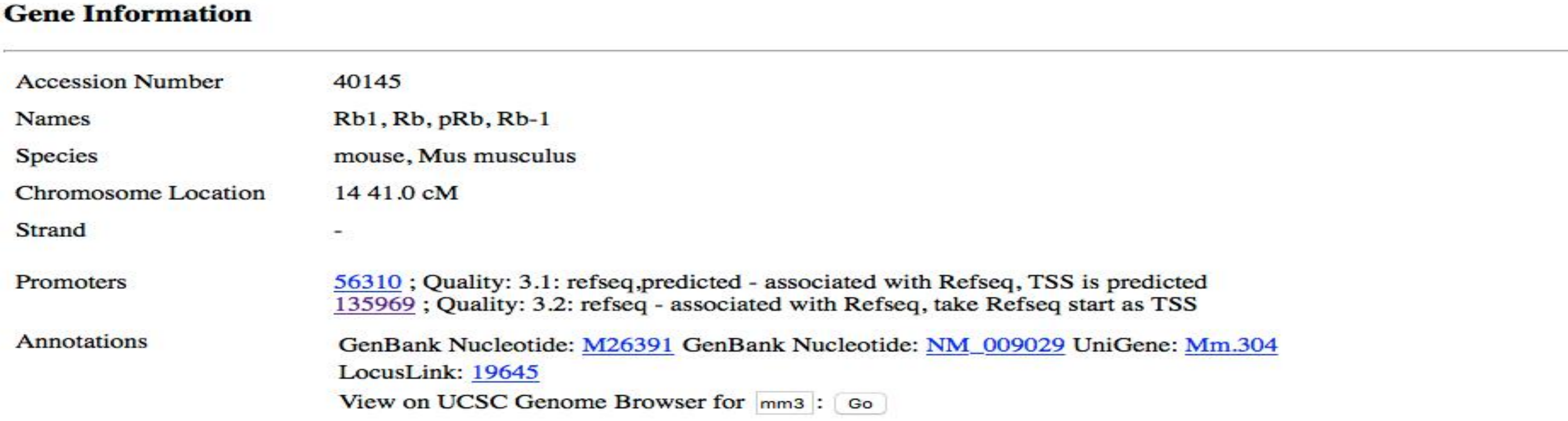
Human and mouse RB1 promoters found in Transcriptional Regulatory Element Database

(https://cb.utdallas.edu/cgi-bin/TRED/tred.cgi?process=searchPromForm)

Gene Information

Accession Number	7507
Names	RB1, RB
Species	human, Homo sapiens
Chromosome Location	13q14.2
Strand	+
Promoters	10832 ; Quality: 2: known - stated explicitly in GenBank records 10833 ; Quality: 2: known - stated explicitly in GenBank records 10834 ; Quality: 2: known - stated explicitly in GenBank records
Annotations	GenBank Nucleotide: BC039060 GenBank Nucleotide: BC040540 GenBank Nucleotide: L41870 GenBank Nucleotide: M15400 GenBank Nucleotide: M19701 GenBank Nucleotide: M28419 GenBank Nucleotide: M33647 GenBank Nucleotide: NM_000321 GeneCards: GC13P046675 GeneCards: GC13P046877 UniGene: Hs.408528 LocusLink: 5925 View on UCSC Genome Browser for hg15 : Go

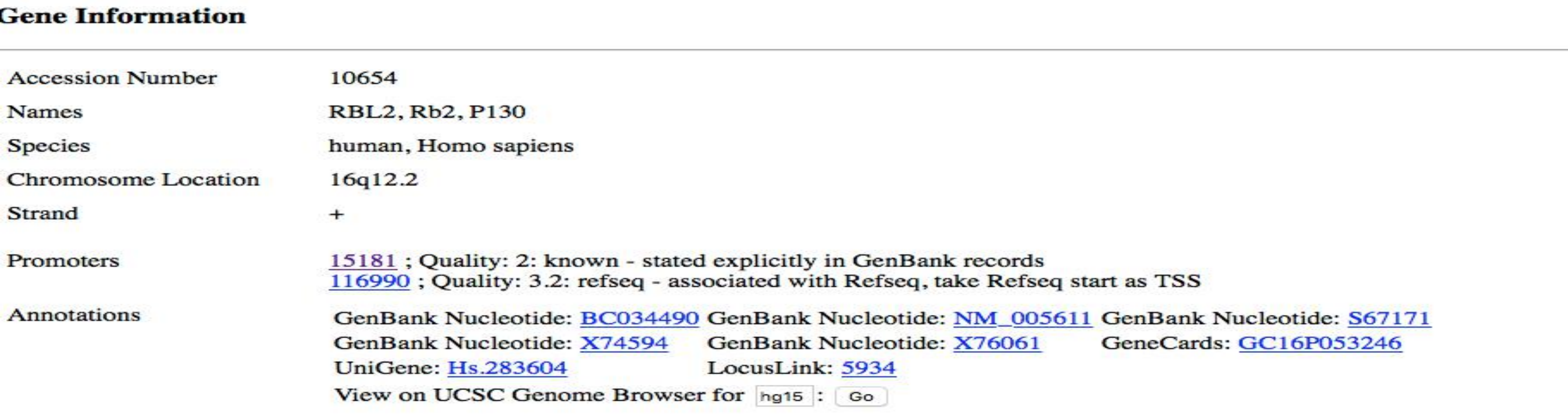


Gene Information

Accession Number	40145
Names	Rb1, Rb, pRb, Rb-1
Species	mouse, Mus musculus
Chromosome Location	14 41.0 cM
Strand	-
Promoters	56310 ; Quality: 3.1: refseq,predicted - associated with Refseq, TSS is predicted 135969 ; Quality: 3.2: refseq - associated with Refseq, take Refseq start as TSS
Annotations	GenBank Nucleotide: M26391 GenBank Nucleotide: NM_009029 UniGene: Mm.304 LocusLink: 19645 View on UCSC Genome Browser for mm3 : Go

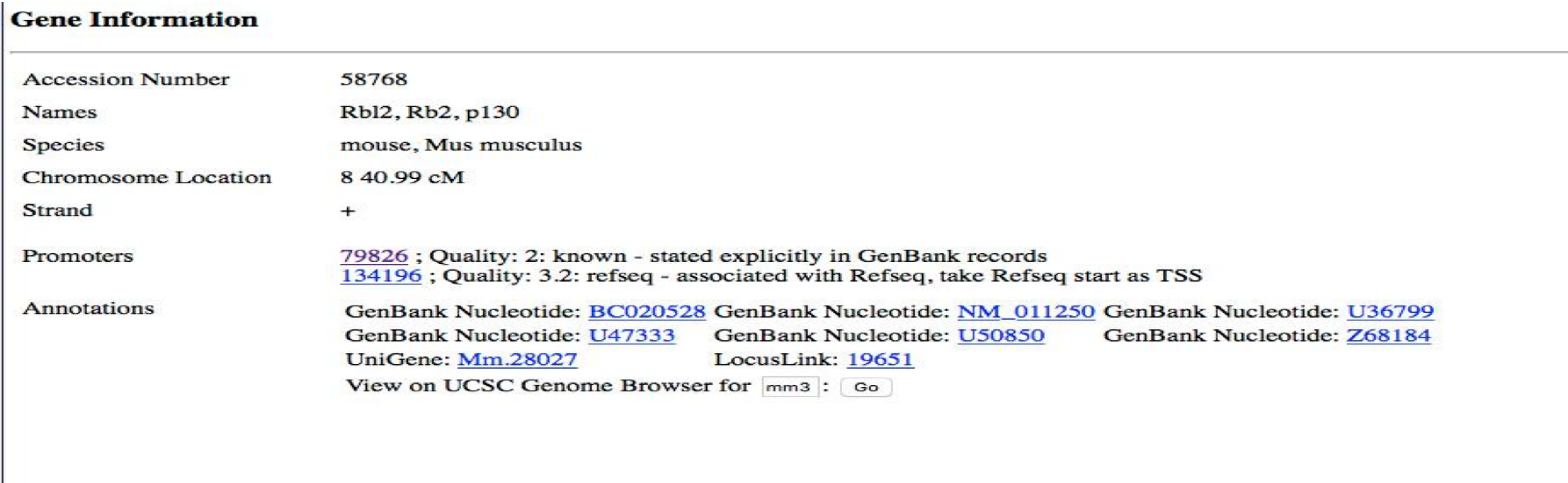
Human and mouse RB2 promoters found in Transcriptional Regulatory Element Database

(https://cb.utdallas.edu/cgi-bin/TRED/tred.cgi?process=searchPromForm)



Gene Information

Accession Number	10654
Names	RBL2, Rb2, P130
Species	human, Homo sapiens
Chromosome Location	16q12.2
Strand	+
Promoters	15181 ; Quality: 2: known - stated explicitly in GenBank records 116990 ; Quality: 3.2: refseq - associated with Refseq, take Refseq start as TSS
Annotations	GenBank Nucleotide: BC034490 GenBank Nucleotide: NM_005611 GenBank Nucleotide: S67171 GenBank Nucleotide: X74594 GenBank Nucleotide: X76061 GeneCards: GC16P053246 UniGene: Hs.283604 LocusLink: 5934 View on UCSC Genome Browser for hg15 : Go

