701 ggtcgagggc ggcctctcc ccttcgctt cgacatcctg gctactagct tctctacgg cagcaagacc ttcataacc acacccaggg catccccgac
4801 ttctcaagc agtcctccc tgagggttc acatgggaga gagtccacc atacgaagac gggggcgtgc tgaccctac ccaggacacc agcctcagg
4901 acggctgctt catctacaac gtcaagatca gaggggtgaa cttcacatcc aacggcctg tgatgcagaa gaaaacactc ggctgggagg cttcaccga
5001 gacgctgtac cccgctgacg gcggcctgga aggcagaac gatagggccc tgaagctcgt gggcgggagc catctgatcg caaacatca gaccacat
5101 agatccaaga aaccgctaa gaacctcaag atgcctggcg tctactatgt ggactacaga ctggaagaa tcaaggaggc caacaacgag acctacgtg
5201 agcagcacga ggtggcagtg gccagatact gcgacctccc tagcaaatg gggcacaagc ttaattgatt ctagagtca cagacatct taccgcat
5301 tataccata tttgtctgt tttctgtat ttgggtatac atttaagt taatagaaca aatgggtgg gcaatcatt acatttttag ggatattgaa
5401 ttactagttc aggtgtattg ccacaagaca aacatgttaa gaaacttcc cgttattac gctctgtcc tgtaataca cctctggatt acaaaattg
5501 tgaagattg actgatattc ttaactatgt tgctctttt acgctgtgtg gatagtgc tttatagcct ctgtatctag ctattgctt ccgtacggc
5601 ttctttttt cctcttga taaactcgtg ttgtgtctc ttttagagga gttgtggccc gttgtccgc aactggcgt ggtgtctct gtgtttgtg
5701 acgcaacccc cactggctgg gcattgcca ccactgtca actccttct gggactttc cttccccct cccgatcgc acggcagaac tcacgccg
5801 ctgcttgc cgctgctgga caggggctag gttgctggc actgataatt ccgtgggtt gtcacggta ctttttaa agaaaaggg ggactggaag
5901 ggctaattca ctccaacga agacaagata tcaacttc gtatagcata cattataca agttataatt ttttggaa atttggatg ctattgctt
6001 atttgaacc atatgttat ttgtgaaatt tgtgatgcta ttgtttatt tgtaaccatt gcttttctg ttactgggt ctctctggt agaccagat
6101 tgagcctgg agctctctg ctaactagg aaccactgc ttaagctca ataaagctg cctgaccag cctcactgt gcctctagt tgccagccat
6201 ctgtgtttg cccctcccc gtccttct tgacctgga aggtgccact cccactgtc tttcctaata aatgaggaa attgcatgc attgtctgag
6301 taggtgtcat tctattctg ggggtgggt ggggcaggac agcaagggg aggtggga agacaatagc aggcagctg gggatcggt gggctctatg
6401 gcctgacgt gcattaatga atcgccaac gcgcggggag aggcggttg cgtattggc gctctccg tctctgctc actgactgc tgcctcgtg
6501 cgttggctg cggcagcgg tatcagctca ctcaaaggcg gtaatacgt tatccacaga atcaggggat aacgcaggaa agaactgtg agcaaaaggc
6601 cagcaaaagg ccaggaaccg taaaaaggcc gcgttctgg cgttttcca taggctcgc cccctgacg agcatcaaa aatcgacgc tcaagtca
6701 ggtggcga cccgacagga ctataaagat accaggcgt tccccgga agctccctg tgcctctcc tttccgacc ctgccctta ccggatact
6801 gtccgctt ctcctcgg gaagcgtggc gctttctat agctcagct gtaggtatct cagttcgtg taggtcttc gctcaagct gggctgtg
6901 cacgaacccc ccgttcagc gcacgctgc gccttatcg gtaactatg tcttgatcc aaccggtaa gacacgact atgccactg gcagcagca

7001 ctggaacag gattagcaga gcgaggatg taggcggtc tacagagttc tgaagtgtt gccctaacta cggctacact agaaggacag tatttggtat
7101 ctgcgctctg ctgaagccag ttaccttcgg aaaaagagtt ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtggttttt tgttgcaag
7201 cagcagatta cgcgcagaaa aaaaggatct caagaagatc cttgatctt ttctacgggg tctgacgctc agtggaacga aaactcacgt taagggattt
7301 tggatcatgag attatcaaaa aggatcttca cctagatcct tttaaattaa aatgaagtt ttaaatacaat ctaaagtata tatgagtaaa ctggctga
7401 cagttaccaa tgctaatca gtgaggcacc tatctcagcg atctgtctat ttgttcatc catagttgcc tgactccccg tcgtgtagat aactacgata
7501 cgggagggtc taccatctgg cccagtgct gcaatgatac cgcgagacc acgctcaccg gctccagatt tatcagcaat aaaccagcca gccggaaggg
7601 ccgagcgcag aagtgttctt gcaacttat ccgctccat ccagtctatt aattgttgc ggaagctag agtaagtagt tcgccagta atagtttgcg
7701 caactgtgtt gccattgcta caggcatcgt ggtgtcacgc tcgtcgttg gtatggcttc atcagctcc ggtccaac gatcaaggcg agttacatga
7801 tccccatgt tgtcaaaaa agcgggttagc tccttcggtc tcccgatct gtgcagaagt aagttggccg cagtgttatc actcatggtt atggcagcac
7901 tgcataattc tcttactgtc atgccatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc atctgagaa tagtgtatgc ggcgaccgag
8001 ttgtcttgc ccgctgcaa tacgggataa taccgcgcca catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt cttcggggcg aaaacttca
8101 aggatcttac cgtgttgag atccagttcg atgtaacca ctgtgcacc caactgatct tcagcatctt ttactttcac cagcgtttct gggtgagcaa
8201 aaacaggaag gcaaaatgcc gcaaaaaagg gaataagggc gacacggaaa tgtgaatac tcatactctt ctttttcaa tattattgaa gcatttatca
8301 gggtattgt ctcatgagcg gatacatatt tgaatgtatt tagaaaaata acaaaatagg ggttcgctc acatttccc gaaaagtccc acct

pCVL.SFFV.HA.NLS.Sce(Opt)D44A.T2A.Trex2.IRES.mTagBFP



General Description

DNA Plasmid pCVL.SFFV.HA.NLS.SceOptD44A.T2A.Trex2.IRES.mTagBFP

Entire molecule length: 8394 bp

Feature Map

CDS (5 total)

Gag (SL4)

Start: 572 End: 924

Original Location Description:

572..924

coSce

Start: 2438 End: 3139

Original Location Description:

2438..3139

mTagBFP

Start: 4567 End: 5268

Original Location Description:

4567..5268

wPRE-O

Start: 5283 End: 5863

Original Location Description:

5283..5863

AP(R)

Start: 7404 End: 8264 (Complementary)

bla gene- Ap(r) determinant

Original Location Description:

complement(7404..8264)

LTR (4 total)

RU5

Start: 236 End: 417

Original Location Description:

236..417

SFFV

Start: 1946 End: 2355

Original Location Description:

1946..2355

Qualifiers:

/gene="MESV"

/product="#AJ224005"

/SECDrawAs="Gene"

SIN U3

Start: 5895 End: 6076

Original Location Description:

5895..6076

R

Start: 6077 End: 6166

Original Location Description:

6077..6166

Misc. Feature (11 total)

PBS (SL123)

Start: 418 End: 571

Original Location Description:

418..571

RRE

Start: 1081 End: 1322

Original Location Description:

1081..1322

cPPT

Start: 1806 End: 1929

Original Location Description:

1806..1929

kozak

Start: 2366 End: 2374

Original Location Description:

2366..2374

ATG

Start: 2375 End: 2377

Original Location Description:

2375..2377

HA

Start: 2381 End: 2407

Original Location Description:

2381..2407

2ndGenNLS

Start: 2408 End: 2431

Original Location Description:

2408..2431

Trex2

Start: 3218 End: 3925

Original Location Description:

3218..3925

IRES

Start: 3966 End: 4551

Original Location Description:

3966..4551

PolyA Signal (1 total)

BGH pA

Start: 6168 End: 6401

Original Location Description:

6168..6401

PolyA Site (1 total)

pA

Start: 6150 End: 6155

Original Location Description:

6150..6155

Primer (1 total)

CVL-34

Start: 1671 End: 1692

Original Location Description:

1671..1692

Promoter Prokaryotic (2 total)

RSV

Start: 7 End: 235

Original Location Description:

7..235

pr

Start: 8329 End: 8334 (Complementary)

Original Location Description:

complement(8329..8334)

Replication Origin (1 total)

ori

Start: 6583 End: 7256 (Complementary)

Original Location Description:

complement(6583..7256)

mRNA (1 total)

TSS

Start: 2330 End: 2355

Original Location Description:

