Drosophila hawaiiensis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > grimshawi group > hawaiiensis subgroup **Assembly:** GCA 037043685.1 ASM3704368v1 genomic

Dro_haw1 | JBAMBA010000213.1:2182102-2183120 (-) | 1019 nt | IncRNA:noe consensus e-value: 8e-165

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Dro_haw2 | JBAMBA010000107.1:3697545-3697954 (-) | 410 nt | IncRNA:noe consensus e-value: 6.2e-15

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 1.00

| | Dro_haw1 | Dro_haw2 |
|----------|----------|----------|
| Dro_haw1 | - | 25 |
| Dro_haw2 | | - |

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.