Fig. S13. Flowchart for multispecies analysis. An overview of the pipeline and methods used for exploring the conservation of homologous cell types and tissues among tomato, Arabidopsis and rice. Ath=*Arabidopsis thaliana*; Osa=*Oryza sativa*; Sly=*Solanum lycopersicum*; IQR= interquartile range; TPM=transcript per million; GO=gene ontology; CTEG=cell type/tissue enriched genes.