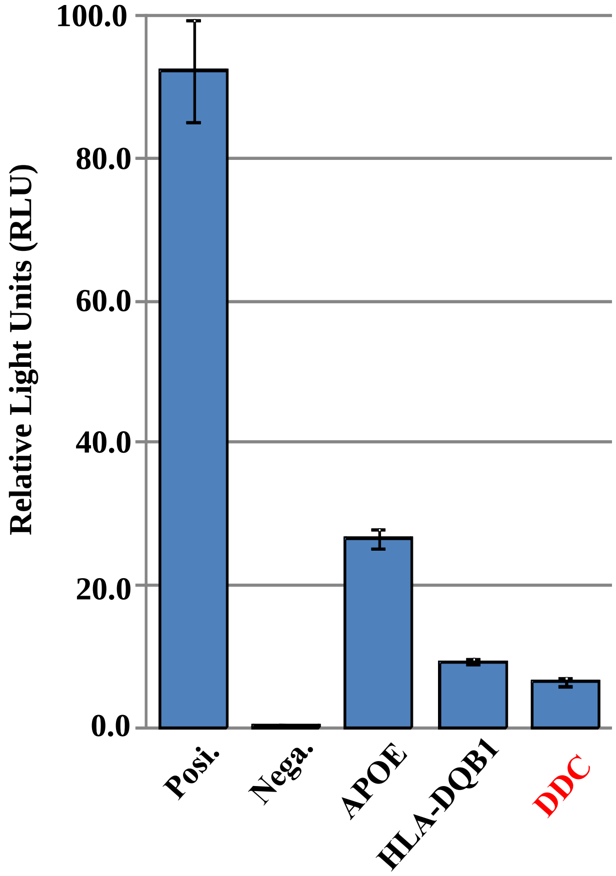
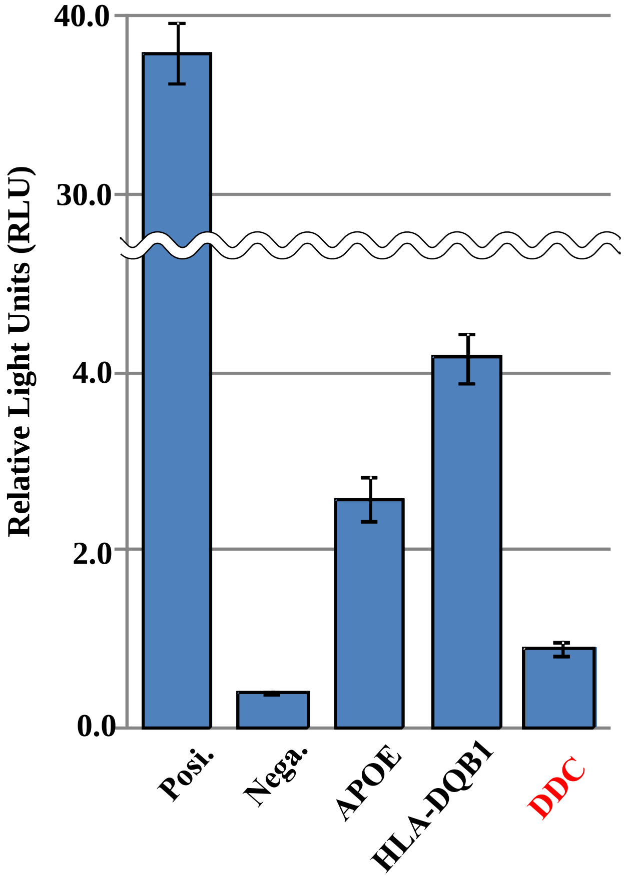
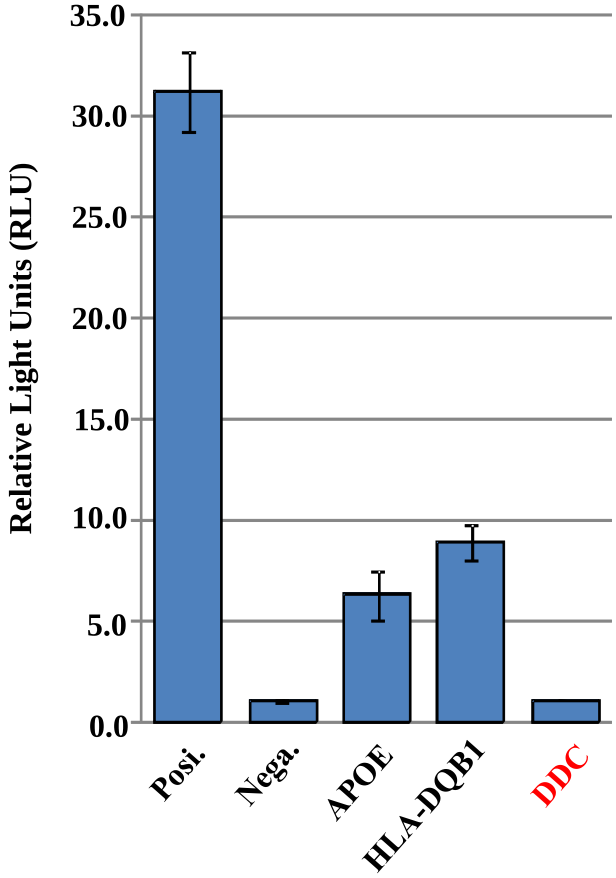
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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 : 2009.11.11

