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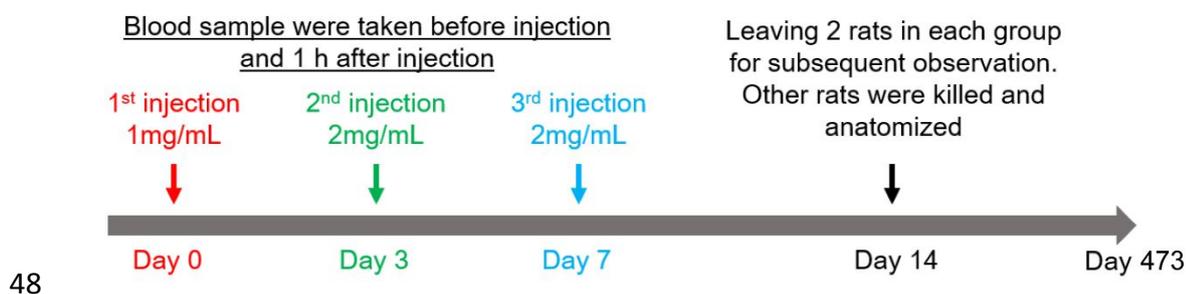
## Supporting Information

### 30 **MicroRNA extraction and qRT-PCR**

31 Total RNAs in the blood samples, including microRNAs, were extracted using Trizol  
32 reagent (Sigma Aldrich, USA) according to the manufacturer's instructions.  
33 Subsequently, the purified RNAs were polyadenylated through a poly(A) polymerase  
34 reaction and was then reversed-transcribed into complementary DNA (cDNA).  
35 TIANGEN® miRcute Plus miRNA First-Strand cDNA Kit (Code No. KR211) was used in  
36 the reverse transcriptional reaction system of total 10  $\mu$ L, including 5  $\mu$ L 2X miRNA RT  
37 Reaction Buffer, 1  $\mu$ L miRNA RT Enzyme Mix and 4  $\mu$ L RNA sample. The reaction  
38 conditions are 40 °C for 60 mins and 95 °C for 3 mins. The cDNA was quantified in real-  
39 time SYBR Green RT-qPCR reactions with the specific microRNA qPCR Assay Primers.  
40 TIANGEN® miRcute Plus miRNA qPCR Kit (SYBR Green) (Code No. FP411) was used in  
41 the qPCR reaction system of total 10  $\mu$ L, including 5  $\mu$ L 2X miRcute Plus miRNA PreMix  
42 (SYBR&ROX), 0.2  $\mu$ L Forward Primer, 0.2  $\mu$ L Reverse Primer, 1  $\mu$ L 50X ROX Reference  
43 Dye, 1  $\mu$ L DNA Sample and 2.6  $\mu$ L ddH<sub>2</sub>O. The cycling conditions are 95°C for 15min,  
44 followed by 40 cycles at 94°C for 20s, 60°C for 15s and 72°C for 30s. The primers used  
45 for qPCR are presented in Table S1.

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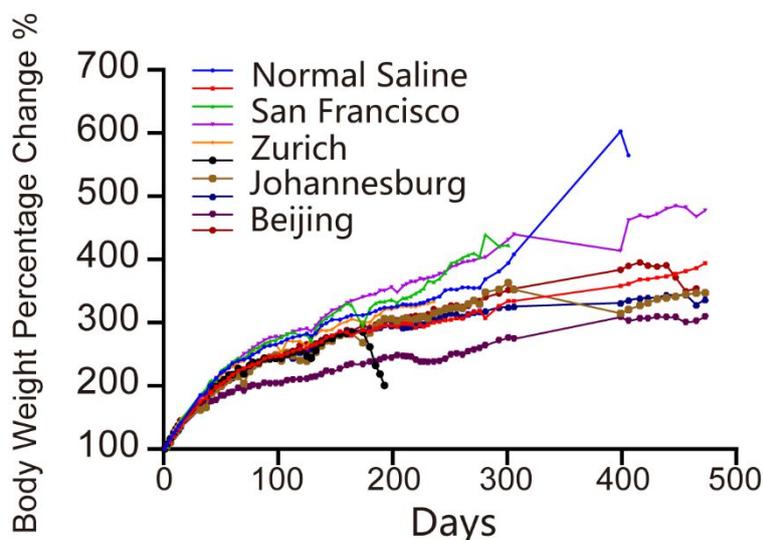
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49 **Figure S1.** Experimental procedure of this work. Three injections were performed  
50 successively for all groups of rats (n=30) on day 0, 3 and 7. Blood samples were taken  
51 before injection and 1 hour after injection. 20 rats (4 rats for each group) were killed  
52 and anatomized on day 14 for the histopathological analysis and the other 10 rats (2  
53 rats for each group) were kept for the follow-up observation till day 473.

