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. The gray lines at $y = 2x$ and $x = 2y$ identify the genes in which tissue-explained variability is two fold greater than developmental stage-explained variability, and in which developmental stage-explained variability is two fold greater than tissue-explained variability, respectively. We restricted to the genes for which either tissue or stage explains at least 75% of the variability (*gray line* at $x + y = 0.75$). We defined 4 sets of genes: (i) genes whose expression varies considerably across stages and little across tissues, SGs (*gray*); (ii) genes whose expression varies considerably across tissues and little across stages, TGs (*pink*); (iii) genes whose expression varies considerably across tissues as well as across stages, TSGs (*purple*); and (iv) genes with variation due to interaction tissues:stages, iTSGs (*dark pink*). (**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 variability than tissue or the interaction tissue:stage. (**c**) Number of transcription factors that are differentially expressed across tissues (TGs), stages (SGs) and both tissue and stage (TSGs). (**d**) Heatmap of DEG across tissues, stages and both tissue and stage. 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. (**e**) Dynamics of DEG across fly development. Notably there are more eye, leg and wing-specific genes, respectively, at the late stage.