## Cochliomyia hominivorax

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

Assembly: GCA\_051144965.1\_Cochliomyia\_hominivorax\_M2\_hap1\_scaffolds\_genomic

## Coc\_hom1 | CM118040.1:83436098-83436635 (+) | 538 nt | IncRNA:noe consensus e-value: 1.3e+00

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 10nt PSE: 0.92



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.