

Assembly: GCA_951800035.1_idLinTess1.1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.86

GCGGGGCTGATGTTCCACCTGACCTTGGAGTATGAGGATATCCCCATATGATGTTGATACCAAAATGAACTTAATAAAACCTTCGTCAAAAAGATTAATGAAACAAACATATGCAACTTAACCTATGAAATATATTTAAAGAACTACCAATGGAA
 AACCAATTAATTTAAATGTCCGGGGTGTAGGTATGATAGCAATATATATAAAAAAGAACAAATCCAAATGAAATATAATATAAAAAATCATCTCTCAGTCAGCAGCATTTGTGTATGAGACAGAGGGGGTACCAACTTTCGCACTTAATCATGAT
 TGTAAATGATCTTGGAGATACATGATGTTCTCAGTTGAGAGAGAAATCTTAAGCAGATTTCAAAAAAATGGTCAAAACAAAAATATAAATCAAAAGATGAAATAAACCATAGACATTTGTGGCAAAAAATAAAATAGCAATAAATAT
 ACCGGGTCAAAAAATATCAAACTCAAGCTGGAACATGTTGTGATGTCGCCCTTTTTTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.95

CGCGTCTGGCATCCCTGTTGACAAAGTTTACAACGCCCTCAATTGCGATACAAATAAGCAGACAAATACCCATCCATGTCACTGTGTAATCGTGATATGACGACAAATTTGTAATTTCTACCTTTTCAAAATTTGGCTCCGGGAAAAGGACAG
ATTATAAATTTGACATGCGCTTTTATGAAAACAAATAGAAAATTTGAAAAATCTCTGTATGTCTGATGCTTCTGATGACAGCGGATCCGATAATACAAATTTATGACGAAATAAAACAGACCAAAATTACTCTGCATCTCCACAAAC
CTGTCATGATTTGACACGATCAAGAATAAATACAAATTTGCGGGGGGATTTCCGGGAGGAGGATGGCCCGCATATACATCTGTGATGACAGCTTTTAT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.96

5GCGGGTTCATAACCTCTGCATTGAAGGGGTGTTCCATTTCCTTAACCAATTGTGAACAACAAAAACAAAAATCCTCTCGCTAAGGCGTCTCAACACGACGCTGAACCTCTGAAAAATGATACAAATTCCTCCACAAAAACAAATCTCTCTGATCTCATGTTTACATGCAAAAGAAAAACCTTTGAATATGCAACTAAAAAGGCTTCAACACAAATTCCTCAATACAAATCCAGTCTCAATTCTAAAACTAAACAAAAACACACACATCCCAATCAATCTTCAACTCAAAATGACGCGCTTCAGATGAAATAAATCTCGGGCCGTTTGAACAAATTCAACTGACAGGGTACTAAACGCGTATATCCCAATTTTTTTTTTTT

| | Lin_tes1 | Lin_tes2 | Lin_tes3 |
|----------|----------|----------|----------|
| Lin_tes1 | - | 45 | 45 |
| Lin_tes2 | | - | 47 |
| Lin_tes3 | | | - |

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.