

Assembly: GCA_965649395.1_idWinCrue1.hap1.1_genomic

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

GGCGGTGGAGTGTCCAAATTTGATATGGGGTGTGACACCGCATCAATTTGTTGAAATGTAACCTAAATCTCTGCTCAAAATGATGCAATCAATATGCAACCAACACTCTTGATGATATATGAAAGACAGATATGGAAATATGCGGCGGCTGCTGATATGGAAATATATAAAAAAACATCCAAATGAAATGAAATATATATCATCTCTCTGCTGACAGATGATGTTGTGTGATATGACAGAGAGGCTGAAACAGTGTGCAATGTGACATGCTTTCTGGAATACAGATGCTCTCTCAATGAGAGAGAAATTTAGACAGATTTCAATGGCAAAATCAAAAAACATAAACCAAAAAAAATGAAATAAACCATAGACATTTGTGACCAAAATATAAATACGAAAAATAGCAATAAAAATGGCAGGCTCAAAATATCATCTAAAGTGTGGAGACATCGTGTGTGTCGCCCAATTTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.90

56CGGTTCTGAACCTCGATTGAAAGGGTTGTTCACTTCCTAAACCAATTGTGAAATTTGCAAAACAAAATTCCTCTTGAAGTCGTTTTTAAAAAGCGACAAAATTTCTGAGACATTACATTTACATAACCGGCCAAATCTGTACT
AAAAAGTTCTCTTGCAAGTTGAAACAAATTTACCTTTTCAAAACAAACGCAAAAATGTGCAACAAATTTCAACACAAATTTCAACACAAATTTCAAACTTTAAAAAAAACATGTCAAAACTTTGCAAACTTTGCAAACTTTCAACT
AATGAGCGCGCGACAAATTAACAAAAACACATGACCAACAAATTTGAAATTTCTAATGTGACAGAGTTACAAACAAAGGATGAGTATTCGCGCAATTTT

	Win_cru1	Win_cru2
Win_cru1	-	48
Win_cru2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[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.