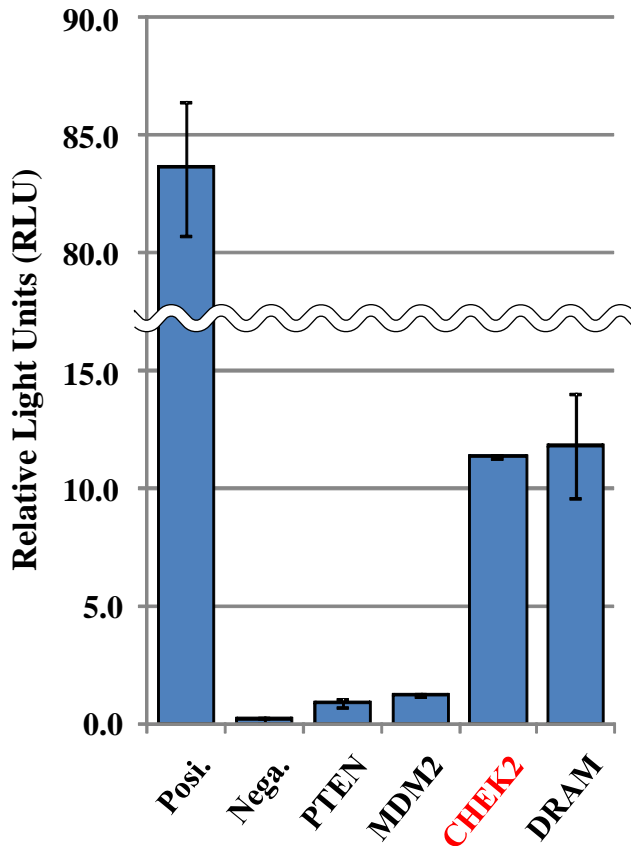
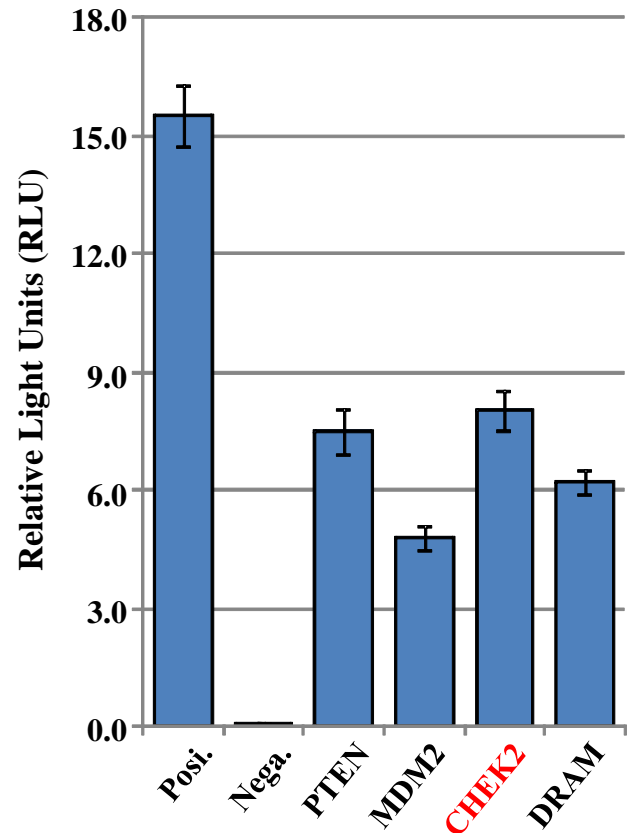


