Brachyopa scutellaris

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Brachyopa

Assembly: GCA 949775065.1 idBraScut1.1 genomic

Bra_scu1 | OX459113.1:103460445-103460750 (+) | 306 nt | IncRNA:noe consensus e-value: NA

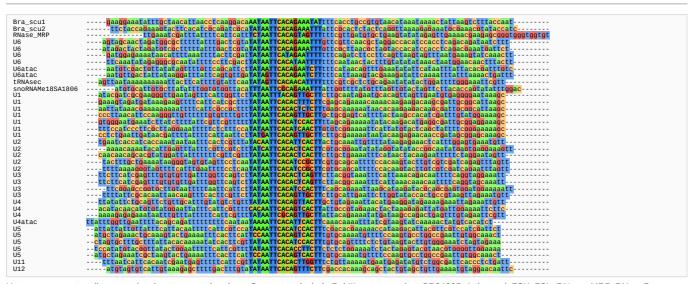
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.88

Bra_scu2 | OX459112.1:38464874-38465137 (-) | 264 nt | IncRNA:noe consensus e-value: 3.5e-10

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

	Bra_scu1	Bra_scu2
Bra_scu1	-	48
Bra_scu2		-

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