Winthemia cruentata

Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Tachinidae > Winthemia

Assembly: GCA 965649395.1 idWinCrue1.hap1.1 genomic

Win_cru1 | OZ287662.1:43112092-43112594 (+) | 503 nt | IncRNA:noe consensus e-value: 1.9e-01

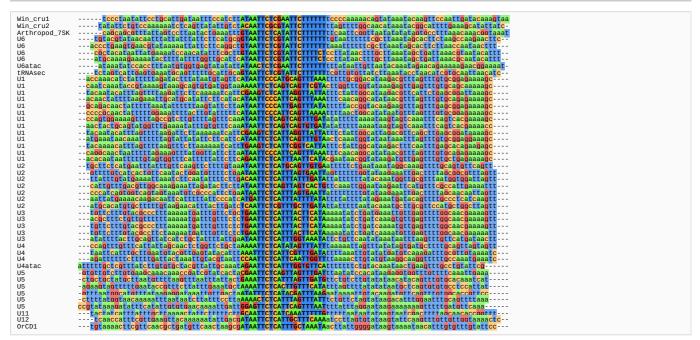
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.98

Win_cru2 | OZ287660.1:119870930-119871327 (+) | 398 nt | IncRNA:noe consensus e-value: 8.1e-02

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

	Win_cru1	Win_cru2
Win_cru1	-	48
Win_cru2		-

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



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.