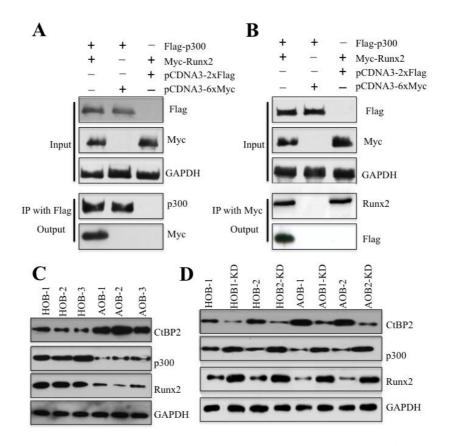


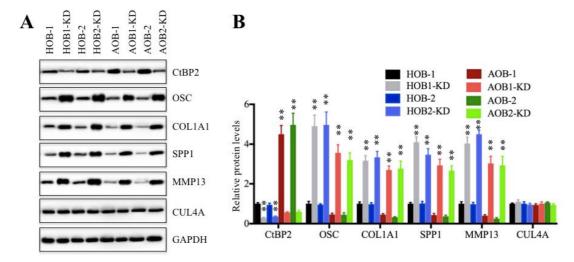
Supplementary Figure 1. CtBP2 is overexpressed in primary osteoblast cells from atrophic nonunion tissues.

The primary osteoblast cells from four normal fracture healing tissues (HOB-1, -2, -3 and -4) and four atrophic nonunion tissues (AOB-1, -2, -3 and -4) were isolated, followed by determining mRNA levels of CtBP1 (**A**) and CtBP2 (**B**) by qRT-PCR, and examining their protein levels (**C**) by western blot in these cells. *P<0.05 and **P<0.001. (**D**) Statistical analysis of the protein levels in (C). *P<0.05, **P<0.001.



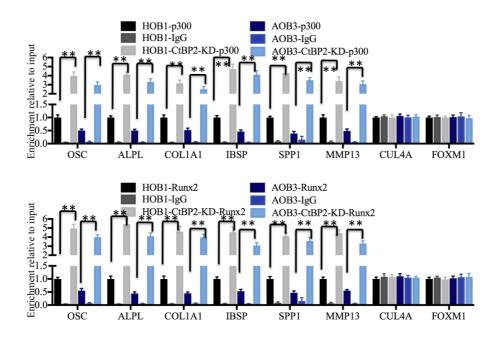
Supplementary Figure 2. p300 directly interacts with Runx2 in HOB-1 cells.

(A and B) p300 directly interact with Runx2 in HOB-1 cells. The HOB-1 cells were cotransfected with pCDNA3-Flag-Runx2 pCDNA3-Myc-p300, pCDNA3-Flag-Runx2 + pCDNA3-Myc, or pCDNA3-Flag + pCDNA3-Myc-p300. After 48 hours, cells were lysed and subjected to IP analysis with either anti-Flag-agarose (A) or anti-Myc-agarose (B). The pull-down products were then subjected to western blot with antibodies indicated in figures. (C) The protein levels of p300 and Runx2 were markedly decreased in AOB cells. Cell lysates from three HOB (1, 2 and 3) and AOB (1, 2 and 3) cells were subjected to western blot to examine p300 and Runx2 levels. CtBP2 and GAPDH were used as controls. (D) The protein levels of p300 and Runx2 were negatively correlated with CtBP2 level. The HOB-1, HOB-2, AOB-1 and AOB-2 cells were transfected with control-siRNA or CtBP2-siRNA, respectively. After 48 hours, cells were lysed and subjected western blot with antibodies against CtBP2, p300, Runx2 and GAPDH.



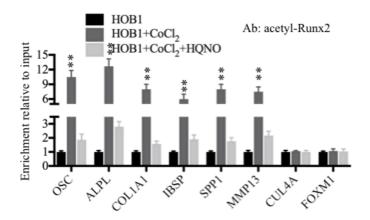
Supplementary Figure 3. Protein levels of Runx2 target genes in AOB cells.

(A) The protein levels of Runx2 target genes were dependent on the CtBP2 level. The HOB-1, HOB-2, AOB-1 and AOB-2 cells were transfected with control-siRNA or CtBP2-siRNA, respectively. After 48 hours, the cells were subjected to protein isolation, followed by measuring the protein levels of Runx2 target genes by western blots. GAPDH was used as a loading control. (B) Statistical analysis of the protein levels in (A). **P<0.001.



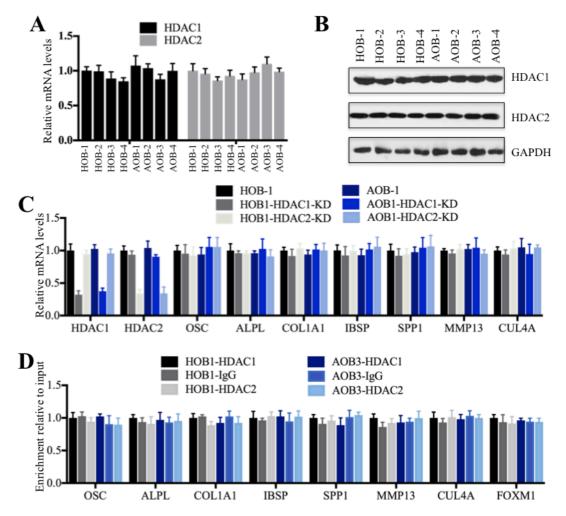
Supplementary Figure 4. CtBP2 knockdown enhances the binding of p300 and Runx2 on the promoters of *Runx2* target genes.

(A) The binding of p300 on the promoters of *Runx2* target genes was significantly increased in CtBP2-KD cells. The HOB-1, HOB1-CtBP2-KD, AOB3 and AOB3-KD cells were subjected to ChIP assays with p300 and IgG antibodies, followed by analysis with qRT-PCR to evaluate their binding to the promoters of Runx2 target genes including *OSC*, *ALPL*, *SPP1*, *COL1A1*, *IBSP* and *MMP13*. *CUL4A* and *FOXM1* were used as controls. **P<0.001. (B) The binding of Runx2 on the promoters of *Runx2* target genes was significantly increased in CtBP2-KD cells. The HOB-1, HOB1-CtBP2-KD, AOB3 and AOB3-KD cells were subjected to ChIP assays with Runx2 and IgG antibodies, followed by analysis with qRT-PCR to evaluate their binding to the promoters of Runx2 target genes including *OSC*, *ALPL*, *SPP1*, *COL1A1*, *IBSP* and *MMP13*. *CUL4A* and *FOXM1* were used as controls. **P<0.001.



