

Ornithomya chloropus

Taxonomic lineage: Brachycera > Muscomorpha > Hippoboscoidea > Hippoboscidae > Ornithomya

Assembly: GCA_963971445.1_idOrnChlo1.1_genomic

Orn_chl1 | OZ020529.1:55424106-55424379 (+) | 274 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.99

GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT

Orn_chl1	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U6	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U6atac	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
tRNAsec	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U1	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U1	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U2	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U2	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U3	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U3	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U4	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U4	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U4atac	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U5	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U5	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U11	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT
U12	----	GGGCGGTTGGTTCCTCATTTGTTGAAAAAGTTGGCCGATCCCTCGAAGTGAATTGTGGCAGCAAAATGAAGTTGCAAAAGCATAAGAAACAACAATATATAATTAAATAAATAGCACGAGAGATCTGTAATCACGAAAAATCATTTCTAAATATCAATACGAAACGAAGCTTGTGTCGGTTCCTGCTGGAGAGAGTGAATTTTCAGACAAATCGAAAAACAAATTAACACTCAGACTAGCACGAGAGGGACGCCGTGATCGCCCATTTTTT

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.