Nowickia ferox

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

Assembly: GCA 936439885.1 idNowFero1.1 genomic

Now_fer1 | OW387024.1:92396286-92396856 (-) | 571 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.95

Now_fer2 | OW387024.1:107641673-107642210 (+) | 538 nt | IncRNA:noe consensus e-value: 3.9e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

Now_fer3 | OW387023.1:99357525-99357934 (-) | 410 nt | IncRNA:noe consensus e-value: 1.8e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.93

Now_fer4 | OW387025.1:59225814-59226123 (+) | 310 nt | IncRNA:noe consensus e-value: 6.8e-04

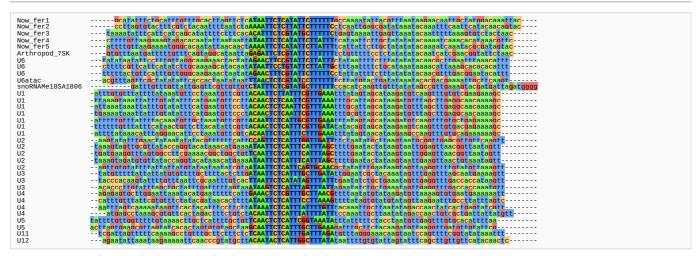
5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.94

Now_fer5 | OW387024.1:92751493-92751815 (-) | 323 nt | IncRNA:noe consensus e-value: 1.4e-01

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.94

		Now_fer1	Now_fer2	Now_fer3	Now_fer4	Now_fer5
	Now_fer1	-	46	40	39	41
	Now_fer2		-	44	41	43
	Now_fer3			-	46	50
	Now_fer4				-	81
	Now_fer5					-

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.