Rhagoletis cerasi

Taxonomic lineage: Brachycera > Muscomorpha > Tephritoidea > Tephritidae > Rhagoletis

Assembly: GCA 029783565.1 ASM2978356v1 genomic

Rha_cer1 | JAPVRG010261024.1:5489-6317 (+) | 829 nt | IncRNA:noe consensus e-value: 2.5e-17

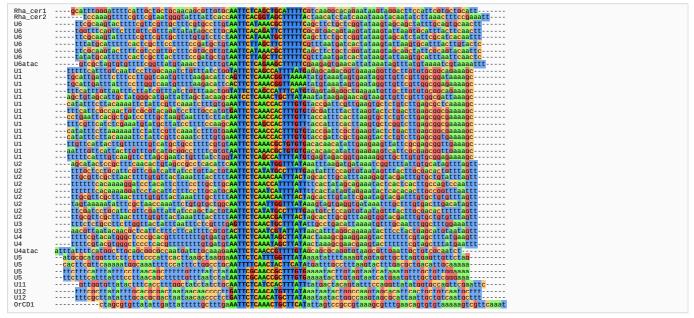
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.93

Rha_cer2 | JAPVRG010231674.1:9877-10198 (-) | 322 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.83

	Rha_cer1	Rha_cer2
Rha_cer1	-	26
Rha_cer2		-

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.