

Assembly: GCA_027943255.1_idAnaObli1_1.0_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.94

GGGCGTCTCGG16TCCGCGACACATCG81GGGCAACACCG6TCAAAAAT16GCCACCAACATACATACAAAC16GATAGACATAAACAAAT16GAACTAC16GAAAC16GCAAAATAGATATGAAT17TAATATACATACATACATACAT
 CAGATCGAATTCAGCAAT17C8TCAACATATGGAATAAAT16T17ACAGT16CAAAATGACACACACCAAAATAT16GATTCGACTACACCAAAAT17CTCATATACATAGGGCAACGATAGAAACCAAGCAATGAAATAGATAT16GCG
 AAAATCAACATATATGACAT17AATGACATGCAAAAAAAAGATTATCAATAGAAAGCCACAT16T8CAAAAATCGAAAAATCGACT17CAAGATACCCGAGGAAGACCGATCACT17AATATAGAAATAGAT17CAAAAAATTCGCACTCGG16TGTG
 T16GATCAAAACCAAGATCGATACCGCG16TCT16G16GCGGCAACACCCCAACAT16TACGCGAT17TGGGCGAGATACAT16TCTGAT17TGTGCC17GGAT17GT16GCAAG17GT16GGAAG16TCACTAGGAGAGAT17CGCCTACAG
 CAGAGATGATCAAAAT16T8CCAAACGGCGCGCGAAAT16GAT16TCTGAAAAAT17AAAAACATAGAT16T17GAGATTAAT16TCAACCAAAAT16GAAACCGAAAAACACCACTAAAT16TCAAGATGAAAAAAATTCGCACTAACAAAAACACA
 CAAAAAGTCGATACAGATGAAACAGATCAAAAAAAATCGAT16GCAAAATCGACGACGATCAAAATCTGTGG16TGTCCCGCTTTT17

[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.