

Supplementary Materials for

Differential regulation of miRNA and protein profiles in human plasma-derived extracellular vesicles by continuous aerobic and high intensity interval training

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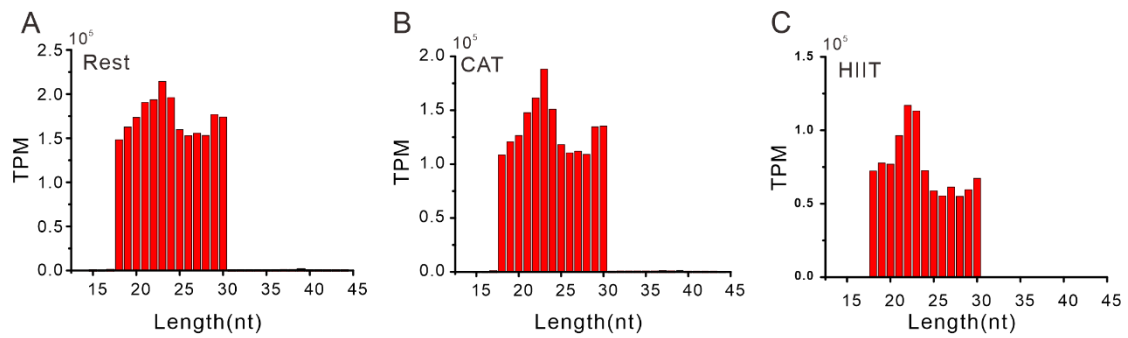


Figure S1. The length distributions of the EV-miRNAs in the three study groups.

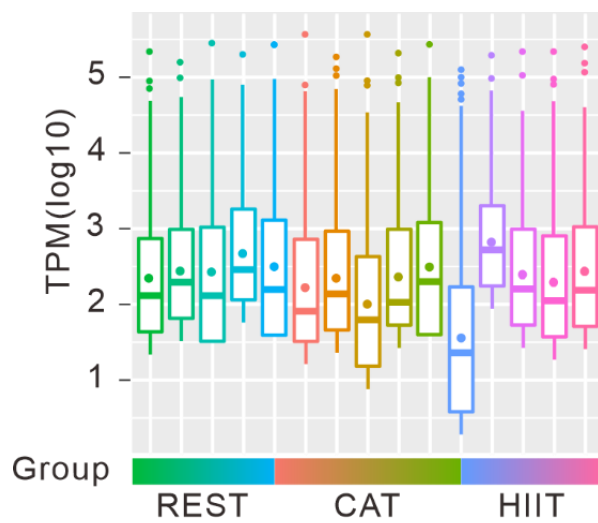


Figure S2. The transcripts per Kilobase Per Million mapped read (TPM) of EV-miRNAs in all tested samples.

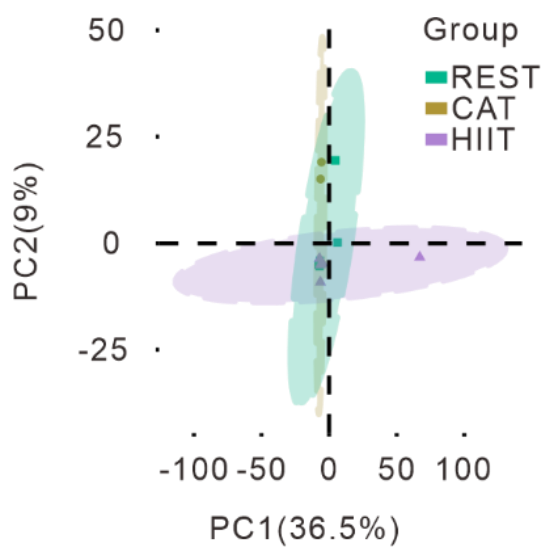


Figure S3. PCA of miRNA expression profiles in the three study groups.

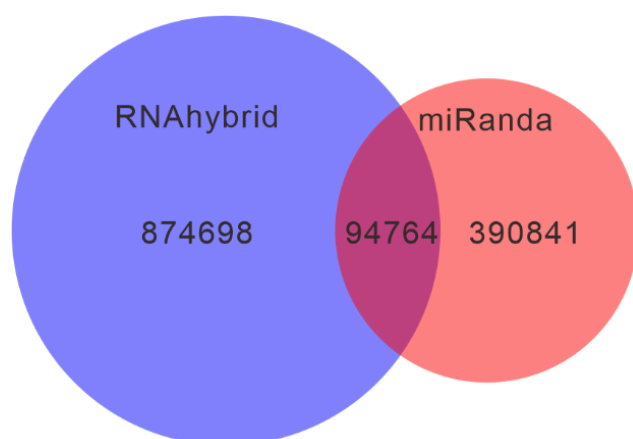


Figure S4. Venn diagram of predicted target genes of the DE EV-miRNAs based on RNAhybrid database and miRanda database.

