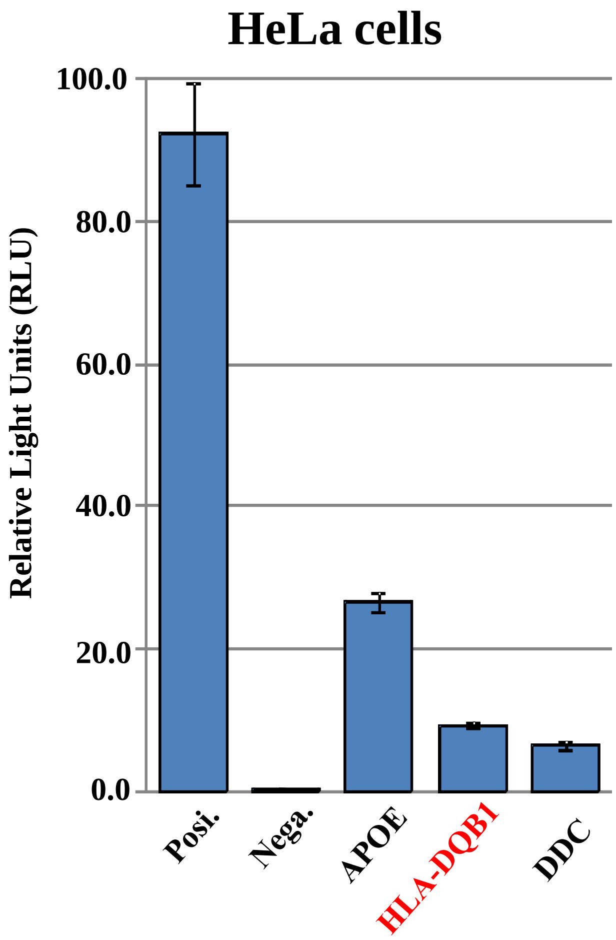
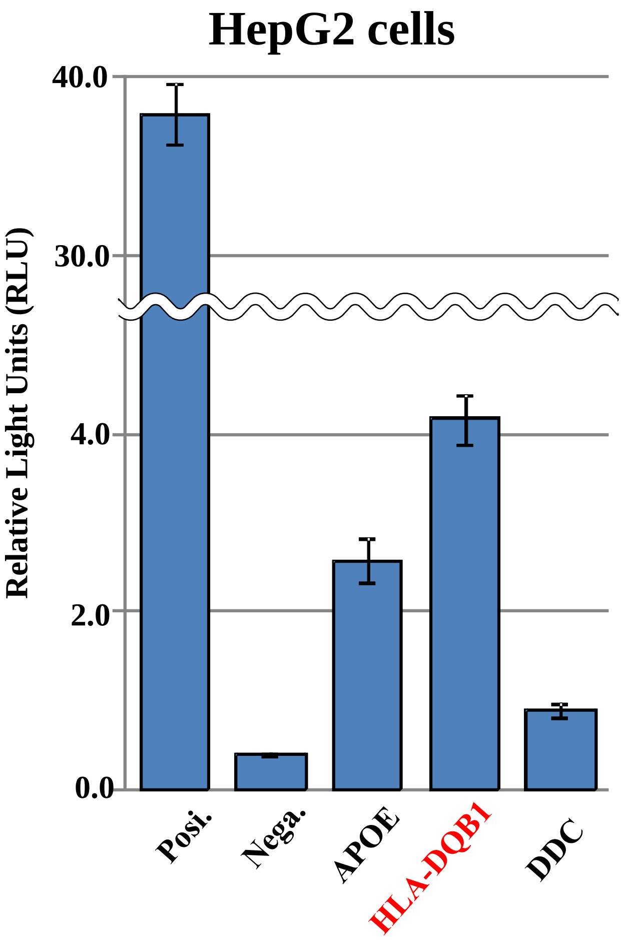
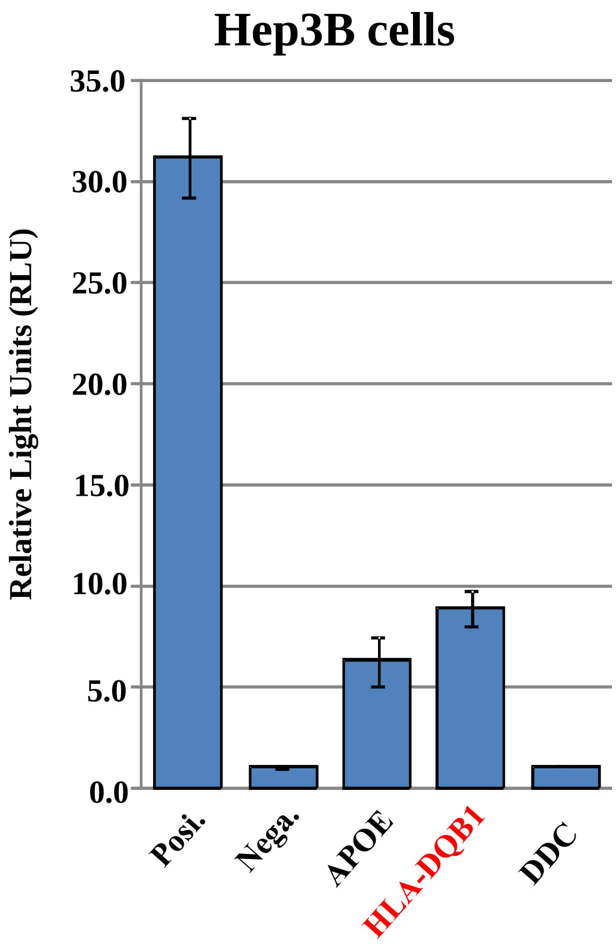
# The Promoter Activities of Reporter Constructs







