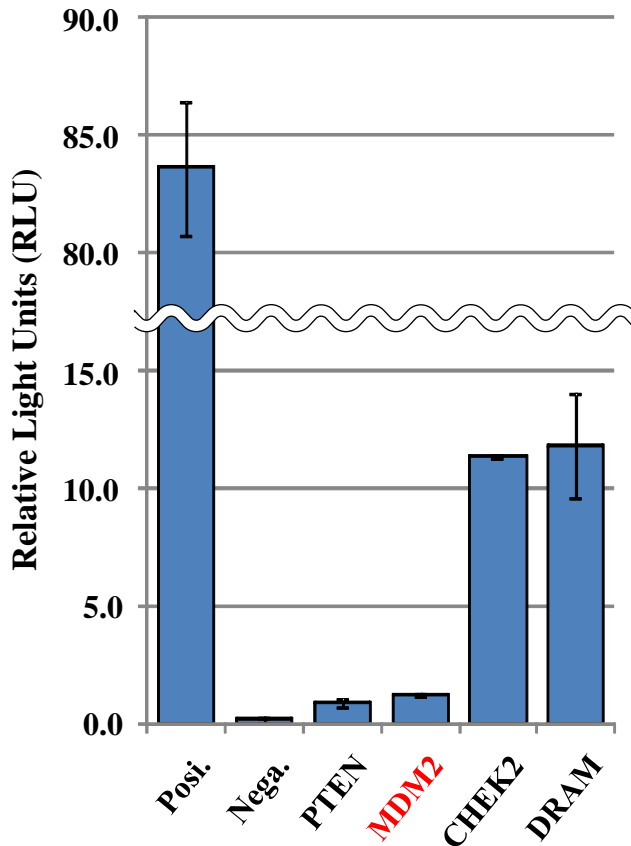
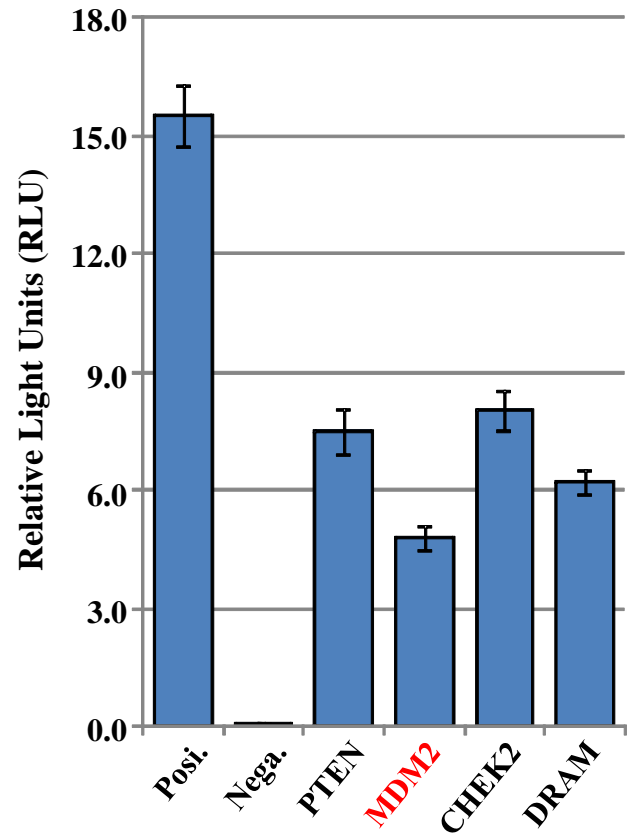


