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

 1701 tcaagagccc actaatgaag cagagcgtca agaagccccc gcccggggag gccgcccggg aggagctgcg caatggcaag ctggaggagg cccccccgcc

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 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

 2301 acagcaccat caaccctgcc tgctatgctc tgtgcaacgc cacctttaaa aagaccttcc ggcacctgct gctgtgccag tatcggaaca tcggcactgc

 2401 caggtaggcg gccgctcgag tctagagggc ccgtttaaac ccgctgatca gcctcgactg tgccttctag ttgccagcca tctgttgttt gcccctcccc

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 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

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 3001 tataggaact tccttggcca aaaagcctga actcaccgcg acgtctgtcg agaagtttct gatcgaaaag ttcgacagcg tctccgacct gatgcagctc

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 3201 atgtttatcg gcactttgca tcggccgcgc tcccgattcc ggaagtgctt gacattgggg aattcagcga gagcctgacc tattgcatct cccgccgtgc

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 4001 ggaaaccgac gccccagcac tcgtccgagg gcaaaggaat agcacgtact acgagatttc gattccaccg ccgccttcta tgaaaggttg ggcttcggaa

 4101 tcgttttccg ggacgccggc tggatgatcc tccagcgcgg ggatctcatg ctggagttct tcgcccaccc caacttgttt attgcagctt ataatggtta

 4201 caaataaagc aatagcatca caaatttcac aaataaagca tttttttcac tgcattctag ttgtggtttg tccaaactca tcaatgtatc ttatcatgtc

 4301 tgtataccgt cgacctctag ctagagcttg gcgtaatcat ggtcatagct gtttcctgtg tgaaattgtt atccgctcac aattccacac aacatacgag

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 5301 agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt aagggatttt

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Component Fragments

