

Assembly: GCA_047663935.1_ASM4766393v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.87

[illegible]

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.98

TGGCGGCTCATCTGTCACAAATGACAAATGGGTTCTCATCATCCGCAATCCGCAATGTGTATGATACCAATAGCACTTACCAAACTTGTATACAAATTCACAAACCAACCAACCAACAACTTCTTGTAAAGATATG
 AATGATACCAATCAATCAATCAATCAATGACCAATGCTCCGCGCTTTGTATGATGACCAACCAAAATAATACCAATATCCCACTTCTCGGATGTGTAGTATACACACGAAGATCTGCTGTTTGGATACATACATACACGGTGGGAGAGAGAGC
 GAAACCTTAACCTACCAAGACATCAAAATGAGTGCAGATCAAAACCTTATAAAACTATAAAAAAAATAAACCAATAGCAATTTGTGGCAAAAAAAATATAAAAAATACCAAAATGCAATTAAAAAATGGCGGGTCAAAAAAATATCAAAATTCAAAGTGT
 TTTGGACATACGCTGTGATCGCCTTTTTTTT

	Mus_aut1	Mus_aut2
Mus_aut1	-	49
Mus_aut2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

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.