

Assembly: GCA_035045125.1_ASM3504512v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Hyp_gut2 | JAWNNJ010001046.1:214853-215119 (+) | 267 nt | lncRNA: noe consensus e-value: 7.7e-09

	Hyp_gut1	Hyp_gut2
Hyp_gut1	-	18
Hyp_gut2		-

[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.