

Processed sequence:

```
1      CTTTCGATGGAGTCTCGCTCTGTACACAGGCTGGAGTGCAGTGGTGCGA
51     TCTCAGCTCACCACAACCTCCGCCTCCCAGTTTCAAGCGATTCTCCTGCC
101    TTAGCCTCCCAAGTAGCTGAACTACAGGTGCCACCATGCCCCGGCTAATTA
151    TTGTATTTTTTGGTAGAGATGGGGTTTACCATGCTGTCCAGGCTGGTTTC
201    AAACCTCCTGACCTCTCGATCCTCCCGCCTCCGCCTCCCAAAGTACTGGGA
251    TTATATGCGTGAGTCACTGCGCCTGGCCGGTGATATAATTAATTTTTTTC
301    CTAGCTGAATAGCAATCTCTGCTCACTGCAACCTCTGCCTCACGGGTTTC
351    AAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCAAGC
401    GCCACCATGCCTGGCTAATTTTTTGTATTTTTTTTTTTTTTTAGCAGAGACG
451    GGGTTTCACCATGTTGGTCAGGCTAGACTCGAACTCCTAACCTCGTGATC
501    CACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCAGGAGCCACAGC
551    ACCTGGCTGAACTCTTTCTTTTACATAATTAACTTATTTGCTCCTGGTG
601    GCAGGGACCTCTTGCCCCCTCTTCTCCAACCCCTTTACAATAACTGAAA
651    TACTCTGATGTCCTGCAATATTCTTACTATTTATTTATTTTTTGTAAAAA
701    GCTTTTAATACTACTCAACTGCAGTAGTGAGGGGGGGGGGAAGTAGAGC
751    AAGGAGTATGATCTGTAACCTGATCCTGAACAATCAATTGGGATAACTCAC
801    TGCCTAGATAATTCATATTTAGATGCTGTATTATTAGGGTCAACAGCTA
851    ACTGGAGCAACAGCTAAAGTCAAGATAAGAGAATTGTCATAGGTGCTGGA
901    CTTTTCTCTCCTCAACATCATCACTTCACCTTCCTGAACTCCGCCACAT
951    GTTCTTCTTCTCCTCTTCTCTAACACCTACTGAGAAAATTGAGAAGGCGATT
1001   CTCTTCTGGCCAATAATATTATACTATTTTCAGAGCAAGGTTCTATATGCT
1051   AAACTTTGGAAGGCATTCTTAGATATTCCTCCTCCCTGCGGGCTAGACTT
1101   ACTAGGGGTTAAAAAGAAATCCCTTTTTTACATTGGGTCAAAGTCCCCTG
1151   AGGGTAGGGTGGGAAGGAGGAAGTCATAAATACCCTGGCAACAATAGTGT
1201   TGGTCAAGGTGAGGACCATTTTTTTTTTCTCCTATTTTTTCAGGAACCAA
1251   AAATGGTCAGGACTATTTTTTGACAATTCGGCTTGATGGTTTAGTCTTCTG
1301   AACTCTCCAGTAGACCTTAGAACTTGGTATACATAGTAATTCAGTCCTTG
1351   AATATTAAGGCCTTTAGTTAGAGTAAGATCTGACAAATTCAAAGCTGAG
1401   CCGTGAGTCAGAAATTTTTTCTCAGCACCATAGGAAAAAAATCATAATA
1451   AAAAAATTAAGAGAAGAAATGTGTTGTTTTGTTTTGGGTATTTTTTTGA
1501   GACGGAATTTGCTCTTGTGTTGCCAGGCTGGAGGGCAATGGCGTGATCTT
1551   GGCTCACCGCAACCTCTGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAG
1601   CCTCCTGAGTAGCTGGAATTACAAACACATGCCACCATCCTTGGCTAATT
1651   TTTGTATTTTTTAGTAGAGACAGGATTTTACCATGTTGGTCAGGCTGGTCT
1701   CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGG
1751   ATTACAGGCGTGAGCCACTGCACCTAGCTGCTTGTGTTTTTATAGGTATA
1801   ACAGGCAAAATAAGTGAAGAATATGCTGTATAATTCCATCTGTAATCTTC
1851   AAACCTAGCAGTTTCCGTAGCTGTGGTGTTCATCTTCCCATCATTTGGTAAT
1901   TGGAGAGTAACTCTACCTCCCAGAGGAAGGAGGACTGTTGTAAATTAAAG
1951   GCTCATTTGTTCAAGCCTCATTTGAATTGTCAGTGTAGGGGACCTGAGGCAA
2001   AGAGCATTTGTTGTTTTCAAGAGTTATTCTGTATATCACATTGATGTGCAG
2051   TTCAATATTTAAATGTAAGGAAATGACTCCTACTCTCTATTTGTTTACAA
2101   AACCTAGTTCTCATTTATGCCCATTCCTTCATCAACAAATAATGATTTT
2151   CTACTTTTTGCCTGGTTCTCTCTAGAAGAGTAGTTCTTAAACAATAGCAT
2201   TCAGAAAAATCACCTGGTTTCAATGGTAGGCTGTCATGAAAAAAAAAAAAA
2251   AAATCACAGGGAGAATTTTAAACACAGATTCCTGGTCCCAACCACCAA
2301   GATTCCTATTCAGTGGTGAAGCCCATCAATCAGCATCTCTAACAAGCTTC
2351   CAAGTGGTGCTGAGGATGCTGGTGAATGATCCATTCTACTCTTCTAGGG
2401   CTGTAGATAATAAATTAAACAGGCAAAATAAAAAATAGGCTGGCGCGGTG
2451   GCTTACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGTGGACCAC
2501   CTGAGGTCAGGAGTTCTAGACCAGCCTGGCCAACATGGTGAACCCCGTCT
2551   CTACTAAAAATACAAAAAAATTAGCTAGGCATGGTGGTGTGTGCCTGTAA
2601   TCCCAGCTACTCTGGAGGCTGAGGCAGAAGAATCGCTTGAACCCAGAAGG
2651   CGGAGGTTGCGGTGAGCCGAGATTGCGCCATTACACTGTAGCCTGGGCAA
2701   CAAGAGGGAACCTCCATCTCAAAAAAAAAAAAAAAAAAAATGCCCCTACA
2751   GAGCTTATATTCTAGTGGTAGTAGGGGGATAAATCAGATAGGTAGCTAGC
2801   TAGCTAGCTAGATAAATAGATAGATAGACAGATAGTATATTACCTGTGTC
2851   GCCTGGCCAAAGGGTAGGTTACATTTGGCATGTGTGTCAACTCAAGCTG
```

