



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

CD55: pGL4-phCD55(RDB# 7539)

LEF1 : pGL4-phLEF1(RDB# 7553)

MET : pGL4-phMET(RDB# 7554)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.11.19

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5723

2nd Nucleotide Sequence

File Name : RDB7554F.fasta
Sequence Size : 651

Unit Size to Compare = 1

Pick up Location = 1

[92.434% / 608 bp] INT/OPT. Score : < 490/ 2035 >

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1' GGCCTAACTG G-CCGGTACC TGAGCTCGCT AGCCTCGAGG ATCCTGCAA ATGGTTCAAT
    **** * ***** ***** ***** ***** ***** *****
1"  ACTG GTCCGGTACC TGAGCTCGCT AGCCTCGAGG ATCCTGCAA ATGGTTCAAT

60' GCAAGACTTT AGTAACGTAA TGGNAACTT TCCTTTTCCA TAAACTGGG GAATCAAGAG
    ***** ***** **** ***** ***** ***** *****
55" GCAAGACTTT AGTAACGTAA TGG-AACTT TCCTTTTCCA TAAACTGGG GAATCAAGAG

120' GTAATCTCTT TTGAGNGACT GAAATCACTC TTATGTAACC TCTGGTTACA TTATCATTTTC
    ***** ***** **** ***** ***** ***** *****
114" GTAATCTCTT TTGAG-GACT GAAATCACTC TTATGTAACC TCTGGTTACA TTATCATTTTC

180' CAAGTGNCT GGCCTTGGG AAATGATAAC TATTCTTACT ACATTTTCT ATGTTTCNAT
    ***** ** ***** ***** ***** ***** ***** **
173" CAAGTG-CCT GGCCTTGGG AAATGATAAC TATTCTTACT ACATTTTCT ATGTTTC-AT

240' TCTGTAGTAA ATAAGAACTG AACCTGCATA GTAAGTGTTA TTTAACCNC ATGACTTTCA
    ***** ***** ***** ***** ***** * *****
231" TCTGTAGTAA ATAAGAACTG AACCTGCATA GTAAGTGTTA TTTAACC-C ATGACTTTCA

300' ATAACGAAGA TATCTATGTC TCATTATCTA TTGCCATGAN TTGAACAAGT TGGTATGAGA
    ***** ***** ***** ***** ***** *****
290" ATAACGAAGA TATCTATGTC TCATTATCTA TTGCCATGA- TTGAACAAGT TGGTATGAGA
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360' GCCGGAACGA ACTCAAGTTC TAACCGGCAA NTGCCCGTTC CTTAGATCCT ATTACCTTTG
*****
349" GCCGGAACGA ACTCAAGTTC TAACCGGCAA -TGCCCGTTC CTTAGATCCT ATTACCTTTG

420' AGTGTTTCATT TACTCTTGTA GNGTGCCAAT TTTTATAGCG AAATACAAAG TTATCCCAAC
*****
408" AGTGTTTCATT TACTCTTGTA AGGTGCCAAT TTTTATAGCG AAATACAAAG TTATCCCACC

480' ACAATTACTC CTNAATAGAG TTCACCGAGG CCCCAAAGC TC-TTTTTTA AAAATCATCA
*****
468" ACAATAACTC CT-AATAGAG TTCACCGAGG CCCCAAAGC TCTTTTTTTT AAAATCATCA

539' TAAGNATTC AACAT-TCAA G-AATTAAG- CTTTTGTTCT GTTGTGCTTA TTCATGCGNT
****. ** * ** * ** * ***** ***** ** * ** **
527" TAAGATTTCA ACCATGCCAA GAAATTAAC CTTTTGGTCC CTGGTTGTTG CCTTAATTCA

596' ATTTGCCAG TTATTAATC AGCCTGCTTC CGGCTATGGA AAAAAAAAAAN AAAGAAAAAA
** *** * ** *
587" ATCCGCCTAT TTTTGCCCC CGTTAAATNT AAAATCAAGC CCCTGCCTTT CCCGGCCTAA

656' AGAAATGGAA GTCTCCTCAG GGTTAAACTC CTCTGTTGTT NCTTCCTTGC AGAAATTTGA

647" TGGGG

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1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5723

