

# Functional annotation of the transcriptome of the pig, *Sus scrofa*, based upon network analysis of an RNAseq transcriptional atlas.

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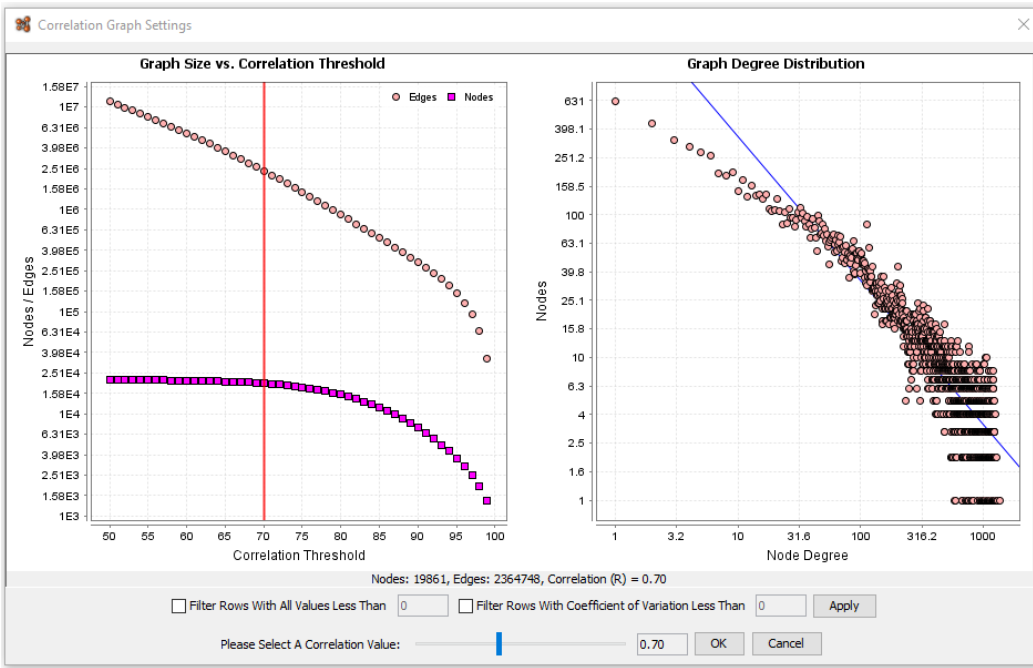
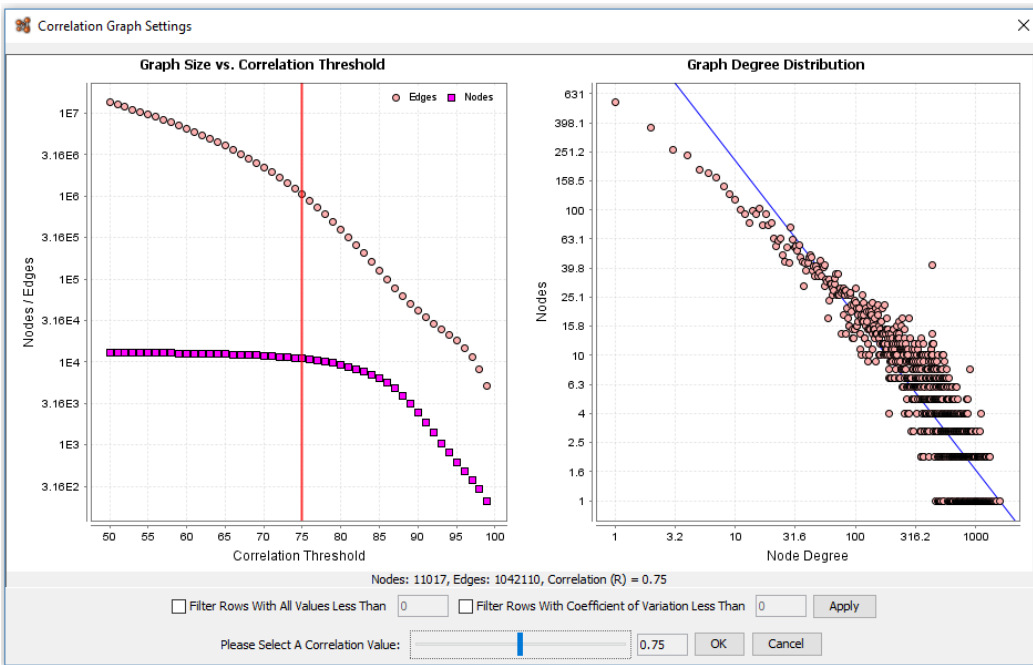
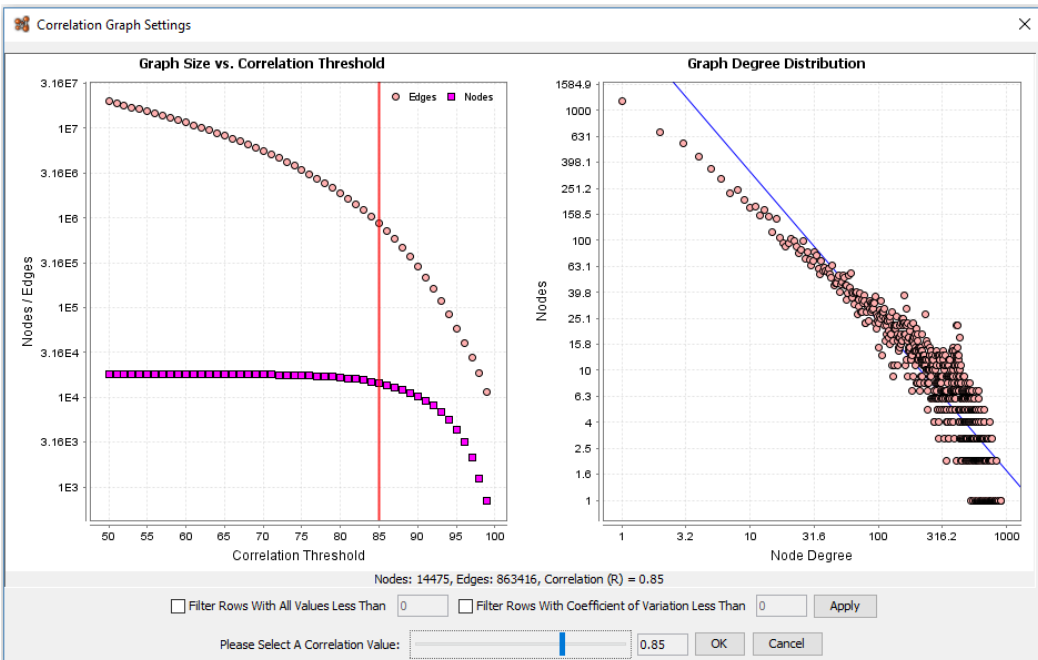
#### Figure S1. Correlation graph settings for network analysis with Graphia Professional

