Processed sequence:

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1       CTTTCGATGGAGTCTCGCTCTGTCACACAGGCTGGAGTGCAGTGGTGCGA
51      TCTCAGCTCACCACAACCTCCGCCTCCCAGTTTCAAGCGATTCTCCTGCC
101     TTAGCCTCCCAAGTAGCTGAACTACAGGTGCCACCATGCCCGGCTAATTA
151     TTGTATTTTTGGTAGAGATGGGGTTTCACCATGCTGTCCAGGCTGGTTTC
201     AAACTCCTGACCTCTCGATCCTCCCGCCTCCGCCTCCCAAAGTACTGGGA
251     TTATATGCGTGAGTCACTGCGCCTGGCCGGTGATATAATTAATTTTTTTC
301     CTAGCTGAATAGCAATCTCTGCTCACTGCAACCTCTGCCTCACGGGTTTC
351     AAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCAAGC
401     GCCACCATGCCTGGCTAATTTTTGTATTTTTTTTTTTTTTTAGCAGAGACG
451     GGGTTTCACCATGTTGGTCAGGCTAGACTCGAACTCCTAACCTCGTGATC
501     CACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCAGGAGCCACAGC
551     ACCTGGCTGAACTCTTTCTTTTACATAATTAAACTTATTTGCTCCTGGTG
601     GCAGGGACCTCTTGCCCCCTCTTCCTCCAACCCCTTTACAATAACTGAAA
651     TACTCTGATGTCCTGCAATATTCTTACTATTTATTTATTTTTTGTAAAAA
701     GCTTTTAATACTACTCAACTGCAGTAGTGAGGGGGGGGGGAAGTAGAGC
751     AAGGAGTATGATCTGTAACTGATCCTGAACAATCAATTGGGATAACTCAC
801     TGCCTAGATAATTCACTATTTAGATGCTGTATTATTAGGGTCAACAGCTA
851     ACTGGAGCAACAGCTAAAGTCAAGATAAGAGAATTGTCATAGGTGCTGGA
901     CTTTTCTCTCCTCAACATCATCACTTCACCTTCCTGAACTCCGCCCACAT
951     GTTCTTCTTCCTCCTTCTCTAACACCTACTGAGAAATTGAGAAGGCGATT
1001    CTCTTCTGGCCAATAATATTATACTATTTCAGAGCAAGGTTCTATATGCT
1051    AAACTTTGGAAGGCATTCTTAGATATTCCTCCTCCCTGCGGGCTAGACTT
1101    ACTAGGGGTTAAAAAGAAATCCCTTTTTACATTGGGTCAAAGGTCCCCTG
1151    AGGGTAGGGTGGGAAGGAGGAAGTCATAAATACCCTGGCAACAATAGTGT
1201    TGGTCAAGGTCAGGACCATTTTTTTTTCCTCCTATTTTTCAGGAACCAAA
1251    AAATGGTCAGGACTATTTTTGACAATTCGGCTTGATGGTTTAGTCTTCTG
1301    AACTCTCCAGTAGACCTTAGAACTTGGTATACATAGTAATTCAGTCCTTG
1351    AATATTAAAAGCCTTTAGTTAGAGTAAGATCTGACAAATTCAAAGCTGAG
1401    CCGTGAGTCAGAAATTTTTTTCTCAGCACCATAGGAAAAAAATCATAATA
1451    AAAAAATTAAGAGAAGAAATGTGTTGTTTTGTTTTGGGTTATTTTTTTGA
1501    GACGGAATTTCGCTCTTGTTGCCCAGGCTGGAGGGCAATGGCGTGATCTT
1551    GGCTCACCGCAACCTCTGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAG
1601    CCTCCTGAGTAGCTGGAATTACAAACACATGCCACCATCCTTGGCTAATT
1651    TTTGTATTTTTAGTAGAGACAGGATTTTACCATGTTGGTCAGGCTGGTCT
1701    CGAACTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGG
1751    ATTACAGGCGTGAGCCACTGCACCTAGCTGCTTGTGTTTTTATAGGTATA
1801    ACAGGCAAAATAAGTGAAGAATATGCTGTATAATTCCATCTGTAATCTTC
1851    AAACTAGCAGTTTCCGTAGCTGTGGTGTTCATCTTCCCATCATTGGTAAT
1901    TGGAGAGTAACTCTACCTCCCAGAGGAAGGAGGACTGTTGTAAATTAAAG
