Leucophora obtusa

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

Assembly: GCA 949987735.1 idLeuObtu2.1 genomic

Leu_obt1 | OX465295.1:70579120-70579293 (+) | 174 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.93

Leu_obt2 | OX465295.1:70599863-70600035 (-) | 173 nt | IncRNA:noe consensus e-value: 1.4e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.88

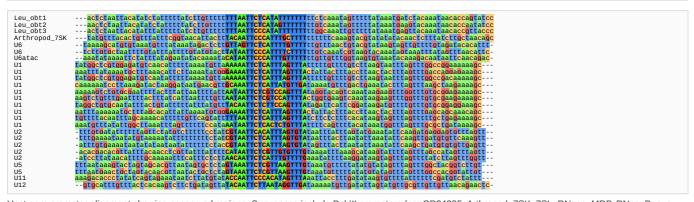
GEGETETEACTCTCTCCASASACTASGTTETACACATCCCTTAATTETEGATTTAETEAAASATAAAAAAETETTEGTAAAATTAATAACETTCAGCTAAGATTTCAAGCTTTAETAGGCAGCTCETTAAGTACACAAAGCTTTAGGAGA AGGGTTECTATCECCCCTATTTT

Leu_obt3 | OX465295.1:70584883-70585068 (+) | 186 nt | IncRNA:noe consensus e-value: 2.2e-01

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.94

| | Leu_obt1 | Leu_obt2 | Leu_obt3 |
|----------|----------|----------|----------|
| Leu_obt1 | - | 97 | 84 |
| Leu_obt2 | | - | 85 |
| Leu_obt3 | | | - |

Pairwise sequence identity matrix (%) showing similarity between IncRNA sequences.



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.