**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)**

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.12.03

1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5739

2nd Nucleotide Sequence
  File Name        : RDB7557F.fasta
  Sequence Size    : 736

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.003% / 734 bp]     INT/OPT.Score : <    336/  2654 >

      1'                 GGCCT AACTGGCCGG TACCTGAGCT CGCTAGCCTC GAGGATGGCT
                         ***** ********** ********** ********** **********
      1" CAGAACATTG TCTCTGGCCT AACTGGCCGG TACCTGAGCT CGCTAGCCTC GAGGATGGCT

     46' CAACGCTTTC ATGTGCCACT ATTGCAAACC TCTTGCTGTN TGCCTCTTCC CTGCTTCTTT
         ********** ********** ********** *********  ********** **** *****
     61" CAACGCTTTC ATGTGCCACT ATTGCAAACC TCTTGCTGT- TGCCTCTTCC CTGC-TCTTT

    106' TTACCTGGTA AACTTATATT CTGATTTTAG NATTGTA-TT CTCTACTTTA AAAGCAGAAC
         ********** ********** **********  ****** ** ********** **********
    119" TTACCTGGTA AACTTATATT CTGATTTTAG -ATTGTATTT CTCTACTTTA AAAGCAGAAC

    165' CTAAAATTTT GGGAAAAGAA AGNAGAGAAA GGGAGAGAAG AAGAGAGGTG GAGATATTTA
         ********** ********** ** ******* ********** ********** **********
    178" CTAAAATTTT GGGAAAAGAA AG-AGAGAAA GGGAGAGAAG AAGAGAGGTG GAGATATTTA

    225' TTGTCTTGGT TGGNGGTCAG AAGTAATGTT TGCCAGGCAT TGTTCTAATT GCTTTATAAC
         ********** *** ****** ********** ********** ********** **********
    237" TTGTCTTGGT TGG-GGTCAG AAGTAATGTT TGCCAGGCAT TGTTCTAATT GCTTTATAAC
```

```
285' CATTNAGTAC TGTCCCTAGT CACTGCCAAG AGGAGCTTGA TAAGTTATGC TTATTNTATA
     **** ***** ** ******* ********** ********** ********** ***** ****
296″ CATT-AGTAC TGCCCCTAGT CACTGCCAAG AGGAGCTTGA TAAGTTATGC TTATT-TATA

345' AAAACACATT GATGTAGATA TGTCCATGAG GAACTGTTAA ATAAAANAAT ACATAGAATT
     ********** ********** ********** ********** ****** *** **********
354″ AAAACACATT GATGTAGATA TGTCCATGAG GAACTGTTAA ATAAAA-AAT ACATAGAATT

405' GAAAAAAACC ACATTGATAC CTCTGCCACT TGGGATTNTG ATGTTTAGGG CTGGCACAGT
     ********** ********** ******** * ******* ** ********** **********
413″ GAAAAAAACC ACATTGATAC CTCTGCCATT TGGGATT-TG ATGTTTAGGG CTGGCACAGT

465' ACAATCTGTG ACTCTAAACA TTTTCTCCNA TCATTAATAC TATTCAGGAC CTAGGAAATG
     ********** ********** ******** * ********** ********** * ********
472″ ACAATCTGTG ACTCTAAACA TTTTCTCC-A TCATTAATAC TATTCAGGAC CCAGGAAATG

525' CTTCTCCACA GCTTTTGCTN CTCTCTCCTC AAATCTAGAC ATGACTATAT CTGAATACTG
     ********** *********  ********** ********** ******** * **********
531″ CTTCTCCACA GCTTTTGCT- CTCTCTCCTC AAATCTAGAC ATGACTATGT CTGAATACTG

585' TAAAGGTTTG NTGTATTGTG CCTTTGCTGA TATCAGATGC ACCTATTTCA TGGTTCAGAG
     **********  ********* ********** ********** ********** ******** *
590″ TAAAGGTTTG -TGTATTGTG CCTTTGCTGA TATCAGATGC ACCTATTTCA TGGTTCAGGG

645' ANGGATTTAA ACAGCTGAAG AACTTAGAAA AGGAATGTCA ACTTAATTAA CTNTTTCAAA
     * ******** ********** ********** ********** ********** ** *******
649″ A-GGATTTAA ACAGCTGAAG AACTTAGAAA AGGAATGTCA ACTTAATTAA CT-TTTCAAA

