General Description

DNA pcDNA5/FRT-HA-hM3D

Entire molecule length: 6832 bp

Feature Map

CDS (2 total)

Hygro(R) (no ATG)

Start: 3353 End: 4375

Original Location Description:

3353..4375

Qualifiers:

/invitrogen="1190000"

Amp(R)

Start: 5836 End: 6696 (Complementary)

Original Location Description:

complement(5836..6696)

Qualifiers:

/invitrogen="1020000"

Homeodomain (1 total)

HA tag

Start: 941 End: 967

Original Location Description:

941..967

Insertion (1 total)

hM3D

Start: 968 End: 2740

Original Location Description:

968..2740

PolyA Signal (1 total)

SV40 pA

Start: 4505 End: 4635

Original Location Description:

4505..4635

Qualifiers:

/invitrogen="1840000"

PolyA Site (1 total)

BGH pA

Start: 2791 End: 3015

Original Location Description:

2791..3015

Qualifiers:

/invitrogen="1870000"

Primer (8 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"

Seq-hM3D begin REV (F)

Start: 1318 End: 1339

Original Location Description:

1318..1339

hACAM3-1

Start: 1351 End: 1370

Original Location Description:

1351..1370

hACAM3-2

Start: 1754 End: 1779

Original Location Description:

1754..1779

Se-hM3D-middle

Start: 1963 End: 1981

Original Location Description:

1963..1981

Seq-hM3D-end

Start: 2503 End: 2521

Original Location Description:

2503..2521

BGH reverse primer

Start: 2785 End: 2802 (Complementary)

Original Location Description:

complement(2785..2802)

Qualifiers:

/invitrogen="1910000"

Primer Binding Site (1 total)

Seq-hM3D-begin (R)

Start: 1114 End: 1132

Original Location Description:

1114..1132

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: 6697 End: 6795 (Complementary)

Original Location Description:

complement(6697..6795)

Qualifiers:

/invitrogen="2330000"

Replication Origin (1 total)

pUC origin

Start: 5018 End: 5691 (Complementary)

Original Location Description:

complement(5018..5691)

Qualifiers:

/invitrogen="2540000"

Mutation (2 total)

Y148C

Start: 1412 End: 1413

Original Location Description:

1412..1413

A238G

Start: 1682 End: 1684

Original Location Description:

1682..1684

Misc. Recombination (1 total)

FRT

Start: 3298 End: 3345

Original Location Description:

3298..3345

Qualifiers:

/invitrogen="2710000"

Imported Features Not Shown on Map

Source (1 total)

Source\_1

Start: 1 End: 6832

Original Location Description:

1..6832

Qualifiers:

/invitrogen="191"

Restriction/Methylation Map

|  |  |  |
| --- | --- | --- |
| **Enzyme** | **# of cuts** | **Positions** |
| BamHI | 1 | 930 |
| EcoRI | 1 | 3594 |
| HindIII | 4 | 912 2076 2234 2244 |
| NheI | 1 | 896 |
| XhoI | 2 | 1096 2749 |

No cuts: AscI

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 atccaccatg tacccatacg atgttccaga ttacgctatg accttgcaca ataacagtac aacctcgcct

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1101 cagctggcaa tttctcctct ccagacggta ccaccgatga ccctctggga ggtcataccg tctggcaagt ggtcttcatc gctttcttaa cgggcatcct

1201 ggccttggtg accatcatcg gcaacatcct ggtaattgtg tcatttaagg tcaacaagca gctgaagacg gtcaacaact acttcctctt aagcctggcc

1301 tgtgccgatc tgattatcgg ggtcatttca atgaatctgt ttacgaccta catcatcatg aatcgatggg ccttagggaa cttggcctgt gacctctggc

1401 ttgccattga ctgcgtagcc agcaatgcct ctgttatgaa tcttctggtc atcagctttg acagatactt ttccatcacg aggccgctca cgtaccgagc

1501 caaacgaaca acaaagagag ccggtgtgat gatcggtctg gcttgggtca tctcctttgt cctttgggct cctgccatct tgttctggca atactttgtt

1601 ggaaagagaa ctgtgcctcc gggagagtgc ttcattcagt tcctcagtga gcccaccatt acttttggca cagccatcgc tggtttttat atgcctgtca

1701 ccattatgac tattttatac tggaggatct ataaggaaac tgaaaagcgt accaaagagc ttgctggcct gcaagcctct gggacagagg cagagacaga

1801 aaactttgtc caccccacgg gcagttctcg aagctgcagc agttacgaac ttcaacagca aagcatgaaa cgctccaaca ggaggaagta tggccgctgc

1901 cacttctggt tcacaaccaa gagctggaaa cccagctccg agcagatgga ccaagaccac agcagcagtg acagttggaa caacaatgat gctgctgcct

2001 ccctggagaa ctccgcctcc tccgacgagg aggacattgg ctccgagacg agagccatct actccatcgt gctcaagctt ccgggtcaca gcaccatcct

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Component Fragments

