

**Supplementary Figure 1** Mass spectrometry of decellularized ECM scaffolds derived from porcine kidney. Heat map analysis following SDS decellularization depicting proteins with spectral counts between 10-100 in at least one decellularization condition. Heat map analysis data was grouped using hierarchical clustering. Spectral counts were used to create heat map.

**Supplementary Figure 2** Mass spectrometry of decellularized ECM scaffolds derived from human kidney. Heat map analysis following SDS decellularization depicting proteins with spectral counts between 10-100 in at least one decellularization condition. Heat map analysis data was grouped using hierarchical clustering. Spectral counts were used to create heat map.

**Supplementary Figure 3** Protein array analysis of whole porcine kidney. Growth factors and cytokines are present and quantifiable in the native kidney prior to decellularization. Error bars represent SEM. N = 3.

**Supplementary Figure 4** Selected GO terms indicating biological, cellular, and molecular functions of retained cytokines.

**Supplementary Figure 5** H&E staining of decellularization of 300  $\mu\text{m}$  x 6mm porcine kidney cortex sections using (a) 0.03% and (b) 0.04% SDS. Presence of hematoxylin staining in glomeruli indicates incomplete decellularization. Scale bars – 100  $\mu\text{m}$ .

**Supplementary Table 1** Mass spectrometry of whole porcine kidney. N = 1.