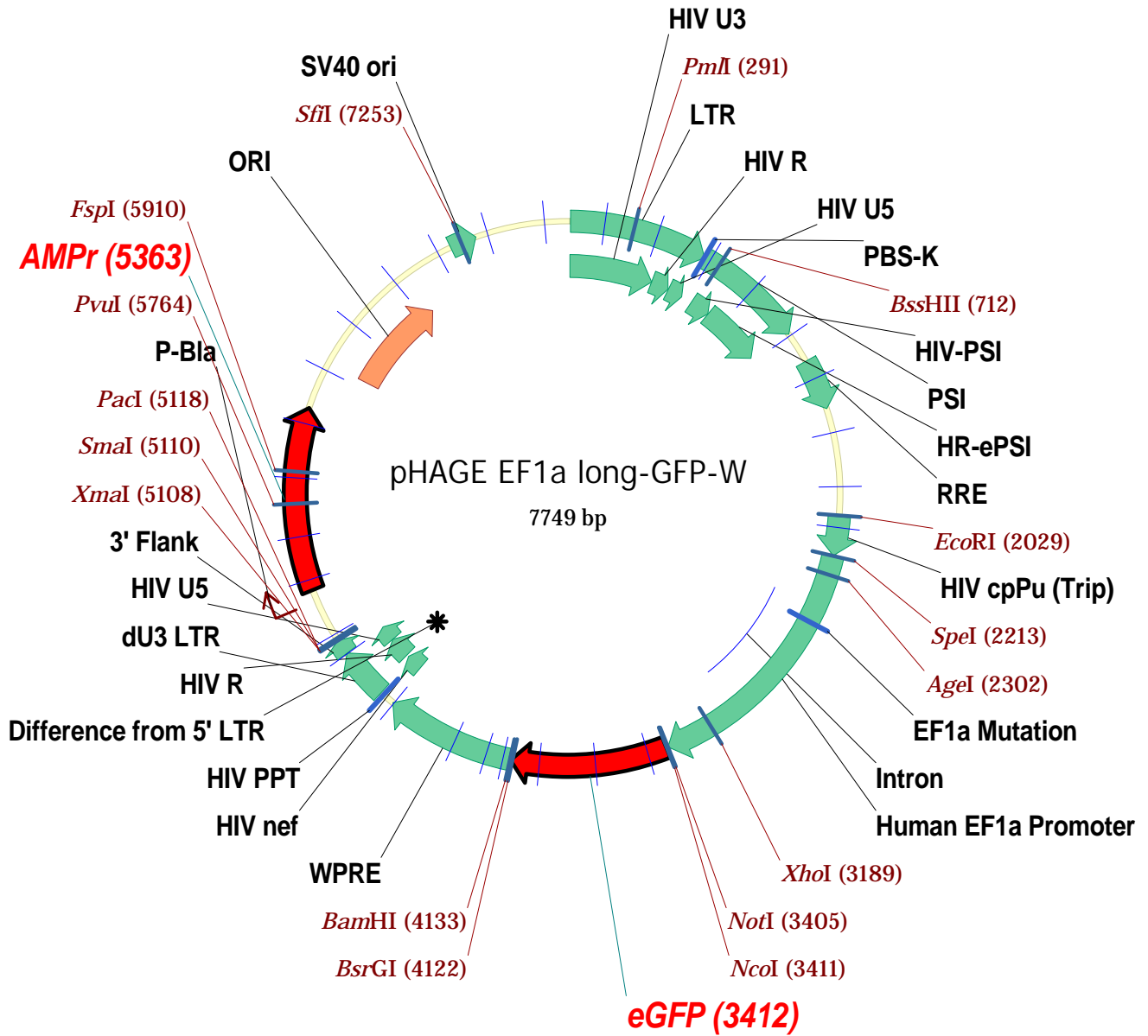


pHAGE EF1a long-GFP-W



General Description

DNA pHAGE EF1a long-GFP-W
Entire molecule length: 7749 bp

Standard Fields

User Fields

Author(s)

Author

Original author

A Omari

References

Comments

Feature Map

CDS (2 total)

eGFP

Start: 3412 End: 4131

Enhanced Green Fluorescent Protein (Mammalian Codon Optimized)

Original Location Description:

2837..3556

Qualifiers:

/gene="eGFP"

AMPr

Start: 5363 End: 6202

Ampicillin Resistance Gene

Original Location Description:

6153..6992

Qualifiers:

/gene="AMPr"

/product="beta-lactamase (mature form)"

Intron (1 total)

Intron

Start: 2454 End: 3045

Human EF1a Intron

Misc. Feature (19 total)

LTR

Start: 1 End: 636

Long Terminal Repeat

Original Location Description:

1..636

Qualifiers:

/gene="LTR"

HIV U3

Start: 1 End: 453

Full Length HIV U3

HIV R

Start: 454 End: 551
HIV Repeat Region

HIV U5

Start: 552 End: 636
HIV U5

PBS-K

Start: 636 End: 658
tRNA binding site for Lysine tRNA

PSI

Start: 637 End: 1155
PSI Packaging Sequence
Original Location Description:
637..1155
Qualifiers:
/gene="psi"
/product="pbs-gag"

HIV-PSI

Start: 697 End: 806

HR-ePSI

Start: 807 End: 1144

RRE

Start: 1303 End: 1536
Rev Responsive Element
Original Location Description:
1303..1536
Qualifiers:
/gene="rre"
/product="minimal RRE"

HIV cpPu (Trip)