1951    GCTCATTGTTCAAGCCTCATTGAATTGTCAGTGTAGGGGACCTGAGGCAA
2001    AGAGCATTGTTGTTTTCAAGAGTTATTCTGTATATCACATTGATGTGCAG
2051    TTCAATATTTAAATGTAAGGAAATGACTCCTACTCTCTATTTGTTTACAA
2101    AACCCTAGTTCTCATTTATGCCCATTCCTTCATCAACAAATAATGATTTT
2151    CTACTTTTTGCCTGGTTCTCTCTAGAAGAGTAGTTCTTAAACAATAGCAT
2201    TCAGAAAAATCACCTGGTTTCAATGGTAGGCTGTCATGAAAAAAAAAAAA
2251    AAATCACAGGGAGAATTTTAAAACACAGATTCCTGGTCCCAACCACCAAA
2301    GATTCCTATTCAGTGGTGAAGCCCATCAATCAGCATCTCTAACAAGCTTC
2351    CAAGTGGTGCTGAGGATGCTGGTGAATGATCCATTCATACTCTTCTAGGG
2401    CTGTAGATAATAAATTAAACAGGCAAAAATAAAAATAGGCTGGCGCGGTG
2451    GCTTACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGTGGACCAC
2501    CTGAGGTCAGGAGTTCTAGACCAGCCTGGCCAACATGGTGAACCCCGTCT
2551    CTACTAAAAATACAAAAAAATTAGCTAGGCATGGTGGTGTGTGCCTGTAA
2601    TCCCAGCTACTCTGGAGGCTGAGGCAGAAGAATCGCTTGAACCCAGAAGG
2651    CGGAGGTTGCGGTGAGCCGAGATTGCGCCATTACACTGTAGCCTGGGCAA
2701    CAAGAGGGAAACTCCATCTCAAAAAAAAAAAAAAAAAAATTGCCCTCACA
2751    GAGCTTATATTCTAGTGGTAGTAGGGGGATAAATCAGATAGGTAGCTAGC
2801    TAGCTAGCTAGATAAATAGATAGATAGACAGATAGTATATTACCTGTGTC
2851    GCCTGGCCAAAGGGTAGGTTCACATTTGGCATGTGTGTCAACTCAAGCTG
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2901 CACTTGACCTTTCCTAATCATCTCCAACACTACCTATTGCCCTATCCAAA
2951 TCCTATCACTTGAATTATTCAAAAAGTCTCCCATCTTCATTTTGGTGGGA
3001 TTTGGTCAGCTCCTTTACTGCAACCTGTTTTATCAGGAAGGTCTTTATGA
3051 CCTGTATTTTGTGCTGACCTCCTATCTCATCCTATGACTTAGAACACCTT
3101 AACCATCTGGGAATGCAGCCCAGTAGGTTTCAGCCTCATTTTACCCAGCT
3151 CCTATTGAAGATGGAGTCGTTCTGGTTCACACAGCTCTGATAGTAATCTG
3201 CTCACTAAGTGTTAGTTGCCGTGTTCTCTCCCACAACTCCCTCCTGTTGC
3251 ACCCCTGCCTTTGAGTCCTGCTAAACAACAGTATTGGAACCCATCATTTT
3301 CTCTCATGCCTTTACCCAAACTGTTAGTTTTCTGGTATTCCCTTCTCTCC
3351 ACATTTTTCCTTCTCAGATCACTGAGGATCGTCCAATCTTCCCTGCCCAT
3401 CCCTCCCCTACCCCAACCTCCATTATTTGTACTCTCTTAGCATCCAGTGC
3451 ACTTTTTTTCCTTACTTATTACACAACTTTACACTTACAATTAACATTAT
3501 AATTGTCTTTTTGGTCTATTTGATCTACTCTACTAAATCTTTTTTTTTTT
3551 TTTTTTGAGACAAGGTCTCACTGTGCCTCCTCGGCTGGAGTGCAGTGGCG
3601 TGATCTCGGCTCGCTGCAACCTCCGCCTCTGGAGTTCAAGTGATTCTCCT
3651 GTCTCAGCCTCCCTAGTAGATGGGATTACAGGCGTGCACCACCACGCCCA
3701 GCCCAGTTAATTTTTGTATTTTTAGTACAGACAGGGTTTCACCATGTTGG
3751 TCAGGCTGGTCTTGAACTCCTGATCTCAGATGATGCACCTGGCTCGGCCT
3801 CGCAAAGTGCTGGGATTACAGGTGTGAGCCACCGTGCCCAGCCGTTAGCT
3851 CATTTTAACACATCCTTAGTCCAGCCTGTTCCAAAAAATCTAAAGTCAGA
3901 TAGCTTCCTAAACCTCAACTTTATTCCAATTGCTTTCCTTGGCGAAGAAT
3951 GTAGTAAGTCGGCCTTCCAGCCACCAGCCCCTTCCCTTTGGTCTTTCACT
