



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

ESR1: pGL4-phESR1(RDB# 7528)

HNF4A146: pGL4-phHNF4A 146(RDB# 7534)

TNFRSF11B: pGL4-phTNFRSF11B(RDB# 7533)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.10.29

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5708

2nd Nucleotide Sequence

File Name : RDB7528F.fasta
Sequence Size : 757

Unit Size to Compare = 1
Pick up Location = 1

[94.195% / 758 bp] INT/OPT. Score : < 383/ 2552 >

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1'          GGCCTAA CTGGCCGGTA CCTGAG-CTC GCTAGCCTCG AGGATTTGCT
          ***** ***** ***** *** ***** * *****
1'' CCGAACTTTC TCTGGCCTAA CTGGCCGGTA CCTGAGACTC GCTAGACCTC AGGATTTGCT

47' GGCATAAAG GGAAATATCT GCGATGCACC TAATGTGTTT TTANACCCTT TATTTGCTGA
          ***** ***** ***** ***** *** ***** *****
61'' GGCATAAAG GGAAATATCT GCGATGCACC TAATGTGTTT TTA-ACCCTT TATTTGCTGA

107' CAATCTATAG TCATTAATGC TAAACTCGAT TTTGNGCTTC AGCTACATTT GCATATTGTC
          ***** ***** ***** ***** ***** ***** *****
120'' CAATCTATAG TCATTAATGC TAAACTCGAT TTTG-GCTTC AGCTACATTT GCATATTGTC

167' CAACAATGGT CTATTTTGT AAGAANTTAG ATAAAATGTA TACTTGATAT AAAATAGTCA
          ***** ***** ***** ***** ***** ***** *****
179'' CAACAATGGT CTATTTTGT AAGAA-TTAG ATAAAATGTA TACTTGATAT AAAATAGTCA

227' AAAATGTAAC TCTTAGNTAA CAGTAAGCTT GGCATTTAGA TAGACCATGA ACACTTCGTC
          ***** ***** ***** ***** ***** ***** *****
238'' AAAATGTAAC TCTTAG-TAA CAGTAAGCTT GGCATTTAGA TAGACCATGA ACACTTCGTC
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287' AGATACTNCT GTTGGGTGTT TGGGATAGCA ATTAACAACAA AGTATTGATA GTTGTATCNA
***** ** ***** ***** ***** ***** ***** *
297'' AGATACT-CT GTTGGGTGTT TGGGATAGCA ATTAACAACAA AGTATTGATA GTTGTATC-A

347' GAGTCTATTA GGCTGCAGCA AAGGAAGTTT ATTCAAAGT ATAACTATN CCAAGATTAT
***** ***** ***** ***** ***** *****
355'' GAGTCTATTA GGCTGCAGCA AAGGAAGTTT ATTCAAAGT ATAACTAT- CCAAGATTAT

407' AGACGCATGA TATACTTCAC CTATTTTTTG TCTCCTTAAT -NATGTATAT ATATATATAT
***** ***** ***** ***** . * *****
414'' AGACGCATGA TATACTTCAC CTATTTTTTG TCTCCTTAAT ATGTATATAT ATATATATAT

466' ATATATATAT ATACACATAT ATGTGTGTGT GTNATGTGCG TGTGCATGTT TAACTTTTAA
***** ***** ***** ** ***** ***** *****
474'' ATATATATAT ATACACATAT ATGTGTGTGT GT-ATGTGCG TGTGCATGTN TAACTTTTAA

526' TTCAGTAAA AACTTTTTTC TATNTTGTGTT TTCATCTGGA TATTTGATTC TGCATATCCT
***** ***** ** . ** * ***** *****
533'' TTCAGTAAA AACTTTTTTC TAT-NTGTNT TTCATCTGGA TATTTGATTC TGCATATCCT

586' AGCCCAAGTG AACCNGAGAA GATCGAGTTG TAGGACTAAA GGATAGACAT GCAGAAATGC
***** **** ***** ***** ***** *****
592'' AGCCCAAGTG AACC-GAGAA GATCGAGTTG TAGGACTAAA CGATAGACAT GCAGAAATGC

646' ATTTTNAAAA ATCTGTTAGC TGGACCAGAC CGACAATGTA ACATAATTGC CAAAGCNTTT
***** ** ***** **** ***** ***** ** * **** **
651'' ATTTT--AAA ATCTGTTAGC TGGA-CAGA- CGACAATGT- ACATAA-TGC C-AAGC--TT

706' GGTTTCGTGAC CTGAGTTAT GTTTGGTATG AAAAGGTCAC ATTTTATNAT TCAGTTTTCT
** ***** ***** ** **** ***** ** . ** ** ** *
702'' GGGTCGTGA- CTGAGG-TAT GTTT-GTATG -AAANGTCCA TTTATATCAG TTTCTGAGTT

