



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

ABCB1: pGL4-phABCB1 (RDB#7315)

APCS: pGL4-phAPCS (RDB# 7317)

KLK3: pGL4-phKLK3 (RDB# 7324)

MYC: pGL4-phMYC (**RDB#7325**)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5509

2nd Nucleotide Sequence

File Name : RDB7325F.fasta
Sequence Size : 699

Unit Size to Compare = 1
Pick up Location = 1

[98.834% / 686 bp] INT/OPT.Score : < 2344/ 2649 >

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1'          GGC CTAAGTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCA
          *** *****
1" TGCCAGAACA TTTCTCTGGC CTAAGTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCA

44' CAAGGGTCTC TGCTGACTCC CCCGGCTCGG TCCACAAGCT CTCCACTTGC CCCTTTTAGG
          *****
61" CAAGGGTCTC TGCTGACTCC CCCGGCTCGG TCCACAAGCT CTCCACTTGC CCCTTTTAGG

104' AAGTCCGGTC CCGCGGTTTC GGTACCCCT GCCCCTCCA TATTCTCCG TCTAGCACCT
          *****
121" AAGTCCGGTC CCGCGGTTTC GGTACCCCT GCCCCTCCA TATTCTCCG TCTAGCACCT

164' TTGATTTCTC CCAAACCCGG CAGCCCGAGA CTGTTGCAA CCGGCGCCAC AGGGCGCAA
          *****
181" TTGATTTCTC CCAAACCCGG CAGCCCGAGA CTGTTGCAA CCGGCGCCAC AGGGCGCAA

224' GGGGATTTGT CTCTTCTGAA ACCTGGCTGA GAAATTGGGA ACTCCGTGTG GGAGGCGTGG
          *****
241" GGGGATTTGT CTCTTCTGAA ACCTGGCTGA GAAATTGGGA ACTCCGTGTG GGAGGCGTGG
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284' GGGTGGGACG GTGGGGTACA GACTGGCAGA GAGCAGGCAA CCTCCCTCTC GCCCTAGCCC
*****
301" GGGTGGGACG GTGGGGTACA GACTGGCAGA GAGCAGGCAA CCTCCCTCTC GCCCTAGCCC

344' AGCTCTGGAA CAGGCAGACA CATCTCAGGG CTAACAGAC GCCTCCCGCA CGGGGCCCA
*****
361" AGCTCTGGAA CAGGCAGACA CATCTCAGGG CTAACAGAC GCCTCCCGCA CGGGGCCCA

404' CGGAAGCCTG AGCAGCGGG GCAGGAGGG CGGTATCTGC TGCTTTGGCA GCAAATTGGG
*****
421" CGGAAGCCTG AGCAGCGGG GCAGGAGGG CGGTATCTGC TGCTTTGGCA GCAAATTGGG

464' GGACTCAGTC TGGGTGAAG GTATCCAATC CAGATAGCTG TGCATACATA ATGCATAATA
*****
481" GGACTCAGTC TGGGTGAAG GTATCCAATC CAGATAGCTG TGCATACATA ATGCATAATA

524' CATGACTCCC CCCAACAAAT GCAATGGGAG TTTATTCATA ACGCGCTCTC CAAGTATACG
*****
541" CATGACTCCC CCCAACAAAT GCAATGGGAG TTTATTCATA ACGCGCTCTC CAAGTATACG

584' T-GGCAATGC GTTGCTGGGT TATTTAATC ATTCTAGGCA TCGTTTTCTT CCTTATGCCT
* *****
601" TGGGCAATGC GTTGCTGGGT TATTTAATC ATTCTAGGCA TCGTTTTCTT CC-TATGCCT

643' CTATCATTCC TCCCTATCTA CACTAACATC CCACGCTCTG AACGCGGCC CATTAAATACC
***** * * *.***** * ***** ***** *** ***
660" CTATCATT-C T-CCNATCTA CCCTAACAT- CCACGCCCTG AAC

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1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5509

2nd Nucleotide Sequence

File Name : RDB7325R. fasta (Complementary)
Sequence Size : 359



Unit Size to Compare = 1

Pick up Location = 1

[100.000% / 353 bp] INT/OPT. Score : < 1412/ 1412 >

1021' TGCCCGGCTG AGTCTCTCC CCACCTTCCC CACCCTCCCC ACCCTCCCA TAAGCGCCC

* ***** ***** ***** *****

1" NNNTCTC CCACCTTCCC CACCCTCCCC ACCCTCCCA TAAGCGCCC

1081' TCCCGGGTTC CAAAGCAGA GGGCGTGGG GAAAAGAAA AAGATCTCT CTCGTAATC

***** ***** ***** ***** ***** *****

48" TCCCGGGTTC CAAAGCAGA GGGCGTGGG GAAAAGAAA AAGATCTCT CTCGTAATC

1141' TCCGCCACC GGCCTTTAT AATGCGAGG TCTGGACGGC TGAGGACCC CGAGCTGTGC

***** ***** ***** ***** ***** *****

108" TCCGCCACC GGCCTTTAT AATGCGAGG TCTGGACGGC TGAGGACCC CGAGCTGTGC

1201' TGCTCGCGC CGCCACGCC GGGCCCGGC CGTCCCTGGC TCCCCTCTG CCTCGAGAAG

***** ***** ***** ***** ***** *****

168" TGCTCGCGC CGCCACGCC GGGCCCGGC CGTCCCTGGC TCCCCTCTG CCTCGAGAAG

1261' GGCAGGGCTT CTCAGAGGCT TGGCGGAAA AAGAACGGAG GGAGGATAT CAAGATCTGG

***** ***** ***** ***** ***** *****

228" GGCAGGGCTT CTCAGAGGCT TGGCGGAAA AAGAACGGAG GGAGGATAT CAAGATCTGG

1321' CCTCGGCGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA

***** ***** ***** ***** ***** *****

288" CCTCGGCGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA

1381' AAACATTAAG AAGGGCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA

***** **

348" AAACATTAAG AA