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56 **Figure S2.** Body weight percentage change of single rat (five groups, two rats left for  
57 each group for longer time period observation after the exposure experiment).

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59 **Video S1.** Surveillance video of the rats before and after the injection of PM extracts  
60 from different cities.

61

62 **Table S1** Primers used for RT-qPCR of microRNA. The reverse primers are included in  
63 the TIANGEN® miRcute Plus miRNA qPCR Kit (SYBR Green) (Code No. FP411).

microRNA	Forward primers
miR-146a-5P	GAGAACTGAATTCCATGGGTT
miR-125b-5P	CCTGAGACCCTAACTTGTGA
miR-126	GTACCGTGAGTAATAATGCG
miR-132	ACAGTCTACAGCCATGGTCTG
miR-155	TTAATGCTAATTGTGATAGGGGT
miR-21-5P	TAGCTTATCAGACTGATGTTGA
miR-223	TGTCAGTTTGTCAAATACCCC
miR-26a	CAAGTAATCCAGGATAGGCT

64

65 **Table S2** The sample size of biomarker analysis in each group on each time injections  
66 after excluding outliers (the Grubbs test).

Biomarker	Group	1 <sup>st</sup> injection	2 <sup>nd</sup> injection	3 <sup>rd</sup> injection
TNF- $\alpha$	Normal saline	6	6	4

	San Francisco	6	6	5
	Zurich	6	6	4
	Johannesburg	6	6	5
	Beijing	6	6	6
IL-1 $\alpha$	Normal saline	6	5	6
	San Francisco	5	5	5
	Zurich	6	6	4
	Johannesburg	6	6	4
	Beijing	6	6	6
MCP-1	Normal saline	6	6	6
	San Francisco	6	6	5
	Zurich	6	6	4
	Johannesburg	6	5	5
	Beijing	6	5	6

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68 **Table S3** The top 20 potential mRNAs targeted by miR-125b and miR-155 and their  
69 genes' information. The potential targets were accessed from miRanda database  
70 (microRNA.org). The full name descriptions were accessed from RGD (rat genome  
71 database, <https://rgd.mcg.edu>).

Potential targets	Full name	Original description extracted from rgd.mcg.edu
MiR-125b		
Wee 1	WEE1 G2 checkpoint kinase	Predicted to have protein tyrosine kinase activity. Predicted to be involved in several processes, including mitotic cell cycle checkpoint; neuron projection morphogenesis; and peptidyl-tyrosine phosphorylation. Predicted to localize to cytoplasm and nucleolus. Orthologous to human WEE1 (WEE1 G2 checkpoint kinase); PARTICIPATES IN cell cycle pathway, mitotic;
H3f3b	H3 histone family member 3B	Predicted to have RNA polymerase II cis-regulatory region sequence-specific DNA binding activity; RNA polymerase II core promoter sequence-specific DNA binding activity; and nucleosomal DNA binding activity. Involved in brain development and response to hormone. Predicted to localize to nuclear chromosome, telomeric region and nuclear nucleosome. Orthologous to human H3-3B (H3.3 histone B); PARTICIPATES IN histone

