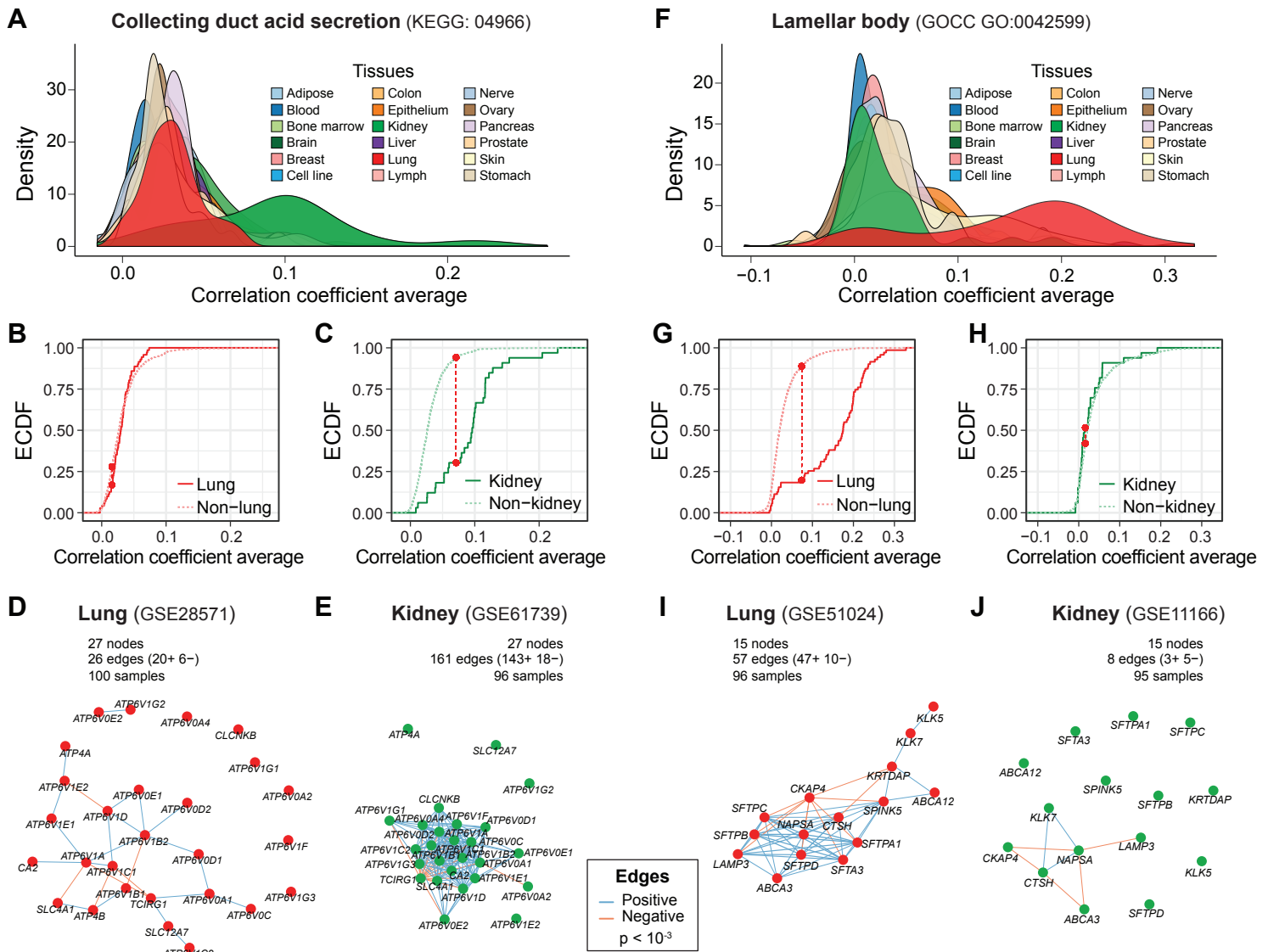# Figure S5

Figure S5. Tissue specific co-expression of modules.
A, F, Distribution of the co-expression of genes in the "collecting duct acid secretion" (**A**) or "lamellar body" (**F**) module across tissues in human. The average correlation coefficient of the gene pairs of the module in 1,300 human expression datasets from 18 major tissues was used to illustrate the co-expressions of this module across tissues. Genes in "collecting duct acid secretion" (**A**) and "lamellar body" (**F**) module have higher co-expression in datasets from kidney and lung, respectively, indicating the potential to assign tissue-specificity.
B-C, G-H, The tissue specificity of "collecting duct acid secretion" (**B-C**) or "lamellar body" (**G-H**) module in lung (**B, G**) and kidney (**C, H**) is illustrated by the empirical cumulative distribution function (ECDF). The red dotted lines indicate the Kolmogorov–Smirnov statistic, which is based on the maximum distance between the two curves. Curves shifting towards the right indicate that datasets from the respective tissue have a higher correlation coefficient, therefore greater specificity for this tissue. In this case, the steeply rising part of the ECDF, also shown as the peak of the density of the correlations in Fig. **S5A, F** is shifted towards higher correlations.
D-E, I-J, Pearson correlation network of genes in the "collecting duct acid secretion" (**D, E**) or "lamellar body" (**I, J**) module in representative datasets of lung (**D, I**) and kidney (**E, J**). The number of genes (nodes) and gene pairs (edges) that survive the indicated threshold of correlation significance are shown. Genes in the "collecting duct acid secretion" module have higher co-expression in datasets from the kidney (**E**) than the lung (**D**), while genes in the "lamellar body" module have higher co-expression in datasets from the lung (**I**) than the kidney (**J**).