

Assembly: GCA_017309665.1_UL_Cfrigida_v1.1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.89

Coe_fri2 | CM029564.1:19457773-19458051 (+) | 279 nt | lncRNA: noe consensus e-value: 1.4e-11

	Coe_fri1	Coe_fri2
Coe_fri1	-	34
Coe_fri2		-

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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