		modification pathway; systemic lupus erythematosus pathway;
APOOL	apolipoprotein O like	Predicted to be involved in cristae formation. Predicted to localize to MICOS complex. Orthologous to human APOOL (apolipoprotein O like); PARTICIPATES IN mitochondrial protein import pathway;
TSPYL1	TSPY like 1	Predicted to have enzyme binding activity. Predicted to be involved in nucleosome assembly. Predicted to localize to nucleolus and nucleoplasm. Human ortholog(s) of this gene implicated in gonadal dysgenesis and sudden infant death syndrome. Orthologous to several human genes including TSPYL1 (TSPY like 1);
CHMP5	charged multivesicular body protein 5	Predicted to be involved in several processes, including cellular response to muramyl dipeptide; midbody abscission; and regulation of microtubule cytoskeleton organization. Predicted to localize to cytosol and nucleus. Orthologous to human CHMP5 (charged multivesicular body protein 5); PARTICIPATES IN endocytosis pathway; INTERACTS WITH acrylamide; amphetamine; benzo[a]pyrene.
LOC304000	immunoglobulin superfamily, member 5	Predicted to have PDZ domain binding activity. Predicted to be involved in cell-cell adhesion. Predicted to localize to bicellular tight junction and cell surface. Orthologous to human IGSF5 (immunoglobulin superfamily member 5);
Cacnb2	calcium voltage-gated channel auxiliary subunit beta 2	Exhibits several functions, including actin filament binding activity; calcium channel regulator activity; and identical protein binding activity. Contributes to voltage-gated calcium channel activity. Involved in positive regulation of calcium ion transmembrane transport via high voltage-gated calcium channel; positive regulation of high voltage-gated calcium channel activity; and protein localization to plasma membrane. Localizes to L-type voltage-gated calcium channel complex. Human ortholog(s) of this gene implicated in Brugada syndrome 4; hypertension; and hypertrophic cardiomyopathy. Orthologous to human CACNB2 (calcium voltage-gated channel auxiliary subunit beta 2); PARTICIPATES IN calcium transport pathway; calcium/calcium-mediated signaling pathway;

		calcium/calmodulin dependent kinase 2 signaling pathway;
Wdr89	WD repeat domain 89	Predicted to be involved in corpus callosum development and ventricular system development. Orthologous to human WDR89 (WD repeat domain 89);
Slc4a10	solute carrier family 4 member 10	Exhibits sodium:bicarbonate symporter activity. Predicted to be involved in several processes, including brain development; growth; and locomotory exploration behavior. Localizes to apical plasma membrane and basolateral plasma membrane. Orthologous to human SLC4A10 (solute carrier family 4 member 10);
Egr2	early growth response 2	Exhibits HMG box domain binding activity. Involved in learning or memory; regulation of neuronal synaptic plasticity; and response to insulin. Predicted to localize to cytoplasm and nucleoplasm. Biomarker of middle cerebral artery infarction. Human ortholog(s) of this gene implicated in Charcot-Marie-Tooth disease type 1D; Charcot-Marie-Tooth disease type 3; Charcot-Marie-Tooth disease type 4E; and motor peripheral neuropathy. Orthologous to human EGR2 (early growth response 2); PARTICIPATES IN interleukin-4 signaling pathway;
LOC498400	HORMA domain containing 2	Predicted to be involved in meiotic sister chromatid cohesion. Predicted to localize to synaptonemal complex. Orthologous to human HORMAD2 (HORMA domain containing 2)
Stk39	serine threonine kinase 39	Exhibits protein kinase binding activity and protein serine/threonine kinase activity. Involved in activation of MAPK activity; positive regulation of ion transport; and protein autophosphorylation. Localizes to cytoskeleton; cytosol; and extrinsic component of membrane. Orthologous to human STK39 (serine/threonine kinase 39);
Dnm3	dynamamin 3	Exhibits G protein-coupled glutamate receptor binding activity; GTPase activity; and nitric-oxide synthase binding activity. Involved in several processes, including positive regulation of synaptic vesicle recycling; postsynaptic neurotransmitter receptor internalization; and regulation of plasma membrane bounded cell