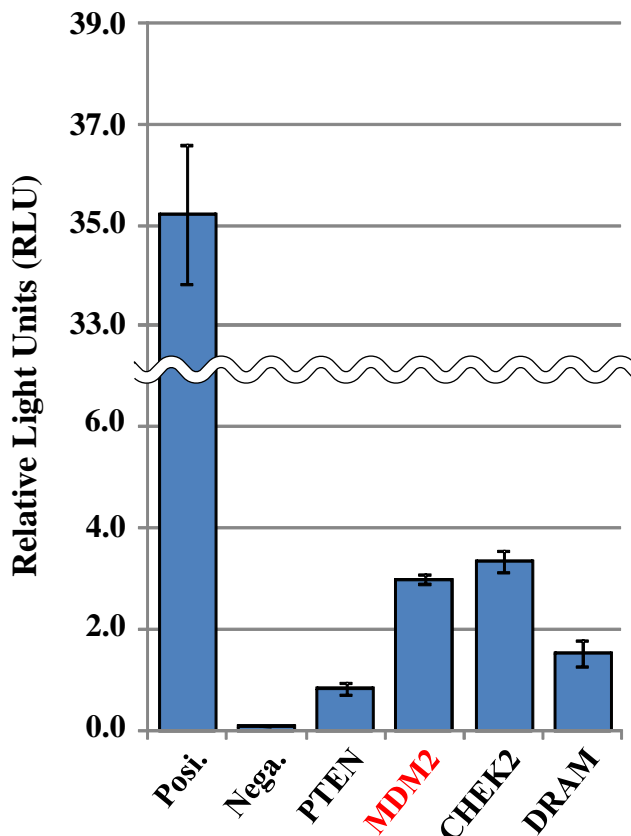
HeLa cells



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 : 2009.06.26

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 3018

2nd Nucleotide Sequence

File Name : RDB7403F.fasta
Sequence Size : 400

Unit Size to Compare = 1
Pick up Location = 1

[99.499% / 399 bp] INT/OPT. Score : < 1584/ 1584 >

```
42' GAAGCGGGAG AAGGGAAGGA TATAACTTTA TAAAAAATAA AAAGCTGCAG AAGGGAAGGA
                                     **** * ** *****
61''                                     GAAGCGGGAG AAGGGAAGGA

102' TATAACTTTA TAAAAAAGG TCCTTGTTCA CAAGGAGCTA ATCACTTACT GGCCAGAGAA
***** ***** ***** ***** ***** *****
81'' TATAACTTTA TAAAAAAGG TCCTTGTTCA CAAGGAGCTA ATCACTTACT GGCCAGAGAA

162' GAAACGTGTT CCTTCTTTC AATGGCTGTG TTTTGGGTT TAGCTAACTC AATCCTTTAT
***** ***** ***** ***** ***** *****
141'' GAAACGTGTT CCTTCTTTC AATGGCTGTG TTTTGGGTT TAGCTAACTC AATCCTTTAT

222' GTCCTCAATT TATGAGACCG CATCAAAAAC GTTTTGCCA CATCTCTGTG GGAAAGTAGG
***** ***** ***** ***** ***** *****
201'' GTCCTCAATT TATGAGACCG CATCAAAAAC GTTTTGCCA CATCTCTGTG GGAAAGTAGG

282' TGAGTCAGAA TGAGTGCATA ATATATAAGT ATATATTTTA ATGATAATGA ATGTGTAGAT
***** ***** ***** ***** ***** *****
261'' TGAGTCAGAA TGAGTGCATA ATATATAAGT ATATATTTTA ATGATAATGA ATGTGTAGAT
```



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342' TAACAAACCC AAAC TTGTT TTTGTTTTT TGAGAGTCTT GCCCTGTCGC CCAGGCTGGA
*****
321" TAACAAACCC AAAC TTGTT TTTGTTTTT TGAGAGTCTT GCCCTGTCGC CCAGGCTGGA

402' GTGCAATGGC ATGATCTTGG CTCACTGCAG CCTCTGCCTC CCGGGTTCAC AGGATTGTCC
*****
381" GTGCAATGGC ATGATCTTGG CTCACTGCAG CCTCTGCCTC CCGGGTTCAC AGGATTGTCC

462' TGCCTCAGCC TCCGGAGTAG AGTAGCTGGG ATTACAGGTG ACCGCCACCA CGCCCGACTA
*****
441" TGCCTCAGCC TCCGGAGTAG

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5561

2nd Nucleotide Sequence

File Name : RDB7403R. fasta (Complementary)
Sequence Size : 311

Unit Size to Compare = 1
Pick up Location = 1

[99.357% / 311 bp] INT/OPT. Score : < 1232/ 1232 >

```

1021' GGCCGAGCCC CACCCTCTCA GCTCGGGGCC AACACCCCA CCCCCTCA CAGCCGCGG
* *****
85" C CACACCCCA CCCCCTCA GAGCCGCGG

1081' CGCCGCGGG GCGACACCC CCACTCCATC ATCCGGAGG TGGTGGGCC GAGCCCGGA
*****
116" CGCCGCGGG GCGACACCC CCACTCCATC ATCCGGAGG TGGTGGGCC GAGCCCGGA

```



1141' CCAATTGGC GGAAGCGGG CCGTTGTGT GCGCGGCAC AAATGCCCG ATGCGCCGG

 176'' CCAATTGGC GGAAGCGGG CCGTTGTGT GCGCGGCAC AAATGCCCG ATGCGCCGG

 1201' ACGACCCGG CGTCCCCTC GGGCGGTAGG GGGCGGCAC CGAGGCACG CGGCGAGCTT

 236'' ACGACCCGG CGTCCCCTC GGGCGGTAGG GGGCGGCAC CGAGGCACG CGGCGAGCTT

 1261' GGCTGCTTCT GGGCCTGTG TGGCCTGTG TGTCGAAAG ATGGAGCAAG AAGCCGAGCC

 296'' GGCTGCTTCT GGGCCTGTG TGGCCTGTG TGTCGAAAG ATGGAGCAAG AAGCCGAGCC

 1321' CGAGGGGCG CCGGACCCC TCTGACGAG ATCCTGCTGC ATCAAGATCT GGCCTGGCG

 356'' CGAGGGGCG CCGGACCCC TCTGACGAG ATCCTGCTGC