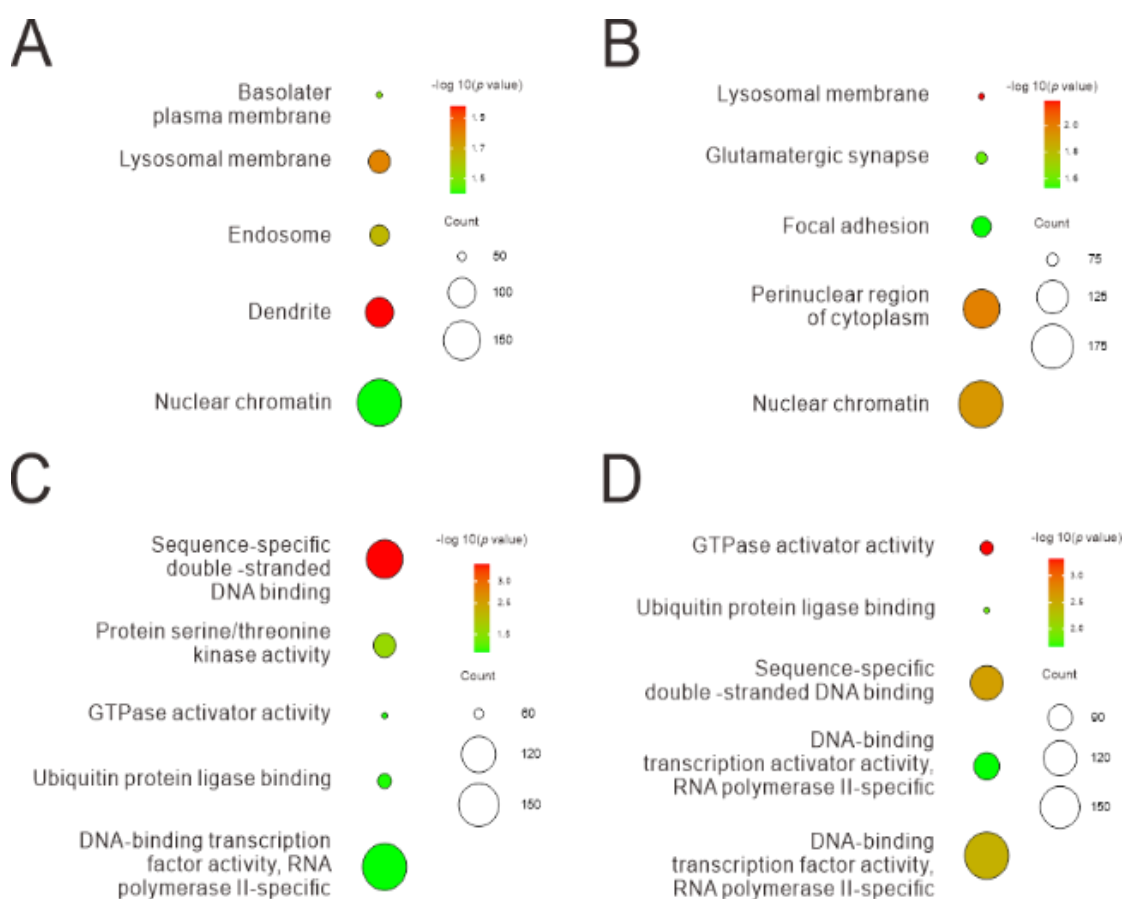
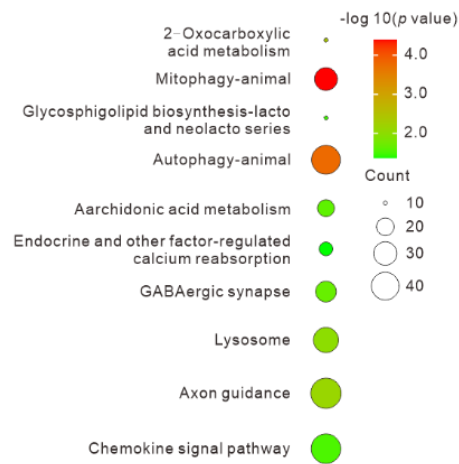


Figure S5. GO Enrichment analysis of the DE EV-miRNAs. (A) Enrichment analysis for GO-CC (the CAT group vs the Rest group). (B) Enrichment analysis for GO-CC (the HIIT group vs the Rest group). (C) Enrichment analysis for GO-MF (the CAT group vs the Rest group). (D) Enrichment analysis for GO-MF (the HIIT group vs the Rest group).

