

**Assembly:** GCA\_035045625.1\_ASM3504562v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.98

GGGGCGGGTCTGCATTTCGCACGAACGACGGTGGACACATCCCCTCTACCCAAATCTGAATTTGTCTCCGTTGGATGGCAGTGCAGAGGAAGTTACCCAAAACCTTTGGGCGAAATCTGAAGCGAATCGCAAAATTCAGATTCGA  
AATGCAGAAATTAACGACAGAGCAAAACCACTATATATACACACATAATTAACAAAAAGCAAGCAAGCAAGCAAAATCTATAGAAATATGCACAAAGAACTTTAAACCAAGAAATTCGACAAACCGAAATGAAGAATATACCAAGAACGACAA  
AATGCAGAAAAAGCAGAAAAATCTATCGACCAAAATATCAATGACAAAAACCTATATAAGACGATAAAAAAATACCAAAAAACCACTAATTTAACTGTACATTAAGTAAATGATCATCATCTGTGTAAATACGAGCAGACA  
ACCAAAATCTCTGCACAAAAATCTCCAAAAATATTTAAAAATCTCAAAATTCATTTGGTGTGTGTCTCCCTCTGTCGAAATCTGCGTGGCGCCGCTCTCTGGCTAAATCTGGCCCCCAAGCGCGCGCTGGGAAGAGAGCTCGGGCTCTGT  
TGGGCTCTCTCTGGCAACGACCAACCATCGATCGGATGGGACTGAGGCGGATCTGTGGATGATGGATGGACCATATCTCCAGCTCCGCTTGAGGACTACCTCTGGCTGGGGGGGGCGGCTCCACAAAAAATACCCATAGACATTTAA  
TGGCAATTTCTAAGTACGAAAAAATATAAACCAATCAAAATTTGACGAGAGAAAAAGCAATCAAAAAATGAGCAATATGAGCAAACTACTTAATATTTGGCAAAAAAGAAAAATGAAAAATGCAAAATACGACCAACCTTT  
CGAAAAAGCTCTCAATATATACATATATCTGGGTCTCGCAAGGAATGCCCTGGCTGTCTGCCCTTTTTT

[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.