

Assembly: GCA_035044965.1_ASM3504496v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.85

Lor_and2 | JAWNMM010003314.1:38838-39313 (+) | 476 nt | lncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.85

Lor_and3 | JAWNMM010003214.1:36845-37130 (+) | 286 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 7nt PSE: 0.85

Lor_and4 | JAWNMM010003214.1:51112-51397 (-) | 286 nt | lncRNA: no consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.80

Lor_and5 | JAWNMM010002855.1:17068-17312 (-) | 245 nt | lncRNA: noe consensus e-value: 3.7e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 11nt PSE: 0.82

GGCGGGTCGAACATCTCAACAGCTTCAAAGGGTTGGTCTCGTCCCCGACTAATTGAGGGCGACCCGACGAACCAACCAAGTTAAGAGAAAGAAACAAAGTTACGTTAAATGAGTGGAGAGAAATCAATATAAGTGAAACATAATTACGTAAATCTACTGAAATTTATCAACCGCTGTTGAGATGATTTGGGAGGACTGACTGCTGGAATACCCCTTCTCCCCCAAAATGATCGCGGTTTTTTTTTTTT

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.