

Assembly: GCA_048593825.1_USP_Cbez_1.1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

GCGGCTTCATCAACCTCGCATTTGAAAGGGGTTGTCTACGACGGGTCTGAAACATTTGTAAGATTCCTGTAAGACGAATTTAAATCTCTCTCCCAAGTCAACAAAAAGTTAAAGTCTTATGCTCTGCTCATAGCAATGACAAAAAT
 TCAAAAATTAACAAAAATAAAAAACAAATCTCCCAAGATAAAAAATATTTCTCTCTCAAAAATTAATAAAAATAAGACAAAAATTAATAAAAAATTCGTTTAAATTAATTTCTCAATATAAAAAATAAAAAATATATGTCTC
 AAAAAATCAACAAAAATCTCAATTCGCAAAACCTTCCCAAAAAACAATTTCTCAACTCAAAATTCGGCAACTTTAAAAAGAGATTTGAAAAATTTAAAAACAACAAACAAATTAAGAGCCCAATTTGAAATTTAATTCGATTAAGAAATTCAGAGGTTAC

[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.