# Supplemental Table 1.

Top 15 canonical pathways representing differentially expressed genes between ShCTR and ShTonEBP, as identified by Ingenuity Pathway Analysis

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Hepatic Fibrosis / Hepatic Stellate Cell Activation	4.97E00	1.46E-01	MMP9,IL6R,COL27A1,EDNRB,COL5A3,LBP,COL1A1,IL6,Flt1,ECE1,NFKB1,BAMBI,LAMA1,IL1B,VEGFA,TGFB2,COL1A2,MMP13,COL5A1,COL5A2,COL11A1,CXCL3,TIMP1,COL11A2,MMP1
Role of Tissue Factor in Cancer	4.8E00	1.75E-01	GNA11,LIMK2,CSF2,RRAS2,IL1B,VEGFA,PAK1,GNA12,LIMK1,PIK3R5,PIK3C2B,EGR1,MMP13,ARRB1,PTPN11,CASP3,ITGB3,MMP1
Colorectal Cancer Metastasis Signaling	4E00	1.22E-01	MMP9,WNT5A,FZD2,IL6R,PIK3R5,RHOQ,IL6,ARRB1,WNT11,E2F4,RHOT1,PRKAR1B,TLR2,NFKB1,MMP11,RRAS2,VEGFA,ADCY5,TGFB2,PIK3C2B,MMP13,MMP19,GNG12,CASP3,MMP10,MMP1,MMP14,WNT9A
Inhibition of Matrix Metalloproteases	3.89E00	2.5E-01	MMP11,MMP9,MMP19,MMP10,TFPI2,TIMP1,MMP13,MMP1,MMP14
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	3.71E00	1.21E-01	BIRC2,CSF2,WNT5A,FZD2,PIK3R5,COL1A1,BMP2,IL6,NFKBIA,BIRC3,WNT11,IL11,IL1RN,ITGB3,NFAT5,SPP1,IL18R1,NFKB1,IL1B,PIK3C2B,MMP13,BMPR2,BMP1,MMP1,MMP14,WNT9A
Xenobiotic Metabolism Signaling	3.63E00	1.14E-01	FTL,PIK3R5,IL6,NQO1,SUMO1,CAT,ALDH1L2,ARNT,MAOA,CHST2,NFKB1,NDST3,RRAS2,NCOA1,IL1B,MAP3K11,HSP90B1,PPM1L,PIK3C2B,HMOX1,CHST11,MAP3K9,Gsta1,SOD3,HS6ST2,MAP3K4,HS3ST1,EIF2AK3,CHST15
HIF1α Signaling	3.49E00	1.55E-01	MMP11,RRAS2,NCOA1,MMP9,VEGFA,EGLN3,PIK3R5,PIK3C2B,SLC2A1,MMP13,MMP19,MMP10,ARNT,MMP1,MMP14
Axonal Guidance Signaling	3.48E00	9.88E-02	EFNA4,GNA11,MMP9,TUBB3,WNT5A,SEMA4C,FZD2,PAPPA,LIMK1,GNA12,PIK3R5,ADAMTS8,WIPF1,BMP2,EPHA2,PLXNB1,WNT11,GNAI2,PTPN11,PRKAR1B,EFNA1,NFAT5,PLCL1,STK36,GLIS2,SEMA6B,LIMK2,MMP11,RRAS2,VEGFA,GNAT2,PAK1,PIK3C2B,EPHB2,MMP13,PLXND1,BMP1,GNG12,MMP10,PLCZ1,WNT9A
Molecular Mechanisms of Cancer	3.48E00	1.03E-01	BIRC2,GNA11,APAF1,WNT5A,FZD2,GNA12,PIK3R5,IRS1,RHOQ,BMP2,NFKBIA,BIRC3,WNT11,E2F4,GNAI2,CFLAR,PTPN11,CDKN1A,RHOT1,PRKAR1B,RAPGEF1,STK36,NFKB1,RRAS2,NOTCH1,ADCY5,GNAT2,PAK1,RBPJ,TGFB2,PIK3C2B,BMPR2,CDKN1B,BMP1,CASP3,WNT9A
Germ Cell-Sertoli Cell Junction Signaling	3.12E00	1.27E-01	LIMK2,RRAS2,TUBB3,MAP3K11,PAK1,LIMK1,JUP,PVRL2,PIK3R5,TGFB2,PIK3C2B,FER,RHOQ,MAP3K9,ZYX,MYO7A,CLINT1,RHOT1,MAP3K4
Chondroitin Sulfate Biosynthesis	2.9E00	1.88E-01	B4GALT7,CHST2,NDST3,B3GAT3,HS6ST2,HS3ST1,CHST11,CHPF,CHST15
IL-6 Signaling	2.74E00	1.32E-01	NFKB1,RRAS2,IL1B,SOCS3,VEGFA,IL6R,PIK3R5,PIK3C2B,COL1A1,LBP,IL6,NFKBIA,MAPKAPK2,IL1RN,PTPN11
Heparan Sulfate Biosynthesis	2.71E00	1.76E-01	B4GALT7,CHST2,NDST3,B3GAT3,HS6ST2,HS3ST1,CHST11,EXTL3,CHST15
Dermatan Sulfate Biosynthesis	2.71E00	1.76E-01	B4GALT7,CHST2,NDST3,B3GAT3,HS6ST2,HS3ST1,CHST11,CHPF,CHST15
Leukocyte Extravasation Signaling	2.71E00	1.12E-01	F11R,MMP11,MMP9,PIK3R5,ARHGAP1,PIK3C2B,FER,WIPF1,MMP13,EDIL3,GNAI2,MMP19,PTPN11,DLC1,MMP10,ITGB3,TIMP1,JAM3,MAP3K4,MMP1,MMP14

