

### ■ Table S1 Mapping Statistics

Statistics for sample mapping to the mouse genome, using Bowtie2.

Statistics	WT			WT Stress			<i>Ccnc</i> <sup>-/-</sup>		
	1	2	3	1	2	3	1	2	3
Total Paired Reads Mapped	2.18E7	2.29E7	2.31E7	2.41E7	2.62E7	1.89E7	2.35E7	2.44E7	2.37E7
Alignment Rate (%)	81.2	78.8	84.0	78.8	85.0	80.1	80.7	83.4	79.6

■ **Table S2 WT Stress DGE Data**

Top 50 repressed and induced genes in WT Stress MEFs, using DESeq2.

Repressed Genes	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Induced Genes	Log <sub>2</sub> FC	FDR
<i>Col3a1</i>	-3.08	1.55E-27	<i>Inka2</i>	3.80	1.34E-69
<i>F2rl1</i>	-2.86	3.24E-49	<i>Ovgp1</i>	3.73	3.09E-38
<i>Prelp</i>	-2.69	1.43E-17	<i>Btnl9</i>	3.54	1.88E-23
<i>Tmem119</i>	-2.63	2.29E-150	<i>Evpl</i>	3.47	1.39E-24
<i>Angptl4</i>	-2.62	8.35E-94	<i>Zfp750</i>	3.31	1.54E-23
<i>Cmklr1</i>	-2.53	5.05E-16	<i>Sec14l5</i>	3.15	7.42E-18
<i>Serpinb1a</i>	-2.49	1.69E-13	<i>Trp53inp1</i>	3.15	7.42E-18
<i>Thbs1</i>	-2.34	4.25E-274	<i>Ddit4l</i>	3.03	6.19E-48
<i>Zfp608</i>	-2.33	4.22E-89	<i>Efcab8</i>	2.98	3.26E-24
<i>Gas1</i>	-2.26	3.29E-246	<i>Cyp27b1</i>	2.87	8.81E-16
<i>Wisp2</i>	-2.23	2.56E-35	<i>Gpr152</i>	2.87	5.92E-15
<i>Apln</i>	-2.20	1.31E-55	<i>Atg9b</i>	2.86	9.84E-37
<i>Angptl7</i>	-2.16	3.10E-14	<i>Slc23a3</i>	2.70	9.64E-13
<i>Gper1</i>	-2.11	7.06E-11	<i>Pmaip1</i>	2.64	3.25E-23
<i>Cd248</i>	-2.10	1.39E-209	<i>Gm29106</i>	2.60	6.52E-16
<i>9930111J21Rik2</i>	-2.10	2.11E-10	<i>Rprm</i>	2.59	2.21E-13
<i>Soon2</i>	-2.08	1.07E-10	<i>Grin3b</i>	2.58	1.27E-37
<i>Emilin</i>	-2.06	7.29E-108	<i>Slc16a8</i>	2.55	6.06E-15
<i>Styk1</i>	-2.06	5.42E-17	<i>Tcam1</i>	2.53	7.65E-20
<i>Cx3cl1</i>	-2.06	2.00E-162	<i>Fscn2</i>	2.52	7.82E-14
<i>Mme</i>	-2.05	4.97E-29	<i>Il17f</i>	2.46	8.77E-11
<i>Lipg</i>	-2.04	1.73E-49	<i>Hic1</i>	2.45	1.07E-14
<i>Clmp</i>	-2.03	4.87E-11	<i>Alpk3</i>	2.42	3.64E-10
<i>Sned1</i>	-2.03	9.06E-12	<i>Sptbn2</i>	2.41	2.21E-28
<i>Plxna2</i>	-2.03	7.24E-132	<i>Gas2l1</i>	2.34	3.22E-15
<i>Ptgfr</i>	-2.01	6.66E-9	<i>Olfra461</i>	2.37	3.45E-9
<i>Tgfb1</i>	-1.96	4.35E-21	<i>H2-DMA</i>	2.31	1.33E-14
<i>Bmp2</i>	-1.95	1.63E-70	<i>Rsph10b</i>	2.30	1.70E-9
<i>Scd2</i>	-1.95	1.10E-299	<i>Slc7a3</i>	2.30	3.71E-9
<i>Dchs2</i>	-1.95	9.60E-25	<i>Mmp15</i>	2.26	3.93E-14
<i>S1pr3</i>	-1.94	4.43E-53	<i>Chrn2</i>	2.24	3.52E-15
<i>Cdh3</i>	-1.89	2.06E-30	<i>Ermap</i>	2.24	1.27E-8
<i>Itgbl1</i>	-1.89	2.30E-14	<i>Creb3l3</i>	2.24	1.22E-9
<i>Lfng</i>	-1.87	1.28E-40	<i>Sapcd1</i>	2.22	1.15E-8
<i>Angpt1</i>	-1.87	3.62E-9	<i>Wfikkn1</i>	2.21	4.13E-19
<i>Dhrs1</i>	-1.86	9.77E-7	<i>Sesn2</i>	2.20	2.40E-203
<i>Wisp1</i>	-1.86	1.97E-111	<i>Fam186a</i>	2.18	2.71E-8
<i>Elovl6</i>	-1.86	1.14E-214	<i>Kcnj4</i>	2.17	4.08E-17

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

■ **Table S2 Continued WT Stress DGE Data**

Top 50 repressed and induced genes in WT Stress MEFs, using DESeq2.

Repressed Genes	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Induced Genes	Log <sub>2</sub> FC	FDR
<i>Pcdh19</i>	-1.85	3.99E-45	<i>Arhgef6</i>	2.16	2.53E-8
<i>Ntn4</i>	-1.84	9.42E-29	<i>Rbm3</i>	2.14	1.45E-26
<i>Ngnf</i>	-1.84	5.99E-15	<i>Dpx1</i>	2.13	3.25E-23
<i>Gm14137</i>	-1.82	3.20E-48	<i>Mdm2</i>	2.12	4.61E-8
<i>Plat</i>	-1.81	1.93E-28	<i>Tex52</i>	2.10	1.15E-7
<i>Setbp1</i>	-1.81	2.07E-24	<i>Slc26a8</i>	2.09	3.41E-8
<i>Fat4</i>	-1.81	1.69E-86	<i>Gng3</i>	2.09	2.40E-20
<i>Pappa</i>	-1.79	1.70E-14	<i>Aen</i>	2.07	3.51E-39
<i>Adamts5</i>	-1.79	6.99E-76	<i>Rho</i>	2.02	3.28E-7
<i>Ephb6</i>	-1.78	4.78E-41	<i>Gzmm</i>	2.02	2.99E-9
<i>Zfp36l2</i>	-1.77	6.90E-229	<i>Pmm1</i>	2.02	6.67E-8

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.

