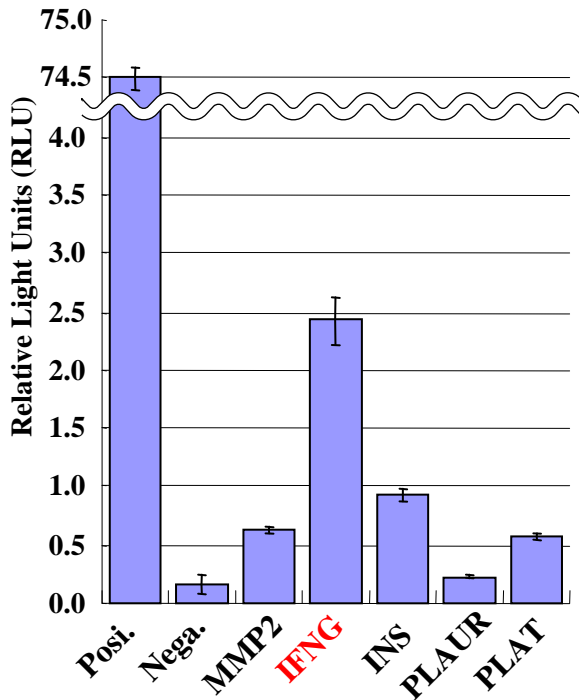
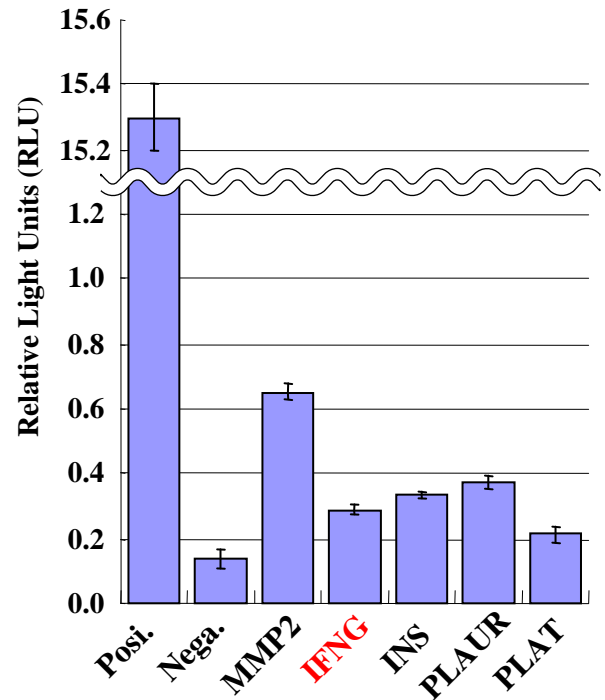


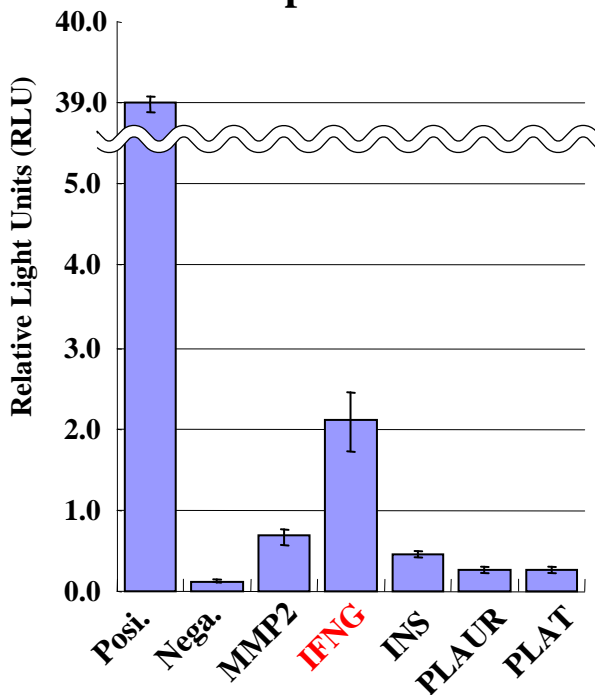
HeLa cells



HepG2 cells



Hep3B cells



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

MMP2: pGL4-phMMP2 (RDB#7314)

IFNG: pGL4-phIFNG (RDB#7297)

INS: pGL4-phINS (RDB#7387)

