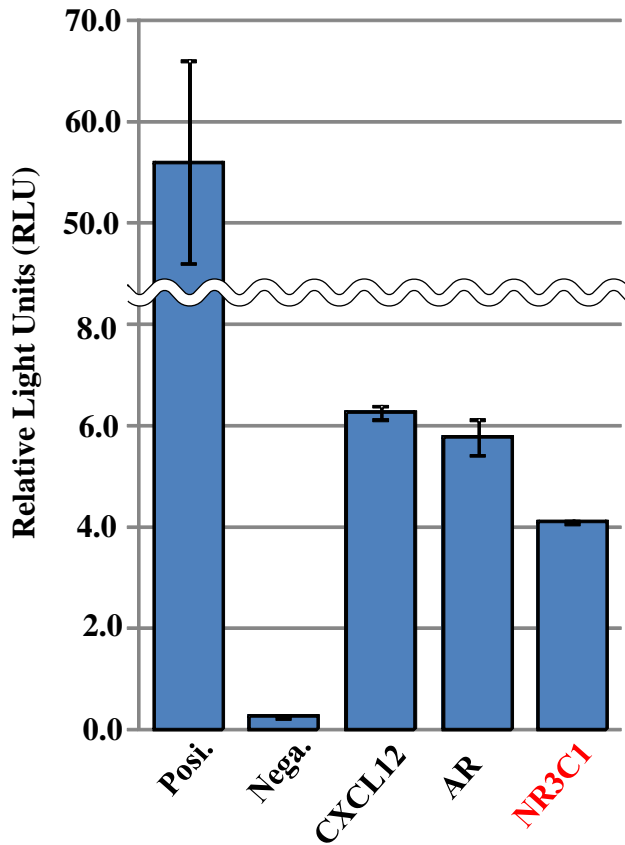
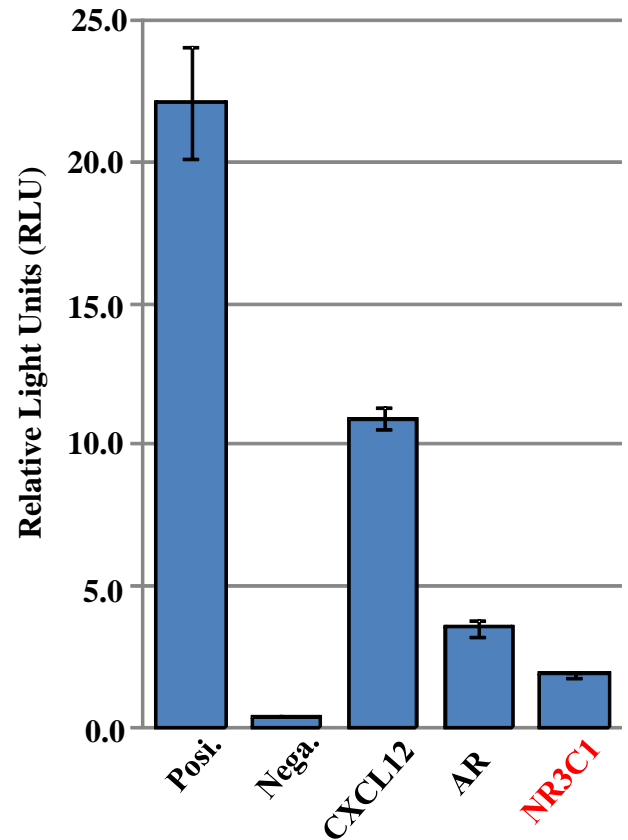