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5708



2nd Nucleotide Sequence

File Name : RDB7528R.fasta (Complementary)

Sequence Size : 747

Unit Size to Compare = 1

Pick up Location = 1

[96.615% / 768 bp] INT/OPT. Score : < 468/ 2710 >

781' TAACCAACCT GTGGAAGGCA TGANACACCC ATGTGCGCCC TAACCAAAGG TTTTCTGAA

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

1''

GGCCC T-ACC-AAGG GTTTTCT-NA

841' TCATCCTCA CATGNAGAAT TCCTAATGGG ACCAAGTACA GTACTGTGGT CCAACATAAA

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

23'' TCATCC-TCA CATG-AG-AT TCCTAAT-GG ACC-AGTACA GTACTGT-GT CCAACATAAA

901' CACACNAAGT CAGGCTGAGA GAATCTCAGA AGGTTGTGGA AGGGTCTATC TACTTTNGGG

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

77'' CACNC--AGT CAGGCTGAGA GAATCTCAGA AGGTTGTGGA AGGGTCTATC TACTTT-GGG

961' AGCATTTCG AGAGGAAGAA ACTGAGGTCC TGGCAGGTTG CATTCTCNCT GATGGCAAAA

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

134'' AGCATTTCG AGAGGAAGAA ACTGAGGTCC TGGCAGGTTG CATTCTC-CT GATGGCAAAA

1021' TGCAGCTCTT CCTATATGTA TACCCTGAAT CTCCGCCNC CTTCCCCTCA GATGCCCCCT

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

193'' TGCAGCTCTT CCTATATGTA TACCCTGAAT CTCCGCC-C CTTCCCCTCA GATGCCCCCT

1081' GTCAGTCCC CCAGCTGCTA AATATAGCTN GTCTGTGGCT GGCTGCGTAT GCAACCGCAC

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

252'' GTCAGTCCC CCAGCTGCTA AATATAGCT- GTCTGTGGCT GGCTGCGTAT GCAACCGCAC

1141' ACCCATTCT ATCTGCCCTA NTCTCGGTTA CAGTGTAGTC CTCCCAGGG TCATCCTATG

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

311'' ACCCATTCT ATCTGCCCTA -TCTCGGTTA CAGTGTAGTC CTCCCAGGG TCATCCTATG



1201' TACACACTAC GNTATTTCTA GCCAACGAGG AGGGGGAATC AAACAGAAAG AGAGACAAAC
 ***** * ***** ***** ***** ***** *****
 370" TACACACTAC G-TATTTCTA GCCAACGAGG AGGGGGAATC AAACAGAAAG AGAGACAAAC

 1261' AGNAGATATA TCGGAGTCTG GCACGGGGCA CATAAGGCAG CACATTAGAG AAANGCCGGC
 ** ***** * ***** ***** ***** ***** ** *****
 429" AG-AGATATA TTGGAGTCTG GCACGGGGCA CATAAGGCAG CACATTAGAG AAA-GCCGGC

 1321' CCCTGGATCC GTCTTTGCGG TTTATTTTAA GCCCAGTCTT CCCTNGGGCC ACCTTTAGCA
 ***** ***** ***** ***** ***** *****
 487" CCCTGGATCC GTCTTTGCGG TTTATTTTAA GCCCAGTCTT CCCT-GGGCC ACCTTTAGCA

 1381' GATCCTCGTG CGCCCCGCC CCCTGGCCGT GAAACNTCAG CCTCTATCCA GCAGCGACGA
 ***** ***** ***** ***** ** * ***** *****
 546" GATCCTCGTG CGCCCCGCC CCCTGGCCGT GAAAC-TCAG CCTCTATCCA GCAGCGACGA

 1441' CAAGTAAAGT AAAGTTCAGG GAAGCTNGCT CTTTGGGATC GCTCCAAATC GAGTTGTGCC
 ***** ***** ***** ** ***** ***** *****
 605" CAAGTAAAGT AAAGTTCAGG GAAGCT-GCT CTTTGGGATC GCTCCAAATC GAGTTGTGCC

 1501' TGGAGTGATC AAGATCTGGC CTCGGCGGCC AAGCTTGCA ATCCGGTACT GTTGGTAAAG
 ***** ***** ***** ***** ***** *****
 664" TGGAGTGATC AAGATCTGGC CTCGGCGGCC AAGCTTGCA ATCCGGTACT GTTGGTAAAG

 1561' CCACCATGGA AGATGCCAAA AACATTAAGA AGGGCCCAGC GCCATTCTAC CCACTCGAAG
 ***** ***** ****
 724" CCACCATGGA AGATGCCAAA AACA