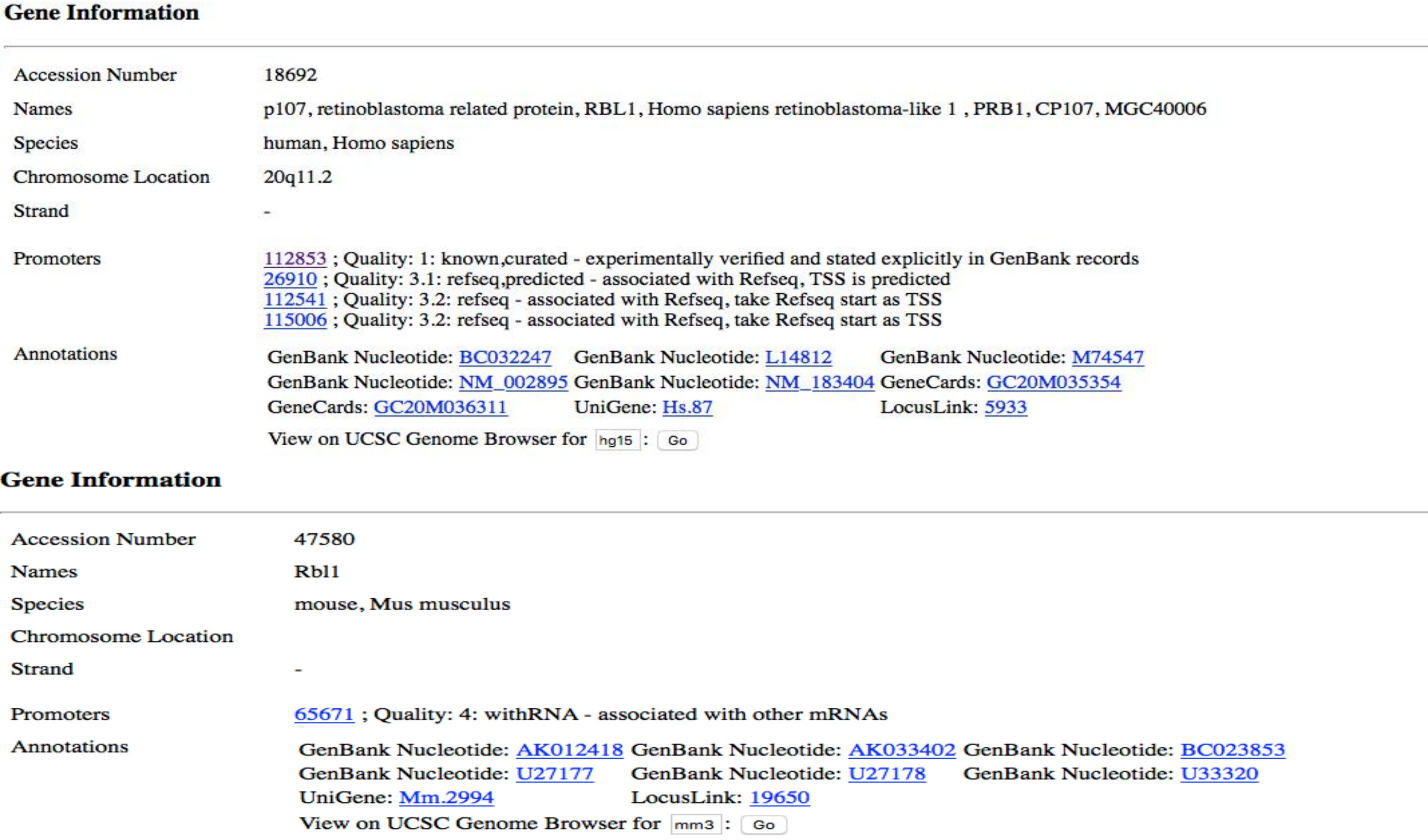


Gene Information

Accession Number	58768
Names	Rbl2, Rb2, p130
Species	mouse, Mus musculus
Chromosome Location	8 40.99 cM
Strand	+
Promoters	79826 ; Quality: 2: known - stated explicitly in GenBank records 134196 ; Quality: 3.2: refseq - associated with Refseq, take Refseq start as TSS
Annotations	GenBank Nucleotide: BC020528 GenBank Nucleotide: NM_011250 GenBank Nucleotide: U36799 GenBank Nucleotide: U47333 GenBank Nucleotide: U50850 GenBank Nucleotide: Z68184 UniGene: Mm.28027 LocusLink: 19651 View on UCSC Genome Browser for mm3 : Go

Human and mouse p107 promoters found in Transcriptional Regulatory Element Database

(https://cb.utdallas.edu/cgi-bin/TRED/tred.cgi?process=searchPromForm)



Gene Information

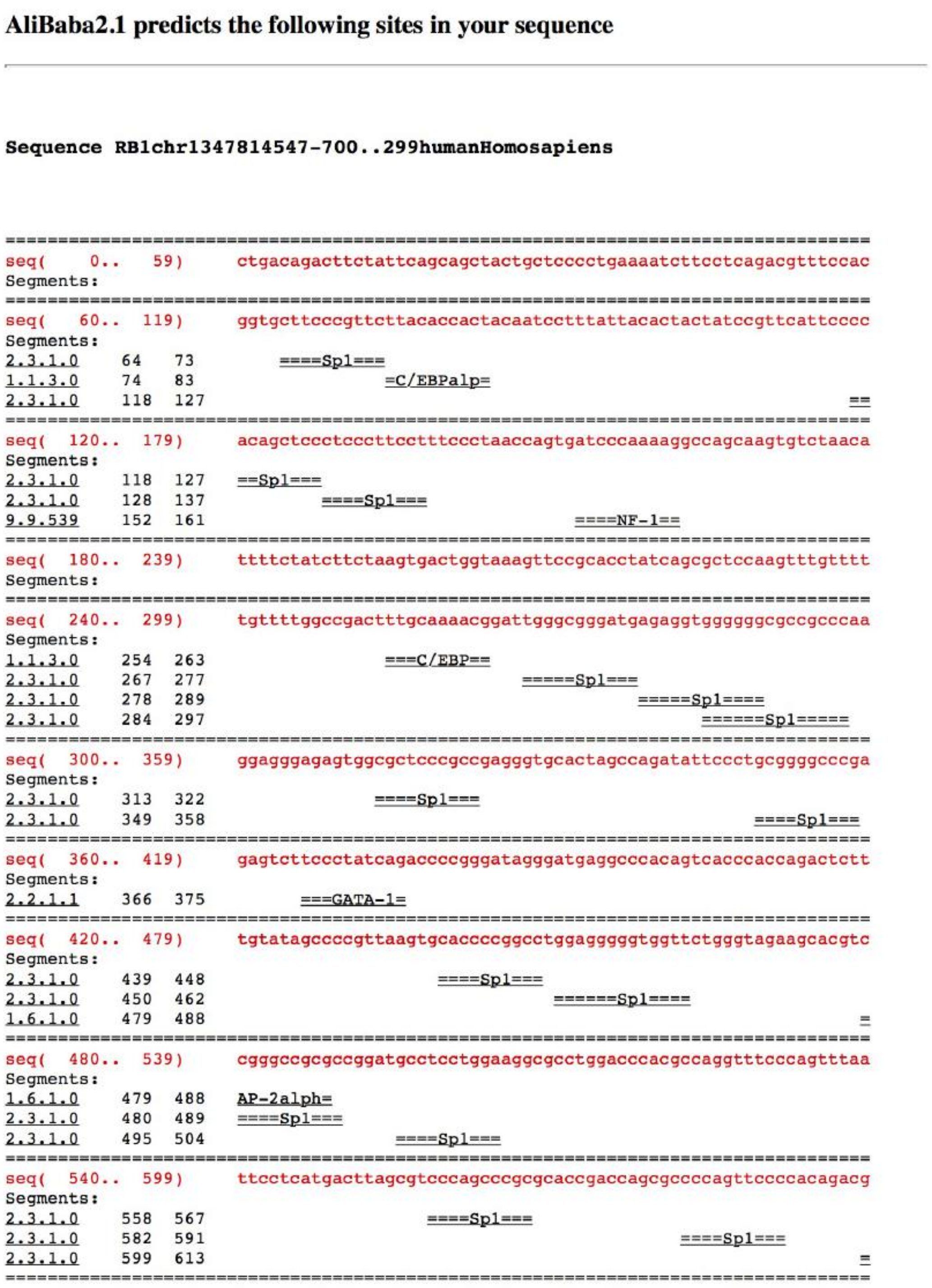
Accession Number	18692
Names	p107, retinoblastoma related protein, RBL1, Homo sapiens retinoblastoma-like 1 , PRB1, CP107, MGC40006
Species	human, Homo sapiens
Chromosome Location	20q11.2
Strand	-
Promoters	112853 ; Quality: 1: known,curated - experimentally verified and stated explicitly in GenBank records 26910 ; Quality: 3.1: refseq,predicted - associated with Refseq, TSS is predicted 112541 ; Quality: 3.2: refseq - associated with Refseq, take Refseq start as TSS 115006 ; Quality: 3.2: refseq - associated with Refseq, take Refseq start as TSS
Annotations	GenBank Nucleotide: BC032247 GenBank Nucleotide: L14812 GenBank Nucleotide: M74547 GenBank Nucleotide: NM_002895 GenBank Nucleotide: NM_183404 GeneCards: GC20M035354 GeneCards: GC20M036311 UniGene: Hs.87 LocusLink: 5933 View on UCSC Genome Browser for hg15 : Go

Gene Information

Accession Number	47580
Names	Rbl1
Species	mouse, Mus musculus
Chromosome Location	
Strand	-
Promoters	65671 ; Quality: 4: withRNA - associated with other mRNAs
Annotations	GenBank Nucleotide: AK012418 GenBank Nucleotide: AK033402 GenBank Nucleotide: BC023853 GenBank Nucleotide: U27177 GenBank Nucleotide: U27178 GenBank Nucleotide: U33320 UniGene: Mm.2994 LocusLink: 19650 View on UCSC Genome Browser for mm3 : Go