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5769

2nd Nucleotide Sequence
  File Name        : RDB7555F.fasta
  Sequence Size    : 574

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.053% / 565 bp]     INT/OPT.Score : <    337/  2094 >

     1'                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT
                           ** ********** ********** ********** **********
     1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATT

    43' GTCCCCTCCC ACAGACCTCC AATGCTCACG GCTGGGGCCT GNCCTCTCCT CTGTGGTCAT
        ********** ********** ********** ********** * ******** **********
    61″ GTCCCCTCCC ACAGACCTCC AATGCTCACG GCTGGGGCCT G-CCTCTCCT CTGTGGTCAT

   103' GGCTGAACTC ACAGTGTTTG GGGGGATGAG CCNACCTTGC TGCTGGCTTC TGGCTCCCCC
        ********** ********** ********** ** ******* ********** **********
   120″ GGCTGAACTC ACAGTGTTTG GGGGGATGAG CC-ACCTTGC TGCTGGCTTC TGGCTCCCCC

   163' TGGATGGTGA CGCTTGGGCA GCTNCCCATC TTGCCCTCTG TGCAGATGGG GCCTAATCTC
        ********** ********** *** ****** ********** ********** **********
   179″ TGGATGGTGA CGCTTGGGCA GCT-CCCATC TTGCCCTCTG TGCAGATGGG GCCTAATCTC

   223' CTTACTGCCT CCATNTGTCC ACATGGCTGC TGCCTGCAGG TCCCTGCACG GCTGCTGGAG
        ********** **** ***** ** ******* ********** ********** **********
   238″ CTTACTGCCT CCAT-TGTCC ACGTGGCTGC TGCCTGCAGG TCCCTGCACG GCTGCTGGAG
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283’ GGAGCNTGCT TATGCACAGG CTGAGACCAG GATCCCCTCA CTTGTACCAC CTGCCANGGT
     ***** **** ********** ********** ********** ********** ****** ***
297″ GGAGC-TGCT TATGCACAGG CTGAGACCAG GATCCCCTCA CTTGTACCAC CTGCCA-GGT

343’ CCCCGCCCTG CAGCCCCTGC ACTCATGGCA TGTTCTGCTG CCTGGAANGG CCGCTGCCTC
     ********** ********** ********** ********** ******* ** **********
355″ CCCCGCCCTG CAGCCCCTGC ACTCATGGCA TGTTCTGCTG CCTGGAA-GG CCGCTGCCTC

403’ TGTCCCAGTT CCATGGGGAT CTCTGCTCTA GAGGGGTANG CTTCTTCCTT GAAAAGATGC
     ********** ********** ********** ******** * ********** **********
414″ TGTCCCAGTT CCATGGGGAT CTCTGCTCTA GAGGGGTA-G CTTCTTCCTT GAAAAGATGC

463’ TGCTTAAAGT CAGAGGATGG ATGGCTCTCN CTTGGGGCAT TTCTAGCTCT GGACTGTGCC
     ********** ********** *********  ********** ********** **********
473″ TGCTTAAAGT CAGAGGATGG ATGGCTCTC- CTTGGGGCAT TTCTAGCTCT GGACTGTGCC

523’ ACAAGCCCTG GATGTGGTAT NGTGTATGTG TGTGTATGCA TGCACTTAGG TATGTGTGTG
     ********** **********  ********* ********** ***
532″ ACAAGCCCTG GATGTGGTAT -GTGTATGTG TGTGTATGCA TGCC
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1st Nucleotide Sequence
  File Name          : Reference Seq.gnu
  Sequence Size      : 5769

2nd Nucleotide Sequence
  File Name          : RDB7555R.fasta (Complementary)
  Sequence Size      : 758

  Unit Size to Compare = 1
  Pick up Location     = 1
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[96.104% / 770 bp]     INT/OPT.Score : <    392/  2745 >

 841' TCAGGAGANA ACGGAGTCCT GCTCCTTCTA TTGCACCCAT CAACCAGGAG TGGGGGGAGN
                                                      ** ** *********.
    1″                                            AAGAAG TGGGGGGAGG