2901 CACTTGACCTTTTCCTAATCATCTCCAACACTACCTATTGCCCTATCCAAA
 2951 TCCTATCACATTGAATTATTCAAAAAGTCTCCCATCTTCATTTTGGTGGGA
 3001 TTTGGTCAGCTCCTTTACTGCAACCTGTTTTATCAGGAAGGTCCTTTATGA
 3051 CCTGTATTTTGTGCTGACCTCCTATCTCATCCTATGACTTAGAACACCTT
 3101 AACCATCTGGGAATGCAGCCAGTAGGTTTCAGCCTCATTTTACCCAGCT
 3151 CCTATTGAAGATGGAGTCGTTCTGGTTCACACAGCTCTGATAGTAATCTG
 3201 CTCACCTAAGTGTTAGTTGCCGTGTTCTCTCCCAAACTCCCTCCTGTTGC
 3251 ACCCCTGCCTTTGAGTCCTGCTAAACAACAGTATTGGAACCCATCATTTT
 3301 CTCTCATGCCTTTACCCAAACTGTTAGTTTTCTGGTATTCCCTTCTCTCC
 3351 ACATTTTTCCTTCTCAGATCACTGAGGATCGTCCAATCTTCCCTGCCCAT
 3401 CCCTCCCTACCCCAACCTCCATTATTTGTACTCTCTTAGCATCCAGTGC
 3451 ACTTTTTTTCCTTACTTATTACACAACCTTTACACTTACAATTAACATTAT
 3501 AATTGTCCTTTTTGGTCTATTTGATCTACTCTACTAAATCTTTTTTTTTTT
 3551 TTTTTTGAGACAAGGTCTCACTGTGCCTCCTCGGCTGGAGTGCAGTGGCG
 3601 TGATCTCGGCTCGCTGCAACCTCCGCCTCTGGAGTTCAAGTGATTCTCCT
 3651 GTCTCAGCCTCCCTAGTAGATGGGATTACAGGCGTGCACCACCACGCCCA
 3701 GCCCAGTTAATTTTTGTATTTTTTAGTACAGACAGGGTTTCACCATGTTGG
 3751 TCAGGCTGGTCTTGAACCTCTGATCTCAGATGATGCACCTGGCTCGGCCT
 3801 CGCAAAGTGCTGGGATTACAGGTGTGAGCCACCGTGCCCAGCCGTTAGCT
 3851 CATTTTAACACATCCTTAGTCCAGCCTGTTCCAAAAAATCTAAAGTCAGA
 3901 TAGCTTCCTAAACCTCAACTTTATTCCAATTGCTTTCCTTGGCGAAGAAT
 3951 GTAGTAAGTCGGCCTTCCAGCCACCAGCCCCTTCCCTTTGGTCTTTCACT
 4001 CCGGAGGCTCTTACCCTAGACACAATGGGACAGGGAGCGGGGGATGGGGG
 4051 AATTCAGCTCAGGCTTTTATGCAAAGACCCCCTTCTGCAAAGAACAAGC
 4101 TTCTGGTACCTGCCCTTTGGAGAGCTGCGGGCAAGCTCAGCCTCGGTGAG
 4151 TCTTGGTGGCCTTGACAGCCCCACTTAACAAACTGTGCTGATTAAAGAGA
 4201 GACAGGAGGGCAAGTTTTTCCCTTCTTTTAAAGAAATCATCCTATTTCTC
 4251 ACGAGACATAGACTATCTGCCTGAAGCATGATGTACTAGCCCCACTCACC
 4301 GGCTCCCTGATGCCCTTATGCTTAATCTTCTCCGGAATGGTAGTCTGAGA
 4351 AGAAAAAAGATTACGCCCAATTTCAATTTCTTGTTCACATCAAGCAATA