PLAUR: pGL4-phPLAUR (RDB#7312)

PLAT: pGL4-phPLAT (RDB#7295)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.07.13

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5481

2nd Nucleotide Sequence

File Name : RDB7297F.fasta
Sequence Size : 765

Unit Size to Compare = 1
Pick up Location = 1

[96.447% / 760 bp] INT/OPT. Score : < 462/ 2644 >

```
1'          GCC TAAC TGGCCG GTACCTGAGC TCGCTAGCCT CGAGGAT-AT
          **** *****
1" GCCAGAACAT TTCTCTGGCC TAAC TGGCCG GTACCTGAGC TCGCTAGCCT CGAGGATAAT

44' TGAGATGCAC CGTAGGCTTA AAATATACAC TGTATTTTNT TTCCTTTTTT CTTTTTTTCT-
          ***** ***** ***** ***** * ***** *****
61" TGAGATGCAC CGTAGGCTTA AAATATACAC TGTATTTTCT TTCCTTTTTT CTTTTTTTCT

103' TTTTTTTTTT TTTGAGACGG AATCTTACTC NTGTCACCTA GGCTGGAGTG TAGTGGCGCG
          ***** ***** ***** ***** ***** *****
120" TTTTTTTTTT TTTGAGACGG AATCTTACTC -TGTACCTA GGCTGGAGTG TAGTGGCGCG

163' ATCTCGGCTC ACTGCAACCT CNCACCTTCT GGGTTCAAGC CATTCTCCTG CCTCAGCCTC
          ***** ***** * ***** ***** ***** *****
179" ATCTCGGCTC ACTGCAACCT C-CACCTTCT GGGTTCAAGC CATTCTCCTG CCTCAGCCTC

223' CCTAGTAGCT GANGATTACA GGCATACACC ACCATGCCTG GCTAATTTTT TTGTATTTTT
          ***** ** ***** ***** ***** ***** *****
238" CCTAGTAGCT GA-GATTACA GGCATACACC ACCATGCCTG GCTAATTTTT TTGTATTTTT
```



283' AGTNAGAGAT GGGGTTTCAC CATATTGGCT AGGCTGGTCT CAAACTCCTG ACCTNTGTGA
 *** ***** ***** ***** ***** ***** ***** *****

297" AGT-AGAGAT GGGGTTTCAC CATATTGGCT AGGCTGGTCT CAAACTCCTG ACCT-TGTGA

343' TCCACCCGCC TCAACCTCCC AAAGTGCTGG GATTACAGGT GTGAGNCCAC TCGTCTGGA
 ***** ***** ***** ***** ***** ***** *****

355" TCCACCCGCC TCAACCTCCC AAAGTGCTGG GATTACAGGT GTGAG-CCAC TCGTCTGGA

403' ACTCCCCCTG GGAATATTCT CTACACTGTA TTTCAANGGA TTTAATATGA CAAAAAGAAT
 ***** ***** ***** ***** ** ***** ***** *****

414" ACTCCCCCTG GGAATATTCT CTACACTGTA TTTCAA-GGA TTTAATATGA CAAAAAGAAT

463' GTCAAATACC TTATTAACAA TGTAGTANTA TTGATGCATA CTGAAGTACT ATTTGGGATA
 ***** ***** ***** ** ***** ***** ***** *****

473" GTCAAATACC TTATTAACAA TGTAGTA-TA TTGATGCATA CTGAAGTACT ATTTGGGATA

523' TATTGGTTTA AATACAATNA TATTTAAAA TTATATTAC CTTTTAAAA AACTTTTATT
 ***** ***** * ***** ***** ***** ***** *****

532" TATTGGTTTA AATACAAT-A TATTTAAAA TTATATTAC CTTTTAAAA AACTTTTATT

583' AATGAGGCTN ACTAGATCAT TAAATTTAC CTGTGTGGCT TGTATTGTAT TTCTACTGGG
 ***** ***** ***** ***** ***** ***** *****

591" AATGAGGCT- ACTAGATCAT TAAATTTAC CTGTGTGGCT TGTATTGTAT TTCTACTGGG

643' NCAGTGCTGA TCTAGAGCAA TTTGAAACTT GTGGTAGATA -TTTTACTAA CCNAACTCTG
 ***** ***** ***** ***** ***** ** *****

650" -CAGTGCTGA TCTAGAGCAT TTTGAAACTT GTGGTAGATA TTTTTACTAA CCAACTCTG

702' A-TGAA-GGA CTT-CCTCA- CAAA-TTG- TTC-TTTAA -CCGCA-TTC TTNTCCTTGC
 * **** ** ** ***** ***** ** ** ***** ***** ** ** **