 901' GGGGTGGAGG TGGGGAAGAT GATCCTCCCT GTTGCTGCCC CATGGTGGGA NGGAGAGACT
      **** ***** *********. *********  ********** ***** ****  *********
  17″ GGGG-GGAGG TGGGGAAGAN GATCCTCCCC GTTGCTGCCC CATGGGGGGA -GGAGAGACT

 961' GAGCCCAAAC CATGTTTTAG ATGCTGATAG GCTTAAGGGT ANACAGCACA GGAGTTTGAG
      *.*****.** ********** **** ***** *********   .******** **********
  75″ GNGCCCANAC CATGTTTTAG ATGCGGATAG GCTTAAGGG- GTACAGCACA GGAGTTTGAG

1021' ATGCATGCGG CTCAACACCT AATCTACATC TCNACTTCAC TTTCTCATCT GGGGAAGTGG
      ********** ********** **** ***** ** ******* ********** **********
 134″ ATGCATGCGG CTCAACACCT AATCAACATC TC-ACTTCAC TTTCTCATCT GGGGAAGTGG

1081' GCTTGGGACC CTGAGCCTCC CGGNGTATCA CAGGGTCCTA ATAGTCCCTC ACAGAAGGAG
      ********** ********** *** ****** *********  ******* ** **********
 193″ GCTTGGGACC CTGAGCCTCC CGG-GTATCA CAGGGTCCTT ATAGTCCTTC ACAGAAGGAG

1141' CAGACCCAGA GTGANGCACT CCCCAAATGC CACGCCGTCC CTTCCTCACC CTTGGAGTGG
      ********** **** ***** ********** ********** ********** **********
 252″ CAGACCCAGA GTGA-GCACT CCCCAAATGC CACGCCGTCC CTTCCTCACC CTTGGAGTGG

1201' AGCCTNGGTC GTTC-TCAAA GTTGCTGGGA GAGTCCCAGG AGCCCTGGCC CCAAATCNTG
      ***** **** **** ***** ********** ********** ********** ******* **
 311″ AGCCT-GGTC GTTCTTCAAA GTTGCTGGGA GAGTCCCAGG AGCCCTGGCC CCAAATC-TG

1260' CATCCTACAC AGTGCCTGGG AACACAGGGC CCA-TTTTTT CCTTGGCCTN CTCGCCAGTC
      ********** ********** ********** *** ****** *********  **********
 369″ CATCCTACAC AGTGCCTGGG AACACAGGGC CCATTTTTTT CCTTGGCCT- CTCGCCAGTC

1319' CCAGCAGGCC CTGATGCTCC TCTCCATCCT GCTAGGATGG NCTCTCTCCC CCTGGGGGCA
      ********** ********** ********** **********  ********* **********
 428″ CCAGCAGGCC CTGATGCTCC TCTCCATCCT GCTAGGATGG -CTCTCTCCC CCTGGGGGCA
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1379' GAGTGGGGGC AGGAGGTGGT GGGAGGGTGG ANGGGATGCT GCTCAGTAAA TAATGCAGAG
      ********** ********** ********** * ******** ********** **********
 487″ GAGTGGGGGC AGGAGGTGGT GGGAGGGTGG A-GGGATGCT GCTCAGTAAA TAATGCAGAG

1439' CCGGCAGCTC TGATTGGCTT CGNGGGAGGC AGACACTCTG TCTACATAAA TGGCAATCAC
      ********** ********** ** ******* ********** ********** **********
 546″ CCGGCAGCTC TGATTGGCTT CG-GGGAGGC AGACACTCTG TCTACATAAA TGGCAATCAC

1499' ATCTTCTGTG CCTNCTTAAC TGTCACTGTG GAGAGGAGAG AGAGAGGACA GAGAGCAAGT
      ********** *** ****** ********** ********** ********** **********
 605″ ATCTTCTGTG CCT-CTTAAC TGTCACTGTG GAGAGGAGAG AGAGAGGACA GAGAGCAAGT

1559' CACTCCCGGC ATCAAGATCT GGCCTCGGCG GCCAAG-CTT GGCAATCCGG TACTGTTGGT
      ********** ********** ********** ****** *** ********** **********
 664″ CACTCCCGGC ATCAAGATCT GGCCTCGGCG GCCAAGTCTT GGCAATCCGG TACTGTTGGT

1618' AAAGCCACCA TGGAAGATG- CCAAAAACAT TAAGAAGGGC CCAGCGCCAT TCTACCCACT
      ********** *********  ********** *****
 724″ AAAGCCACCA TGGAAGATGT CCAAAAACAT TAAGA
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