



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

E2F4: pGL4-phE2F4 (RDB# 7714)

IFNGR1: pGL4-phIFNGR1(RDB# 7708)

ATF2: pGL4-phATF2 (RDB# 7712)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.09

1st Nucleotide Sequence

File Name : Reference Seq (inset)
Sequence Size : 1470

2nd Nucleotide Sequence

File Name : RDB7714F.fasta
Sequence Size : 656

Unit Size to Compare : 6

Percent Similarity : 98.8

Percent Identity : 98.8

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1' GGGAGATTAC AGGCGTGAGT CACCGCAACT GGCAGCTGT GTTTATCTTG AGAGTTATAG
*****
59" GGGAGATTAC AGGCGTGAGT CACCGCAACT GGCAGCTGT GTTTATCTTG AGAGTTATAG

61' GGAGCCAGGG AAGGGACTAT AAGGTGGTAA TTATTTAGTG GATGTTGAGT CCACCACCA
*****
119" GGAGCCAGGG AAGGGACTAT AAGGTGGTAA TTATTTAGTG GATGTTGAGT CCACCACCA

121' AATCCACCCT TCAGGACAGA AGTGCTCATT CTCCAGCTGC CAGGAGTGTA GGCTACTGAG
*****
179" AATCCACCCT TCAGGACAGA AGTGCTCATT CTCCAGCTGC CAGGAGTGTA GGCTACTGAG

181' ATCACACCAC TGAGTCTCTC AGTCAATATT GGGGTGCAA AGCATGGTAC CATCGTGTGA
*****
239" ATCACACCAC TGAGTCTCTC AGTCAATATT GGGGTGCAA AGCATGGTAC CATCGTGTGA

241' ACATGAACCC TTCAGAAGTG CTACCCCAAT TTCAGAGATC CTAGTGGGAT AGGCTGAGGC
*****
299" ACATGAACCC TTCAGAAGTG CTACCCCAAT TTCAGAGATC CTAGTGGGAT AGGCTGAGGC
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301' CTATAATATA ATTGCATCTG CTCAATTCTG CTTGTCTTAA TCCCTTAAAG GTGTGGATCC
*****
359" CTATAATATA ATTGCATCTG CTCAATTCTG CTTGTCTTAA TCCCTTAAAG GTGTGGATCC

361' TGACCAGGTG CGGTGGCTCA CACCGGTCAT CCCAGCATTG TGGGAGGCTG AGGTGGGAGG
*****
419" TGACCAGGTG CGGTGGCTCA CACCGGTCAT CCCAGCATTG TGGGAGGCTG AGGTGGGAGG

421' ATCTCTT-GA GCCCA---CG AGTTCAAGAC TAGCCTGGGC AATATAGTGA GACCCACATC
***** ** * ** *****
479" ATCTCTTCGA GCAAAAACCG AGTTCAAGAC TAGCCTGGGC AATATAGTGA GACCCACATC

477' TCTAAAAAAC TAAAAATAAA TGAGCCGGGC ATGGTG-GTG CATGCCTGTG GTCCCAGCTA
*****
539" TCTAACAAAC CTAAAAATAAA TGAGCCGGGC ATGGTGCGTG CATGCCTGTG GTCCCAGCTA

536' CTTGGGAGGC TGAGGTGGGA GAATCGCTTG GGCCAGGAA GCTGAGACGG CATTGATC
*****
599" CTTGGGAGGC TGAGGTGGGA AAATCGCTTG GGCCAGGAA GCTGAGACGG CATTGATT

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1st Nucleotide Sequence

File Name : Reference Seq (inset)
Sequence Size : 1470

2nd Nucleotide Sequence

File Name : RDB7714R.fasta (Complementary)
Sequence Size : 678

Unit Size to Compare : 6

Percent Similarity : 99.7
Percent Identity : 99.7



871' TGAGCACTGT ACTGTGAGGA CAAGACGAGC GAAAGATGAG GCTAGGACCA TGGGTGGAAC
 ***** * ***** * ***** * ***** * ***** * *****

678" GGAGCACTGT ACTGTGAGAA CAAGACGAGC GAAAGATGAG GCTAGGACCA TGGGTGGAAC

931' AAGGTGGACA AGGTAGATAT AGTTAGTGCT TGCTGTTTGG CAGGAAGTGA GGGATAGGAA
 ***** * ***** * ***** * ***** * ***** * *****

618" AAGGTGGACA AGGTAGATAT AGTTAGTGCT TGCTGTTTGG CAGGAAGTGA GGGATAGGAA

991' TAGATGGGGT GACCCCAAGA CAGTAGGGCA GCCTTTAGGA ACAGGTTTGA TGTGGCAGTA
 ***** * ***** * ***** * ***** * ***** * *****

558" TAGATGGGGT GACCCCAAGA CAGTAGGGCA GCCTTTAGGA ACAGGTTTGA TGTGGCAGTA

1051' AAATGAGTTT GAAATATATA AAAGAATAAA TAAAGAGAAA AAAATGGAAA AGGAACAGGT
 ***** * ***** * ***** * ***** * ***** * *****

498" AAATGAGTTT GAAATATATA AAAGAATAAA TAAAGAGAAA AAAATGGAAA AGGAACAGGT

1111' TTGAGGGAGC AGATTGGATT AGTCAGGTAG TGTGGTCTCC TCTCCAAGA TGGGGACTAG
 ***** * ***** * ***** * ***** * ***** * *****

438" TTGAGGGAGC AGATTGGATT AGTCAGGTAG TGTGGTCTCC TCTCCAAGA TGGGGACTAG

1171' GCAGAGTTAG TGATGTTGGG GCAGATTGGC AAGGAAAGTT CCGATGGCGT CCCCTTCTCT
 ***** * ***** * ***** * ***** * ***** * *****

378" GCAGAGTTAG TGATGTTGGG GCAGATTGGC AAGGAAAGTT CCGATGGCGT CCCCTTCTCT

1231' ACTGCCAGGG CGGCCACTG ACGCCCTTCT CATTCTCCC CAACTTCATC CCAACTCCCC
 ***** * ***** * ***** * ***** * ***** * *****

318" ACTGCCAGGG CGGCCACTG ACGCCCTTCT CATTCTCCC CAACTTCATC CCAACTCCCC

1291' GGTCTACCCA GGTAGTTTTC GTCTTATTCG GAGGCTGGAC ATTTGCTACT GGTCCCTGAA
 ***** * ***** * ***** * ***** * ***** * *****

258" GGTCTACCCA GGTAGTTTTC GTCTTATTCG GAGGCTGGAC ATTTGCTACT GGTCCCTGAA

1351' GTTTTGCGGC TGCACCACA GACAGCAATA GCGCCACGTT CCCTGGAAGG CGCACGGGAC
 ***** * ***** * ***** * ***** * ***** * *****

198" GTTTTGCGGC TGCACCACA GACAGCAATA GCGCCACGTT CCCTGGAAGG CGCACGGGAC

1411' GGAAGCGGAA GCAGTAACGC TGGCTCCGGC TGCCCGGCGG CCAGGAACGG AAGCGGAAGT
 ***** * ***** * ***** * ***** * ***** * *****

138" GGAAGCGGAA GCAGTAACGC TGGCTCCGGC TGCCCGGCGG CCAGGAACGG AAGCGGAAGT