Supplementary Figure 5. The CoCl₂ treatment significantly increases the binding of acetylated-Runx2 to Runx2 target gene promoters.

The HOB-1 cells treated with CoCl₂ or CoCl₂+HQNO were subjected to ChIP assays with the anti-acetyl Runx2 antibody, followed by analysis with qRT-PCR to evaluate its binding to the promoters of Runx2 target genes including *OSC*, *ALPL*, *SPP1*, *COL1A1*, *IBSP* and *MMP13*. *CUL4A* and *FOXM1* were used as controls. **P<0.001.



Supplementary Figure 6. HDAC1 and 2 are not required for the regulation of Runx2 target gene expression.

(A) The mRNA levels of HDAC1 and 2 were not changed in HOB and AOB cells. The mRNAs from four HOB cell lines (1-4) and four AOB cell lines (1-4) were subjected to qRT-PCR analysis to determine the expression of *HDAC1* and 2. (B) The HDAC1 and 2 protein levels were not changed in HOB and AOB cells. Cells used in (A) were subjected to western blot to examine HDAC1 and 2 levels. GAPDH was used as a loading control. (C) Knockdown of HDAC1 and 2 did not change the expression of Runx2 target genes. The HOB-1 and AOB-1 cells were knockdowned with HDAC1-siRNA and HDAC2-siRNA, respectively. After 48 hours, cells were used to isolate RNA and then were subjected to qRT-PCR analysis to determine the expression of *HDAC1* and 2, as well as Runx2 target genes including *OSC*, *ALPL*, *SPP1*, *COL1A1*, *IBSP* and *MMP13*. *CUL4A* was used a control. (D) HDAC1 and 2 did not bind to the promoters of Runx2 target genes. The HOB-1 and AOB-1 cells were subjected to ChIP assays with HDAC1, HDAC2 and IgG antibodies, followed by analysis with

qRT-PCR to evaluate their bindings to the promoters of Runx2 target genes. CUL4A and FOXM1 were used as controls.

Supplementary Table-1. The basic information of patients (HC represents normal fracture healing patients; AN represents atrophic nonunion patients)

Patients	Age	Sex
HC-1	34	Male
HC-2	45	Female
HC-3	37	Male
HC-4	40	Female
HC-5	22	Female
HC-6	29	Female
HC-7	34	Female
HC-8	55	Male
НС-9	54	Male
HC-10	60	Female
HC-11	32	Male
HC-12	46	Female
HC-13	55	Male
HC-14	44	Male
HC-15	47	Female
HC-16	50	Male
HC-17	34	Female
HC-18	37	Female
HC-19	25	Male
HC-20	29	Male
HC-21	33	Female
HC-22	35	Female
HC-23	57	Female
HC-24	63	Male
AN-1	31	Female
AN-2	25	Male
AN-3	34	Female
AN-4	45	Female

<u> </u>		
AN-5	44	Female
AN-6	42	Male
AN-7	40	Male
AN-8	56	Female
AN-9	36	Female
AN-10	38	Female
AN-11	44	Male
AN-12	35	Female
AN-13	48	Male
AN-14	66	Male
AN-15	63	Female
AN-16	29	Female
AN-17	26	Male
AN-18	35	Male
AN-19	38	Female
AN-20	40	Male
AN-21	42	Female
AN-22	46	Female
AN-23	48	Male
AN-24	20	Male

Supplementary Table-2. Primers used for qRT-PCR analyzes

Gene	Forward Primers	Reverse primers
CtBP1	5'- AGATGCGAGAGGAGGCGCAC-3'	5'- TATAGGCAGCCCCATTGAGCT-3'
CtBP2	5'- AATCCGAAGACCCTCTGGCA-3'	5'- TATTCCAGATTCTGGGCAG-3'
SPHK1	5'- GGCTCTGGCAACGCGCTGGCA-3'	5'- CTAGGTCCACATCAGCAA-3'
DKK1	5'- GCTGCATGCGTCACGCTAT-3'	5'- AACAGAACCTTCTTGTCC-3'
CDH2	5'-GCATTCAGAAGCTAGGC -3'	5'- AAACTAATTCCAATCTGAA-3'
P300	5'- TATGCTCCCAAATCAGGCCC -3'	5'- CAGTCCAGGATGTGGGGA -3'
Runx2	5'- TGTTCTCTGGTCCTTCT -3'	5'- TTGGTATACGGCCTTTA-3'
BMP2	5'- ATTGTCCAATCCATGAGA-3'	5'- TTCCTGCAGGTTCATCGTT-3'
OSC	5'-GCAGCAGAGGGCCGATG-3'	5'-TGTTATGGATCTGGGACT-3'
ALPL	5'-CCCTGCTGCTCGCGCTG-3'	5'-GGCAGACTTTGGTTTCTT-3'
COL1A1	5'-ACACACTCTTCACATCT-3'	5'-GACCCTTCATGTCAG-3'
IBSP	5'-GAGCCAATGCAGAAGAC-3'	5'-TTTCATATCCATTGTC-3'
SPP1	5'-AGTTGAATGGTGCATAC-3'	5'-CTATCAATCACATCGG-3'
MMP13	5'-TGGGACACATGGTCTGT-3'	5'-GTCTATTATTACAGAC-3'
CUL4A	5'-AAGAAGGAATTCCAGGT-3'	5'-ATCAGCACACGTGCTT-3'
□-Actin	5'-GATGAGATTGGCATGGC-3'	5'-CACCTTCACCGTTCCAGTTT-3'

