

Drosophila erecta

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > melanogaster subgroup

Assembly: GCA_003286155.2_DereRS2_genomic

Dro_ere1 | QMER02000005.1:16739303-16740385 (+) | 1083 nt | lncRNA: no consensus e-value: 2e-198

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

GGGGCGGTCSTGCAATTCGCGACCAACGACGGGTTGGGCGCATCCCGCTCATCCCGCATCTCCAAATTTGCCCGCTGGTACGCGAATGTACGATTCGCAAAATCTTGGTATCTCTCTCCATCTCTGATGACCAAGCCCCCAAGGCGGGAAG
 CAGCGCTACATAGGCGGGGACCCCCCATCAAGGGGGGGGGGGTGGTGGACGGCAATTCGACGGGCGACAGGACGACGATCAATAAAGCAACCAATCAACCAACCGCAAAAGTCTAAGACATCTGTATACGAAATTTGAATATGATG
 TCGCAAAATTAAGAAAAACCAATATCAGACAAATTTGTATATCAATGCGAAACAAAAAATTTTAAAAATGACATCAATAATATCAAAAAAGAGAACGATCTTAAATATGTCAGCTAGTATAGTAATATCCCATCTGTTGTCATGGACACAG
 CCGCAAAATATCTTGTAATATCGTAATATGATATTAATACCTCAAAATGCGTGGTGGTGTGTCGCTGTCGTGATATCGTGGCGGCGGCGCCGCCGCGCCGACCAGCGGCTCATGTGTGCCCATCTGCGCCGCGGCCCCCAATTTGCCCGCG
 CCAATGATCTGCGGGGACGATGGACACGTGGGGGCGACCCACAGGACATCTGATGGTACCAAGCGGCGGCGCCCAATTTGATCGGCCCTCTCGCGGGGAGAGCTTGTCGTGGGCGGCGACAGGAACGCGTCCGGGAAGCGGGCG
 GAGAGTGGAGAGCAAGAACCGGAGACGGGCGACCAAAATGGTGGTGGTCGGTACCGGGGCGGACGCGGCGGCGCTCCAAAAAATTAACCATGACGAGGCTTTAAGGCAAAATCTCAAAATGAACAAACATATTAACCAAAATATTTGACACAG
 AAAACAAGACGAATTCATAAATGAGCAATATGACACACCAATTAATAATGGCAAAAAGCAAAAACGCGGCTCAAAATTCACGACCAACACGTCGAAAAAGCCTCAGTAATAATTAATACCCACCAAAAACACCGTAATTCGTTGGTGGCTG
 CAAAGGAATGCGCTTCAATATCGCCCTTTT

Dro_ere2 | QMER02000016.1:1946567-1947053 (-) | 487 nt | IncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 1.00

[illegible]

	Dro_ere1	Dro_ere2
Dro_ere1	-	29
Dro_ere2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

