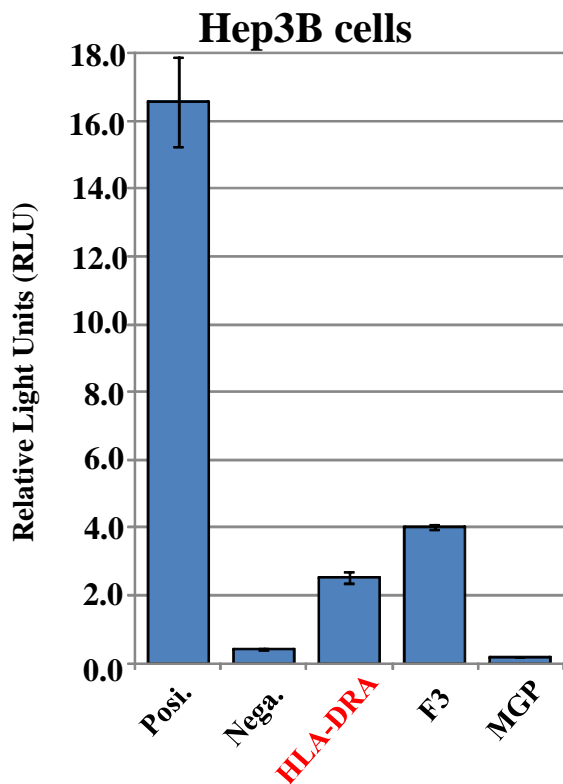
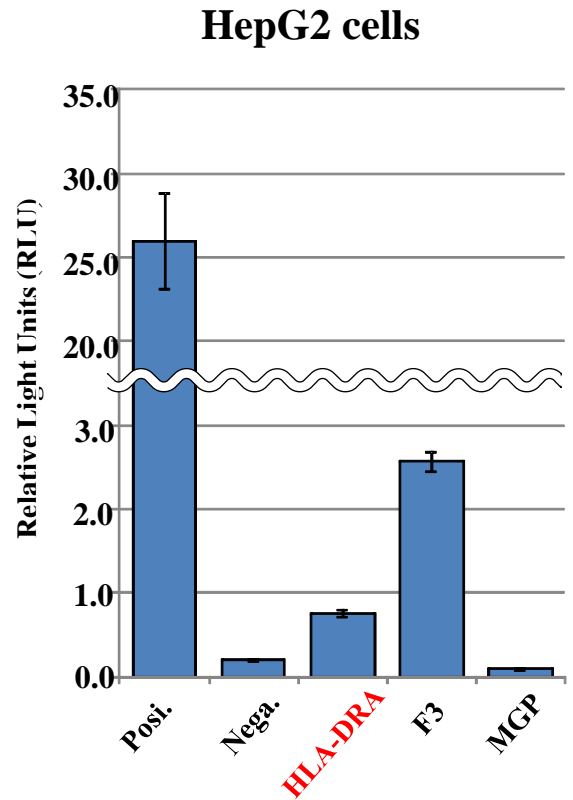
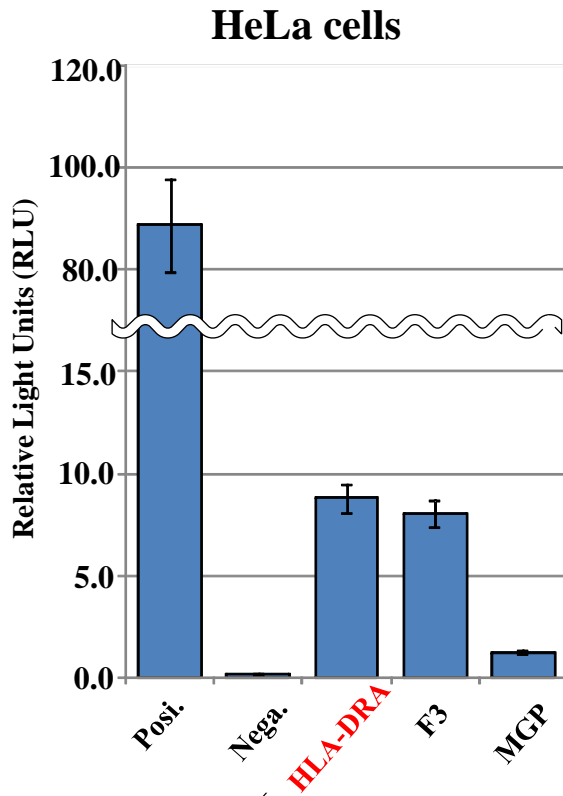


