

Eristalinus sepulchralis

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Eristalinus

Assembly: GCA_944738645.1_idEriSepu1.1_genomic

Eri_sep1 | OX122884.1:16895940-16896219 (+) | 280 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 5nt PSE: 0.89

GGGCGGTTCAATACCTCACAGTGTTCBGGTTGGTCACACCCGTTTCCCACTAATTGCAGCTCTAAATTCBAAAGCTTCGACATCCATACCAAAATAAATGCGAAAAAAGTGTGACGCGCACGCAAGGTTTTTCAAGAAAAAGCCGAAATTTGAAAACTCCTTTCTTCATCATATTATAATATATAGAATATAAGCAAAATCAATAAATGAGGAAATAACGTTTAAAACTAATTAAAGCTAAGTTTGTCTGCTGAGGTAAGTGCATTCGCCCTTTTT

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Eri_sep1      -----GTacatccadcdacacaaactcdacattctctTATACTTCACAGAAATTCattctccattctctttacataaaaaacaaacacdaaacctattccctc-----
Arthropod_7SK -----GcaaaagaaatctctctctctctctctctctctCACAAATTCACAGTTACTTtttcattcgatgctatggcaagtagaagttttaaacatggaataac-----
RNase_MRP     -----TgaatatataatctttccattcgatTATAGTTCBAGATTTTTTttcaagagctgccacacgggtatacagtaaatcaatgtgaagcgggaggcgtt-----
U6            -----TcaataaaaaacattgaatgaaatattatataaaataTATAATTCBAGAAATATcttcadattctcttttcaacaadacaadattatataaaacacaaattt-----
U6            -----TggaactagatgacgcagactcttcacactcgataTATAATTCACAGAAATTTgttttaaggagccggtacatatacctttatgaaatcatgaacatc-----
U6            -----TtagacaattgatagatggcgtttattattattaagaTATAATTCACAGAAATTTttaccgcaattgttggtataagatgattagtggacataaaacatt-----
U6atac        -----TttatccaatctcacaattcaacacacattttattctTATAATTCACAGATTTTTTttcaaaaattttaaadatoottaotttttatataaaaaadaaattt-----
tRNAsec       -----aaattgttaactactgattggaattcgttttcattggtTATAATTCACAGAAATTTattcagctgtcttttcttaattctctactatgtgaaagttttgt-----
U1            -----TcacagtcagtataggagaaaaaatttcatttccctttTATACTTCACAGTTAGTTTcttcttagacgagcattgtagttcgaaggagcaaaaggaaagc-----
U1            -----caacaacaaaacacattctctctctctctctctctCACAAATTCACACTCAGTTctctatgtttddadacaaadadadadacaaagacaaagaaagc-----
U1            -----TgcacaagactttgaaatgaaatgttaattcgttcgcacATAATTCACAGAGTCTTcgagcagagagttctgtatgacataaaaggagagcgaagaaagc-----
U1            -----GcaacactgatagattacagctactttctttcattcaTAAATTCACACTCTTGTtctgcatgaggaatgcatacgttagttcagcgaagcagaataaagc-----
U1            -----TccgaaggaggagatggatcagtttgcgttagttggTAAATTCACAGTTAGTTTgggcatgagaattcgtatgatttcagcgaagcaggagaagc-----
U1            -----TccctttctcccccgaattcaattttccatccctTATAATTCACAGTTACTTctctcgaadtaaaacctaadaadcaattattcccccadaaaac-----
U1            -----GacagacacaaatgtgtgaaatctttcttcagcgaTATAATTCACAGTTTGTtctgcttgcagtcgcgtgataacgggatctatgagcggcgttaaagc-----
U1            -----CattttgtgaaataggattttctctttgcattttTACAGTTACAGTTAGTTTgacaggaaggtgggttaagcaataagagatggcgggaagc-----
U2            -----TcaactcaacgaacaatttataaattcaattcgaatTATAATTCACAGTCCACTTctcgaadattatctccattttacccctcgaatgttccgtatagtt-----
U2            -----ccctgtatagggtgtttcagaattatcgttcgctTACAGTTACAGTTCACTTtctgcatggcatcccggaagctctctgttgagcgtgagtcagtt-----
