KEGG Pathways

ABC transporters
Area under the curve = 0.83

Adherens junction
Area under the curve = 0.79

Alanine, aspartate, and glutamate metabolism
Area under the curve = 0.79

Cell cycle
Area under the curve = 0.84

Cysteine and methionine metabolism
Area under the curve = 0.80

Focal adhesion
Area under the curve = 0.89

Lysine degradation
Area under the curve = 0.90

MAPK signaling pathway
Area under the curve = 0.87

Notch signaling pathway
Area under the curve = 0.80

Oocyte meiosis
Area under the curve = 0.82

Oxidative phosphorylation
Area under the curve = 0.82

Phosphatidylinositol signaling system
Area under the curve = 0.84

Protein processing in endoplasmic reticulum
Area under the curve = 0.82

Purine metabolism
Area under the curve = 0.84

Regulation of actin cytoskeleton
Area under the curve = 0.78

Ribosome
Area under the curve = 0.83

RNA transport
Area under the curve = 0.83

RNA degradation
Area under the curve = 0.87

Spliceosome
Area under the curve = 0.87

Ubiquitin mediated proteolysis
Area under the curve = 0.92

Wnt signaling pathway
Area under the curve = 0.88
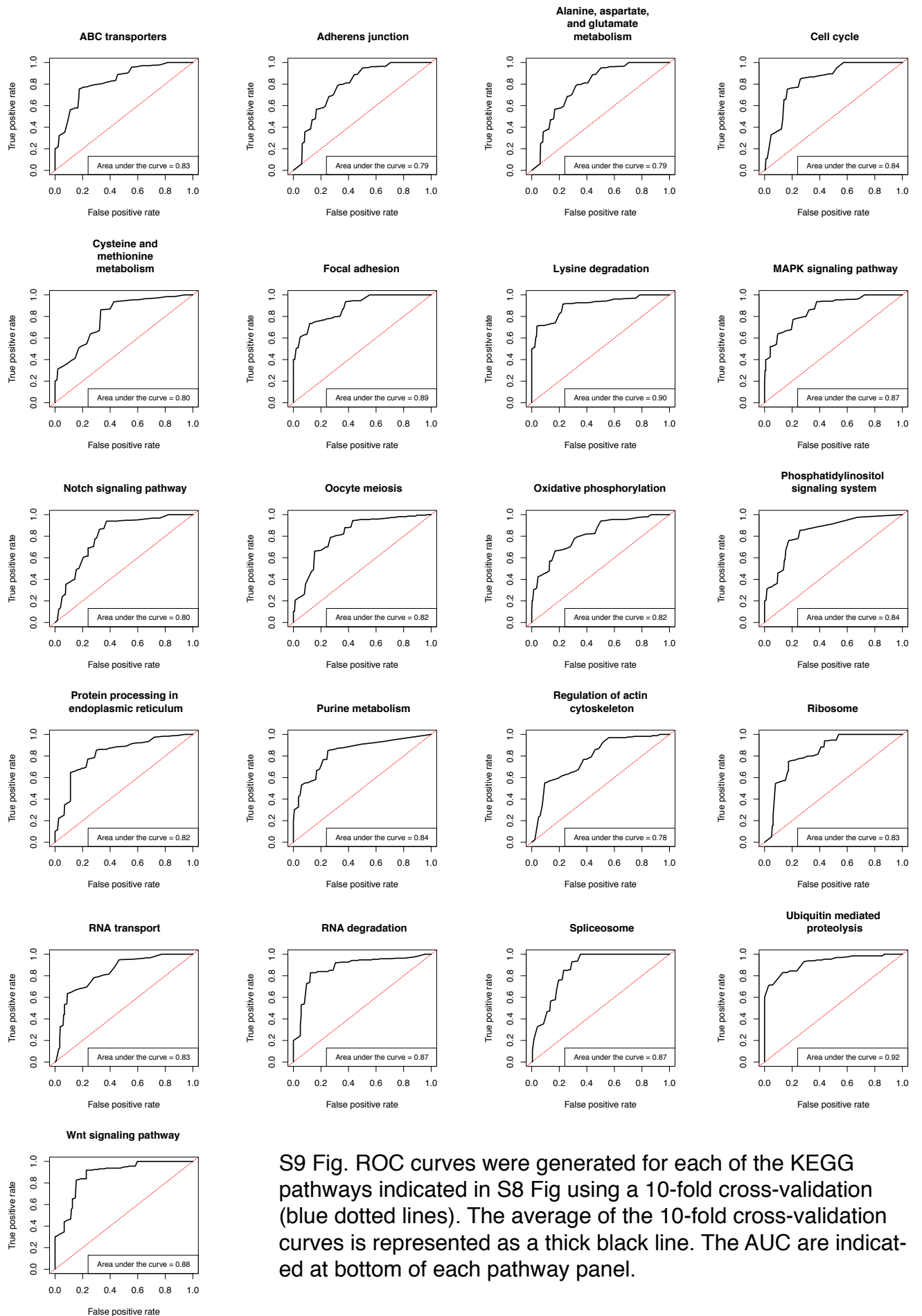
S9 Fig. ROC curves were generated for each of the KEGG pathways indicated in S8 Fig using a 10-fold cross-validation (blue dotted lines). The average of the 10-fold cross-validation curves is represented as a thick black line. The AUC are indicated at bottom of each pathway panel.