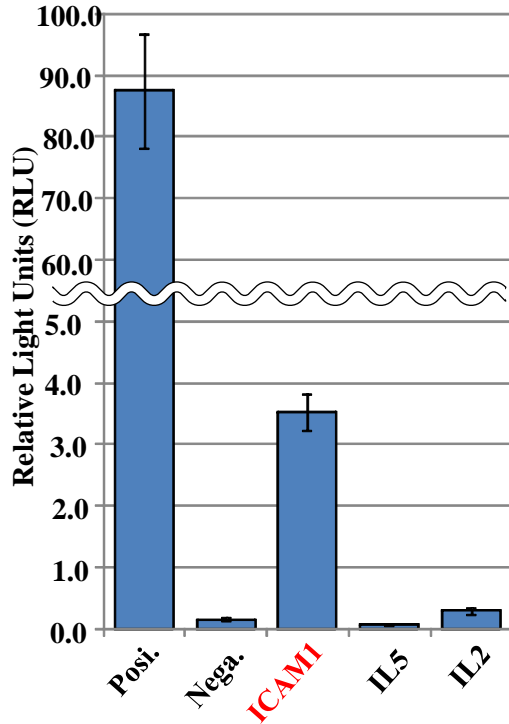
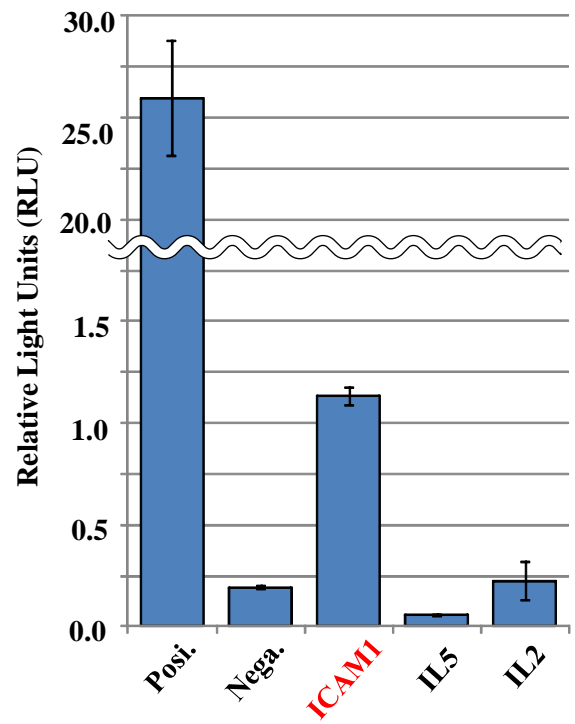