The Promoter Activities of Reporter Constructs



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

HLA-DRA: pGL4-phHLA-DRA(RDB# 7389)

F3: pGL4-phF3 (RDB# 7458)

MGP: pGL4-phMGP (RDB# 7394)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.01.25

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5665

2nd Nucleotide Sequence

File Name : RDB7389F.fasta
Sequence Size : 579

Unit Size to Compare = 1
Pick up Location = 1

[94.301% / 544 bp] INT/OPT.Score : < 838/ 1760 >

```
1'                               GGCCTAA CTG-GCCGGT -ACCTGAG-C
                               ***** *
1" ACCGATGCTT TAGCTGGTGC GAAACTTATC TCTGGCCAAC CTGTGCCGGT AACCTGAGAC

25' TCG-CTAGCC TCGAGGATCA CTGCCAGGTC ACTCTTCATG GAAGTATTTG TATTCCAGTC
   *** **** *      ***** ***** ***** ***** *****
61" TCGACTAGAC CTCAGGATCA CTGCCAGGTC ACTCTTCATG GAAGTATTTG TATTCCAGTC

84' CTTTCTGTGG AAAGAACTTA ACATTCT-CC TTTTCATAAC ACTGTATCTT CAGAAACAAG
   ***** ***** ***** ** ***** ***** *****
121" CTTTCTGTGG AAAGAACTTA ACATTCTCCC TTTTCATAAC ACTGTATCTT CAGAAACAAG

143' AGAGTCGAAG TCTCCTAATT TTCAGGAGTG TCTATGTTGA ACATCAAAT ATATTCTTTA
   ***** ***** ***** ** ***** ***** *****
181" AGAGTCGAAG TCTCCTAATT TTCAGGACTG TCTATGTTGA ACATCAAAT ATATTCTTTA

203' GAGCAGATCT TTAATAATCA TATGACAAGA GAAAACTTT CATAATCTTA TGACATGAGG
   ***** ***** ***** ***** ***** *****
241" GAGCAGATCT TTAATAATCA TATGACAAGA GAAAACTTT CATAATCTTA TGACATGAGG
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263' GAAGGAATAT TAAAGCCGTT CTGTGGGTTA TTATCTCTAA CGTTCCCAAT AGAATAGGC-
*****
301" GAAGGAATAT TAAAGCCGTT CTGTGAGTTA TTATCTCTAA CGTTCCCAAT AGAATAGGCA

322' TTTGCC-AGC -TGGGTGC-G GTGGCTCATG CCTGTAATCC C-AGC-ACTT TG-AGAGGCC
*****
361" TTTGCCAAGC ATGGGTGCAG GTGGCTCATG CCTGTAATCC CAAGCAACTT TGCAGAGGCC

376' AAGGC-GGGC -AAATCAGC- AGGTCAGGAG TCTGAGACC- AGCCTGACC- AAC-ATGGTG
*****
421" AAGGCAGGGC AAAATCACGA AGGTCAGGAG TCTGAGACCA AGCCTGACCA AACAATGGTG

430' -AAACCCCGT CTCTAC-TAA AAATAC-AAA AATTAGCCGG GCATGGTGGT GGGC-GCCTG
*****
481" AAAACCCCGT CTCTACATAA AAATACAAA AATTAGCCGG GCATGGTGGT GGGCAGCCTG

486' TAATCCCAGC TACTCAGGAG GC-TGAGGCA GGAGAATCGC TTGAACCCGG GAGGCGGAGA
*****
541" TAATCCCAGC TACTCAGGAG GCATGAGGCA GGAGAATTT