<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

**Table S3 Oxidative Stress-Repressed Genes in WT MEFs**

GO-Functional Annotation Clusters for repressed genes in WT MEFs following oxidative stress. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes repressed (1,966 genes).

Cluster	ES <sup>a</sup>	Category <sup>b</sup>	Associated Terms	p-value	Number of Genes Involved
1	12.41	GOTERM MF DIRECT	Cadherin binding involved in cell-cell adhesion	8.73E-17	76
		GOTERM CC DIRECT	Cell-cell adherens junction	3.83E-15	78
		GOTERM BP DIRECT	Cell-cell adhesion	1.80E-7	43
2	6.88	GOTERM MF DIRECT	Transferase Activity	5.38E-9	210
		GOTERM BP DIRECT	Protein phosphorylation	1.28E-8	99
		GOTERM MF DIRECT	ATP binding	1.42E-8	212
		GOTERM BP DIRECT	Phosphorylation	1.93E-8	103
		GOTERM MF DIRECT	Kinase activity	3.07E-8	111
3	6.84	UP KEYWORDS	Cell cycle	4.25E-10	102
		UP KEYWORDS	Cell division	1.93E-9	69
		GOTERM BP DIRECT	Cell cycle	1.64E-7	100
		GOTERM BP DIRECT	Cell division	1.81E-7	69
		UP KEYWORDS	Mitosis	9.54E-6	45
		GOTERM MF DIRECT	Mitotic nuclear division	4.06E-5	49
4	5.90	UP KEYWORDS	Oxidoreductase	1.69E-7	95
		GOTERM BP DIRECT	Oxidation-reduction process	2.55E-6	100
		GOTERM MF DIRECT	Oxidoreductase activity	4.73E-6	94

<sup>a</sup> ES = Enrichment score produced by Functional Annotation Clustering in DAVID.

<sup>b</sup> Category Terms Defined: GOTERM MF DIRECT = GO Term for Direct Involvement in Molecular Function; GOTERM CC DIRECT = GO Term for Direct Localization to Cellular Compartment; GOTERM BP DIRECT = GO Term for Direct Involvement in Biological Process; UP Keywords = Uniprot Keywords

■ **Table S4 Oxidative Stress-Induced Genes in WT MEFs**

GO-Functional Annotation Clusters for induced genes in WT MEFs following oxidative stress. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes induced (1,875 genes).

Cluster	ES <sup>a</sup>	Category <sup>b</sup>	Associated Terms	p-value	Number of Genes Involved
1	6.38	GOTERM BP DIRECT	Cellular response to DNA damage stimulus	1.86E-8	72
		UP KEYWORDS	DNA damage	6.44E-8	58
		GOTERM BP DIRECT	DNA repair	1.82E-6	54
		UP KEYWORDS	DNA repair	1.36E-5	45
2	4.93	UP KEYWORDS	Ubl conjugation pathway	4.44E-9	95
		GOTERM BP DIRECT	Protein ubiquitination	4.68E-6	58
		GOTERM MF DIRECT	Ubiquitin-protein transferase activity	1.50E-4	49
		GOTERM MF DIRECT	Ubiquitin protein ligase activity	6.26E-3	29
3	4.15	GOTERM BP DIRECT	Autophagy	8.16E-6	30
		GOTERM CC DIRECT	Autophagosome	2.05E-4	16
		GOTERM BP DIRECT	Autophagosome assembly	3.38E-3	11
4	3.46	UP KEYWORDS	Protein Transport	4.47E-6	79
		GOTERM BP DIRECT	Protein transport	4.43E-5	80
		UP KEYWORDS	Transport	4.55E-3	185
		GOTERM BP DIRECT	Transport	1.55E-2	182

<sup>a</sup> ES = Enrichment score produced by Functional Annotation Clustering in DAVID.

<sup>b</sup> Category Terms Defined: GOTERM BP DIRECT = GO Term for Direct Involvement in Biological Process; UP Keywords = Uniprot Keywords; GOTERM MF DIRECT = GO Term for Direct Involvement in Molecular Function; GOTERM CC DIRECT = GO Term for Direct Localization to Cellular Compartment

■ **Table S5 *Ccnc*<sup>-/-</sup> DGE Data**Top 50 repressed and induced genes in *Ccnc*<sup>-/-</sup> MEFs, using DESeq2.