705' TACTTTCACT CGAAGAGTAT AAATACAATA TATTCTTGCG TAANTGAAGA ATCATTTACC
     ********** ********** ** *** **
707″ TACTTTCACT CGAAGAGTAT AATTACCATT
```

```
1st Nucleotide Sequence
  File Name        : Reference Seq.GNU
  Sequence Size    : 5739
```

```
2nd Nucleotide Sequence
  File Name        : RDB7557R.fasta (Complementary)
  Sequence Size    : 698

  Unit Size to Compare = 1
  Pick up Location     = 1



[94.225% / 710 bp]     INT/OPT.Score : <    425/  2443 >

 901’ NATCTAGATG TAAAATGCAT GA-AACATGA T-CCACATTT TACAAAGAGA AGCNCTGGGG
                  ********* ** ******* * ******** * ** *****  **. *****
   1″          A AAAAATGCAT GAGAACATGA TGCCACATTT TGCAGAGAGA GGCG-TGGGG

 959’ CAAAAATAAA TTCAGTAATT TGTTGACTCT CATAAAGCAC ATTANGTGGT GGAACTGCAA
      **** **  *  ***** *** ********** * ******** **** ***** ******** *
  51″ CAAAGATGGA GTCAGTGATT TGTTGACTCT CCTAAAGCAC ATTA-GTGGT GGAACTGCGA

1019’ CTCACCATTA TTTCCTTCTA AGAACTTTGC TCTTTNTCAC CAAAACTTAA GGCTCCTCAG
      ********** ********** ***** **** * ***.**** ********** *********
 110″ CTCACCATTA TTTCCTTCTA AGAACCTTGC T-TTTTTCAC CAAAACTTAA GGCTCCTCAA

1079’ GGTGTGTCTA AGACAACAGC AGTAAANAAT GTCTATGACA GCAATTTTCT CTCCCCTGAA
       ********* ********** ******. ** ********** ** ******* **********
 169″ AGTGTGTCTA AGACAACAGC AGTAAAG-AT GTCTATGACA GCGATTTTCT CTCCCCTGAA

1139’ ATATGATCCC CACTTAANTT TGCCCTATTG AAAGAATCCC AAGTATAAGA ACAACTGGTT
      ********** ***** * ** ********** ********** ****** * * **********
 228″ ATATGATCCC CACTTGA-TT TGCCCTATTG AAAGAATCCC AAGTATGAAA ACAACTGGTT

1199’ TTTAATCANA TATTACAAAG ATGTTTACTG TTGAATCGCA TTTTTCTTTG GCTTCTTAAN
      ******** * ********** ********** ********** ***** **** *********
 287″ TTTAATCA-A TATTACAAAG ATGTTTACTG TTGAATCGCA TTTTT-TTTG GCTTCTTAA-

1259’ AATCCCTTAG GCATTCAATC TTCAGCTCTT CCATAATTGA GAGGAAATTT NTCACCTCAA
      ********** ******* ** ********** ********** **********  *********
 344″ AATCCCTTAG GCATTCAGTC TTCAGCTCTT CCATAATTGA GAGGAAATTT -TCACCTCAA
```

```
1319' ATGTTCATCC AGTGCAATTG AAAGACGTCA CAGTGCCAGG CNACTGGATT CAGAACCTTC
      ********** **********  ********* ********** * ********  *********
 403″ ATGTTCATCC AGTGCAATTG GAAGACGTCA CAGTGCCAGG C-ACTGGATT GAGAACCTTC

1379' ACAAAAAAAA AATCTGCCCA GAGACAGCTG AGNGTCCTTC AGCTCCAGTG CTGATTGGTT
      ** ******* ********** ******* ** ** ******* ********** **********
 462″ AC-AAAAAAA AATCTGCCCA GAGACAGATG AG-GTCCTTC AGCTCCAGTG CTGATTGGTT

1439' CCTTTCCAAG GGACCATCCA ATCNCTACCA CGCATGGAAA CATCCACAGA TTTTTATTCT
      ********** ********** *** ****** ********** *********  **********
 520″ CCTTTCCAAG GGACCATCCA ATC-CTACCA CGCATGGAAA CATCCACAGG TTTTTATTCT

1499' TTCTGCCAGG TACANTCAGA TCCATCAGGT CCGAGCTGTG ATCAAGATCT GGCCTCGGCG
      ********** **** ***** ********** ********** ********** **********
 579″ TTCTGCCAGG TACA-TCAGA TCCATCAGGT CCGAGCTGTG ATCAAGATCT GGCCTCGGCG

1559' GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA
      ********** ********** ********** ********** ********** **********
 638″ GCCAAGCTTG GCAATCCGGT ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA

1619' AGAAGGGCCC AGCGCCATTC TACCCACTCG AAGACGGGAC CGCCGGCGAG CAGCTGCACA
      *
 698″ A
```