## Hirtodrosophila caputudis

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

Assembly: GCA\_037075125.1\_ASM3707512v1\_genomic

## $\label{lin_cap1} \textbf{Hir\_cap1} \ | \ \textbf{JBAMCO010051726.1:155-507} \ (\textbf{+}) \ | \ \textbf{353} \ \text{nt} \ | \ \textbf{IncRNA:} \\ \textbf{noe consensus e-value: 1.0e-08} \\ \textbf{-0.06} \ | \ \textbf{-0.06} \ | \\ \textbf{-0.06} \ | \ \textbf{-0.$

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 12nt PSE: 0.91



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.