General Description

DNA pcDNA5/FRT-HA-GsD

Entire molecule length: 6441 bp

Standard Fields

Original Source Database: GenBank

Division: SYN

Modification Date in the Original DB: 17-DEC-2007

User Fields

Author(s)

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References

Comments

Feature Map

CDS (2 total)

Hygro(R) (no ATG)

Start: 2962 End: 3984

Original Location Description:

2962..3984

Qualifiers:

/invitrogen="1190000"

Amp(R)

Start: 5445 End: 6305 (Complementary)

Original Location Description:

complement(5445..6305)

Qualifiers:

/invitrogen="1020000"

Insertion (1 total)

from pCD-GsD (BsPMI)

Start: 965 End: 2336

Original Location Description:

965..2336

Misc. Binding Site (1 total)

Gs DREADD

Start: 1037 End: 2272

Original Location Description:

1037..2272

Misc. Feature (1 total)

start

Start: 1007 End: 1009

Original Location Description:

1007..1009

PolyA Signal (1 total)

SV40 pA

Start: 4114 End: 4244

Original Location Description:

4114..4244

Qualifiers:

/invitrogen="1840000"

PolyA Site (1 total)

BGH pA

Start: 2400 End: 2624

Original Location Description:

2400..2624

Qualifiers:

/invitrogen="1870000"

Primer (5 total)

CMV forward primer

Start: 769 End: 789

Original Location Description:

769..789

Qualifiers:

/invitrogen="1930000"

T7 primer

Start: 863 End: 882

Original Location Description:

863..882

Qualifiers:

/invitrogen="2100000"

GsD begin-F

Start: 1182 End: 1200

Original Location Description:

1182..1200

Seq-Gs Dread-b1 i3 loop

Start: 1787 End: 1807

Original Location Description:

1787..1807

BGH reverse primer

Start: 2394 End: 2411 (Complementary)

Original Location Description:

complement(2394..2411)

Qualifiers:

/invitrogen="1910000"

Primer Binding Site (1 total)

GsD begin (R)

Start: 1301 End: 1318

Original Location Description:

1301..1318

Promoter Eukaryotic (1 total)

CMV promoter

Start: 232 End: 819

Original Location Description:

232..819

Qualifiers:

/invitrogen="2180000"

Promoter Prokaryotic (2 total)

T7 promoter

Start: 863 End: 879

Original Location Description:

863..879

Qualifiers:

/invitrogen="2370000"

bla promoter

Start: 6306 End: 6404 (Complementary)

Original Location Description:

complement(6306..6404)

Qualifiers:

/invitrogen="2330000"

Replication Origin (1 total)

pUC origin

Start: 4627 End: 5300 (Complementary)

Original Location Description:

complement(4627..5300)

Qualifiers:

/invitrogen="2540000"

Mutation (4 total)

Y148C

Start: 1475 End: 1477

Original Location Description:

1475..1477

turkey b1 i2 loop

Start: 1544 End: 1579

Original Location Description:

1544..1579

A238G

Start: 1745 End: 1747

Original Location Description:

1745..1747

turkey b1 i3 loop

Start: 1787 End: 1969

Original Location Description:

1787..1969

Misc. Recombination (1 total)

FRT

Start: 2907 End: 2954

Original Location Description:

2907..2954

Qualifiers:

/invitrogen="2710000"

Old Sequence (1 total)

HA Tag

Start: 1010 End: 1036

Original Location Description:

1010..1036

Restriction/Methylation Map

|  |  |  |
| --- | --- | --- |
| **Enzyme** | **# of cuts** | **Positions** |
| BamHI | 1 | 930 |
| EcoRI | 2 | 953 3203 |
| HindIII | 1 | 912 |
| NheI | 2 | 896 1991 |
| NotI | 1 | 2352 |
| XbaI | 2 | 2364 2935 |
| XhoI | 2 | 1579 2358 |

No cuts: XmaI

Sequence

1 gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt

101 ggaggtcgct gagtagtgcg cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc ttagggttag gcgttttgcg

201 ctgcttcgcg atgtacgggc cagatatacg cgttgacatt gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata

301 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc cccgcccatt gacgtcaata atgacgtatg ttcccatagt

401 aacgccaata gggactttcc attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt atcatatgcc aagtacgccc

501 cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca

601 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg actcacgggg atttccaagt ctccacccca ttgacgtcaa

701 tgggagtttg ttttggcacc aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg gtaggcgtgt acggtgggag

801 gtctatataa gcagagctct ctggctaact agagaaccca ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc

901 gtttaaactt aagcttggta ccgagctcgg atccactagt ccagtgtggt ggaattctgc agataagctg ctgcaggtcg tcctgggact atgtcagaga

1001 gtcacaatgt acccctacga cgtccccgac tacgccacct tgcacagtaa cagtacaacc tcgcctttgt ttcccaacat cagctcttcc tgggtgcaca

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1301 gtggccttca aggtcaacaa acagctgaag acagtcaaca actacttcct cttaagcctg gcctgtgcag acctgatcat cggggtcatt tccatgaacc

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2201 aggcgcaaac agcagtacca gcagagacag tcggtcattt ttcacaagcg agtgccggag caggccttgt agaaaagggg tatgttgaga gcagtgacca

2301 cgcaagcgcg tcagcccaca cagcctagca ggagtcatcc agcacagtgg cggccgctcg agtctagagg gcccgtttaa acccgctgat cagcctcgac

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Component Fragments

