

# Scaptomyza flava

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Scaptomyza > Scaptomyza subgenus Scaptomyza

Assembly: GCA\_030179655.1\_sfla\_v2\_genomic

Sca\_fla2 | JARNME010000404.1:9068014-9069082 (+) | 1069 nt | lncRNA: noe consensus e-value: 3e-167

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.87

GGGGCGGTCGTCGATTCGCGCAGATAGAAACGGTTGGGCGATCCCGTTTAAACCCACAACTTGAATTTGTCACCCCTTGGGTTCAAAACGCAAAATTTACGATTGAAATACAAATCGCGTCGCTGGCAAAACATTTCTGCTCAT  
TCTCTGAAGCAAAATCCAAAGCAAGATAAAAACATGAAAAAATATGCAAAATGAAACACAAACAAACAAACATATAAAATGAAATGAATCAACAAAAATCTAATGCAAAAAGAAATCACGAATCGCAAAAGATAAAAAATAA  
AGACAAACAAAAATATCAGACCAAAAAAGTTTATCCAAATGCAAAACAAAAAATATAAAAACATACATAAAACACTAAAAAATATGCAACTTAAATGTGAACCTTAGTAGATAAAATCATCGTGTATCAGGACGACAAAAAATCTCTG  
AAAAAATCTTAAAACAAAAAAACAATAAAACTGCAAAAAAATCTGCAATGGTGTGTGTGTCCTGTTTCTGTAATCGCTGACGCGCAAGGGCGGCCCAATCCAAATGTGGCCGGCTCGGGTGGGAAGGGGATGTCCAAATGGG  
GGAACTTTGGCTCTTCAGACCCCAAACTACTACTTTACCAACACAAACAAATCTGCTCGGGCAGAGGATATTAGTGGATGAGAAAGATATATGGTGAATATCGGTCTACTACTATGTCTCTAAACACTCTAAAGCCATTGTAG  
TGGAGTCAACTACCAAGACGGTTTCAATAGCTTGGGACAGGCTGGCTGGGTGCTCCACAAAAAATACCATAGAGACCTTTAAAGGCAAAATCTAAAGAACAAAAATATAAACCAAAATAAACGGAAAAAACAAGATATTC  
AAAAAATAGCAATATTGAGCAACCACTACTAATAATGGCAAAAAAGAAAACTGCAAAATACGACACACACCTTCGAAAAATGACCTCAGTTGATTGATATATATAAATACTACACCAATTAATGTTGGGTACTGCGTAGGAATGCCTCG  
TTGTATCGCCCTTTTTTT

