



S1 Fig. Validation of genes of interest by quantitative real-time reverse transcriptase polymerase chain reaction analysis similar to Fig 1C, but with data for each target gene normalized to *HMBS* (hydroxymethylbilane synthase). Data are represented graphically as the fold changes (FC) as compared to control cell lines. Lines represent means and each dot represents an individual cell line. ADC, adenocarcinoma; IPF, idiopathic pulmonary fibrosis.