Supplemental Table 2.
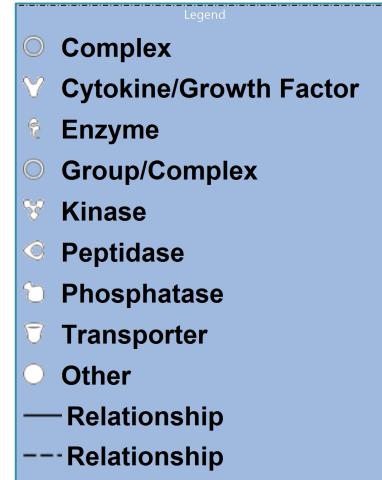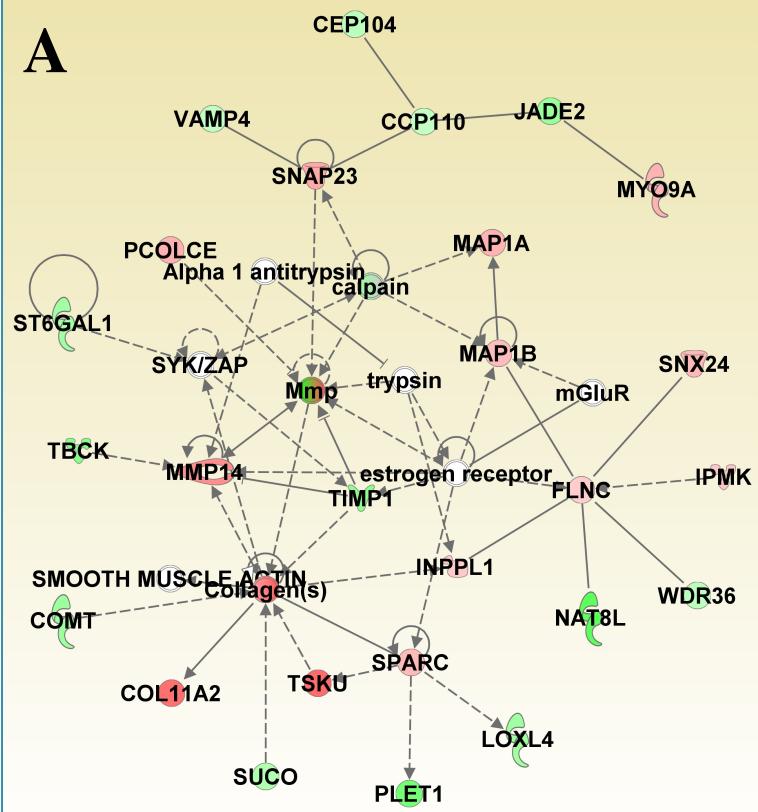
Top biological functions representing differentially expressed genes between ShCTR and ShTonEBP, as identified by Ingenuity Pathway Analysis

