Supplement

Oligos used to generate templates for immobilized template pulldown

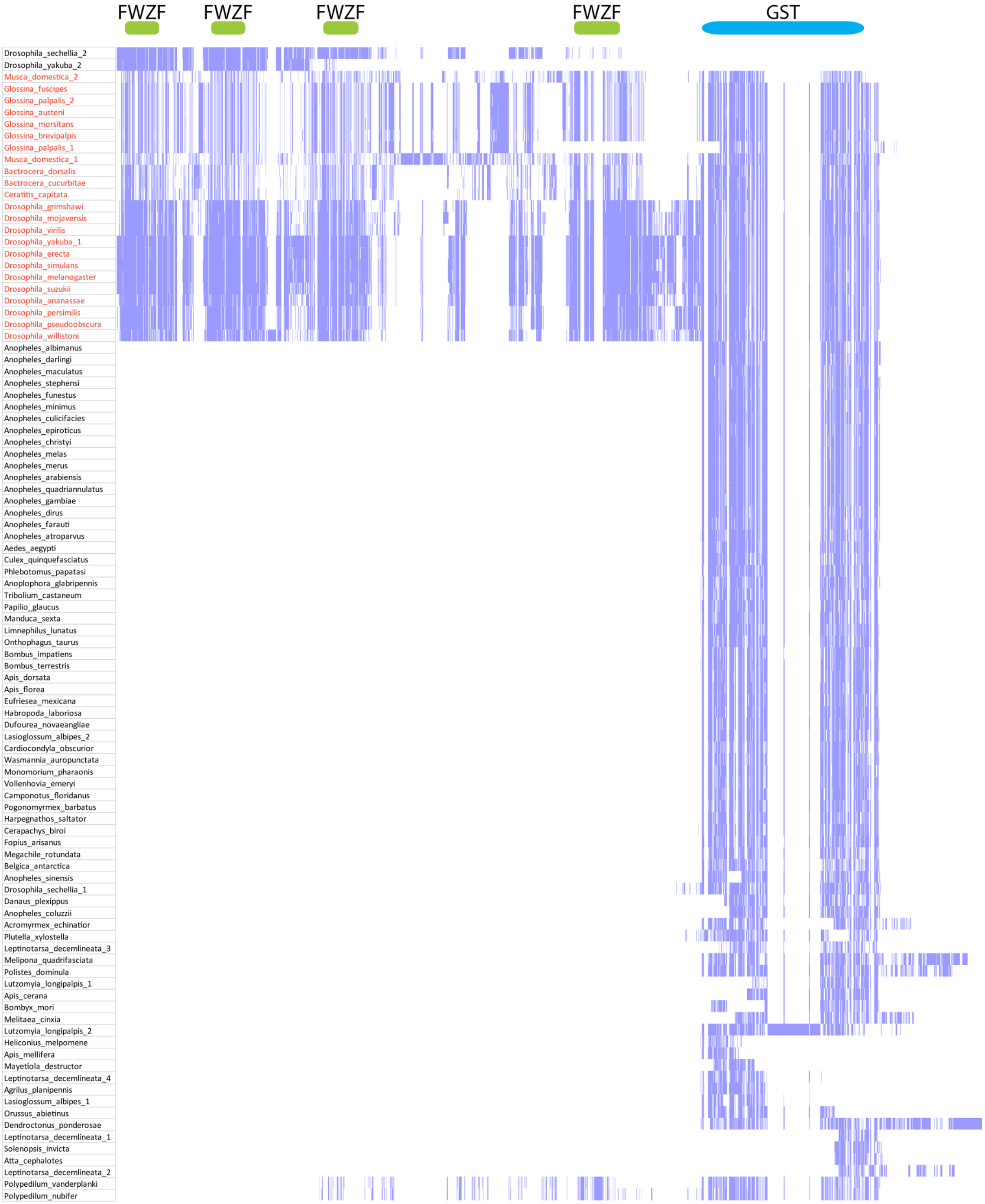
Name	Sequence
mRpS30_wtMotif1(+)	ATCCAGCGTGCGGTCACACTGCAGCAATGACATAACCTAGTTATTGTCAA/3InvdT/
Biotin-mRpS30_wtMotif1(-)	/5Biosg/TTGACAATAACTAGGTTATGTCATTGCTGCAGTGTGACCGCACGCTGGAT/3InvdT/
mRpS30_mutMotif1(+)	ATCCAGCGTGCCGTCAGAGTGCAGCAATGACATAACCTAGTTATTGTCAA/3InvdT/
Biotin-mRpS30_mutMotif1(-)	/5Biosg/TTGACAATAACTAGGTTATGTCATTGCTGCACTCTGACGGCACGCTGGAT/3InvdT/
RpLP1_wtMotif1(+)	TTCGTCATCGGCGCGGTCACACTGCATATCAACTGCTCTTTCCGGTTTAG
Biotin-RpLP1_wtMotif1(-)	/5Biosg/CTAAACCGGAAAGAGCAGTTGATATGCAGTGTGACCGCGCCGATGACGAA
RpLP1_mutMotif1(+)	TTCGTCATCGGCGCCGTCAGAGTGCATATCAACTGCTCTTTCCGGTTTAG
Biotin-RpLP1_mutMotif1(-)	/5Biosg/CTAAACCGGAAAGAGCAGTTGATATGCACTCTGACGGCGCCGATGACGAA