 4401 CTTTTCGAGTCTTTGCATTGTGAACAAAAGTCAGCTTGTGTGGGAGCAAA
 4451 GCCAGCTGCTCTGGGTGCAGACCCAGGAGCAGAGTGCAGAGGAGAATGAG
 4501 TCAAAGAGTTTTGTCTTCAAAAAATTACATAATCGGGATTTGCTAAGAGTT
 4551 TACTTTTCGGTATGGAAGACTGGAAGAGAGAAAGAAATCTTAGGTTTCTT
 4601 GAATGTTGGGTTTGGGAATAGGAAGGAAATCGAAAACCTGTAGACTTTGT
 4651 CCATAAATGTTAGTGCTGGAACCCCACTCTAAAAACTTTGTTCCTTTGGA
 4701 AAACACCTCCCTTCCCCCAGAAACACACACACCCACACGAGATGGGCACG
 4751 GAGTAGTCTTGAAAGACATGACAAATCACCAGACCTGGGAAGAAGCTAAA
 4801 GAGCCAGAGGGAAAAAGCCAGAAGTCGACTACCTGGGAGGAGGGATAGAC
 4851 AAGAAACCAAACTAAAGGAACTAAGGTAGGTGCTGAAAAAAGTACCAT
 4901 TTTCAACATTAACTGATGCCTTGGCTTCATGCTATAATGCCATGTTGTGT
 4951 TTCACTATAACCTCAGAGTGAATGAAAGAGGAAAAATGGAGCTAGTTGAAA
 5001 TTTCTGCCTAAACTAGCCAGATTTTGAGACACTAAGTTATCTCAAATCAA
 5051 GAAATCACCCCTAATGAGAATTTCAATAACCTCAGGAATTTAAGGTGCATG
 5101 CATCCCCCACCCCCCTTTTTTTTTTTGAGACGTAGTCCCGCTCTGTTGC
 5151 CCAGGCTGGAGTACAGTGGCGCGATATCGGCTCACCACAACCTCTGCCTC
 5201 CCAGGTTCAAGGGATTCTCCCGCTCAGCTTCCAGAGTAGCTGGGACTAC
 5251 AGACACCCACCACCATGCGTGGCTAATTTTTGTATTTTAGTAGAGAGGG
 5301 GGTTTCGCCATGTTGGCCAGGCTGGTTTCAAACCTCCTGACTTCAGGTGAT
 5351 CCGCTGCCACGGCCTCCCAATTTACTGGGATTACAGGGGTGGGCCACCG
 5401 CGCCCGCCTTTTTCTTAATTTTTTAAAAATATTAAAGTTTTATCCCATT
 5451 CTGTTGAACCATATTCTGATTTTAAAGTTTGAAACGTGGTGAACCTAGA
 5501 AGTATTTGTTGCTGGGTTTGTCTTCAGGTTCTGTTGCTCGGTTTCTAGT
 5551 TCCCCACCTAGTCTGGGTTACTCTGCAGCTACTTTTGCATTACAATGGCC
 5601 TTGGTGAGACTGGTAGACGGGATTAACCTGAGAATTCAAGGGTGGGTCA
 5651 GTAGGGGTGTGCCCGCCAGGAGGGGTGGGTCTAAGGTGATAGAGCCTTC
 5701 ATTATAAATCTAGAGACTCCAGGATTTTAAAGTTCTGCTGGACTGAGCTG
 5751 GTTGCTCATGTTATTATGCAGGCAACTCACTTTATCCCAATTTCTTGAT
 5801 ACTTTTCTTCTGGAGGTCTTATTTCTCTAACATCTTCCAGAAAAGTCTT
 5851 AAAGCTGCCTTAACCTTTTTTCCAGTCCACCTCTTAAATTTTTTCTCCT
 5901 CTCTCTTATACTAACATGAGTGTGGATCCAGCTTGTCCCCAAAGCTTGC