	Category	*P*-value	No. Molecules
Diseases and Disorders	Inflammatory Response	3.59E-11-3.61E-04	225
	Connective Tissue Disorders	5.14E-09-3.06E-04	168
	Skeletal and Muscular Disorders	5.14E-09-3.84E-04	207
	Organismal Injury and Abnormalities	1.2E-08-3.85E-04	872
	Renal and Urological Disease	1.2E-08-2.56E-04	80
Molecular and Cellular Functions	Cellular Movement	2.38E-16-3.55E-04	269
	Cell Death and Survival	2.95E-15-3.44E-04	380
	Cellular Growth and Proliferation	1.58E-11-3.06E-04	422
	Cellular Development	1.75E-09-3.06E-04	339
	Cell Morphology	4.74E-08-3.84E-04	253
Physiological System Development and Function	Cardiovascular System Development and Function	1.23E-12-3.13E-04	215
	Organismal Development	1.23E-12-3.77E-04	353
	Hematological System Development and Function	3.59E-11-3.77E-04	202
	Immune Cell Trafficking	3.59E-11-3.55E-04	111
	Organismal Survival	5.37E-10-7.22E-07	273
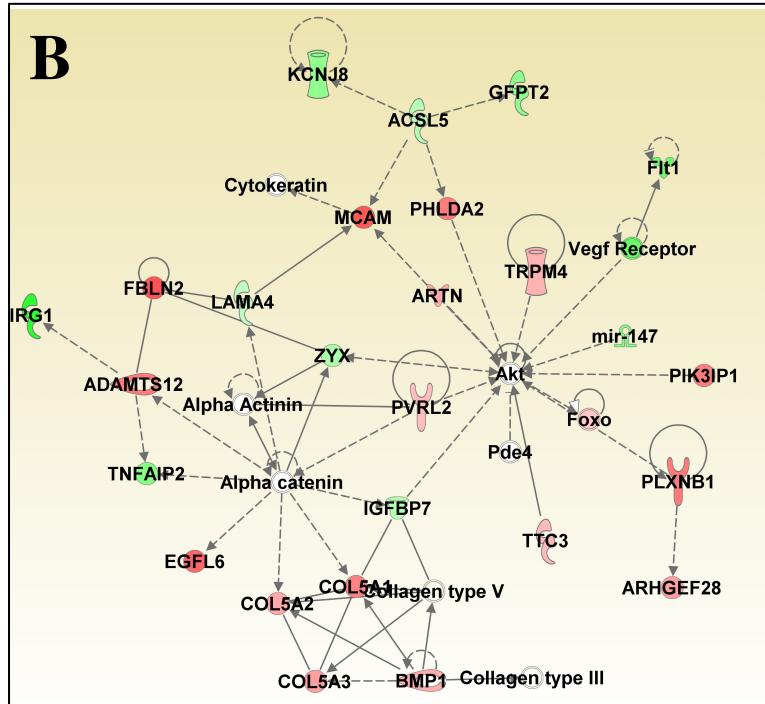
Supplemental Figure 1

IPA Network Diagrams

Supplemental Figure 1. Functional gene network identified using Ingenuity Pathway Analysis (IPA) software from differentially expressed genes between ShCTR and ShTonEBP-transduced NP cells under hypertonic conditions. (A) Network diagram of Skeletal and Muscular Disorders, Connective Tissue Disorders, Cell-to-Cell Signaling and Interaction (score 25, focus molecules: 26). (B) Connective Tissue Disorders, Dermatological Diseases and Conditions, Developmental Disorder (score 25, focus molecules: 26). Each node represents a single gene; node shape denotes functional class of the gene product (i.e., cytokine/ growth factor, kinase, transporter). Intensity of node color indicates degree of overexpression (red) or degree of downregulation (green). Uncolored nodes indicate genes that were not differentially expressed between experimental groups, but were incorporated into the network based on information in the IPA database. Edges indicate direct (solid) and indirect (dashed) interactions based on information in the IPA database.