

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > immigrans group > nasuta subgroup

**Assembly:** GCA\_019972355.1\_D\_kohkoa\_1.0\_genomic

Dro\_koh1 | BJEL01000052.1:2240073-2241242 (-) | 1170 nt | lncRNA: noe consensus e-value: 2e-164

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.89

[illegible]

Dro\_koh1  
Arthropod\_75K

RNase\_MRP

U6

U6

U6

U6atc

tRNAsec

tRNAsec

mRNAME18SA1906

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.