

Table SI. Sequences of vectors in this study.

Primer	Sequences
miR-182-5p mimic (double strand)	5'-UUUGGCAAUGGUAGAACUCACACU-3' 5'-UGUGAGUUCUACCAUUGCCAAAUU-3'
Mimic-NC (double strand)	5'-UUCUCCGAACGAACGUGUCACGUUU-3' 5'-ACGUGACACGUUCGGAGAAUU-3'
miR-182-5p inhibitor	5'-AGUGUGAGUUCUACCAUUGCCAAA-3'
Inhibitor-NC si-BNIP3	5'-CAGUACUUUUGUGUAGUACAA-3'
Forward sequence	5'-GAAAGUAAAUACUAUUUAUAUA-3'
Reverse sequence	5'-UAUAAUAGUAUUUACUUUCAG-3'
si-NC	5'-UUCUUCGAACGUGUCACGUUU-3'

miR, microRNA; si, small interfering; NC, negative control.

Table SII. The identified 53 DEGs from GSE48053 data profile with the selection criteria of adjusted P-value <0.05.

Probe ID	Adjusted P-value	logFC	Gene symbol	Gene title
204614_at	0.0218	-3.07	SERPINB2	Serpin family B member 2
209351_at	0.0268	-2.75	KRT14	Keratin 14
228956_at	0.0289	-2.7	UGT8	UDP glycosyltransferase 8
213764_s_at	0.0485	-2.62	MFAP5	Microfibrillar associated protein 5
1555854_at	0.0406	-2.34	LOC101930400	Aldo-keto reductase family 1 member C2-like
237552_at	0.0452	-2.28	LOC100505817	Uncharacterized LOC100505817
204823_at	0.0406	-1.75	NAV3	Neuron navigator 3
201825_s_at	0.0289	-1.71	SCCPDH	Saccharopine dehydrogenase (putative)
218435_at	0.0495	-1.67	DNAJC15	DnaJ heat shock protein family (Hsp40) member C15
1556097_at	0.0357	-1.62	HOMER2	Homer scaffolding protein 2
228850_s_at	0.0374	-1.49	SLIT2	Slit guidance ligand 2
224032_x_at	0.0406	-1.49	SPANXA2	SPANX family member A2
209125_at	0.0495	-1.46	KRT6A	Keratin 6A
223784_at	0.0406	-1.42	TMEM27	Transmembrane protein 27
227037_at	0.0452	-1.38	PLD6	Phospholipase D family member 6
239108_at	0.0452	-1.37	FAR2	Fatty acyl-CoA reductase 2
1569582_at	0.0455	-1.28	AADACP1	Arylacetamide deacetylase pseudogene 1
207526_s_at	0.0495	-1.23	IL1RL1	Interleukin 1 receptor like 1
202784_s_at	0.0488	-1.2	NNT	Nicotinamide nucleotide transhydrogenase
207543_s_at	0.0455	1.17	P4HA1	Prolyl 4-hydroxylase subunit alpha 1
201848_s_at	0.0455	1.19	BNIP3	BCL2 interacting protein 3
219147_s_at	0.0452	1.27	NMRK1	Nicotinamide riboside kinase 1
201811_x_at	0.0406	1.34	SH3BP5	SH3 domain binding protein 5
209173_at	0.0406	1.34	AGR2	Anterior gradient 2, protein disulphide isomerase family member
223571_at	0.0452	1.35	C1QTNF6	C1q and tumor necrosis factor related protein 6
209118_s_at	0.0374	1.43	TUBA1A	Tubulin alpha 1a
219806_s_at	0.0406	1.46	SMCO4	Single-pass membrane protein with coiled-coil domains 4
222088_s_at	0.0455	1.5	SLC2A14	Solute carrier family 2 member 14
202769_at	0.0374	1.53	CCNG2	Cyclin G2
219232_s_at	0.0374	1.54	EGLN3	Egl-9 family hypoxia inducible factor 3
204298_s_at	0.0357	1.55	LOX	Lysyl oxidase
202022_at	0.0406	1.55	ALDOC	Aldolase, fructose-bisphosphate C
204595_s_at	0.0406	1.59	STC1	Stanniocalcin 1
202619_s_at	0.0383	1.62	PLOD2	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
243386_at	0.0452	1.62	CASZ1	Castor zinc finger 1
205319_at	0.0289	1.7	PSCA	Prostate stem cell antigen
226535_at	0.0455	1.73	LOC100505984	Uncharacterized LOC100505984
202499_s_at	0.0406	1.74	SLC2A3	Solute carrier family 2 member 3
213397_x_at	0.0357	1.79	RNASE4	Ribonuclease A family member 4
226325_at	0.0258	1.86	ADSSL1	Adenylosuccinate synthase like 1
242907_at	0.0374	1.87	GBP2	Guanylate binding protein 2
218901_at	0.0374	1.92	PLSCR4	Phospholipid scramblase 4
209189_at	0.0452	2.13	FOS	Fos proto-oncogene, AP-1 transcription factor subunit
202912_at	0.0495	2.15	ADM	Adrenomedullin
203980_at	0.0419	2.21	FABP4	Fatty acid binding protein 4
201313_at	0.0218	2.32	ENO2	Enolase 2
230748_at	0.0258	2.47	SLC16A6	Solute carrier family 16 member 6
202238_s_at	0.0374	2.71	LOC101928916	Uncharacterized LOC101928916
207761_s_at	0.0218	2.87	METTL7A	Methyltransferase like 7A
215444_s_at	0.0455	2.92	TRIM31	Tripartite motif containing 31
212143_s_at	0.0406	3.2	IGFBP3	Insulin like growth factor binding protein 3
1558034_s_at	0.0455	3.4	CP	Ceruloplasmin (ferroxidase)
218729_at	0.0257	4.51	LXN	Latexin

FC, fold change; bold, gene of interest.

Table SIII. Top conserved targets of BNIP3 predicted by TargetScan Human 7.2.

miRNA	Position in the UTR	Seed match	Context++ score	Context++ score percentile	Weighted context++ score
hsa-miR-182-5p	824-831	8mer	-0.42	98	-0.36
hsa-miR-411-5p.1	783-789	7mer-m8	-0.3	98	-0.26
hsa-miR-96-5p	825-831	7mer-1A	-0.23	91	-0.2
hsa-miR-1271-5p	825-831	7mer-1A	-0.17	86	-0.15

miRNA, microRNA; has, human.