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Dro_ere1      ---- gggaaagctctctcgttttctcactgctctccgcTTATAATCCCAAGTGGAAATCagcaggacacagcttaaaaccctcgttctgaaggaacccacgc-
Dro_ere2      ---- lacgctcagctatttattatctgattgagttttTATAATCCCAACGTCttttcggcgttgtgcctataaagacacctcaaaactctgtgactt-
Arthropod_7SK ---- ggTggcgcacccacacacttadctacttgcacactTATAATCCCAAGTGCttATtcaaaaaatoodatataataaaacacccccccttcttttactc-
RNaSe_MRP     ----          ggcctatttctatcacaccgcctcgtTATAATCCCAACGTCgttttcgcagatagccgctttaaataccgctatgacatgagcagtgatgccggtt
U6            ---- actctgccagagggcgccgtgcctcactattttTAAATCCCAACTATttttCgggtgtttttctatataataaaaaatttcgaacgttacttc-
U6            ---- gcttttcccaaaadccccttccctctactattttTATAATCCCAACTCTGtttcgaatcctctctctatataataaaaaatttcacaaacttacttc-
U6            ---- aacactacacaccccctacacttctctgcactctTATAATCCCAAGTCTGttCaaacaaagtgcctataataataaaaaagatccaccattgaacttctc-
U6            ---- tttaaacgaagggctctcacaagacattcaaatctTATAATCCCAAGTCTGttCagagtggttaattatataatagacacatttccacacatttccac-
U6atac        ---- gacagctctccatctactctctcTAAAAATCCCAAGTCTGtttcccaaaagctgagctctcctcctcctcctcctcctcctcctcctcctcctc-
tRNAseC       ---- gtcagatcttctggaattcccccacagctactTAAAAATCCCAAGTGCttATtCagcacacgctgcatataaagtaagaaattctacaactgtaaat-
snorNAME18SA1806 ---- gaatttttctttataaaaaaagctgcattTATAATCCCAAGTGCttTtatcgcgctcgttctgataaaaaagacacacgctcgtcttcaaatctctc-
U1            ---- ttcgaaggtatttgaggtgattttctgtcagaagacgacTGAATCCCAACAGGtTtGGCagttttctctgtgaaaacctcgcagctcagcgcgggaagac-
U1            ---- ttcatctctctctctctcttcttctctatccacacTATAATCTTAAGTtTCTAGctcccccctatodaaaacctcttcccaactctctctctctctct-
U1            ---- cctcagacacaaattcgaactcacaagcgtatgcacatTATAATCCCAAGTtTATGttgcgccctctatgaaaaccccccttcccaagctcgaatgaagc-
U1            ---- atactctgaagggctctctctctctccgacgctctTATAATCCCAAGTtTCTAGctctctctgagcagtgagacccctcgcgcgcagacacaaagc-
U1            ---- acccaactctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U1            ---- gcatcatcttctcgttgaataatctctgcacactctcTGAATCCCAAGCAGtTtGGCagatctctcaaggaacccccaaggttggtgcgtctggaagc-
U1            ---- ctttcgggggtctctctctcagcagctttctcTAAACATCCCAAGTGCtTtGGccgccctctctatgagaaacctccccacggcggaagc-
U1            ---- catactctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U2            ---- gccatagaaggtctgataacttctctacttccattTATAATCCCATCTGGTtCAAGcggtttgctatgagaacccctgtcttcttctcgaatt-
U2            ---- accgctcatttgatgcacattctgagtggtgcatactTATAATCCCAACGTCtTtGGctgtgtctctatgagaacccctgtcttcttctctctacttt-
U2            ---- tctatcaaaatgcacaactatccctccacacTCTATCTTAAGTtTCTAGctctctctctctctctctctctctctctctctctctctctctctctct-
U2            ---- accaggttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U2            ---- ttcatcaccatttttgattctgaaactctacatattTATAATCTTAAGTGCttTtAGctgcaatgcataaagctctcttcttcttcttcttctctctct-
U2            ---- ccccaactcacacaataattctccatctatctatctTATAATCCCAAGTGCtTtGGcccttctctatodaaacccctctcttcttctctctctct-
U3            ---- cgcgcgctcgtcttcaattctctgtcggcgcagctctTATAATCCCAACTGTCtTtGGccctcggcgacacaaagctcagaggtgggcacagaaaaggt-
U3            ---- cgcgcgctcgtcttcaatttctctgtcggcgcagctctTATAATCCCAACTGTCtTtGGccctatgcacacaaagctcagaggtgggcacagaaaaggt-
U4            ---- caaacctcttccatctctctatctctctctctctctTATAATCCCAAGTtTCTtGGctctctctctctctctctctctctctctctctctctctct-
U4            ---- actcgtctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U4            ---- ggttctctgctctctctctctctctctctctctTATAATCCCAAGTGCtTtGGcacaactcgaactagagagctatgattctctgatttgaggactcaac-
U4atac        ---- tctcaattctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U5            ---- aaaaatttttaacgttgtcgtcttttctcagctcgcacTATAATCCCAACAGTCTtGGcagatttgagctctatctctctctctctctctctctct-
U5            ---- tctctaccataaggtctataaatttctctctcgaatctcccTATAATCCCAAGAGTCTAGctcgaatcgaatagatgacacctctctctctctctct-
U5            ---- atcttctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U5            ---- gccacagtttttaataaagaactccagcctctctctctTATAATCCCAACATGTTCTGcaccaccccatctatgacacataaaaaatctatctct-
U5            ---- tctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctctct-
U11           ---- Tctcccaatctcaacaaacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacacac-
U11           ---- tctctctcaaaagctttctcaactcgcacactctctctTATAATCCCAAGTGCtTtGGgttaactctcatatgcctctccatcccaacccaadcaattc-
ORC1          ---- gtgcatacaaaaatttccaccacacgcgggtgcTATAATCCCAAGCAGtTtGGcccgccgtgagtggttactcagcgaactcttctggaatttctt-

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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.