

**Assembly:** GCA\_963971545.1\_idPhiCaes1.1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.94

GGGCGGTCTGGTGTTCGCGAGTACATATCGGTGGACAAACCCGTTTCAAAATTTGTGCCACCTAACTAACTACAACACTGAGTAACATAAAACCACTGAATACTGATGAATTTACTGAAATACACATGGCAACCGATGAATGAAATTTAA  
 AACATACATACCAATGGCAAACTTTGCGCAATCAAAATGGAAATGATTTCAGTTCAAAATGGACACACACACACAGCAAGAAAGATGAAATCTGACTCAGCGCAAACTCTCATATAAGGGCAACGATAAAAACGAAATTTATA  
 TAAATTTGCGAAAGATTAACATCTAATGACATTAATCAGATGCAAAATAAAGACGATTTACACAAAGCAAAAAACCAACTCATGAAATGGAAATCAATTTCAAAATACAGGCAACATCAATGAATCTTAATGAAAAAATAA  
 CTGTCAGAAATCGCGTGTCTCCGCTTTGTGATAAAGCAAAATGCATATACCGCTCGCATCGGCCGCGATCAGCAAGCAAGTAGCAGCAGGACACACACATCACTCAACACACACACAGCTGCCACATCATTCAGCCGATTT  
 CTGTGAAAAATGGCCGCGATGTGGGTGTGTGTGTACBCTTGAAGTTGTGCGCGCGATGAGGAGGCGGAGAGTACAAAGCGCTCAAAACGGCGCGCAATTTGGATCTGCAAAAATTTAAACCAATAGCATGTGTGAGAGATTAATTTCT  
 AGTAAATGAAATGAAAAAATAACACCAACTAAATGGCAAAATATGAACAAAAAATACTAAACAAAAAATCACTAAAAAAGCTGCACAAAACAATGGAAACCAATAAACATAGGTAAACTGCCGGAAACACAAACAGTAT  
 CGCCCTTTTTTTTT

[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.