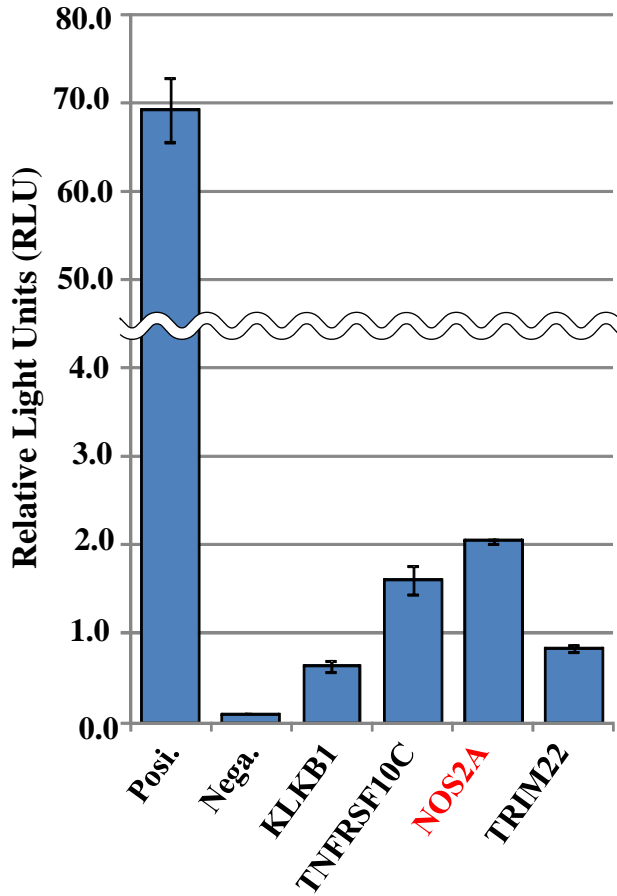
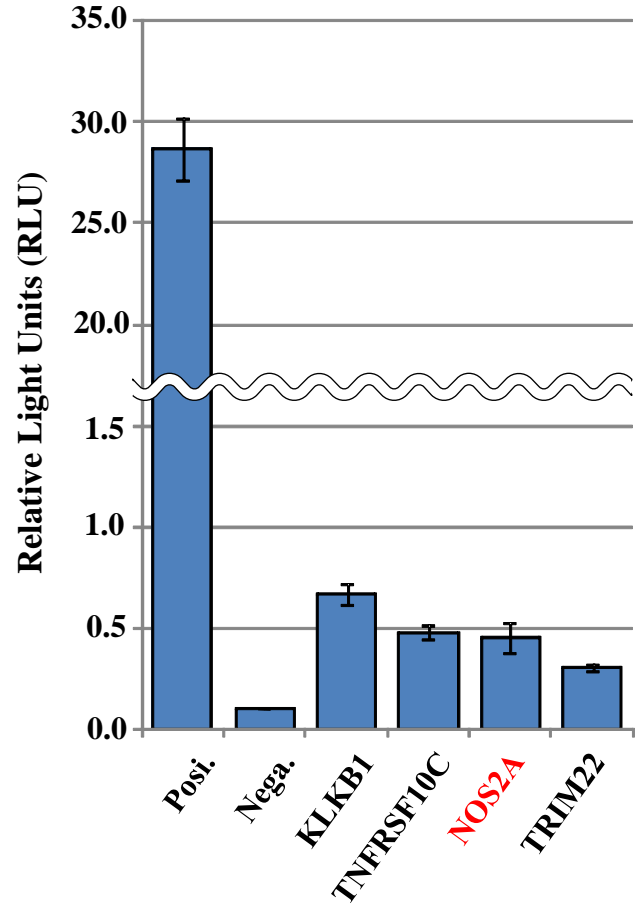


