## Drosophila athabasca

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > obscura group > affinis subgroup

Assembly: GCA\_008121215.1\_UCBerk\_Dath\_EB\_1.0\_genomic

## Dro\_ath1 | CM017796.1:60045569-60046840 (-) | 1272 nt | IncRNA:noe consensus e-value: 3e-178

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

## Dro\_ath2 | CM017794.1:1516556-1517149 (-) | 594 nt | IncRNA:noe consensus e-value: 7.0e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.97

	Dro_ath1	Dro_ath2
Dro_ath1	-	31
Dro_ath2		-

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



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.