Tachina grossa

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

Assembly: GCA_949987645.1_idTacGros1.1_genomic

Tac_gro1 | OX465276.1:57664909-57665463 (-) | 555 nt | lncRNA:noe consensus e-value: 9.5e+00

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 4nt   PSE: 0.94

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GGCGGTCTTGATATTCTCCTTGAAAAGGTTGCAAGCAACCCTTAATTGCTTTTAAAATTCTCCACCATTATCACCCAATAGAATCTCAATACACATCTTGTGTGCTTCCATTTACAATACATCTCAAAATTAGGCTTAGGGAAGTACATA
ATCAAACCATAGCCATAATAGAGCTCAAGCTTTGTTGTGATATTAGTAATTAGTATTAATTATTAGTAACATAGATACATACAAAAACCAAAAAATGATCTCAAAATACAACACATATACGATCGTTGCATTGCGTAGCCGCCACTG
ATTTCAAGGAGAGGGGCGTGTATGCTGCTTCACTCTCACTCCTTGTTAAAAGTGGAAATGTATATATTCAAACGTAATGCAGCGAAGCTCAGCTTCGACGTTGTGATAAATAGTAAAATAGTGTGAAAAACTACTTGCCATCCGTTGCCA
ATATCAATACACCGGCAGCGTTAGATATGTGATAAAATAGGATGGATGATTTATAGGGAATATCCAACAACAAACACCATCATGTTGTCGATCGCCAAATATTTT
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Tac_gro2 | OX465276.1:30956773-30957303 (+) | 531 nt | lncRNA:noe consensus e-value: 2.1e-01

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 6nt   PSE: 0.93

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GGCGGTCTTGATATTCTCCACTTTGAAATTAGGTTTTTACACATCCCTACAAATAAATTGTGTTAAAAATGAACTTAAGTAAAACTTTCGTCAAAAATTAATAATTGCAACCAACCAACTAATTGAATATATAATTTAAAGAACTACAATGAAA
AAACTTAAATTTAAATGAATGTCCCGGCTTGTATATGGAATAAAATAAATAATAATCAAAAACATCAAAAATGAATAAAAAAAAAATCATCTCTTCTCAGTCAGTAGTAGATAGATATTGCAGTATAGACCAGAAGGCGTAACTAATTGCAAC
TACAAACGATTGTCACACTTTCTGGAATACATACATGATGTCCGTCAATTGAGAGAGATAGAGCTTAAGCAGATTTAAAAAAAATGGTCAAATCAAAAAAACCGATAAACTAAAATGAAAAATGAAATAAACCATAGACATTTGTGGCAA
AAAACCAAAAATAGCAATAAAAATAGCGGGCCAAAAATATCAACAAAAGTGGTTGGAACATCTTGTGATCGCCCATTTTTT
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Tac_gro3 | OX465274.1:155956826-155957242 (-) | 417 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 7nt   PSE: 0.85

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GGCGGTTCGTGATCTCTGCATTGAAGGGGTTGTTCACATTCCCTAAACAATTGTGAGTGAAAATTAGCAAAATGTTAATAAAAAAAAATCCAACCAAAGCCAGCCATCATCTCTCAAAGTGATGACTACAATTTCTGAAATATTAAATGA
ATAACACAAATTCACTTTCTCTCTCTCTGTCCTCTTTCGCAAGTTTAAAAACATTGATACTCAAATAGAAAAACTTAAAACCAAAAAAAGTATTCTTCTTCCTTCGATAGAAAATTCAGTTCAGTTCAATTCCAAACTTTACAAAAATCTG
TGTCAAAACATTCCAAAAACTTTCAACTCAAATGAGCGCGCAAGATTTAAATAAATTTCGAGCCAATTTGAAAAATTCATATGCGAGATTACAAAAAGGGTTAATCGCCATTTTTTT
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Tac_gro4 | OX465277.1:72930441-72930755 (+) | 315 nt | lncRNA:noe consensus e-value: 2.0e-02

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

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GGTGGTCTGGTTACTCCTTGTCGAAACGGTTGGTCACAATTCCATTAATTGCGACAAAATATACTTTGATATAAAACTACCATCTAATTATATACTAAGATATTTCTTCCAGAAAAAACAAAACAACAAACAAAATGAAAACAAACAAAC
AAAACAAAACAAAACAAATGAAAACAATTGAAAACAAACAAAAAACTTCTTCTTGATCACTTGTGATCAGGAAAACTAATTAACGTAAGTTAATATAATTTAATAATAAACTGGAGTAACTAAAATGTAAACACACTTGTTTGTGTGTTTGT
GATCACCATTTTTTTT
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	Tac_gro1	Tac_gro2	Tac_gro3	Tac_gro4
Tac_gro1	-	47	43	39
Tac_gro2		-	46	41
Tac_gro3			-	46
Tac_gro4				-

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.