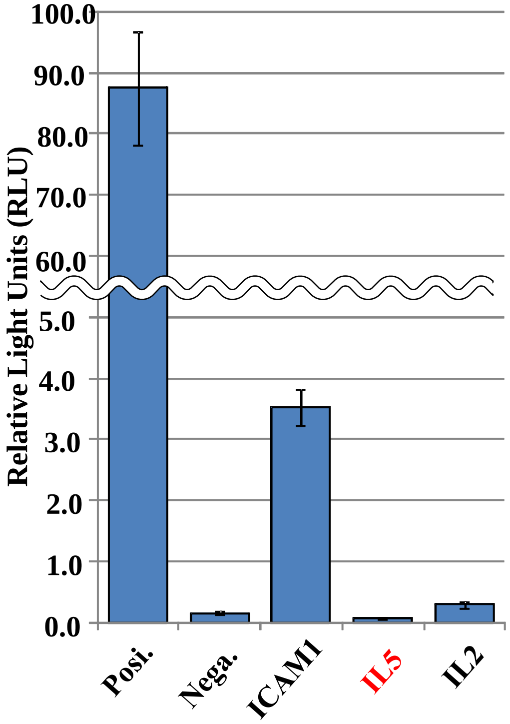
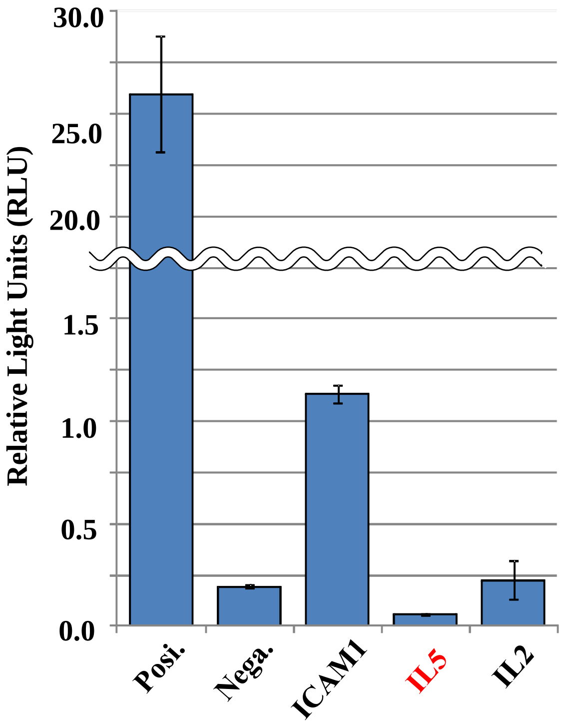
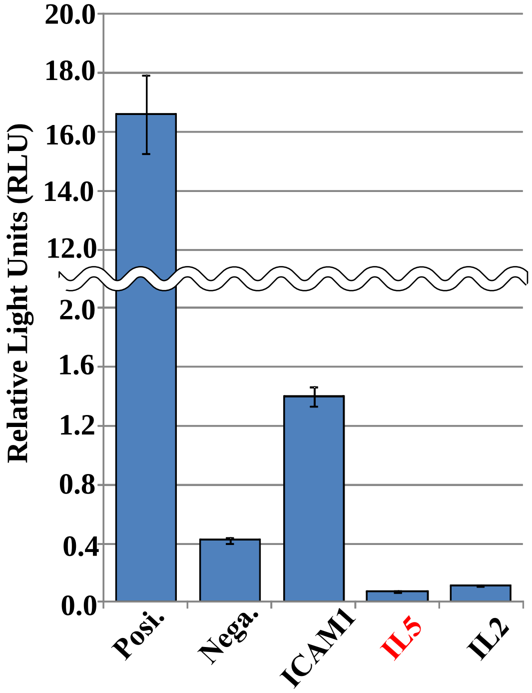
The Promoter Activities of Reporter Constructs


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)

