## Neoceratitis asiatica

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Tephritidae > Neoceratitis

Assembly: GCA 030068015.2 ASM3006801v2 genomic

## Neo\_asi1 | CM061526.1:41814302-41815284 (-) | 983 nt | IncRNA:noe consensus e-value: 9.2e-18

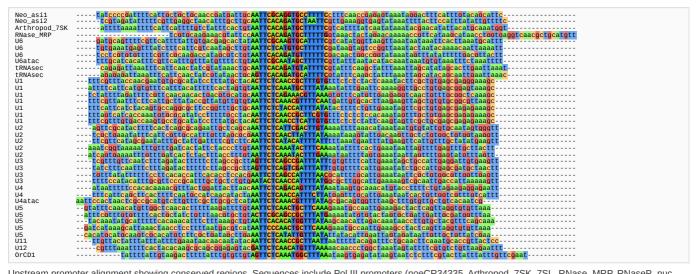
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.95

## Neo\_asi2 | CM061525.1:63830223-63830496 (-) | 274 nt | IncRNA:noe consensus e-value: 5.5e-05

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

	Neo_asi1	Neo_asi2
Neo_asi1	-	21
Neo_asi2		-

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.