Bellardia bayeri

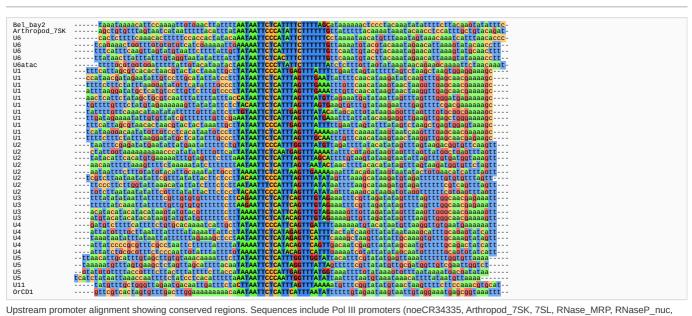
Taxonomic lineage: Brachycera > Muscomorpha > Oestroidea > Calliphoridae > Bellardia

Assembly: GCA 950370525.1 idBelBaye1.1 genomic

Bel_bay2 | OX493267.1:81435192-81435432 (+) | 241 nt | IncRNA:noe consensus e-value: 2.7e-02

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

GGCSATCTTGGCTACTCAASASAAATGGTTGTTCACAACCCTTAATTGTSATACCTTCAAATTGCTAAACTCTTTGCTTCAAAATAAAATAGAATTTTAAATSAATTTCTSAATACGTGTTATAAACACAATTTTAGTTCTTAATAA
TCACACCACTAAGATTTCAAGCTTTGGTAGATAGTTGTGTATAAAAATACAAAGCTTATAGAGCAACTAAAAAAGTGATCGCTGCTTTTTTT



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.