Dryomyza anilis

Taxonomic lineage: Brachycera > Muscomorpha > Sciomyzoidea > Dryomyzidae > Dryomyza

Assembly: GCA 951804985.1 idDryAnil2.1 genomic

Dry_ani1 | OX638131.1:43055348-43055851 (+) | 504 nt | IncRNA:noe consensus e-value: 4.7e-03

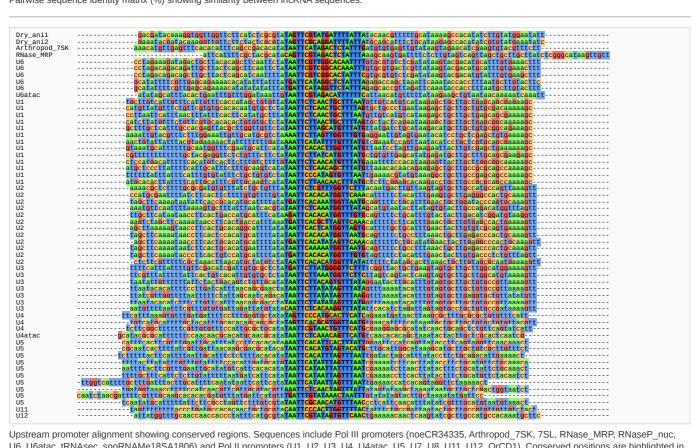
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.82

Dry_ani2 | OX638131.1:43053480-43053953 (+) | 474 nt | IncRNA:noe consensus e-value: 1.5e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.82

	Dry_ani1	Dry_ani2
Dry_ani1	-	77
Dry_ani2		-

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.