PID Pathways

BARD1 — Area under the curve = 0.78

Canonical Wnt signaling pathway — Area under the curve = 0.90

CDC42 Signaling — Area under the curve = 0.80

Class I PI3K — Area under the curve = 0.72

CXCR4–mediated signaling events pathway — Area under the curve = 0.80

Degradation of beta catenin — Area under the curve = 0.87

Direct p53 effectors — Area under the curve = 0.87

ErbB1 downstream signaling — Area under the curve = 0.84

Insulin Pathway — Area under the curve = 0.83

Neurotrophic factor-mediated Trk — Area under the curve = 0.83

p75 (NTR) - mediated signaling — Area under the curve = 0.85

PDGFR–beta signaling pathway — Area under the curve = 0.90

Presenilin action in Notch and Wnt signaling — Area under the curve = 0.84

Regulation of CDC42 activity — Area under the curve = 0.86

Regulation of nuclear beta catenin signaling and target gene transcription — Area under the curve = 0.86

Regulation of Telomerase — Area under the curve = 0.87

Signaling events mediated by Hepatocyte Growth Factor Receptor c-Met — Area under the curve = 0.86
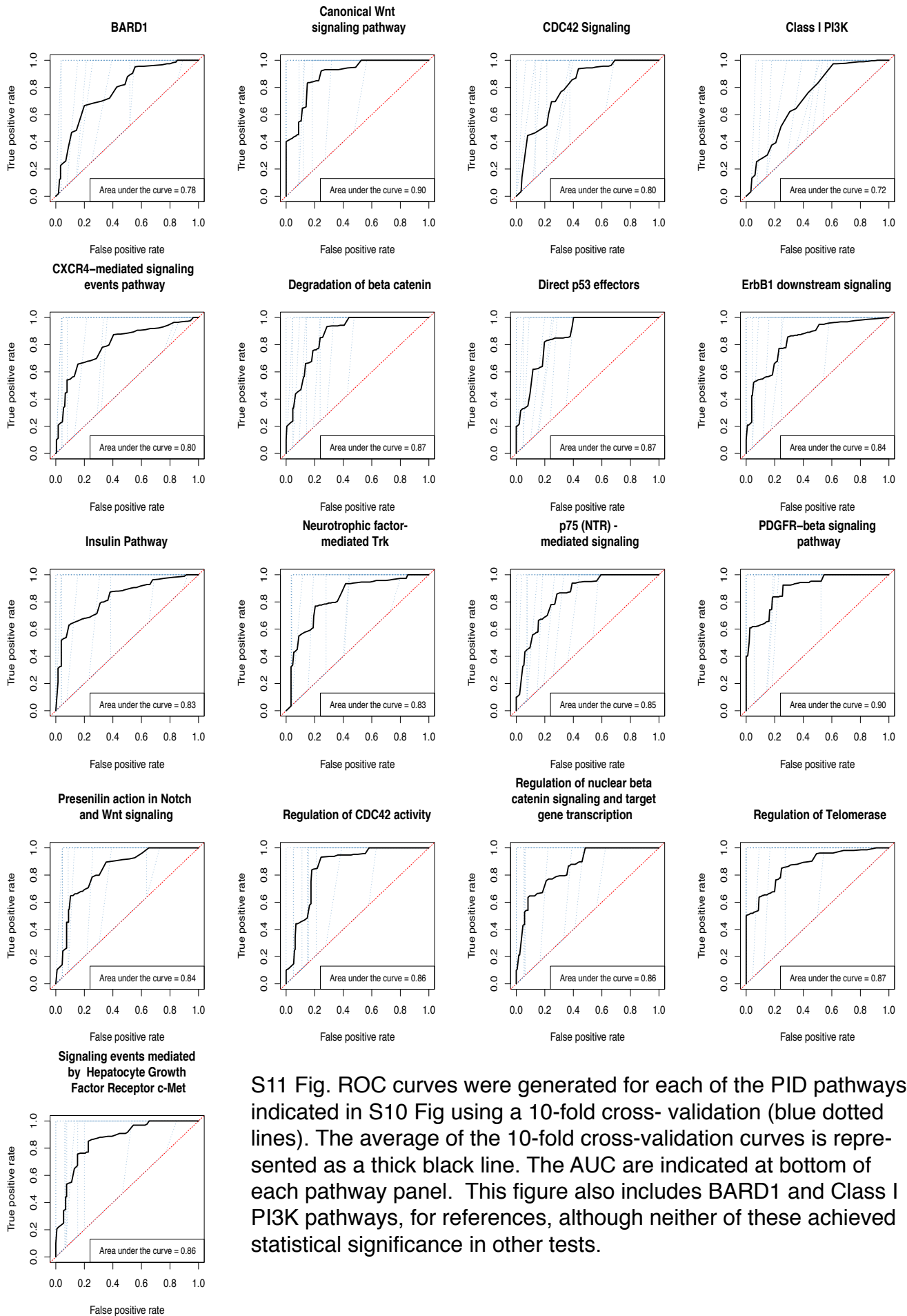
S11 Fig. ROC curves were generated for each of the PID pathways indicated in S10 Fig using a 10-fold cross- validation (blue dotted lines). The average of the 10-fold cross-validation curves is represented as a thick black line. The AUC are indicated at bottom of each pathway panel. This figure also includes BARD1 and Class I PI3K pathways, for references, although neither of these achieved statistical significance in other tests.