Primers to generate PCR template for dsRNA production

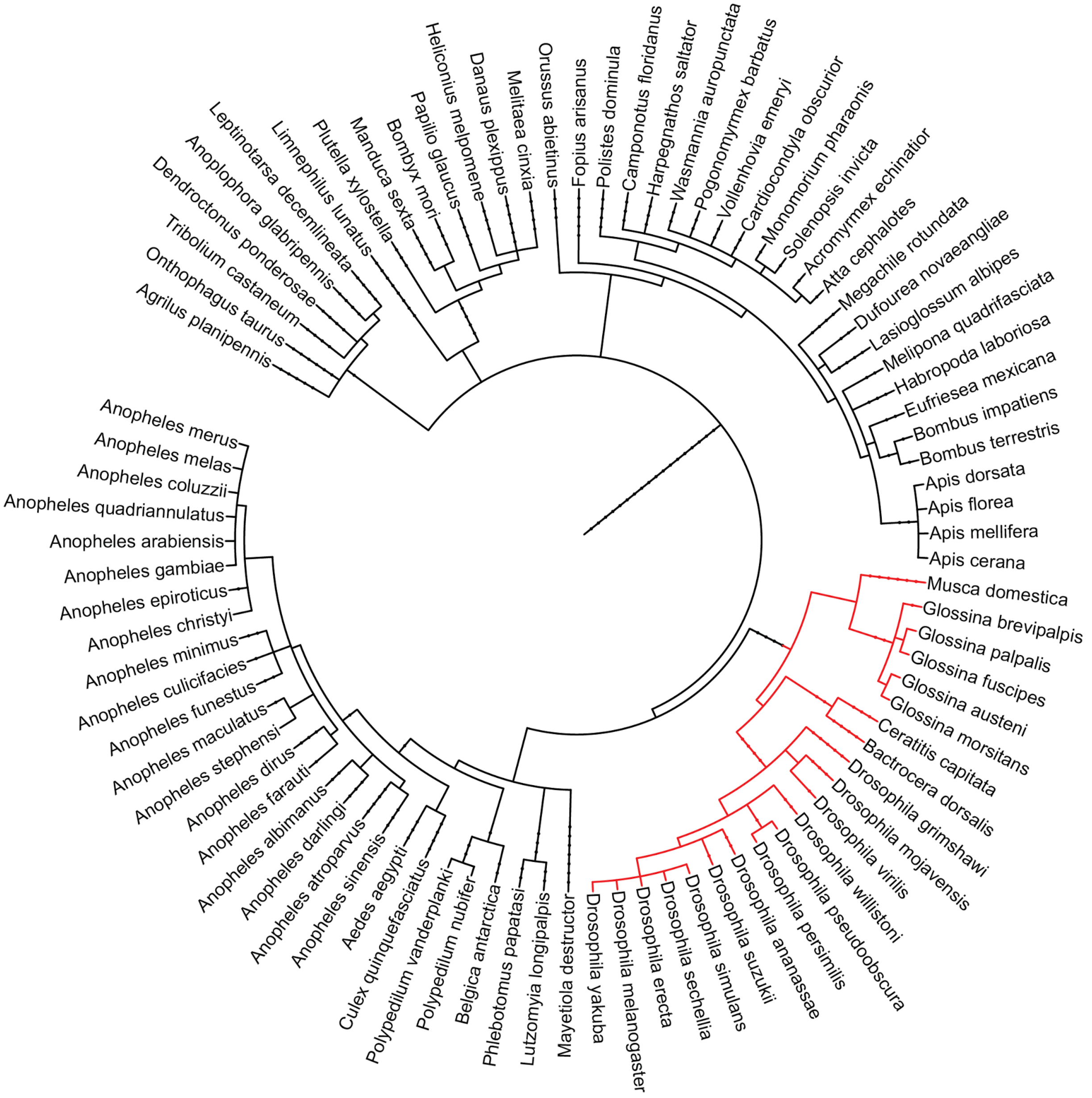
Name	Sequence
lacZ RNAi Fwd	GAATTAATACGACTCACTATAGGGAGATGAAAGCTGGCTACAGGA
lacZ RNAi Rev	GAATTAATACGACTCACTATAGGGAGAGCAGGCTTCTGCTTCAAT
GFZF RNAi Exon 2 Fwd	GAATTAATACGACTCACTATAGGGAGATCAGCATCTGTTCCACTTCG
GFZF RNAi Exon 2 Rev	GAATTAATACGACTCACTATAGGGAGAGTGTGTGAATGTGGGTCGAG
GFZF RNAi 5’UTR Fwd	GAATTAATACGACTCACTATAGGGAGAGCATAGCTCGCAGCCCTCGTATCC
GFZF RNAi 5’UTR Rev	GAATTAATACGACTCACTATAGGGAGAGGCCCGAGCCCGGAATTCAGC

