## Delia radicum

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Anthomyiidae > Delia

Assembly: GCA 021234595.1 iDiv DRa 1.0 genomic

## Del\_rad1 | CM037851.1:256701124-256701389 (+) | 266 nt | IncRNA:noe consensus e-value: 1.7e+00

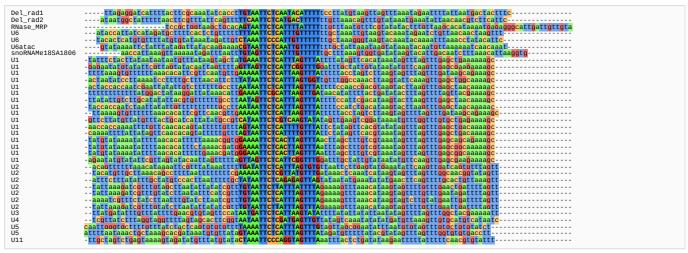
5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.89

## Del\_rad2 | CM037851.1:256675704-256675886 (-) | 183 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.81

	Del_rad1	Del_rad2
Del_rad1	-	44
Del_rad2		-

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.