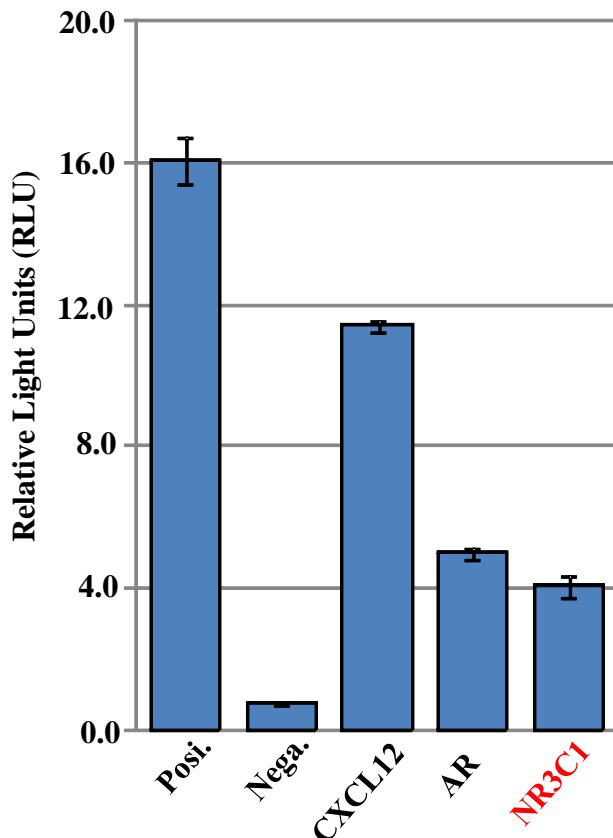
### HeLa cells



### HepG2 cells



### Hep3B cells



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

CXCL12: pGL4-phCXCL12 (RDB# 7687)

AR: pGL4-phAR(RDB# 7690)

NR3C1: pGL4-phNR3C1 (RDB# 7689)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.21

1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5734

2nd Nucleotide Sequence

File Name : RDB7689F.fasta (Complementary)  
Sequence Size : 721

Unit Size to Compare = 1  
Pick up Location = 1

[97.920% / 721 bp] INT/OPT. Score : < 2062/ 2724 >

```
901' CCCGCAGGG CACTGGCGGC GCTTGCCGCC AAGGGCAGA GCGAGCTCCC GAGTGGGTCT
      **** ** ***** ***** ***** *****
1''   TGGC-GC GCTTGCCGCC AAGGGCAGA GCGAGCTCCC GAGTGGGTCT

961' GGAGCCGCG AGCTGGGCGG GGGCGGAAG GAGGTAGCGA GAAAAGAAAC TGGAGAACT
      ***** ***** ***** ***** ***** *****
47'' GGAGCCGCG AGCTGGGCGG GGGCGGAAG GAGGTAGCGA GAAAAGAAAC TGGAGAACT

1021' CGGTGGCCCT CTTAACGCCG CCCAGAGAG ACCAGGTCGG CCCCCGCCG TGCCGCCGCC
      ***** ***** ***** ***** ***** *****
107'' CGGTGGCCCT CTTAACGCCG CCCAGAGAG ACCAGGTCGG CCCCCGCCG TGCCGCCGCC

1081' ACCCTTTTTC CTGGGAGTT GGGGCGGGG GGCGAAGCGC GGCGACCGG GCGGGCGGG
      ***** ***** ***** ***** ***** *****
167'' ACCCTTTTTC CTGGGAGTT GGGGCGGGG GGCGAAGCGC GGCGACCGG GCGGGCGGG

1141' CAGCCAGGG GACCGGGCG TGCAGGCGCC GTCGGGCGG GGTGGCGGG GCCCGCGGG
      ***** ***** ***** ***** ***** *****
227'' CAGCCAGGG GACCGGGCG TGCAGGCGCC GTCGGGCGG GGTGGCGGG GCCCGCGGG
```



```

1201' AGGGCGTGGG GGCAGGGACC GCGGGCGCCC CTGCAGTTGC CAAGCGTCAC CAACAGGTTG
*****
287" AGGGCGTGGG GGCAGGGACC GCGGGCGCCC CTGCAGTTGC CAAGCGTCAC CAACAGGTTG

1261' CATCGTTCCT CGCGGCCGCC GCGGGGCCCT TCGGGCGGGG AGCGGCCGGG GGTGGAGTGG
*****
347" CATCGTTCCT CGCGGCCGCC GCGGGGCCCT TCGGGCGGGG AGCGGCCGGG GGTGGAGTGG

1321' GAGCGCGTGT GTGCGAGTGT GTGCGGCGCG TGGCGCCGCC TCCACCCGCT CCCCGCTCGG
*****
407" GAGCGCGTGT GTGCGAGTGT GTGCGGCGCG TGGCGCCGCC TCCACCCGCT CCCCGCTCGG

1381' TCCCGCTCGC TCGCCAGGC CGGGCTGCC TTTGCGTGT CCGCGCTCTC -TTCCCTCCG
*****
467" TCCCGCTCGC TCGCCAGGC CGGGCTGCC TTTGCGTGT CCGCGCTCTC TTTCCCTCCG

1440' CCGCCGCCTC CTCCATTTG CGAGCTCGTG TCTGTGACGG GAGCCCGAGT CACCGCC-TG
*****
527" CCGCCGCCTC CTCCATTTG CGAGCTCGTG TCTGTGACGG GAGCCCGAGT CACCGCCTTG

1499' CCCGTCGGGG ACGGATTCTG TGGGTGGAAG GAGACATCAA GATCTGGCCT CGGCGGCCAA
*****
587" CCCGTCGGGG ACGGATTCTG TGGGTGGAAG GAGACATCAA GATCTGGCCT CGGCGGCCAA

1559' GCTTGGCAAT CCGTACTGT TGGTAAAGCC ACCATGGAAG A-TGCCAAA A-CA-TTAAG
** *****
647" GC-TGGCAAT CCGTACTGT TGGTAAAGCC ACCCAGGAAG AGTTCCAAA ACCACTTAAG

1616' AAGGGCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA GCTGCACAAA
**** ** * **
706" AAGGCACCG TTCCCC