Repressed Genes	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Induced Genes	Log <sub>2</sub> FC	FDR
<i>Cxcl5</i>	-8.85	1.46E-292	<i>Pitx1</i>	7.90	3.49E-175
<i>Efemp1</i>	-7.89	1.65E-191	<i>Sall1</i>	7.60	1.74E-168
<i>Sox2</i>	-6.92	1.20E-112	<i>Acta2</i>	6.45	1.20E-298
<i>Grem1</i>	-6.89	7.74E-115	<i>Scara3</i>	6.41	4.81E-92
<i>Vldlr</i>	-6.87	7.67E-111	<i>Galm</i>	5.96	2.37E-105
<i>Pcdh17</i>	-6.60	6.38E-130	<i>Sim2</i>	5.80	4.78E-70
<i>Tbx5</i>	-6.53	7.24E-86	<i>Pcolce2</i>	5.80	5.40E-122
<i>Ston2</i>	-6.19	2.10E-122	<i>Ltbr</i>	5.75	2.78E-226
<i>Igfbp4</i>	-5.90	1.67E-96	<i>Hoxb4</i>	5.73	1.68E-75
<i>Penk</i>	-5.82	9.01E-92	<i>Sox11</i>	5.14	1.89E-185
<i>Igfbp3</i>	-5.80	5.10E-148	<i>Mmp2</i>	5.05	1.75E-84
<i>Foxg1</i>	-5.74	2.55E-67	<i>Meox2</i>	4.98	2.38E-46
<i>Sfrp2</i>	-5.66	1.14E-188	<i>Hoxc13</i>	4.92	3.53E-45
<i>Ackr3</i>	-5.24	1.75E-140	<i>Peg12</i>	4.92	1.78E-48
<i>Slc16a2</i>	-5.17	8.83E-260	<i>Hoxb13</i>	4.91	9.55E-48
<i>Acot1</i>	-5.05	7.24E-48	<i>Trim71</i>	4.87	8.26E-83
<i>Pik3r5</i>	-5.00	1.30E-297	<i>Plekha2</i>	4.86	6.54E-45
<i>Slc22a4</i>	-4.73	9.73E-42	<i>Nid2</i>	4.84	1.54E-221
<i>Nfatc4</i>	-4.64	7.78E-95	<i>Boc</i>	4.70	7.25E-52
<i>Arap2</i>	-4.63	1.30E-55	<i>Six2</i>	4.68	6.07E-41
<i>Klf12</i>	-4.62	8.09E-38	<i>Bicc1</i>	4.62	1.31E-229
<i>4930452B06Rik</i>	-4.59	3.51E-37	<i>Trim30a</i>	4.42	2.28E-39
<i>Mab21l1</i>	-4.53	6.94E-52	<i>Myl9</i>	4.39	1.02E-68
<i>S1pr3</i>	-4.53	2.00E-173	<i>Ifnlr1</i>	4.38	1.47E-42
<i>Pappa</i>	-4.43	5.93E-42	<i>Rsad2</i>	4.38	1.73E-45
<i>Zic2</i>	-4.37	2.07E-93	<i>Gpnmb</i>	4.30	1.20E-299
<i>Sp9</i>	-4.20	2.51E-43	<i>Lgals3bp</i>	4.19	6.48E-190
<i>Kcnj2</i>	-4.15	3.25E-192	<i>Flt4</i>	4.18	1.33E-48
<i>Cd34</i>	-4.14	1.35E-29	<i>Slc2a10</i>	4.15	3.68E-29
<i>Nid1</i>	-4.14	1.00E-298	<i>Gsdmd</i>	4.14	1.68E-31
<i>Fgf5</i>	-4.14	6.29E-28	<i>Paqr9</i>	4.05	3.95E-29
<i>Osr1</i>	-4.09	1.30E-296	<i>Cplx2</i>	4.00	1.88E-138
<i>Lonrf3</i>	-4.00	8.01E-28	<i>Fam217b</i>	3.92	8.64E-41
<i>Sema4f</i>	-4.00	3.50E-32	<i>Lifr</i>	3.89	4.71E-130
<i>Zic5</i>	-3.96	1.38E-40	<i>Mrgpre</i>	3.89	1.26E-56
<i>Gnai1</i>	-3.90	2.79E-32	<i>Evx2</i>	3.86	1.35E-36
<i>Enpp2</i>	-3.86	2.95E-49	<i>Armcx4</i>	3.79	4.54E-142
<i>Pcdhgb5</i>	-3.85	1.95E-39	<i>Flrt2</i>	3.78	1.32E-108

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

■ **Table S5 Continued *Ccnc*<sup>-/-</sup> DGE Data**

Top 50 repressed and induced genes in *Ccnc*<sup>-/-</sup> MEFs, using DESeq2.

Repressed Genes	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Induced Genes	Log <sub>2</sub> FC	FDR
<i>Fam110c</i>	-3.85	8.29E-24	<i>P4ha3</i>	3.77	6.02E-34
<i>Gm43517</i>	-3.80	2.77E-23	<i>Msx1</i>	3.77	4.40E-65
<i>Tubb3</i>	-3.76	1.30E-55	<i>2310030G06Rik</i>	3.75	3.53E-24
<i>Bmp6</i>	-3.73	1.61E-23	<i>Lmcd1</i>	3.75	4.84E-26
<i>Itgbl1</i>	-3.72	1.63E-35	<i>Selp</i>	3.74	1.12E-22
<i>Fgf7</i>	-3.66	1.12E-40	<i>Asxl2</i>	3.73	5.33E-36
<i>Ar</i>	-3.62	8.35E-22	<i>Sgcd</i>	3.73	5.34E-23
<i>Dlx3</i>	-3.61	3.52E-24	<i>Esr1</i>	3.72	1.04E-24
<i>Slit3</i>	-3.60	2.41E-21	<i>Ulbp1</i>	3.65	2.45E-68
<i>Prelp</i>	-3.55	1.39E-28	<i>Oas1a</i>	3.59	6.96E-26
<i>Zdhhc15</i>	-3.53	9.39E-66	<i>Hoxb7</i>	3.59	1.38E-20
<i>Pkp1</i>	-3.48	2.28E-49	<i>Hoxb7</i>	3.59	1.60E-43

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.

<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

**Table S6 Cyclin C-Dependent Genes**

GO-Functional Annotation Clusters for repressed genes in *Ccnc*<sup>-/-</sup> MEFs. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes repressed (2,353 genes).

Cluster	ES <sup>a</sup>	Category <sup>b</sup>	Associated Terms	p-value	Number of Genes Involved
1	19.06	UP KEYWORDS	Mitochondrion	1.52E-26	222
		GOTERM CC DIRECT	Mitochondrion	1.68E-25	327
		UP KEYWORDS	Transit peptide	4.91E-19	121
2	6.78	UP KEYWORDS	Oxidoreductase	8.07E-8	109
		GOTERM BP DIRECT	Oxidation-reduction process	1.91E-7	121
		GOTERM MF DIRECT	Oxidoreductase activity	3.16E-7	110
3	4.49	GOTERM MF DIRECT	Cadherin binding involved in cell-cell adhesion	2.44E-6	59
		GOTERM CC DIRECT	Cell-cell adherens junction	2.67E-5	60
		GOTERM BP DIRECT	Cell-cell adhesion	5.11E-4	38
4	3.23	UP KEYWORDS	Cell cycle	3.32E-7	105
		GOTERM BP DIRECT	Cell cycle	1.76E-5	104
		UP KEYWORDS	Cell division	1.85E-3	57
		GOTERM BP DIRECT	Cell division	1.02E-2	58
		GOTERM BP DIRECT	Mitotic nuclear division	1.73E-2	44
		UP KEYWORDS	Mitosis	2.16E-2	38

<sup>a</sup> ES = Enrichment score produced by Functional Annotation Clustering in DAVID.

<sup>b</sup> Category Terms Defined: UP Keywords = Uniprot Keywords; GOTERM CC DIRECT = GO Term for Direct Localization to Cellular Compartment; GOTERM BP DIRECT = GO Term for Direct Involvement in Biological Process;; GOTERM MF DIRECT = GO Term for Direct Involvement in Molecular Function



■ **Table S7 Cyclin C-Repressed Genes**

GO-Functional Annotation Clusters for induced genes in *Ccnc*<sup>-/-</sup> MEFs. The following clusters (1-4) resulting from DAVID-GO Functional Annotation Clustering, represent the genes induced (2,482 genes).

