

Control of seminal fluid protein expression via regulatory hubs in *D. melanogaster*

Irina Mohorianu^{1,2*}, Emily Fowler^{1*}, Tamas Dalmay¹, Tracey Chapman^{1,#}

¹School of Biological Sciences, University of East Anglia, Norwich Research Park, Norwich, NR4 7TJ, UK.

²School of Computing Sciences, University of East Anglia, Norwich Research Park, Norwich, NR4 7TJ, UK.

*Joint first authors

SI Figures

Figure S1. miRNA regulation of the transferome genes. Network of putative interactions between miRNAs (colourless nodes) and transferome genes whose products have a function in: development/cellular organisation (red), gene expression (orange), post-mating behaviour/response (green), response to stimulus (purple), metabolic process (yellow), protein processing (blue), unknown function (grey). Node size is directly proportional to the number of edges.

Figure S2. Summary of the similarity (proportional identity) in pairwise comparisons of sets of UTRs potentially targeted by the same miRNAs. The similarity analysis was conducted where there were sets of at least 3 transcripts targeted by the same miRNA (the 87 such 3p/5p miRNAs potentially targeting >3 transcripts are shown on the X axis). Proportional identities (Y axis) are summarised by the median \pm IQR similarity of all pairwise comparisons between transcripts targeted by the same miRNA. Overall, the median identity across all sets of transcripts oscillated in the 45-55% range, with the maximum identity exceeding 70% for only 11/87 sets. Hence for the majority of transcripts predicted to be targeted by the same miRNA, the similarity was < 60%, giving no evidence that they were paralogues. The inset shows an example weighted scatterplot for the 5 transcripts potentially targeted by miR-972-3p, calculated using Clustal Omega, reported as a proportion of the length of the shortest transcript in each case - the transcripts are presented in the same order on the X and Y axes, hence the diagonal values illustrate the comparison of each sequence against itself (100% similarity (proportional identity)).