709" ATTGAAGGA CTTCCCTCAC CAAATTTGT TTCTTTTAA CCCGCATTC TTTCCC

1st Nucleotide Sequence

File Name : Reference Seq. GNU
 Sequence Size : 5481



2nd Nucleotide Sequence

File Name : RDB7297R.fasta (Complementary)

Sequence Size : 690

Unit Size to Compare = 1

Pick up Location = 1

[97.293% / 702 bp] INT/OPT.Score : < 501/ 2527 >

661' AATTTGAAAC -TTGTGGTAG ATATTTACT AACNAACTC TGATGAAGGA CTCCTCACC

***** ***** ** .***** **** ***** ***** * *****

1" TTGAAAC TTTGTGGTAG AT-NTTTACT AACC-AACTC TGATGAAGAA CTCCTCACC

720' AAATTGTTCT TTTAACCGCA TTCTNTCCT TGCTTTCTGG TCATTGCAA GAAAAATTTT

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

56" AAATTGTTCT TTTAACCGCA TTCTT-TCCT TGCTTTCTGG TCATTGCAA GAAAAATTTT

780' AAAAGGCTGC CCCTTNGTA AAGGTTGAG AGGCCCTAGA ATTCGTTTT TCACTTGTTT

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

115" AAAAGGCTGC CCCTT-GTA AAGGTTGAG AGGCCCTAGA ATTCGTTTT TCACTTGTTT

840' CCAACCANCA AGCAAATGAT CAATGTGCTT TGTGAATGAA GAGTCAACAT TTTACCAGNG

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

174" CCAACCA-CA AGCAAATGAT CAATGTGCTT TGTGAATGAA GAGTCAACAT TTTACCAG-G

900' GCGAAGTGGG GAGGTACAAA AAAATTTCCA GTCCTTGAAT GGTGTGAAGN TAAAAGTGCC

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

232" GCGAAGTGGG GAGGTACAAA AAAATTTCCA GTCCTTGAAT GGTGTGAAG- TAAAAGTGCC

960' TTCAAAGAAT CCCACCAGAA TGGCACAGGT GGCATAATG NGGTCTGTCT CATCGTCAAA

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

291" TTCAAAGAAT CCCACCAGAA TGGCACAGGT GGCATAATG -GGTCTGTCT CATCGTCAAA

1020' GGACCCAAGG AGTCTAAAGG AACTCTAAC TNACAACACC CAAATGCCAC AAAACCTTAG

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

350" GGACCCAAGG AGTCTAAAGG AACTCTAAC T-ACAACACC CAAATGCCAC AAAACCTTAG



1080' TTATTAATAC AAACATCAT CCNCTGCCTA TCTGTCACCA TCTCATCTTA AAAAATTGT

 409" TTATTAATAC AAACATCAT CC-CTGCCTA TCTGTCACCA TCTCATCTTA AAAAATTGT

 1140' GAAAATACGT AATNCCTCAG GAGACTTCAA TTAGGTATAA ATACCAGCAG CCAGAGGAGG

 468" GAAAATACGT AAT-CCTCAG GAGACTTCAA TTAGGTATAA ATACCAGCAG CCAGAGGAGG

 1200' TGCANGCACA TTGTTCTGAT CATCTGAAGA TCAGCTATTA GAAGAGAAAG ATCAGTTAAG

 527" TGCA-GCACA TTGTTCTGAT CATCTGAAGA TCAGCTATTA GAAGAGAAAG ATCAGTTAAG

 1260' TCCTTTGGAC -CTGATCAGC TTATCAAGAT CTGGCCTCGG CGGCCAAGCT TGGCAATCCG

 586" TCCTTTGGAC ACTGATCAGC -TATCAAGAT CTGGCCTCGG CGGCCAAGCT TGGCAATCCG

 1319' GTACTGTTGG TAAAGCCACC ATGGAA-GAT GCCAAA-AAC ATTAAGAAGG GCCCAGCGCC

 645" GTACTGTTGG TAAAGCCACC ATGGAACGAT GCCAAACAAC ATTAAG