Cluster	ES <sup>a</sup>	Category <sup>b</sup>	Associated Terms	p-value	Number of Genes Involved
1	8.39	UP KEYWORDS	Lysosome	3.03E-11	65
		GOTERM CC DIRECT	Lysosomal membrane	1.80E-8	59
		GOTERM CC DIRECT	Lysosome	1.23E-7	73
2	6.68	UP KEYWORDS	Ubl conjugation pathway	3.14E-12	128
		GOTERM MF DIRECT	Ubiquitin-protein transferase activity	2.27E-6	70
		GOTERM BP DIRECT	Protein ubiquitination	3.31E-6	75
		GOTERM MF DIRECT	Ligase activity	8.38E-5	70
3	6.56	UP KEYWORDS	Protein transport	1.35E-10	115
		GOTERM BP DIRECT	Protein transport	5.34E-9	121
		UP KEYWORDS	Transport	9.79E-6	265
		GOTERM BP DIRECT	Transport	8.34E-4	264
4	3.51	KEGG PATHWAY	Melanogenesis	3.80E-6	29
		GOTERM BP DIRECT	Canonical Wnt signaling pathway	2.80E-4	24
		KEGG PATHWAY	Wnt signaling pathway	1.22E-3	30
		KEGG PATHWAY	Basal cell carcinoma	6.99E-3	14

<sup>a</sup> ES = Enrichment score produced by Functional Annotation Clustering in DAVID.

<sup>b</sup> Category Terms Defined: UP Keywords = Uniprot Keywords; GOTERM CC DIRECT = GO Term for Direct Localization to Cellular Compartment; GOTERM MF DIRECT = GO Term for Direct Involvement in Molecular Function; GOTERM BP DIRECT = GO Term for Direct Involvement in Biological Process; KEGG PATHWAY = KEGG Pathway Association

■ **Table S8 Overlapping DGE Data**Overlapping repressed and induced genes in WT Stress and *Ccnc*<sup>-/-</sup> MEFs, as determined using DESeq2.

	<i>Ccnc</i> <sup>-/-</sup>		WT Stress			<i>Ccnc</i> <sup>-/-</sup>		WT Stress	
Repressed Genes	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Log <sub>2</sub> FC	FDR	Induced Genes	Log <sub>2</sub> FC	FDR	Log <sub>2</sub> FC	FDR
<i>Cxcl5</i>	-8.85	1.50E-292	-1.64	3.70E-126	<i>Pla2g16</i>	2.99	8.75E-16	1.01	1.91E-2
<i>Sox2</i>	-6.92	1.20E-112	-1.23	1.93E-28	<i>Cfap53</i>	2.91	2.83E-13	1.62	5.81E-05
<i>Pcdh17</i>	-6.60	6.40E-130	-1.01	2.47E-23	<i>Eda2r</i>	2.26	3.74E-15	1.02	6.66E-3
<i>Sfrp2</i>	-5.66	1.1E-188	-1.33	4.61E-32	<i>Ikzf4</i>	2.02	1.50E-06	1.28	1.67E-3
<i>Ackr3</i>	-5.24	1.7E-140	-1.74	4.70E-47	<i>Tbx2</i>	2.02	3.29E-07	1.52	1.41E-4
<i>S1pr3</i>	-4.53	2.00E-173	-1.94	4.43E-53	<i>Fbxl22</i>	1.90	3.37E-07	1.22	2.59E-3
<i>Pappa</i>	-4.43	5.93E-42	-1.79	1.70E-14	<i>Rab11b</i>	1.87	3.71E-73	1.55	2.25E-47
<i>Kcnj2</i>	-4.15	3.30E-192	-1.42	4.92E-36	<i>Rprm</i>	1.83	5.90E-06	2.59	2.21E-13
<i>Osr1</i>	-4.09	1.02E-299	-1.11	4.66E-74	<i>Lims2</i>	1.82	1.52E-05	1.25	2.88E-3
<i>Gm43517</i>	-3.80	2.77E-23	-1.13	2.60E-4	<i>Ephb2</i>	1.76	2.04E-11	1.41	4.79E-7
<i>Itgbl1</i>	-3.72	1.63E-35	-1.89	2.30E-14	<i>Srrm4</i>	1.65	6.97E-10	1.13	1.99E-4
<i>Fgf7</i>	-3.66	1.12E-40	-1.42	6.97E-12	<i>Nat8f4</i>	1.60	4.34E-07	1.14	1.30E-3
<i>Prep</i>	-3.55	1.39E-28	-2.69	1.43E-17	<i>Slc16a8</i>	1.56	8.31E-5	2.55	6.06E-15
<i>Pkp1</i>	-3.48	2.28E-49	-1.17	5.50E-11	<i>Olf920</i>	1.49	3.76E-4	1.08	5.41E-3
<i>Trib2</i>	-3.39	8.31E-54	-1.63	1.44E-18	<i>Gas2l1</i>	1.49	3.79E-05	2.34	3.22E-15
<i>Slit2</i>	-3.30	1.09E-28	-1.32	2.17E-08	<i>Fermt3</i>	1.46	2.12E-05	1.35	7.23E-05
<i>Fgf10</i>	-3.18	9.59E-50	-1.52	3.31E-18	<i>Hypk</i>	1.44	7.21E-05	1.89	5.24E-09
<i>Adora2b</i>	-3.13	4.56E-25	-1.08	1.06E-05	<i>Inha</i>	1.44	5.19E-10	1.16	3.45E-06
<i>Foxq1</i>	-3.10	5.38E-61	-1.09	6.45E-11	<i>Prob1</i>	1.39	3.34E-06	1.26	4.97E-05
<i>Ephb6</i>	-3.05	6.11E-93	-1.78	4.78E-41	<i>Mmp15</i>	1.39	1.17E-4	2.26	3.93E-14
<i>Lypd6b</i>	-3.04	4.26E-16	-1.46	9.93E-06	<i>Garem2</i>	1.35	6.92E-08	1.24	1.84E-06
<i>Cd248</i>	-3.03	1.22E-298	-2.10	1.40E-209	<i>Mpeg1</i>	1.30	1.94E-3	1.36	7.15E-4
<i>Bdkrb2</i>	-3.00	4.13E-77	-1.23	6.76E-15	<i>Arhgef6</i>	1.29	3.18E-3	2.16	2.53E-08
<i>Cdh3</i>	-2.98	2.14E-60	-1.89	2.06E-30	<i>Car14</i>	1.27	3.75E-3	1.57	9.64E-05
<i>Ndnf</i>	-2.90	9.64E-29	-1.84	5.99E-15	<i>Gpr156</i>	1.24	3.41E-3	1.49	1.60E-4
<i>Cspg4</i>	-2.81	1.23E-297	-1.17	7.51E-56	<i>Rbm7</i>	1.22	5.92E-3	1.05	1.53E-2
<i>Adm</i>	-2.76	7.07E-12	-1.41	2.64E-4	<i>Zc3h12c</i>	1.21	1.84E-4	1.01	3.36E-3
<i>Spon2</i>	-2.75	1.04E-15	-2.08	1.07E-10	<i>Nptn</i>	1.20	3.58E-4	1.06	2.86E-3
<i>Dcdc2c</i>	-2.74	2.26E-11	-1.57	5.12E-05	<i>Plekhhg6</i>	1.17	2.82E-3	1.90	1.24E-08
<i>Angptl4</i>	-2.68	5.49E-95	-2.62	8.35E-94	<i>Chrnb2</i>	1.16	7.11E-4	2.24	3.52E-15
<i>Cavin4</i>	-2.67	2.10E-127	-1.67	6.39E-69	<i>Gabarap</i>	1.15	9.60E-5	1.69	4.11E-11
<i>Rgs2</i>	-2.64	2.75E-20	-1.21	2.28E-06	<i>Depdc7</i>	1.11	2.92E-08	1.32	2.38E-10
<i>Ahr</i>	-2.63	6.70E-146	-1.28	9.11E-43	<i>Zfr2</i>	1.11	1.95E-4	1.42	2.64E-07
<i>Arsj</i>	-2.62	1.10E-42	-1.76	5.36E-25	<i>Blzf1</i>	1.09	7.32E-3	1.06	8.25E-3
<i>Epha8</i>	-2.57	3.34E-11	-1.51	3.43E-05	<i>Rasl11a</i>	1.08	1.27E-4	1.07	2.66E-4
<i>Fam43a</i>	-2.49	2.60E-193	-1.04	7.18E-49	<i>Nat8l</i>	1.06	1.74E-2	1.01	1.63E-2
<i>Ptgr</i>	-2.44	1.05E-11	-2.01	6.66E-09	<i>Grin3b</i>	1.06	1.29E-4	2.58	1.27E-37