		projection organization. Localizes to several cellular components, including apical tubulobulbar complex; basal tubulobulbar complex; and dendritic spine head. Orthologous to human DNMT3 (dynamain 3); PARTICIPATES IN clathrin-dependent synaptic vesicle endocytosis; endocytosis pathway; Fc gamma receptor mediated signaling pathway;
Elavl2	ELAV like RNA binding protein 2	Predicted to have RNA binding activity. Predicted to be involved in cellular response to leukemia inhibitory factor. Predicted to localize to synapse. Orthologous to human ELAVL2 (ELAV like RNA binding protein 2);
Ing3	inhibitor of growth family, member 3	Predicted to contribute to histone acetyltransferase activity. Predicted to be involved in histone H2A acetylation; histone H4 acetylation; and positive regulation of apoptotic process. Predicted to localize to Piccolo NuA4 histone acetyltransferase complex and Swr1 complex. Used to study hepatocellular carcinoma. Orthologous to human ING3 (inhibitor of growth family member 3); PARTICIPATES IN INO80 family mediated chromatin remodeling pathway
Pnrc1	proline-rich nuclear receptor coactivator 1	Predicted to localize to nucleus. Orthologous to human PNRC1 (proline rich nuclear receptor coactivator 1)
Tsc22d3	TSC22 domain family, member 3	Predicted to have MRF binding activity. Involved in body fluid secretion. Predicted to localize to cytoplasm and nucleus. Orthologous to human TSC22D3 (TSC22 domain family member 3)
Tmem39a	transmembrane protein 39a	Predicted to localize to integral component of membrane. Orthologous to human TMEM39A (transmembrane protein 39A)
Syp	synaptophysin	Exhibits protein domain specific binding activity and syntaxin-1 binding activity. Involved in endocytosis; regulation of opioid receptor signaling pathway; and response to amyloid-beta. Localizes to several cellular components, including integral component of synaptic vesicle membrane; postsynaptic density; and presynaptic active zone. Biomarker of Alzheimer's disease. Human ortholog(s) of this gene implicated in non-syndromic X-linked

		intellectual disability. Orthologous to human SYP (synaptophysin);
Zfand6	zinc finger AN1-type containing 6	Predicted to have polyubiquitin modification-dependent protein binding activity. Predicted to be involved in several processes, including cellular response to tumor necrosis factor; protein targeting to peroxisome; and regulation of I-kappaB kinase/NF-kappaB signaling. Predicted to localize to cytoplasm. Orthologous to human ZFAND6 (zinc finger AN1-type containing 6); miR-155
Asf1a	anti-silencing function 1A histone chaperone	Predicted to have chromatin binding activity and histone binding activity. Predicted to be involved in several processes, including DNA repair; nucleosome assembly; and osteoblast differentiation. Predicted to localize to nuclear chromatin; nucleoplasm; and protein-containing complex. Orthologous to human ASF1A (anti-silencing function 1A histone chaperone); PARTICIPATES IN histone modification pathway;
Arid2	AT-rich interaction domain 2	Predicted to have DNA binding activity. Predicted to be involved in several processes, including heart development; nucleosome disassembly; and positive regulation of double-strand break repair via homologous recombination. Predicted to localize to nucleoplasm and plasma membrane. Human ortholog(s) of this gene implicated in Coffin-Siris syndrome 6. Orthologous to human ARID2 (AT-rich interaction domain 2); PARTICIPATES IN SWI/SNF family mediated chromatin remodeling pathway;
TYRP1	tyrosinase-related protein 1	Predicted to have monophenol monooxygenase activity; protein heterodimerization activity; and protein homodimerization activity. Predicted to be involved in several processes, including acetoacetic acid metabolic process; melanosome organization; and positive regulation of melanin biosynthetic process. Predicted to localize to clathrin-coated endocytic vesicle membrane; endosome membrane; and melanosome membrane. Human ortholog(s) of this gene implicated in

