Sphaerogastrella javana

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Sphaerogastrella

Assembly: GCA_037040025.1_ASM3704002v1_genomic

Sph_jav1 | JBANCZ010004095.1:8590-9010 (-) | 421 nt | lncRNA:noe consensus e-value: 1.5e-03

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 10nt   PSE: 0.95

GGCGGTCGAACGCCTCACAGTCATAAGGGTTGGTCACACTTCCCGACTAATTGTGATGACATAACAAAAATACACACACACACACAACGCTCTCTAGAGTTAAGCGCAAAGTTTAAATTTAGATTTAGTTGCTCTATAGATATAAGAC
AAAACAACACAAACAACACCAACAACACACACATTAATGTACACGAATGCCAGAACAAATGAACAGAACACAGTACAGAATGTAGTTAATAGTTAGTACAGAATGCACAAACACAAATCAGTAAGCCAAAGCATTATAATAACAATTAGA
GAAAAGAAATTGAATGATATGAGCAGAAGAGAACAAAGGGGAAAGAAAGGTGAGTGGTACAGAGTGGGGAAGGAACTGTGAGTCGCGTGATCAACAACAACTGATCGCCGCTTTTTTTTTT

Sph_jav2 | JBANCZ010002911.1:10478-10869 (+) | 392 nt | lncRNA:noe consensus e-value: 1.5e-10

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 9nt   PSE: 0.90

GGCGGTCGAGCGCCTCACAGCACGAAGGGTTGGTCACACTACCCGACTGATTGTGACAAACCAACCCCTGTAGAACACTGTCGAAAGATAATATTCAATGTTTGAAATGTAATTTGTCCCCTAATTTCAATGTTAAACCAAAAAGAGTTT
AACATTGAAATTGTAGTTAAAACACACACATAGAGATAGAGAGGTAACACATAAGAAGAGAGGAATTTCCAGAACAAGAACAACAAACAAATGAACATATAAAAACACAAATGAAGAAATCTACAAAACAAAAACAAAAACACCACTAAAC
CGAGTCAGAATTGGATTGAATTGAAAGAAAAAAACGGGTGTTAGAAGAAGGTGGGTAGCTGTGAGTCGCGATCGAATGATCGCTTTTTTTTTT

Sph_jav3 | JBANCZ010001526.1:16992-17333 (-) | 342 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 8nt   PSE: 0.81

GGCGGTCGAGCTTCTTACAGCGCTTAAGGGTTAATCACATCCCCGAACCAATTGTGATGTTGGAGAGCCTTCTAAAACAACGTTATCCACCTAAATATTTCTTAGAGTAGTTAAGTTTTAGTGATATGCAATCAGTTAACAATCCACATA
TAGCACTAGCATTCGTTGATACCTTAAGCACACACACAAACACACATTCAAGCAATAACTCTAAGGAGTGACAGGGAAAAAAGTTCCCAAGCAGTAAGTCGCAGTTATGAGCCCCGGTTGAGAGGATTATATGATTATTGTTAAGGGTAA
ACTTATAGTCCTCTTGACTTACACTGATCGCCACTTTTTTTT

Sph_jav4 | JBANCZ010001526.1:12213-12482 (-) | 270 nt | lncRNA:noe consensus e-value: 2.2e-04

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 6nt   PSE: 0.85

GGCGGTCGAACGCCTCACAGTAAAAAGGGTTGGTCACACTTCCCAACGGATTGTGAAGCATTTCATCTAATTAGAGTCTAAGTTGAAAAGTTGCAATTAGAAATAAGTATAATAACAAAGTAGAAATCGTTTTCAGTAAGGCGATAATAA
TAATAATCAGTAATATATCAATAAGGAATTCAATGGAAGTAAAAGAGGGGGGGAGGGGTATAAATAATGTGGTCGGGGTGCATTAAAACTGTGAGTCGTGTGATCAGAGATCGCTTTTTT

	Sph_jav1	Sph_jav2	Sph_jav3	Sph_jav4
Sph_jav1	-	53	47	47
Sph_jav2		-	48	45
Sph_jav3			-	50
Sph_jav4				-

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.