## Baccha elongata

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

Assembly: GCA 951217065.2 idBacElon1.2 genomic

## Bac\_elo1 | OX578274.2:35235065-35235380 (+) | 316 nt | IncRNA:noe consensus e-value: 3.3e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.87

## Bac\_elo2 | OX578273.2:114832725-114833037 (+) | 313 nt | IncRNA:noe consensus e-value: 2.8e-10

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

## Bac\_elo4 | OX578274.2:35230360-35230635 (+) | 276 nt | IncRNA:noe consensus e-value: 1.1e-02

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.87

GGCGGTCTATTGTCTCTCATTAACAAGGTTGAACACATCCCTCAAATTGTGTATGTGGAAGCGTCGGAAGATATTCGTAGAGCGCAATCGTTTATGTCTTACCGTACGCCTTATTCAAGTTGTTTCT. ATACCCATGTGTGTTCCCGATCGAAGGGAAAATACGTTCCCCGTGATTGAAGGGGAGGAAGAACGGACGCGACAGCGCGTATAAAATAAAATGATGTTGAGACAATGCGAGAAAGGATCGCTTTTTT

	Bac_elo1	Bac_elo2	Bac_elo4
Bac_elo1	-	46	56
Bac_elo2		-	43
Bac_elo4			-

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.