Potential transcription factor binding sites found on -700 + 299 region of human RB1 promoter found in ALIBABA2 software

(https://www.generegulation.com)



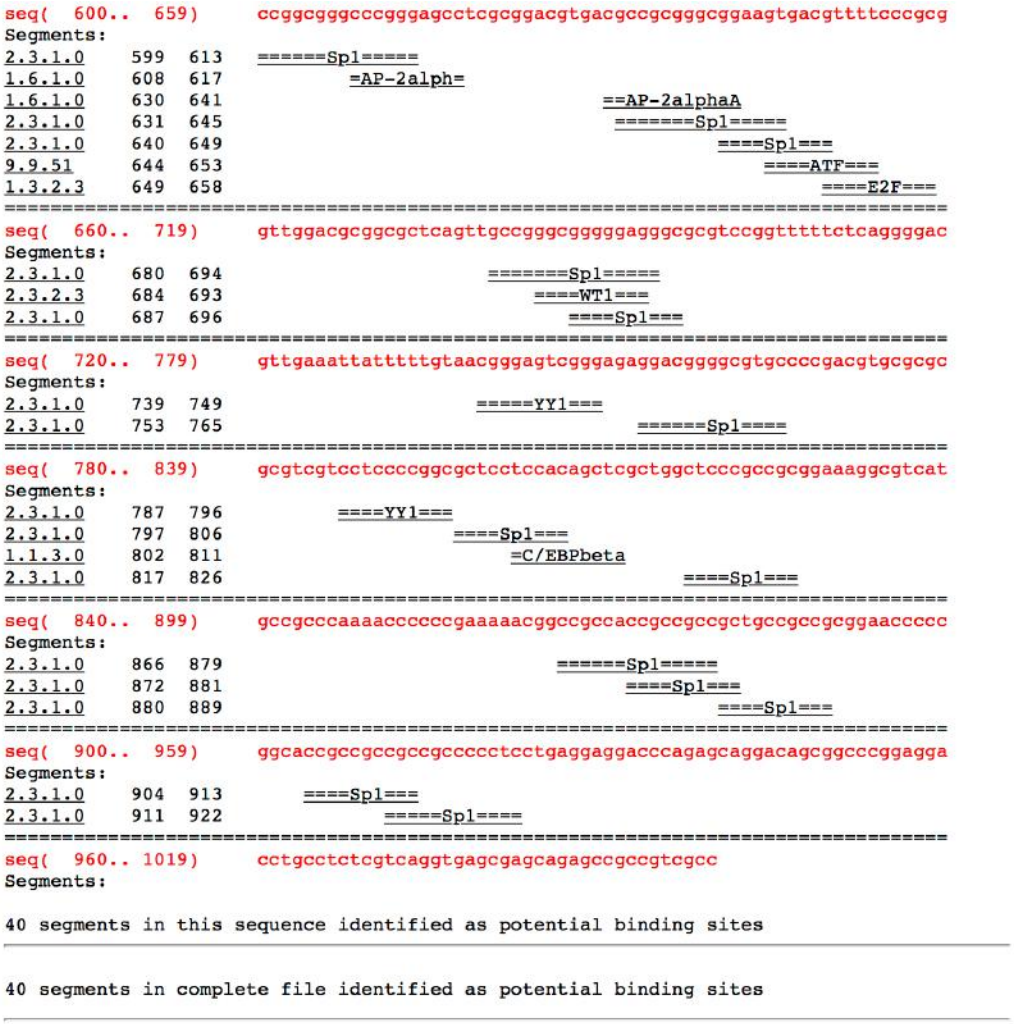
AliBaba2.1 predicts the following sites in your sequence

```
Sequence RB1chr1347814547-700..299humanHomosapiens


==================================================================================
seq(    0..   59)     ctgacagacttctattcagcagctactgctcccctgaaaatcttcctcagacgtttccac
Segments:
==================================================================================
seq(   60..  119)     ggtgcttcccgttcttacaccactacaatcctttattacactactatccgttcattcccc
Segments:
2.3.1.0    64   73        ====Sp1===
1.1.3.0    74   83                  =C/EBPalp=
2.3.1.0    118  127                                                             ==
==================================================================================
seq(  120..  179)     acagctccctcccttcctttccctaaccagtgatcccaaaaggccagcaagtgtctaaca
Segments:
2.3.1.0    118  127   ==Sp1===
2.3.1.0    128  137           ====Sp1===
9.9.539    152  161                                   ====NF-1==
==================================================================================
seq(  180..  239)     ttttctatcttctaagtgactggtaaagttccgcacctatcagcgctccaagtttgtttt
Segments:
==================================================================================
seq(  240..  299)     tgttttggccgactttgcaaaacggattgggcgggatgagaggtgggggcgccgcccaa
Segments:
1.1.3.0    254  263                 ===C/EBP==
2.3.1.0    267  277                              =====Sp1===
2.3.1.0    278  289                                         =====Sp1====
2.3.1.0    284  297                                               ======Sp1=====
==================================================================================
seq(  300..  359)     ggagggagagtggcgctcccgccgagggtgcactagccagatattccctgcggggcccga
Segments:
2.3.1.0    313  322                ====Sp1===
2.3.1.0    349  358                                                    ====Sp1===
==================================================================================
seq(  360..  419)     gagtcttccctatcagaccccgggatagggatgaggcccacagtcacccaccagactctt
Segments:
2.2.1.1    366  375         ===GATA-1=
==================================================================================
seq(  420..  479)     tgtatagccccgttaagtgcaccccggcctggaggggtggttctgggtagaagcacgtc
Segments:
2.3.1.0    439  448                      ====Sp1===
2.3.1.0    450  462                                 ======Sp1====
1.6.1.0    479  488                                                              =
==================================================================================
seq(  480..  539)     cgggccgcgccggatgcctcctggaaggcgcctggacccacgccaggtttcccagtttaa
Segments:
1.6.1.0    479  488   AP-2alph=
2.3.1.0    480  489   ====Sp1===
2.3.1.0    495  504                  ====Sp1===
==================================================================================
seq(  540..  599)     ttcctcatgacttagcgtcccagcccgcgcaccgaccagcgccccagttccccacagacg
Segments:
2.3.1.0    558  567                     ====Sp1===
2.3.1.0    582  591                                             ====Sp1===
2.3.1.0    599  613                                                              =
==================================================================================
```

Potential transcription factor binding sites found on -700 + 299 region of human RB1 promoter found in ALIBABA2 software

(https://www.generegulation.com)



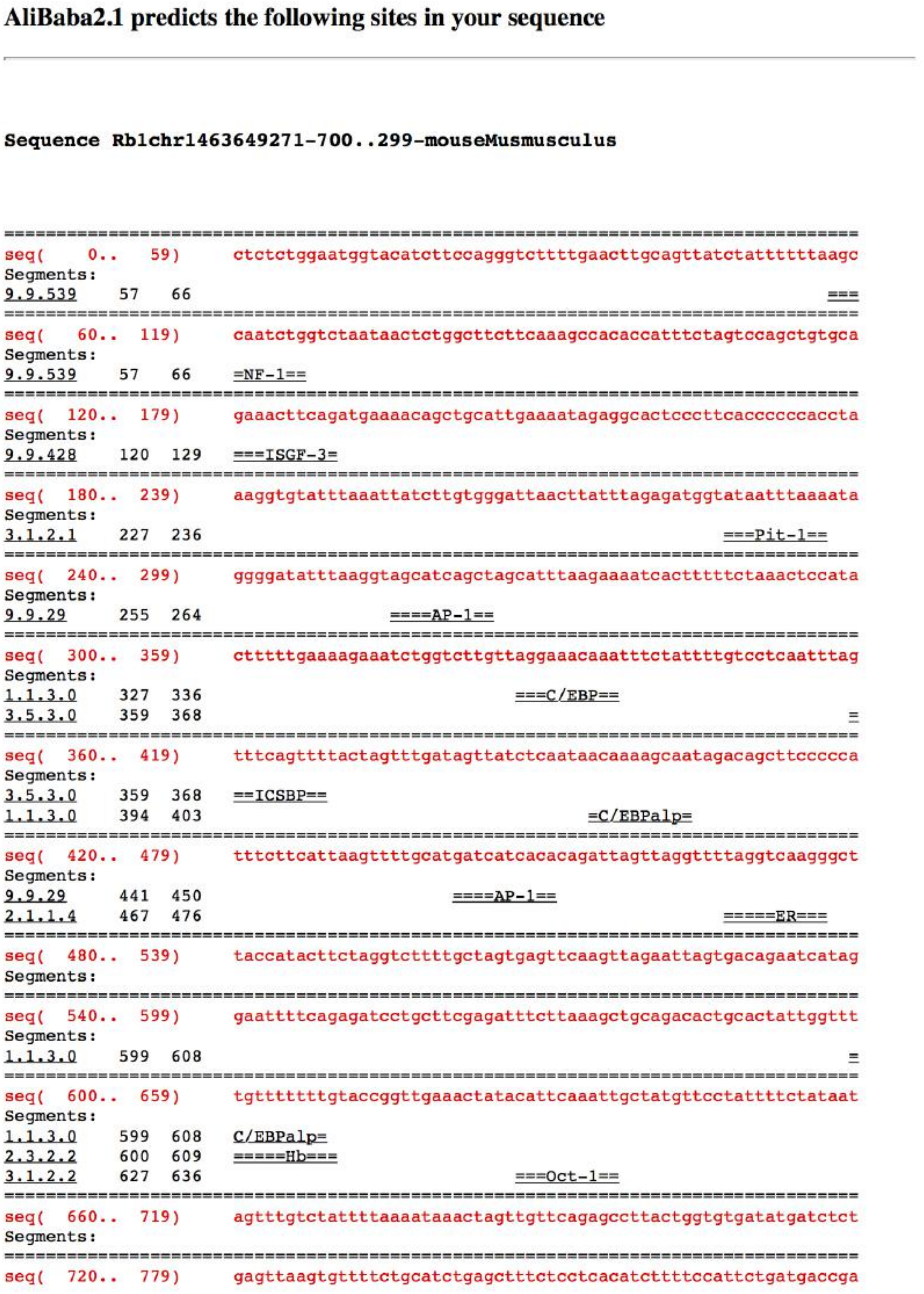
```
seq(  600..  659)     ccggcgggcccgggagcctcgcggacgtgacgccgcgggcggaagtgacgttttcccgcg
Segments:
2.3.1.0    599  613   ======Sp1=====
1.6.1.0    608  617           =AP-2alph=
1.6.1.0    630  641                                 ==AP-2alphaA
2.3.1.0    631  645                                  =======Sp1=====
2.3.1.0    640  649                                           ====Sp1===
9.9.51     644  653                                               ====ATF===
1.3.2.3    649  658                                                    ====E2F===
==================================================================================
seq(  660..  719)     gttggacgcggcgctcagttgccgggcgggggagggcgcgtccggtttttctcaggggac
Segments:
2.3.1.0    680  694                       =======Sp1=====
2.3.2.3    684  693                           ====WT1===
2.3.1.0    687  696                              ====Sp1===
==================================================================================
seq(  720..  779)     gttgaaattatttttgtaacgggagtcgggagaggacggggcgtgccccgacgtgcgcgc
Segments:
2.3.1.0    739  749                      =====YY1===
2.3.1.0    753  765                                    ======Sp1====
==================================================================================
seq(  780..  839)     gcgtcgtcctccccggcgctcctccacagctcgctggctcccgccgcggaaaggcgtcat
Segments:
2.3.1.0    787  796          ====YY1===
2.3.1.0    797  806                    ====Sp1===
1.1.3.0    802  811                         =C/EBPbeta
2.3.1.0    817  826                                        ====Sp1===
==================================================================================
seq(  840..  899)     gccgcccaaaacccccgaaaaacggccgccaccgccgccgctgccgccgcggaacccccc
Segments:
2.3.1.0    866  879                             ======Sp1=====
2.3.1.0    872  881                                   ====Sp1===
2.3.1.0    880  889                                           ====Sp1===
==================================================================================
seq(  900..  959)     ggcaccgccgccgccgcccccctcctgaggaggacccagagcaggacagcggcccggagga
Segments:
2.3.1.0    904  913       ====Sp1===
2.3.1.0    911  922              =====Sp1====
==================================================================================
seq(  960.. 1019)     cctgcctctcgtcaggtgagcgagcagagccgccgtcgcc
Segments:

40 segments in this sequence identified as potential binding sites
________________________________________________________________________________________

40 segments in complete file identified as potential binding sites
________________________________________________________________________________________
```

