

В

Brain.e10.5	Brain.e12.5	Brain.e13.5	Brain.e14.5	Brain.e15.5	Brain.e16.5	Brain.e17.5	Brain.e18.5	Brain.P0.1	Brain.P3.1	
Heart.e10.5	Heart.e12.5	Heart.e13.5	Heart.e14.5	Heart.e15.5	Heart.e16.5	Heart.e17.5	Heart.e18.5	Heart.P0.1	Heart.P3.1	value
Kidney.e11.5	Kidney.e12.5	Kidney.e13.5	Kidney.e14.5	Kidney.e15.5	Kidney.e16.5	Kidney.e17.5	Kidney.e18.5	Kidney.P0.1	Kidney.P3.1	0 -2 -4
Liver.e10.5	Liver.e12.5	Liver.e13.5	Liver.e14.5	Liver.e15.5	Liver.e16.5	Liver.e17.5	Liver.e18.5	Liver.P0.1	Liver.P3.1	
С										



Fig. 5 Conservation of differentiation regulatory program in mouse. (**a**) Orthologs of differentiation genes in mouse RNASeq data (brain, heart, kidney and liver at different developmental time points. (**b**) The orthologs of *Drosophila* Early and Late genes cluster separately regarding gene expression along mouse tissue development using self-organizing maps. (**c**) Number of Early and Late orthologs in the different mouse tissues. Venn diagrams show the number of Early and Late orthologs that show the same expression profiles in the mouse RNA-seq compared to the fly in the different tissues. The bar plots show the Early and Late orthologs classified by the expression profile in the mouse RNA-seq data per tissue.