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

■ **Table S8 Continued Overlapping DGE Data**

Overlapping repressed and induced genes in WT Stress and *Ccnc*<sup>-/-</sup> MEFs, as determined using DESeq2.

Repressed Genes	<i>Ccnc</i> <sup>-/-</sup>		WT Stress		Induced Genes	<i>Ccnc</i> <sup>-/-</sup>		WT Stress	
	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Log <sub>2</sub> FC	FDR		Log <sub>2</sub> FC	FDR	Log <sub>2</sub> FC	FDR
<i>Ch25h</i>	-2.43	3.22E-10	-1.30	4.97E-4	<i>Lrp2bp</i>	1.04	1.03E-2	1.25	1.52E-3
<i>Serpina3i</i>	-2.42	5.05E-13	-1.12	1.99E-4	<i>D630039A03Rik</i>	1.04	1.85E-2	1.68	3.09E-05
<i>9930111J21Rik2</i>	-2.39	7.35E-14	-2.10	2.12E-10	<i>Duox1</i>	1.01	1.97E-2	1.24	1.69E-3
<i>Car5b</i>	-2.38	8.70E-77	-1.41	6.22E-31	<i>Cfp</i>	0.995	1.29E-05	1.05	3.72E-06
<i>Tmem45a</i>	-2.38	2.38E-23	-1.09	1.18E-07	<i>Ccdc188</i>	0.990	2.11E-2	1.07	8.55E-3
<i>Mme</i>	-2.36	1.43E-37	-2.05	4.97E-29	<i>Zfp444</i>	0.960	2.41E-2	1.52	4.62E-05
<i>Tspan11</i>	-2.34	1.89E-08	-1.26	2.20E-3	<i>Dtx3</i>	0.946	9.42E-3	1.28	1.16E-4
<i>Ptx3</i>	-2.29	1.24E-299	-1.74	3.10E-220	<i>Klhl24</i>	0.937	1.03E-32	1.10	3.17E-43
<i>Mbp</i>	-2.27	4.16E-13	-1.06	2.57E-4	<i>Pmaip1</i>	0.931	2.36E-09	2.64	3.25E-23
<i>Pcdh19</i>	-2.25	3.37E-62	-1.85	3.99E-45	<i>Ptbp1</i>	0.897	3.26E-2	1.05	7.29E-3
<i>Tnfrif6</i>	-2.19	2.74E-10	-1.52	4.73E-06	<i>Sec14l5</i>	0.893	3.58E-2	3.15	7.42E-18
<i>Rnf39</i>	-2.15	1.56E-34	-1.02	4.01E-11	<i>Wfikkn1</i>	0.888	1.18E-2	2.21	4.13E-19
<i>Zbtb7c</i>	-2.12	1.23E-32	-1.36	8.56E-16	<i>Gtf2h1</i>	0.882	9.01E-13	0.862	5.35E-12
<i>Angptl7</i>	-2.11	4.05E-13	-2.16	3.10E-14	<i>Crebrf</i>	0.880	1.78E-20	1.08	2.36E-29
<i>Tlr6</i>	-2.06	1.91E-09	-1.01	3.51E-3	<i>Tbc1d8</i>	0.864	3.53E-2	1.93	5.18E-10
<i>Rnf150</i>	-2.01	2.10E-22	-1.18	3.20E-10	<i>Jmy</i>	0.827	1.93E-28	0.663	2.01E-18
<i>Ankrd63</i>	-1.98	2.29E-06	-1.26	2.18E-3	<i>H2-DMA</i>	0.821	4.44E-2	2.31	1.33E-14
<i>Sema3d</i>	-1.97	1.21E-20	-1.47	3.84E-13	<i>Fam89a</i>	0.813	2.84E-2	1.90	1.62E-11
<i>A930002H24Rik</i>	-1.96	4.97E-09	-1.04	1.15E-3	<i>Galr2</i>	0.806	4.42E-2	1.69	7.99E-08
<i>Gcnt4</i>	-1.96	1.73E-60	-1.56	2.27E-36	<i>Tma16</i>	0.789	7.19E-06	1.11	1.87E-12
<i>Hlf</i>	-1.90	3.13E-11	-1.12	4.10E-05	<i>Mafk</i>	0.784	9.43E-3	1.43	4.62E-09
<i>Fam84b</i>	-1.89	1.30E-20	-1.06	3.08E-08	<i>Enc1</i>	0.784	7.56E-41	1.10	1.00E-66
<i>Twist1</i>	-1.89	7.60E-195	-1.14	6.59E-76	<i>Plpp3</i>	0.731	1.17E-4	2.00	3.92E-54
<i>Mgp</i>	-1.85	3.41E-06	-1.59	3.77E-05	<i>Far2</i>	0.680	2.17E-2	1.58	1.14E-11
<i>Cacna1i</i>	-1.73	9.97E-09	-1.41	1.85E-06	<i>C1qtnf12</i>	0.677	2.81E-2	1.32	4.83E-07
<i>Egr3</i>	-1.73	1.54E-05	-2.51	1.35E-55	<i>Polk</i>	0.660	5.70E-05	1.73	4.18E-37
<i>Cp</i>	-1.72	1.15E-14	-1.11	5.48E-07	<i>Amt</i>	0.637	1.38E-2	1.12	6.90E-07
<i>Plpp3</i>	-1.66	1.18E-30	-1.20	1.06E-16	<i>Znrf3</i>	0.589	1.82E-4	0.388	2.21E-2
<i>Lox</i>	-1.61	1.92E-36	-1.48	1.40E-41	<i>Rev1</i>	0.550	1.19E-06	1.08	1.91E-26
<i>Col6a2</i>	-1.60	1.35E-12	-1.18	1.22E-07	<i>Ccdc39</i>	0.547	3.43E-2	1.08	1.74E-06
<i>Plxna2</i>	-1.58	4.86E-96	-2.03	7.20E-132	<i>Aen</i>	0.535	2.60E-2	2.07	3.51E-39
<i>Tcf7</i>	-1.58	1.21E-26	-1.02	5.24E-13	<i>Mast1</i>	0.451	1.74E-2	1.42	3.68E-23
<i>Zc3h12a</i>	-1.56	1.25E-61	-1.06	4.33E-30	<i>Fnip1</i>	0.447	2.93E-10	1.09	6.26E-69
<i>Bmp2</i>	-1.51	2.18E-64	-1.95	1.63E-70	<i>Mthfsd</i>	0.444	2.85E-2	1.54	5.85E-24
<i>Ccl2</i>	-1.48	1.50E-225	-1.11	1.40E-130	<i>Leng8</i>	0.418	3.25E-3	1.28	1.26E-26