2330..2355

Sequence

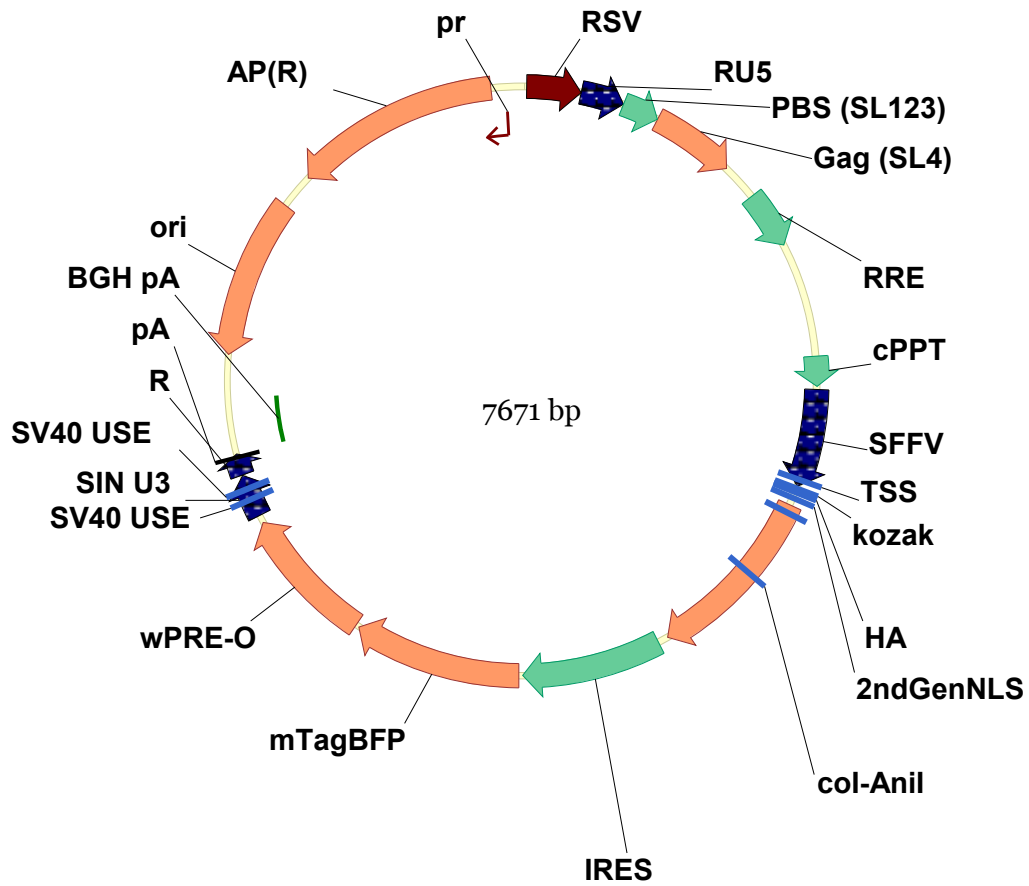
1 gacgtcaatg tagtcttatg caatactctt gtagtcttgc aacatggtaa cgatgagtta gcaacatgcc ttacaaggag agaaaaagca ccgtgcatgc
101 cgattggtgg aagtaagggtg gtacgatcgt gccttattag gaaggcaaca gacgggtctg acatggattg gacgaaccac tgaattgccattgcagag
201 atattgtatt taagtgccta gctcgataca taaacgggtc tctctgtta gaccagatct gagcctggga gctctctggc taactagga acccactgct
301 taagcctcaa taaagcttgc ctgagtgct tcaagtagtg tgtgccgctc tgttgtgta ctctgtaac tagagatccc tcagaccctt ttagtcagtg
401 tggaaaatct ctacgagtg cgcccgaaca gggacttgaa agcgaagggg aaaccagagg agctctctcg acgcaggact cggcttctgaagcgcgcac
501 ggcaagaggc gagggcgcc gactggtgag tacgccaaaa atttgacta gcggaggcta gaaggagaga gatgggtcgc agagcgtcag tattaagcgg
601 gggagaatta gatgcgatg ggaaaaaatt cggtaaggc cagggggaaa gaaaaatat aaataaac atatagtatg ggcaagcagg gagctagaac
701 gattcgact taatcctgct ctgttagaaa catcagaagg ctgtagacaa atactgggac agctacaacc atccctcag acaggatcag aagaactag
801 atcattat aatacagtag caacctcta ttgtgtgcat caaaggatag agataaaga caccaaggaa gcttagaca agatagga agagcaaac
901 aaaagtaaga ccaccgaca gcaagggcc ctgatctta gactggagg aggagatag agggacaatt ggagaagtga attatataa tataaagtag
1001 taaaaattga accattagga gtgacacca ccaaggcaaa gagaagagt gtgcagagag aaaaaagagc agtgggaata ggagcttctg tcttgggtt
1101 cttgggagca gcaggaagca ctatggcgc agcgtcaatg acgctgacgg tacagccag acaattattg tctggtatag tgcagcagca gaacaattg
1201 ctgagggcta ttgaggcgca acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa gaatcctggc tgtggaaaga tacctaaagg
1301 atcaacagct cctggggatt tgggttgct ctgaaaact catttcacc actgctgtgc ctggaatgc tagttggagt aatgaatctc tggaacagat
1401 ttggaatcac acgacctgga tggagtggga cagagaaatt aacaattaca caagcttaac acactcctta attgaagaat cgcaaaacca gcaagaaaag
1501 aatgaacaag aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata acaaatggc tgtgtatataaaaattatc ataatgatag

1601 taggaggctt ggtaggtta agaatgttt ttgctgtact ttctatagtg aatagagtta ggcaggata ttaccatta tcgttcaga cccactccc
1701 aaccccagg ggaccggaca ggcccgaagg aatagaagaa gaaggtggag agagagacag agacagatcc attcgattag tgaacggatc tcgacggat
1801 cggtaactt ttaaagaaa aggggggatt ggggggtaca gtgcagggga aagaatagta gacataatag caacagacat acaactaaa gaattacaaa
1901 aacaattac aaaaattcaa aattttatcg attacgctc acgtgctagc tgcagtaacg ccattttgca aggcattggaa aaatacaaaa ccaagaatag
2001 agaagttcag atcaaggcgc ggtacatgaa aatagctaac gttgggcaac acaggatc tgcggtgagc agtttcggcc cggccggg gccaagaaca
2101 gatggtcacc gcagtttcgg ccccgcccg aggccaagaa cacatgtcc ccagatcgg ccaaccctc agcagttct taagccat cacatgttc
2201 caggctccc caaggacctg aatgacctc gcgcctatt tgaattaacc aatcagcctg cttctgctt ctgttcgctc gcttctgct cccgagctc
2301 ataaagagc tcacaaccc tctctggcg gcgcagctc cgcagacact gactgcccc ctgcagccg caccatggga tatccatag atgtcccaga
2401 ttatcgcca cctaagaaga aacgcaaagt cgaattcaag aatcaaga agaaccaggt catgaacctg ggcccaaca gcaagctgct gaaggagta
2501 aagagccagc tgatcgact gaacatcgag cagttcagg ccggcatcg cctgacctg ggcgctgct acatcaggag caggacgag gccaagacct
2601 actgcatca gttcagtg aagaacaagg cctacatgga ccagctgct ctgctgacg accagtggt gctgagcccc cccacaaga agggaggggt
2701 gaaccacctg gccaacctg tcatcacctg gggcgccag acctcaagc accaggcctt caacaagctg gccaacctg tcatctgaa caacaagaag
2801 accatccca acaacctgt ggaactac ctgacccca tgagctggc ctactggtt atggacgac gcgcaagtg ggactacaac aagaacagca
2901 ccaacaagag catctgctg aacaccaga gttcacctt cgaggagtg gactacctg tgaaggcct gaggaacaag ttccagctga actgctact
3001 gaagatcaac aagaacaagc ccacatcta catcgacagc atgagctacc tgatcttca caacctgac aagccctacc tgatccca gatgatgac
3101 aagctccca acaccatcag cagcgagacc ttctgaagg gcggcgccg atccggtgag ggcagaggaa gtcttcaac atgcggtgac gtggaggaga
3201 atccggccc ctcggatct gagccactc gggctgagac cttgtattc ctggacctag aagccactg gctcccaac atggacctg agattgaga
3301 gatatcctt ttgtgctt ccctcttc cctggagaac ccagaacgg atgattctg ttcttggtg ctgccccg ttctggaca gctcacactg
3401 tgatgtgcc cggagcggc cttactgcc aaggccagtg agattactg ttgagcagc gaaagcctga tgcactcgg gaaggctggt tcaatggcg
3501 ctgtgtaag gacactcag ggcttctaa gccccagga gggcccatc tccttggtg cccacaatg cttcgattat gactccac tgctgtcac
3601 ggagctaca cgtctgggt cccatctgc ccaagacact gctgctg acacactg tgcattcgg ggcctggacc gtgctcacag ccacggcacc
3701 agggctcaag gcccaaaag ctacagcctg gccagtctt tccaccgta cttcaggct gaaccagtg ctgccatc agcagaaggt gatgtgaca
3801 ccctgctt gatcttctg catctgctc ctgagctc gcctgggca gatgagcagg ccgacagtg ggctcatatt gagccatgt acgtgccacc
3901 tgatgtcca agcctgaag cctgacctg aggtcgagca tgcactagg gcgccaatt ccgcccctt cctcccccc ccccaactg tactggcca
4001 agcccttg aataaggcc gtgtgctt gtctatatgt gattttcac catattgctg tctttggca atgtgaggc ccggaacct ggcctgtct
4101 tcttgacgag cattctagg ggtctttccc ctctccca agaatgcaa ggtctgtta atgtctgaa ggaagcagtt ccttggaag cttctgaa
4201 acaacaacg tctgtagca cctttgag cgagcgaac cccccactg gcgacagtg cctctcggc caaaagccac ggtataaga tacactgca
4301 aaggcggcac aacccagtg ccacgttg agttggatag ttggaag agtcaaatg ctctctca gcgtattca caagggctg aaggatgcc
4401 agaagttacc ccattgatg ggatctgac tgggacctg gtgcacatgc ttacatgtg tttagtcgag gtaaaaaa cgtctaggcc cccgaacca
4501 cggggactg gtttcttt gaaaaacag atgataagct tgccacaacc cttaccgct gccacatga gcgagctg taaggagaac atgcacatga
4601 agctgtacat ggaggcacc gttgacaacc atcactca gtcacatcc gagggcgaag gcaagccca cagggcacc cagacatga gaatcaagtt