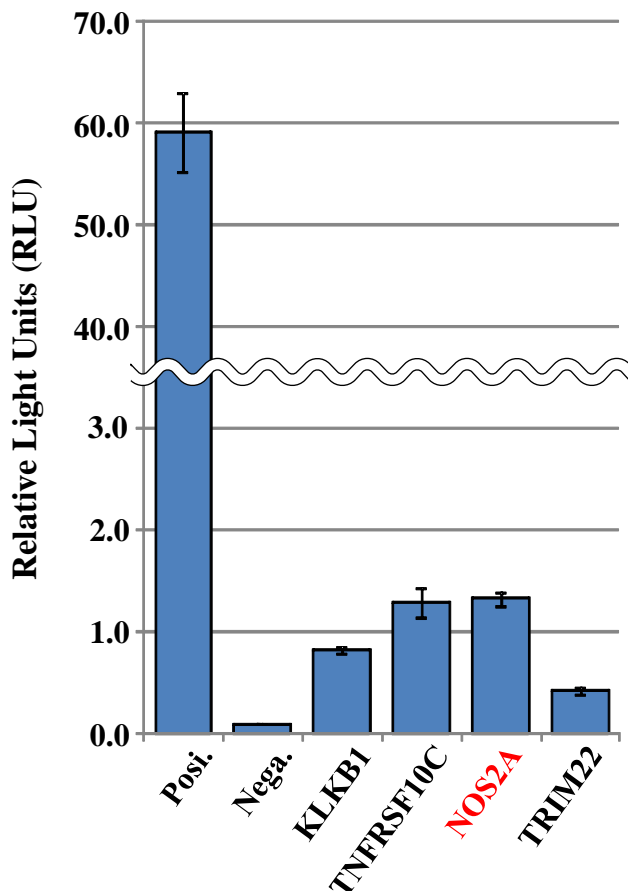
HeLa cells



HepG2 cells



Hep3B cells



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

KLKB1: pGL4-phKLKB1 (RDB# 7373)

TNFRSF10C: pGL4-ph TNFRSF10C (RDB# 7375)

NOS2A: pGL4-phNOS2A (RDB# 7377)

TRIM22: pGL4-phTRIM22 (RDB#7382)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5546

2nd Nucleotide Sequence

File Name : RDB7377F.fasta
Sequence Size : 461

Unit Size to Compare = 1
Pick up Location = 1

[99.544% / 439 bp] INT/OPT. Score : < 1536/ 1734 >

```
1'          GGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG
          *****
1" AGGTGCCAGA ACATTTTCTC TGGCCTAACT GGCCGGTACC TGAGCTCGCT AGCCTCGAGG

40' ATCGGTGAGA TCAA-GGGTG ACTTTTTTTC CCTTTGCTTC TCAACTTCTC CCTAATGTAG
          *****
61" ATCGGTGAGA TCAAGGGTG ACTTTTTTTC CCTTTGCTTC TCAACTTCTC CCTAATGTAG

99' TTGTTATTTT ACTTTTATGA TGGAAAAATG CATATGTATG GGAATACTGT ATTCAGGCA
          *****
121" TTGTTATTTT ACTTTTATGA TGGAAAAATG CATATGTATG GGAATACTGT ATTCAGGCA

159' TTATAAGGAA TGA AATTATA GGCCGGGCAT GGTGGCTAAC CCTTGTAATC CTAGCACTTT
          *****
181" TTATAAGGAA TGA AATTATA GGCCGGGCAT TGTGGCTAAC CCTTGTAATC CTAGCACTTT

219' GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA TGGACAACAT
          *****
241" GAGAGGCTGA AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA TGGACAACAT
```



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279' GGTGAAACCC AGTCTCTACC AAAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC
*****
301" GGTGAAACCC AGTCTCTACC AAAAACACAA AAATATTAGC TGGGTGTGGT GGTGCATGCC

339' TGTAGTCCCA GCTACTCAGG AGGCTGAGGT GGGAGGATCG CTTGAGCCTG GGAGGCAGAA
*****
361" TGTAGTCCCA GCTACTCAGG AGGCTGAGGT GGGAGGATCG CTTGAGCCTG GGAGGCAGAA

399' GTTGCAATGA GCAGAGATCG TGCCACTCCG CTCCAGTCTT GGTGACAGAA TGAGACTCCA
*****
421" GTTGCAATGA GCAGAGATCG TGCCACTCCG CTCCAGTCTT T

```

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5546

2nd Nucleotide Sequence

File Name : RDB7377R.fasta (Complementary)
Sequence Size : 795

Unit Size to Compare = 1
Pick up Location = 1

[98.363% / 794 bp] INT/OPT. Score : < 1878/ 3062 >