Primers used for qPCR analysis of ChIP material

Name	Sequence	Product Size	Flybase Gene Accession
RpLP1-Fwd (-10)	ATCAACTGCTCTTTCCGGTT	78 bp	FBgn0002593
RpLP1-Rev (+68)	TGTTTATAACAAATGGCCTTAGCTC		
awd-Fwd (-84)	ATTCACCTTGCCGGCATTTC	125 bp	FBgn0000150
awd-Rev (+41)	TCCTTGTTAGCCGCCATTGT		
hsp70Bc-Fwd (-72)	GAGAGCGCGCCTCGAAT	101 bp	FBgn0013279
hsp70Bc-Rev (+29)	CGTGTTCACTTTGCTTGTTTGAA		
roX2-Fwd (-52)	AGTGTGGCCAAAACTCGAAAA	121 bp	FBgn0019660
roX2-Rev (+69)	TTCGCTTACCTAAACGCTCG		
sxl-Fwd (-56)	TTAGCCACCGTAAAGCCACC	99 bp	FBgn0264270
sxl-Rev (+43)	TTCACTGCGCGACTTTCCTT		



Supplemental Figure S1. Orthologs of the entirety of GFZF are restricted to Schizophora. GFZF orthologs and sequences were obtained from OrthoDB (1) by providing the amino acid sequence of GFZF. Sequence alignments were generated using Clustal Omega (2). The image was generated using Jalview with the “Blosum62” coloring mode (3). The FLYWCH zinc finger (FWZF) and GST domains are delineated above the alignments.



Supplemental Figure S2. Orthologs of the entirety of GFZF are restricted to Schizophora. Cladogram showing Schizophora cladogram was generated with Interactive Tree of Life (iTOL) server (4) by feeding the phyloT server with the list of organisms that possess GFZF orthologs according to OrthoDB as shown in Supplemental Figure S1. Species with orthologs possessing N-terminal FLYWCH zinc fingers, like GFZF, are highlighted in red.

References

1. Zdobnov EM, Tegenfeldt F, Kuznetsov D, Waterhouse RM, Simão FA, Ioannidis P, Seppey M, Loetscher A, Kriventseva EV. 2017. OrthoDB v9.1: cataloging evolutionary and functional annotations for animal, fungal, plant, archaeal, bacterial and viral orthologs. Nucleic Acids Res 45:D744–D749.

2. Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, Lopez R, McWilliam H, Remmert M, Söding J, Thompson JD, Higgins DG. 2011. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Mol Syst Biol 7:539.

3. Waterhouse AM, Procter JB, Martin DMA, Clamp M, Barton GJ. 2009. Jalview Version 2--a multiple sequence alignment editor and analysis workbench. Bioinformatics 25:1189–1191.

4. Letunic I, Bork P. 2016. Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. Nucleic Acids Res 44:W242–5.