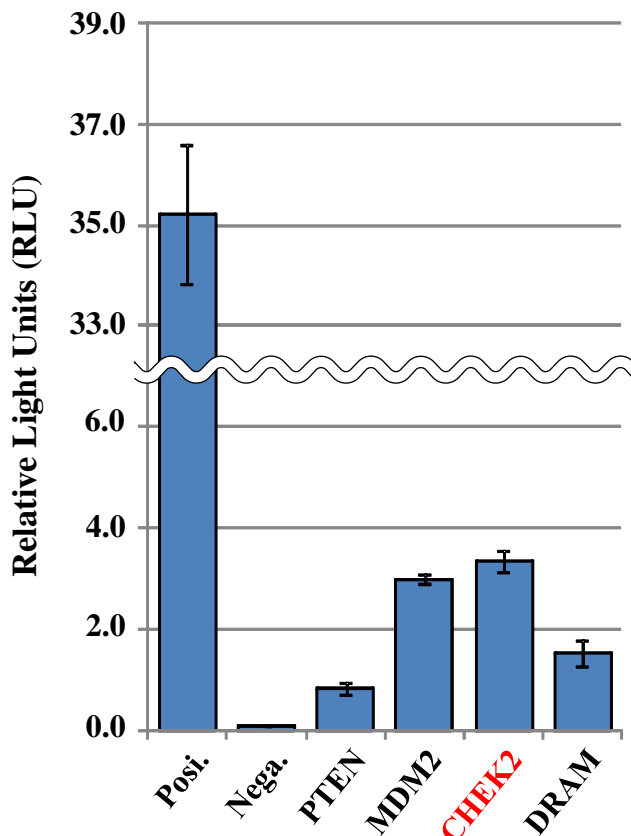
HeLa cells



HepG2 cells



Hep3B cells



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

PTEN: pGL4-phPTEN (RDB# 7400)

MDM2: pGL4-phMDM2 (RDB# 7403)

CHEK2: pGL4-phCHEK2 (RDB# 7407)

DRAM: pGL4-phDRAM (RDB#7412)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.06.30

