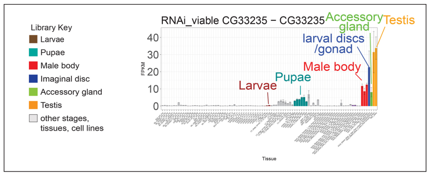
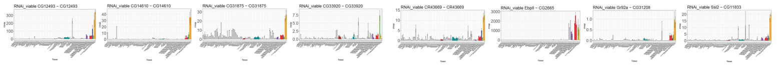
Spatial expression of 136 young “RNAi viable” genes classified by Chen et al Science 2010

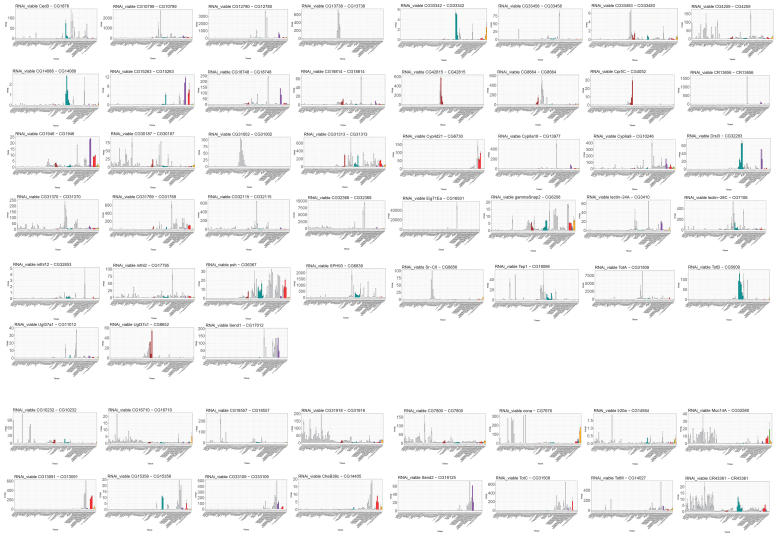


Testis expression > 2X higher than the next highest expressed tissue

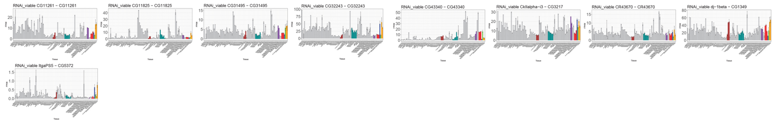
Testis highest expressed tissue (”Xmax”),
but <2X higher than the next highest expressed tissue/stage/cell line



Xmax in non-testis tissue/stage/cell line



Ubiquitous



Supplementary Figure 2. Spatiotemporal expression patterns of recently emerged “RNAi-viable” genes.

Chen et al (Science 2010) used RNAi assays to deplete 195 genes that had emerged recently in the lineage towards D. melanogaster, resulting in classification of 59 “RNAi-lethal” and 136 “RNAi-viable” young genes. We analyzed their expression patterns across the diversity of developmental stage, dissected tissue, and cell line RNA-seq datasets reported by the modENCODE project. The 59 “RNAi-lethal” loci are presented in Supplementary Figure 1 and the 136 “RNAi-viable” young genes are summarized here.

(Boxed legend) Selected tissues and stages are colored to enable browsing of spatiotemporal expression patterns. Mean RPKM values and standard deviation from replicate RNA-seq datasets is potted. In particular, the datasets that are most relevant to the male reproductive system are placed at the far right of each gene summary; e.g. testis, accessory gland, male body. Also included with these is unsexed larval imaginal disc/gonad library data, which we have previously observed is rich in testis-specific transcripts and likely represents developmental expression of genes that are also expressed in the adult male reproductive system. For this reason, we also highlight larval and pupal libraries, which although unsexed undoubtedly include expression from developing male gonads.

(Below) Spatiotemporal expression patterns of 136 “RNAi-viable” young genes. More than half of these genes are highly restricted to the male reproductive system, which is not needed for viability. Many other genes exhibit expression pattterns and/or levels that are not overtly expected for lethal phenotypes. These spatiotemporal expression patterns mirror those of the 59 “RNAi-lethal” genes (Supplementary Figure 1), suggesting that the RNAi lethality might not be due to suppression of the intended loci.

Kondo et al,
Supplementary Figure 2