

Table SI. Baseline clinical characteristics of the present study population.

Characteristic	Control (n=50)	AF (n=50)	CKD (n=48)	AF + CKD (n=47)	P-value
Age, years	59.5 (39-76)	62.0 (40-82)	61.0 (46-84)	62.0 (45-85)	0.79
Men, n (%)	30 (60.0)	31 (62.0)	30 (62.5)	31 (66.0)	0.96
BMI, kg/m ²	24.2±2.8	24.9±3.0	24.6±2.9	24.0±3.1	0.72
Hypertension, n (%)	20 (40.0)	23 (46.0)	23 (47.9)	24 (51.1)	0.68
AF type, persistent, n (%)	-	50 (100)	-	47 (100)	-
CKD stage, n (%)	-	-	-	-	-
Stage 2	-	-	12 (25.0)	10 (21.3)	-
Stage 3	-	-	14 (29.2)	12 (25.5)	-
Stage 4	-	-	12 (25.0)	12 (25.5)	-
Stage 5	--	-	10 (20.8)	13 (27.7)	-
Diabetes mellitus, n (%)	12 (24.0)	14 (28.0)	13 (27.1)	15 (31.9)	0.89
Coronary artery disease, n (%)	10 (20.0)	13 (26.0)	12 (25.0)	13 (27.7)	0.86
Heart failure, n (%)	7 (14.0)	9 (18.0)	8 (16.7)	11 (23.4)	0.79
Smoking, n (%)	15 (30.0)	16 (32.0)	15 (31.3)	15 (31.9)	0.99
Serum creatinine, µmol/l	73.4±15.2	79.1±17.6	140.6±34.5	172.3±39.8	0.0003
eGFR, ml/min/1.73 m ²	91.8±13.9	88.5±15.6	49.2±11.8	39.6±10.5	0.0007
ACEI/ARB use, n (%)	15 (30.0)	17 (34.0)	17 (35.4)	17 (36.2)	0.93
Anticoagulant use, n (%)	0 (0.0)	46 (92.0)	0 (0.0)	43 (91.2)	0.0006

Data are presented as mean ± SD or n (%), as appropriate. Age (years) are presented as median (range). AF, atrial fibrillation; CKD, chronic kidney disease; eGFR, estimated glomerular filtration rate; ACEI, angiotensin-converting enzyme inhibitor; ARB, angiotensin receptor blocker.

Table SII. Primer sequences used for reverse transcription-quantitative PCR.

Gene	Primer name	Sequence (5'-3')	Amplicon, bp
ZFP36	ZFP36-F	GACCTTCCACTGTCACCCTC	117
	ZFP36-R	CCAGACGCTGATAGGAGTGG	
BTG2	BTG2-F	GGCACTCACAGAGCACTACAAAC	291
	BTG2-R	ACTTGTTCTTGCAGGTGAGG	
GAPDH	GAPDH-F	GGAAGCTTGTCATCAATGGAAATC	168
	GAPDH-R	TGATGACCCTTTTGGCTCCC	

All sequences are shown as 5'-3'. F, forward; R, reverse; BTG2, BTG anti-proliferation factor 2; ZFP36, ZFP36 zinc finger CCCH-type.

Table SIII. Key target genes, TFs and miRNAs in the regulatory network.

Name	Regulatory network component
BTG2	Target gene
ZFP36	Target gene
NPPB	Target gene
JUN	TF
EGR1	TF
TP53	TF
FOS	TF
YY1	TF
USF1	TF
TAL1	TF
2623	TF
STAT3	TF
SRF	TF
SP1	TF
SMAD4	TF
SMAD3	TF
REST	TF
RELA	TF
NFKB2	TF
NFKB1	TF
MYC	TF
MYB	TF
MXI1	TF
23601	TF
MEF2A	TF
MAX	TF
JUND	TF
JUNB	TF
GABPA	TF
FOSL1	TF
FOSB	TF
ELK1	TF
CUX1	TF
CREB1	TF
BPTF	TF

BACH2
BACH1
ATF2
CNOT7
CNOT8
EWSR1
HOXB9
HOXC8
SMAD1
SMAD9
hsa-let-7e
hsa-let-7g
hsa-let-7i
PICK1
PRKCA
PRMT1
CCDC85B
EDC3
EXOSC6
EXOSC8
HMGB1
MAPK1
MAPKAPK2
NUP214
SFN
UPF2
XRN1
YWHAB
YWHAG
YWHAH
hsa-miR-21
hsa-miR-27a
hsa-miR-27b
hsa-miR-98
hsa-miR-103
hsa-miR-107
hsa-miR-124

hsa-miR-128	miRNA
hsa-miR-128b	miRNA
hsa-miR-132	miRNA
hsa-miR-140-3p	miRNA
hsa-miR-142-5p	miRNA
hsa-miR-149	miRNA
hsa-miR-15a	miRNA
hsa-miR-15b	miRNA
hsa-miR-16	miRNA
hsa-miR-182	miRNA
hsa-miR-195	miRNA
hsa-miR-200a	miRNA
hsa-miR-202	miRNA
hsa-miR-212	miRNA
hsa-miR-218	miRNA
hsa-miR-219-1-3p	miRNA
hsa-miR-220c	miRNA
hsa-miR-25	miRNA
hsa-miR-26a	miRNA
hsa-miR-26b	miRNA
hsa-miR-296-3p	miRNA
hsa-miR-29a	miRNA
hsa-miR-29b	miRNA
hsa-miR-29c	miRNA
hsa-miR-300	miRNA
hsa-miR-31	miRNA
hsa-miR-32	miRNA
hsa-miR-323-5p	miRNA
hsa-miR-330-3p	miRNA
hsa-miR-340	miRNA
hsa-miR-361-3p	miRNA
hsa-miR-363	miRNA
hsa-miR-367	miRNA
hsa-miR-374a	miRNA
hsa-miR-381	miRNA
hsa-miR-383	miRNA
hsa-miR-409-3p	miRNA

hsa-miR-421	miRNA
hsa-miR-424	miRNA
hsa-miR-492	miRNA
hsa-miR-495	miRNA
hsa-miR-497	miRNA
hsa-miR-506	miRNA
hsa-miR-515-5p	miRNA
hsa-miR-520g	miRNA
hsa-miR-520h	miRNA
hsa-miR-551a	miRNA
hsa-miR-551b	miRNA
hsa-miR-562	miRNA
hsa-miR-567	miRNA
hsa-miR-568	miRNA
hsa-miR-576-3p	miRNA
hsa-miR-577	miRNA
hsa-miR-582-5p	miRNA
hsa-miR-590-5p	miRNA
hsa-miR-591	miRNA
hsa-miR-617	miRNA
hsa-miR-622	miRNA
hsa-miR-623	miRNA
hsa-miR-632	miRNA
hsa-miR-633	miRNA
hsa-miR-638	miRNA
hsa-miR-646	miRNA
hsa-miR-650	miRNA
hsa-miR-656	miRNA
hsa-miR-877	miRNA
hsa-miR-9	miRNA
hsa-miR-92	miRNA
hsa-miR-92b	miRNA
hsa-miR-940	miRNA

miR/miRNAs, microRNAs; TF, transcription factor.