2010, DNA Bank, RIKEN BioResource Center

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.25

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5544

2nd Nucleotide Sequence
  File Name         : RDB7392F.fasta
  Sequence Size     : 648

  Unit Size to Compare = 1
  Pick up Location     = 1



[96.970% / 627 bp]     INT/OPT.Score : <    442/  2264 >

  1’                                     GGCCTAAC TGGCCGGTAC CTGAGCTCGC
                                         * * *** ** ***  ** * ********
  1″ TTANTAAGGC TAGCGGGGAC TAAACTNATA CGCGTCCAAC TGACCGTCAC C-GAGCTCGC

 29’ TAGCCTCGAG GATGGCTGCA ACATAGAGCC ACTCTGGGAT GCTC-ACTGA ANGCACTCTA
     ********** ********** ********** ********** **** ***** * ********
 60″ TAGCCTCGAG GATGGCTGCA ACATAGAGCC ACTCTGGGAT GCTCTACTGA A-GCACTCTA

 88’ TTAAAAACAA TGAGCCACAT ACACCTCCAT CATATGTGTT CANGGCCAGG GAAAAAGGAA
     ********** ********** ********** ********** ** ******* **********
119″ TTAAAAACAA TGAGCCACAT ACACCTCCAT CATATGTGTT CA-GGCCAGG GAAAAAGGAA

148’ GTGTGTGATC TAGGAGGGGG CCTCATTTGT ACCNTTTCTG GGATTACAGG TCTGAGCCTA
     ********** ********** ********** *** ****** ********** **********
178″ GTGTGTGATC TAGGAGGGGG CCTCATTTGT ACC-TTTCTG GGATTACAGG TCTGAGCCTA

208’ AGGAACAAAG GCTGATTCCC CTAANTTTCA TGGCCCGCCC AAGGTGTGAA AGGACACCTC
     ********** ********** **** ***** ********** ********** **********
237″ AGGAACAAAG GCTGATTCCC CTAA-TTTCA TGGCCCGCCC AAGGTGTGAA AGGACACCTC
```

```
268’ CACCCTTATG GGACANTAAA GGAGAGGACA CATCCATGTA TTGTGTATCT GTGACAGATA
     ********** ***** **** ********** ********** ** ******* **********
296″ CACCCTTATG GGACA-TAAA GGAGAGGACA CATCCATGTA TTATGTATCT GTGACAGATA

328’ TTTATTNGGT TGCCTTCCTA GAATCTGTGT CCCCCTTACT ACTGGGACCC CACATTTNCT
     ****** *** ********** ********** ********** ********** ******* **
355″ TTTATT-GGT TGCCTTCCTA GAATCTGTGT CCCCCTTACT ACTGGGACCC CACATTT-CT

388’ AAGCTATGCA GTTGAGGTAG GATTAGGGTC ACCTCTAGCT CCAGGGAGNA GCCAATCAGT
     ********** ********** ********** ********** ******** * **********
413″ AAGCTATGCA GTTGAGGTAG GATTAGGGTC ACCTCTAGCT CCAGGGAG-A GCCAATCAGT

448’ ATATACTACA CCCTGGTCAC AGTTCAAGGA TGAACATGTN GACCCTTGTC AGAAAGAGAC
     ********** ********** ********** *********  ********** **********
472″ ATATACTACA CCCTGGTCAC AGTTCAAGGA TGAACATGT- GACCCTTGTC AGAAAGAGAC

508’ TGAATTTGAA AGCTTTTGAT TAAACAATCA NGAAAAGCAC AGCTTGCTTT TTCCTGCTGC
     ********** ********** **********  ********* ********** **********
531″ TGAATTTGAA AGCTTTTGAT TAAACAATCA -GAAAAGCAC AGCTTGCTTT TTCCTGCTGC

