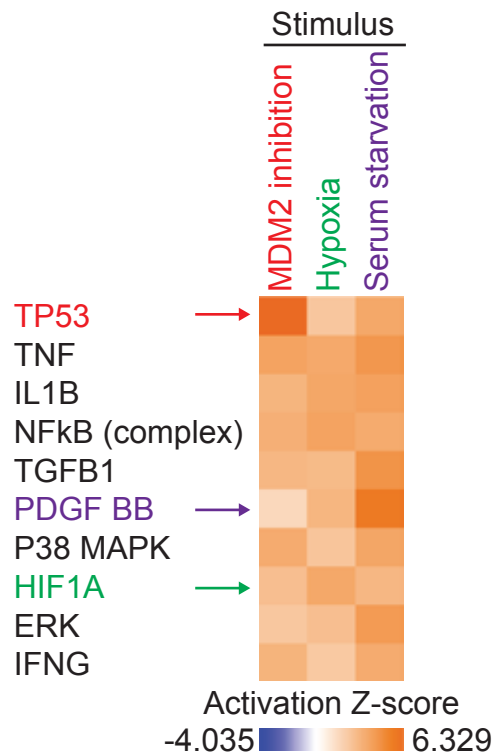


A



B

Pathway	# Genes in Pathway	# Observed	# Expected	adjusted p-value
Signaling mediated by p38-gamma and p38-delta	11	6	0.34	0.0001
Interferon Signaling	98	14	3.05	0.0003
Interferon alpha/beta signaling	77	12	2.4	0.0005
Cytokine Signaling in Immune system	193	19	6	0.0008
Signaling events mediated by focal adhesion kinase	1288	56	40.07	0.0483
Thrombin/protease-activated receptor (PAR) pathway	1300	60	40.44	0.0483
FOXA1 transcription factor network	44	6	1.37	0.0483
S1P1 pathway	1288	56	40.07	0.0483
IGF1 pathway	1291	56	40.16	0.0483
Alpha9 beta1 integrin signaling events	1305	57	40.6	0.0483
IFN-gamma pathway	1296	56	40.32	0.0483
EGFR-dependent Endothelin signaling events	1289	56	40.1	0.0483
BMP receptor signaling	226	15	7.03	0.0483
Arf6 trafficking events	1288	56	40.07	0.0483
EGF receptor (ErbB1) signaling pathway	1288	56	40.07	0.0483

C

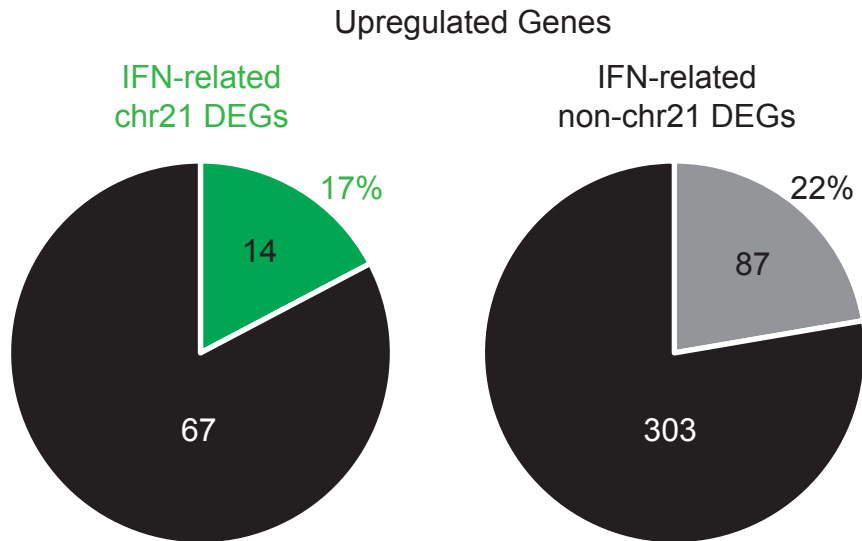


Figure 2 – figure supplement 1. Network analysis confirms IFN activation signature in T21 cells. (A) IPA upstream regulator analysis of genes activated upon MDM2 inhibition with Nutlin-3, hypoxia (1% O₂), and serum stimulation in HCT116 colorectal cancer cells correctly identifies the transcription factor p53, the transcription factor HIF1A, and the growth factor PDGF, as the key upstream regulators in each scenario. (B) Top 15 deregulated pathways in T21 cells identified by Pathway Commons Analysis in WebGestalt. IFN-related pathways are highlighted in red. (C) Pie charts showing the percentage of chr21 and non-chr21 upregulated genes in the interferon pathway.