4701 ggtcagggc gccctctcc ccttcgctt cgacatcctg gctactagct tcctctacgg cagcaagacc ttcacacacc acaccaggg catccccgac
4801 ttcttcaagc agtccttccc tgagggttc acatgggaga gagtccaccac atacgaagac gggggcgtgc tgaccgctac ccaggacacc agcctccagg
4901 acggctgctt catctacaac gtaaatgca gagggtgaa cttcacatcc aacggcctg tgatgcagaa gaaaacactc ggctgggagg ccttcaccga
5001 gacgctgtac cccgctgacg gcggcctgga aggcagaaac gacatggccc tgaagctcgt gggcgggagc catctgatcg caaacatcaa gaccacat
5101 agatccaaga aaccgctaa gaacctcaag atgcctggcg tctactatgt ggactacaga ctgaaagaa tcaaggaggc caacaacgag acctacgtc
5201 agcagcacga ggtggcagtg gccagatact gcgacctccc tagcaactg gggcacaagc ttaattgatt ctgagctga ccgagcatct taccgccatt
5301 tataccata ttgttctgt tttcttcat ttgggtatac atttaagt taatagaaca aatgggtggg gcaatcatt acatttttag ggatattgaa
5401 ttactagtc aggtgtattg ccacaagaca aacatgtaa gaaacttcc cgttattac gctctgttcc tgtaataca cctctggatt acaaaattg
5501 tgaagattg actgatattc ttaactatgt tgctctttt acgctgtgtg gatagtcgc tttatagcct ctgtatctag ctattgctc ccgtacggg
5601 ttcttttct cctcttcta taaactcgg ttgctgtctc ttttagagga gttgtggccc gttgtccgc aactggcgt ggtgtctct gtgttctg
5701 acgcaacccc cactggctgg ggcatgcca ccactgtca actccttct gggacttcc ctttccccct cccgatgcc acggcagaa tcacgccc
5801 ctgcttgc cgctgctga cagggtctag gttgctggc actgataatt ccgtgggtt gtcacgga ctttttaa agaaaaggg gactggaag
5901 ggctaattca ctccaacga agacaagata tcataactc gtatagcata cattatacga agttataatt ttttggaa atttggatg ctattgctt
6001 atttgaacc atatgttt ttgtgaatt tgtgatgcta ttgcttatt tgaaccatt gcttttctg tctactggg ctctctggt agaccagatc
6101 tgaccctgg agctctctgg ctaactaggg aaccactgc ttaagctca ataaagctg cctcgaccag cctcactgt gccttctag tgccagccat
6201 ctgtgtttg cccctcccc gtgccttct tgacctgga aggtgccact cccactgtc tttcctaata aatgaggaa attgcatgc attgtctgag
6301 taggtgtcat tctattctgg ggggtgggt gggcaggac agcaagggg aggtggga agacaatagc aggcactgt gggatgctg gggctctatg
6401 gcctgcact gcattatga atcgccaac gcgcggggag agcggttg cgtattggc gctctccg ttcctgctc actgactgc tgcctctg
6501 cgttcgctg cgcgagcgg tatcagctca ctcaaaggc gtaatacgt tatccagaa atcaggggat aacgaggaa agaactgtg agcaaaagg
6601 cagcaaaagg ccaggaacc taaaaaggc gcgttctg cgttttcca taggctccg cccctgacg agcatcaaa aatcgacg tcaagtca
6701 ggtggcga cccgacagga ctataaagat accaggcgt tccccgga agctccctg tgcctctcc tgtccgacc ctgcccta ccggatact
6801 gtccgctt cctcttcc gaagcgtggc gcttctcat agctcagct gtaggtatc cagtccggt taggtcttc gctccaagc gggctgtg
6901 cacgaaccc cgttcagcc cgaccgctgc gcctatcgc gtaactatc tcttagtcc aaccgtaa gacagactt atgccactg gcagaccca
7001 ctgtaacag gattagcaga gcgaggtat taggcggtc tacagagtc tgaagtgt ggccaacta cggctacact agaaggacag tatttggat
7101 ctgcctct ctgaagccag ttacctcg aaaaagagt gtagctct gatccgcaa acaaccacc gctgtagcg gtgttttt tttttcaag
7201 cagcagatta cgcgagaaa aaaagatc caagaagat ctttatct tctacggg tctgacgct agtgaacga aaactacgt taaggatt
7301 tggctatg attatcaaaa aggatctca cctagatct ttaaatata aatgaagt taaatcaat cttaagtata tatgataa ctgtctga
7401 cagttacaa tgctaatca gtgaggcacc tatctcagc atctgtct ttcgttcat catagttcc tgactcccc tctgtatag aactacgata
7501 cgggaggct taccatctg cccagctg gcaatgata cgcgagacc acgctaccg gctccagatt tatcagcaat aaaccagca gccggaagg
7601 ccgagcag aagtgtct gcaacttat ccgctccat ccagtctatt aattgttcc gggaagctag agtaagtag tccagctta atagttg
7701 caactgtt gccattgta caggcatct ggtgtcagc tcgtcttg gtatggctc attcagctc gttccaac gatcaaggc agttacatga

7801 tccccatgt tgtcaaaaa agcggtagc tccttcggtc ctccgatcgt tgtcagaagt aagttggccg cagtgttatc actcatggtt atggcagcac
7901 tgcataattc tcttactgtc atgcatccg taagatgctt ttctgtgact ggtgagtact caaccaagtc attctgagaa tagtgtatgc ggcgaccgag
8001 ttgctcttgc ccggcgtcaa tacgggataa taccgcgcca catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt ctcggggcg aaaacttca
8101 aggatcttac cgctgttgag atccagttcg atgtaacca ctctgcacc caactgatct tcagcatctt ttactttcac cagcgtttct gggtagcaa
8201 aaacaggaag gcaaaatgcc gcaaaaaagg gaataagggc gacacggaaa tgtgaatac tcatactctt ctttttcaa tattattgaa gcatttatca
8301 gggttattgt ctcatgagcg gatacatatt tgaatgtatt tagaaaaata acaaatagg ggtccgcgc acatttccc gaaaagtgcc acct

pCVL.SFFV.HA.NLS.I-AniI.IRES.mTagBFP



General Description

DNA Plasmid pCVL.SFFV.HA.NLS.I-Ani I.IRES.mTagBFP

Entire molecule length: 7671 bp

Feature Map

CDS (5 total)

Gag (SL4)

Start: 572 End: 924

Original Location Description:

572..924

coAnil

Start: 2438 End: 3199

Original Location Description:

2438..3199

mTagBFP

Start: 3844 End: 4545

Original Location Description:

3844..4545

wPRE-O

Start: 4560 End: 5140

Original Location Description:

4560..5140

AP(R)

Start: 6681 End: 7541 (Complementary)

bla gene- Ap(r) determinant

Original Location Description:

complement(6681..7541)

LTR (4 total)

RU5

Start: 236 End: 417

Original Location Description:

236..417

SFFV

Start: 1946 End: 2355

Original Location Description:

1946..2355

Qualifiers:

/gene="MESV"

/product="#AJ224005"

/SECDrawAs="Gene"

SIN U3

Start: 5172 End: 5353

Original Location Description:

5172..5353

R

Start: 5354 End: 5443

Original Location Description:

5354..5443

Misc. Binding Site (1 total)

loxP

Start: 5210 End: 5243

Original Location Description:

5210..5243

Qualifiers:

/gene="(null)"

/product="loxP"

Misc. Feature (10 total)

PBS (SL123)

Start: 418 End: 571

Original Location Description:

418..571

RRE

Start: 1081 End: 1322

Original Location Description:

1081..1322

cPPT

Start: 1806 End: 1929

Original Location Description:

1806..1929

kozak

Start: 2366 End: 2374

Original Location Description:

2366..2374

ATG

Start: 2375 End: 2377

Original Location Description:

2375..2377

HA

Start: 2381 End: 2407

Original Location Description:

2381..2407

2ndGenNLS

Start: 2408 End: 2431

Original Location Description:

2408..2431

Y13F

Y111S

IRES

Start: 3243 End: 3828

Original Location Description:

3243..3828

Misc. Marker (3 total)

junction

SV40 USE

Start: 5246 End: 5289

Original Location Description:

5246..5289

SV40 USE

Start: 5293 End: 5336

Original Location Description:

5293..5336

PolyA Signal (1 total)

BGH pA

Start: 5445 End: 5678

Original Location Description:

5445..5678

PolyA Site (1 total)

pA

Start: 5427 End: 5432

Original Location Description:

5427..5432

Primer (1 total)

CVL-34

Start: 1671 End: 1692

Original Location Description:

1671..1692

Promoter Prokaryotic (2 total)

RSV

Start: 7 End: 235

Original Location Description:

7..235

pr

Start: 7606 End: 7611 (Complementary)

Original Location Description:

complement(7606..7611)

Replication Origin (1 total)

ori

Start: 5860 End: 6533 (Complementary)

Original Location Description:

complement(5860..6533)

mRNA (1 total)

TSS

Start: 2330 End: 2355

Original Location Description:

2330..2355

Mutation (1 total)

