SUPPLEMENTARY TABLES

Supplementary Table 1. Characteristics of 3 hypertensive patients and 5 normotensive individuals of sequencing.

Characteristics Gender (M/F)	Hypertension (n=3) 1/2	Normotension (n=5) 3/2
Age (years)	59.73 ± 6.08	60.17 ± 4.10
SBP (mmHg)	161.00 ± 15.10**	114.70 ± 7.40
DBP (mmHg)	98.77 ± 5.40**	78.97 ± 6.16
BMI (kg/m^2)	25.81 ± 3.29	24.17 ± 2.30
FBG (mmol/L)	5.36 ± 1.04	5.08 ± 1.16
TG (mmol/L)	1.67± 1.09	1.17 ± 0.86
LDL (mmol/L)	2.97 ± 0.91	2.80 ± 0.73
HDL (mmol/L)	1.14 ± 0.12	1.32 ± 0.27
CHO (mmol/L)	4.93 ± 1.02	4.71 ± 0.79

[#]Data are mean ±standard deviation (SD).
[##] M, male; F, female; SBP, systolic blood pressure; DBP, diastolic blood pressure; BMI, body mass index; FBG, fasting blood glucose; TG, triglycerides; LDL, low density lipoprotein; HDL, high density lipoprotein; CHO, cholesterol.
**P<0.01 vs. normotensive individuals.

Supplementary Table 2. Correlation between the most significant DE lncRNAs, circRNAs and mRNAs.

Name	mRNA	Pearson	P-value	FDR
LOC646616	WNT3	0.999888	0.009524	0.048855
	CAMK2N2	0.999920	0.008051	0.047351
LAP3P2	WNT3	0.999691	0.015827	0.048855
	CAMK2N2	0.999996	0.001748	0.044093
hsa_circ_0039388	WNT3	0.999898	0.009100	0.045505
	CAMK2N2	0.999122	0.026675	0.048718
hsa_circ_0038648	WNT3	0.999998	0.001173	0.041120
	CAMK2N2	0.999668	0.016402	0.048514
WNT3	CAMK2N2	0.999619	0.017575	0.048855

[#]FDR: false discovery rate.

Supplementary Table 3. Expression data (in units of FPKM) for the most significant DE lncRNAs and circRNAs.

	FPKM	FPKM	FPKM	FPKM	FPKM	FPKM	FPKM	FPKM	EH1/2/3 vs NC1/2/3/4/5	
gene type	EH_1F	EH_1M	EH_2F	NC_1M	NC_2F	NC_2M	NC_3M	NC_3F	EH average	NC average
LOC646616	23.32145695	22.82128303	19.68736046	1.43010615	1.863003619	0.90103621	1.722328318	1.744558523	21.94336681	1.532206564
LAP3P2	0.916949814	0.268886904	0.451702508	0	0.177244944	0	0	0	0.5458464	0.035449
circ_0039388	7.792171867	1.559141998	3.09035545	0	0	0	0.270651619	0	4.147223105	0.054130324
circ_0038648	3.896085934	1.133921453	1.85421327	0.116586733	0.117713797	0	0	0	2.29474	0.04686

Supplementary Table 4. Characteristics of 60 hypertensive patients and 60 normotensive individuals.

Characteristics	Hypertension	Normotension
Gender (M/F)	(n=60) 26/34	(n=60) 30/30
Age (years)	54.33± 8.94	53.37± 9.18
SBP (mmHg)	158.33± 13.16**	119.60± 9.59
DBP (mmHg)	96.20± 5.46**	79.53± 5.75
Family history (%)	36.67	26.67
Smoking (%)	43.33	46.67
Drinking (%)	53.33	50.00
BMI (kg/m^2)	26.29±3.21	25.39±2.81
FBG (mmol/L)	5.16±0.64	4.99±0.51
TC (mmol/L)	4.57±0.98*	4.07±0.60
TG (mmol/L)	1.87±0.14	1.55±0.09
HDL (mmol/L)	1.06±0.22	1.16±0.19
LDL (mmol/L)	2.81±0.90	2.58±0.78

[#]Data are mean ± SD.
*P<0.05, **P <0.01 vs. normotensive individuals.

Supplementary Table 5. Whole gene sequencing results of 7 DE lncRNAs and 2 DE cicRNAs.

Test_id	EH	NH	Log$_2$ FC	FDR	Style	Length
DE lncRNAs						
SCARNA7	12882.37	338.65	5.25	0.000072	up	329
RPS3AP20	223.78	9.59	4.55	0.009161	up	858
LOC646616	13.56	0.92	3.89	0.038099	up	1346
RPL34P25	7.39	39.60	-2.42	0.003287	down	436
RPSAP16	31.19	64.98	-1.06	0.006135	down	986
RPSAP36	6.47	24.99	-1.95	0.024000	down	1010
LAP3P2	12.83	0.75	4.09	0.006210	up	1695
DE circRNAs						
hsa_circ_0039388	26.09	1.06	4.63	0.000000	up	381
hsa_circ_0038648	15.90	0.79	4.33	0.000000	up	533

*The screening criteria were log$_2$ FC >1 or <-1, FDR<0.05.

