

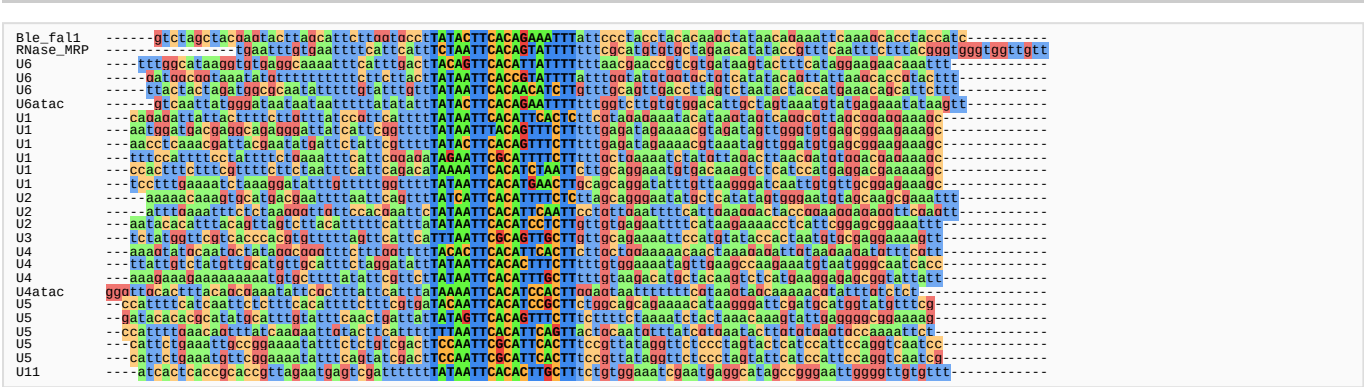
Blera fallax

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

Assembly: GCA_946965025.1_idBleFall4.1_genomic

Ble_fal1 | OX337248.1:52476978-52477240 (-) | 263 nt | lncRNA: noe consensus e-value: 7.3e-10
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.93

GGGCGGTTGATGCTTCACAGTTGTTGCGGTTAGCTACATCCGTTCCGCCAATTGTAGCAATCTAAATCGTATGCTTTGACATCCATACATAATAAAATGCAAAAGTGTGTTTGAATAAAATGTTTACCATAAAACGACGCAAGCAAAAAACAAAAATCTTTCTCTATCATAGATTAATATAGAAATAAGCAATTCAATAAAATGAGAAAAAAAGTTTATCTAAACGGTTCTGCTGAGGTAGATGCGATCGCCTTTTT



Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.