Potential transcription factor binding sites found on -700 + 299 region of mouse RB1 promoter found in ALIBABA2 software

(https://www.generegulation.com)



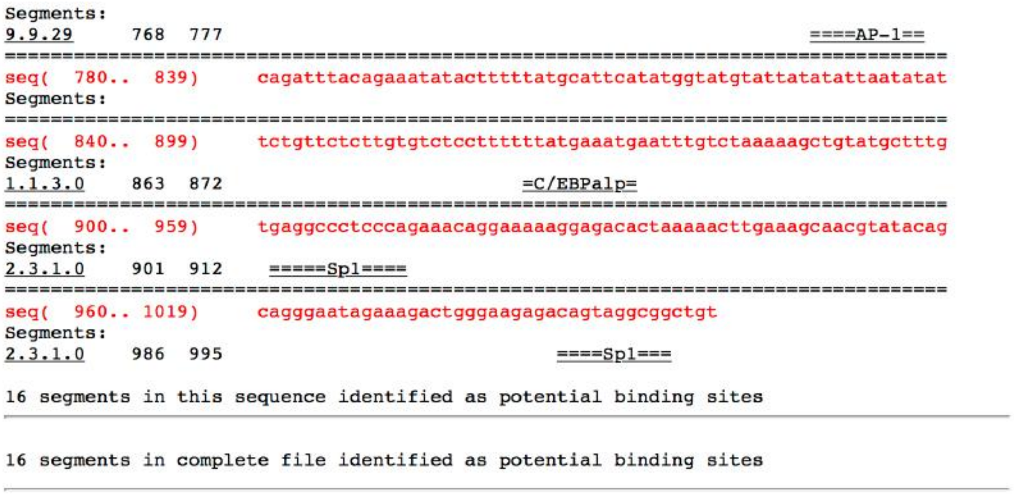
AliBaba2.1 predicts the following sites in your sequence

```
Sequence Rb1chr1463649271-700..299-mouseMusmusculus


==================================================================================
seq(    0..   59)     ctctctggaatggtacatcttccaggtcttttgaacttgcagttatctatttttaagc
Segments:
9.9.539    57   66                                                             ===
==================================================================================
seq(   60..  119)     caatctggtctaataactctggcttcttcaaagccacaccatttctagtccagctgtgca
Segments:
9.9.539    57   66    =NF-1==
==================================================================================
seq(  120..  179)     gaaacttcagatgaaaacagctgcattgaaaatagaggcactcccttcaccccccaccta
Segments:
9.9.428    120  129   ===ISGF-3=
==================================================================================
seq(  180..  239)     aaggtgtatttaaattatcttgtgggattaacttatttagagatggtataatttaaaata
Segments:
3.1.2.1    227  236                                                  ===Pit-1==
==================================================================================
seq(  240..  299)     ggggatatttaaggtagcatcagctagcatttaagaaaatcacttttttctaaactccata
Segments:
9.9.29     255  264                  ====AP-1==
==================================================================================
seq(  300..  359)     ctttttgaaaagaaatctggtcttgttaggaaacaaatttctattttgtcctcaatttag
Segments:
1.1.3.0    327  336                              ===C/EBP==
3.5.3.0    359  368                                                              =
==================================================================================
seq(  360..  419)     tttcagttttactagtttgatagttatctcaataacaaaagcaatagacagcttccccca
Segments:
3.5.3.0    359  368   ==ICSBP==
1.1.3.0    394  403                                     =C/EBPalp=
==================================================================================
seq(  420..  479)     tttcttcattaagttttgcatgatcatcacacagattagttaggttttaggtcaagggct
Segments:
9.9.29     441  450                        ====AP-1==
2.1.1.4    467  476                                                  =====ER===
==================================================================================
seq(  480..  539)     taccatacttctaggtcttttgctagtgagttcaagttagaattagtgacagaatcatag
Segments:
==================================================================================
seq(  540..  599)     gaattttcagagatcctgcttcgagatttcttaaagctgcagacactgcactattggttt
Segments:
1.1.3.0    599  608                                                              =
==================================================================================
seq(  600..  659)     tgtttttttgtaccggttgaaactatacattcaaattgctatgttcctattttctataat
Segments:
1.1.3.0    599  608   C/EBPalp=
2.3.2.2    600  609   =====Hb===
3.1.2.2    627  636                              ===Oct-1==
==================================================================================
seq(  660..  719)     agtttgtctattttaaaataaactagttgttcagagccttactggtgtgatatgatctct
Segments:
==================================================================================
seq(  720..  779)     gagttaagtgttttctgcatctgagctttctcctcacatcttttccattctgatgaccga
```

Potential transcription factor binding sites found on -700 + 299 region of mouse RB1 promoter found in ALIBABA2 software

(https://www.generegulation.com)



