Drosophila cracens

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified tarsi group > split tarsi subgroup **Assembly:** GCA 035042505.1 ASM3504250v1 genomic

Dro_cra1 | JAWNLF010000188.1:75829-76842 (-) | 1014 nt | IncRNA:noe consensus e-value: 1e-157

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

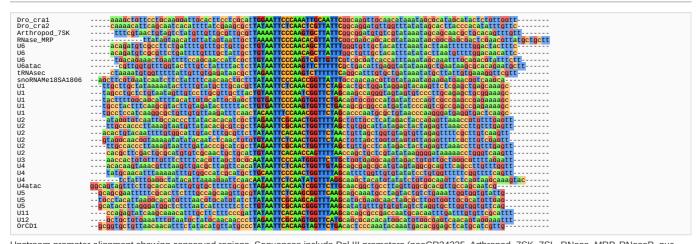
Dro_cra2 | JAWNLF010001081.1:324087-324327 (-) | 241 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.95

ATACBACAAACTAAAAAAAAABABTACABCCACBBABBABTBCTCGCTGCBABTTBTBTTTCABBABBBTCATTTCCTTBATCGCTTTTTT

	Dro_cra1	Dro_cra2
Dro_cra1	-	17
Dro_cra2		-

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.