Beris morrisii

Taxonomic lineage: Brachycera > Stratiomyomorpha > Stratiomyidae > Beris

Assembly: GCA_951812415.1_idBerMorr1.1_genomic

Ber_mor1 | OX638310.1:26839098-26839503 (-) | 406 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 5nt   PSE: 1.00

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GCGGTCTAAATTTACCATCACATTCTAGATGCCTGGTTGTGCATCCCACTAATTGCACGTAGGAACCCTAACCTCTCTAAATATAAATTTACATACACTGCCTAATTTCTAGTTACCATTTCAGTATTAATTTCTAAATTAAGAAAAGGC
GTCAAAATTCTAAATTAGTATCTAGTTATCCTCTTTAAAGGATTGTATAATAATTGTATATAAAAGTAGTTATTGATGGTTCATGTTAGCAAGCACTGTTCCCTGCTCGTTAGTTAGATCCGTTACAAACACGCTTTGTAGATAATATAGA
ATGCACCTTTAGGGCCAGTTTAGTTCCTACTAGTTTCACCTTAGTTCGTTAAGGGAGTTGGGGAATTCACGGTATTCTAGAATGGAATATGGTGATCGCACTTTTT
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Ber_mor2 | OX638310.1:26831179-26831583 (-) | 405 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 3nt   Trailing-T: 6nt   PSE: 1.00

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GCGGTCTAAATTTACCATCACATTCTAGATGCCTGGTTGTGCATCCCACTAATTGCACCGTAGGAACCCAAACCTCTCTAAATATAAATTTACATACACTGCCTAATTTCTAGTTACCATTTCAGTATTAATTTCTAAATTAAGCCAAGG
CGTCAATATTCTAAATTAGTATCTAGTCGTCCTTTAAAGGATTGTATAATAATTGTATATAAAAGTAGTTATTGATGGTTCATGTTAGCAAGCACTGTTCCCTGTTCGTTAGTTAGATCCGTTACAAACACGCTTTGTAGATAATATAGAA
TGCACCTTTAGGGCCAGTTTAGTTCCTACTAGTTTCACCTTAGTTCGTTAAGGGAGTTGGGGAATTCACGGTATTCTAGAATGGAATATGGTGATCGCATTTTTT
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Ber_mor3 | OX638310.1:26851140-26851519 (-) | 380 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT   3' motif: ATCGC   Internal max. Poly-T: 4nt   Trailing-T: 6nt   PSE: 1.00

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GCGGTCACATTCTAGATGCCTGGTTGTGCATCCCACTAATTGCACCGTAGGAACCCAAACTTTCTAAATATAAATACACTCCTAATTTCCATTTTCAGTATTAATTTCTAAATTAATAAAAGGCGTCAAAATTCTAAATTAGTATCTAGT
TATCCTCTTTAAAGGATTGTATAATATTGTATATAAAAGTAGTTATTGATGGTTCATGTTAGCAAGCACTGTTCCCTGTTCGTTAGTTAGATCCGTTACAAACACGCTTTGTAGATGATATAGAATGCACCTTTAGGGCCAGTTTAGTTC
CTACTAGTTTCACCTTAGTTCGTTAAGGGAGTTGGGGAATTTACGGTTTTCTAGAATGGAATATGGTGATCGCATTTTTT
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	Ber_mor1	Ber_mor2	Ber_mor3
Ber_mor1	-	97	91
Ber_mor2		-	90
Ber_mor3			-

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.