Drosophila trichaetosa

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified tarsi group > bristle tarsi subgroup **Assembly:** GCA 035043205.1 ASM3504320v1 genomic

Dro_tric1 | JAWNNE010000074.1:13279722-13280739 (-) | 1018 nt | IncRNA:noe consensus e-value: 1e-156

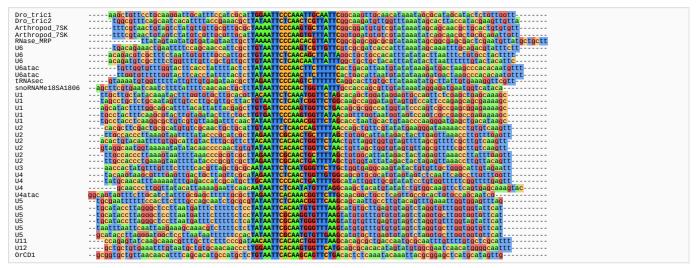
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.84

Dro_tric2 | JAWNNE010000072.1:792891-793169 (-) | 279 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

	Dro_tric1	Dro_tric2
Dro_tric1	-	17
Dro_tric2		-

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.