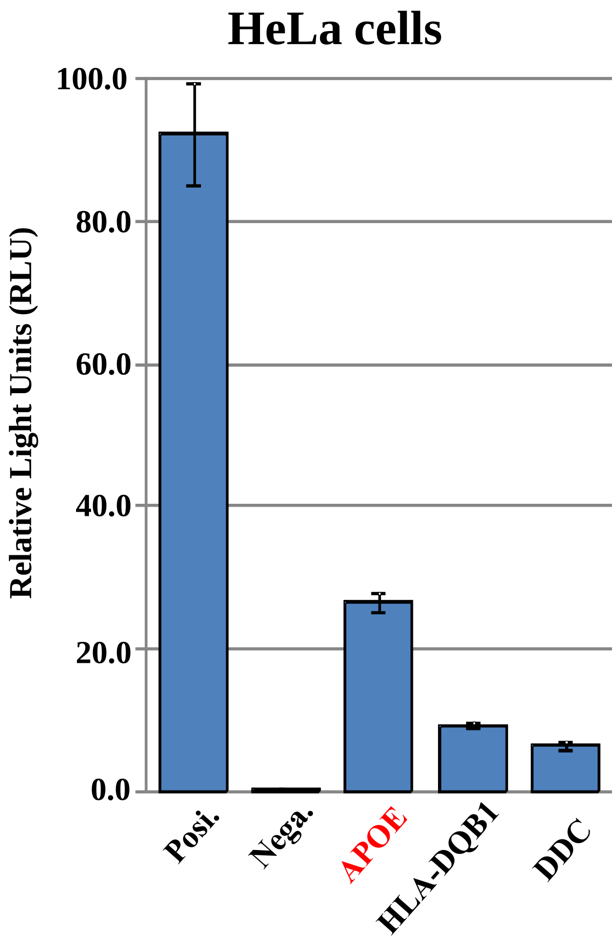
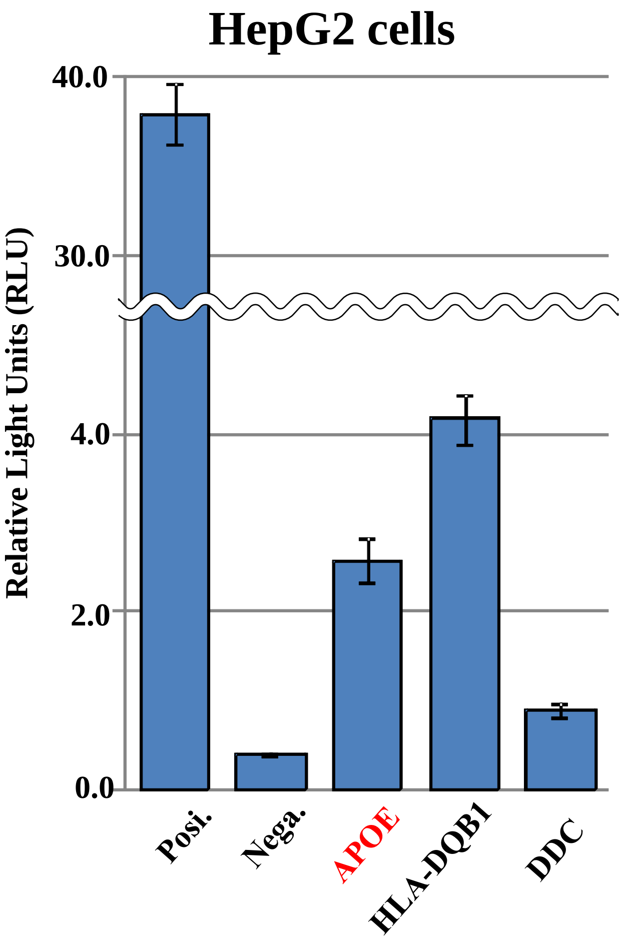
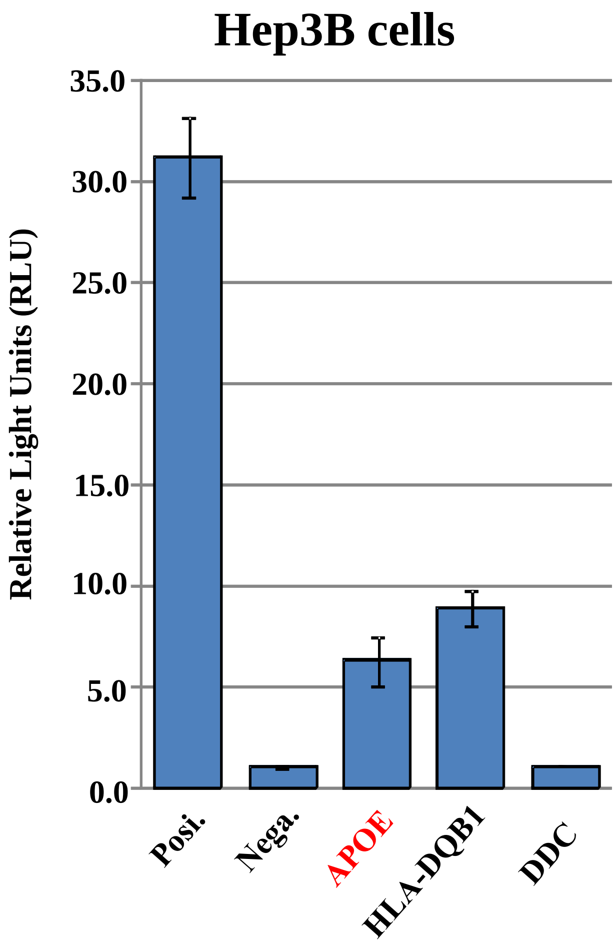
# The Promoter Activities of Reporter Constructs