Supplementary Table-3. Primers used for ChIP qRT-PCR analyzes

Gene	Forward Primers	Reverse primers	
OSC	5'-CCTGAGGCTCTCACAGGT-3'	5'-CATGGGGACACTTCT-3'	
ALPL	5'-ACATGCAGTACGAGCTGA-3'	5'-GAATGGTCCGCAGTGAC-3'	
COL1A1	5'-GTGGACACCACCCTCAAG-3'	5'-CACGCAGGTCTCACCA-3'	
IBSP	5'-AGATGACAGTTCAGAAGA-3'	5'-ATATCCCCAGCCTTCTT-3'	
SPP1	5'-GCAACCGAAGTTTTCAC-3'	5'-GCGTTCAGGTCCTGGGC-3'	
MMP13	5'-TGTGACCCTTCCTTATC-3'	5'-GTGCTCATATGCAGCA-3'	
CUL4A	5'-TGGGCTACTGGCCAACATAC-3'	5'-TTCCTTCTTCCCTTC-3'	
FOXM1	5'-CAGCCTGGGGAGGAAATG-3'	5'-AATCACAAGCATTTCC-3'	

Supplementary Table-4. Genes that consistently aberrant expression in three atrophic nonunion tissues

Gene	Gene Description	Average	P Value	Expression
		fold change		
CtBP2	C-terminal-binding protein 2	7.5	0.0000032	Upregulation
GDF5	Growth differentiation factor 5	7.4	0.0000083	Upregulation
GDF6	Growth differentiation factor 6	7.4	0.0000062	Upregulation
GDF7	Growth differentiation factor 7	7.2	0.0000045	Upregulation
DRM	Down-regulated in mos-transformed cells	7.1	0.000080	Upregulation
Follistatin	FSH-suppressing protein	7.1	0.000074	Upregulation
Noggin	Also known as NOG	7.1	0.000036	Upregulation
DKK1	Dickkopf-related protein 1	7.0	0.000067	Upregulation
SPHK1	sphingosine kinase 1	7.0	0.0000091	Upregulation
PHLDA2	Pleckstrin homology-like domain family A	7.0	0.000085	Upregulation
	member 2			
ARHGAP22	Rho GTPase Activating Protein 22	7.0	0.000063	Upregulation
SERPINE1	Plasminogen activator inhibitor-1	7.0	0.000072	Upregulation
CDH2	Cadherin-2	6.8	0.000056	Upregulation
SRF	Serum response factor	6.7	0.000069	Upregulation
SPHK2	Sphingosine kinase 2	6.7	0.000052	Upregulation
TFP12	Tissue Factor Pathway Inhibitor 2	6.7	0.000043	Upregulation
MFAP2	Microfibrillar-associated protein 2	6.6	0.000063	Upregulation
HBEGF	Heparin-binding EGF-like growth factor	6.6	0.000077	Upregulation
VEGFB	Vascular endothelial growth factor B	6.4	0.000086	Upregulation
XPO4	Exportin 4	6.3	0.000092	Upregulation
GJB2	Gap junction beta-2 protein	6.2	0.000054	Upregulation
CUL1	Cullin 1	6.2	0.000058	Upregulation
CUL4A	Cullin 4A	6.2	0.000055	Upregulation
MDA7	Melanoma differentiation associated	6.1	0.000085	Upregulation
	gene-7			
NM23	Nucleoside diphosphate kinase A	6.1	0.000075	Upregulation
MKK4	Mitogen-activated protein kinase kinase 4	6.1	0.000057	Upregulation
KAI1	Also known as CD82, Cluster of	6.1	0.000064	Upregulation

	Differentiation 82			
BRMS1	Breast cancer metastasis-suppressor 1	6.1	0.000066	Upregulation
CRSP3	Mediator Complex Subunit 23	6.0	0.000076	Upregulation
GAS1	Growth arrest-specific protein 1	6.0	0.000058	Upregulation
EEF1A2	Eukaryotic Elongation Factor 1 A-2	6.0	0.000099	Upregulation
СКВ	Choline Kinase B	6.0	0.000081	Upregulation
GAL	Galanin	5.9	0.000065	Upregulation
TTC39C	Tetratricopeptide repeat protein 39C	5.9	0.000042	Upregulation
EBP	Emopamil binding protein	5.8	0.000015	Upregulation
HBQ1	Hemoglobin Subunit Theta-1	5.8	0.000032	Upregulation
NPM3	Nucleoplasmin 3	5.8	0.000043	Upregulation
PLCXD1	Phosphatidylinositol Specific	5.6	0.000054	Upregulation
	Phospholipase C X Domain Containing 1			
FAM69B	Family With Sequence Similarity 69,	5.6	0.0000041	Upregulation
	Member B			
SNRPA1	Small Nuclear Ribonucleoprotein	5.5	0.000032	Upregulation
	Polypeptide A			
LIN28B	Lin-28 Homolog B	5.5	0.0000023	Upregulation
COMTD1	Catechol-O-methyltransferase domain	5.5	0.000037	Upregulation
	containing 1			
TUBB4	Tubulin Beta 4A	5.5	0.0000044	Upregulation
TRAP1	TNF Receptor Associated Protein 1	5.3	0.0000053	Upregulation
RPL29	Ribosomal Protein L29	5.3	0.0000056	Upregulation
RPL11	Ribosomal Protein L11	5.2	0.000065	Upregulation
RPL23	Ribosomal Protein L23	5.1	0.0000021	Upregulation
RPL6	Ribosomal Protein L6	5.1	0.000059	Upregulation
IL6	Interleukin 6	5.1	0.000019	Upregulation
IL10	Interleukin 10	5.0	0.00015	Upregulation
IL15	Interleukin 15	5.0	0.0000048	Upregulation
IL23	Interleukin 23	4.9	0.0000025	Upregulation
CAV1	Caveolin 1	4.9	0.0000043	Upregulation
MT2A	Metallothionein 2A	4.9	0.000028	Upregulation