```

1st Nucleotide Sequence

File Name : Reference Seq. GNU  
Sequence Size : 5734



2nd Nucleotide Sequence

File Name : RDB7689R.fasta

Sequence Size : 569

Unit Size to Compare = 1

Pick up Location = 1

[99.262% / 542 bp] INT/OPT. Score : < 1796/ 2117 >

```
1' G GCCTAACTGG CCGGTACCTG AGCTCGCTAG
    * *****
1" ATGCATGTGC AGGTGCCGAA CTTTACTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG

32' CCTCGAGGAT GAGGGGGAAG CTCCTAACAG GAACATCTGT AGGGAGTTGA ACGCTGGCAT
    **** *****
61" CCTC-AGGAT GAGGGGGAAG CTCCTAACAG GAACATCTGT AGGGAGTTGA ACGCTGGCAT

92' TTTAAAGCTG CCTGTATTTT GTTTATTTG TAGGGGCAGG GGCCTATGA ACGTGATAGG
    *****
120" TTTAAAGCTG CCTGTATTTT GTTTATTTG TAGGGGCAGG GGCCTATGA ACGTGATAGG

152' GTGAGCAACG CACAGAGTCG AGGCAGCAA ATGTCAAGAT TCGGGGTGG GGCCTGCACC
    *****
180" GTGAGCAACG CACAGAGTCG AGGCAGCAA ATGTCAAGAT TCGGGGTGG GGCCTGCACC

212' GGGAACTTGG ACGCGGGCCC TGGCCGGGGT GGAAGAAGAG GTCAGGAGTT TCGGAAGGGG
    *****
240" GGGAACTTGG ACGCGGGCCC TGGCCGGGGT GGAAGAAGAG GTCAGGAGTT TCGGAAGGGG

272' GGCTATATTT CGCCAGCAAC TTAATATTTT GCCTGCAACT TGCTTTTAAG CCTGCCGCC
    *****
300" GGCTATATTT CGCCAGCAAC TTAATATTTT GCCTGCAACT TGCTTTTAAG CCTGCCGCC

332' CCTGCTTTCC TTAATCATAA TAATAAAAAA AAAGTGCAA GAAATCCAGC TCGCTGGAGG
    *****
360" CCTGCTTTCC TTAATCATAA TAATAAAAAA AAAGTGCAA GAAATCCAGC TCGCTGGAGG
```



392' TTTTGCATTT GCGTGCAAC TTCCTTCGAG TGTGAGCACA TTGGGCGGGA GGGGTGGGG  
\*\*\*\*\*  
420'' TTTTGCATTT GCGTGCAAC TTCCTTCGAG TGTGAGCACA TTGGGCGGGA GGGGTGGGG  
  
452' TTGAACTTG CAGGCGGCGC CTCCTTCTGC CG-CCGCCGC CGCCTCGCAG ACTCGGGAA  
\*\*\*\*\*  
480'' TTGAACTTG CAGGCGGCGC CTCCTTCTGC CGCCCGCCGC CGCCTCGCAG ACTCGGGAA  
  
511' GAGGTGGGG GACGGTCGGG GCGCGGGGA GGGTGGGTTG TGCTTTGCAA CTTCTCTCC  
\*\*\*\*\*  
540'' GAGGTGGGG GACNGTC-GG GCGCGGGGA G