

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 1.00

GGGCGGTTCTGCTCACAGTTGATACGGTGGCTACAATCCGTTCCCAAAATTGTAGCATCTAAAATCGTATGCTTTGACATCCATACAAAAACGAAAAACAAAAAACACTGCAAAATTGTGTTTGAGAAATAAAATATAAGTTTCACC
AAAAACAACACGCAACAAAAAACTTCTCCCTCTATCTATAAGATATCTATAATATAGACTTAAAGCCCAATTCAATAAAATTTAGAAAAAAATCTATCAAAAATGATATCTGCTGAGGTAGATGTGATCGCCTTTT

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.

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.