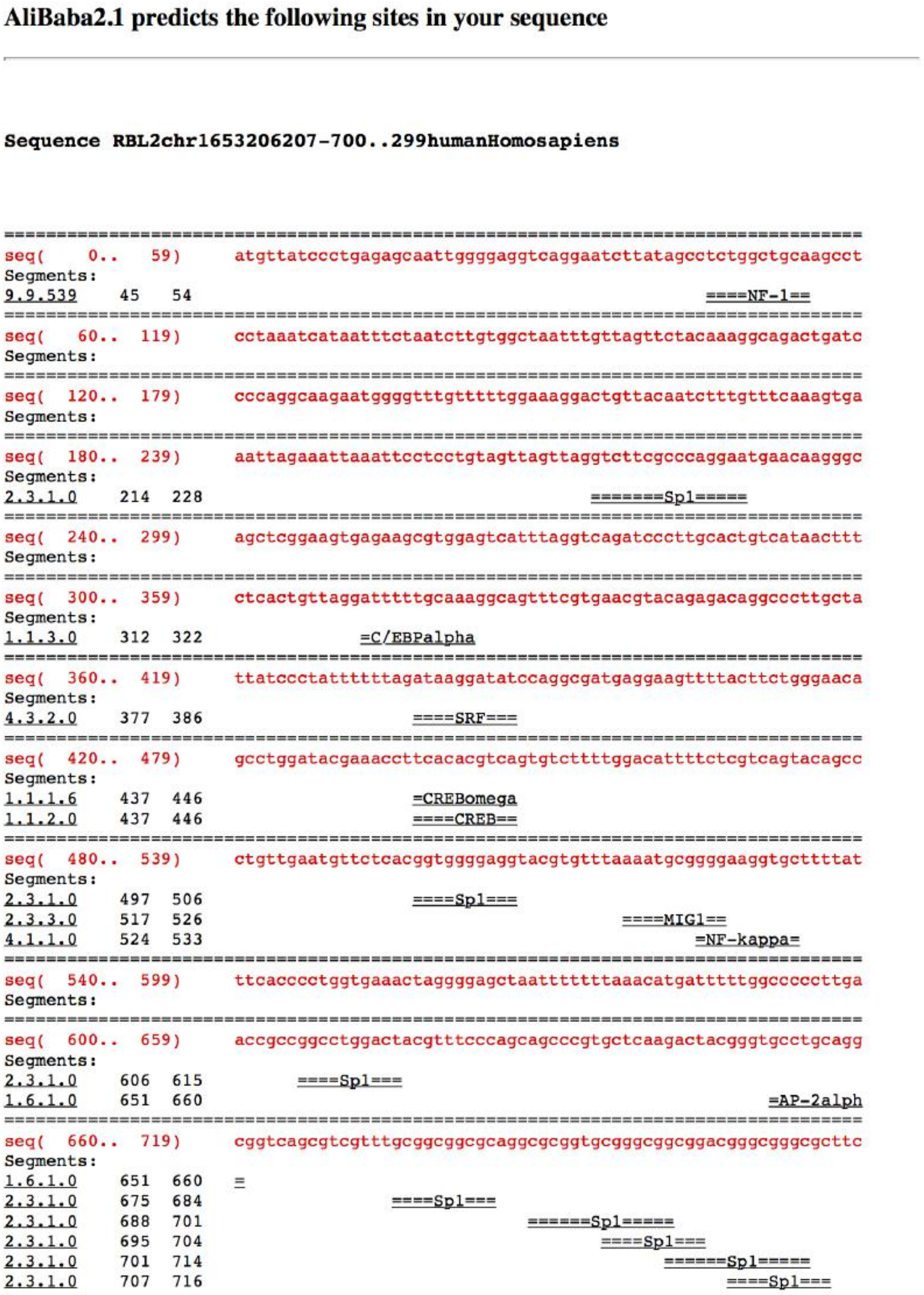
```
Segments:
9.9.29     768  777                                                   ====AP-1==
==================================================================================
seq(  780..  839)     cagatttacagaaatatacttttatgcattcatatggtatgtattatatattaatatat
Segments:
==================================================================================
seq(  840..  899)     tctgttctcttgtgtctccttttttatgaaatgaatttgtctaaaaagctgtatgctttg
Segments:
1.1.3.0    863  872                          =C/EBPalp=
==================================================================================
seq(  900..  959)     tgaggccctcccagaaacaggaaaaaggagacactaaaaacttgaaagcaacgtatacag
Segments:
2.3.1.0    901  912     =====Spl====
==================================================================================
seq(  960.. 1019)     cagggaatagaaagactgggaagagacagtaggcggctgt
Segments:
2.3.1.0    986  995                             ====Spl===

16 segments in this sequence identified as potential binding sites

16 segments in complete file identified as potential binding sites
```

Potential transcription factor binding sites found on -700 + 299 region of human RB2/P130 promoter found in ALIBABA2 software

(https://www.generegulation.com)



AliBaba2.1 predicts the following sites in your sequence

```
Sequence RBL2chr1653206207-700..299humanHomosapiens

==================================================================================
seq(    0..   59)     atgttatccctgagagcaattggggaggtcaggaatcttatagcctctggctgcaagcct
Segments:
9.9.539    45   54                                                 ====NF-1==
==================================================================================
seq(   60..  119)     cctaaatcataatttctaatcttgtggctaatttgttagttctacaaaggcagactgatc
Segments:
==================================================================================
seq(  120..  179)     cccaggcaagaatggggtttgtttttggaaaggactgttacaatctttgtttcaaagtga
Segments:
==================================================================================
seq(  180..  239)     aattagaaattaaattcctcctgtagttagttaggtcttcgcccaggaatgaacaagggc
Segments:
2.3.1.0    214  228                                     =======Sp1=====
==================================================================================
seq(  240..  299)     agctcggaagtgagaagcgtggagtcatttaggtcagatcccttgcactgtcataacttt
Segments:
==================================================================================
seq(  300..  359)     ctcactgttaggattttgcaaaggcagtttcgtgaacgtacagagacaggcccttgcta
Segments:
1.1.3.0    312  322               =C/EBPalpha
==================================================================================
seq(  360..  419)     ttatccctatttttagataaggatatccaggcgatgaggaagttttacttctgggaaca
Segments:
4.3.2.0    377  386                    ====SRF===
==================================================================================
seq(  420..  479)     gcctggatacgaaaccttcacacgtcagtgtcttttggacattttctcgtcagtacagcc
Segments:
1.1.1.6    437  446                    =CREBomega
1.1.2.0    437  446                    ====CREB==
==================================================================================
seq(  480..  539)     ctgttgaatgttctcacggtggggaggtacgtgtttaaaatgcggggaaggtgcttttat
Segments:
2.3.1.0    497  506                    ====Sp1===
2.3.3.0    517  526                                        ====MIG1==
4.1.1.0    524  533                                               =NF-kappa=
==================================================================================
seq(  540..  599)     ttcacccctggtgaaactaggggagctaatttttttaaacatgattttggccccccttga
Segments:
==================================================================================
seq(  600..  659)     accgccggcctggactacgtttcccagcagcccgtgctcaagactacgggtgcctgcagg
Segments:
2.3.1.0    606  615         ====Sp1===
1.6.1.0    651  660                                                      =AP-2alph
==================================================================================
seq(  660..  719)     cggtcagcgtcgtttgcggcggcgcaggcgcggtgcgggcggcggacgggcgggcgcttc
Segments:
1.6.1.0    651  660   =
2.3.1.0    675  684                  ====Sp1===
2.3.1.0    688  701                               ======Sp1=====
2.3.1.0    695  704                                      ====Sp1===
2.3.1.0    701  714                                            ======Sp1=====
2.3.1.0    707  716                                                  ====Sp1===
```

Potential transcription factor binding sites found on -700 + 299 region of human RB2/P130 promoter found in ALIBABA2 software

(https://www.generegulation.com)

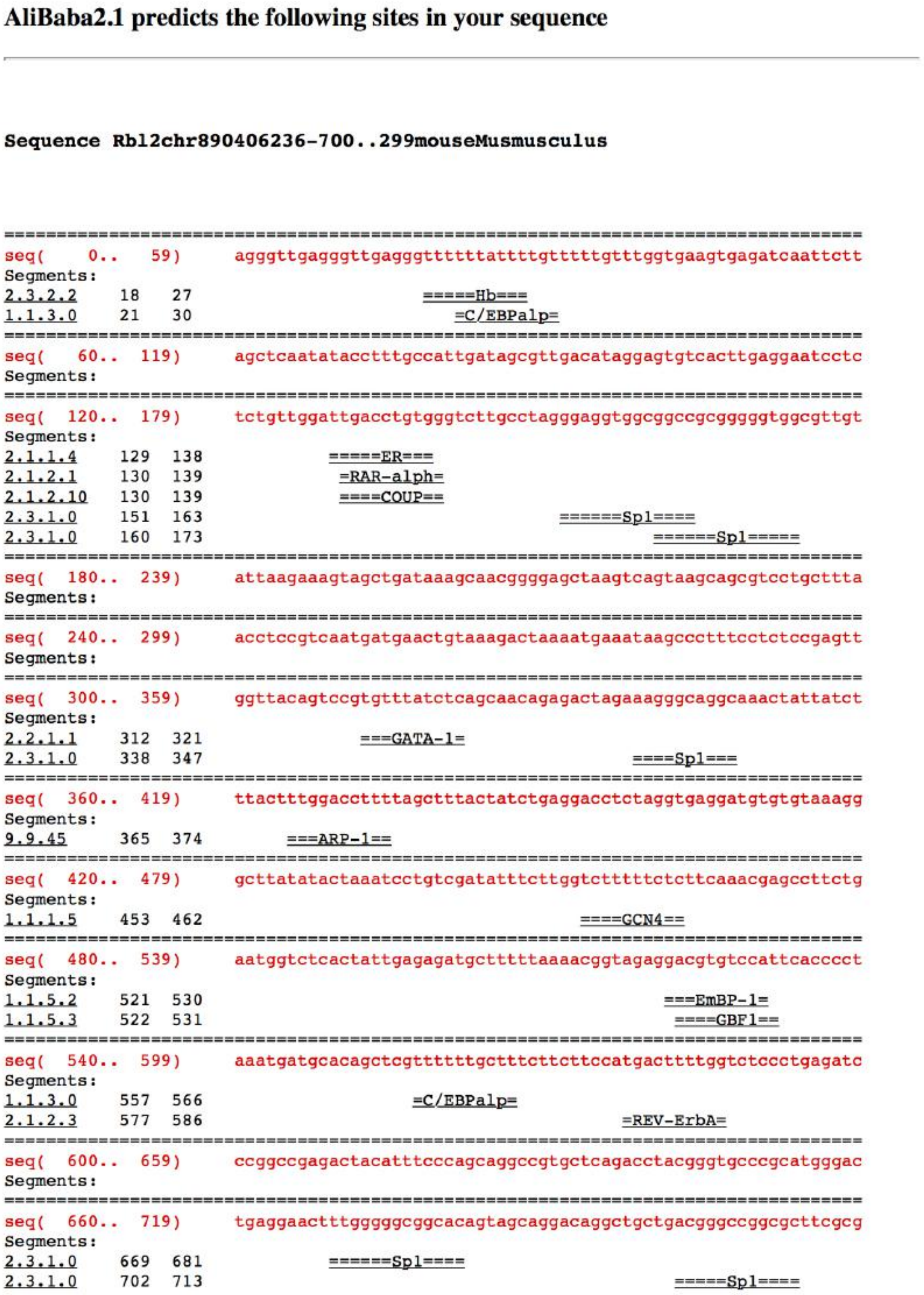
```
==================================================================================
seq(  720..  779)     gccgtttgaatggctgcgggcccgggccctcacctcacctgaggtccggccgcccagggg
Segments:
2.3.1.0    735  748                  ======Sp1=====
2.3.1.0    746  755                             ====Sp1===
2.3.1.0    767  776                                                  ====Sp1===
2.3.1.0    774  785                                                         =====S
==================================================================================
seq(  780..  839)     tgcgctatgccgtcgggaggtgaccagtcgccaccgcccccgcctccccctccggcggcg
Segments:
2.3.1.0    774  785   p1====
2.3.1.0    811  825                                  =======Sp1=====
2.3.2.3    813  822                                    ====WT1===
2.3.2.1    814  823                                     ==Krox-20=
2.3.1.0    817  831                                        =======Sp1=====
2.3.1.0    831  841                                                      =====Sp1=
==================================================================================
seq(  840..  899)     gcagcctcggatgaggaggaggaggacgacggcgaggcggaagacgccgcgccgcctgcc
Segments:
2.3.1.0    831  841   ==
2.3.1.0    854  864                 =====Sp1===
2.3.1.0    870  880                                 =====Sp1===
2.3.1.0    886  895                                                 ====Sp1===
==================================================================================
seq(  900..  959)     gagtcgcccacccctcagatccagcagcggttcgacgagctgtgcagccgcctcaacatg
Segments:
2.3.1.0    905  915        =====Sp1===
==================================================================================
seq(  960.. 1019)     gacgaggcggcgcgggccgaggcctgggacagctaccgca
Segments:
2.3.1.0    963  977      =======Sp1=====
2.3.2.1    966  975         ===Egr-1==
2.3.1.0    972  983               =====Sp1====

32 segments in this sequence identified as potential binding sites

32 segments in complete file identified as potential binding sites
```

