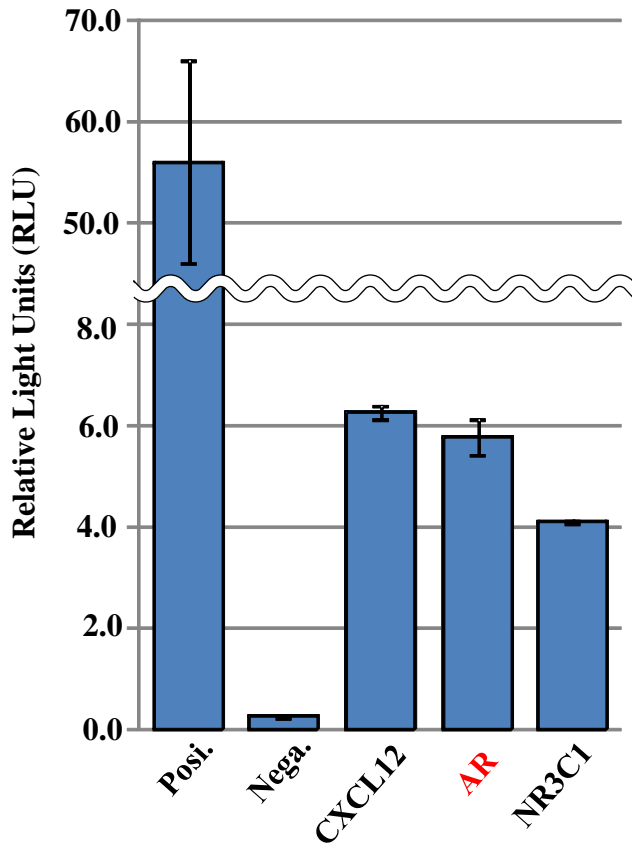
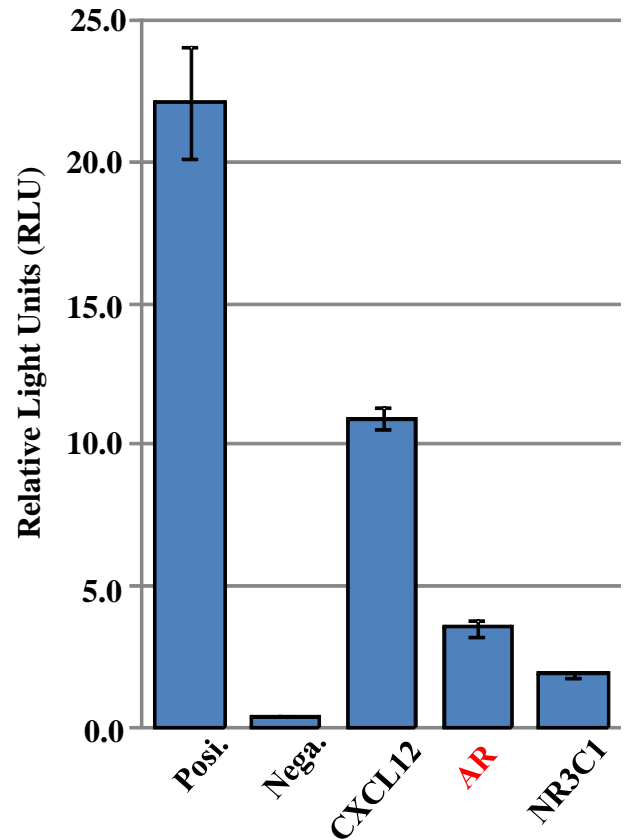