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Sca_fla2      -----a d c t d c c a d t o c a c a d t t o c a t t t c c t o d d c t T A T A A T T C C C A A A T T G T A A T T C c c a a g a t o c a d c a t a a a t a d c c a t a c a t t t c c c a d t t t o t t -----
Arthropod_7SK  -----c c g t t g t c a d t t g t c t g t g g c a d c t t c a c a t T A T A A T T C C C A A G T G C T G G T T T g g c g t a t a t g c g t a t a a a t c a a g t t a c c t g c a c t g t g t t -----
RNase_MRP     -----c t a a t c a g c c c c a g c g t c g c t t g c t T A T A A T T C C C A A C T C G T A T T C a c g c a c t o g t g c g t a t a a a t a g c g c a a g c t a t t t c a c c g c a g g c g t t t -----
U6            -----a a a c a t c c c t a a a t a t c a d c f c a c t c c c t T A T A A T T C C C A A G T G A C T A T T C c c c o d t a c a t a a a t a a a t a c t a o t a o c c t t a c c a t t t -----
U6            -----g a a c c a c a g a t g c c t a g t t t a c t a a c a a a t g c t T G T A A T T C G C A A G T G C T A T T C g g c a t g t g c t a c a t t t a a a t a g c a c a a a t t c c t t c t a c a t t c -----
U6atac       -----c t c a a c a c a g t t c g a g t a c c t g t c a a a t g c t c c t T A T A A T T C G C A A G T G C T A T T C g g c g a t g t g c t a c a c t t a a a t a g c a c a a a t t c c t t c t a c a t t c -----
tRNAsec      -----c a a t a t a a c g a c a c t g a t a g c g a t t t g g t c t T A T A A T T C G C A A G T G C T A T T C g g c g a c g c t g g c t a t a a c g a g g g t g a g c t a a c a t g t t a t t t -----
snoNAME18SA1806 -----a c a d d c a d a t t a c a t a t o t a t a t o t a t t c c c t T A T A A T T C C C A A G T A A T T T T C c a d c t t o t o t a t o t t t a t a t a c c o c t a t t a d c c c t a d t t a c a t t -----
U1            -----g a a t t a t a a t c a t t g t c g t a t t a c t t a c c t g a t t g c c t T A T A A T T C C A A C T G C T A T T C c c c a g t c g c g a g t a t a a a t a a a g c t g g c a g t c g a g c a t -----
U1            -----t t g c t g c a t t c c t t g t g c a c a c a a t t g t g a a t a a a a a t T C T A A C T G A T T C A g c t c t t t g g g a g t a g t g g g t t g t g a g c t g a a c a a g c -----
U1            -----t c c c t o c c c a a a a a t o t t c t a t a t o c a c a c a t T A A A A T T C C C A A C T G A T T C A g c c c a t a a o o t a o t a o d o c t o t t o t t a n c t a a c a a a g c -----
U1            -----t t a t g t g c a c t t t a g t t g c a t a c t a c t t g c g a g t T G G A A T T C C C A A C T G G T T C T A g c a t t g a g a g c a t g g a a t g c t a c g g t c t g a g c t g a c g a a a g c -----
U1            -----t t a c c t a c t t t c t g c a a a c t t a a c a t a t t g c c t c c t T A T A A T T C T C A A C T G G T T C A A G c a a t g t g c a t a g g a a t c t a g g a t t t g g c c a g t c a a g c -----
U2            -----t t t c a c t c a c a t t c a a a t a t t t o a t a t t t c c c t T A T A A T T C C C A A C T G G T T T A g c a t t t o t a t a t o a t t c c a a o o c t a o c c a d t t c a d c -----
U2            -----c t t g c g a g t t c g c a c g a t c g c a g c a c a a a t g c a c T A T A A T T C A C A A C T G G T T C A g t t t t a g c t c a t g a t g g t a g g a a a a a t t t a t g t c a a g t t -----
U2            -----c a c c a t g t g a t t g a t a t g c g t g c a c a a t a g T A T A A T T C A C A A C T G G T T T G A c t g t t g g g g t c a c t g t t g g a g c t c t g a g a t t a a a g t t -----
U2            -----a a a t t a t a c t c a o d t a a o t t g c a c a d a c a t a a c a T A T A A T T C A C A A C T G G T T T T A g c a c a c c a c c t a a a t t a c c t o a a c a a a c t c o d t t a c a d t t -----
U2            -----t t c a c a c t c c a t c g a t t t t t g c a t t t g c g t g c t T A A A A T T C A C A A C T G G T T T T G A c t g t g c g a g g g t c a g t g t g g g g t c t a t t c a t a t t a g t t -----