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.

<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

■ **Table S8 Continued Overlapping DGE Data**

Overlapping repressed and induced genes in WT Stress and *Ccnc*<sup>-/-</sup> MEFs, as determined using DESeq2.

Repressed Genes	<i>Ccnc</i> <sup>-/-</sup>		WT Stress		Induced Genes	<i>Ccnc</i> <sup>-/-</sup>		WT Stress	
	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Log <sub>2</sub> FC	FDR		Log <sub>2</sub> FC	FDR	Log <sub>2</sub> FC	FDR
<i>Pdgfra</i>	-1.42	6.87E-4	-1.03	1.28E-2	<i>Apobr</i>	0.411	4.43E-2	1.40	1.43E-19
<i>Tmem119</i>	-1.42	1.13E-62	-2.63	2.30E-150	<i>Dpp7</i>	0.371	4.76E-4	1.32	3.29E-53
<i>Adra1d</i>	-1.42	3.49E-4	-1.22	2.96E-3	<i>Rnf169</i>	0.314	7.60E-3	1.44	6.33E-61
<i>Cdc42ep2</i>	-1.42	1.53E-41	-1.27	2.69E-32	<i>Pdrg1</i>	0.289	4.59E-2	1.05	9.30E-18
<i>Cemip</i>	-1.40	8.12E-09	-1.22	4.58E-06	<i>Phlda3</i>	0.259	1.18E-3	1.60	1.32E-85
<i>Epb414b</i>	-1.39	2.27E-06	-1.35	6.42E-07					
<i>Twist2</i>	-1.38	2.27E-33	-1.48	2.58E-36					
<i>Serpinb1a</i>	-1.38	1.46E-05	-2.49	1.69E-13					
<i>Gas1</i>	-1.36	1.80E-100	-2.26	3.30E-246					
<i>Gabrb2</i>	-1.34	2.08E-3	-1.18	4.75E-3					
<i>Snai2</i>	-1.34	2.21E-30	-1.40	1.16E-33					
<i>Wisp2</i>	-1.33	1.92E-17	-2.23	2.56E-35					
<i>Tgfb1</i>	-1.33	2.97E-11	-1.96	4.35E-21					
<i>Medag</i>	-1.32	2.68E-3	-1.50	2.39E-4					
<i>Gpr39</i>	-1.31	5.72E-07	-1.17	1.60E-06					
<i>Arhgef19</i>	-1.31	1.41E-18	-1.04	1.30E-13					
<i>Zfp36l2</i>	-1.30	1.30E-151	-1.77	6.90E-229					
<i>Plxdc2</i>	-1.29	2.23E-3	-1.63	5.79E-05					
<i>Bmf</i>	-1.28	9.29E-06	-1.31	4.86E-06					
<i>Tspan13</i>	-1.28	3.13E-4	-1.10	2.81E-3					
<i>Clmp</i>	-1.28	1.15E-05	-2.03	4.87E-11					
<i>Gdpd5</i>	-1.26	2.91E-10	-1.10	1.15E-08					
<i>Cx3cl1</i>	-1.26	2.83E-75	-2.06	3.62E-162					
<i>Fam20a</i>	-1.25	1.15E-07	-1.64	2.08E-12					
<i>Flt1</i>	-1.24	2.64E-24	-1.58	1.96E-35					
<i>Ldlrad4</i>	-1.23	4.83E-21	-1.74	1.15E-35					
<i>Ccl7</i>	-1.22	5.22E-30	-1.30	8.87E-34					
<i>Gjb5</i>	-1.22	2.37E-3	-1.12	5.37E-3					
<i>Itgb8</i>	-1.21	1.76E-11	-1.11	1.44E-10					
<i>Pdgfb</i>	-1.16	6.19E-29	-1.32	7.02E-32					
<i>Nedd4l</i>	-1.16	2.88E-05	-1.33	2.70E-06					
<i>Hipk2</i>	-1.15	2.01E-43	-1.42	1.59E-74					
<i>Igf1</i>	-1.10	2.04E-05	-1.36	2.56E-06					
<i>Pdp1</i>	-1.08	1.28E-4	-1.20	4.73E-05					
<i>Pik3ip1</i>	-1.07	2.27E-11	-1.10	2.59E-10					
<i>6030445D17Rik</i>	-1.07	1.30E-2	-1.05	1.29E-2					

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.

