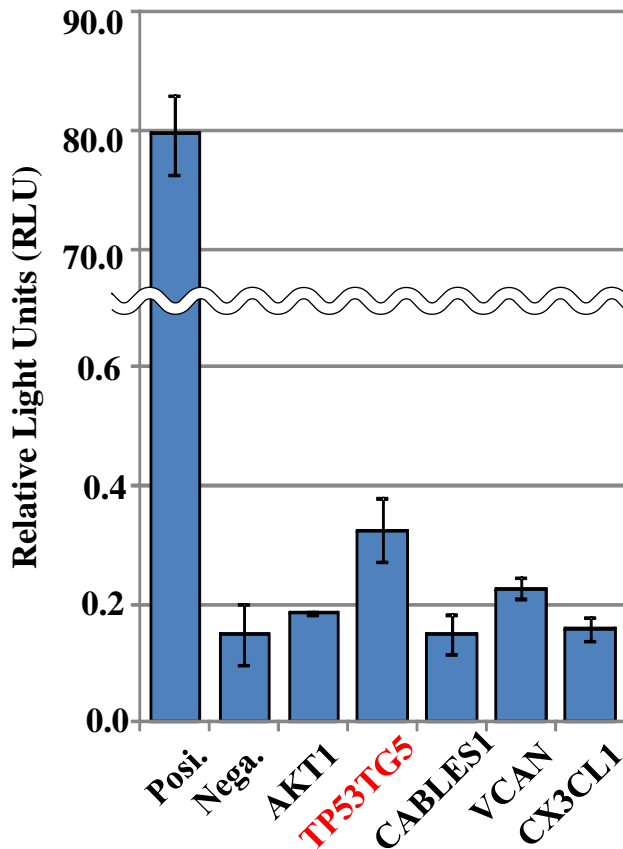
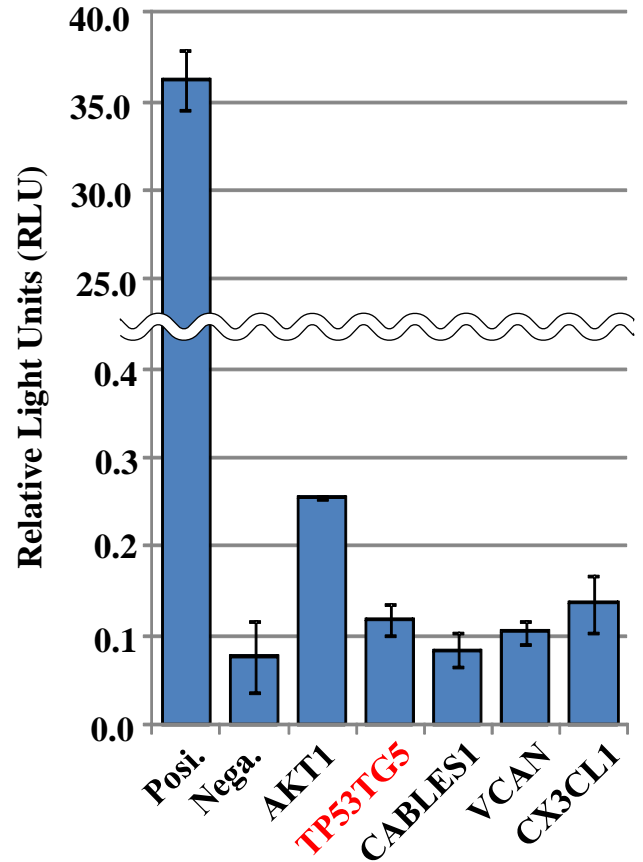