The correlation threshold for each gene-to-gene analysis was chosen to optimise the number of nodes and edges in order to generate meaningful clusters.

A. Settings for the overall atlas.

B. Settings for the analysis of liver samples.

C. Settings for the analysis of central nervous system samples.

**A****B****C**

## Figure S2. Sample to sample networks

A. Networks generated for the overall atlas. Colours show the organ system of the samples. Upper panel shows the result for all nodes (samples) at  $R \geq 0.38$ ; lower panel shows the network at  $R \geq 0.85$ , which clusters samples of related origin together. Note that muscle, heart, spleen, liver and testis samples from BioProject PRJNA297855 are separated from the other samples of the same tissues. These samples are from a study of Guizhou minipigs which may be very different from the full sized breeds of the other samples.

B. Network generated for the liver analysis. Colours indicate the BioProject from which the samples were drawn.

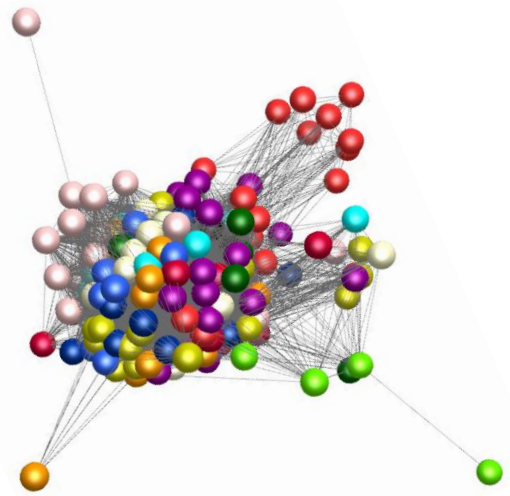
C. Network generated for the central nervous system analysis.

### A. Overall atlas

Node colour	Organ system
Red	Cardiovascular system
Light red	Endocrine system
Pink	Female reproductive system
Orange	Gastrointestinal tract
Yellow-green	Immune system
Yellow	Integumentary system
Green	Male reproductive system
Black	Mixture of multiple tissues
Purple	Muscular system
Dark green	Nervous system
Dark blue	Cells, cell lines, embryo
Cyan	Renal system
Blue	Respiratory system

