Tachina lurida

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

Assembly: GCA_944452675.1_idTacLuri1.1_genomic

Tac_lur1 | OX101754.1:106855010-106855566 (-) | 557 nt | lncRNA:noe consensus e-value: NA

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

GGCGGTCTTGATATTCTCCTTGAACAGGTTGCAAGCAACCCTTAATTGCTTTTAAACTTCTCCTTAATTATCACCCCATAGAATCTCAATAAGCATCTTGTGTGCTTCCATTAACAATAATACATCTCAATATAGGCTTAGGGAAGTACA
TAATCAAACTAAAGCCATAATAGAGCTCAAGCTTTGTTGTGATATTAGTAATTAGTATTAATAATTAGTACATACATACATAGATAAACCAAAAAACGATCTCAGAATACAATATATATACGATCGTTGCATTGCGTAGTTACCGCTGATT
TCAGGGAGAGGGGCGTGTATGCTGCCTCACTCTCACTCCTTGTTAAAAGTGGAAATGTATATATTAAATCGTAATGCAGCGAAGCTAACTAACCATCGATGTTGTGATAAATAGTTAATAAATATGTGATAAAAACTACTTGCCATCCGT
TGCCAATACTAACACACCGGCAGCGTTAGAAATGTGATAAAAAAAGGATGATTTATAGGGAATATCCAACGACAAACACCATCATGTTGTCGATCGCCAAATTTTTT

Tac_lur2 | OX101754.1:136805743-136806264 (-) | 522 nt | lncRNA:noe consensus e-value: 7.8e-01

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

GCGGTCTGATGTTCCACTTTGAAATTAGGTTGTACACATCCCCACAAATAAATTGTGTTAAAAATGAACTTAATTGAAACTTTCGTCAAAAATTAATAATTGCAACCAACCAACTACTTGAATATATAATTTAAAGAACTACAATGGAA
AACTTAATTTAAATGATGTCCCGGCTTGTATATGGAATAAAATAATTAATATTATCAAAAGCAAACAAAATGAAAAAAAAACTCATCTCTTCTCAGTCAGTAGATGTTGCAGTATAGACCAGAAGGCGTAACTAATTGCACCTACAAAACG
ATTGTCACACTTTCTGGAATACAAACATGATGTCCTTCAATTGAGAGAGAGAGCTTAAGCAGATTTAAAAAAATGGTCAAATCAAAAACCGATAAACTAAAATGAAAAATGAAATAAACCATAGACATTTGTGGCAAAAAAAATACCAAA
AATAGCAATAAAAATAGCGGGTCAAAAATATCAACAAAAGTGGTTGGAACATCTTGTGATCGCCCATTTTTT

Tac_lur3 | OX101752.1:142795812-142796231 (-) | 420 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 6nt   PSE: 0.89

GGCGGTTAGTAATCTCTGCATTGAAGGGGTTGTTCACATTCCCTAAACAATTGTGAAAATTAGCAAACATGTTAATAAAAGAAATTCCAACCAAAGCCAGTTAGCAGCTCTCAAACTGATGACTACAATTTCTGAAATATTAAATAACAC
AAATTCAATTTCTCTCTCTCTTTCTTTCGCAAGTTTAAAAACACTGATGCTCAAATAGAAAAACTTAAAACTATGAAACTAAAAAAAGCCTTCTTCCTCCTTCGATAGAAATTCATTTCAGTTCAATTCCAAACTTTACAAAAAT
ATGCGTGTCAAAACATTCCAAACACTTTCAACTCCAATGAGCGCGCAAGATTTGAATAAATTTCGAGCCAATTTGAAAAATTCATATGCGAGATTACAAAAGGGGTAATCGCCATTTTTT

Tac_lur4 | OX101755.1:79101634-79101936 (+) | 303 nt | lncRNA:noe consensus e-value: 1.1e-04

5' motif: GTGGT   3' motif: ATCAC   Internal max. Poly-T: 3nt   Trailing-T: 7nt   PSE: 0.90

GGTGGTCTGATTACTCCTTGTTGAAACGGTTGGTCACATCCCATTAATTGTGACAAAATATACTTTGATATAAACTACCATCATATATATACTAAGATATTTCTTCCAAGAAAACACAAAACAAATGAAAAAACCAACAACAAACAATTC
AAAAACAAACAAAAAACTTCTCTTGATCACTTTCTGTTGCCGTGTGGTGGCAGGCTGTGATCAAGAACCAATTGACGTAAGTTAATATAAATTTAATAAACTGGAGTAACTAAAGTGAACACACTTGTCTGTGTTTGTGATCACCACTTTT TTT

	Tac_lur1	Tac_lur2	Tac_lur3	Tac_lur4
Tac_lur1	-	50	40	37
Tac_lur2		-	47	41
Tac_lur3			-	43
Tac_lur4				-

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.