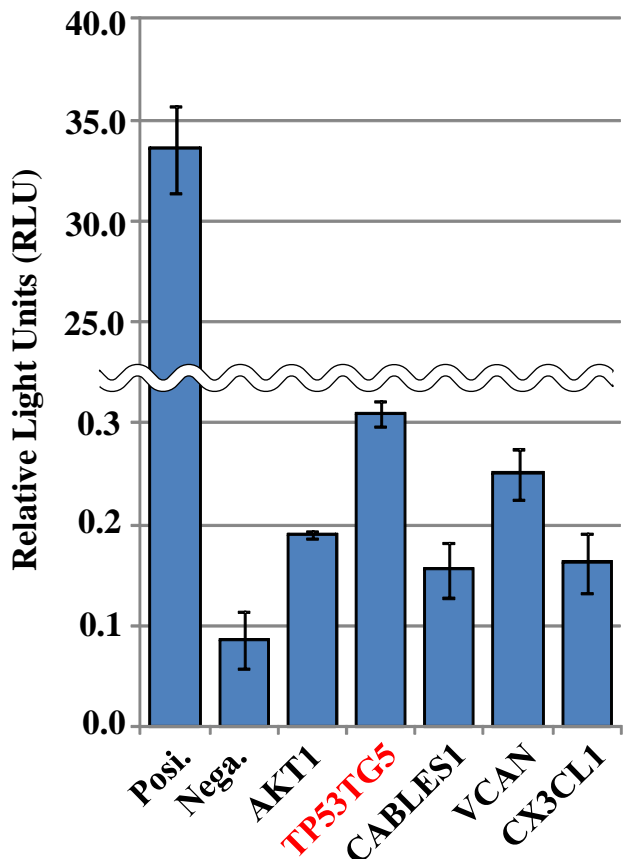
HeLa cells



HepG2 cells



Hep3B cells



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

AKT1: pGL4-phAKT1 (RDB# 7331)

TP53TG5: pGL4-phTP53TG5 (RDB# 7336)

CABLES1: pGL4-phCABLES1 (RDB# 7337)

VCAN: pGL4-phVCAN (RDB#7339)

CX3CL1: pGL4-phCX3CL1 (RDB#7340)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq 0.gnu
Sequence Size : 5512

2nd Nucleotide Sequence

File Name : RDB7336F.fasta
Sequence Size : 624

Unit Size to Compare = 1
Pick up Location = 1

[99.669% / 604 bp] INT/OPT. Score : < 2404/ 2404 >

```
1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA
          ** *****
1'' GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA

43' GCAAGTGTCC TGCCCATAGC TATTCGATTG TAAATAACAA AAAGAATCTG AGAAATATAT
          *****
61'' GCAAGTGTCC TGCCCATAGC TATTCGATTG TAAATAACAA AAAGAATCTG AGAAATATAC

103' CTCCAGTATT CAAAACTAT GGTCTAATTC AGCAAATAGG TCAATGAAAT CATTGATAAA
          *****
121'' CTCCAGTATT CAAAACTAT GGTCTAATTC AGCAAATAGG TCAATGAAAT CATTGATAAA

163' TGAGTTAAAT TTCAATATCT CTGTTGTTTC ACTTTTTCAC CTTCTTCTTA CTGTTTAGTG
          *****
181'' TGAGTTAAAT TTCAATATCT CTGTTGTTTC ACTTTTTCAC CTTCTTCTTA CTGTTTAGTG

223' TAAATGAAAA TACAAACATT AATGTTGGTA TTATACTTGT TTATCCATTA CAACCATAGG
          *****
241'' TAAATGAAAA TACAAACATT AATGTTGGTA TTATACTTGT TTATCCATTA CAACCATAGG
```



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283' TTGGCTATAA ATGGAGGGGT TAGGCAAAAT CCAAGAAAAG CATACTATAA GAAGCAACTC
*****
301" TTGGCTATAA ATGGAGGGGT TAGGCAAAAT CCAAGAAAAG CATACTATAA GAAGCAACTC

343' ACTAATAGAA GTTACAATAA AGAGTATTAT AGGATTCTAT TATTTGTTGA TTTCTATCAG
*****
361" ACTAATAGAA GTTACAATAA AGAGTATTAT AGGATTCTAT TATTTGTTGA TTTCTATCAG

403' TAAAATTTAT AATACAAACA CATATACATT TTGCTTCAGA GAGCCAATTA TTAACATTT
*****
421" TAAAATTTAT AATACAAACA CATATACATT TTGCTTCAGA GAGCCAATTA TTAACATTT

463' ACAAGTACAC ACACTGTTTC CCCTCCACTA GAATGTAAGC TTGAGGGCAA GAATTTTCTG
*****
481" ACAAGTACAC ACACTGTTTC CCCTCCACTA GAATGTAAGC TTGAGGGCAA GAATTTTCTG

