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)

 Author

 NCBI Entrez

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 EMAIL: bioinfosales@invitrogen.com

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

 1101 gtccctcgga ggcagggctg cccttgggga cagtcactca gttgggcagc tacaacattt cacaagaaac tgggaatttc tcctcaaacg acacctccag

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 1801 ggccaaggag cagatcagga agatcgaccg ctgcgagggc cggttctatg gcagccagga gcagccgcag ccacccccgc tcccccaaca ccagcccatc

 1901 ctcggcaacg gccgtgccag caagaggaag acgtcccgtg tcatggccat gagggaacac aaagctctgc agacgctcag tgccatcttg ctagccttca

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Component Fragments