<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

**Table S8 Continued Overlapping DGE Data**

Overlapping repressed and induced genes in WT Stress and *Ccnc*<sup>-/-</sup> MEFs, as determined using DESeq2.

Repressed Genes	<i>Ccnc</i> <sup>-/-</sup>		WT Stress				
	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Log <sub>2</sub> FC	FDR			
<i>Kitl</i>	-1.06	4.28E-50	-1.47	3.29E-89			
<i>Nr2f2</i>	-1.06	1.97E-40	-1.55	1.45E-16			
<i>Errfi1</i>	-1.06	1.38E-4	-1.17	7.31E-07			
<i>Foxn1</i>	-1.05	1.77E-2	-1.00	2.01E-283			
<i>Lurap1l</i>	-1.05	4.75E-43	-1.29	3.29E-54			
<i>Rad51b</i>	-1.04	2.11E-2	-1.05	1.50E-2			
<i>Tnfrsf1b</i>	-1.01	1.87E-40	-1.01	8.94E-44			
<i>Spn</i>	-1.01	8.25E-05	-1.64	9.66E-10			
<i>Apcdd1</i>	-0.991	6.80E-09	-1.05	1.03E-09			
<i>Ccnd1</i>	-0.986	8.51E-48	-1.36	5.79E-56			
<i>Rubcnl</i>	-0.979	1.81E-2	-1.59	3.42E-05			
<i>Ccdc80</i>	-0.975	1.93E-05	-1.05	5.22E-06			
<i>Jup</i>	-0.975	1.23E-17	-0.568	2.37E-9			
<i>Agap1</i>	-0.950	1.05E-05	-1.08	2.37E-06			
<i>Syne3</i>	-0.949	1.78E-3	-1.25	1.13E-3			
<i>Samd12</i>	-0.924	3.41E-4	-1.02	1.30E-4			
<i>Gjb2</i>	-0.912	2.08E-2	-1.37	3.72E-06			
<i>Gas7</i>	-0.907	2.67E-12	-1.62	2.44E-28			
<i>Col8a2</i>	-0.893	1.60E-3	-1.31	6.85E-06			
<i>Trmt61a</i>	-0.853	3.72E-2	-1.01	1.17E-2			
<i>Cyp51</i>	-0.846	1.20E-121	-1.41	5.80E-206			
<i>Ssbp3</i>	-0.820	1.65E-26	-1.43	1.15E-62			
<i>Klhdc8a</i>	-0.803	2.10E-09	-1.11	6.36E-15			
<i>Sned1</i>	-0.790	7.32E-3	-2.03	9.06E-12			
<i>Aacs</i>	-0.759	7.56E-41	-1.28	1.74E-94			
<i>Tsc22d3</i>	-0.757	1.13E-4	-1.04	9.54E-08			
<i>Col1a2</i>	-0.754	3.19E-72	-1.39	8.70E-304			
<i>Igfbp6</i>	-0.737	4.56E-3	-1.02	8.21E-05			
<i>Map6</i>	-0.709	1.35E-06	-1.32	1.08E-18			
<i>Nfil3</i>	-0.697	6.39E-13	-1.19	2.33E-38			
<i>Nsdhl</i>	-0.696	5.33E-19	1.44	2.18E-71			
<i>Fam171a2</i>	-0.692	4.60E-15	-1.17	2.66E-41			
<i>Fhdc1</i>	-0.688	3.02E-2	-1.32	3.53E-05			
<i>Per2</i>	-0.687	1.40E-3	-1.49	6.38E-11			
<i>Gramd2</i>	-0.681	2.57E-3	-1.05	2.73E-05			
<i>Mgst3</i>	-0.677	2.53E-3	-1.26	1.45E-06			
<i>Hoxa13</i>	-0.673	1.89E-05	-1.08	4.86E-11			

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.

<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

**Table S8 Continued Overlapping DGE Data**

Overlapping repressed and induced genes in WT Stress and *Ccnc*<sup>-/-</sup> MEFs, as determined using DESeq2.

Repressed Genes	<i>Ccnc</i> <sup>-/-</sup>		WT Stress				
	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Log <sub>2</sub> FC	FDR			
<i>Nrn1</i>	-0.673	6.59E-4	-1.09	1.32E-08			
<i>Maml3</i>	-0.665	3.28E-2	-1.19	1.06E-4			
<i>Fam69a</i>	-0.655	1.68E-4	-1.03	2.72E-10			
<i>Tspyl4</i>	-0.653	6.49E-05	-1.04	2.23E-09			
<i>Cxcl1</i>	-0.646	1.20E-25	-1.70	6.11E-150			
<i>Msmo1</i>	-0.637	1.79E-49	-1.26	4.30E-148			
<i>Dhcr24</i>	-0.617	7.56E-46	-1.53	1.20E-202			
<i>Zfp608</i>	-0.615	4.98E-11	-2.33	4.22E-89			
<i>Col6a1</i>	-0.612	5.45E-20	-1.22	1.66E-52			
<i>Adh7</i>	-0.610	3.19E-14	-1.14	1.51E-41			
<i>Bmper</i>	-0.592	3.16E-2	-1.10	6.66E-05			
<i>Plec</i>	-0.578	1.21E-2	-1.26	2.67E-07			
<i>Bhlhe40</i>	-0.571	5.64E-11	-1.01	7.10E-18			
<i>Dhrs9</i>	-0.569	8.29E-3	-1.86	9.77E-07			
<i>Amot</i>	-0.569	1.44E-12	-1.30	1.88E-51			
<i>Eppk1</i>	-0.562	2.90E-2	-1.05	1.02E-4			
<i>Irs1</i>	-0.560	2.74E-08	-1.18	1.37E-31			
<i>Rdh10</i>	-0.556	1.68E-09	-1.09	1.09E-27			
<i>Slc1a3</i>	-0.551	3.51E-2	-1.29	5.36E-07			
<i>Vegfd</i>	-0.544	9.96E-05	-1.65	5.21E-28			
<i>Frmd6</i>	-0.533	1.64E-18	-1.14	2.95E-84			
<i>Tgfb3</i>	-0.522	2.92E-08	-1.71	1.96E-58			
<i>Ankrd35</i>	-0.517	4.16E-2	-1.19	1.10E-05			
<i>Vcam1</i>	-0.511	1.29E-15	-1.54	1.80E-111			
<i>Osbpl3</i>	-0.510	5.08E-07	-1.33	2.55E-35			
<i>Zfp827</i>	-0.491	8.60E-4	-1.30	3.53E-17			
<i>Idi1</i>	-0.476	4.20E-06	-1.30	4.80E-26			
<i>Stard4</i>	-0.475	1.99E-18	-1.06	3.40E-127			
<i>Oaf</i>	-0.463	1.42E-05	-1.27	6.64E-31			
<i>Bpgm</i>	-0.460	3.04E-08	-1.29	3.10E-46			
<i>Prrx2</i>	-0.445	3.53E-3	-1.21	8.60E-16			
<i>Lfng</i>	-0.426	5.48E-4	-1.87	1.28E-40			
<i>Slc22a23</i>	-0.387	9.58E-06	-1.21	2.33E-40			
<i>Timp3</i>	-0.375	3.76E-18	-1.65	2.90E-198			
<i>Kif21b</i>	-0.375	3.01E-3	-1.58	4.74E-31			
<i>Bnip3</i>	-0.371	2.20E-2	-1.59	3.49E-19			