A->G

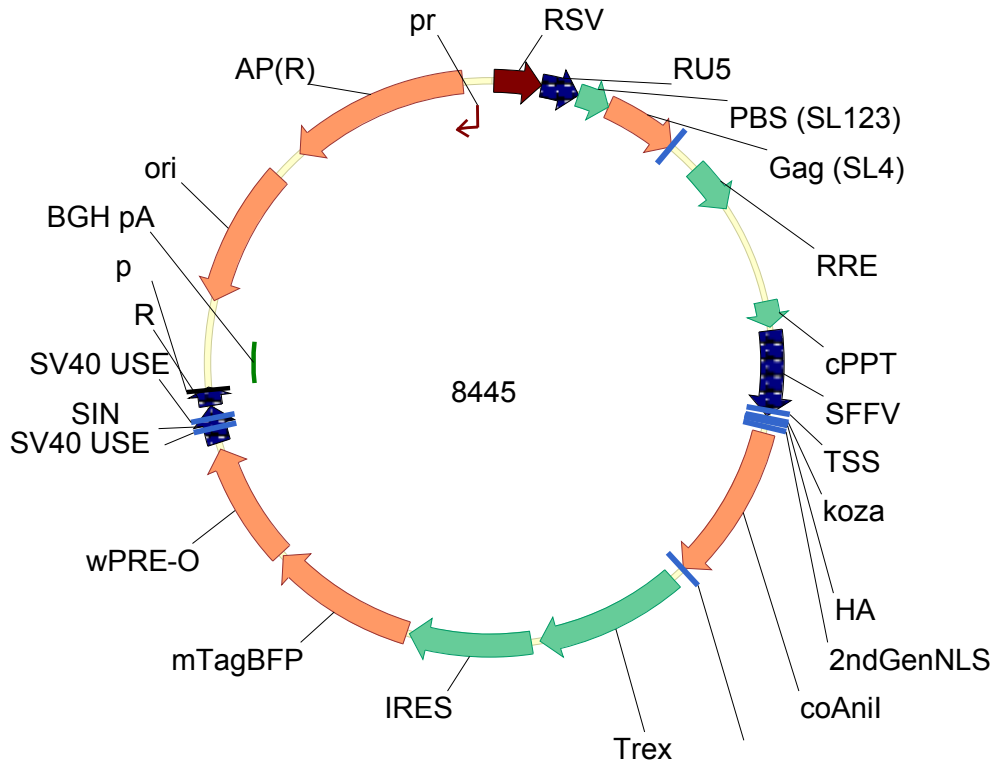
Sequence

1 gacgtcaatg tagtcttatg caataactctt gtagtcttgc aacatggtaa cgatgagtta gcaacatgcc ttacaaggag agaaaaagca ccgtgcatgc
101 cgattggtgg aagtaagggtg gtacgatcgt cccttattag gaaggcaaca gacgggtctg acatggattg gacgaaccac tgaattgccg cattgcagag
201 atattgtatt taagtcctta gctcgataca taaacgggtc tctctggta gaccagatct gagcctggga gctctctggc taactagga acccactgt
301 taagcctcaa taaagcttgc cttgagtgt tcaagtagtg tgtgccctg tgttgtgta ctctggtaac tagagatccc tcagaccctt ttagtcatg
401 tggaaaatct ctacagtggtg cgcccgaaca gggacttgaa agcgaaggg aaaccagagg agctctctcg acgcaggact cggcttctg aagcgcgcac
501 ggcaagaggc gagggcgccg gactggtgag tacccaaaa atttgacta gcggaggcta gaaggagaga gatgggtgag agagcgtcag tattaagcgg
601 gggagaatta gatcgcgatg gaaaaaatt cggttaaggc cagggggaaa gaaaaatat aaattaaac atatatatg ggcaagcagg gagctagaac
701 gattcgcagt taatcctggc ctgttagaaa catcagaagg ctgtagaca atactgggac agctacaacc atcccttag acaggatcag aagaacttag
801 atcattatat aatacagtag caacctcta ttgtgtcat caaagatag agataaaga caccaaggaa gcttagaca agatagga agagcaaac
901 aaaagtaaga ccaccgaca gcaagcggcc ctgatctca gacctggagg aggagatag agggacaatt ggagaagtga attatataa tataaagtag
1001 taaaaattga accattagga gtacaccca ccaaggcaaa gagaagatg gtgcagagag aaaaagagc agtgggaata ggagcttctg tccttgggt
1101 cttgggagca gcaggaagca ctatggcgcg agcgtcaatg acgctgacgg tacaggccag acaattatg tctggtatag tgcagcagca gaacaattg
1201 ctgagggcta ttgaggcga acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa gaatcctggc tgtgaaaga tacctaaagg
1301 atcaacagct cctgggatt tggggttct ctgaaaact catttcacc actgctgtgc cttggaatg tagttggagt aatgaatctc tggacagat
1401 ttggaatcac acgacctgga tggagtggga cagagaaatt aacaattaca caagctaat acactccta attgaagaat cgcaaaacca gcaagaaaag
1501 aatgaacaag aattattgga attagataaa tgggcaagt tgtggaattg gtttaacata acaattggc tgtgtatat aaaattatc ataagatag
1601 taggaggctt ggtaggttta agaatagtt ttgtgtact ttctatagtg aatagatga ggcaggata ttcaccatta tctttcaga cccactccc
1701 aacccgagg ggaccgaca ggcccgaagg aatagaaga gaaggtggag agagagacag agacagatcc attcgattag tgaacggatc tcgacggtat
1801 cgttaactt taaaagaaa aggggggatt ggggggtaca gtgcaggga aagaatagta gacataatag caacagacat acaactaaa gaattacaaa
1901 aaaaattac aaaaattcaa aattttatcg attacgctc acgtgctagc tgcagtaacg ccattttgca agcatggaa aatacaaaa ccaagaatag
2001 agaagttcag atcaaggcgc ggtacatgaa aatagctaac gttggccaa acaggatatt tgcggtgagc agtttcggcc ccgcccggg gccaaaga
2101 gatggtcacc cgatttctcg ccccgcccaggccaagaa cagatggtcc ccagatattg cccaacctc agcagttct taagacccat cagatgtttc
2201 caggctccc caaggacctg aatgacctc gcgcttatt tgaattaacc aatcagcctg cttctcctt ctgttcgagc gcttctgctt cccagctct
2301 ataaaagagc tcacaaccc tcaactggcg cgccagtct ccgacagact gactgcccc ctcgagccc caccatggga tatcatac atgtcccaga
2401 ttatgcgcca cctaagaaga aacgcaagt cgaattcggc agcagatcga cctacgcta tctggtggc ctgttcgagg gcgacggata ttttccatc
2501 actaaaagg gcaagtacct gacatagag ctggaattg aactgtctat caagatgtg cagctgatc acaagatcaa gaagatcctg gggatcggca

2601 ttgtgagcct caggaagaga aacgagattg aaatggtggc cctgaggatc agggataaga atcacctgaa atctaagatt ctgccatct tcgagaagta
2701 tcctatgttt agtaacaac agtacgacta tctgaggttt agaaatgctc tgctgagcgg catcatctcc ctggaggatc tgccagacta taccgggtcc
2801 gacgagcccc tgaacagcat cgaatccatc attaatacat cttacttcag tgcctggctg gtgggcttca tcgaggctga aggggtcttc tctgtgtaca
2901 aactgaacaa ggacgatgac tatctgattg ccagtttga tatcgtcag agggatggag acatcctgat tagcctcctc agaaagtacc tgcctctc
3001 cacaaagtg tatctggaca aaacaaatg tagcaaatg aaggtcacta gcgtgcctc cgtggagaac atcattaagt tcctcgagaa tgcctctgtg
3101 aaactgctgg gcaacaaaa gctgcagtac aaactgtggc tgaagcagct gcggaaaatc tctcctaca gtgaaaaat caagattcca tccaattatt
3201 aacctgcagg tcgagcatgc atctagggcg gccaaatccg cccctctccc tcccccccc ctaacgttac tggccgaagc cgcttggat aagccgggtg
3301 tgcgtttgtc tatatgtat ttccaccat attccgtct tttgcaatg tggggcccc gaaacctggc cctgtctctc tgacgagcat tcttaggggt
3401 ctttcccc tcgcaaaag aatgcaaggt ctgtgaaatg tctgaaagga agcagttct ctggaagctt ctgaaagaca aacaactctc gtagcgacc
3501 ttgcaaggca gcggaacccc ccactggcg acaggtcct ctgcggcaa aagccactg tataagatac acctgcaag gcgcacacac cccagtcca
3601 cgttgtgagt tggatagttg tggaaagagt caaatggctc tcctcaagcg tattcaaca ggggctgaag gatgccaga aggtaccca ttgtatgga
3701 tctgatctgg ggcctcggc cacatgctt acatgtgtt agtcgaggt aaaaaactg ctagccccc cgaaccacgg ggactgtgtt ttctttgaa
3801 aaacacgatg ataacttgc cacaacctt accggtgcc accatgagcg agctgattaa ggagaacatg cacatgaagc tgtacatgga gggaccgtg
3901 gacaaccatc actcaagtg cacatcgag ggcgaaggca agcctcaca gggcaccag accatgagaa tcaaggtgt cgagggggc cctctcccc
4001 tcgccttca catcctggct actagcttc tctacggcag caagacctc atcaaccaca cccaggcat ccccgactc ttcaagcagt cttccttga
4101 gggcttaca tgggagagag tcaccacata cgaagacggg ggcgtctga ccgctacca ggacaccagc ctccaggacg gctgcctcat ctacaactc
4201 aagatcagag gggggaact cacatcaac ggcctgtga tgcagaagaa aactcggc tgggagcct tcaccgagc gctgtacccc gctgagggc
4301 gcctggaagg cagaacgac atggcctga agctcgtgg cgggagcat ctgatcga acatcaagac cacatataga tccaagaac ccgctaagaa
4401 cctaagatg cctggctct actatgtgga ctacagactg gaaagaatca aggggcca caacgagacc tacgtcagc agcacaggt ggagtgcc
4501 agatactcg acctccctag caaactgggg cacaagctta atgtattca gactgaccg agcatctac cgccattat acctatatt gtctgttt
4601 tcttgattg ggtatacat taaatgtaa tagaacaaa tggggggca atcattaca ttttaggga tatgtaata ctagtcagg tttattcca
4701 caagacaaac atgtaagaa actttccgt tattacgct gtgtctgt taatcaacct ctggattaca aaatttga aagattgact gatattcta
4801 actatgttc tcctttacg ctgtgtgat atgtcttt atagcctc tatctagta ttgctccc tacggcttc gtttctct cttgtataa
4901 atcctggtg ctgtcttt tagaggagt gtggccgt gtcgtcaac gtggctgtg gtgctctg tttgctgac caacccac tggctgggc
5001 attgccaca cctgcaact ctttctggg acttctcct tccccccc gatcacaag gcagaacta tcgccctg cctgcccgc tctggagac
5101 gggctaggtt gctggcact gataattccg tgggtgtc atcggtact ttttaaaaga aaagggggga ctggaaggc taattcact ccaacgaaga
5201 caagatata taactccta tagcacaat tacaagaat tataattat ttgtgaaat tgtgatgta ttgcttatt tgaaccata ttttattg
5301 tgaattgt gatgctatt ctttattgt aaccattgt tttgctgt actgggtctc tctggtaga ccagatcga gcctgggagc tctctgcta
5401 actaggaac cactgcta agcctcaata aagcttgcct cgaccagct cactgtgccc ttctagttc cagcatctg ttgttccc cccccctg
5501 ccttctga ccctggaag tgccactccc actgtcctt cctaataaaa tgaggaaat gcatcgact gtctgagtag gtgtcattc attctgggg
5601 gtgggtggg gcaggacagc aagggggagg attgggaaga caatagcagg catgctggg atcggtggg ctctatggc tgcagctga ttaatgaat