Potential transcription factor binding sites found on -700 + 299 region of mouse RB2/P130 promoter found in ALIBABA2 software

(https://www.generegulation.com)



AliBaba2.1 predicts the following sites in your sequence

```
Sequence Rbl2chr890406236-700..299mouseMusmusculus

==================================================================================
seq(    0..   59)     agggttgagggttgagggtttttatttttgtttttgtttggtgaagtgagatcaattctt
Segments:
2.3.2.2    18   27                      =====Hb===
1.1.3.0    21   30                         =C/EBPalp=
==================================================================================
seq(   60..  119)     agctcaatatacctttgccattgatagcgttgacataggagtgtcacttgaggaatcctc
Segments:
==================================================================================
seq(  120..  179)     tctgttggattgacctgtgggtcttgcctagggaggtggcggccgcgggggtggcgttgt
Segments:
2.1.1.4    129  138            =====ER===
2.1.2.1    130  139             =RAR-alph=
2.1.2.10   130  139             ====COUP==
2.3.1.0    151  163                                  ======Sp1====
2.3.1.0    160  173                                           ======Sp1=====
==================================================================================
seq(  180..  239)     attaagaaagtagctgataaagcaacggggagctaagtcagtaagcagcgtcctgcttta
Segments:
==================================================================================
seq(  240..  299)     acctccgtcaatgatgaactgtaaagactaaaatgaaataagccctttcctctccgagtt
Segments:
==================================================================================
seq(  300..  359)     ggttacagtccgtgtttatctcagcaacagagactagaaagggcaggcaaactattatct
Segments:
2.2.1.1    312  321               ===GATA-1=
2.3.1.0    338  347                                         ====Sp1===
==================================================================================
seq(  360..  419)     ttactttggaccttttagctttactatctgaggacctctaggtgaggatgtgtgtaaagg
Segments:
9.9.45     365  374        ===ARP-1==
==================================================================================
seq(  420..  479)     gcttatatactaaatcctgtcgatatttcttggtctttttctcttcaaacgagccttctg
Segments:
1.1.1.5    453  462                                    ====GCN4==
==================================================================================
seq(  480..  539)     aatggtctcactattgagagatgcttttttaaaacggtagaggacgtgtccattcacccct
Segments:
1.1.5.2    521  530                                            ===EmBP-1=
1.1.5.3    522  531                                             ====GBF1==
==================================================================================
seq(  540..  599)     aaatgatgcacagctcgtttttttgctttcttcttccatgactttttggtctccctgagatc
Segments:
1.1.3.0    557  566                    =C/EBPalp=
2.1.2.3    577  586                                        =REV-ErbA=
==================================================================================
seq(  600..  659)     ccggccgagactacatttcccagcaggccgtgctcagacctacgggtgcccgcatgggac
Segments:
==================================================================================
seq(  660..  719)     tgaggaactttgggggcggcacagtagcaggacaggctgctgacgggccggcgcttcgcg
Segments:
2.3.1.0    669  681            ======Sp1====
2.3.1.0    702  713                                             =====Sp1====
```

Potential transcription factor binding sites found on -700 + 299 region of mouse RB2/P130 promoter found in ALIBABA2 software

(https://www.generegulation.com)

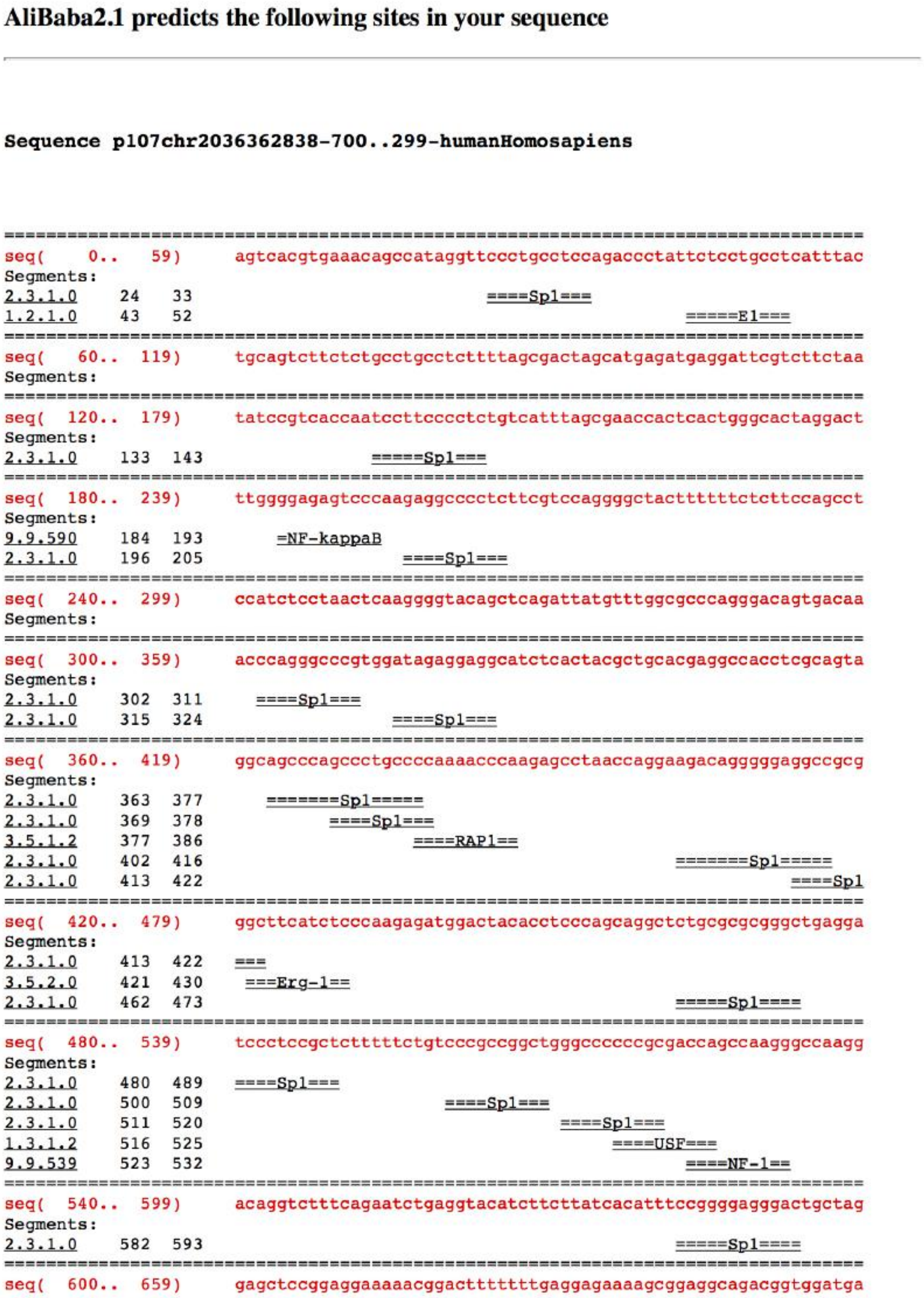
```
==================================================================================
seq(  720..  779)     gtttgaatggctgcgggcccgggccctgagcgcatctgaagagccgcggcctcggggtgc
Segments:
2.3.1.0    732  745               ======Sp1=====
2.3.1.0    738  747                     ====Sp1===
==================================================================================
seq(  780..  839)     gccatggcatctggaggcaaccagtcgccaccgcctcctccagctgctgcagccagctcg
Segments:
2.3.1.0    808  819                               =====Sp1====
3.5.1.2    820  829                                           ===Adf-1==
==================================================================================
seq(  840..  899)     gaggaagaggaggaggatggcgacgccgcggatcgcgcgcagcccgcggggtccccgagc
Segments:
2.3.1.0    840  854   =======Sp1=====
3.5.1.2    855  864                  ===Adf-1==
==================================================================================
seq(  900..  959)     catcagatccagcagcggttcgaggagctgtgcagccgcctcaacatggacgaggcggcg
Segments:
2.3.1.0    951  960                                                      ====Sp1==
==================================================================================
seq(  960.. 1019)     cgcgccgaggcctggagcagctaccgcagcatgagcgaga
Segments:
2.3.1.0    951  960   =

24 segments in this sequence identified as potential binding sites

24 segments in complete file identified as potential binding sites
```