DCN	Bone Proteoglycan II	4.9	0.000046	Upregulation
PTRF	Caveolae Associated Protein 1	4.9	0.000035	Upregulation
THBS1	Thrombospondin 1	4.9	0.000046	Upregulation
S100A6	S100 Calcium Binding Protein A6	4.9	0.000042	Upregulation
S100A8	S100 Calcium Binding Protein A8	4.8	0.000067	Upregulation
S100A9	S100 Calcium Binding Protein A9	4.8	0.000055	Upregulation
DCN	Decorin	4.7	0.000043	Upregulation
SPARC	Secreted Protein Acidic And Cysteine	4.7	0.000027	Upregulation
	Rich			
DHCR7	Delta-7-Dehydrocholesterol Reductase	4.7	0.00065	Upregulation
SC4MOL	Methylsterol Monooxygenase 1	4.7	0.000043	Upregulation
SQLE	Squalene Epoxidase	4.7	0.00087	Upregulation
FDFT1	Farnesyl-Diphosphate Farnesyltransferase	4.7	0.000073	Upregulation
	1			
CYP51A1	Cytochrome P450 Family 51 Subfamily A	4.6	0.000044	Upregulation
	Member 1			
DHCR24	24-Dehydrocholesterol Reductase	4.6	0.00035	Upregulation
INSIG1	Insulin Induced Gene 1	4.6	0.000084	Upregulation
SCD	Stearoyl-CoA Desaturase	4.5	0.0000065	Upregulation
HMGCS1	3-Hydroxy-3-Methylglutaryl-CoA	4.5	0.000054	Upregulation
	Synthase 1			
NSDHL	NAD(P) Dependent Steroid	4.5	0.000069	Upregulation
	Dehydrogenase-Like			
SREBF2	Sterol Regulatory Element Binding	4.5	0.000078	Upregulation
	Transcription Factor 2			
FASN	Fatty Acid Synthase	4.5	0.000083	Upregulation
FADS1	Fatty Acid Desaturase 1	4.5	0.000021	Upregulation
ZCCHC2	Zinc finger CCHC domain-containing	4.4	0.000043	Upregulation
	protein 2			
IDI1	Isopentenyl-Diphosphate Delta Isomerase	4.4	0.000036	Upregulation
	1			

FDPS	Farnesyl Diphosphate Synthase	4.3	0.000022	Upregulation
RCC2	Regulator of chromosome condensation 2	4.3	0.000019	Upregulation
PSRC1	Proline/serine-rich coiled-coil protein 1	4.3	0.000024	Upregulation
RNF200	RING finger protein 220	4.3	0.000004	Upregulation
DBT	dihydrolipoamide branched chain	4.3	0.000032	Upregulation
	transacylase E2			
EXTL1	Exostosin like glycosyltransferase 1	4.3	0.000046	Upregulation
EXTL2	Exostosin like glycosyltransferase 2	4.3	0.000065	Upregulation
LRRC39	Leucine-rich repeat-containing protein 39	4.2	0.000067	Upregulation
LRRC40	Leucine-rich repeat-containing protein 40	4.2	0.000037	Upregulation
USP1	Ubiquitin carboxyl-terminal hydrolase 1	4.2	0.000014	Upregulation
L1TD1	LINE-1 type transposase domain	4.1	0.000025	Upregulation
	containing 1			
DDX59	DEAD-box helicase 59	4.1	0.000046	Upregulation
CREG1	Cellular repressor of E1A stimulated genes	4.0	0.000054	Upregulation
	1			
CSRP1	Cysteine and glycine rich protein 1	4.0	0.000026	Upregulation
SCAMP3	Secretory carrier-associated membrane	4.0	0.000029	Upregulation
	protein 3			
SLC50A1	Solute carrier family 50 member 1	4.0	0.000045	Upregulation
GPR37L1	G protein-coupled receptor 37 like 1	4.0	0.000084	Upregulation
ZBED6	Zinc finger, BED-type containing 6	4.0	0.000068	Upregulation
LINGO2	Leucine rich repeat and Ig domain	4.0	0.000055	Upregulation
	containing 2			
CAAP1	caspase activity and apoptosis inhibitor 1	4.0	0.000064	Upregulation
CCL21	Chemokine (C-C motif) ligand 21	4.0	0.000057	Upregulation
UBAP1	Ubiquitin-associated protein 1	4.0	0.000087	Upregulation
TSC1	Tuberous sclerosis complex 1	4.0	0.000091	Upregulation
NRBP1	Nuclear receptor-binding protein 1	3.9	0.000053	Upregulation
PCYOX1	Prenylcysteine oxidase 1	3.9	0.000031	Upregulation
MTIF2	Mitochondrial translational initiation	3.9	0.000036	Upregulation
	factor 2			

	1			1
GKN1	Gastrokine 1	3.9	0.000039	Upregulation
COL4A4	Collagen, type IV, alpha 4	3.9	0.000054	Upregulation
INPP1	Inositol polyphosphate 1-phosphatase	3.9	0.00032	Upregulation
UBXD2	UBX domain-containing protein 4	3.8	0.000065	Upregulation
TDGF1	Teratocarcinoma-derived growth factor 1	3.8	0.000043	Upregulation
CPN2	Carboxypeptidase N subunit 2	3.7	0.000069	Upregulation
SOX2	Sex Determining Region Y-Box 2	3.7	0.000043	Upregulation
SERP1	Stress-associated endoplasmic reticulum	3.6	0.000037	Upregulation
	protein 1			
AMOTL1	Angiomotin-like protein 1	3.6	0.000035	Upregulation
CDHR5	Cadherin related family member 5	3.5	0.000055	Upregulation
FAR1	Fatty acyl-coA reductase 1	3.4	0.000088	Upregulation
GLYAT	Glycine-N-acyltransferase	3.4	0.000093	Upregulation
USP47	Ubiquitin specific peptidase 47	3.3	0.000065	Upregulation
LRG1	Leucine-rich alpha-2-glycoprotein 1	3.3	0.00043	Upregulation
P14K2B	Phosphatidylinositol 4-kinase type 2-beta	3.3	0.00056	Upregulation
UGT8	UDP glycosyltransferase 8	3.3	0.000067	Upregulation
INTS12	Integrator complex subunit 12	3.2	0.000022	Upregulation
FGFRL1	Fibroblast growth factor receptor-like 1	3.2	0.000025	Upregulation
DHX16	DEAH-box helicase 16	3.2	0.00094	Upregulation
GMDS	GDP-mannose 4,6-dehydratase	3.1	0.000062	Upregulation
NQO2	N-ribosyldihydronicotinamide:quinone	3.1	0.000032	Upregulation
	reductase 2			
PFDN6	Prefoldin subunit 6	3.0	0.000054	Upregulation
PKHD1	Polycystic kidney and hepatic disease 1	3.0	0.000016	Upregulation
ARG1	Arginase 1	-11.2	0.0000012	Downpregulation
MCDR1	Macular dystrophy, retinal, 1	-11.1	0.0000019	Downpregulation
MOXD1	Monooxygenase DBH like 1	-11.1	0.0000011	Downpregulation
CDCA7L	Cell division cycle-associated 7-like	-11.0	0.0000015	Downpregulation
	protein			
CROT	Peroxisomal carnitine	-11.0	0.0000024	Downpregulation