**Posi.: pGL3 Control Vector**
**(SV40 promoter)**
**Nega.: Empty Vector**

**APOE: pGL4-phAPOE (RDB# 7556)**
**HLA-DQB1: pGL4-phHLA-DQB1 (RDB# 7557)**
**DDC: pGL4-phDDC (RDB# 7555)**

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.12.03

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5720

2nd Nucleotide Sequence
  File Name        : RDB7556F.fasta
  Sequence Size    : 580

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.255% / 573 bp]     INT/OPT.Score : <    281/  2132 >

      1’                   GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCC
                           *** ********** ********** ********** **********
      1″ TGCCAGAACA TTTCTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCC

     44’ TTGCCAGCCA AAGCAAACAG GCCCGNGCCC GGCACTGGGG GTTCCTTCTC GAACCAGGAG
         ********** ********** ***** **** ********** ********** **********
     61″ TTGCCAGCCA AAGCAAACAG GCCCG-GCCC GGCACTGGGG GTTCCTTCTC GAACCAGGAG

    104’ TTCAGCCTCC CCTGACNCCG CAGAATCTTC TGATCCCACC CGCTCCAGGA GCCAGGAATG
         ********** ****** *** ********** ********** ********** **********
    120″ TTCAGCCTCC CCTGAC-CCG CAGAATCTTC TGATCCCACC CGCTCCAGGA GCCAGGAATG

    164’ AGTCCCANGT CTCTCCCAGT TCTCACTGTG TGGTTTTGCC ATTCGTCTTG CTGCTGAANC
         ******* ** ********** ********** ********** ********** ******** *
    179″ AGTCCCA-GT CTCTCCCAGT TCTCACTGTG TGGTTTTGCC ATTCGTCTTG CTGCTGAA-C

    224’ CACGGGTTTC TCCTCTGAAA CATCTGGGAT TTATAACAGG GCTTAGGAAN AGTGACAGCG
         ********** ********** ********** ********** *********  **********
    237″ CACGGGTTTC TCCTCTGAAA CATCTGGGAT TTATAACAGG GCTTAGGAA- AGTGACAGCG
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284’ TCTGAGCGTT CACTGTGGCC TGTCCATTGC TAGCCCTAAC NATAGGACCG CTGTGTGCCA
     ********** ********** ********** **********  ********* **********
296″ TCTGAGCGTT CACTGTGGCC TGTCCATTGC TAGCCCTAAC -ATAGGACCG CTGTGTGCCA

344’ GGGCTGTCCT CCATGCTCAA TACACGTTAG CNTTGTCACC AAACATACCC GTGCCGCTGC
     ********** ********** ********** * ******** ********** **********
355″ GGGCTGTCCT CCATGCTCAA TACACGTTAG C-TTGTCACC AAACATACCC GTGCCGCTGC

404’ TTTCCCAGTC TGATGAGCAA AGNGAACTTG ATGCTCAGAG AGGACAAGTC ATTTGCCCAA
     ********** ********** ** ******* ********** ********** **********
414″ TTTCCCAGTC TGATGAGCAA AG-GAACTTG ATGCTCAGAG AGGACAAGTC ATTTGCCCAA

464’ GGTCACACAG CTGNGCAACT GGCAGAGCCA GGATTCACGC CCTGGCAATT TGACTCCAGA
     ********** *** ****** ********** ********** ********** **********
473″ GGTCACACAG CTG-GCAACT GGCAGAGCCA GGATTCACGC CCTGGCAATT TGACTCCAGA

524’ ATCCNTAACC TTAACCCAGA AGCACGGCTT CAAGCCCCTG GAAACCACAA TACCTNGTGG
     **** ***** ********** ********** ********** **********
532″ ATCC-TAACC TTAACCCAGA AGCACGGCTT CAAGCCCCTG GAAACCACAA
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1st Nucleotide Sequence
  File Name         : Reference Seq.GNU
  Sequence Size     : 5720

2nd Nucleotide Sequence
  File Name         : RDB7556R.fasta (Complementary)
  Sequence Size     : 767