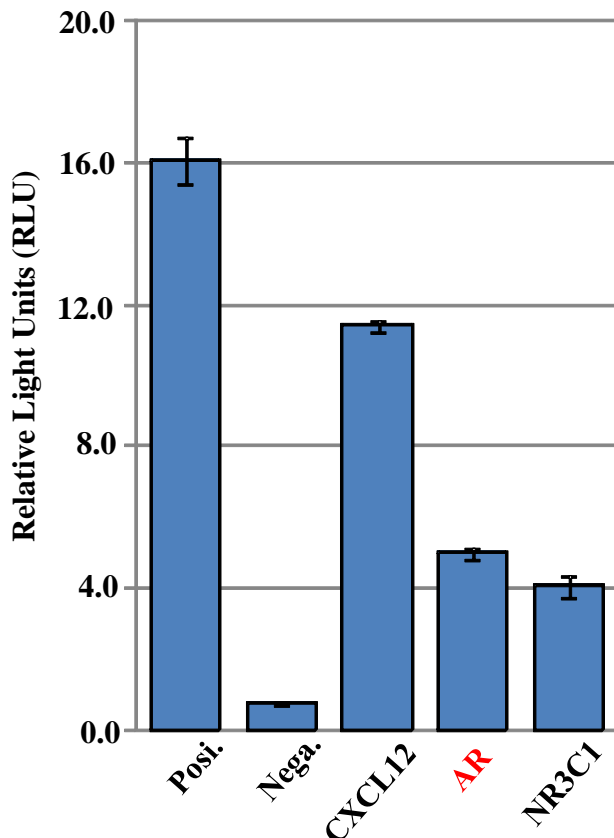
HeLa cells



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 : 2010.01.12

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5732

2nd Nucleotide Sequence

File Name : RDB7690F.fasta
Sequence Size : 743

Unit Size to Compare = 1
Pick up Location = 1

[96.936% / 718 bp] INT/OPT. Score : < 2380/ 2620 >

```
1'          GGCC TAACTGGCCG GTACCTGAG- CTCGCTAGCC
          **** *****
1'' CAGTGCATGT GCCAGAACAT TTCTCTGGCC TAACTGGCCT GTACCTGAGC CTCGCTAGCC

34' TCGAGGATTG TTTGGCTGTG CACAAGATAA AGCTACAACA AAGCTACAAC CCATCTTTTC
          ***** ***** ***** ***** ***** *****
61'' TCGAGGATTG TTTGGCTGTG CACAAGATAA AGCTACAACA AAGCTACAAC CCATCTTTTC

94' TCTGTAGAAG ACTGCAAAAA GCAAAAGAGA CCCAGGCAAA AATCTCGGAA TGACTTTTGG
          ***** ***** ***** ***** ***** *****
121'' TCTGTAGAAG ACTGCAAAAA GCAAAAGAGA CCCAGGCAAA AATCTCGGAA TGACTTTTGG

154' AACAGAGAGC CTCCCAGAA TCAGAAGTCA AAGGAATTTA AAACATAGGG AGGCCCAGGG
          ***** ***** ***** ***** ***** *****
181'' AACAGAGAGC CTCCCAGAA TCAGAAGTCA AAGGAATTTA AAACATAGGG AGGCCCAGGG

214' TCTCTACTGA CATAAAGGAA AGATGTTTTC CTTATAGGTT TACGTTTACA TTTTCTCTCT
          ***** ***** ***** ***** ***** *****
241'' TCTCTACTGA CATAAAGGAA AGATGTTTTC CTTATAGGTT TACGTTTACA TTTTCTCTCT
```



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274' CTTTCCATTG CCACTTGCAT CTCCACCTTT ACACAGGGCT TATGGGACCT CCTCCACAAA
*****
301" CTTTCCATTG CCACTTGCAT CTCCACCTTT ACACAGGGCT TATGGGACCT CCTCCACAAA

334' AGAGCAGTTG CAGTAACCCA CATCATCCTC TAGGCCTGGC TGTCCATCAA GAGGCGAAAA
*****
361" AGAGCAGTTG CAGTCACCCA CATCATCCTC TAGGCCTGGC TGTCCATCAA GAGGCGAAAA

394' GCAGCCCTAT ATAGTTCTA TCCTTGATA GTTCCAGTTG TAAAGTTAA AATATGCGAA
*****
421" GCAGCCCTAT ATAGTTCTA TCCTTGATA GTTCCAGTTG TAAAGTTAA AATATGCGAA

454' GGCAACTTGG AAAAGCAAGC GGCTGCATAC AAAGCAAACG TTTACAGAGC TCTGGACAAA
*****
481" GGCAACTTGG AAAAGCAAGC GGCTGCATAC AAAGCAAACG TTTACAGAGC TCTGGACAAA

514' ATTGAGCGCC TATGTGTACA TGGCAAGTGT TTTTAGTGTT TGTGTGTTA CCTGCTTGTC
*****
541" ATTGAGCGCC TATGTGTACA TGGCAAGTGT TTTTAGTGTT TGTGTGTTA CCTGCTTGTC

574' TGGGTGATTT TGCCTTTGAG AGTCTGGATG AGAAATGCAT GGTAAAGGC AATCCAGAC
*****
601" TGGGTGATTT TGCCTTTGAG AGTCTGGATG AGAAATGCAT GGT-AAGGC AATCCAGAC

634' AGGAAGAAAG GCAGAGAAGA GGTAGAAAT GACCTCTGAT TCTTGGGGCT GAGGGTTCCT
*****
660" AGGAAGAAA- GCAGAGAAGA -GGTAG-AAT GA-CTCTGA- TC-TGGGGCT GA-GGTT-CT