Potential transcription factor binding sites found on -700 + 299 region of human P107 promoter found in ALIBABA2 software

(https://www.generegulation.com)



AliBaba2.1 predicts the following sites in your sequence

```
Sequence p107chr2036362838-700..299-humanHomosapiens


==================================================================================
seq(    0..   59)     agtcacgtgaaacagccataggttccctgcctccagaccctattctcctgcctcatttac
Segments:
2.3.1.0    24   33                            ====Sp1===
1.2.1.0    43   52                                               =====E1===
==================================================================================
seq(   60..  119)     tgcagtcttctctgcctgcctcttttagcgactagcatgagatgaggattcgtcttctaa
Segments:
==================================================================================
seq(  120..  179)     tatccgtcaccaatccttcccctctgtcatttagcgaaccactcactgggcactaggact
Segments:
2.3.1.0    133  143                =====Sp1===
==================================================================================
seq(  180..  239)     ttggggagagtcccaagaggcccctcttcgtccaggggctactttttctcttccagcct
Segments:
9.9.590    184  193       =NF-kappaB
2.3.1.0    196  205                   ====Sp1===
==================================================================================
seq(  240..  299)     ccatctcctaactcaaggggtacagctcagattatgtttggcgcccagggacagtgacaa
Segments:
==================================================================================
seq(  300..  359)     acccagggcccgtggatagaggaggcatctcactacgctgcacgaggccacctcgcagta
Segments:
2.3.1.0    302  311     ====Sp1===
2.3.1.0    315  324                  ====Sp1===
==================================================================================
seq(  360..  419)     ggcagcccagccctgccccaaaacccaagagcctaaccaggaagacaggggaggccgcg
Segments:
2.3.1.0    363  377      =======Sp1=====
2.3.1.0    369  378            ====Sp1===
3.5.1.2    377  386                    ====RAP1==
2.3.1.0    402  416                                             =======Sp1=====
2.3.1.0    413  422                                                        ====Sp1
==================================================================================
seq(  420..  479)     ggcttcatctcccaagagatggactacacctcccagcaggctctgcgcgcgggctgagga
Segments:
2.3.1.0    413  422   ===
3.5.2.0    421  430    ===Erg-1==
2.3.1.0    462  473                                             =====Sp1====
==================================================================================
seq(  480..  539)     tccctccgctctttttctgtcccgccggctgggcccccgcgaccagccaagggccaagg
Segments:
2.3.1.0    480  489   ====Sp1===
2.3.1.0    500  509                       ====Sp1===
2.3.1.0    511  520                                  ====Sp1===
1.3.1.2    516  525                                       ====USF===
9.9.539    523  532                                              ====NF-1==
==================================================================================
seq(  540..  599)     acaggtctttcagaatctgaggtacatcttcttatcacatttccggggagggactgctag
Segments:
2.3.1.0    582  593                                             =====Sp1====
==================================================================================
seq(  600..  659)     gagctccggaggaaaaacggactttttttgaggagaaaagcggaggcagacggtggatga
```

Potential transcription factor binding sites found on -700 + 299 region of human P107 promoter found in ALIBABA2 software

(https://www.generegulation.com)

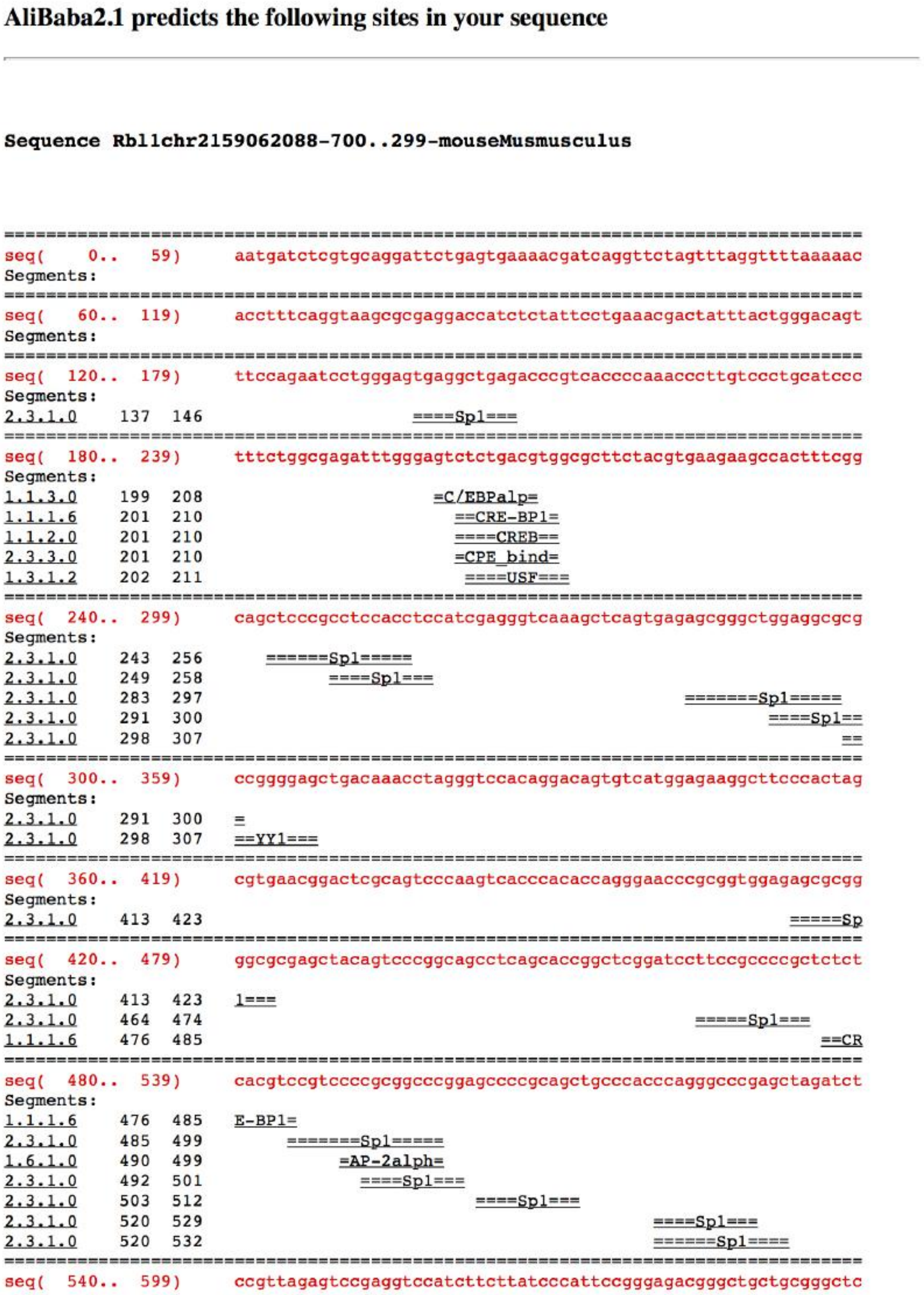
```
Segments:
2.3.1.0    637  646                                        ====Sp1===
==================================================================================
seq(  660..  719)     caacacgtcccgcagctgcagattttcgcgcgctttggcgcaggtggttgtgggtagcgc
Segments:
2.3.1.0    663  672      ====Sp1===
==================================================================================
seq(  720..  779)     gcctgggagggagaaagaagtcgggggccgtggcgcgcagcccgcggggcctgaagggat
Segments:
2.3.1.0    720  731   =====Sp1====
2.3.1.0    742  751                         ====Sp1===
2.3.1.0    762  771                                             ====Sp1===
==================================================================================
seq(  780..  839)     gttcgaggacaagccccacgctgagggggcggcggtggtcgccgcagccggggaggcgct
Segments:
2.3.1.0    802  813                         =====Sp1====
2.3.1.0    826  839                                                 ======Sp1=====
==================================================================================
seq(  840..  899)     acaggccctgtgccaggagctgaacctggacgaggggagcgcggccgaagccctggacga
Segments:
2.3.1.0    840  849   ====Sp1===
2.3.1.0    871  880                                  ====Sp1===
==================================================================================
seq(  900..  959)     ctttactgccatccgaggcaactacagcctagaggtgagcggcagcaggtggggcggccg
Segments:
2.3.1.0    939  948                                          ====Sp1===
1.2.1.0    941  950                                            =====E1===
1.2.2.0    941  950                                            ====MRF4==
2.3.1.0    945  958                                                ======Sp1=====
==================================================================================
seq(  960.. 1019)     gaccctaccctcgccaggccccacccctgccccgcccct
Segments:
2.3.1.0    962  971     ====Sp1===
2.3.1.0    972  986               =======Sp1=====
2.3.1.0    985  997                            ======Sp1====
2.3.2.1    988  997                               ==Krox-20=
2.3.2.3    988  997                               ====GLI3==

38 segments in this sequence identified as potential binding sites

38 segments in complete file identified as potential binding sites
```

Potential transcription factor binding sites found on -700 + 299 region of mouse P107 promoter found in ALIBABA2 software

(https://www.generegulation.com)