	O-octanoyltransferase			
p300	Histone Butyryltransferase P300	-10.8	0.0000032	Downpregulation
DDX56	DEAD-box helicase 56	-10.7	0.0000017	Downpregulation
Runx2	Runt Related Transcription Factor 2	-10.5	0.0000028	Downpregulation
COL1A1	Collagen Type I Alpha 1	-10.4	0.0000015	Downpregulation
MMP13	Matrix Metallopeptidase 13	-10.3	0.0000026	Downpregulation
SPP1	Secreted Phosphoprotein 1	-10.1	0.0000045	Downpregulation
OSC	OxidosqualeneLanosterol Cyclase	-10.1	0.0000025	Downpregulation
FOXM1	Forkhead Box M1	-9.7	0.0000047	Downpregulation
BMP2	Bone Morphogenetic Protein 2	-9.5	0.0000019	Downpregulation
BMP4	Bone Morphogenetic Protein 4	-9.5	0.0000013	Downpregulation
BMP7	Bone Morphogenetic Protein 7	-9.2	0.00000067	Downpregulation
VCAM1	Vascular Cell Adhesion Molecule 1	-9.1	0.0000054	Downpregulation
CD45	Protein Tyrosine Phosphatase, Receptor	9.1	0.0000032	Downpregulation
	Туре С			
CDH22	Cadherin 22	-9.0	0.0000025	Downpregulation
FBN1	Fibrillin 1	-8.9	0.0000028	Downpregulation
FBN2	Fibrillin 2	-8.9	0.0000065	Downpregulation
GERM1	Gremlin 1	-8.8	0.0000047	Downpregulation
Col5a3	Collagen Type V Alpha 3	-8.7	0.0000067	Downpregulation
DLX5	Distal-Less Homeobox 5	-8.7	0.0000035	Downpregulation
LGALS3	Galectin 3	-8.6	0.0000056	Downpregulation
IGFBP1	Insulin Like Growth Factor Binding	-8.5	0.0000069	Downpregulation
	Protein 1			
IGFBP2	Insulin Like Growth Factor Binding	-8.5	0.00000035	Downpregulation
	Protein 1			
SFXN1	Sideroflexin 1	-8.5	0.0000045	Downpregulation
SOCS2	Suppressor Of Cytokine Signaling 2	-8.4	0.0000036	Downpregulation
NUPL1	Nucleoporin Like 1	-8.4	0.0000025	Downpregulation
XPD	Xeroderma Pigmentosum Complementary	-8.4	0.0000043	Downpregulation
	Group D			

Г			1	,
DDB1	Damage Specific DNA Binding Protein 1	-8.2	0.00000032	Downpregulation
KAL1	Anosmin 1	-8.2	0.0000028	Downpregulation
CPT2	Carnitine Palmitoyltransferase 2	-8.1	0.0000019	Downpregulation
CCL2	C-C Motif Chemokine Ligand 2	-8.1	0.0000077	Downpregulation
ING3	Inhibitor of growth protein 3	-8.1	0.0000057	Downpregulation
NUPL2	Nucleoporin-like 2	-8.0	0.0000098	Downpregulation
METTL2B	Methyltransferase-like protein 2B	-8.0	0.0000054	Downpregulation
LAPTM4B	Lysosomal-associated transmembrane	-7.8	0.0000032	Downpregulation
	protein 4B			
NDRG1	N-myc downstream regulated gene 1	-7.8	0.0000047	Downpregulation
ODF1	Outer dense fiber protein 1	-7.8	0.0000067	Downpregulation
PKIA	cAMP-dependent protein kinase inhibitor	-7.8	0.0000054	Downpregulation
	alpha			
RRS1	Ribosome biogenesis regulator homolog	-7.7	0.0000048	Downpregulation
RUNX1T1	Runt-related transcription factor 1	-7.7	0.0000033	Downpregulation
TRMT12	tRNA methyltransferase 12 homolog	-7.5	0.0000056	Downpregulation
INTS8	Integrator complex subunit 8	-7.4	0.0000053	Downpregulation
EMP2	Epithelial membrane protein 2	-7.4	0.0000043	Downpregulation
TELO2	Telomere length regulation protein TEL2	-7.4	0.0000066	Downpregulation
	homolog			
CARHSP1	Calcium-regulated heat stable protein 1	-7.3	0.0000045	Downpregulation
NUBP2	Nucleotide-binding protein 2	-7.2	0.0000062	Downpregulation
UNKL	RING finger protein unkempt-like	-7.2	0.0000044	Downpregulation
CST9L	Cystatin-9-like	-7.2	0.0000065	Downpregulation
ENTPD6	Ectonucleoside triphosphate	-7.2	0.0000063	Downpregulation
	diphosphohydrolase 6			
GSS	Glutathione synthetase	-7.1	0.0000043	Downpregulation
NAPB	Beta-soluble NSF attachment protein	-7.1	0.0000069	Downpregulation
NRSN2	Neurensin-2	-7.1	0.0000087	Downpregulation
TASP1	Threonine aspartase 1	-7.0	0.0000064	Downpregulation
UCKL1	Uridine-cytidine kinase-like 1	-7.0	0.0000039	Downpregulation
CBS	cystathionine-beta-synthase	-7.0	0.0000045	Downpregulation

