

**Assembly:** GCA\_030448955.1\_ASM3044895v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.90

GGCGGTCCCGTTACTCTCAGTGGATACGGTTGGCCACAACCCGTAAATGTGCGAAAAATATACTTTGATATAAATATCTATGACTAAGAATATTTCTTCCATAAAACAAAAAAATCAAAACAAAAAAACAAAAAACAAATTTCAAAAC  
ACAAAAACTTTCAAATCATTGTCCAAATTAATAAATAAGTTGAGACTAAGAACACAATTAACAGATGTTAATAAAAAAATACACTTTAGAACTGGAGAGCAACAATTATGATCGCCTTCCTTTTTT

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

GGCGGCTCTGCCCCCTCTTGATCTGGTTGCCACAACCCATAATTGTGGAGTCTCTTACAAAACATATAAATCTATAAAACCGTAAATTATGAATCGTAAACATTATGAATCGTAAAAACACCAATAAATCTTGGACTTTTGGATTGGT  
GCGCTTAATAAATTCAGAGGGGGGGCTGAAAACAATGATCGCGCTCTTTTTTT

	Tri_pen253	Tri_pen290
Tri_pen253	-	46
Tri_pen290		-

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, snoRNAm18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.