  Unit Size to Compare = 1
  Pick up Location     = 1


[96.915% / 778 bp]     INT/OPT.Score : <    446/  2802 >
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 781' TTNTTTTCTT TTTTTGAGAC AGTCTCCCTC TTGCTGAGGC TGGAGTGCAG TGGNCGAGAT
                                                 *** **** ***. **  *
   1″                                          G CTGAGGGCAG TGGCGGA-TT

 841' CTCGGCTCAC TGTAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCNCTGCC TCAGCCTCCC
      ********** ********** ********** .********* **** ***** **********
  21″ CTCGGCTCAC TGTAACCTCC GCCTCCCGGG NTCAAGCGAT TCTC-CTGCC TCAGCCTCCC

 901' AAGTAGCTAG GATTACAGGC GCCCGCCACC ACGCCNTGGC TAACTTTTGT ATTTTTAGTA
      ********** ********** ********** ***** **** ********** **********
  80″ AAGTAGCTAG GATTACAGGC GCCCGCCACC ACGCC-TGGC TAACTTTTGT ATTTTTAGTA

 961' GAGATGGGGT TTCACCATGT TGGCCANGGC TGGTCTCAAA CTCCTGACCT TAAGTGATTC
      ********** ********** ****** *** ********** ********** **********
 139″ GAGATGGGGT TTCACCATGT TGGCCA-GGC TGGTCTCAAA CTCCTGACCT TAAGTGATTC

1021' GCCCACTGTG GCCTCCCNAA AGTGCTGGGA TTACAGGCGT GAGCTACCGC CCCCAGCCCC
      ********** ******* ** ********** ********** ********** **********
 198″ GCCCACTGTG GCCTCCC-AA AGTGCTGGGA TTACAGGCGT GAGCTACCGC CCCCAGCCCC

1081' TCCCATCCNC ACTTCTGTCC AGCCCCCTAG CCCTACTTTC TTTCTGGGAT CCAGGAGTCN
      ******** * ********** ********** ********** ********** *********
 257″ TCCCATCC-C ACTTCTGTCC AGCCCCCTAG CCCTACTTTC TTTCTGGGAT CCAGGAGTC-

1141' CAGATCCCCA GCCCCCTCTC CAGATTACAT TCATCCAGGC ACAGGAAAGG NACAGGGTCA
      ********** ********** ********** ********** **********  *********
 315″ CAGATCCCCA GCCCCCTCTC CAGATTACAT TCATCCAGGC ACAGGAAAGG -ACAGGGTCA

1201' GGAAAGGAGG ACTCTGGGCG GCAGCCTCCA CATTCCCCTT CNCACGCTTG GCCCCCAGAA
      ********** ********** ********** ********** * ******** **********
 374″ GGAAAGGAGG ACTCTGGGCG GCAGCCTCCA CATTCCCCTT C-CACGCTTG GCCCCCAGAA

1261' TGGAGGAGGG TGTCTGTATT ACTGGGCGAG GTNGTCCTCC CTTCCTGGGG ACTGTGGGGG
      ********** ********** ********** ** ******* ********** **********
 433″ TGGAGGAGGG TGTCTGTATT ACTGGGCGAG GT-GTCCTCC CTTCCTGGGG ACTGTGGGGG

1321' GTGGTCAAAA GACCTCTATG CCCNCACCTC CTTCCTCCCT CTGCCCTGCT GTGCCTGGGG
      ********** ********** *** ****** ********** ********** **********
 492″ GTGGTCAAAA GACCTCTATG CCC-CACCTC CTTCCTCCCT CTGCCCTGCT GTGCCTGGGG
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1381' CAGGGGGAGA ACAGNCCCAC CTCGTGACTG GGGGCTGGCC CAGCCCGCCC TATCCCTGGG
      ********** **** ***** ********** ********** ********** **********
 551″ CAGGGGGAGA ACAG-CCCAC CTCGTGACTG GGGGCTGGCC CAGCCCGCCC TATCCCTGGG

1441' GGAGGNGGGC GGGACAGGGG GAGCCCT-AT AATTGGACAA GTCTGGGATC CTTGAGTNCC
      ***** **** ********** ******* ** ********** ********** ******* **
 610″ GGAGG-GGGC GGGACAGGGG GAGCCCTAAT AATTGGACAA GTCTGGGATC CTTGAGT-CC

1500' TACTCAGCCC CAGCGGAGGT ATCAAGATCT GGCCTCGGCG GCCAAGCTTG GCAATCCGGT
      ********** ********** ********** ********** ********** **********
 668″ TACTCAGCCC CAGCGGAGGT ATCAAGATCT GGCCTCGGCG GCCAAGCTTG GCAATCCGGT

1560' ACTGTTGGTA AAGCCACCAT GGAA--GATG CCAAA-AACA TTAAGAAGGG CCCAGCGCCA
      ********** ********** ****   *** ***** ****
 728″ ACTGTTGGTA AAGCCACCAT GGAACGAATG CCAAACAACA
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