DGCD1	D 0 1 1		0.000054	D 1.:
DSCR1	Down Syndrome critical region 1	-6.9	0.0000054	Downpregulation
PCNE1	Potassium voltage-gated channel,	-6.9	0.0000032	Downpregulation
	Isk-related family, member 1			
PCNE2	Potassium voltage-gated channel,	-6.8	0.00000055	Downpregulation
	Isk-related family, member 2			
PCNT	Pcentrosomal pericentrin	-6.8	0.0000098	Downpregulation
CRELD2	Cysteine-rich with EGF-like domain	-6.7	0.000035	Downpregulation
	protein 2			
DGCR6	DiGeorge Syndrome critical region gene 6	-6.7	0.0000043	Downpregulation
IGLJ3	Immunoglobulin lambda joining 3	-6.6	0.000064	Downpregulation
PI4KA	Phosphatidylinositol 4-kinase alpha	-6.5	0.0000078	Downpregulation
THAP7	THAP domain-containing protein 7	-6.5	0.000072	Downpregulation
TTC28	Tetratricopeptide repeat domain 28	-6.5	0.000065	Downpregulation
SSR4	Translocon-associated protein subunit	-6.3	0.000036	Downpregulation
	delta			
TCEAL1	Transcription elongation factor A	-6.3	0.000054	Downpregulation
	protein-like 1			
TCEAL2	Transcription elongation factor A	-6.2	0.000042	Downpregulation
	protein-like 2			
USP51	Ubiquitin carboxyl-terminal hydrolase 51	-6.2	0.000046	Downpregulation
TSPYL2	Testis-specific Y-encoded-like protein 2	-6.1	0.000054	Downpregulation
TREX2	Three prime repair exonuclease 2	-6.1	0.0000063	Downpregulation
ABI3	ABI gene family member 3	-6.1	0.000054	Downpregulation
AZI1	5-azacytidine-induced protein 1	-6.1	0.000035	Downpregulation
GGT6	Gamma-glutamyltransferase 6	-6.0	0.000039	Downpregulation
IBD22	Inflammatory bowel disease-22	-5.9	0.0000064	Downpregulation
OMG	Oligodendrocyte-myelin glycoprotein	-5.8	0.000013	Downpregulation
PNPO	Pyridoxine-5'-phosphate oxidase	-5.7	0.000018	Downpregulation
SLFN11	Schlafen family member 11	-5.7	0.000087	Downpregulation
TAC4	Tachykinin-4	-5.7	0.000056	Downpregulation
GLOD4	Glyoxalase domain containing 4	-5.7	0.000043	Downpregulation
GRB7	Growth factor Receptor-Bound protein 7	-5.6	0.000067	Downpregulation

EDD 1	Ecc.	<i>5</i> (0.0000054	D
EPR1	Effector cell peptidase receptor 1	-5.6	0.0000054	Downpregulation
PRPSAP2	Phosphoribosyl pyrophosphate	-5.6	0.000045	Downpregulation
	synthetase-associated protein 2			
TBC1D3	TBC1 domain family member 3E/3F	-5.6	0.000067	Downpregulation
VPS25	Vacuolar protein-sorting-associated	-5.6	0.000042	Downpregulation
	protein 25			
YBX2	Y-box-binding protein 2	-5.5	0.0000035	Downpregulation
MSI2	Musashi RNA binding protein 2	-5.4	0.0000066	Downpregulation
TCL1B	T-cell leukemia/lymphoma protein 1B	-5.4	0.0000021	Downpregulation
TMED10	Transmembrane emp24	-5.4	0.000029	Downpregulation
	domain-containing protein 10			
ZBTB1	Zinc finger and BTB domain containing 1	-5.3	0.000084	Downpregulation
CIDEB	Cell death-inducing DFFA-like effector b	-5.3	0.000032	Downpregulation
CRIP2	Cysteine-rich protein 2	-5.3	0.000036	Downpregulation
HKDC1	Hexokinase domain containing 1	-5.3	0.000021	Downpregulation
MTG1	Mitochondrial GTPase 1	-5.2	0.00016	Downpregulation
NPM3	Nucleoplasmin-3	-5.1	0.00042	Downpregulation
NRBF2	Nuclear receptor-binding factor 2	-5.0	0.00056	Downpregulation
PLXDC2	Plexin domain-containing protein 2	-4.9	0.000042	Downpregulation
SMNDC1	Survival motor neuron domain containing	-4.9	0.000021	Downpregulation
	1			
TCTN3	Tectonic family member 3	-4.8	0.000015	Downpregulation
UTF1	Undifferentiated embryonic cell	-4.8	0.000056	Downpregulation
	transcription factor 1			
WBP1L	WW domain binding protein 1-like	-4.7	0.000034	Downpregulation
GGT6	Gamma-glutamyltransferase 6	-4.7	0.00039	Downpregulation
MSI2	Musashi RNA binding protein 2	-4.7	0.00089	Downpregulation
VPS25	Vacuolar protein-sorting-associated	-4.7	0.00037	Downpregulation
	protein 25			
YBX2	Y-box-binding protein 2	-4.5	0.00025	Downpregulation
ARPP19	cAMP-regulated phosphoprotein 19	-4.4	0.00078	Downpregulation
ELL3	Elongation factor RNA polymerase II-like	-4.4	0.00047	Downpregulation

