

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified tarsi group > spoon tarsi subgroup
Assembly: GCA_035043855.1_ASM3504385v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

GGGGCGGTCGTGTATCCGCGAGTAAAAAGACGGTGTGGACATCCGCTCTCATACCAAGCAAACTCAGAAATGTGTCTCTTTGGGTTACAAACGACGAAGATTCAGATTGAAAAAAACAATATCACCTTCGTATTCTCTGAAGCAAA
 AACTCCAAAACCAAACTCAAGCAGAAATTGCAAAATATAAAAACAACATATAAAAAACGAAATACACAGCAAAATGCTAAAAACAGAAATCCAGATTCGCAAGATTAATATCAGACAAAAAAATATCCAAATGCAACAAAAAAATACAA
 AAAACCAAGACATAATCAAAAAAATGCACTAACTTGTGAACTAGSTATAAATACATCGTGTATTATTCAGGACGCAAAAAAATCTGAAAAAATCTGAAAAAAATCTAAATAACTACAAAACTGATCGTGGTGTGTGTCT
 CGCTTCTGTGAATCGCTCTGACGCGCCAGAGTCCGCCCAATCAATCGGGTGTGCTGACTACTATCAATGAGAGGGGGTCCCAATCAGGGACGCGTGAACCTCTCTGACAGCAGCTCTGACGAGGACAGCACTACTGAGAAAGAGCAAC
 ACACACACATCTGCTGCTCTGACTGAGGAGGAGAACCAACATCACTGTGTGTGGGTGACTCGGTGCTGCAATTTGGGGCTGAGTCACTGTCTCCCTCTCTTGACCATCTCTACAGCAGTGTGTATTTGGAGTCAAGTGGTCAATGTGTGACCT
 CAGACAGCTTCTGGGAAAAAGGCTGGCTCGGCGGCTCACAACAAATATCAATACAGAGACGTCTTAAGGCAAAATCTAAATAGACAGAAATGATAAACCAAGAAACAAACAAAAAAACAAAGATTTCAAGAAAAATGCAACAACTACTTAATAC
 TGGCAAAAGGCTGCAAAATACGACACACACCTCTGAAAAATGACCTCAAGTAAATACACACACATATGTGGTGGGTGCTGGAGATGTGATGTTGTCTGCCCTTCTG

rro_per1
 Arthropod_7SK
 RNase_MRP
 U6
 U6
 U6atac
 tRNAsec
 snoRNAme18S1806
 U1
 U1
 U1
 U1
 U1
 U2
 U2
 U2
 U2
 U2
 U2
 U2
 U3
 U3
 U4
 U4
 U4atac
 U5
 U5
 U5
 U5
 U5
 U5
 ORC1

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.