



Fig. 2 RNA dynamics through tissues along fly development. **(a)** Proportion of the gene expression variation explained by tissues (x -axis) and by developmental stages (y -axis) for 9334 genes (*dots*; *i.e.* genes expressed at least 5 TPMs in two samples) using linear models. **(b)** Box plot representing the distribution of the proportion of gene expression variation across stages and tissues, where stages show higher contribution to gene expression variation than tissue or the interaction tissue:stage. **(c)** Heatmap of DEG across tissues (334 TGs), stages (1445 SGs) and both tissue and stage (255 TSGs). Gene expression values are normalized to z -scores. There are more stage-specific genes than tissue-specific genes. Genes were further classified in subgroups based on upregulation in precise tissues/stages. **(d)** Dynamics of DEG across fly development. Notably there are more eye, leg and wing-specific genes, respectively, at the late stage. Overall, the transcriptome diverges as tissues become more specified.