		oculocutaneous albinism; oculocutaneous albinism type III; and pigmentation disease. Orthologous to human TYRP1 (tyrosinase related protein 1); PARTICIPATES IN tyrosine metabolic pathway;
Hivep2	human immunodeficiency virus type I enhancer binding protein 2	Exhibits DNA-binding transcription activator activity, RNA polymerase II-specific and RNA polymerase II cis-regulatory region sequence-specific DNA binding activity. Involved in positive regulation of transcription by RNA polymerase II. Predicted to localize to nucleoplasm. Human ortholog(s) of this gene implicated in autosomal dominant non-syndromic intellectual disability 43. Orthologous to human HIVEP2 (HIVEP zinc finger 2);
Kat2b	lysine acetyltransferase 2B	Exhibits chromatin binding activity; enzyme binding activity; and transcription factor binding activity. Involved in several processes, including cellular response to parathyroid hormone stimulus; positive regulation of chromatin binding activity; and positive regulation of histone acetylation. Localizes to cytosol and nuclear chromatin. Orthologous to human KAT2B (lysine acetyltransferase 2B); PARTICIPATES IN histone modification pathway; p53 signaling pathway; RNA polymerase II transcription initiation pathway;
Arhgap10	Rho GTPase activating protein 10	Predicted to have GTPase activator activity. Predicted to be involved in cytoskeleton organization and negative regulation of apoptotic process. Predicted to localize to cytosol. Orthologous to human ARHGAP10 (Rho GTPase activating protein 10);
TLE4	TLE family member 4, transcriptional corepressor	Predicted to have several functions, including DNA-binding transcription factor activity, RNA polymerase II-specific; repressing transcription factor binding activity; and transcription corepressor activity. Predicted to be involved in several processes, including cellular response to leukemia inhibitory factor; negative regulation of canonical Wnt signaling pathway; and negative regulation of transcription by RNA polymerase II. Localizes to nucleus. Orthologous to human TLE4 (TLE family member 4, transcriptional corepressor);

RIF1	replication timing regulatory factor 1	Predicted to be involved in several processes, including cellular response to leukemia inhibitory factor; positive regulation of histone H3-K9 methylation; and regulation of nucleobase-containing compound metabolic process. Predicted to localize to several cellular components, including chromosome; nucleus; and spindle midzone. Orthologous to human RIF1 (replication timing regulatory factor 1); PARTICIPATES IN ataxia telangiectasia-mutated (ATM) signaling pathway; non-homologous end joining pathway of double-strand break repair;
GABRA1	gamma-aminobutyric acid type A receptor subunit alpha 1	Exhibits drug binding activity. Contributes to GABA receptor activity. Involved in GABAergic synaptic transmission and cellular response to histamine. Localizes to GABA receptor complex; GABA-ergic synapse; and integral component of postsynaptic specialization membrane. Biomarker of hepatic encephalopathy. Human ortholog(s) of this gene implicated in early infantile epileptic encephalopathy 19 and idiopathic generalized epilepsy 13. Orthologous to human GABRA1 (gamma-aminobutyric acid type A receptor subunit alpha1);
IGJ	joining chain of multimeric IgA and IgM	Predicted to contribute to several functions, including immunoglobulin receptor binding activity; peptidoglycan binding activity; and phosphatidylcholine binding activity. Predicted to be involved in several processes, including defense response to other organism; glomerular filtration; and positive regulation of respiratory burst. Predicted to localize to monomeric IgA immunoglobulin complex; pentameric IgM immunoglobulin complex; and secretory dimeric IgA immunoglobulin complex. Orthologous to human JCHAIN (joining chain of multimeric IgA and IgM);
PICALM	phosphatidylinositol binding clathrin assembly protein	Exhibits several functions, including SH3 domain binding activity; identical protein binding activity; and phosphatidylinositol binding activity. Involved in several processes, including generation of neurons; regulation of synaptic vesicle cycle; and regulation of terminal button organization. Localizes to several cellular components, including Schaffer collateral - CA1 synapse; cytoplasmic vesicle; and synaptic membrane. Predicted to colocalize

