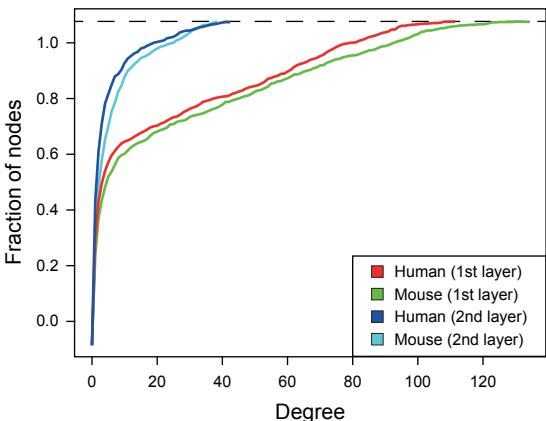
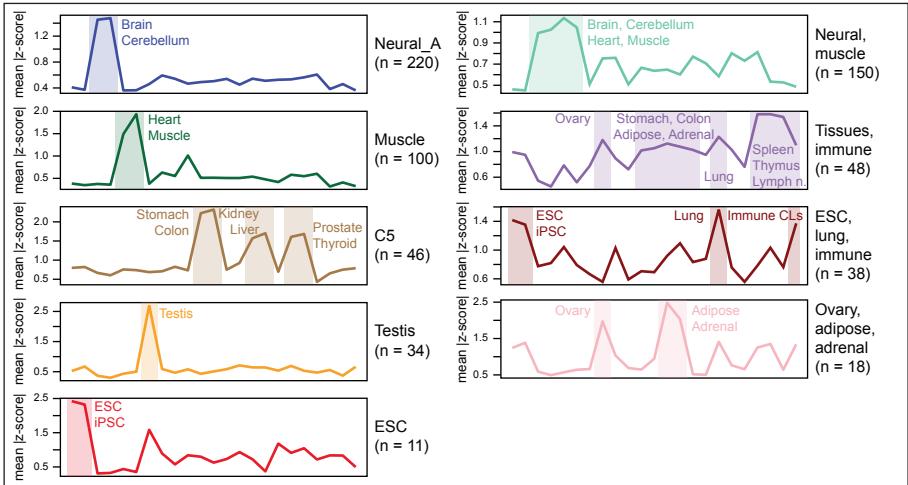
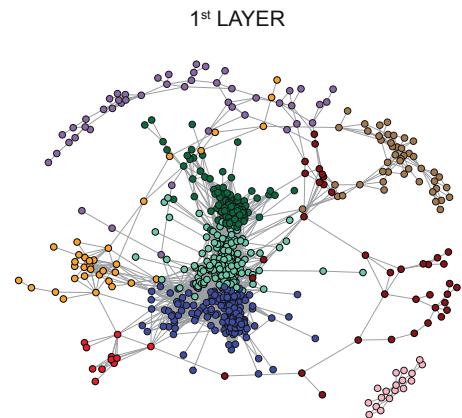
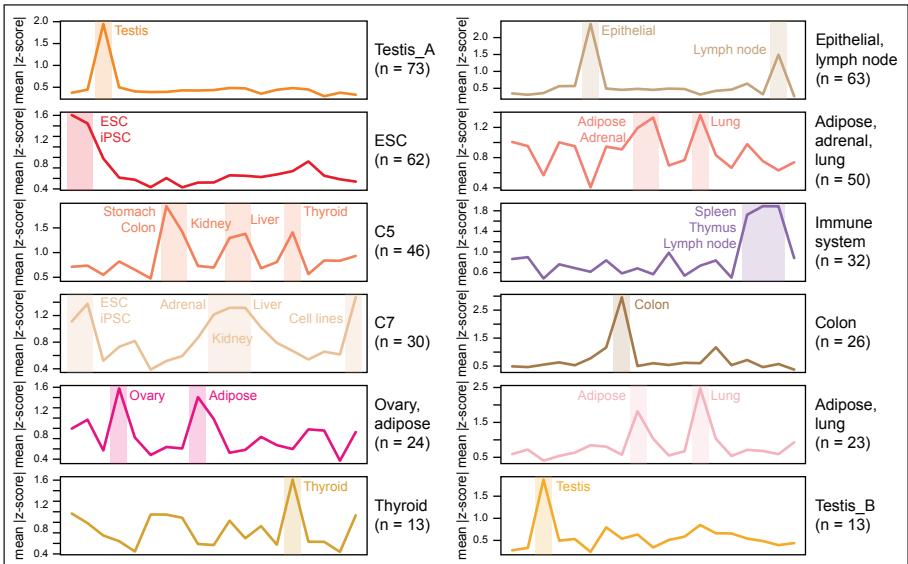
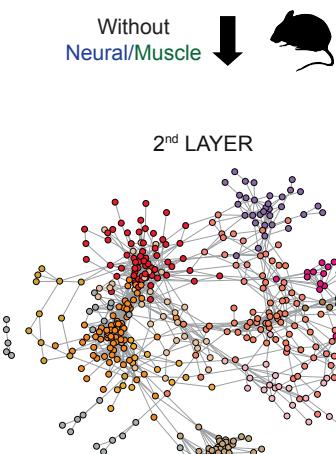


A

Tissue	ESC	IPS	Brain	Cerebellum	Heart	Muscle	Testis	Ovary
Human	4	2	5	2	3	3	3	2
Mouse	6	2	5	3	4	3	3	2

Tissue	Placenta	Epithelial	Stomach	Colon	Adipose	Adrenal	Kidney	Liver
Human	3	2	2	3	3	2	3	3
Mouse	3	3	3	3	3	3	3	3

Tissue	Lung	Prostate	Spleen	Thymus	Lymph_Node	CL_Immune	Thyroid	Total
Human	3	3	2	2	2	2	3	62
Mouse	3	2	3	3	2	2	2	69

B**C****D**

Supplemental Figure S17 – Mouse co-regulated splicing network analysis

A) Matched tissue and cell types in human and mouse and corresponding number of replicates in each species used in the network analysis. B) Cumulative plot of the degree for the resulting splicing network for 1,033 conserved and highly alternatively spliced exons in human (red, dark blue) and mouse (green, light blue) including (1st layer) or excluding (2nd layer) neural and muscle tissues. C-D) Left: Graphical representation of the mouse splicing networks, highlighting the different exon communities for the 1st (C) and 2nd (D) layer networks. Right: Plot of the mean absolute Z-score across tissues for each community of the 1st (A) and 2nd (B) layer mouse networks. Dominant tissues are highlighted. Communities were named based on dominant tissues, when possible. For simplicity, only communities with 10 or more AS events are displayed.