5701 ggccaacgcg cggggagagg cggtttgcgt attgggcgct ctccgcttc ctcgctcact gactcgtgc gctcggctgt tcggctcgg cgagcggat
5801 cagctcactc aaaggcggta atacggtat ccacagaatc aggggataac gcaggaaaga acatgtgagc aaaaggccag caaaaggcca ggaaccgtaa
5901 aaaggccgcg ttgctggcgt ttttccatag gctccgccc cctgacgagc atcaaaaaa tcgacgctca agtcagaggt ggcgaaaccc gacaggacta
6001 taaagatacc aggcgtttcc ccctggaagc tccctcgtgc gctctcctgt tccgacctg ccgcttaccg gatacctgtc cgcctttctc ccttcgggaa
6101 gcgtggcgtc ttctcatagc tcacgctgta ggtatctcag ttcgggtgag gtcgttcgct ccaagctggg ctgtgtgcac gaacccccg ttcagccccg
6201 ccgctcgcgc ttatccggta actatcgtct tgagtccaac ccgtaagac acgacttatc gccactggca gcagccactg gtaacaggat tagcagagcg
6301 aggtatgtag gcggtgctac agagtcttg aagtgggtgc ctaactacgg ctacactaga aggacagtat ttggtatctg cgctctgctg aagccagtta
6401 ccttcgaaa aagagttggt agctcttgat ccggcaaa aaccaccgct gtagcgggtg gttttttgt ttgcaagcag cagattacgc gcagaaaaa
6501 aggatctcaa gaagatcctt tgatctttc tacggggtct gacgctcgtg ggaacgaaaa ctacggttaa gggattttg tcatgagatt atcaaaaaa
6601 atctcacct agatcctttt aaataaaaa tgaagtttta aatcaatcta aagtatatat gaggtaactt ggtctgacag ttaccaatgc ttaatcagt
6701 aggcacctat ctcagcgtc tgctatttc gttatccat agttgctga ctccccgctg ttagataac tacgatacgg gagggttac catctgccc
6801 cagtgctgca atgataccgc gagaccacg ctcaccgct ccagattat cagcaataa ccagccagcc ggaaggccg agcgagaag tggctctgca
6901 acttatccg cctccatca gtctattaat tgttccggg aagctagagt aagtagttc ccagtaata gtttgcgcaa cgttgttcc attgctacag
7001 gcatcgtggt gtcacgctc tcgtttgta tggcttatt cagctcgggt tccaacgat caaggcagat tacatgatcc ccatgttgt gcaaaaaagc
7101 ggttagctcc ttccgtctc cgatcgttgc cagaagtaag ttggccgag tttatcact catggttatg gcagcactgc ataattctt tactgtcatg
7201 ccatccgtaa gatcctttc tgtgactggt gactactcaa ccaagtcatt ctgagaatag ttagtcggc gaccgagttg ctctgccc gcgtcaatac
7301 gggataatac cgcgccatc agcagaactt taaaagtgt catcattgga aaacttctt cggggcgaaa actctcaagg atctaccgc tttgagatc
7401 cagttgatg taaccactc gtcacccaa ctgatctca gcatcttta cttcaccag cgttctggg tgagcaaaa caggaaggca aaatgccgca
7501 aaaaaggaa taaggcgac acgaaatgt tgaatactca tactcttct tttcaatat tattgaagca tttacaggg ttattgtctc atgagcggat
7601 acatattga atgtattag aaaaataaac aaatagggt tccgcgaca tttccccgaa aagtccacc t

pCVL.SFFV.HA.NLS.IAni-I.T2A.Trex2.IRES.mTagBFP



General Description

DNA Plasmid pCVL.SFFV.HA.NLS.IAni-I.T2A.Trex2.IRES.mTagBFP

Entire molecule length: 8445 bp

Feature Map

CDS (5 total)

Gag (SL4)

Start: 572 End: 924

Original Location Description:

572..924

coAnil

Start: 2438 End: 3199

Original Location Description:

2438..3199

mTagBFP

Start: 4618 End: 5319

Original Location Description:

4618..5319

wPRE-O

Start: 5334 End: 5914

Original Location Description:

5334..5914

AP(R)

Start: 7455 End: 8315 (Complementary)

bla gene- Ap(r) determinant

Original Location Description:

complement(7455..8315)

LTR (4 total)

RU5

Start: 236 End: 417

Original Location Description:

236..417

SFFV

Start: 1946 End: 2355

Original Location Description:

1946..2355

Qualifiers:

/gene="MESV"

/product="#AJ224005"

/SECDrawAs="Gene"

SIN U3

Start: 5946 End: 6127

Original Location Description:

5946..6127

R

Start: 6128 End: 6217

Original Location Description:

6128..6217

Misc. Binding Site (1 total)

loxP

Start: 5984 End: 6017

Original Location Description:

5984..6017

Qualifiers:

/gene="(null)"

/product="loxP"

Misc. Feature (13 total)

PBS (SL123)

Start: 418 End: 571

Original Location Description:

418..571

RRE

Start: 1081 End: 1322

Original Location Description:

1081..1322

cPPT

Start: 1806 End: 1929

Original Location Description:

1806..1929

kozak

Start: 2366 End: 2374

Original Location Description:

2366..2374

ATG

Start: 2375 End: 2377

Original Location Description:

2375..2377

HA

Start: 2381 End: 2407

Original Location Description:

2381..2407

2ndGenNLS

Start: 2408 End: 2431

Original Location Description:

2408..2431

Y13F

Y111S

Trex2

Start: 3269 End: 3976

Original Location Description:

3269..3976

K77 (to A = dimerization defect (K59A in human))

D193 (to N = catalytically inactive dominate negative)

IRES

Start: 4017 End: 4602

Original Location Description:

4017..4602

Misc. Marker (3 total)

junction

Start: 927 End: 930

Original Location Description:

927..930

SV40 USE

Start: 6020 End: 6063

Original Location Description:

6020..6063

SV40 USE

Start: 6067 End: 6110

Original Location Description:

6067..6110

PolyA Signal (1 total)

BGH pA

Start: 6219 End: 6452

Original Location Description:

6219..6452

PolyA Site (1 total)

pA

Start: 6201 End: 6206

Original Location Description:

6201..6206

Primer (1 total)

CVL-34

Start: 1671 End: 1692

Original Location Description:

1671..1692

Promoter Prokaryotic (2 total)

RSV

Start: 7 End: 235

Original Location Description:

7..235

pr

Start: 8380 End: 8385 (Complementary)

Original Location Description:

complement(8380..8385)

Replication Origin (1 total)

ori

Start: 6634 End: 7307 (Complementary)

Original Location Description:

complement(6634..7307)

mRNA (1 total)

TSS

Start: 2330 End: 2355

Original Location Description:

2330..2355

Mutation (1 total)

Misc. Signal (1 total)

T2A

Start: 3203 End: 3262

Original Location Description:

3203..3262

Sequence

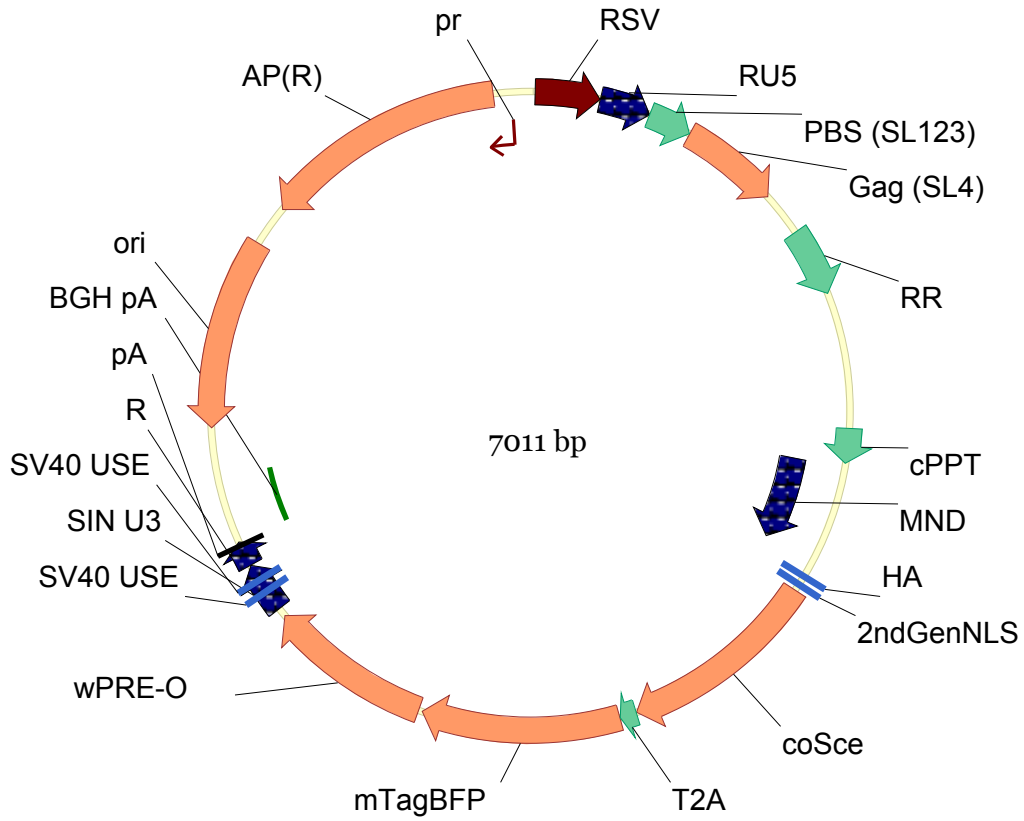
1 gacgtcaatg tagtcttatg caatactctt gtagtcttgc aacatggtaa cgatgagtta gcaacatgcc ttacaaggag agaaaaagca ccgtgcatgc
101 cgattgggtgg aagtaagggtg gtacgatcgt cccttattag gaaggcaaca gacgggtctg acatggattg gacgaaccac tgaattgccg cattgcagag
201 atattgtatt taagtcccta gctcgatata taaacgggtc tctctgtta gaccagatct gagcctggga gctctctggc taactagga acccactgct
301 taagcctcaa taaagcttgc cttgagtgtc tcaagtagtg tgtcccctc tgttgtgtga ctctgtaac tagagatccc tcagaccctt ttagtcaatg
401 tggaaaatct ctgacgtgg cgcccgaaca gggacttgaa agcgaagggg aaaccagagg agctctctcg acgcaggact cggcttgctg aagcgcgcac
501 ggcaagaggc gagggcgccg gactgggtgag tacgccaaaa attttgacta gcggaggcta gaaggagaga gatgggtgcg agagcgtcag tattaagcgg
601 gggagaatta gatcgcatg ggaaaaaatt cggtaaggc cagggggaaa gaaaaatat aaattaaac atatagtagt ggcaagcagg gagctagaac
701 gattcgcagt taatcctggc ctgttagaaa catcagaagg ctgtagacaa atactgggac agctacaacc atccctttag acaggatcag aagaacttag
801 atcattatat aatacagtag caacctcta ttgtgtgcat caaaggatag agataaaga caccaaggaa gcttagaca agatagaggag agagcaaac
901 aaaaagtaaga ccaccgcaca gcaagcggcc ctgatctta gacttggagg aggagatag agggacaatt ggagaagtga attatataa taaaagtga
1001 taaaattga accattagga gtgacacca ccaaggcaaa gagaagagtg gtgcagagag aaaaaagagc agtgggaata ggagctttgt tccttgggtt
1101 cttgggagca gcaggaagca ctatggcgcg agcgtcaatg acgctgacgg tacaggccag acaattattg tctggtatag tgcagcagca gaacaatttg
1201 ctgagggcta ttgagcgcga acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa gaatcctggc tgtggaaaga tacctaaagg
1301 atcaacagct cctggggatt tggggttct ctggaaaact catttgacc actgctgtgc cttggaatgc tagttggagt aatgaatctc tggacagat
1401 ttggaatcac acgacctgga tggagtggga cagagaaatt aacaattaca caagctaat acactcctta attgaagaat cgcaaaacca gcaagaaaag

1501 aatgaacaag aattattgga attagataaa tggcaagtt tgtggaattg gtttaacata acaaattggc tgtggtatat aaaattattc ataattgatg
1601 taggaggctt ggtaggttta agaatagttt ttctgtact ttctatagtg aatagagtta ggcagggata ttcaccatta tcgttcaga cccactccc
1701 aaccccaggg ggaccgcaca ggcccgaagg aatagaagaa gaaggtggag agagagacag agacagatcc attcgattag tgaacggatc tcgacggat
1801 cggtaactt ttaaagaaa aggggggatt ggggggtaca gtgcagggga aagaatagta gacataatag caacagacat acaaactaaa gaattacaaa
1901 aacaattac aaaaattcaa aattttatcg attacgcgtc acgtgctagc tgcagtaacg ccatittgca aggcattgaa aaataccaaa ccaagaatg
2001 agaagttcag atcaaggcgc ggtacatgaa aatagctaac gttgggcaa acaggatc tgcggtgagc agtttcggcc cggcccggg gccaagaaca
2101 gatggtcacc gcagtttcgg ccccgcccg aggccaagaa cagatggccc ccagatatgg cccaaccctc agcagtttct taagacccat cagatgttc
2201 caggctccc caaggacctg aatgaccct gcgccttatt tgaattaacc aatcacctg cttctgctt ctgttcgagc gcttctgctt cccgagctc
2301 ataaaagagc tcacaacccc tctactggcg cgcagctct cgcagacact gactgcccc ctcgagccgc caccatggga tatccatagc atgtcccaga
2401 ttatcgcca cctaagaaga aacgcaaagt cgaattcggc agcagctgaa cctacgcta tctggtggc ctgttcgagg gcgacggata ttttccatc
2501 actaaaagg gcaagtacct gacatagag ctgggaattg aactgtctat caaggatg cagctgatc acaagatcaa gaagatcctg gggatcgcca
2601 ttgtgagctt caggaagaga aacgagattg aatgggtggc cctgaggatc agggataaga atcacctgaa atctaagatt ctgcccactc tcgagaagta
2701 tcctatgttt agtaacaac agtacgacta tctgagttt agaaatgctc tctgagcgg catcatctcc ctggaggatc tgccagacta taccggctc
2801 gacgagccc tgaacagcat cgaatccatc attaatacat cttactcag tgcctggctg gtggcttca tcgaggctga agggctctc tctgtgata
2901 aactgaacaa ggacgatgac tatctgattg ccagtttga tatcgtcag agggatggag acatcctgat tagcggccatc agaaagtacc tgtcctcac
3001 cacaaagggt tatctggaca aaacaaattg tagcaactg aaggtcacta gcgtgcgctc cgtggagaac atcattaagt tctgcagaa tgcctctgtg
3101 aaactgctgg gcaacaaaaa gctgcagtac aaactgtggc tgaagcagct cgggaaaaatc tctgctaca gtgaaaaat caagattcca tccaattatg
3201 gatccgtga gggcagagga agtcttctaa catcgggtga cgtggaggag aatccggccc cctccggatc tgagccacct cgggctgaga ctttgtatt
3301 cctggaccta gaagccactg ggctcccaaa catggaccct gagattgcag agatatcctt tttgctgtt caccgctt cctggagaa cccagaacgg
3401 gatgattctg gttccttgg gctccccgt gttctggaca agctcacact gtgcatgtgc ccggagcgc ctttactgc caaggccagt gagattactg
3501 gtttgagcag cgaagcctg atgcactgcg ggaaggctgg tttcaatggc gctgtgtaa gacactgca gggcttcta agccccagg agggccccat
3601 ctgcttctg gcccaaatg gcttgatta tgactccca ctgctgtgca cggagctaca acgtctgggt gccatctgc ccaagacac tgtctgctg
3701 gacacactgc ctgattcgc gggcctggac cgtctcaca gccacggcac cagggtcaa ggccgcaaaa gctacagcct ggccagctc tccaccgct
3801 actccaggc tgaaccagct gctgccatt cagcagaagg tgatgtcac accctcttc tgatcttct gcactgtct cctgagctgc tcgctggc
3901 agatgagcag gcccgactg gggctcatat tgagccatg tacgtccac ctgatgtcc aagcctgaa gcctgacctg caggtcagc atgcatctag
4001 gggcgccaat tcccccctc tccctcccc ccccctaagc ttactggccg aagccgctt gaaataaggcc ggtgtgctt tcttatatg tgatttcca
4101 ccatattgcc gcttttggc aatgtgaggg cccgaaacc tggcctgtc ttctgacga gcattcctag ggtctttcc cctctgcca aaggaatgca
4201 aggtctgtt aatgtctga aggaagcagt tctctggaa gcttctgaa gacaaacac gctgtagc acccttgc ggcagcgaa cccccact
4301 ggcgacaggt gcctctcgg ccaaaagcca cgtgtataag atacactgc aaaggcggca caacccagt gccacgtgt gagttggata gttgtgaaa
4401 gagtcaaatg gctctctca agcgtattca acaagggct gaaggtgcc cagaaggtac cccattgtat gggatctgat tggggcctc ggtgcacatg
4501 cttacatgt gtttagtga ggttaaaaa acgtctaggc ccccgaaac acggggactg gttttctt tgaaaaacac gatgataagc ttgccacaac