Start: 2034 End: 2211
Central Poly Purine Track
Original Location Description:
2034..2211
Qualifiers:
/gene="cppt"

Human EF1a Promoter

Start: 2218 End: 3402
Human Elongation Factor 1 alpha promoter

WPRE

Start: 4138 End: 4729
Woodchuck Hepatitis Virus Posttranscriptional Regulatory Element
Original Location Description:
3563..4154
Qualifiers:
/gene="WPRE"

HIV nef

Start: 4735 End: 4823
HIV nef

HIV PPT

Start: 4785 End: 4799
Polypurine Tract (Not degraded by RNaseH so it can serve as a primer for + strand DNA

dU3 LTR

Start: 4800 End: 5035
Deleted U3 Long-Terminal Repeat
Original Location Description:
4225..4460
Qualifiers:
/gene="dU3 LTR"

HIV R

Start: 4837 End: 4952
HIV Repeat Region

HIV U5

Start: 4953 End: 5035
HIV U5

3' Flank

Start: 5036 End: 5106
Chromosomal 3' Flanking Sequence carried over from original HIV integration site

SV40 ori

Start: 7201 End: 7324
Original Location Description:
7991..8114
Qualifiers:
/gene="SV40 ori"

Modified Base (1 total)

Difference from 5' LTR

Start: 4848 End: 4848
This T is a C in the 5' LTR

Primer Binding Site (28 total)

pHAGE-A0050-8050

Start: 158 End: 179 (Complementary)

pHAGE-S501-1000

Start: 401 End: 421

pHAGE-A0550-0050

Start: 667 End: 690 (Complementary)

pHAGE-S1001-1500

Start: 898 End: 919

pHAGE-A1050-0550

Start: 1166 End: 1189 (Complementary)

pHAGE-S1501-2000

Start: 1391 End: 1417

pHAGE-A1550-1050

Start: 1650 End: 1678 (Complementary)

pHAGE-S2001-2500

Start: 1898 End: 1922

pHAGE-A2050-1550

Start: 2084 End: 2112 (Complementary)

pHAGE-S3001-3500

Start: 3501 End: 3518

pHAGE-A3050-2550

Start: 3744 End: 3764 (Complementary)

pHAGE-S3501-4000

Start: 3999 End: 4020

pHAGE 3' CDS

Start: 4166 End: 4200 (Complementary)

pHAGE-A3550-3050

Start: 4244 End: 4267 (Complementary)

pHAGE-S4001-4500

Start: 4397 End: 4417

pHAGE-A4050-3550

Start: 4725 End: 4747 (Complementary)

pHAGE-S4501-5000

Start: 5033 End: 5064

pHAGE-S6001-6500

Start: 5139 End: 5161

pHAGE-A6050-5550

Start: 5412 End: 5435 (Complementary)

pHAGE-S6501-7000

Start: 5612 End: 5636

pHAGE-A6550-6050

Start: 5881 End: 5904 (Complementary)

pHAGE-S7001-7500

Start: 6132 End: 6156

pHAGE-A7050-6550

Start: 6392 End: 6413 (Complementary)

pHAGE-S7501-8000

Start: 6636 End: 6660

pHAGE-A7550-7050

Start: 6903 End: 6924 (Complementary)

pHAGE-S8001-8500

Start: 7139 End: 7158

pHAGE-A8050-7550

Start: 7379 End: 7405 (Complementary)

pHAGE-S1-500

Start: 7644 End: 7672

Promoter Prokaryotic (1 total)

P-Bla

Start: 5310 End: 5344

Beta Lactamase Promoter

Replication Origin (1 total)

ORI

Start: 6431 End: 6964

Bacterial Origin of Replication

Original Location Description:

7221..7754

Qualifiers:

/gene="ORI"
/product="ColE1 origin of replication"

Mutation (1 total)

EF1a Mutation

Start: 2531 End: 2531

Missing GCCC according to Genbank and Celera sequences

Restriction/Methylation Map

Enzyme	# of cuts	Positions
AfIII	2	2857 7021
AgeI	1	2302
ApaLI	3	4349 5461 6707
AvaI	8	296 1928 2269 2371 2557 3072 3189 5108
BamHI	1	4133
BglIII	5	474 2790 4768 4834 4875
BsrGI	1	4122
BssHII	1	712
DraI	7	2062 2725 4785 5555 6247 6266 7707
EagI	3	1145 1149 3405
EcoRI	1	2029
EcoRV	3	36 115 334
FseI	2	1151 2928
FspI	1	5910
HindIII	4	532 1088 1676 4933
NaeI	3	1149 2926 4654
NarI	2	639 3163
NcoI	1	3411
NotI	1	3405
PacI	1	5118
PmlI	1	291
PstI	2	2540 3045
PvuI	1	5764
PvuII	2	436 4763
SacI	4	492 683 3052 4893
SacII	3	2478 2825 4643
SfiI	1	7253
SmaI	1	5110
SpeI	1	2213
StuI	3	2595 2638 7299
XhoI	1	3189
XmaI	1	5108

No cuts: Acc65I, AfeI, AscI, BclI, ClaI, HpaI, KpnI, MluI, MscI, NdeI, NheI, PmeI, Sall, SbfI, SrfI, Swal,

Sequence

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cacaaggcta cttccctgat tagcagaact acacaccagg
101 gccaggggtc agatatccac tgacctttgg atgggtgtac aagctagtagc cagttgagcc
agataaggta gaagaggcca ataaaggaga gaacaccagc
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Component Fragments