U2            -----CTcgaactcgaacagattttaaaattccattcaaaTATAATTCACACTTCACTTTgtgcaggagcaactgtgaagttagctgatgaggagttttcagtt-----
U2            -----aaatgaaaaactattttcaaaaattttttdaaatTATAATTCACAGTTGCTTtcttcataaatttccctcaaatctcacttccaaaadadaaaatt-----
U2            -----ccgtgatattagggtgttttcggaattatcatctgcctTACAGTTACAGTTCACTTTgtgcattggcatcccggaagctctctgttgagcgggagttagtt-----
U2            -----acaacaatttatcattgttttctcattctgctctTATGATTACAGTTCAGTTTgagcaaatgtaccfacaTgtagtcgcatatttgcataggagagtt-----
U3            -----TagtctgaactcgaatgtaattacattctttTACGATTACAGTTCAGTTcatccctgtatctctctttagatcccatccctccctcccaactt-----
U3            -----cagttctgagacttcgaggttgattacattcgtttTACGATTACAGTTCAGTTcatcagttgtagtctgtttagacgcgcatcgaggcactgaaaagtt-----
U3            -----TagtgtgattcagaagttgtttacattcgtttcaaTACAATTCACACTCAGTTcagctgtttgtatctatcagatgccgatcgctggcgttgaagatt-----
U3            -----GtcatccdcacdaatctctctcttccattcattctTACAATTCACAGTTCAGTTtcccccgaadattctataacaadccaattccctcccttgaatt-----
U3            -----acagactctcttggtcagatttctgcatctgattTACAATTCACAGTTCAGTTcagtcgcatcaccattctcagtcagatcgttggtagaggagact-----
U4            -----GacaaggactcgttatttattctctagttttactgtTATAATTCACAGTTAGTTTtgacagacagttctcaagagagaaaaatttagcagatgagtt-----
U4            -----GaaaacdaaadtatggaagaaatgatttctcattcTATAATTCACAGTTGCTTcaagcaaatcccatctaaadacaadccctccctcttgaattctt-----
U4            -----TgcaatggaattatgtgaggaattctcattcagattTATAATTCACAGTTGCTTgcgcaagatgtcagattagacgaatcagcagattttgttaagtt-----
U4atac       attgaaatcatttctggttgaataaaattttgcatttgcaTGAATTCACACTCAGTTTcaagccaatttcacgtatgtacaaaaaacctcagtcattct-----
U5            -----CotttctctctctctctctctctctctctctctTATGATTACAGTTCAGTTTadacattcttttaadtaadadadacotccaaocatttgaat-----
U5            -----TgcaacactgaaagggaagcattttgtgcactcgtttTATAATTCACAGTAACTTtgacagaggttcagtgtaagaatttgtctggggacbtgggtct-----
U5            -----TgcatcacctagtggtgaaattctttgtctctcattTATAATTCACACTTACTTcggtaaatatctgtacagagactatgtctaccacatttttgag-----
U5            -----CotttttaacatttaataataacactcttttacttTATAATTCACAGCATCATGaacatgattgaaggttaagatttgaaccctccctccctgaat-----
U5            -----TcttaagaatacagcggaacacgatttttattcattTATAATTCACAGCATCATGaacatgatttagggtaagattgaagcggcagtggtatgact-----
U5            -----attttcaacaagtgaaataaaagatcccttttctcgtTATAATTCACAGCATCATGaacatgatttagggtaagattgaagcggcagtggtatgact-----
U11           -----atttgaattctctctcttctctctctctctctctctTATGATTTCGATTGAGTTTctcgaaaaaatataaaaaacacacccaatccctccctccctt-----
U12           -----agctttctctctccgaaaacttttttcgattcgtTATGATTTCAGATTACTCTctcgccgtacagttacagtagagaaagaaacggacttggattct-----
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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, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.