

**Assembly:** GCA\_958431115.1\_idSyrVitr1.1\_genomic

5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.86

GGTGGTCAATTATCTCACAATCGTGAAGGTTGGTCAATCCCTTAATTGTGACAAACCAAAAGACACAGGGCTTATAAAACGGCTTAACATAAGCAAAACAAACCCAAAAACATACTCATACATTCACTGATTGACGTGAAGTTTGAGT  
GAGCTACAAAAACCTCTCGTGTACAAACAAAACACCTTTGAATAAGACCGAAATTTGAATTAAATTATCGACCTTAAATTTGAAAAATGTGACAGGATTTAAATAAATTTGTACTTTCAAAACAAATGGTGCATTGAGATAAAACGGGATCACCC

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

GGGGCGGTTCAATGCCTCACAGTTGATACGGTTGGTTACAAGTCCGTTCCCAAAATTGTAACTTCAAAATCGTATGCTTTGACATCCATACAAAAACGAAAAACAAAAACACACTGCAAAAACAACTGTGTGTTTGAGAAATATAAAATATAAGTTT  
TCACCAAAAAAAAAACAAATGACGCAAAACAAAAAATTCTCCACTCTATCGTATATAAGATATCTATAATATAGAAATTAAGCCAAATCAATAAAAAATTGAGAAAAAATCTATCAAAAAATGATATCTGCTGAGGTAAGATGTGATCGCCCTT TTT

	Syr_vit1	Syr_vit2
Syr_vit1	-	52
Syr_vit2		-

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, snoRNAme18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.