



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

SSTR2: pGL4-phSSTR2 (RDB# 7378)

TERT: pGL4-phTERT (RDB# 7379)

TNFRSF10B: pGL4-phTNFRSF10B (RDB# 7380)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.06.04

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5583

2nd Nucleotide Sequence

File Name : RDB7379F.fasta
Sequence Size : 400

Unit Size to Compare = 1
Pick up Location = 1

[99.750% / 400 bp] INT/OPT. Score : < 1594/ 1594 >

```
1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TCAAGACGAG GCTAACCTCC
                                     ***** *****
77"                                     CAAGACGAG GCTAACCTCC

61' AGCGAGCGTG ACAGCCCAGG GAGGGTGCGA GGCCTGTTCA AATGCTAGCT CCATAAATAA
    ***** ***** ***** ***** ***** *****
96" AGCGAGCGTG ACAGCCCAGG GAGGGTGCGA GGCCTGTTCA AATGCTAGCT CCATAAATAA

121' AGCAATTTCC TCCGGCAGTT TCTGAAAGTA GGAAAGGTTA CATTAAAGGT TCGTTTTGTT
     ***** ***** ***** ***** ***** *****
156" AGCAATTTCC TCCGGCAGTT TCTGAAAGTA GGAAAGGTTA CATTAAAGGT TCGTTTTGTT

181' AGCATTTCAG TGTTTGCCGA CCTCAGCTAC AGCATCCCTG CAAGGCCTCG GGAGACCCAG
     ***** ***** ***** ***** ***** *****
216" AGCATTTCAG TGTTTGCCGA CCTCAGCTAC AGCATCCCTG CAAGGCCTCG GGAGACCCAG

241' AAGTTTCTCG CCCCTTAGAT CCAAACCTGA GCAACCCGGA GTCTGGATTC CTGGGAAGTC
     ***** ***** ***** ***** ***** *****
276" AAGTTTCTCG CCCCTTAGAT CCAAACCTGA GCAACCCGGA GTCTGGATTC CTGGGAAGTC
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301' CTCAGCTGTC CTGCGGTTGT GCCGGGGCCC CAGGTCTGGA GGGGACCAGT GGCCGTGTGG
*****
336'' CTCAGCTGTC CTGCGGTTGT GCCGGGGCCC CAGGTCTGGA GGGGACCAGT GGCCGTGTGG

361' CTTCTACTGC TGGGCTGGAA GTCGGGCCTC CTAGCTCTGC AGTCCGAGGC TTGGAGCCAG
*****
396'' CTTCTACTGC TGGGCTGGAA GTCGGGCCTC CTAGCTCTGC AGTCCGAGGC TTGGAGCCAG

421' GTGCCTGGAC CCCGAGGTTG CCCTCCACCC TGTGCGGGCG GGATGTGACC AGATGTTGGC
*****
456'' GTGCCTGGAC CCCGAGGCTG C

```

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5583

2nd Nucleotide Sequence

File Name : RDB7379R.fasta (Complementary)
Sequence Size : 160

Unit Size to Compare = 1
Pick up Location = 1

[95.625% / 160 bp] INT/OPT. Score : < 586/ 597 >

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1201' TGCCCTTCA CCTCCAGCT CCGCCTCCTC CGCGCGGACC CCGCCCGTC CCGACCCCTC
          ** **** .***. * ** ***** *.*****
93''          GCGGTCCT- NGCGNGACCC CCGCCCGTC CNGACCCCTC

1261' CCGGGTCCCC GGCCAGCCC CCTCGGGCC CTCCCAGCCC CTCCCCTTCC TTTCCGGGGC
*****
131'' CCGGGTCCCC GGCCAGCCC CCTCGGGCC CTCCCAGCCC CTCCCCTTCC TTTCCGGGGC

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1321' CCGGCCCTCT CCTCGCGGCG CGAGTTTCAG GCAGCGCTGC GTCCTGCTGC GCACGTGGGA

191" CCGGCCCTCT CCTCGCGGCG CGAGTTTCAG GCAGCGCTGC GTCCTGCTGC GCACGTGGGA

1381' AGATCAAGAT CTGGCCTCGG CGGCCAAGCT TGGCAATCCG GTACTGTTGG TAAAGCCACC
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251" AG