U2            -----a a a a t g a a a c c t g t a g t t a t c a a c g t c t t t c a c t T A T A A T T C A C A A C T G G C T C T A g c c g c a a c t a c a t a a g t a g a a a t a a t c c a t a t c c a g t t -----
U2            -----a a a o t a a a t c t o t t a o d t a c a a c a c t t t c a c t T A T A A T T C A C A A C T G G C T C T A g c c c a a c t a c a d a a o t c t a d a a a t o t a t t c a d t t c c a o t t -----
U3            -----a g a a t g t g g c t g t t a t t t t g a c t t t g g t g c g g T A T A A T T C C C A A C T G G T T C A g t t t g a t g c a t g a t g c t c a t g a c t t t g c t g t t c a a t t -----
U3            -----t t c g t a c c g t t g a t t a t t t g a t a t t t g t g g g g T A T A A T T C C C A A C T G G T T T T G c t t g a c g a c a t g a g t g c t a g a c t t t g c t g t t c a a t t -----
U3            -----g c a t t a t a c a a t t t o t t t a c c t t a c o t t a c t a c c t T A A A T T C C C A A G T T G T T C T A g c t t a t o a c t a o t a a a c c a a c t o t t o o c a t t o o t a a a t t -----
U4            -----c t a t c g t a c g t t a a a t t t c g t t g c t a g g t a c t T A T A A T T C T A A C T G G T T C A A T t t t t t c g c a t g g a g t a g c a g c a g c t g g c g t t t a c a g g t t -----
U4            -----t c c a t t a a a t g c t t t a g t t t t a a a g t t t c a c a T A C A A T T C T C A A G C C G T T C A T G c a c t t c t g t a t a t c a g c a t a a t g g t t c a g t g a t t c a a a t a c -----
U4            -----g t t c a t a a o d t a a d c a a t t a t a a c a t t o t t o c c T G T A A T T C A C A A C T G G T T C T A g t a t o t c o t t a a o t a o t c a n t c o a t g t c a d t t a a a g t t -----
U4atac       -----t t c a a t g c a a t t c c c t g a t c a t a g c a c a c a g a t c g c t T A A A A T T C A C A A G T G G T T C A A G t t t c g t c a g a a a g a g t c g c a c t t g c a g c a a t c h -----
U5            -----t t g c a t t c a c t g c t t a a g c g c a a t g c a t g t t t c t T A C A A T T C C C A A C A G T T T C A A G c a g a t g g g t a g a g g c g g t t g a t t c c t t c a a a -----
U5            -----g o d t t o c t t c a t t a t c t t a a d o t a t c t a t t t c c t T A T A A T T C C C A A C A G T T T C A A G t a t a t a t t c o o t a t a o t c o a c t o c c a d c c t c a t t c a a -----
U5            -----g c a a c g c a g t g c t g t t t t t t t c a a c a g c t g c t c g c T A A A A T T C C C A A C A G T T T T A G c a g t g g c c g a t g g t g t g t g g a a g t t g c c t t c t c a a -----
U5            -----g a a c g t g c c t a c c t t a g g g c t t g c a g g t g t t g t t c t T A G A A T T C C C A A C A G T T T T A G c g t t g c t c a g c a a g g t c t g g c t c a a t c a a t t t c a a -----
U7            -----t a c a t g t c t o t c o o t a a t c t o a t a a c a d a a t t t o t T A G T T C T C A A C A A G T T C A A G t a d c c t a t o d c c t t o o t c t a o c t o t t a o c t a o t t c a a -----
U11          -----t t g c t a t t a a c t g c c c t c a c t t g c c a t a a a t t c c a a T A A A T T C C C A A G T G G T T C A A G c a c t t t c a a c a c a g t t a g g a g t t g t t t g c c a t g a a a a c a t t g a -----
U12          -----c t a t a a c a a a t t g t a t g a t a t t c a t a a a g c c c t T A T A A T T C T C A A C A C T T T A A G c a t a a t g c c a g a t a t g c a t t g c a t g c a c a t t a t t -----
OrCD1        -----t a t c t a t t c o t t t o c t c a t t t a a a t a t c a c c c t T A C A A T T C A C A A A T G G T T C T A G c a c c a c a a a t o t c t t o t t o c a a t c o o c t c a t t o t a t t c -----
               -----a g c t a t g c t a a a a c a a a t g t t c a a c a t t t g a c g c c T A T A A T T C A C A A C A G G T T C A A C t c g c c g t a c g a a a t g c c c t g a c t c g t t t g a c a a c t g -----
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Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod\_7SK, 7SL, RNase\_MRP, RNaseP\_nuc, U6, U6atac, tRNAsec, snoNAME18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.