Linnaemya tessellans

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

Assembly: GCA 951800035.1 idLinTess1.1 genomic

Lin_tes1 | OX637535.1:19678515-19679019 (-) | 505 nt | IncRNA:noe consensus e-value: 5.9e-01

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

Lin_tes2 | OX637535.1:33314945-33315337 (-) | 393 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.95

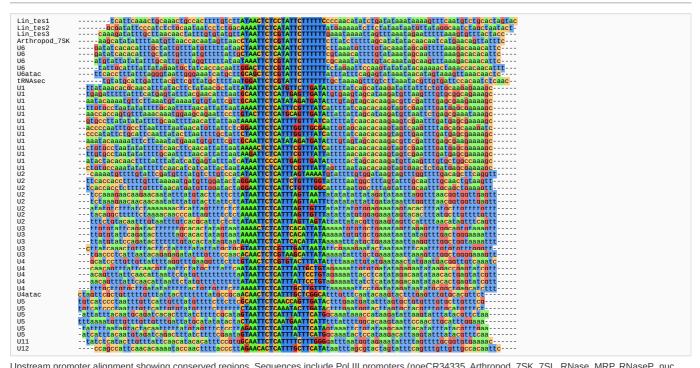
Lin_tes3 | OX637532.1:149242285-149242675 (-) | 391 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.96

GGCGGTTCATAACCTCTGCATTGAAAGGGTTGTTCACCATTGCTAACCAATTGTGAACCACAAAATACCAAAATTCCTTCTGGCTAAAGGCGTCTCACCAGAGGCGCTGAACTTCTGAAAATGATACAAATTCCTCCACCAAAAACCAAA TTTCTCTCTTCTCTCTGTGTTTACATGCAAAAGAAAAACTTTGAATATGCAACTAAAAAGCCTTCAACACAATTCCAATTCCAATTCCAGTTCAAATCCAAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCAAATCAAAATCAAAACCAAAAACACAAATCCAAAAACCAAAAATCCAAAATCCAAAAACCAAAATCCAAAAACCAAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAAATCCAAATCCAAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAAATCCAAATCCAAATCCAAAATCCAAAATCCAAAATCCAAAAATCCAAAATCCAAATCAAATCCAAATCCAAATCCAATCCAAATCCAAATCCAAATCCAAAATCCAAATCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCAAATCAAATCAAATCAAATCAAATCAAAATCAAAATCAA

	Lin_tes1	Lin_tes2	Lin_tes3
Lin_tes1	-	45	45
Lin_tes2		-	47
Lin_tes3			-

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.