5951 CTTGCTTTGAAGCATCCGACTGTAAAGAATCTTCACCTATGCCTGTGATT
 6001 T

Proscan: Version 1.7

Processed Sequence: 6001 Base Pairs

Promoter region predicted on forward strand in 947 to 1197

Promoter Score: 56.27 (Promoter Cutoff = 53.000000)

TATA found at 1174, Est.TSS = 1204

Significant Signals:

Name	TFD #	Strand	Location	Weight
Sp1	S00064	-	947	5.934000
Sp1	S01542	-	947	3.608000
junB-US2	S01738	+	1008	2.717000
JCV_repeated_sequenc	S01193	-	1086	1.658000
PuF	S02016	+	1157	1.082000
JCV_repeated_sequenc	S01193	+	1157	1.427000

Promoter region predicted on forward strand in 5474 to 5724

Promoter Score: 54.96 (Promoter Cutoff = 53.000000)

TATA found at 5702, Est.TSS = 5732

Significant Signals:

Name	TFD #	Strand	Location	Weight
SIF	S02021	-	5621	1.161000
PuF	S02016	+	5641	1.082000
Sp1	S00801	+	5663	2.755000
Sp1	S00781	-	5668	2.772000
SDR_RS	S01561	+	5671	1.554000
AP-2	S01936	-	5680	1.091000
TFIID	S00087	+	5703	2.618000
TFIID	S01540	+	5703	1.971000

Promoter region predicted on reverse strand in 1186 to 936

Promoter Score: 57.47 (Promoter Cutoff = 53.000000)

Significant Signals:

Name	Strand	Location	Weight
JCV_repeated_sequenc	+	1157	1.658000
PuF	+	1157	1.391000
JCV_repeated_sequenc	-	1086	1.427000
junB-US2	+	1008	1.510000
Sp1	-	947	6.661000
Sp1	-	947	10.681000
Sp1	-	947	17.211000
JCV_repeated_sequenc	-	946	1.427000
Sp1	-	946	7.086000
Sp1	-	946	3.013000
Sp1	+	941	3.061000
EARLY-SEQ1	+	939	5.795000
