## Drosophila nikananu

**Taxonomic lineage:** Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > montium subgroup

Assembly: GCA\_008042635.1\_UCB\_Dnik\_1.0\_genomic

## Dro\_nik1 | VNJV01000004.1:52381-53609 (-) | 1229 nt | IncRNA:noe consensus e-value: 1e-191

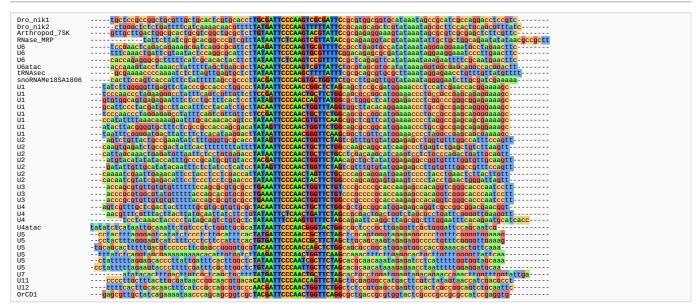
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.91

## Dro\_nik2 | VNJV01011790.1:3136-3626 (+) | 491 nt | IncRNA:noe consensus e-value: 1.3e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.99

	Dro_nik1	Dro_nik2
Dro_nik1	-	22
Dro_nik2		-

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.