

Assembly: GCA_018150835.1_ASM1815083v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.90

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row_rep1          -gcgtcagctctttttgtgcgcacaaagctcaagcgtATAAATTCGAAGTCGAATCGgaagatgttgcataaaatcagcagtcagcatttctgttgat-
Arthropod_75K    -tatagctactctcctccctactcgtttgtaattATAATTCGAAGTCGTAGTCGgcagtagcagctatgataaaacagcagcaggttgatgacatt-
Rnase_MRP        -taccactattttatatttttttctctTAGAATTCCCAACGTCGTTTTCCcattgcctccacataaaataacccacattatttactcttctgctgtatt-
U6               -caaaacgaacacacagagcgcctcactagttgttATAATTCGCAACGCTATTCTGcattttgttcattataaagaagaaattttgacacatcct-
U6              -cctgactactgaagcctgaacctcctgtctgtccttATAATTCGCAAGTCGTTATTCgcaggttgcaacataataatagacacatttttagctcactct-
U6              -ctctctcctaccctacccaaataccttataatcctATAAATCCCAACGTGTGTAATTCcactctctctcatataaaatcaattttttcccaactctct-
U6              -cacacgtcagtagctcgtatagccctgagcctcctcctATAATTCGCAAGTCGTTATTCgcagctatgaggttataaagaggttaattgacagaaattt-
t6eac            -gataagcattttctgtttgtgtgtgtgtATAAATTCGCAAGTCGTTATTCgacttttacttactccttataaagccttctgtgtgtgtgtgtgt-
tRNAsec          -cgcctgaacttttttttaccctctctcctATAAATCGCAACGCTTTTTCAcctcctctctcacttaaaacacataataaacacatttttagctcttga-
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U1              -tctatgcctgttttctcctcagatagaaatttgacattATAAATTCGAACGGCTCTAGTaaatttttctgtgtatcctctctcagagacagagaaaagc-
U1              -ttgctcactttttcggcctctctacagctctctcctATAAATTCGAACGGCTCTAGTaaatttttctgtgtatcctctctcagagacagagaaaagc-
U1              -cgadaaatttgaattttataacacagctttcctATAAATTCGCAACGCTCAAGcagcagctatgagacccctaggcgcagagccgagaaaagc-
U2              -cacacaaaaattctctaccataacacagcgtttcctATAAATTCGCAACGCTTTAAAGctgaatttgatgagcctgggttatctctgcttaatt-
U2              -cacacaaaaattctcttaggttgacacacagcttttctAAAAATCGCAACGAGTCTAGctgataatttagtggtatgcgcagacttacccttttgaatt-
U2              -aaatctctctctctctctctctctctctctctATAAATTCGCAACGAGTTTAAAGctgataatttagttaaattctctctctctctctctct-
U2              -aaatctctctctctctctctctctctctctctATAAATTCGCAACGAGTCTAGctgataatttagtggtatgcgcagacttattcctcttgaatt-
U2              -acaaaaatacatcaagatatttatacaaaatttgcATAAATTCGAACGAGTTTAAAGctgattttcccaagttgtgtgtccattatcccttttaagtt-
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U3              -attgtacacacacattttattataatagctctATAAATTCGAACGCTTTTAAAGctgagcctgagcagaaabaatttgaagggcagcagcagcagc-
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U4              -ccctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U4              -acctttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U4              -gcctataattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U4atc            -tgaagaattcgaatgctctttttctctatttttctctcaacGTCAAAATCCCAACGGTCTCAGcagcagctcttgaggtctgaaggtctgcacacatg-
U5              -tctcactttatgaggtttttttaaagagttctctcGTCAAAATCCCAACGAGTTAAAGcctcttttcaodtaaatctaatatttaccacttacc-
U5              -tgccctacttttaggggtgtttttaaagaggtgtctctGTCAAAATCCCAACGAGTTAAAGcctcttttcaagtgaggtcaggtatttcccgatttct-
U5              -caacatttttttctcttttttttctcttgcaatccaggtGTAAATTCGCAATGGTCTAGcgtgagtcctcagttatgtcccccgaagccttggtaaaa-
U5              -tacttttaggtgtgtttattttgtcctcctgtttgtctGTCAAAATCCCAACGAGTCAAGcagcagctaggtagcaatctgaattgtgttccaaatgt-
U5              -tctcacttttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U5              -ctctactctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U7              -caagcgcgtttttatacaacctgcgcgtGTCAAAATCCCAACGGTCTCAGcgcgcctatgagagccctatgaagcgcctttgtctctcagactttatatatga-
U11             -ttctcccaaaaaaaaaaacctttcacatattctcctATAAATTCGAACGGTCTCAAGcctctccacacacaaactctcacaactcaactctctct-
U12             -gttgcctcgtttgggaattttaaagcttctctcctctAAAAATCCCAACGGTCTAGcgcgcctctcagatcagctcgcctcagcactgttgaatttt-
OrCD1           -tgttatgtgtaatttcagttattttgtgtgtcctGTCTAATTCGCAATGGTCTAGcctcagaaatgaacacacagcagcgtgttatgtatgtg

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Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNAme18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.