Germaria angustata

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Tachinidae > Germaria

Assembly: GCA_963681545.1_idGerAngu1.1_genomic

Ger_ang1 | OY813000.1:22530794-22531226 (+) | 433 nt | lncRNA:noe consensus e-value: 2.8e-06

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 5nt   PSE: 0.94

Ger_ang2 | OY813000.1:41734992-41735383 (+) | 392 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATTGC   Internal max. Poly-T: 4nt   Trailing-T: 8nt   PSE: 0.87

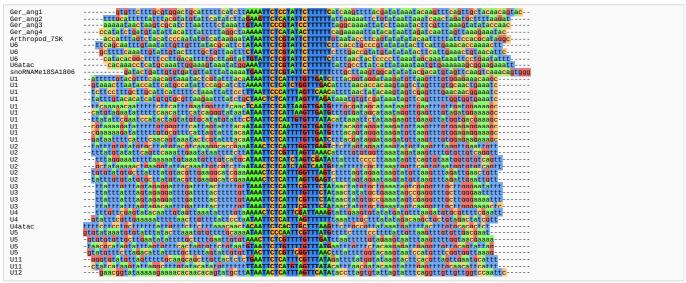### Ger_ang3 | OY812998.1:44672214-44672584 (+) | 371 nt | lncRNA:noe consensus e-value: 1.5e-01

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 6nt   PSE: 0.86

Ger_ang4 | OY813000.1:41743740-41743967 (+) | 228 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 5nt   PSE: 0.90

	Ger_ang1	Ger_ang2	Ger_ang3	Ger_ang4
Ger_ang1	-	49	50	37
Ger_ang2		-	45	42
Ger_ang3			-	36
Ger_ang4				-

Pairwise sequence identity matrix (%) showing similarity between lncRNA 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.