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.

<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

■ **Table S8 Continued Overlapping DGE Data**

Overlapping repressed and induced genes in WT Stress and *Ccnc*<sup>-/-</sup> MEFs, as determined using DESeq2.

Repressed Genes	<i>Ccnc</i> <sup>-/-</sup>		WT Stress				
	Log <sub>2</sub> FC <sup>a</sup>	FDR <sup>b</sup>	Log <sub>2</sub> FC	FDR			
<i>Cdk6</i>	-0.367	9.85E-07	-1.21	7.98E-74			
<i>Lss</i>	-0.351	4.96E-11	-1.19	1.37E-94			
<i>Nrp1</i>	-0.348	7.08E-3	-1.22	1.13E-22			
<i>Sh3pxd2b</i>	-0.341	1.16E-13	-1.28	2.00E-133			
<i>Rnd3</i>	-0.338	1.37E-06	-1.33	3.86E-61			
<i>Fads2</i>	-0.314	6.84E-05	-1.26	4.99E-49			
<i>Sh3bp4</i>	-0.298	1.83E-06	-1.32	1.32E-80			
<i>Trps1</i>	-0.287	2.23E-3	-1.72	1.79E-59			
<i>Gxylt2</i>	-0.253	4.75E-4	-1.57	1.31E-82			
<i>Cnp</i>	-0.248	1.72E-2	-1.22	1.01E-30			
<i>Thbs1</i>	-0.238	9.75E-06	-2.34	4.30E-274			
<i>Slc2a1</i>	-0.235	8.62E-05	-1.05	7.58E-61			
<i>Acat2</i>	-0.167	3.51E-2	-1.33	4.89E-36			
<i>Scd1</i>	-0.143	1.90E-4	-1.28	1.30E-222			
<i>Col5a1</i>	-0.125	2.33E-2	-1.07	1.64E-73			

<sup>a</sup> Log<sub>2</sub>FC = Fold change as expressed as log base 2.

<sup>b</sup> FDR = Adjusted p-value using Benjamini and Hochberg method in DESeq2.

■ Table S9 RT-qPCR Primers

Primer	Gene	Strand	Sequence (5'-3')
KCO2012	<i>Igfbp4</i>	Sense	CCATTCCAAACTGTGACCGC
KCO2013	<i>Igfbp4</i>	Antisense	CCCTGTCTTCCGATCCACAC
KCO2080	<i>Cd34</i>	Sense	GTCTGCTCCCTGCTTCTAGC
KCO2081	<i>Cd34</i>	Sense	GGAATAGCTCTGGTGGCTCC
KCO2082	<i>Nfatc4</i>	Sense	GCAGAGCAGTGAGGTGACAT
KCO2083	<i>Nfatc4</i>	Antisense	GGCTCCTCCTTGAAGACCAC
KCO2090	<i>Gpnmb</i>	Sense	TGCCTGCTGTCTGTGAGAAG
KCO2091	<i>Gpnmb</i>	Antisense	CAGCCGATGGAGATCAGGAC
KCO2092	<i>Ltbr</i>	Sense	CAGAGAGCTGGAGGCTGAAC
KCO2093	<i>Ltbr</i>	Antisense	TCAGGAGTGGGGTATGGAGG
KCO2094	<i>Pcolce2</i>	Sense	CAACTGGCCAGACCGAGATT
KCO2095	<i>Pcolce2</i>	Antisense	GTCATTGACTTCCCCACCGT
KCO2106	<i>Atg9b</i>	Sense	GGTTCCTGGCATCACATCCA
KCO2107	<i>Atg9b</i>	Antisense	CAGCGAAGGAGGAAGGTTGT
KCO2108	<i>Pmaip1</i>	Sense	GCCCAGATTGGGGACCTTAG
KCO2109	<i>Pmaip1</i>	Antisense	TCTTCCTGAGTTGAGCTGCG
KCO2110	<i>F2rl1</i>	Sense	GAGTAGGGCTCCGAGTTTCG
KCO2111	<i>F2rl1</i>	Antisense	CAGTGATTGGAGGCTGGGTT
KCO2112	<i>Tmem119</i>	Sense	GTCCTTCACCCAGAGCTGTC
KCO2113	<i>Tmem119</i>	Antisense	CCCGGTGAAGAGCTGTCATT
KCO2114	<i>Thbs1</i>	Sense	AGTGTCAGTCCAGAACTCG
KCO2115	<i>Thbs1</i>	Antisense	TCGCATCTGTTGTTGAGGCT
KCO2126	<i>Sfrp2</i>	Sense	AGTTCCTGTGCTCGCTCTTC
KCO2127	<i>Sfrp2</i>	Antisense	CCTTGGGAGCTTCCTCTGTG
KCO2148	<i>Gabarap</i>	Sense	GAAAAAGCCCCCAAAGCTCG
KCO2149	<i>Gabarap</i>	Antisense	CACTGGTGGGTGGAATGAC
KCO2161	<i>Gtf2h1</i>	Sense	GAAGCAGGATGGAGCACTGT
KCO2162	<i>Gtf2h1</i>	Antisense	CCTTCACTGCATCCCCTTCT