4601 ccttaccggt cgccaccatg agcgagctga ttaaggagaa catgcacatg aagctgtaca tggagggcac cgtggacaac catcacttca agtgcacatc
4701 cgagggcgaa ggcaagccct acgagggcac ccagaccatg agaatcaagg tggctgaggg cggccctctc cccttcgctc tcgacatcct ggctactagc
4801 ttctctacg gcagcaagac cttcatcaac cacaccagg gcatccccga cttctcaag cagtccttcc ctgagggctt cacatgggag agagtacca
4901 catacgaaga cggggcgctg ctgaccgcta cccaggacac cagcctccag gacggctgac tcatctaaa cgtcaagatc agagggggta acttcacatc
5001 caacggccct gtgatcaga agaaaact cggctgggag gccttcaccg agacgctgta ccccgctgac ggcggcctgg aaggcagaaa cgacatggcc
5101 ctgaagctcg tgggaggag ccatctgat gcaaacatca agaccacata tagatccaag aaaccgcta agaactcaa gatgcctggc gtctactatg
5201 tggactacag actgaaaga atcaaggagg ccaacaacga gacctacgtc gagcagcacg aggtggcagt ggccagatac tgcgacctc ctagaaact
5301 ggggcacaag cttaatgat tctagatcg accgagcatc ttaccgcat ttataccat atttgtctg ttttcttga tttgggtata cattaaatg
5401 ttaatagaac aaaatggtgg ggcaatcatt tacatttta gggatgta attactagt caggtgtatt gccacaagc aaacatgta agaaacttc
5501 ccgttatta cgctcttctc ctgttaata acctctgat tacaaaatt gtgaaagatt gactgatatt ctaactatg ttgctcttt tacgctgtg
5601 ggatagctg ctttatagc tctgtatc gctattgct cccgtacggc tttcgtttc tctcctgt ataaactcg gttgctgtc ctttagagg
5701 agttgtgccc cgtgtccgt caacgtggcg tgggtgctc tgtgttctc gacgcaacc cactggctg gggcattgcc accactgtc aactccttc
5801 tgggacttcc gctttcccc tcccgatcg caggcagaa ctcatcggc cctgccttc cgctgctgg acaggggcta ggtgctggg cactgataat
5901 tccgtggtg tgcacggt accttttaa aagaaagg gggactgaa gggctaattc actccaacg aagacaagat atcataact cgtatagcat
6001 acattatagc aagtataat ttattgtga aattgtgat gctattgct tattgtaac catatgta tttgtaaat ttgtgatct attgcttat
6101 ttgtaacct tgcttttgc ttgtactgg tctctctgt tagaccagat ctgagcctgg gagctctc gtaactagg gaaccactg cttagcctc
6201 aataaagct gcctcgacca gcctcactg tgcctctag ttgagcca tctgttgtt gccctccc cgtgcctcc ttgacctgg aagggtccac
6301 tccactgtc ctttctaataaaaatgagg aattgcatc cattgtcga gtaggtgca ttctattct ggggtggg tgggcagga cagcaagggg
6401 gaggattggg aagacaatag caggcatgct ggggatcgg tggctctat ggctgcagc tgcattaatg aatcgccaa cgcgaggga gaggcggtt
6501 gcgtattggc cgcttccg cttctcgt cactgactc ctgcctcg tcttccgct cggcgagcg gtatcagct actcaaaggc ggtaatacgg
6601 ttatccacag aatcagggga taacgagga aagaacatg gagcaaaagg ccagcaaaag gccaggaacc gtaaaaaggc cgcgttctg gcgtttttc
6701 ataggctccg cccccctgac gagcatcaca aaaatcagc ctcaagtcag aggtggcgaa acccgacagg actataaaga taccaggcgt tccccctg
6801 aagctcctc gtgcctctc ctgtccgac cctgccctt accgatacc tgcgcctt tctccctc ggaagcgtg cgctttctca tagctcacg
6901 ttaggtatc tcagttcgt gtaggtcgt cgctcaagc tggctgtgt gcacgaacc cccgtcagc ccgacctg cgcctatcc ggtaactatc
7001 gtcttgatc caaccggta agacacgact tatccact ggacgagcc actgtaaca ggattagcag agcgaggtat taggcgggt ctacagagt
7101 cttgaagtgg tggcctaact acggctacac tagaaggaca gttttgta tctgcctc gctgaagcca gttacctc gaaaaagagt tggtagctc
7201 tgatccgca aaaaaccg ctggttagc ggtggtttt ttgttcaa gcagcagatt acgagcagaa aaaaagatc tcaagaagat cttttagct
7301 tttctacggg gtctgacgt cagtggaaacg aaaactcagc ttaagggatt ttggtcatga gattatcaa aaggatctt acctagatcc ttttaatta
7401 aaaatgaagt ttaaatcaa tctaaagt atagatgaa acttgctc acagttacca atgctaatc agtgggac ctatctcagc gatctgtca
7501 tttcttcat ccatagttc ctgactcccc gctgtgtaga taactacat acgggaggc ttaccatctg gccccagtgc tgcaatgata ccgagagac
7601 cagctcacc ggctccagat ttatcagca taaaccagc agccggaagg gccgagcga gaagtgtcc tgcaactta tccgctcca tccagtctat

7701 taattgttc cgggaagcta gagtaagtag ttcgccagtt aatagtttc gcaacgttg tgccattgct acaggcatcg tgggtcagc ctgctgttt
7801 ggtatggctt cattcagctc cggttcccaa cgatcaaggc gaggatcatg atccccatg ttgtgcaaaa aagcggtag ctcttcggt cctccgatcg
7901 ttgtcagaag taagttggcc gcagtgtat cactcatggt tatggcagca ctgcataatt ctctactgt catgcatcc gtaagatgct tttctgtgac
8001 tggtgagtac tcaaccaagt cattctgaga atagtgtatg cggcgaccga gttgctcttg cccggcgtca atacgggata ataccgccc acatagcaga
8101 actttaaag tgctcatcat tggaaaact tctcggggc gaaaactctc aaggatctta ccgctgtga gatccagttc gatgtaacc actcgtgcac
8201 ccaactgac ttcagcatct ttactttca ccagcgttc tgggtgagca aaaacaggaa ggcaaatgc cgcaaaaag ggaataaggc cgacacggaa
8301 atgtgaata ctactactct tctttttca atattatga agcattatc agggttattg tctcatgagc ggatacatat ttgaatgat ttagaaaaat
8401 aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacct

pCVL.MND.SceOPT.2A.TagBFP



General Description

DNA Plasmid (#906) pCVL.MND.SceOPT.2A.TagBFP

Entire molecule length: 7011 bp

Feature Map

CDS (5 total)

Gag (SL4)

Start: 572 End: 924

Original Location Description:

572..924

coSce

Start: 2410 End: 3120

Original Location Description:

2410..3120

mTagBFP

Start: 3184 End: 3885

Original Location Description:

3184..3885

wPRE-O

Start: 3900 End: 4480

Original Location Description:

3900..4480

AP(R)

Start: 6021 End: 6881 (Complementary)

bla gene- Ap(r) determinant

Original Location Description:

complement(6021..6881)

LTR (3 total)

RU5

Start: 236 End: 417

Original Location Description:

236..417

SIN U3

Start: 4512 End: 4693

Original Location Description:

4512..4693

R

Start: 4694 End: 4783

Original Location Description:

4694..4783

Misc. Binding Site (1 total)

Misc. Feature (5 total)

PBS (SL123)

Start: 418 End: 571

Original Location Description:

418..571

RRE

Start: 1081 End: 1322

Original Location Description:

1081..1322

cPPT

Start: 1806 End: 1929

Original Location Description:

1806..1929

HA

Start: 2353 End: 2379

Original Location Description:

2353..2379

2ndGenNLS

Start: 2386 End: 2409

Original Location Description:

2386..2409

Misc. Marker (3 total)

junction

SV40 USE

Start: 4586 End: 4629

Original Location Description:

4586..4629

SV40 USE

Start: 4633 End: 4676

Original Location Description:

4633..4676

PolyA Signal (1 total)

BGH pA

Start: 4785 End: 5018

Original Location Description:

4785..5018

PolyA Site (1 total)

pA

Start: 4767 End: 4772

Original Location Description:

4767..4772

Promoter Prokaryotic (2 total)

RSV

Start: 7 End: 235

Original Location Description:

7..235

pr

Start: 6946 End: 6951 (Complementary)

Original Location Description:

complement(6946..6951)

Replication Origin (1 total)

ori

Start: 5200 End: 5873 (Complementary)

Original Location Description:

complement(5200..5873)

Repeat Region (1 total)

MND

Start: 1942 End: 2288

Original Location Description:

1942..2288

Mutation (2 total)

Misc. Signal (1 total)

T2A

Start: 3124 End: 3183

Original Location Description:

3124..3183

Sequence

1 gacgtcaatg tagtcttatg caatactctt gtagtcttgc aacatggtaa cgatgagtta gcaacatgcc ttacaaggag agaaaaagca ccgtgcatgc
101 cgattggttg aagtaagggtg gtacgatcgt gccttattag gaaggcaaca gacgggtctg acatggattg gacgaaccac tgaattgccg cattgcagag
201 atattgtatt taagtgccta gctcgataca taaacgggtc tctctggta gaccagatct gagcctggga gctctctggc taactagga acccactgt
301 taagcctcaa taaagcttgc cttgagtgt tcaagtagtg tgtcccgct tgttgtgta ctctgtaac tagagatccc tcagaccctt ttagtcagt
401 tggaaaatct ctgacagtgg cgcccgaaca gggacttga agcgaaagg aaaccagagg agctctctg acgcaggact cggcttctg aagcgcgac
501 ggcaagaggc gagggcgcc gactggtgag tacccaata atttgacta gcggaggcta gaaggagaga gatgggtcgc agagctcag tattaagcgg
601 gggagaatta gatcgcatg ggaataaatt cggtaagc caggggaaa gaaaaatat aaataaac atatagtat ggcaagcagg gagctagaac
701 gattcgagt taactctgct ctgttagaaa catcagaagg ctgtagaca atactggac agctacaacc atccctcag acaggatcag aagaacttag
801 atcattatat aatacagtag caacctcta ttgtgcat caaaggatag agataaaga caccaaggaa gcttagaca agatagga agagcaaac
901 aaaagtaaga ccaccgaca gcaagcggc ctgatctca gacctggagg aggagatag agggacaatt ggagaagtga attatataa tataagtag
1001 taaaattga accattagga gtgacacca ccaaggcaaa gagaagagt gtgcagagag aaaaagagc agtgggaata ggagcttctg tccttgggt
1101 cttgggagca gcaggaagca ctatggcgc agcgtcaatg acgctgacg tacaggccag acaattatg tctggtatg tgcagcagca gaacaattg
1201 ctgagggcta ttgagcgc acagcatctg ttgcaactca cagtctggg catcaagcag ctccaggcaa gaatctgct tgtgaaaga tacctaaagg
1301 atcaacagct cctgggatt tggggttct ctgaaaact catttgacc actgctgtg cttggaatg tagttggagt aatgaatct tggacagat
1401 ttggaatcac acgacctgga tggagtggga cagagaaatt aacaattaca caagctaat acactccta attgaagaat cgcaaacca gcaagaaaag
1501 aatgaacaag aattattgga attagataaa tgggcaagt tgtggaattg gtttaacata acaaatggc tgtgtatata aaaattattc ataagtag
1601 taggaggctt ggtagttta agaatagtt ttgctgact ttctatagt aatagagta ggcaggata ttcaccatta tcttctaga cccactccc
1701 aaccccagg ggaccgaca ggcccgaagg aatagaaga gaagtgagg agagagacag agacagatcc attcgattg tgaacggatc tcgacggtat
1801 cggtaactt taaaagaaa aggggggatt ggggggtaca gtgcaggga aagaatagta gacataatag caacagacat acaactaaa gaattacaaa
1901 acaaaattac aaaaattca aattttatcg attacgcta ggaacagaga aacaggagaa tatggccaa acaggatct tgtgtaagc agttcctgcc
2001 ccgctcagg gccaaagca gttggaacag cagaatatg gccaaacagg atatctgtgg taagcagttc ctgcccggc tcagggccaa gaacagatgg
2101 tcccagatg cggctccc ctcagcagtt tctagagaac catcagatgt ttccagggtg ccccaaggac ctgaaatgac cctgtcctt atttgaacta
2201 accaatcagt tgcctctcg cttctgtcg cgcgcttct ctccccgagc tctatataag cagagctctg ttagtaacc gtcagatcgc ctggagcgc
2301 catccacgt tttttgactt ccatagaagg atctcgacc accatggcg tatacccta cgactgccc gactacccc ccggccccc taagaaaaag
2401 aggaaggtga agaacaatca gaagaaccag gtcatgaacc tggcccaaa cagcaagctg ctgaaggagt acaagagcca gctatcgag ctgaacatc
2501 agcagttcga gcccggcatc ggctgatcc tggcgacgc ctacatcagg agcaggagc agggcaagac ctactgcatg cagttcagat ggaagaaca
2601 ggcctacatg gaccacgtgt gcctgtgta cgaccagtgg gtgctgagcc cccccacaa gaaggagagg gtgaaccacc tggcaacct ggtcatcacc
2701 tggggcccc agacctcaa gcaccaggcc ttcaacaagc tggcaacct gttcatcgtg aacaacaaga agaccatccc caacaacctg gtggagaact
2801 acctgacccc catgagcctg gcctactggt tcatggacga cggcgcaag tggactaca acaagaacag caccaacaag agcatcgtgc tgaacaccca
2901 gagcttacc ttcgaggagg tggagtacct ggtgaaggc ctgaggaaca agttccagct gaactgctac gtgaagatca acaagaacaa gccatcatc

3001 tacatcgaca gcatgagcta cctgatcttc tacaacctga tcaagcccta cctgatcccc cagatgatgt acaagctgcc caacaccatc agcagcgaga
3101 ccttcctgaa gggcggcggc ggatccgggt agggcagagg aagtcttcta acatcggtg acgtggagga gaatccgggc cccatgagcg agctgattaa
3201 ggagaacatg cacatgaagc tgtacatgga gggcaccgtg gacaaccatc acttcaagtg cacatccgag ggcaaggca agccctacga gggcaccag
3301 accatgagaa tcaagtggt cgagggcggc cctctcccct tgccttca catcctggct actagcttc tctacggcag caagacctc atcaaccaca
3401 cccagggcat ccccacttc tcaagcagt ccttcctga gggcttaca tgggagagag tcaccacata cgaagacggg ggcgtgctga cgcctacca
3501 ggacaccagc ctccaggacg gctgcctcat ctacaacgc aagatcagag ggggaactt cacatccaac ggccctgta tgcagaagaa aacctcggc
3601 tgggaggcct tcaccgagac gctgtacccc gctgacggcg gcctggaag cagaaacgac atggccctga agctcgtggg cgggagccat ctgatcгаа
3701 acatcaagac cacatataga tcaagaac ccgctaagaa cctcaagatg cctggcgtct actatgtgga ctacagactg gaaagaatca aggaggccaa
3801 caacgagacc tacgtcagc agcacgaggt ggcatggcc agatactcgc acctccctag caaactgggg cacaagctta attgattcta gagtcgaccg
3901 agcatctac cgccattat acctatatt gttctttt tcttgattg ggtatacatt taaatgtaa tagaacaana tggggggca atcattaca
4001 ttttaggga tatgtaatta ctggtcagg tgtattgca caagacaaac atgttaagaa actttcccgt tattacgct ctgttctgt taatcaact
4101 ctggattaca aaattgtga aagattgact gatattcta actatgttc tcttttac ctgtgtgat atgtcctt atagcctctg tatctagcta
4201 ttgctcccg tacggcttc gttttctct cctgtataa atcctgggt ctgtcttt tagaggagt ttggcccgt gtccgcaac gtggcgtgt
4301 gtgctctgt tttgctgac caacccccac tggctgggc atgcca cactgtcaact ctttctggg actttcgt tccccctcc gatgccacg
4401 gcagaactca tgcgcctg cttgcccgc tgctggacag gggctaggt gctggcact gataattcg tgggtgtgc atcggtacct tttaaaaga
4501 aaaggggga ctggaaggc taattact ccaacgaaga caagatca taactcgt tagcatacat tacaagaat tataattat ttgtgaatt
4601 tgtatgcta ttgcttatt tgaaccata tgtttattg tgaattgt gatgctattg ctttattgt aaccattgt tttgctgt actgggtct
4701 tctggtaga ccagatcga ccctgggagc tcttgcta actaggaac cactgcta agcctaata aagctgct cgaccagct cgactgtcc
4801 ttctagtgc cagcatctg ttgttccc cccccgt ccttctga cctggaag tgccactccc actgtcctt ctaataana tgggaaat
4901 gcatcgatt gtctgagtag gtgcttct attctgggg gtgggtgg gcaggacagc aaggggagg attggaaga caatagcagg catgctggg
5001 atcgggtgg ctctatgccc tgacgtgca ttaatgaat gcccaacgc cggggagag cggttgcgt attggcgct cttccgttc ctgctcact
5101 gactcgtc gctggtctg tggctcgg cgagcggat cagctcact aaaggcgta atacgttat ccacagaatc agggataac gcaggaaga
5201 acatgtgagc aaaaggccg caaaaggcca ggaaccgta aaagccgcg ttgctgctg tttccatag gctccccc cctgacgagc atcaaaaa
5301 tcgacgcta agtcagaggt ggcaaaacc gacaggacta taaagatac aggcgttcc cctggaagc tcctcgtg gctctcgt tccacccg
5401 ccgctaccg gatactgct cgccttct cctcggga gcgtggcct ttctatagc tcacgctga ggtatctag ttcggtgag gtcgttctg
5501 ccaagctggg ctgtgtgac gaacccccg ttagccgca cgctcgcg ttatccgta actatctt tgagccaac ccgtaagac acgacttat
5601 gccactgca gcagccactg gtaaccagat tagcagagc aggtatgtag cgggtctac agattctt aagtggtgc ctaactcgg ctactaga
5701 aggacagat ttggtatctg cgctcgtc aagccagta cctcggaaa aagattgt agctctgat ccggcaaca aaccaccgct ggtagcgtg
5801 gttttttg ttcaagcag cagattacg gcagaaaaa aggatctca gaagatcctt tgatcttct tacgggtct gacgctcag gaaacaaaa
5901 ctacgttaa gggatttgg tcatgagatt atcaaaaag atcttacct agatctttt aaataaaaa tgaagttta aatcaatca aagatatat
6001 gataaactt ggtctgacg ttaccaatgc ttaacagtg aggcacat ctacgcatc tcttattc gttcatcat agttgcctga cttccgctg

6101 tgtagataac tacgatacgg gagggcttac catctggccc cagtgtgca atgataccgc gagaccacg ctcaccggct ccagatttat cagcaataaa
6201 ccagccagcc ggaaggccg agcgcagaag tggctctgca acctatccg cctccatcca gtctattaat tggccggg aagctagagt aagtagttcg
6301 ccagttaata gttgcaaa cgtgttgcc atgtctacag gcatcgtgt gtcacgctcg tcgtttgta tggcttcatt cagctccgg tccaacgat
6401 caaggcaggt tacatgatcc cccatgtgt gcaaaaaagc ggtagctcc ttcggctctc cgatcgtgt cagaagtaag ttggccgag tttatcact
6501 catggtatg gcagcactgc ataattctct tactgtcatg ccatccgtaa gatgctttc tgtgactggt gactactca ccaagtcatt ctgagaatag
6601 tgtagcggc gaccgagtg ctctgcccg gcgtcaatac gggataatac cgcgccacat agcagaactt taaaagtct catcattgga aaacttctt
6701 cggggcgaaa actctcaagg atctaccgc tgttgagatc cagttgatg taaccactc gtgcaccaa ctgatctca gcatcttta cttcaccag
6801 cgtttctgg tgagcaaaa caggaaggca aaatccgca aaaaaggaa taaggcgac acggaaatgt tgaatactca tactctctt tttcaatat
6901 tattgaagca tttatcaggg ttattgtctc atgagcggat acatattga atgtattag aaaaataaac aaataggggt tccgcgaca tttcccgaa
7001 aagtccacc t