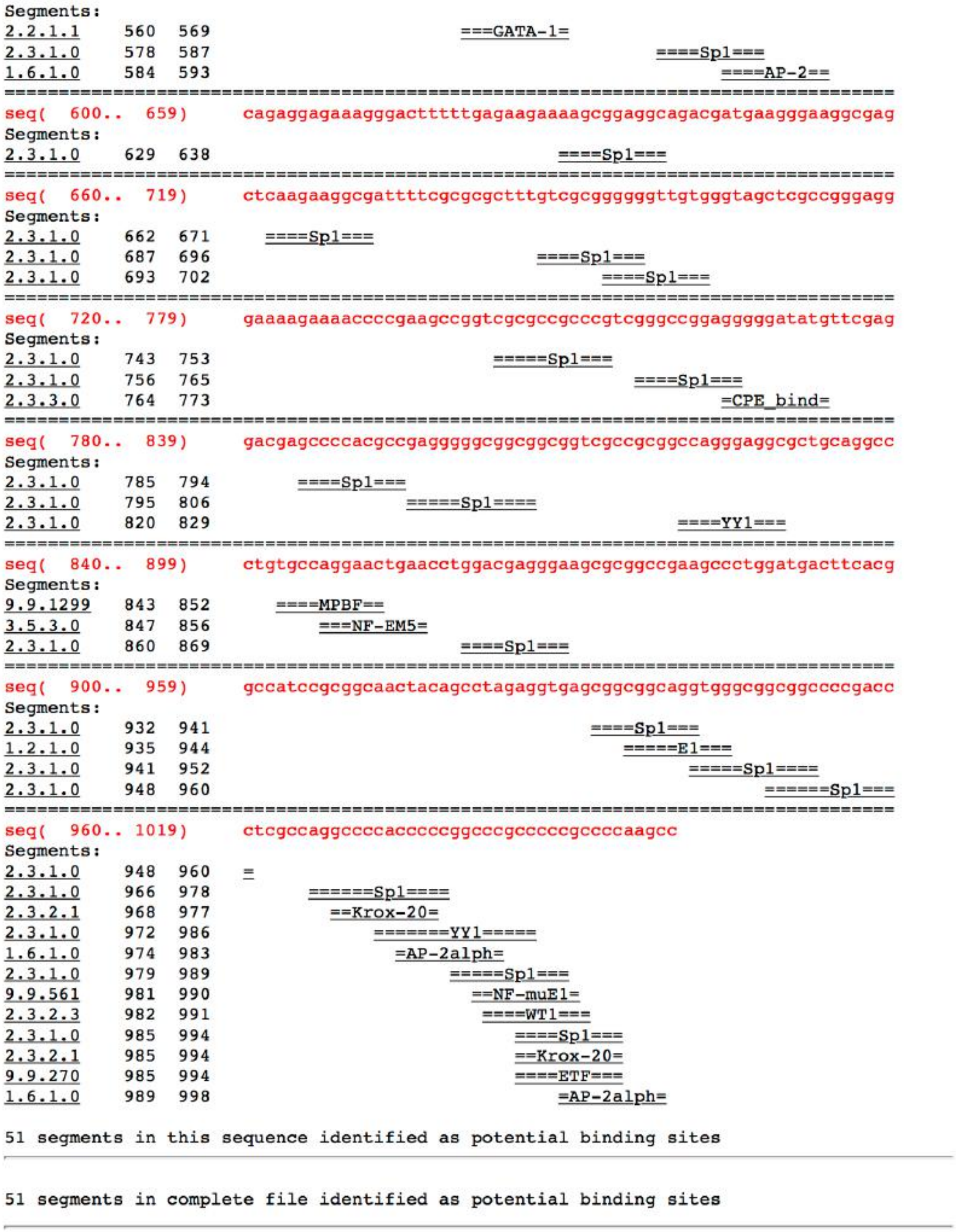
AliBaba2.1 predicts the following sites in your sequence

```
Sequence Rbl1chr2159062088-700..299-mouseMusmusculus


==================================================================================
seq(    0..   59)     aatgatctcgtgcaggattctgagtgaaaacgatcaggttctagtttaggttttaaaaac
Segments:
==================================================================================
seq(   60..  119)     acctttcaggtaagcgcgaggaccatctctattcctgaaacgactatttactgggacagt
Segments:
==================================================================================
seq(  120..  179)     ttccagaatcctgggagtgaggctgagacccgtcaccccaaacccttgtccctgcatccc
Segments:
2.3.1.0    137  146                    ====Sp1===
==================================================================================
seq(  180..  239)     tttctggcgagatttgggagtctctgacgtggcgcttctacgtgaagaagccactttcgg
Segments:
1.1.3.0    199  208                      =C/EBPalp=
1.1.1.6    201  210                        ==CRE-BP1=
1.1.2.0    201  210                        ====CREB==
2.3.3.0    201  210                        =CPE_bind=
1.3.1.2    202  211                         ====USF===
==================================================================================
seq(  240..  299)     cagctcccgcctccacctccatcgagggtcaaagctcagtgagagcgggctggaggcgcg
Segments:
2.3.1.0    243  256      ======Sp1=====
2.3.1.0    249  258            ====Sp1===
2.3.1.0    283  297                                              =======Sp1=====
2.3.1.0    291  300                                                      ====Sp1==
2.3.1.0    298  307                                                             ==
==================================================================================
seq(  300..  359)     ccggggagctgacaaacctagggtccacaggacagtgtcatggagaaggcttcccactag
Segments:
2.3.1.0    291  300   =
2.3.1.0    298  307   ==YY1===
==================================================================================
seq(  360..  419)     cgtgaacggactcgcagtcccaagtcacccacaccagggaacccgcggtggagagcgcgg
Segments:
2.3.1.0    413  423                                                        =====Sp
==================================================================================
seq(  420..  479)     ggcgcgagctacagtcccggcagcctcagcaccggctcggatccttccgccccgctctct
Segments:
2.3.1.0    413  423   1===
2.3.1.0    464  474                                               =====Sp1===
1.1.1.6    476  485                                                           ==CR
==================================================================================
seq(  480..  539)     cacgtccgtccccgcggcccggagccccgcagctgcccacccagggcccgagctagatct
Segments:
1.1.1.6    476  485   E-BP1=
2.3.1.0    485  499        =======Sp1=====
1.6.1.0    490  499             =AP-2alph=
2.3.1.0    492  501               ====Sp1===
2.3.1.0    503  512                          ====Sp1===
2.3.1.0    520  529                                           ====Sp1===
2.3.1.0    520  532                                           ======Sp1====
==================================================================================
seq(  540..  599)     ccgttagagtccgaggtccatcttcttatcccattccgggagacgggctgctgcgggctc
```

Potential transcription factor binding sites found on -700 + 299 region of mouse P107 promoter found in ALIBABA2 software

(https://www.generegulation.com)



```
Segments:
2.2.1.1    560  569                       ===GATA-1=
2.3.1.0    578  587                                         ====Sp1===
1.6.1.0    584  593                                               ====AP-2==
==================================================================================
seq(  600..  659)     cagaggagaaagggacttttgagaagaaaagcggaggcagacgatgaagggaaggcgag
Segments:
2.3.1.0    629  638                                ====Sp1===
==================================================================================
seq(  660..  719)     ctcaagaaggcgatttcgcgcgctttgtcgcgggggttgtgggtagctcgccgggagg
Segments:
2.3.1.0    662  671     ====Sp1===
2.3.1.0    687  696                              ====Sp1===
2.3.1.0    693  702                                    ====Sp1===
==================================================================================
seq(  720..  779)     gaaaagaaaaccccgaagccggtcgcgccgcccgtcgggccggaggggatatgttcgag
Segments:
2.3.1.0    743  753                          =====Sp1===
2.3.1.0    756  765                                       ====Sp1===
2.3.3.0    764  773                                               =CPE_bind=
==================================================================================
seq(  780..  839)     gacgagccccacgccgagggggcggcggcggtcgccgcggccagggaggcgctgcaggcc
Segments:
2.3.1.0    785  794        ====Sp1===
2.3.1.0    795  806                  =====Sp1====
2.3.1.0    820  829                                           ====YY1===
==================================================================================
seq(  840..  899)     ctgtgccaggaactgaacctggacgagggaagcgcggccgaagccctggatgacttcacg
Segments:
9.9.1299   843  852      ====MPBF==
3.5.3.0    847  856          ===NF-EM5=
2.3.1.0    860  869                       ====Sp1===
==================================================================================
seq(  900..  959)     gccatccgcggcaactacagcctagaggtgagcggcggcaggtgggcggcggccccgacc
Segments:
2.3.1.0    932  941                                   ====Sp1===
1.2.1.0    935  944                                      =====E1===
2.3.1.0    941  952                                            =====Sp1====
2.3.1.0    948  960                                                   ======Sp1===
==================================================================================
seq(  960.. 1019)     ctcgccaggccccacccccggcccgcccccgccccaagcc
Segments:
2.3.1.0    948  960   =
2.3.1.0    966  978         ======Sp1====
2.3.2.1    968  977           ==Krox-20=
2.3.1.0    972  986               =======YY1=====
1.6.1.0    974  983                 =AP-2alph=
2.3.1.0    979  989                      =====Sp1===
9.9.561    981  990                        ==NF-muE1=
2.3.2.3    982  991                         ====WT1===
2.3.1.0    985  994                            ====Sp1===
2.3.2.1    985  994                            ==Krox-20=
9.9.270    985  994                            ====ETF===
1.6.1.0    989  998                                =AP-2alph=

51 segments in this sequence identified as potential binding sites

51 segments in complete file identified as potential binding sites
```