523' TTATTCTAGC ACTTAGAAAA AGCACCTGGC AAGGCCAGGC GCGCTGACTC ATGCCTGTAA
*****
541" TTATTCTAGC ACTTAGAAAA AGCACCTGGC AAGGCCAGGC GCACTGACTC ATGCCTGTAA

583' TCCAGCACT GTGGGAGGTG GAGGTGGGCG GATCACAAG TCAAGAGATC GAGACCATCC
*****
601" TCCAGCACT GTGGGAGGTG GAAA

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5512

2nd Nucleotide Sequence

File Name : RDB7336R. fasta (Complementary)
Sequence Size : 658

Unit Size to Compare = 1
Pick up Location = 1



[99.696% / 658 bp] INT/OPT. Score : < 2620/ 2620 >

721' GCTACTTGGG AGGCTGAGGC AGGAAAATCG CTTGAACCCA GGAGGCGGAG GTTGCAGGGA

* * ***** ***** ***** *****

1" GCC AGGAAAATCG CTTGAACCCA GGAGGCGGAG TTTGCAGGGA

781' GCCAAGATCT CACCACTGCA CTCCAGCCTG GCGACAGAGT GAGACTCTGT CTCAAAAAC

***** ***** ***** ***** ***** *****

44" GCCAAGATCT CACCACTGCA CTCCAGCCTG GCGACAGAGT GAGACTCTGT CTCAAAAAC

841' AAAAAACAAA AAAAGAGAAA GAAAAGAAA AGCACCTGGC ATGTAGCAGG CGCCCAGTCA

***** ***** ***** ***** ***** *****

104" AAAAAACAAA AAAAGAGAAA GAAAAGAAA AGCACCTGGC ATGTAGCAGG CGCCCAGTCA

901' AAACAGGCGA CATGACTGAA TGGATGAGCA TGGTTTGGGA ATCCCTGGTT TCATGGGTTG

***** ***** ***** ***** ***** *****

164" AAACAGGCGA CATGACTGAA TGGATGAGCA TGGTTTGGGA ATCCCTGGTT TCATGGGTTG

961' ACTATCAGAC CTTGGTTAGG TTTCCAGCCC ACTATGATCT AGCTGGGCTA GATCTAGTGT

***** ***** ***** ***** ***** *****

224" ACTATCAGAC CTTGGTTAGG TTTCCAGCCC ACTATGATCT AGCTGGGCTA GATCTAGTGT

1021' GGCCTTGAGT AGATTATTCA ACCTCTTTGA ACCCTGGCTT CCTCATTTAA AAAGAGGGGA

***** ***** ***** ***** ***** *****

284" GGCCTTGAGT AGATTATTCA ACCTCTTTGA ACCCTGGCTT CCTCATTTAA AAAGAGGGGA

1081' TAATCCTCTT ACCCCACAGG GAGGTTGTGA CAATGCACAC AGCTGTCTGT CGCCTATTGT

***** ***** ***** ***** ***** *****

344" TAATCCTCTT ACCCCACAGG GAGGTTGTGA CAATGCACAC AGCTGTCTGT CGCCTATTGT

1141' CTATATTTCT TTCTACCCT CTACCCCTCA CCTCTGCCAC ATACACTCCT TGGAGACCCA

***** ***** ***** ***** ***** *****

404" CTATATTTCT TTCTACCCT CTACCCCTCA CCTCTGCCAC ATACACTCCT TGGAGACCCA

1201' GCCCTGCTAC TGTCACATTT CAGTGATGTC ACAGCTGCAG GTGGTACAGA GCCAGCACCA

***** ***** ***** ***** ***** *****

464" GCCCTGCTAC TGTCACATTT CAGTGATGTC ACAGCTGCAG GTGGTACAGA GCCAGCACCA



1261' CCATCTGATG CCCAGCCTGA GTGCTGGCTG AACTGAGAGG AACAGGGTTG GATCAAGATC

524'' CCATCTGATG CCCAGCCTGA GTGCTGGCTG AACTGAGAGG AACAGGGTTG GATCAAGATC

1321' TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT AAAGCCACCA TGGAAAGATGC

584'' TGGCCTCGGC GGCCAAGCTT GGCAATCCGG TACTGTTGGT AAAGCCACCA TGGAAAGATGC

1381' CAAAAACATT AAGAAGGGCC CAGCGCCATT CTACCCACTC GAAGACGGGA CCGCCGGCGA

644'' CAAAAACATT AAGAA