Supplementary Table 6. Multiple stepwise regression analysis showing variables independently associated with LOC646616 and hsa_circ_0038648.

	β	SE	β'	t
LOC646616				
Constant	-0.280	0.276		-0.101
SBP	0.345	0.098	0.421	3.525*
Cys C	0.262	0.123	0.230	2.135*
Hcy	0.317	0.154	0.250	2.051*
hsa_circ_0038648				
Constant	0.162	0.416		0.390
SBP	0.300	0.142	0.364	2.119*
HDL	-0.330	0.161	-0.233	-2.039*

[#]β': standardized β. Variables included in the original model are SBP, DBP, BMI, FBG, TC, TG, HDL, LDL, CRP, Hcy and Cys C. CRP, C-reactive protein; Hcy, homocysteine; Cys C, cystatin C. *P<0.05.

Supplementary Table 7. Primers sequences used for the studies.

Test_id		Primer
RPSAP36	F primer	5'-GCTGAAGACCAGCCTCTCATA-3'
	R primer	5'-CCACATCAAACCCACGGAGT-3'
LOC646616	F primer	5'-ACCGAAGGCACTACACGC-3'
	R primer	5'-GAGATTGGAGCAGCAAATGG-3'
RPS3AP20	F primer	5'-TTTGAATTGGGAAAGCTCATG-3'
	R primer	5'-AACAGATTCTTGGACTGGTGG-3'
RPL34P25	F primer	5'-TCCCAGACCCTTGGTAATAGA-3'
	R primer	5'-ACATGCCACATGCAGATTTT-3'
SCARNA7	F primer	5'-GCTTGTGGTGGCTATGGAA-3'
	R primer	5'-GGTGAGCTGTTCTTGGGTTAT-3'
RPSAP16	F primer	5'-GGGTGCCCTCTGTGCCTAT-3'
	R primer	5'-CCTGAGCAGTGGGAGCTGTA-3'
LAP3P2	F primer	5'-GAGCCCTCAGTCTTCTTG -3'
	R primer	5'-AGATACCACCACTGTCAAA -3'
GAPDH	F primer	5'-TCTCTGCTCCTCCTGTTCGA-3'
	R primer	5'- GCGCCCAATACGACCAAATC-3'
hsa_circ_0039388	F primer	5'-AGGGGAGACCTCATTCAGTTCTACA -3'
	R primer	5'-TGTAGAACTGAATGAGGTCTCCCCT-3'
hsa_circ_0038648	F primer	5'-TTTTTCTCTATGCAGTCAGCTGAAA -3'
	R primer	5'-TTTCAGCTGACTGCATAGAGAAAAA-3'
miR-637	F primer	5'-ACACTCCAGCTGGGACTGGGGGCTTTCGGGCT -3'
	R primer	5'-CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGACGCAGAG-3'
U6	F primer	5'-CTCGCTTCGGCAGCACA-3'
	R primer	5'-AACGCTTCACGAATTTGCGT-3'
miR-637 mimics	Sense	5'-ACUGGGGGCUUUCGGGCUCUGCGU-3'
	Antisense	5'-GCAGAGCCCGAAAGCCCCCAGUUU-3'
miR-637 inhibitor	Sense	5'ACGCAGAGCCCGAAAGCCCCCAGU-3'
WNT3	F primer	5'- CTGCCAGGAGTGTATTCGCATC -3'
	R primer	5'- GAGAGCCTCCCCGTCCACAG -3'
CAMK2N2	F primer	5'- CGCAGACCCCGAAGGTT-3'
	R primer	5'-TTGCCAGCGAAGAAGGAGTT-3'
β-catenin	F primer	5'-GGGACACAGCAGCAATTTGT-3'
	R primer	5'-CAGCTGCACAAACAATGGAA-3'

* RPSAP36, ribosomal protein SA pseudogene 36; LOC646616 transmembrane protein 183A pseudogene; RPS3AP20, ribosomal protein S3a pseudogene 20; RPL34P25, ribosomal protein L34 pseudogene 25; SCARNA7, small Cajal body-specific RNA 7; RPSAP16, ribosomal protein SA pseudogene 16; LAP3P2, leucine aminopeptidase 3 pseudogene 2; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; has_circ_0039388, Homo sapiens_circular RNA_0039388; hsa_circ_0038648, Homo sapiens_circular RNA_0038648; miR-637, microRNA-637; U6, U6 small nuclear RNA; WNT3, Wnt family member 3; CAMK2N2, calcium/calmodulin dependent protein kinase II inhibitor 2.

Supplementary Table 8. siRNA sequences used for the studies.

		Sequence(5'-3')
LOC646616-1	Sense	GCGGCUGGAUUAUAUAUCUTT
	Antisense	AGAUAUAUAAUCCAGCCGCTT
LOC646616-2	Sense	CCAUAUAUGUAUGAGCCAUTT
	Antisense	AUGGCUCAUACAUAUAUGGTT
LOC646616-3	Sense	CAGGAACCAAUGUGGAAAUTT
	Antisense	AUUUCCACAUUGGUUCCUGTT