

Assembly: GCA_035044765.1_ASM3504476v1_genomic

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

GGGCGCGGCTTCGATCCGAGCAATAAGCGGGTGGACATCTCCGCGATCCAAACAAATTTG1GTGCAACATCATAGTACBATTGACAAACCTTGTCAACAACTTCBTAACGCTCAAAAAACATGGACAAAGTACTATAAAATGCAAAAAG
GACCAACGATTAATAATATGACCAAAATGACACAAAGCAGACACATTTATCCAAAGAACACACACATGTABGAAAGAAATGACAAACATACBACAAAAATGTBAAAACCGTTGACAAACAGACCATATATATATTCAT
TCTCTAATATAAACTCTATATAGGCGTCAAAATGAGTTTAAAAACAACAACTACTACTCAATCAATCAGABACCAAAAAAGCAATAAATTCBGCACATGCAAAAATGATTTAAACAAAAATCAAGTCAAAACBGTACCTACTAGTTAA
AAATATATATCAACATGGACATATCTGATATATGATATATATATATATGAGGCTCTCTCAAAAACACACACACACATATGAAACAAAGCAACCAAAAAAGTTTAAAAACAAAGCGATCATGTAGTACAAATCAATATGATTCATGAT
CTAATATATCAATATTAATCTTAACAAACAAATTAATGGTATGACAAAAATATATCTAACCTATATATATAAACAAAAATCBTATATGTGTGTGTCGCGCTGCTTTAAATCBATATGTCCCTGTGTGTGATGTGTCAATCBBAATAT
TCTCATAGAAAGCGGGGCTAGGCGGTTGABCATGAACCTGACBAGCAGCAATCTCTATAATACCATATACAGACGCTTTAAGGCATATCTTAATATACCAATATGACACGCAAAAAATACBACCTTAAGGACAAAAACATATAAAAAAA
ATCCGATAGAACTCAAAAAAAATGTTATAGCTCTAAAAAAAACCAAAAAAATAATATATAGBACAAAGAAAGCAATGACAAACACBGTAGCTGACTAGBGAATGCGCTTATGTGTGATCGCGCGCTTTT

5' motif: GCGGT 3' motif: ACTGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.98

GC GG TCT GG TGT CT CACA AATT AAAC GGG TT GAC CACA TT CCG TGC ATA AAT TGT GG AT G CACA TACT GAC GGAC ATACA AAT TGC ACAA AATT GCT GGG ACC CGT GTG AT CGC ACT AT GAAAA T GCC AAT TT AAAA AT CAAA ACC ATA
AAAC TTCAA AATTAT GTCCAG TTT CCT ATTTT GAA CGTATA GTT GGGG ACC GT CAT GT GACC GACT GCT ATTTT T

	Leu_mon1	Leu_mon2
Leu_mon1	-	15
Leu_mon2		-

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.