

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Zaprionus > Zaprionus subgenus Zaprionus > armatus group > vittiger subgroup

**Assembly:** GCA\_018904035.1\_ASM1890403v1\_genomic

**Zap\_orn1 | JAEIFZ010000023.1:4451834-4453273 (+) | 1440 nt | lncRNA: noe consensus e-value: 5e-170**

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.89

[illegible][illegible]

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.