	3			
IDDM3	Insulin dependent diabetes mellitus 3	-4.2	0.00067	Downpregulation
LCMT2	Leucine carboxyl methyltransferase 2	-4.0	0.00043	Downpregulation
MFAP1	Microfibrillar-associated protein 1	-3.9	0.00056	Downpregulation
SPN1	Snurportin1	-3.9	0.00078	Downpregulation
TMC3	Transmembrane channel like 3	-3.9	0.00046	Downpregulation
EAPP	E2F-associated phosphoprotein	-3.7	0.00037	Downpregulation
TC2N	Tandem C2 domains nuclear protein	-3.7	0.00032	Downpregulation
GPHB5	Glycoprotein hormone beta-5	-3.7	0.000078	Downpregulation
IFI27	Interferon alpha-inducible protein 27	-3.6	0.000042	Downpregulation
PSMG1	Proteasome assembly chaperone 1	-3.6	0.00043	Downpregulation
RRP1B	Ribosomal RNA processing 1 homolog B	-3.6	0.00011	Downpregulation
TJAP1	Tight junction associated protein 1	-3.6	0.00056	Downpregulation
TCF19	Transcription factor 19	-3.5	0.00034	Downpregulation
ZNRD1	Zinc ribbon domain containing 1	-3.5	0.00055	Downpregulation
TRAM2	Translocation associated membrane	-3.5	0.00032	Downpregulation
	protein 2			
MUT	Methylmalonyl Coenzyme A mutase	-3.5	0.00043	Downpregulation
GMDS	GDP-mannose 4,6-dehydratase	-3.5	0.00024	Downpregulation
ELOVL5	ELOVL fatty acid elongase 5	-3.4	0.00037	Downpregulation
COL11A2	Collagen, type XI, alpha 2	-3.4	0.00046	Downpregulation
APOM	Apolipoprotein M	-3.4	0.00016	Downpregulation
CABYR	Calcium-binding tyrosine	-3.3	0.00098	Downpregulation
	phosphorylation-regulated protein			
CXXC1	CXXC-type zinc finger protein 1	-3.2	0.00045	Downpregulation
NPC1	Niemann-Pick disease, type C1	-3.0	0.00032	Downpregulation
NOL4	Nucleolar protein 4	-3.0	0.00021	Downpregulation

Supplementary Table-5. Identification of CtBP2-associating proteins analyzed by LC-MS/MS

Protein	Protein description	Molecular weight	MASCOT scores
CTBP2	C-Terminal Binding Protein 2	49 kDa	4308
GAPDH	Glyceraldehyde 3-phosphate dehydrogenase	36 kDa	4219
KDM1A	Lysine Demethylase 1A	93 kDa	4193
P300	Histone acetyltransferase	264 kDa	4082
PRDX1	Peroxiredoxin-1	22 kDa	4066
FOXP1	Forkhead Box P1	79 kDa	4019
HDAC1	Histone Deacetylase 1	55 kDa	3980
HK2	Hexokinase 2	103 kDa	3855
CTNNB1	Catenin Beta 1	85 kDa	3769
MTA2	Metastasis Associated 1 Family Member 2	75 kDa	3643
POLD	DNA Polymerase Delta 1	124 kDa	3577
CUL7	Cullin 7	192 kDa	3418
POLRA1	RNA Polymerase II Subunit A	217 kDa	3302
HDAC2	Histone Deacetylase 2	55 kDa	3299
MCM7	Minichromosome maintenance complex component 7	81 kDa	3168
ATR	ATR serine/threonine kinase	301 kDa	3083
RAD51	RAD51 Recombinase	37 kDa	3039
PRDX6	Peroxiredoxin 6	25 kDa	2988
DNMT1	DNA Methyltransferase 1	183 kDa	2975
CDC23	Cell Division Cycle 23	69 kDa	2973
PLK1	Polo Like Kinase 1	68 kDa	2910
GALK1	Galactokinase 1	42 kDa	2854
HCFC1	Host Cell Factor C1	215 kDa	2798
RQCD1	Required For Cell Differentiation 1	34 kDa	2649
COPA	Coatomer Protein Complex Subunit Alpha	138 kDa	2587
HIC2	Hypermethylated In Cancer 2	67 kDa	2504
CTBP1	C-Terminal Binding Protein 1	48 kDa	2492
RCOR2	REST Corepressor 2	58 kDa	2483

GATAD2A DLG1 GDF5 ZNRD1 CUL4A	GATA Zinc Finger Domain Containing 2A Discs Large MAGUK Scaffold Protein 1 Growth differentiation factor 5 Zinc ribbon domain containing 1	67 kDa 100 kDa 55 kDa	2415 2359
GDF5 ZNRD1	Growth differentiation factor 5		2359
ZNRD1		55 kDa	
	Zinc ribbon domain containing 1		2321
CUL4A		14 kDa	2304
	Cullin 4A	88 kDa	2295
HIPK2	Homeodomain Interacting Protein Kinase 2	131 kDa	2247
TCF7	Transcription Factor 7	42 kDa	2166
XPO4	Exportin 4	130 kDa	2127
DCN	Bone Proteoglycan II	40 kDa	2095
TCF7L1	Transcription Factor 7 Like 1	63 kDa	2046
ACAT2	Acetyl-CoA Acetyltransferase 2	41 kDa	2037
USP1	Ubiquitin carboxyl-terminal hydrolase 1	88 kDa	2011
MDA7	Melanoma differentiation associated gene-7	24 kDa	2004
NRBP1	Nuclear receptor-binding protein 1	60 kDa	1975
GDF6	Growth differentiation factor 6	51 kDa	1962
CTNNB1	Catenin Beta 1	85 kDa	1911
UGT8	UDP glycosyltransferase 8	61 kDa	1884
AMOTL1	Angiomotin-like protein 1	107 kDa	1862
TCF7L2	Transcription Factor 7 Like 2	68 kDa	1826
SOCS2	Suppressor Of Cytokine Signaling 2	22 kDa	1793
TTC28	Tetratricopeptide repeat domain 28	27 kDa	1732
ABI3	ABI gene family member 3	39 kDa	1703
BIRC5	Baculoviral IAP Repeat Containing 5	16 kDa	1676
YBX2	Y-box-binding protein 2	39 kDa	1548
IGLJ3	Immunoglobulin lambda joining 3	5 kDa	1491
PLXDC2	Plexin domain-containing protein 2	60 kDa	1435
MSI2	Musashi RNA binding protein 2	35 kDa	1407
LCMT2	Leucine carboxyl methyltransferase 2	76 kDa	1357
EAPP	E2F-associated phosphoprotein	33 kDa	1290
IFI27	Interferon alpha-inducible protein 27	11 kDa	1269
TCF19	Transcription factor 19	37 kDa	1202
MUT	Methylmalonyl Coenzyme A mutase	83 kDa	1154

