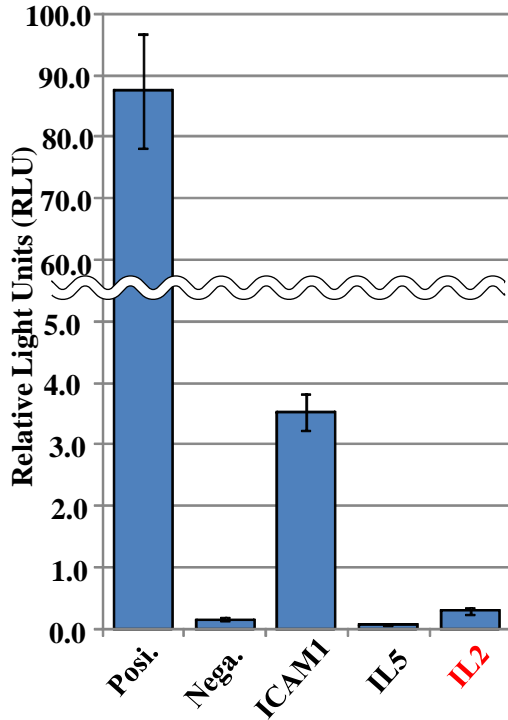
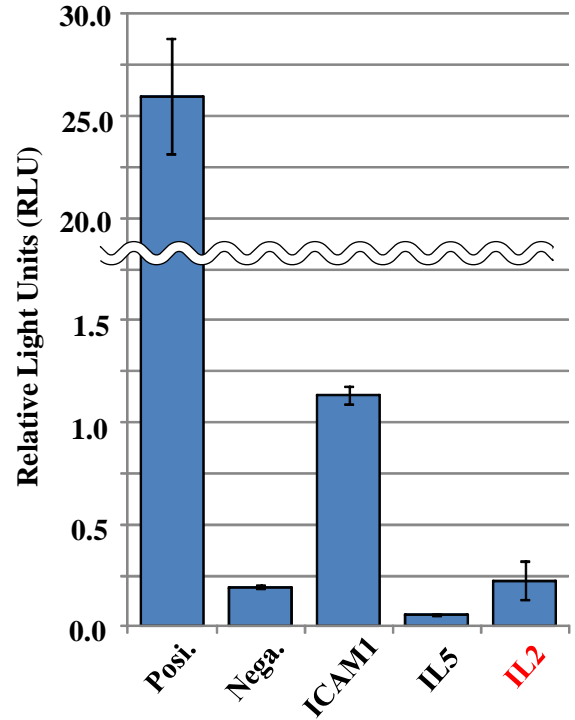


# The Promoter Activities of Reporter Constructs

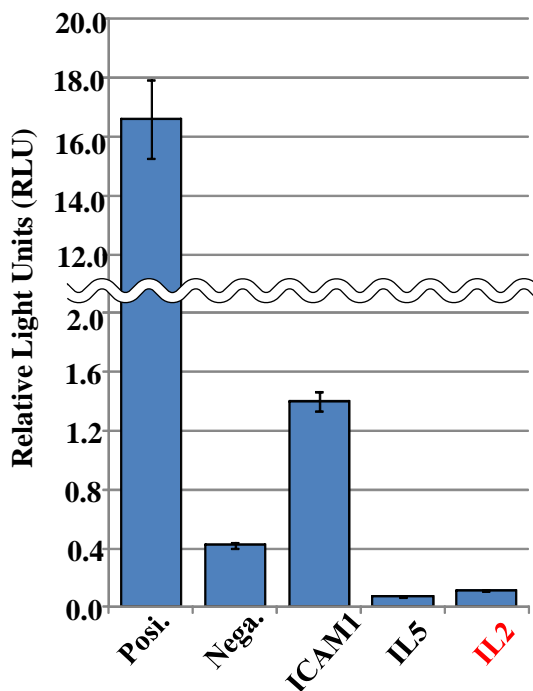
## HeLa cells



## HepG2 cells



## Hep3B cells



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

ICAM1: pGL4-phICAM1(RDB# 7390)

IL5: pGL4-phIL5(RDB# 7392)

IL2: pGL4-phIL2 (RDB# 7391)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.06.11