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5554

2nd Nucleotide Sequence

File Name : RDB7407F.fasta
Sequence Size : 670

Unit Size to Compare = 1

Pick up Location = 1

[98.483% / 659 bp] INT/OPT. Score : < 2232/ 2514 >

```
1'          GGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATTGGCC
          *****
1'' AGAACATTAT CTCTGGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATTGGCC

47' CCTCTACAAG ATGGTCTTGA AGAAAGTCTT TCTGGTGCTT GAACAAGTGT GACTGAATCA
          *****
61'' CCTCTACAAG ATGGTCTTGA AGAAAGTCTT TCTGGTGCTT GAACAAGTGT GACTGAATCA

107' TGTTTTCTTT AATACCACCC TAACTTTTCC ACGGCCCAGG TCCCTTCATC CCTGTCTCTC
          *****
121'' TGTTTTCTTT AATACCACCC TAACTTTTCC ACGGCCCAGG TCCCTTCATC CCTGTCTCTC

167' CCGGTTTATT TTAATTCAGC CCCTTTCACA TTCTACTCCC AGAGTCTGTC CTATTTCTT
          *****
181'' CCGGTTTATT TTAATTCAGC CCCTTTCACA TTCTACTCCC AGAGTCTGTC CTATTTCTT

227' ACCAGTTCAG CTCTATCCAC ACTGCCCGT CTCTCCAAGA ACCTCAGTCT CAGGGGGAAA
          *****
241'' ACCAGTTCAG CTCTATCCAC ACTGCCCGT CTCTCCAAGA ACCTCAGTCT CAGGGGGAAA

287' AACCATTTAT TGGACCCTCT CCCTCCAATT CTCACITTTT CCTCAGGCCT CGCCACAAT
          *****
301'' AACCATTTAT TGGACCCTCT CCCTCCAATT CTCACITTTT CCTCAGGCCT CGCCACAAT
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347' ATTAAGCTTT TCATGCTTTA CTCCTAATC TCGGATCACA CTTCTGCAGT CCTTTCTTAA
*****
361" ATTAAGCTTT TCATGCTTTA CTCCTAATC TCGGATCACA CTTCTGCAGT CCTTTCTTAA

407' ATACATCAAC CCAACTTTAA ACCTTACTCA CCCTATTCAT TCAAGTCTTC CAGTCTCCCA
*****
421" ATACATCAAC CCAACTTTAA ACCTTACTCA CCCTATTCAT TCAAGTCTTC CAGTCTCCCA

467' GGCCTGCC CTCAAGTACC CTTTCTCAA GTTCGGCCCC TCGACTTCTC CTTCCCTTTC
*****
481" GGCCTGCC CTCAAGTACC CTTTCTCAA GTTCGGCCCC TCGACTTCTC CTTCCCTTTC

527' CCGTAGGTAC CGCCCTCAA ATCTCCCT-C CCCTCTAGCC TC-GGCCCC CTATTTCTC
*****
541" CCGTAGGTAC CGCCCTCAA ATCTCCCTCC CCCTCTAGCC TCGGGCCCC CTATTTCTC

585' TAACTTACG GCCCGCCCT CCAGTCCG- TTCGTCTCC TTCTCCACAC CTC AAGTTG
*****
601" TAACTTACG GCCCGCCCC TCAGTCCCGT TTCGTCTCC TTCT-CACAC CTC-ACGTTG

644' CTTCCCTCAG TCCCGCCTC TCAATTTCT CCTGAGAAAT CAAGACACTT CTCTCAGCC
* ***** ***
659" C--TCCTCAG TCCT

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5554

2nd Nucleotide Sequence

File Name : RDB7407R. fasta (Complementary)
Sequence Size : 633

Unit Size to Compare = 1
Pick up Location = 1



[99.681% / 627 bp] INT/OPT. Score : < 2496/ 2496 >

781' CAGACCTCGA CGTGTCTCTC GCCCGGGCCC GTTTCCCGAA ACCGTCGCTC GTACCAGTCC
*** *****
1" CCC GTTTCCCGAA ACCGTCGCTC GTACCAGTCC

841' ATAAGGCTGA AGTAGTCTCG AGTGGGGTCA GGTGCCTGCA GCGCTCGGCA CTGTGGGCAG

34" ATAAGGCTGA AGTAGTCTCG AGTGGGGTCA GGTGCCTGCA GCGCTCGGCA CTGTGGGCAG

901' AAGAACCTGT CCTCCGCCC GGGGCCCAT GGGCCGCCG AGTTCCAACA GCGGGGATAA

94" AAGAACCTGT CCTCCGCCC GGGGCCCAT GGGCCGCCG AGTTCCAACA GCGGGGATAA

961' TTGCTTCCCG CCTGCGACGC AGCATCGCAG CTTAGCGGTC TCCTTCTGGG AACCCCTGTC

154" TTGCTTCCCG CCTGCGACGC AGCATCGCAG CTTAGCGGTC TCCTTCTGGG AACCCCTGTC

1021' GGCCAAAACC CCCACACCCG GAGCAAAGCC CCGGCTCTCC CCCGCCACAT CTGGCCGGCG

214" GGCCAAAACC CCCACACCCG GAGCAAAGCC CCGGCTCTCC CCCGCCACAT CTGGCCGGCG

1081' GCCTATCTAG CCGTGGTCAC TCGTGGGGAA AAGCAAAGAG AGCGTCTAAC CAGACTAATG

274" GCCTATCTAG CCGTGGTCAC TCGTGGGGAA AAGCAAAGAG AGCGTCTAAC CAGACTAATG

1141' TTGCTGATTG GCTGGGGAGT CGAGGGGGCG GGATCACCCG AGGGGAACCC GGGTTCTAAG

334" TTGCTGATTG GCTGGGGAGT CGAGGGGGCG GGATCACCCG AGGGGAACCC GGGTTCTAAG

1201' TTCCGCTCTC CTTTCTAAAC TACAACTCCC AGGAGGCATT GAGGCGGCGC CTGACGGCCA

394" TTCCGCTCTC CTTTCTAAAC TACAACTCCC AGGAGGCATT GAGGCGGCGC CTGACGGCCA

1261' CATCTGCTGC TCCTCATTGG TCCGGCGGCA GGGGAGGGG TTTTGATTGG CTGAGGGTGG



454" CATCTGCTGC TCCTCATTGG TCCGGCGGCA GGGGAGGGGG TTTTGATTGG CTGAGGGTGG

1321' AGTTTGTATC TGCAGGTTTA GCGCCACTCT GCTATCAAGA TCTGGCCTCG GCGGCCAAGC

514" AGTTTGTATC TGCAGGTTTA GCGCCACTCT GCTATCAAGA TCTGGCCTCG GCGGCCAAGC

1381' TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAAACA TTAAGAAGGG

574" TTGGCAATCC GGTACTGTTG GTAAAGCCAC CATGGAAGAT GCCAAACACA TTCAAGCACC