2nd Nucleotide Sequence

File Name : RDB7554R. fasta (Complementary)
Sequence Size : 787

Unit Size to Compare = 1
Pick up Location = 1



[86.100% / 741 bp] INT/OPT. Score : < 656/ 2099 >

781' TACCTCCGCC TCTAACANAT GAACTCCTTG TTTCTGCGGT GCCCAAATCT CTCTAAACCC

1" C

841' GGGTGGGCNG CGGGGCGGTT AGCGGAGACG TGGGAGAGGC CGAGAGCAA GCTCGCGCCN

*** * **.

2" CCCNTTNTN ANAAANTNAA NAAGTCCCA AAACCAAAG CCCCCCCCC CCTCTCCCG

901' CTTCCCGGG TCAGCGAGCG GGGTGCCAGG --AGGGTG-C GCGCCCTGCA TCTNG-AG-C

* *

62" TGAATCAAGC CAAACCCGGG GGTCCAGG AAAGGGGGCC CCCCCCCCC CCTCGAAGCC

956' CCGGGGTG-A CACTCGCC-T CCCAAGCGCC AGGAGGGGGA GACTCGGTNC CCGTTATCT

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

122" CCGGGGGGAA CACTCCCCG CCAAGCCCC AGAAGGGGAA AACTCGATCC CC-CCAACT

1014' CCGGCTGTGC TAACTCAGA CTGCCTGAGC TGGGGAGGN AGAGCGCGCA GCCAGGGCGA

** . * **** *

181" CC-NCCGTGC CAACGTCAA CCG-CTGANC CGACGNAGAA AG-CCGCCA GCCAGGGCTA

1074' GAAAA-CTTC TCCACCTAGA AAG--TTTCA CCTNTGTCGT -GGGC-GGGG CAG-AGGC-G

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

238" GAAAAGGGTC TCCACCTAAA AAGATGTGCA CCCTTTTCGT GGGGCGGGG CAGAAGGCGG

1127' GGAGGAAACG CG---ACCCC CGCGGGGCCA GNGCGC-GGC GCGGAC--GG CAGGAAGGGC

**** * . *** ** ***** ***** . ***** ** ***** ***** ***** ***** *****

298" GGAGTANACG CGAACCCCC CGCGGGGCC AGGCGCGGGC GCGGACGGG CAGGAAGGGC

1181' GGGGGCCGAT TTCCCTCTGG GTGGTNGCCA GTCCCCACCT CAGCGGTCT CGGAACCCGC

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

358" GGGGGCCNAT TTCCCTCTGG GGGT-GCCA GTCCCCACCT CAGCGGTCT CGGAACCCGC

1241' -GGACTAGG GACGGACNAG CACGCGAGGC AGACAGACAC GTGCTGGGC GGGCAGGCGA

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

417" GGGACTAGG GACGGAC-AG CACGCGAGGC AGACAGACAC GTGCTGGGC GGGCAGGCGA



1300' GC-GCC-TCA GTCT-GGTGG CCTGGCGGTG CCTCC-GGCC CCAACGCGCC CGGGCCGCCG
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 476" GCGGCCCTCA GTCTGGGTGG CCTGGCGGTG CCTCCGGGCC CCAACGCGCC CGGGCCGCCG

 1356' CGGGCCGCCG GCGCCGATGC CCGGCTGAGT CACTGGCAGG GCAGCGCGCG TGTGGGAAGG
 ***** ***** ***** ***** ***** *****
 536" CGGGCCGCCG GCGCCGATGC CCGGCTGAGT CACTGGCAGG GCAGCGCGCG TGTGGGAAGG

 1416' GCGGGAGGGA GTGCGGCCGG CGGGCGGGC- GGGGCGCTGG GCTCAGCCCG GCCGCAGGTG
 ***** ***** ***** ***** ***** *****
 596" GCGGGAGGGA GTGCGGCCGG CGGGCGGGCG GGGGCGCTGG GCTCAGCCCG GCCGCAGGTG

 1475' ACCCGGAGGC CCTCGCCGCC CGCGGCGCCC CGAGCGCTTT GTGAGCAGAT CAAGATCTGG
 ***** ***** ***** ***** ***** *****
 656" ACCCGGAGGC CCTCGCCGCC CGCGGCGCCC CGAGCGCTTT GTGAGCAGAT CAAGATCTGG

 1535' CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA
 ***** ***** ***** ***** ***** *****
 716" CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA

 1595' AAACATTAAG AAGGGCCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA
 ***** **
 776" AAACATTAAG AA