



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

NFATC4: pGL4-phNFATC4 (RDB# 7376)

TP73: pGL4-phTP73 (RDB# 7381)

EGFR: pGL4-phEGFR (RDB# 7398)

NFIC: pGL4-phNFIC1 (RDB#7399)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.06.25

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5394

2nd Nucleotide Sequence

File Name : RDB7399F.fasta
Sequence Size : 555

Unit Size to Compare = 1
Pick up Location = 1

[99.629% / 539 bp] INT/OPT. Score : < 2144/ 2144 >

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1'          GGCCT AACTGGCCGG TACCTGAGCT CGCTAGCCTC GAGGATCTGA
          *****
1" CCAGAACATT TCTCTGGCCT AACTGGCCGG TACCTGAGCT CGCTAGCCTC GAGGATCTGA

46' GCTAGCCTGG GAGGATCCAG GGAGTGAACC GGGGGAGGGT TGGGGCCCTG TCATCAGATG
          *****
61" GCTAGCCTGG GAGGATCCAG GGAGTGAACC GGGGGAGGGT TGGGGCCCTG TCATCAGATG

106' CCCTGGGGGC TCAGACGGAG GCAGGCCAGG TCTCTGCCCT GTTACGTCTA GAAGGAGAAC
          *****
121" CCCTGGGGGC TCAGACGGAG GCAGGCCAGG TCTCTGCCCT GTTACGTCTA GAAGGAGAAC

166' AGAATGTGGG CTCCAGGTCC AGATGGCCTG GCTCCAAGCC ACACTTGCCA TACCTCAGTC
          *****
181" AGAATGTGGG CTCCGGGTCC AGATGGCCTG GCTCCAAGCC ACACTTGCCA TACCTCAGTC

226' TTGAGATCTG TGA AAAAGGGC ACACCCCTGA GGCAGGTGGA AATTATTGGA TACCCAGGGG
          *****
241" TTGAGATCTG CGAAAAGGGC ACACCCCTGA GGCAGGTGGA AATTATTGGA TACCCAGGGG
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286' GAGGCTGCAA GGGTTTATCT GGCCAGCTGG AGATCCCGCC TGGACACCGT CCTCCTGGGG
*****
301" GAGGCTGCAA GGGTTTATCT GGCCAGCTGG AGATCCCGCC TGGACACCGT CCTCCTGGGG

346' TGCTGGAGAG ACACACAGGC GAGGCCACCC CTCCCCTGCC CTTGGGTGC TGGGTGAAGA
*****
361" TGCTGGAGAG ACACACAGGC GAGGCCACCC CTCCCCTGCC CTTGGGTGC TGGGTGAAGA

406' GAGCAAATTC TGGAGCCTCC CGTGTTAGCC TGGGCCCTTC TGGCCAAGGA AGGGACAGCT
*****
421" GAGCAAATTC TGGAGCCTCC CGTGTTAGCC TGGGCCCTTC TGGCCAAGGA AGGGACAGCT

466' GCACACAAGC CCCTCTAGCT GGGGACCCGC AGCCCCTGCC TGGCTCTGGG GGGAGAAGGG
*****
481" GCACACAAGC CCCTCTAGCT GGGGACCCGC AGCCCCTGCC TGGCTCTGGG GGGAGAAGGG

526' AGCCAGGGTG CTGTGGGACC AGCTCACCGT GCACCCAGGG TCGTACATCT TTAAGGGGAA
*****
541" AGCCAGGGTG CTGTT

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5394

2nd Nucleotide Sequence

File Name : RDB7399R.fasta (Complementary)
Sequence Size : 654

Unit Size to Compare = 1

Pick up Location = 1

[98.454% / 647 bp] INT/OPT. Score : < 2339/ 2511 >

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601' GGCTCTGCG CACGTCACTT CTCATTCTT TCCCTCCCC CTGGCTCTTT CCTCCAATT

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* * * ***** ***** *** *****
1" TCCTT TCCCTCCCC CTGGCTTTT CCTCCAACT

661' CCCGCCAGC TCGGGGGTG- ATGGGGGGT GGGGAGGGG GGCCTAAAA ATCCACCCT
***** ***** * * ***** ***** ***** ***** *
36" CCCGCCAGC TCGGGGNGA ACGGGGGGT GGGGAGGGG GGCCTAAAA ATCCACCCT

720' GGCCCTCAA TGTCCAGAAA CAACCCTGTC CCCCTCTCC GCTTGATCCG AATTGGGGTC
***** ***** ***** ***** ***** ***** *****
96" GGCCCTCAA TGTCCAGAAA CAACCCTGTC CCCCTCTCC GCTTGATCCG AATTGGGGTC

780' GCCCTGCAGT CCTGGGGTCC TGGTCTAGTG CCCTGGGGCA TTGCGTAAAT ACGGGAGGAG
***** ***** ***** ***** ***** ***** *****
156" GCCCTGCAGT CCTGGGGTCC TGGTCTAGTG CCCTGGGGCA TTGCGTAAAT ACGGGAGGAG

840' CGGGGGGGTC CTGAGACGTC GGGGAGGCT CTCCTTTCTC GCTCGCGCCC TTTTTCCCT
***** ***** ***** ***** ***** ***** *****
216" CGGGGGGGTC CTGAGACGTC GGGGAGGCT CTCCTTTCTC GCTCGCGCCC TTTTTCCCT

900' CGTTTCTTTG AAAGTTGGT GTTGAAGT GGGAGGTCG GGGTGGGAGG GGGAGGGTGT
***** ***** ***** ***** ***** ***** *****
276" CGTTTCTTTG AAAGTTGGT GTTGAAGT GGGAGGTCG GGGTGGGAGG GGGAGGGTGT

960' CAGAGGGTAG AGAGAGAGAC AGAGAGACAG AGACGGGGA GAGAGGAAGA GAGAGACGGA
***** ***** ***** ***** ***** ***** *****
336" CAGAGGGTAG AGAGAGAGAC AGAGAGACAG AGACGGGGA GAGAGGAAGA GAGAGACGGA

1020' GGGAGAGAGG GACAGAGAGC GAGGCGGGCG GCGCGAGAGA GGGAGAGCAG GAGGGAGGAG
***** ***** ***** ***** ***** ***** *****
396" GGGAGAGAGG GACAGAGAGC GAGGCGGGCG GCGCGAGAGA GGGAGAGCAG GAGGGAGGAG

1080' GAGGGAGACC GAGGGAGGAG GCGGCGAGGA GAGCGGCCG GCCGCGGGC GGGGGGGGG
***** ***** ***** ***** ***** ***** *****
456" GAGGGAGACC GAGGGAGGAG GCGGCGAGGA GAGCGGCCG GCCGCGGGC GGGGGGGGGT

1140' GTTGGGGGGG GCGGGGGGT GTTTGAAA AATGACTCAG TAAGTTCAGC GCGCATCAAG
***** ***** ***** ***** ***** ***** *****
516" GTTGGGGGGG GCGGGGGGT GTTTGAAA AATGACTCAG TAAGTTCAGC GCGCATCAAG

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1200' ATCTGGCCTC GCGGCGCAAG CTTGGCAATC CGGTACTGTT GGTAAGCCA CCATGGAAGA

576'' ATCTGGCCTC GCGGCGCAAG CTTGGCAATC CGGTACTGTT GGTAAGCCA CCATGGAAGA

1260' TGCCAAA-AA CATTAAAGAAG GGCCAGCGC CATTCTACCC ACTCGAAGAC GGGACCGCCG
***** ** **

636'' TGCCAAACAA CACGTCAGG