A



B

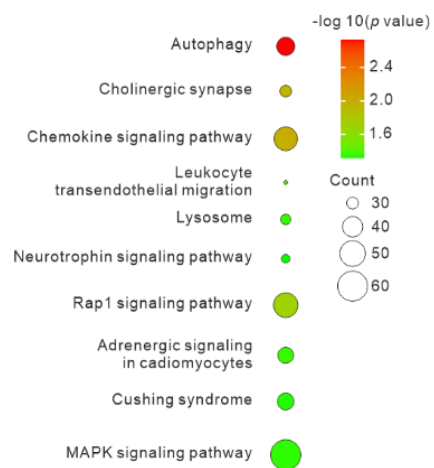


Figure S6. KEGG pathway enrichment analysis of the DE EV-miRNAs. (A) the CAT group vs the Rest group. (B) the HIIT group vs the Rest group.

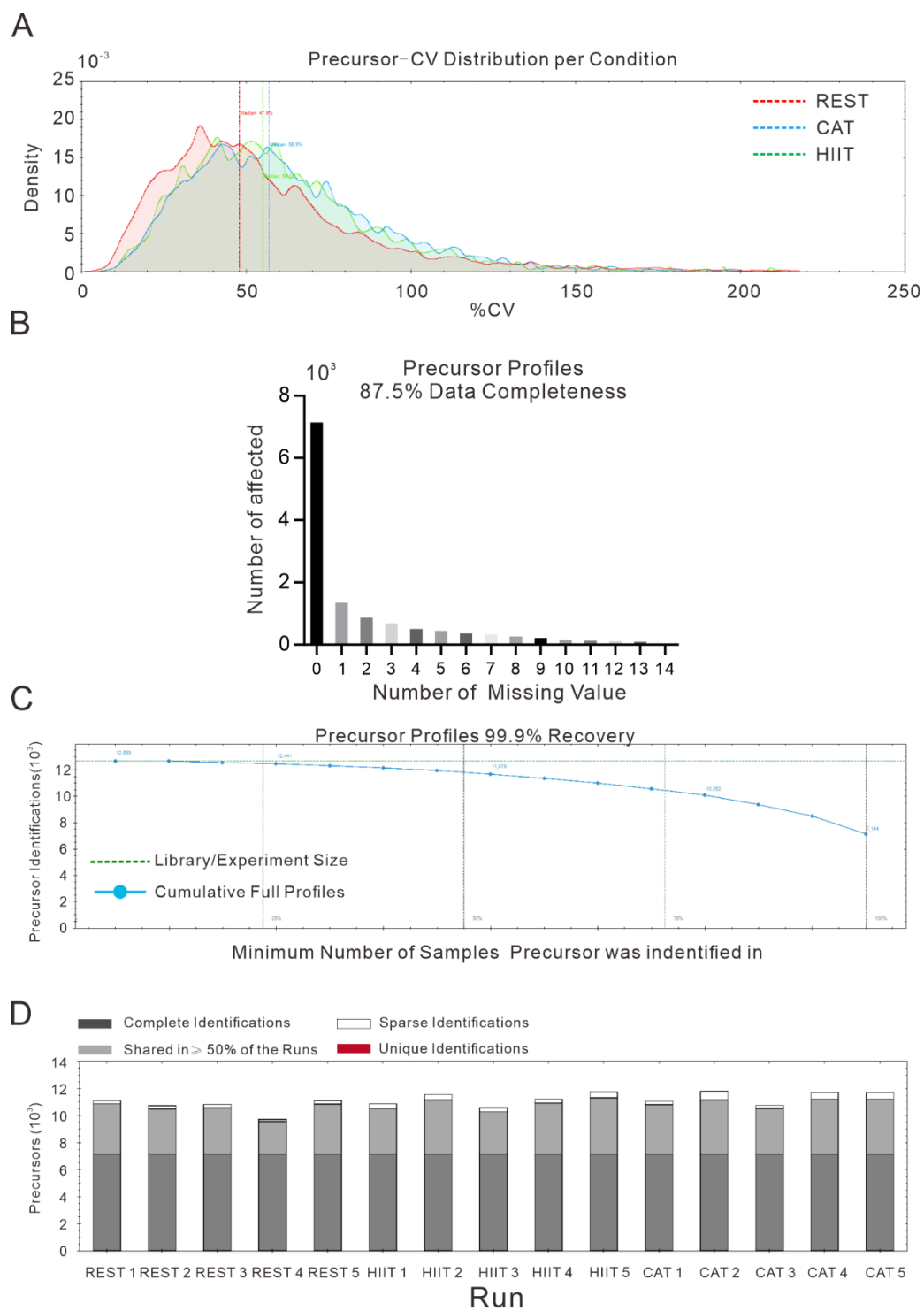


Figure S7. The quality control (QC) assessment of proteomics data. (A) coefficient of variation, (B) data completeness, (C) reproducibility and (D) run identification of proteomics data.

