

Assembly: GCA_949987735.1_idLeuObtu2.1_genomic

GGCGGTGTGACCCCTCTTCAGAGACTAGGTTGTACACATCCCCTTAATTGTGGATTAGTGAAGATAAAAAGTGTGGTAAATAATTGACGTTACGCTAAGATTCAAGCTTTAGTAGGCAGCTCTGTTAAGTACACAAAGCTTTAGGAG
AAGGGTTATTATCGCCGCTATTTT

GGCGGTTGTGACTCTCTCCAGAGACTAGGTTGTACACATCCCCTAATTGTGGATTAGTGAAAGATAAAAAAGTGTGGTAAAAATTAATAACGTTCAGCTAAGATTTCAAGCTTTAGTAGGCAGCTCTGTTAAGTACACAAAGCTTTAGGAAGA
AGGGTTGCTATCCGCCGTATTTT

GGCGGTGTGGCCCTCTCCAGAGACTAGGTTGCACACATCCCCTTAATTGTGAATCATAAAGAGGATTAGTGAAAGATAAAAAACCGTGTGTGAAATAAATAACGTTCAAGCTAAGATTCAAGCTTTAGTAGGCAGCTCTGTTAAATACACA
AAGCTTTAGGAGAAGCGGTTACGATCGCCGCTTTTT

	Leu_obt1	Leu_obt2	Leu_obt3
Leu_obt1	-	97	84
Leu_obt2		-	85
Leu_obt3			-

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.