ELOVL5	ELOVL fatty acid elongase 5	35 kDa	1151
SSX2IP	SSX Family Member 2 Interacting Protein	71 kDa	1088
SOX13	SRY-Box 13	68 kDa	1056
POLA1	DNA Polymerase Alpha 1	167 kDa	1022
FBXW11	F-Box And WD Repeat Domain Containing 11	61 kDa	989
NPEPPS	Aminopeptidase Puromycin Sensitive	103 kDa	955
PBDC1	Polysaccharide Biosynthesis Domain Containing 1	22 kDa	943
PHGDH	Phosphoglycerate Dehydrogenase	57 kDa	921
TTC27	Tetratricopeptide Repeat Domain 27	96 kDa	905
MKLN1	Muskelin 1	85 kDa	889
MAPK6	Mitogen-Activated Protein Kinase 6	82 kDa	868
IPO7	Importin 7	119 kDa	843
DDB1	Damage Specific DNA Binding Protein 1	127 kDa	820
CBS	Cystathionine-beta-synthase	61 kDa	805
CARHSP1	Calcium-regulated heat stable protein 1	16 kDa	759
KAT2B	Lysine Acetyltransferase 2B	93 kDa	740
MAPK8	Mitogen-Activated Protein Kinase 8	48 kDa	719
RUNX1	Runt Related Transcription Factor 1	49 kDa	699
HIST2H3A	Histone Cluster 2 H3 Family Member A	15 kDa	687
MAPK10	Mitogen-Activated Protein Kinase 10	53 kDa	675
P65	NF-Kappa-B Transcription Factor P65	60 kDa	659
P52	Nuclear Factor Kappa B Subunit 2	97 kDa	644
P50	Nuclear Factor NF-Kappa-B P105 Subunit	105 kDa	638
AGXT2	Alanine-glyoxylate aminotransferase 2	57 kDa	629
ARL15	ADP-ribosylation factor-like 15	23 kDa	615
ERAP2	Endoplasmic reticulum aminopeptidase 2	110 kDa	609
PHAX	Phosphorylated adapter for RNA export	44 kDa	603
SLCO4C1	Solute carrier organic anion transporter family	79 kDa	595
	member 4c1		
SMN1	Survival motor neuron 1	32 kDa	588
SMN2	Survival motor neuron 2	32 kDa	577
YIPF5	Yip1 domain family member 5	28 kDa	570

TNFAIP8	Tumor necrosis factor, alpha-induced protein 8	23 kDa	564
CARD19	Caspase recruitment domain family member 19	26 kDa	558
CAAP1	Caspase activity and apoptosis inhibitor 1	38 kDa	553
NUDT2	Nudix hydrolase 2	17 kDa	551
SIT1	Signaling threshold regulating transmembrane	21 kDa	543
	adapter 1		
STOML2	Stomatin-like protein 2	39 kDa	538
UBAC1	Ubiquitin-associated domain containing protein 1	45 kDa	527
UBAP1	Ubiquitin-associated protein 1	55 kDa	518
ZNF79	Zinc finger protein 79	55 kDa	513
TMC1	Transmembrane channel-like 1	88 kDa	510
TTC39B	Tetratricopeptide repeat protein 39B	77 kDa	506
CARHSP1	Calcium-regulated heat stable protein 1	16 kDa	503
TMEM8A	Transmembrane protein 8A	85 kDa	498
IBD8	Inflammatory bowel disease 8	73 kDa	487
GLCE	D-glucuronyl C5-epimerase	70 kDa	476
MFAP1	Microfibrillar-associated protein 1	52 kDa	465
TMC3	Transmembrane channel like 3	126 kDa	462
VPS25	Vacuolar protein-sorting-associated protein 25	21 kDa	455
OMG	Oligodendrocyte-myelin glycoprotein	50 kDa	449
NAPB	Beta-soluble NSF attachment protein	34 kDa	443
STAU1	Double-stranded RNA-binding protein Staufen	63 kDa	428
	homolog 1		
TASP1	Threonine aspartase 1	44 kDa	417
KIZ	Kizuna centrosomal protein	75 kDa	410
NDRG1	N-myc downstream regulated gene 1	43 kDa	405
RECQL4	RecQ protein-like 4	133 kDa	402
UBAP2	Ubiquitin-associated protein 2	117 kDa	398
THAP1	THAP domain containing, apoptosis associated	25 kDa	394
	protein 1		
GDAP1	Ganglioside-induced differentiation-associated	41 kDa	390
	protein 1		

INTS9	Integrator complex subunit 9	74 kDa	388
FBXL1	F-box and leucine rich repeat protein 2	48 kDa	383
TRAK1	Trafficking kinesin-binding protein 1	106 kDa	380
FBP1	Fructose-1,6-bisphosphatase 1	37 kDa	376
IFN1	Interferon, type 1	13 kDa	374
ISCA1	Iron-sulfur cluster assembly 1 homolog	14 kDa	370
GCNT1	Glucosaminyl (N-acetyl) transferase 1	50 kDa	366
DDX31	DEAD box polypeptide 31	94 kDa	363
GPR107	G protein-coupled receptor 107	67 kDa	355
CDKAL1	CDK5 regulatory subunit associated protein 1 like 1	65 kDa	352
NQO2	N-ribosyldihydronicotinamide:quinone reductase 2	26 kDa	348
LST1	Leukocyte specific transcript 1	11 kDa	346
RCD1	Retinal cone dystrophy 1	34 kDa	340
CUL4B	Cullin 4B	104 kDa	336
MOXD1	Monooxygenase DBH like 1	70 kDa	333
SYNJ2	Synaptojanin 2	166 kDa	330
TAAR1	Trace amine associated receptor 1	39 kDa	321
ARHGAP44	Rho GTPase activating protein 44	89 kDa	320
AZI1	5-azacytidine-induced protein 1	122 kDa	317
DPH1	Diphthamide biosynthesis protein 1	49 kDa	315
GGT6	Gamma-glutamyltransferase 6	51 kDa	312
PNPO	Pyridoxine-5'-phosphate oxidase	30 kDa	306
PRCD	Progressive rod-cone degeneration	6 kDa	303
SLFN11	Schlafen family member 11	103 kDa	278
RNMTL1	RNA methyltransferase-like protein 1	47 kDa	254
SECTM1	Secreted and transmembrane protein 1	27 kDa	205