

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > quinaria group

**Assembly:** GCA\_035042165.1\_ASM3504216v1\_genomic

**Dro\_kun1 | JAWNLU010001704.1:2421755-2422717 (-) | 963 nt | lncRNA: noe consensus e-value: 6e-201**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

GGGGCGTGTGCATTTCGCAGTAACGACGGTTGGACACATCCCGTTTACCCAAATCTGAAATTTGTGTCCTTGGATGGCAGAGCAGATAAGTTACGCAAACTTTGGTCAAACTCTGAAAGCAAAAAACAAAGCAAAATCGAAATTCGCAAAATCGCAAAATCGCAAAAGCAAACTACTTATATATATAAAAAAATATAAAACAACAAAGATCTAAACAAGAAATCACGAAACGCTAAGATAAAATAATGACAAAAAAACCTATCAGACCCAAAGAAATATCAATGCAAAACAAAAAAATCTAAAAACAATAAAATACGTAACCACTAACTTAACTTGAATCTTGTAGTAACTATCATCTCTGATTCGCTTATCAGGACAAATGAAAAACCTGAAAAAAAACCTTAAAAAAATATTAATAAACTGCAATTCGATTAATTCGTCGCGACCAATGTCGCGATATCGCCCAAGAGCGCGCTGGGAGABAGACCGCCCGGCTCTTTGGGCTCTCTCTGCGACCTCAACTCCCGCCCAAAACACAAATATACACACACACACATCTGTAGTCGCAATTAAGTCACGCBCTAACTCCCTGTGCCCACTCTCACTTAAGTTTGGTGTACATGGATGTGGATCAATGGGTACCATATGTCAGCTTCBCTTGAAGGAAAAATGCTGGCAGCGCGCGTCCACAAAAAATACCATAGACAGCTTTAAGGCAAAATCTTAAATGACAAAAAAAGTATAAACCAAAATCAATTGTAAACAGAAAAACAAACCAATTCAAAAAAATGAGCAATATGACCAATACAGTAAATATGCAACATACATAATTAATGGCAAAAAACAAAAATGAAAAACTGCAAAATACGACACACACCTTCGAAAAACCTCAGTATAATACACATAATGCTGGGTGCTGCAAAAGGAATGCCTTCGTTGTATCGCCCTTTT

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.