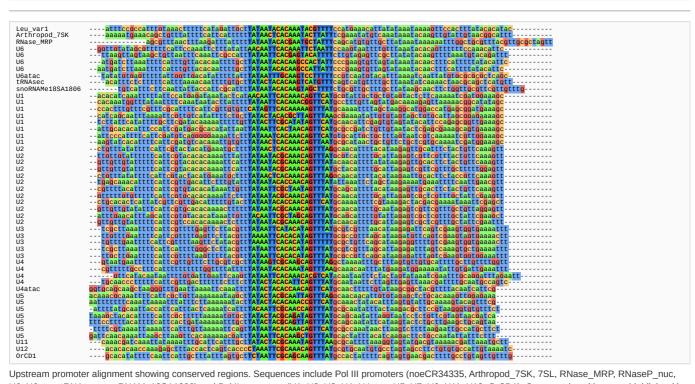
## Leucophenga varia

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Leucophenga

Assembly: GCA 018903435.1 ASM1890343v1 genomic

## Leu\_var1 | JAEIFJ010000200.1:1181927-1183080 (+) | 1154 nt | IncRNA:noe consensus e-value: 2.3e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.95



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.