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5509

2nd Nucleotide Sequence

File Name : RDB7391F.fasta  
Sequence Size : 431

Unit Size to Compare = 1  
Pick up Location = 1

[74.537% / 432 bp] INT/OPT. Score : < 477/ 886 >

```
1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TCCTGCCTGT ACACTGTTCT
      * ** * *   **** ***** *****
1"          CACTA GACCTCAGGA TCCTGCCTGT ACACTGTTCT

61' CTTTTCTCTC TTTCTATATA CCTGAAGGCA TNTATAGGTG -CTAGATGTC TGTTTAAAGA
      ***** ***** ***** * ***** ***** *****
36" CTTTTCTCTC TTTCTATATA CCTGAAGGCA T-TATAGGTG ACTAGATGTC TGTTTAAAGA

120' CCAGACAATA TTGTCTTAAA AAANACAAAC AAAAAC-AC- AGACAATACC ATCTTTAAAA
      ***** ***** *** ***** ***** ** ***** *****
95" CCAGACAATA TTGTCTTAAA AAA-ACAAAC AAAACAACA AGACAATACC ATCTTTAAAA

178' AAAAAAAAAA AGTCCANGGT AAGAAATAAA TAAGG-CCAT AGAATGGAAG -CTTT-ACAA
      ***** * * ***** ***** ***** ***** * *
154" AAAAAAAAAA GATCCAGGAT AAGAAATAAA TAAGGACCAT AGAATGGAAG ACTTTAACAA

235' GGA CTCTCTC NTGAGACAGG ATCTCCTCAA -GTG-TCCCC A-GGTT-AAA TTAGAAGTAT
      ***** ***** ***** *** ***** * ***** *
214" GGA CTCTCTC -TGAGACAGG ATCTCCTCAA GGTGATCCCC AGGGTTAAAA TTAGAAAGAT
```



```

291' ATATCNCGTA CAATTGTTCA GCCAGTTTGT GCACTGTACT GAGGATGAAT GAACACNCTA
    * . * * * * * * * * * * * * * * * * * * * * * * * * * *
273" AGTAGTAATT CCGGTAACAA GTTTGGTT-T ACAAGGACCA GGATTTTGAT GGACAACCT-

351' TCCTAAATAT CCTAGTCTTC TGAATAAAAA CAAGATCATA TTTCATANAC GATTATTGTT
    ****      * * * * * * * * * * * * * * * * * * * * * * *
331" GGATAAACTG GAGGGGAGTG AAAGTGAAAA CAA--CCCTA GTTCCTAAA- -GTAGTTCCT

411' ACATTCATAG TGTCCAGGT GATTAGAGG ATAAATAANA AATCCATTAA AGAGGTAAAG
    * ** ** ** * * * * * * * * * * * * * * * * * * * *
387" A-GGTCTTAC TGAATAAAAA AACAAAGAAG -TAAGTAGTT GTCAGTT

```

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5509

2nd Nucleotide Sequence

File Name : RDB7391R.fasta (Complementary)  
Sequence Size : 638

Unit Size to Compare = 1  
Pick up Location = 1

[97.682% / 647 bp] INT/OPT. Score : < 533/ 2379 >

```

721' TGACATGTAA GAAGCAATCT ATCTTATTGT ATGCNAATTA GCTCATTGTG TGGATAAAAA
    * **** * * * * * * * * * * * * * * * * * * * * * * * * * *
1"      T ATGC-AATTA GCTCATTGTG TGGATAAAAA

781' -GGTAAAACC ATTCTGAAAC AGGAAANCCA ATACACTTCC TGTTTTATCA ACAAATCTAA
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
31" GGGTAAAACC ATTCTGAAAC AGGAAATCCA ATACACTTCC TGTTAATCA ACAAATCTAA

```



840' ACATTTATTC TTTTCATNCT GTTTACTCTT GCTCTTGTCC ACCACAATAT GCTATTCACA  
 \*\*\*\*\* \*\* \*\*\*\*\*  
 91" ACATTTATTC TTTTCAT-CT GTTTACTCTT GCTCTTGTCC ACCACAATAT GCTATTCACA  
  
 900' TGTTTCAGTNG TAGTTTTATG ACAAAGAAAA TTTTCTGAGT TACTTTTGTGTA TCCCCACCCN  
 \*\*\*\*\* \* \*\*\*\*\*  
 150" TGTTTCAGT-G TAGTTTTATG ACAAAGAAAA TTTTCTGAGT TACTTTTGTGTA TCCCCACCC-  
  
 960' CCTTAAAGAA AGGAGGAAAA ACTGTTTCAT ACAGAAGGCG TTAATTGCAT NGAATTAGAG  
 \*\*\*\*\* \*\*\*\*\*  
 208" CCTTAAAGAA AGGAGGAAAA ACTGTTTCAT ACAGAAGGCG TTAATTGCAT -GAATTAGAG  
  
 1020' CTATCACCTA AGTGTGGGCT AATGTAACAA AGAGGGATTT CNACCTACAT CCATTTCAGTC  
 \*\*\*\*\* \*\*\*\*\* \* \*\*\*\*\*  
 267" CTATCACCTA AGTGTGGGCT AATGTAACAA AGAGGGATTT C-ACCTACAT CCATTTCAGTC  
  
 1080' AGTCTTTGGG GGTTTAAAGA AATCCAAAG AGNTCATCAG AAGAGGAAAA ATGAAGGTAA  
 \*\*\*\*\* \*\* \*\*\*\*\*  
 326" AGTCTTTGGG GGTTTAAAGA AATCCAAAG AG-TCATCAG AAGAGGAAAA ATGAAGGTAA  
  
 1140' TGTTTTTCA GACAGGTAAA GTCNTTTGAA AATATGTGTA ATATGTAAAA CATTTTGACA  
 \*\*\*\*\* \*\* \*\*\*\*\*  
 385" TGTTTTTCA GACAGGTAAA GTC-TTTGAA AATATGTGTA ATATGTAAAA CATTTTGACA  
  
 1200' CCCCATAAT ATTTNTTCCA GAATTAACAG TATAAATTGC ATCTCTTGTT CAAGAGTTCC  
 \*\*\*\*\* \*\*\*\* \*\*\*\*\*  
 444" CCCCATAAT ATTT-TTCCA GAATTAACAG TATAAATTGC ATCTCTTGTT CAAGAGTTCC  
  
 1260' CTATCACTCT CTTTAATCAC TACTCACAGT AACCTCAACT CCTGCCACAA --TCAAGATC  
 \*\*\*\*\* \*\*\*\*\*  
 503" CTATCACTCT CTTTAATCAC TACTCACAGT AACCTCAACT CCTGCCACAA TATCAAGATC  
  
 1318' TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT AAAGCCACCA TGAAGATGC  
 \*\*\*\*\* \*\*\*\*\*  
 563" TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT AAAGCCACCA TGAAGATGC  
  
 1378' CAAA-AACAT TAAGAAGGGC CCAGCGCCAT TCTACCCACT CGAAGACGGG ACCGCCGGCG  
 \*\*\*\* \*  
 623" CAAATAACAT TAAGAA