

Assembly: GCA_949628195.1_idPhaObes1.1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.91

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.99

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 8nt PSE: 0.94

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.94

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.96

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.

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