		with AP-2 adaptor complex and perinuclear region of cytoplasm. Human ortholog(s) of this gene implicated in acute myeloid leukemia. Orthologous to human PICALM (phosphatidylinositol binding clathrin assembly protein);
FAR1	fatty acyl CoA reductase 1	Predicted to have fatty-acyl-CoA reductase (alcohol-forming) activity. Predicted to be involved in several processes, including ether lipid biosynthetic process; long-chain fatty-acyl-CoA metabolic process; and wax biosynthetic process. Predicted to localize to integral component of peroxisomal membrane. Orthologous to human FAR1 (fatty acyl-CoA reductase 1);
Bach1	BTB domain and CNC homolog 1	Predicted to have DNA-binding transcription activator activity, RNA polymerase II-specific; DNA-binding transcription repressor activity, RNA polymerase II-specific; and RNA polymerase II cis-regulatory region sequence-specific DNA binding activity. Predicted to be involved in DNA repair and regulation of transcription, DNA-templated. Predicted to localize to nucleus. Orthologous to human BACH1 (BTB domain and CNC homolog 1);
FAM133B	family with sequence similarity 133, member B	Orthologous to several human genes including FAM133B (family with sequence similarity 133 member B);
NCAM1	neural cell adhesion molecule 1	Exhibits LRR domain binding activity and phosphatase binding activity. Involved in several processes, including axon development; positive regulation of cardiac muscle cell proliferation; and thalamus development. Localizes to several cellular components, including Schaffer collateral - CA1 synapse; glutamatergic synapse; and integral component of synaptic membrane. Biomarker of congestive heart failure and hypothyroidism. Human ortholog(s) of this gene implicated in bipolar disorder and pancreatic cancer. Orthologous to human NCAM1 (neural cell adhesion molecule 1); PARTICIPATES IN fibroblast growth factor signaling pathway; prion disease pathway;
MOBKL3	MOB family member 4, phocein	Exhibits kinase binding activity. Predicted to be involved in vesicle budding from membrane. Localizes to several cellular components, including dendritic spine; neuronal cell body;

		and perinuclear region of cytoplasm. Orthologous to human MOB4 (MOB family member 4, phocein);
ZIC3	Zic family member 3	Predicted to have DNA-binding transcription activator activity, RNA polymerase II-specific and RNA polymerase II cis-regulatory region sequence-specific DNA binding activity. Predicted to be involved in several processes, including determination of left/right symmetry; lung development; and positive regulation of transcription by RNA polymerase II. Predicted to localize to cytoplasm and nucleoplasm. Human ortholog(s) of this gene implicated in X-linked VACTERL association; situs inversus; and visceral heterotaxy. Orthologous to human ZIC3 (Zic family member 3);
LRP1B	LDL receptor related protein 1B	Predicted to have Wnt-activated receptor activity and Wnt-protein binding activity. Predicted to be involved in canonical Wnt signaling pathway. Predicted to localize to plasma membrane and receptor complex;
ZMYM6	zinc finger MYM-type containing 6	Predicted to have DNA-binding transcription factor activity, RNA polymerase II-specific. Predicted to be involved in cytoskeleton organization; regulation of cell morphogenesis; and regulation of transcription by RNA polymerase II. Predicted to localize to nucleus. Orthologous to human ZMYM6 (zinc finger MYM-type containing 6);
C3orf58	divergent protein kinase domain 2A	Predicted to be involved in cardiac muscle cell proliferation; negative regulation of smooth muscle cell apoptotic process; and regulation of phosphatidylinositol 3-kinase signaling. Predicted to localize to COPI vesicle coat; Golgi membrane; and extracellular space. Orthologous to human DIPK2A (divergent protein kinase domain 2A);