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

 1001 ttgtttccaa acatcagctc ctcctggata cacagcccct ccgatgcagg gctgcccccg ggaaccgtca ctcatttcgg cagctacaat gtttctcgag

 1101 cagctggcaa tttctcctct ccagacggta ccaccgatga ccctctggga ggtcataccg tctggcaagt ggtcttcatc gctttcttaa cgggcatcct

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 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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 2201 aagagcgtgg acgatggagg cagttttcca aaaagcttct ccaagcttcc catccagcta gagtcagccg tggacacagc taagacttct gacgtcaact

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 2501 ctggtgaaca ccttttgtga cagctgcata cccaaaacct tttggaatct gggctactgg ctgtgctaca tcaacagcac cgtgaacccc gtgtgctatg

 2601 ctctgtgcaa caaaacattc agaaccactt tcaagatgct gctgctgtgc cagtgtgaca aaaaaaagag gcgcaagcag cagtaccagc agagacagtc

 2701 ggtcattttt cacaagcgcg cacccgagca ggccttgtag gcggccgctc gagtctagag ggcccgttta aacccgctga tcagcctcga ctgtgccttc

 2801 tagttgccag ccatctgttg tttgcccctc ccccgtgcct tccttgaccc tggaaggtgc cactcccact gtcctttcct aataaaatga ggaaattgca

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 3001 cggtgggctc tatggcttct gaggcggaaa gaaccagctg gggctctagg gggtatcccc acgcgccctg tagcggcgca ttaagcgcgg cgggtgtggt

 3101 ggttacgcgc agcgtgaccg ctacacttgc cagcgcccta gcgcccgctc ctttcgcttt cttcccttcc tttctcgcca cgttcgccgg ctttccccgt

 3201 caagctctaa atcgggggtc cctttagggt tccgatttag tgctttacgg cacctcgacc ccaaaaaact tgattagggt gatggttcac gtacctagaa

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 4401 ccgccgcctt ctatgaaagg ttgggcttcg gaatcgtttt ccgggacgcc ggctggatga tcctccagcg cggggatctc atgctggagt tcttcgccca

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 6801 gcacatttcc ccgaaaagtg ccacctgacg tc

Component Fragments

