General Description

DNA pcDNA5/FRT-HA-hM4D

Entire molecule length: 6499 bp

Feature Map

CDS (2 total)

Hygro(R) (no ATG)

Start: 3020 End: 4042

Original Location Description:

3020..4042

Qualifiers:

/invitrogen="1190000"

Amp(R)

Start: 5503 End: 6363 (Complementary)

Original Location Description:

complement(5503..6363)

Qualifiers:

/invitrogen="1020000"

Insertion (1 total)

hM4D

Start: 968 End: 2407

Original Location Description:

968..2407

Misc. Feature (2 total)

MCS

Start: 895 End: 2440

Original Location Description:

895..2440

Qualifiers:

/invitrogen="1630000"

HA tag

Start: 941 End: 967

Original Location Description:

941..967

PolyA Signal (1 total)

SV40 pA

Start: 4172 End: 4302

Original Location Description:

4172..4302

Qualifiers:

/invitrogen="1840000"

PolyA Site (1 total)

BGH pA

Start: 2458 End: 2682

Original Location Description:

2458..2682

Qualifiers:

/invitrogen="1870000"

Primer (6 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-hM4D-middle

Start: 1113 End: 1132

Original Location Description:

1113..1132

Seq-hM4-1

Start: 1353 End: 1371

Original Location Description:

1353..1371

Seq-hM4D end

Start: 1954 End: 1975

Original Location Description:

1954..1975

BGH reverse primer

Start: 2452 End: 2469 (Complementary)

Original Location Description:

complement(2452..2469)

Qualifiers:

/invitrogen="1910000"

Primer Binding Site (1 total)

Seq-hM4D-begin (R)

Start: 1144 End: 1165

Original Location Description:

1144..1165

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: 6364 End: 6462 (Complementary)

Original Location Description:

complement(6364..6462)

Qualifiers:

/invitrogen="2330000"

Replication Origin (1 total)

pUC origin

Start: 4685 End: 5358 (Complementary)

Original Location Description:

complement(4685..5358)

Qualifiers:

/invitrogen="2540000"

Mutation (2 total)

Y3.33C

Start: 1304 End: 1306

Original Location Description:

1304..1306

A5.46G

Start: 1574 End: 1576

Original Location Description:

1574..1576

Misc. Recombination (1 total)

FRT

Start: 2965 End: 3012

Original Location Description:

2965..3012

Qualifiers:

/invitrogen="2710000"

Imported Features Not Shown on Map

Source (1 total)

Source\_1

Start: 1 End: 6499

Original Location Description:

1..6499

Qualifiers:

/invitrogen="191"

Restriction/Methylation Map

|  |  |  |
| --- | --- | --- |
| **Enzyme** | **# of cuts** | **Positions** |
| BamHI | 1 | 930 |
| BclI | 1 | 2446 |
| EcoRI | 1 | 3261 |
| NdeI | 2 | 485 3468 |
| NheI | 2 | 896 2186 |
| SacI | 2 | 819 928 |
| SpeI | 1 | 250 |
| XhoI | 1 | 2416 |

No cuts: AgeI, AscI, FseI

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 gccaacttca cacctgtcaa tggcagctcg

1001 ggcaatcagt ccgtgcgcct ggtcacgtca tcatcccaca atcgctatga gacggtggaa atggtcttca ttgccacagt gacaggctcc ctgagcctgg

1101 tgactgtcgt gggcaacatc ctggtgatgc tgtccatcaa ggtcaacagg cagctgcaga cagtcaacaa ctacttcctc ttcagcctgg cgtgtgctga

1201 tctcatcata ggcgccttct ccatgaacct ctacaccgtg tacatcatca agggctactg gcccctgggc gccgtggtct gcgacctgtg gctggccctg

1301 gactgcgtgg tgagcaacgc ctccgtcatg aaccttctca tcatcagctt tgaccgctac ttctgcgtca ccaagcctct cacctaccct gcccggcgca

1401 ccaccaagat ggcaggcctc atgattgctg ctgcctgggt actgtccttc gtgctctggg cgcctgccat cttgttctgg cagtttgtgg tgggtaagcg

1501 gacggtgccc gacaaccagt gcttcatcca gttcctgtcc aacccagcag tgacctttgg cacagccatt gctggcttct acctgcctgt ggtcatcatg

1601 acggtgctgt acatccacat ctccctggcc agtcgcagcc gagtccacaa gcaccggccc gagggcccga aggagaagaa agccaagacg ctggccttcc

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1901 gagctgtcca ccacagaggc caccacgccc gccatgcccg cccctcccct gcagccgcgg gccctcaacc cagcctccag atggtccaag atccagattg

2001 tgacgaagca gacaggcaat gagtgtgtga cagccattga gattgtgcct gccacgccgg ctggcatgcg ccctgcggcc aacgtggccc gcaagttcgc

2101 cagcatcgct cgcaaccagg tgcgcaagaa gcggcagatg gcggcccggg agcgcaaagt gacacgaacg atctttgcca ttctgctagc cttcatcctc

2201 acctggacgc cctacaacgt catggtcctg gtgaacacct tctgccagag ctgcatccct gacacggtgt ggtccattgg ctactggctc tgctacgtca

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2501 cgtgccttcc ttgaccctgg aaggtgccac tcccactgtc ctttcctaat aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg

2601 gggggtgggg tggggcagga cagcaagggg gaggattggg aagacaatag caggcatgct ggggatgcgg tgggctctat ggcttctgag gcggaaagaa

2701 ccagctgggg ctctaggggg tatccccacg cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt tacgcgcagc gtgaccgcta cacttgccag

2801 cgccctagcg cccgctcctt tcgctttctt cccttccttt ctcgccacgt tcgccggctt tccccgtcaa gctctaaatc gggggtccct ttagggttcc

2901 gatttagtgc tttacggcac ctcgacccca aaaaacttga ttagggtgat ggttcacgta cctagaagtt cctattccga agttcctatt ctctagaaag

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3201 atgtttatcg gcactttgca tcggccgcgc tcccgattcc ggaagtgctt gacattgggg aattcagcga gagcctgacc tattgcatct cccgccgtgc

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4101 tcgttttccg ggacgccggc tggatgatcc tccagcgcgg ggatctcatg ctggagttct tcgcccaccc caacttgttt attgcagctt ataatggtta

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Component Fragments