The Promoter Activities of Reporter Constructs

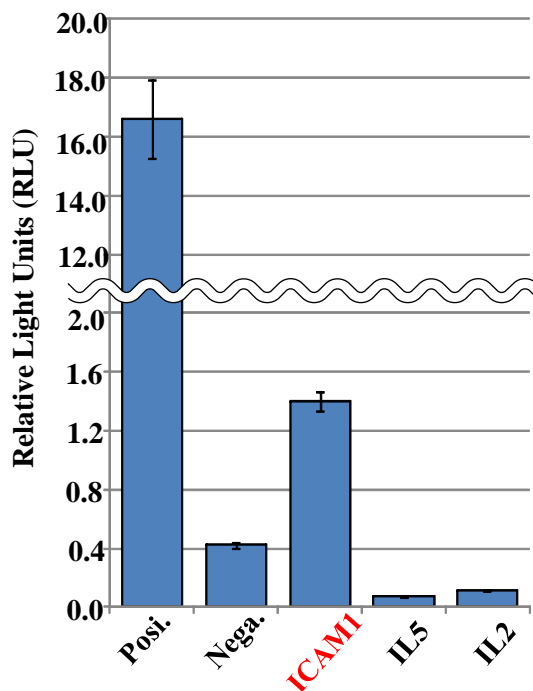
HeLa cells



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 : 2010.01.25

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5569

2nd Nucleotide Sequence

File Name : RDB7390F.fasta
Sequence Size : 404

Unit Size to Compare = 1
Pick up Location = 1

[87.248% / 298 bp] INT/OPT.Score : < 430/ 833 >

```
1'                                     GGCCTAACT
                                     *
1" AAAAAGAGAA TACGTTTTTT CGGTACGCAG AGGCCTTCTC AATATCGCGG TCCAATCTTT

10' GGCCGGTACC TGAG-CTCGC TAGCCTC--G AGGATGGGAA ATATG-CGT- CT-CTGGATG
    **** *.*** ** * * ** *** ***** ***** *** ** *****
61" GGCCTGNACC GCAGTCGCAT CAGACTCAGC AGGATGGGAA ATATGCCGTG CTNCTGGATG

64' GCCAGTGA-- CTCG---CAG CCCCTT-CC CCGA-TAGGA AGGGCCTGCG -CGTCCGGGG
    ** **** *** * * ***** ** ***** ***** ***** *****
121" GCACGTGATC TTCGACACGG CCCCTTCCC CCGACTAGGA AGGGCCTGCG ACGTCCGGGG

116' ACCCTTCGCT TCCCCTTCTG CTGCGCGACC TCCCTGGCCC CTCGGAGAT- -CTCCATGGC
    ***** ***** ***** ***** ***** *****
181" ACCCTTCGCT TCCCCTTCTG CTGCGCGACC TCCCTGGCCC CTCGGAGATA CTTCATGGN

174' GACGCCGCGC GCGCCCCACA ACAGGAAAGC CTTAGGCGGC GCGGCTTGGT GCTCGGAGAC
    ***** ***** ***** ***** ** ***** *****
241" GACGCCGCGC GCGCCCCACA ACAGGAAAGC CTTAGGNGGC GCGGCTTGGT GCTCGGAGAC
```



234' TTAAGAGTAC CCAGCCTCGA CGTGGTGGAT GTCGAG-TCT TGGGGTC-AC ACGCACAGGC

 301" TTAAGAGTAC CCAGCCTCGA CGTGGTGGAT GTCGAGTTCT TGGGGTCAAC AACGACAACA
 292' GGTGGCCAAG CAAACACCCG CTCATATTTA GTGCATGAGC CTGGGTTCGA GTTGCCGGAG
 361" AGGACGGGTG GGGCCAAAGA CAAAAACAN CCCCAGGCCT TCAT

1st Nucleotide Sequence

File Name : Reference Seq. gnu
 Sequence Size : 5569

2nd Nucleotide Sequence

File Name : RDB7390R. fasta (Complementary)
 Sequence Size : 414

Unit Size to Compare = 1
 Pick up Location = 1

[79.758% / 331 bp] INT/OPT. Score : < 96/ 562 >

1081' GGCCGGGAGC AGCCCCGGG GTCATCGCCC TGCCACCGCC GCCCGATTGC TTTAGCTTGG
 1" CCCCTGTCC ACCGCCGTC CCGAATTGCT TTTAGTCTTT GGAAATTTCC
 1141' AAATTCCGGA GCTGAAGCGG CCAGCGAGGG AGG-ATGACC C-TCTCGG-C CCGGG-CACC
 ** *** ** ** * ***** * ***** **
 50" GGTAGTCTTT AAGCGGTCCA GTCGTAGGGT AGGAATAACC CTTCTCGGTC CCGGGTCACC
 1197' CTG-TCA-GT CCGGAAATAA CTGCAG-CAT TTGTTCCGGA GGGG-AAGG- CGCGAGG-TT
 *** ** * ***** ** ***** * ***** **
 110" CTGTTAGGT CCGGAAATAA CTGCAGTCAT TTGTTCCGTA GGGGTAAGGT CTCGAGGTTT



1251' TCGGG--AA AGCAG-CACC -GCCCCTTGG --CCCCA-G GTGGCTAG-C G-CTA-TAAA
 ***** ** ***** ***** ***** ***** * *** ***** * * *** *****
 170" TCGGGTAAA AGCAGTCACC TCCCCTTGG TCCCCCAGG GTGTCTAGTC GTCTATTA

 1301' GGATCAG-C G-CCCCAG-T CG-ACG--CT GAG--CTCCT CTG-CTACTC A-GAG-TTG-
 ***** * * ***** * ** *** * *** ***** ***** * *** ***
 230" GGATCAGTC GTCCCCAGTT CGAACGTCTT GAGTCTTCTT CTGTCTACTC AGGAGTTTGC

 1349' CAACCTCAG- -CCTCG-CTA TGGATCAAGA TCTGG-CCTC GCGGCCAAG --CTTGGCAA
 ***** ** * ***** ***** ***** ***** *****
 290" CAACCTCAGT CAATCGTCTA TGGATCAAGA TCTGGTCCTC GCGGCCAAG TCTTTGGCAA

 1403' TCGGACTG TTGGT----A AAGCCACCAT GGAAG--ATG CCAAAAACAT TAAGAAGGGC
 ***** ***** * ** * *** * *** * ***** ** ***
 350" TCGGACTG TTGGTAACAA AAACACCCAG GTAAGTAGTT CCAAAAACCA TATAGAGGAG

 1457' CCAGCGCCAT TCTACCCACT CGAAGACGGG ACCGCCGGCG AGCAGCTGCA CAAAGCCATG

 410" AATCA