```

601' AAGGATGAGG TGTTAGTAAG ACCAACATCT CAGAGGCCTC TC-TGTGCCA ATAGCCTTCC
**.*.*** ** *****
1" TC AAGNGNCCTT TCGTGTGCCA ATAGCCTTCC

660' TTCCTTTCCC TT-CCAAAAA CCTCAAGTGA CTAGTTCAGA GGCCTGTCTG GAATAATGGC
***** ** *****
33" TTCCTTTCCC TTCCAAAAAC CCTCAAGTGA CTAGTTCAGA GGCCTGTCTG GAATAATGGC

```



719' ATCATCTAAT ATCACTGGCC TTCTGGAACC TGGGCATTTT CCAGTGTGTT CCATACTGTC

 93" ATCATCTAAT ATCACTGGCC TTCTGGAACC TGGGCATTTT CCAGTGTGTT CAATACTGTC

 779' AATATTCCCC CAGCTTCCTG GACTCCTGTC ACAAGCTGGA AAAGTGAGAG GATGGACAGG

 153" AATATTCCCC CAGCTTCCTG AACTCCTGTC ACAAGCTGGA AAAGTGAGAG GATGGACAGG

 839' GATTAACCAG AGAGCTCCCT GCTGAGGAAA AAATCTCCA GATGCTGAAA GTGAGGCCAT

 213" GATTAACCAG AGAGCTCCCT GCTGAGGAAA AAATCTCCA GATGCTGAAA GTGAGGCCAT

 899' GTGGCTTGGC CAAATAAAC CTGGCTCCGT GGTGCCTCTA TCTTAGCAGC CACCCTGCTG

 273" GTGGCTTGGC CAAATAAAC CTGGCTCCGT GGTGCCTCTG TCTTAGCAGC CACCCTGCTG

 959' ATGAACTGCC ACCTTGACT TGGGACCAGA AAGAGGTGGG TTGGGTGAAG AGGCACCACA

 333" ATGAACTGCC ACCTTGACT TGGGACCAGA AAGAGGTGGG TTGGGTGAAG AGGCACCACA

 1019' CAGAGTGATG TAACAGCAAG ATCAGGTCAC CCACAGGCC TGGCAGTCAC AGTCATAAAT

 393" CAGAGTGATG TAACAGCAAG ATCAGGTCAC CCACAGGCC TGGCAGTCAC AGTCATAAAT

 1079' TAGCTAACTG TACACAAGCT GGGGACACTC CCTTTGAAA CCAAAAAAAAA AAAAAAAAAA

 453" TAGCTAACTG TACACAAGCT GGGGACACTC CCTTTGAAA CC—AAAAAA AAAAAAAAAA

 1139' AAGAGACCTT TATGCAAAA CAACTCTCTG GATGGCATGG GGTGAGTATA AATACTTCTT

 511" AAGAGACCTT TATGCAAAA CAACTCTCTG GATGGCATGG GGTGAGTATA AATACTTCTT

 1199' GGCTGCCAGT GTGTTCAATA CTTTGTAGCG AGTCGAAAAC TGAGGCTCCG GCCGCAGAGA

 571" GGCTGCCAGT GTGTTCAATA CTTTGTAGCG AGTCGAAAAC TGAGGCTCCG GCCCCAGAGA

 1259' ACTCAGCCTC ATTCCTGCTT TAAAATCTCT CGGCCACCTT TGATGAGGGG ACTGGGCAGT

 631" ACTCAGCCTC ATTCCTGCTT TAAAATCTCT CGGCCACCTT TGATGAGGGG ACTGGGCAGT

1319' TCTAGACAGT CCCGAAGTTC TCAAGGCATC AAGATCTGGC CTCGGCGGCC AAGCTTGCA

691" TCTAGACAGT CCCGAAGTTC TCAAGGCATC AAGATCTGGC CTCGGCGGCC AAGCTTGCA

1379' ATCCGGTACT GTTGGTAAAG CCAC-CATGG AAGATGCCAA AAACATTAAG AAGGGCCCAG

751" ATCCGGTACT GTTGGTAAAG CCACNCATGG AAGATGCCAA AAACA