694' AGAGCAAATG GCACAATGCC ACGAGGCCCG ATCTATCCCT ATGACGGAAT CTAAGGTTTC
****
712" -GAGC-AATG CCATGCAGAG CCGACATCTT AGGG

```

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5732



2nd Nucleotide Sequence

File Name : RDB7690.fasta (Complementary)

Sequence Size : 798

Unit Size to Compare = 1

Pick up Location = 1

[96.168% / 809 bp] INT/OPT.Score : < 1920/ 2941 >

781' CTTGCTCCTC AGTTTGTAGG AGACTCTCCC ACTCTCCCAT CTGCGCGCTC TTATCAGTCC
* * * * * ***** ** * * * *****
1" TTCC AAT-TTCCAT -TGGGGGGT- TTAT-AGTCC

841' TGAAAAGAAC CCCTGGCAGC CAGGAGCAGG TATTCTATC GTCCTTTTCC TCCCTCCCTC
***** *** ***** ***** ** ***** ***** ***** *****
31" --AAAAA AAC CCCT-GCAGC CA-GAGCAGG GATTCTATT GTCC-TTTCT TCCCTCCCTG

901' GCCTCCACCC TGTTGGTTTT TTAGATTGGG CTTTGAACC AAATTTGGTG AGTGCTGGCC
***** * * ***** ***** * ** ***** ** ***** * * *****
86" GCCTCCACCC CGGT-GTTTT TTAGAAT-GG CTTTGGGACC AAATTTTGGG AGTGCTGGCC

961' TCCAGGAAAT CTGGAGCCCT GGCGCCTAAA CCTTGGTTTA GGAAAGCAGG AGCTATTCAG
* . ***** ***** ***** ***** ***** ***** * * *****
144" TNCAGGAAAT CTGGAGCCCT GGCGCCTAAA CCTTGGTTTA GGAAAGCAGG AGGTATTCAG

1021' GAAGCAGGGG TCCTCCAGGG CTAGAGCTAG CCTCTCCTGC CCTCGCCAC GCTGCGCCAG
***** ***** ***** ***** ***** *****
204" GAAGCAGGGG TCCTCCAGGG CTAGAGCTAG CCTCTCCTGC CCTCGCCAC GCTGCGCCAG

1081' CACTTGTTTC TCCAAAGCCA CTAGGCAGGC GTTAGCGCGC GGTGAGGGGA GGGGAGAAA-
***** ***** ***** ***** ***** *****
264" CACTTGTTTC TCCAAAGCCA CTAGGCAGGC GTTAGCGCGC GGTGAGGGGA GGGGAGAAAT

1140' AGGAAAGGGG AGGGGAGGGA AAAGGAGGTG GGAAGGCAAG GAGGCCGGCC CGGTGGGGGC
***** ***** ***** ***** ***** *****
324" AGGAAAGGGG AGGGGAGGGA AAAGGAGGTG GGAAGGCAAG GAGGCCGGCC CGGTGGGGGC



1200' GGGACCCGAC TCGCAAAGTG TTGCATTTGC TCTCCACCTC CCAGCGCCCC CTCCGAGATC

 384" GGGACCCGAC TCGCAAAGTG TTGCATTTGC TCTCCACCTC CCAGCGCCCC CTCCGAGATC

 1260' CCGGGGAGCC AGCTTGCTGG GAGAGCGGGA CGGTCCGGAG CAAGCCCAGA GGCAGAGGAG

 444" CCGGGGAGCC AGCTTGCTGG GAGAGCGGGA CGGTCCGGAG CAAGCCCAGA GGCAGAGGAG

 1320' GCGACAGAGG GAAAAAGGGC CGAGCTAGCC GCTCCAGTGC TGTACAGGAG CCGAAGGGAC

 504" GCGACAGAGG GAAAAAGGGC CGAGCTAGCC GCTCCAGTGC TGTACAGGAG CCGAAGGGAC

 1380' GCACCAGGCC AGCCCCAGCC CGGCTCCAGC GACAGCCAAC GCCTCTTGCA GCGCGGCGGC

 564" GCACCAGGCC AGCCCCAGCC CGGCTCCAGC GACAGCCAAC GCCTCTTGCA GCGCGGCGGC

 1440' TTCGAAGCCG CCGCCCGGAG CTGCCCTTTC CTCTTCGGTG AAGTTTTTAA AAGCTGCTAA

 624" TTCGAAGCCG CCGCCCGGAG CTGCCCTTTC CTCTTCGGTG AAGTTTTTAA AAGCTGCTAA

 1500' AGACTCGGAG GAAGCAAGGA AAGTGCCTGG TAATCAAGAT CTGGCCTCGG CGGCCAAGCT

 684" AGACTCGGAG GAAGCAAGGA AAGTGCCTGG TAATCAAGAT CTGGCCTCGG CGGCCAAGCT

 1560' TGGCAATCCG GACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT TAAGAAGGGC

 744" TGGCAATCCG GACTGTTGG TAAAGCCACC ATGGAAGATG CCAAAAACAT TAAGA