4001 CCGGAGGCTCTTACCCTAGACACAATGGGACAGGGAGCGGGGGATGGGGG
4051 AATTCAGCTCAGGCTTTTATGCAAAGACCCCCTTCTGCAAAGAACAAAGC
4101 TTCTGGTACCTGCCCTTTGGAGAGCTGCGGGCAAGCTCAGCCTCGGTGAG
4151 TCTTGGTGGCCTTGACAGCCCCCACTTAACAAACTGTGCTGATTAAGAGA
4201 GACAGGAGGGCAAGTTTTTCCCTTCTTTTAAAGAAATCATCCTATTTCCT
4251 ACGAGACATAGACTATCTGCCTGAAGCATGATGTACTAGCCCCACTCACC
4301 GGCTCCCTGATGCCCCTATGCTTAATCTTCTCCGGAATGGTAGTCTGAGA
4351 AGAAAAAAGATTACGCCCAATTTCATTTCCTTGTTTCACATCAAGCAATA
4401 CTTTTCGAGTCTTTGCATTGTGAACAAAAGTCAGCTTGTGTGGGAGCAAA
4451 GCCAGCTGCTCTGGGTGCAGACCCAGGAGCAGAGTGCAGAGGAGAATGAG
4501 TCAAAGAGTTTTGTCTTCAAAAATTACATAATCGGGATTTGCTAAGAGTT
4551 TACTTTTCGGTATGGAAGACTGGAAAAGAGAAAGAAATCTTAGGTTTCTT
4601 GAATGTTGGGTTTGGGAATAGGAAGGAAAATCGAAAACTGTAGACTTTGT
4651 CCATAAATGTTAGTGCTGGAACCCCACTCTAAAAACTTTGTTCCTTTGGA
4701 AAACACCTCCCTTCCCCCAGAAACACACACACCCACACGAGATGGGCACG
4751 GAGTAGTCTTGAAAGACATGACAAATCACCAGACCTGGGAAGAAGCTAAA
4801 GAGCCAGAGGGAAAAAGCCAGAAGTCGACTACCTGGGAGGAGGGATAGAC
4851 AAGAAACCAAACTAAAGGAAACTAAGGTAGGTGCTGAAAACAAGTACCAT
4901 TTTCAACATTAACTGATGCCTTGGCTTCATGCTATAATGCCATGTTGTGT
4951 TTCACTATAACCTCAGAGTGAATGAAAGAGGAAAATGGAGCTAGTTGAAA
5001 TTTCTGCCTAAACTAGCCAGATTTTGAGACACTAAGTTATCTCAAATCAA
5051 GAAATCACCCTAATGAGAATTTCAATAACCTCAGGAATTTAAGGTGCATG
5101 CATCCCCCACCCCCCCCTTTTTTTTTTGAGACGTAGTCCCGCTCTGTTGC
5151 CCAGGCTGGAGTACAGTGGCGCGATATCGGCTCACCACAACCTCTGCCTC
5201 CCAGGTTCAAGGGATTCTCCCGCCTCAGCTTCCAGAGTAGCTGGGACTAC
5251 AGACACCCACCACCATGCGTGGCTAATTTTTGTATTTTTAGTAGAGAGGG
5301 GGTTTCGCCATGTTGGCCAGGCTGGTTTCAAACTCCTGACTTCAGGTGAT
5351 CCGCCTGCCACGGCCTCCCAATTTACTGGGATTACAGGGGTGGGCCACCG
5401 CGCCCGGCCTTTTTCTTAATTTTTAAAAATATTAAAGTTTTATCCCATTC
5451 CTGTTGAACCATATTCCTGATTTAAAAGTTGGAAACGTGGTGAACCTAGA
5501 AGTATTTGTTGCTGGGTTTGTCTTCAGGTTCTGTTGCTCGGTTTTCTAGT
5551 TCCCCACCTAGTCTGGGTTACTCTGCAGCTACTTTTGCATTACAATGGCC
5601 TTGGTGAGACTGGTAGACGGGATTAACTGAGAATTCACAAGGGTGGGTCA
5651 GTAGGGGGTGTGCCCGCCAGGAGGGGTGGGTCTAAGGTGATAGAGCCTTC
5701 ATTATAAATCTAGAGACTCCAGGATTTTAACGTTCTGCTGGACTGAGCTG
5751 GTTGCCTCATGTTATTATGCAGGCAACTCACTTTATCCCAATTTCTTGAT
5801 ACTTTTCCTTCTGGAGGTCCTATTTCTCTAACATCTTCCAGAAAAGTCTT
5851 AAAGCTGCCTTAACCTTTTTTCCAGTCCACCTCTTAAATTTTTTCCTCCT
5901 CTTCCTCTATACTAACATGAGTGTGGATCCAGCTTGTCCCCAAAGCTTGC

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5951   CTTGCTTTGAAGCATCCGACTGTAAAGAATCTTCACCTATGCCTGTGATT
6001   T
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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