568’ TCATGAACAG AATACATATA GNATCCAGGA GTCTGGACAT CATCTTGAGA CCTCAATGGG
     ********** ********** * ******** ********** ********** **********
590″ TCATGAACAG AATACATATA G-ATCCAGGA GTCTGGACAT CATCTTGAGA CCTCAATGGG
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5544

2nd Nucleotide Sequence
  File Name        : RDB7392R.fasta (Complementary)
  Sequence Size    : 565

  Unit Size to Compare = 1
  Pick up Location     = 1
```

```
[95.304% / 575 bp]     INT/OPT.Score : <    363/  1996 >

  841’ TTCNCATTTC AATCACTGTC TTCCCACCAG TATTTTCAAT TTCTTTTAAG ACAGNATTAA
                   ********* ********** ********** ********** **** *****
    1″             ATCACTGTC TTCCCACCAG TATTTTCAAT TTCTTTTAAG ACAG-ATTAA

  901’ TCTAGCCACA GTCATAGTAG AACATAGCCG ATCTGAAAAA AACATNTCCC AATATTTATG
       ********** ********** ********** ********** ***** **** **********
   49″ TCTAGCCACA GTCATAGTAG AACATAGCCG ATCTGAAAAA AACAT-TCCC AATATTTATG

  961’ TATTTTAGCA TAAAATTCTG T-TTAGTGGT CTACCTTNAT ACTTTGTTTT GCACACATCT
       ********** ********** * ******** ******* ** ********** **********
  108″ TATTTTAGCA TAAAATTCTG TGTTAGTGGT CTACCTT-AT ACTTTGTTTT GCACACATCT

 1020’ TTTAAGAGGA AGTTAATTTT CTGATTTTNA AGAAATGCAA ATGTGGGGCA ATGATGTATT
       ********** ********** ******** * ********** ********** **********
  167″ TTTAAGAGGA AGTTAATTTT CTGATTTT-A AGAAATGCAA ATGTGGGGCA ATGATGTATT

 1080’ AACCCAAAGA TTCTTCGTAN ATAGAAAATG TTTTTAAAGG GGGGAAACAG GGATTTTTAT
       ********** *********  ********** ********** ********** **********
  226″ AACCCAAAGA TTCTTCGTA- ATAGAAAATG TTTTTAAAGG GGGGAAACAG GGATTTTTAT

 1140’ TATTAAAAGA NTAAAAGTAA ATTTATTTTT TAAGATATAA GGCATTGGAA ACATTTAGTT
       **********  ********* ********** ********** ********** **********
  285″ TATTAAAAGA -TAAAAGTAA ATTTATTTTT TAAGATATAA GGCATTGGAA ACATTTAGTT

 1200’ TNCACGATAT GCCATTATTA GGCATTCTCT ATCTGATTGT TAGAAATTAT TCNATTTCCT
       * ******** ********** ********** ********** ********** ** *******
  344″ T-CACGATAT GCCATTATTA GGCATTCTCT ATCTGATTGT TAGAAATTAT TC-ATTTCCT

 1260’ CAAAGACAGA CAATAAATTG ACTGGGGACG CAGTCTTGTA CTANTGCACT TTCTTTGCCA
       ********** ********** ********** ********** *** ****** **********
  402″ CAAAGACAGA CAATAAATTG ACTGGGGACG CAGTCTTGTA CTA-TGCACT TTCTTTGCCA

 1320’ AAGGCAAACG CAGAACGTTT CAGAATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC
       ********** ********** ********** *** ****** ********** * ********
  461″ AAGGCAAACG CAGAACGTTT CAGAATCAAG ATC-GGCCTC GGCGGCCAAG C-TGGCAATC
```

```
1380’ CGGTACTGTT --GGTAAAGC CACCATGGAA GATGCCA-AA AACATTAAGA AGGGCCCAGC
      **********   * * *  * ***   ***      **** *  ******
 519″ CGGTACTGTT GTGATTAGAC CACTCAGGAT TTAGCCATAT AACATTT
```