Sample-to-sample analysis by organ system  
 $r \geq 0.38$

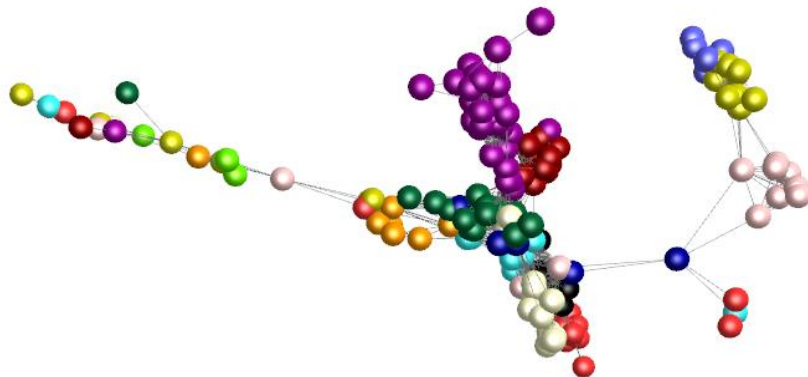
206 nodes, 14,243 edges



Sample-to-sample analysis by organ system

$r \geq 0.85$

188 nodes, 1378 edges

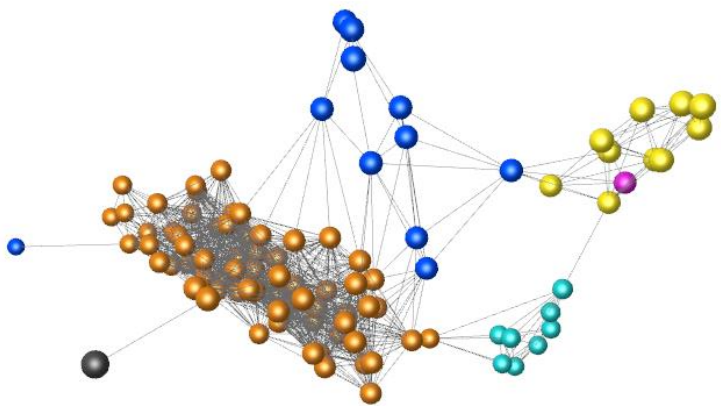


**B. Analysis of liver samples**

$r \geq 0.9$

102 nodes, 1301 edges

Nodes are coloured by BioProject ID



Node colour	BioProject	Description
	PRJNA193204	Berkshire pig, adult (Sodhi et al., 2017)
	PRJNA240332	Yorkshire-Landrace cross pigs, juvenile (15-20 kg), haemorrhagic shock model (Determan et al., 2014)
	PRJNA297855	Guizhou minipig, 240 days postnatal (Tang et al., 2017)
	PRJNA305529	Iberian-Landrace cross, backcrossed to Landrace, 175 days postnatal, low and high growth and fatness (Martinez-Montes 2016)
	PRJNA311523	Various breeds, 60 days postnatal {Li 2017}
	PRJNA451072	Danish Landrace pigs, adult (100 kg), high and medium boar taint (Drag et al., 2017)

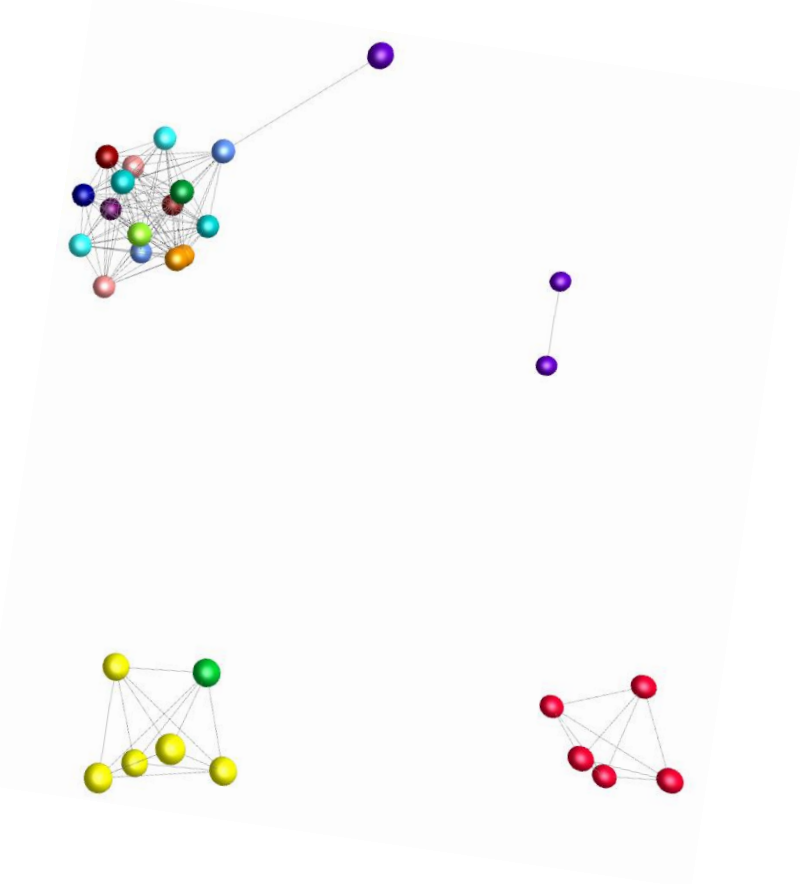
**C. Analysis of central nervous system samples**

$r \geq 0.87$

30 nodes, 142 edges

Nodes are coloured by region

Node colour	Region
	Amygdala
	Brain
	Brainstem
	Corpus callosum
	Cortex
	Thalamus
	Forebrain
	Frontal cortex
	Hippocampal formation
	Hypothalamus
	Medulla oblongata
	Occipital cortex
	Pituitary gland
	Pons



## References for Supplementary Figures

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