```

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5665

2nd Nucleotide Sequence

File Name : RDB7389R.fasta (Complementary)
Sequence Size : 604

Unit Size to Compare = 1

Pick up Location = 1

[86.131% / 548 bp] INT/OPT. Score : < 184/ 1234 >



961' AAAGAGCTTC TTTAGTGAAG CTATGTCTC AGTACTGCCA AAATTCAGAC AATCTCCATG
1" CCCCATG GGCCCTGTA

1021' GCCTGACAAT TTACCTTCTA TTTGGGTAA- TTTATTGTCC CTTACGCAA CT-CTCCAGC
* * * * * ***** ***** ***** * * . * * * *
18" TCTATTTTAG CCTTCCTATT TTGGGGTAAT TTTATTGTCC CTTACGCAA CTNCNCCAAC

1079' TG-TCA-TGG CACAGA-CAT ATGA-TCTGT A-TTTA-GCT CTCA-CTTTA -GGTG-TTTC
** *** ** ***** ** ***** ***** * ***** ** ***** ***** ** * * * *
78" TGTTCAATTGG CACAGACCAT ATGATTCTGT ATTTTAGGCT CTCACCTTTA GGGTGTTTTC

1130' CATTGA-TTC TATT-CT-CA CTAATGT-GC TTCAGGTATA T-CCCTGT-C TAGAACTCAG
****. * *** ***** ** ** ***** ** ***** ***** * ***** * ***** *****
138" CATTNATTC TATTGCTGCA CTAATGTGGC TTCAGGTATA TGCCCTGTGC TAGAAGTCAG

1184' ATTGGGGTTA AAGAGTCTGT CCGTCATTGA CCAACAGT-C TTAATACTT -GATTGTG
***** ***** ***** ***** * ***** * ***** ***** *****
198" ATTGGGGTTA AAGAGTCTGT CCGTGATTGA CTAACAGTGC TTAATACTT GGATTGTG

1242' TCGTTGTTGT -CCTGTTTGT TTAAGAACTT TAG-TTCTTT A-TCCAATGA A-CGGAGTAT
* ***** ***** ***** ***** ***** * ***** * ***** *****
258" TTGTTGTTGT GCCTGTTTGT TTAAGAACTT TACTTTCTTT ATTCCAATGA AGCGGAGTAT

1298' -CTT-GTGT- CCTGGACCCT TTG-CAAGAA CCCTTCCCCT AGCAA-CAGA TCGGT-CATC
*** ***** ***** ***** * ***** ***** ***** ***** *****
318" GCTTGGTGTG CCTGGACCCT TTGTCAAGGA CCCTTCCCCT AGCAAGCAGA TCGGTGCATC

1352' TC--AAAATA TTTTCT-GA TTGGCCAAAG AGTAATTGAT TTGCA-TTTT AAT-GGTCAG
** ***** ***** ** ***** ***** ***** ***** ***** ** *****
378" TCGAGGAATA TTTTCTGGA TTGGCCAAAG AGTAATTGAT TTGCATTTT AATGGGTCAG

1407' ACTCT---AT TACACCCAC ATT-CT-CTT TT-CTTTT-A TT-CTTGT-C TGTT-CT-GC
** ** ***** ***** ** ** ** * ***** * ** ***** * ***** ** **
438" GAGCTGGTAT TACACCCAC ATTGCTGCTT TTGCTTTTGA TTGCTTGTGC TGTTGCTGGC

1456' CT-CACTCCC AT-CAAG-AT -CTGGCCTC- GGCGGCCAAG CTTGGC-AAT CCGGT-ACTG
** ***** ** * ** ** ***** ***** ** ***** ** ***** *****
498" CTACACTCCC ATGCGAGTAT GCTGGCCTCG GGCGGCCGAG CTTGGCGAAT CCGGTGACTG



1509' TTGGTAAAGC C—ACCATGG AAGATGCCAA AAACATTAAG AAGGGCCCAG CGCCATTCTA

***** ** * ***** *

558" GTGGTAACGC CACACCATGG TAAGTATGTC CAATTTAGCA CTTAGTG