## Drosophila arizonae

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > repleta group > mulleri subgroup

Assembly: GCA\_001654025.1\_ASM165402v1\_genomic

## $Dro\_ari1 \mid LSRM01000004.1:4087249-4088176 \text{ (+)} \mid 928 \text{ nt} \mid IncRNA: noe consensus e-value: } 7e-158$

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.78

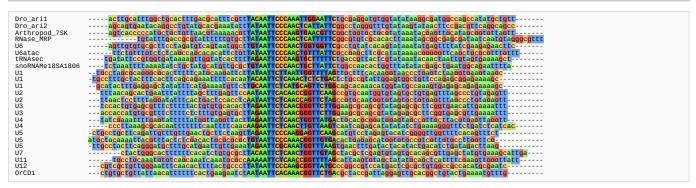
## Dro\_ari2 | LSRM01000001.1:19780883-19781553 (+) | 671 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 18nt PSE: 0.99

GGGCEGT CEAGT GCCCCACAGCAGCAACAGEGT TEATACACT CTCCCCGACTEATT GTEACTTTACACT TAGACT TAGATTT CAAATT TAGATT TAAATTT CAAATT AGATTT ACACT TTACCT TAAATTACACT TTACCT TAAATTACACT TTACCT CAAATTACACAT TACACAT TACACT TACACAT TACACAT TACACAT TACACAT TACACAT TACACAT TACACAT TACACT TACACAT TACACT TACACAT TACACT TACACAT TACA

	Dro_ari1	Dro_ari2
Dro_ari1	-	44
Dro_ari2		-

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.