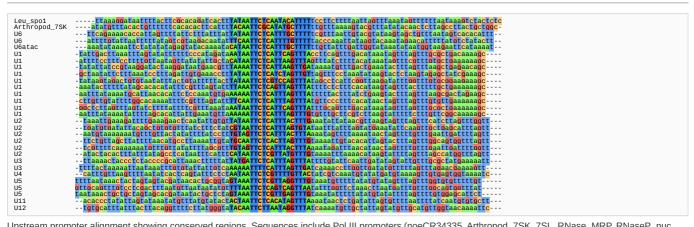
Leucophora sponsa

Taxonomic lineage: Brachycera > Muscomorpha > Muscoidea > Anthomyiidae > Leucophora

Assembly: GCA 965643815.1 idLeuSpon1.hap1.1 genomic

```
Leu_spo1 | OZ286162.1:341095311-341095573 (+) | 263 nt | IncRNA:noe consensus e-value: 5.3e-01
```

5' motif: GCGGT 3' motif: ATCGT Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.80



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.