



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

Jun: pGL4-phJun (RDB#7298)

FOS: pGL4-phFOS(RDB#7292)

CALCA: pGL4-phCALCA (RDB#7291)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.06.25

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5429

2nd Nucleotide Sequence

File Name : RDB7298F.fasta
Sequence Size : 556

Unit Size to Compare = 1
Pick up Location = 1

[97.810% / 548 bp] INT/OPT. Score : < 454/ 2010 >

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1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
          ** *****
1" GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC

43' GGGAGTGCAG AGAT-TTGAA GTCCAGGTTT TACCCCGGNG CTCCGAGTAC TACTGCGTGA
          ***** **** ***** ***** * *****
61" GGGAGTGCAG AGATGTTGAA GTCCAGGTTT TACCCCGG-G CTCCGAGTAC TACTGCGTGA

102' CTTTATGCCA GTGTCCGCCG CTTTCTGGGN CTTGTTTTCC CGGAAGCAAC TCGGCGCGGA
          ***** ***** ***** ***** *****
120" CTTTATGCCA GTGTCCGCCG CTTTCTGGG- CTTGTTTTCC CGGAAGCAAC TCGGCGCGGA

162' TGGAGTGTGT GTGTGCGCGC NGCGCGCGCG TTATGTTGTG CGTGTTGTGT TAAGCGTGTG
          ***** ***** ***** ***** *****
179" TGGAGTGTGT GTGTGCGCGC -GCGCGCGCG TTATGTTGTG CGTGTTGTGT TAAGCGTGTG

222' CGTGTGTGCC GNGGGGCGGG AGGGGGAGTA GACTAACACC GGGGTTCCCC GAGTTTCGGA
          ***** * ***** ***** ***** *****
238" CGTGTGTGCC G-GGGGCGGG AGGGGGAGTA GACTAACACC GGGGTTCCCC GAGTTTCGGA
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282' TCNGCCTACA CGCTTGTTC CATCTGGACC CTGTTACCCA CCAATTGCGC CCANCTATAA
    ** ***** ***** ***** ***** ***** ***** *****
297'' TC-GCCTACA CGCTTGTTC CATCTGGACC CTGTTACCCA CCAATTGCGC CCA-CTATAA

342' AAAGTCCCC TCCGAGCAA AGCTGTGAAC CCGCGGCC TTTCCCCCA CGGTCCCGGA
    ***** ***** ***** ***** ***** ***** *****
355'' AAAGTCCCC TCCGAGCAA AGCTGTGAAC CCGCGGCC TTTCCCCCA CGGTCCCGGA

402' GGATGAAGTG GGGTGCAACG GAGACTCAGC TGAGCNGTCC AGTTTCGGGC AATACAAATC
    ***** ***** ***** ***** ***** ***** *****
414'' GGATGAAGTG GGGTGCAACG GAGACTCAGC TGAGC-GTCC AGTTTCGGGC AATACAAATC

462' TCTCGGCTTC TACGAGCAGC CAGACGNACC CCGCGGACCG TCGCTCCTGA ACTTGACCGA
    ***** ***** ***** ***** ***** ***** *****
473'' TCTCGGCTTC TACGAGCAGC CAGACG-ACC CCGCGGACCG TCGCTCCTGA ACTTGACCGA

522' GATGCAAAC TCGGAGTNGT TCTCAACGTG GGGGGCCGAC TCTCGGAGG CCGCCCCTAA
    ** ***** ***** ** *****
532'' GACGCAAAC TCGGAGT-GT TCTCAA

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5429

2nd Nucleotide Sequence

File Name : RDB7298R.fasta (Complementary)
Sequence Size : 587

Unit Size to Compare = 1

Pick up Location = 1

[97.983% / 595 bp] INT/OPT. Score : < 451/ 2221 >



661' AGTGC GGGGG GGTGGCAGCG TACTTGATT CNTCAGCCTC CAGCCCCGCG CGGTGGCGGC

1" GGGCGGC

721' CGCCGGTGA TGA CTTCGGG CNCCACAAG TGGGAAACA ACAACCACC CTGCGCCGCA
***** ** ***** ***** ***** ***** **
8" CGCCGGTGA TGA CTTCGGG CCCCACAAG TGGGAAACA ACAACCACC TTCGCGGCA

781' CCCCTGGCC AAANACA ACT GGCCAGGTT CCTGGCCTCC CGGGTCCCTG CATCCCCGC
***** ** ***** ***** ***** ***** *****
68" CCCCTGGCC AAA-ACA ACT GGCCAGGTT CCTGGCCTCC CGGGTCCCTG CATCCCCGC

841' ATCNCCGTC CGCAGCCGT AACTTGAGCC CCCCTCCATC AGAGGTTGCG AGCGTNCCGC
**** ***** ***** ***** ***** ***** *****
127" ATCC-CCGTC CGCAGCCGT AACTTGAGCC CCCCTCCATC AGAGGTTGCG AGCGT-CCGC

901' CCGCTCGCG CAGCCACCGT CACTAGACAG TCAAACCCA AGACGTNCAG CCCACAATGC
***** ***** ***** ***** ***** ** *****
185" CCGCTCGCG CAGCCACCGT CACTAGACAG TCAAACCCA AGACGT-CAG CCCACAATGC

961' ACCGGGCGG CCGGAAAAA CGGCCGCGG AGGGGACNCG GGAAGAGAG GCGGAGAGG
***** ***** ***** ***** ** ***** *****
244" ACCGGGCGG CCGGAAAAA CGGCCGCGG AGGGGAC-CG GGAAGAGAG GCGGAGAGG

1021' CGTGCGGCG GGGGAGGGT AGGAGAAANG AAGGGCCCGA CTGTAGGAG GCAGCGGAGC
***** ***** ***** * ***** ***** *****
303" CGTGCGGCG GGGGAGGGT AGGAGAAA-G AAGGGCCCGA CTGTAGGAG GCAGCGGAGC

1081' ATTACCTCAT CCCGTGAGCN CTCCGCGGC CCAGAGAAGA ATCTTCTAGG GTGGAGTCTC
***** ***** ***** ***** ***** *****
362" ATTACCTCAT CCCGTGAGC- CTCCGCGGC CCAGAGAAGA ATCTTCTAGG GTGGAGTCTC

1141' CATGGTGAC NGGCGGGCC GCCCCCTGA GAGCGACGCG AGCCAATGGG AAGCCTTGG
***** ***** ***** ***** ***** *****
421" CATGGTGAC -GGCGGGCC GCCCCCTGA GAGCGACGCG AGCCAATGGG AAGCCTTGG

1201' GNGTGACATC ATGGGCTATT TTAGGGGAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC
* ***** ***** ***** ***** *****
480" G-GTGACATC ATGGGCTATT TTAGGGGAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC

1261' AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA AAACATTAAG AAGGGCCCAG

539" AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA AAACATTAA