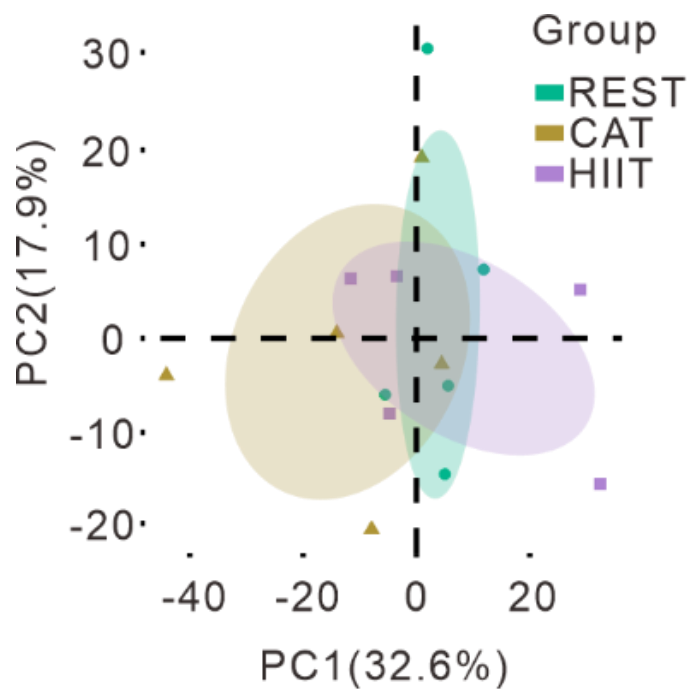


Figure S8. PCA of proteomic profiles in the three study groups.

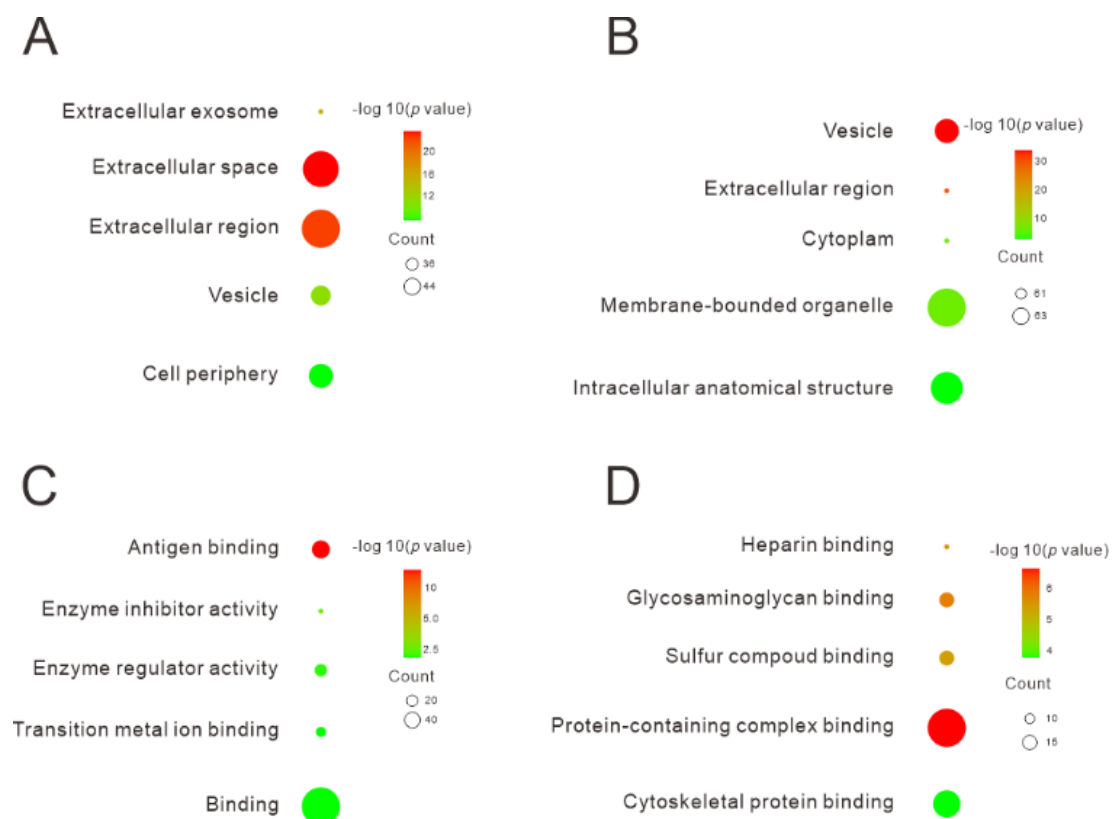
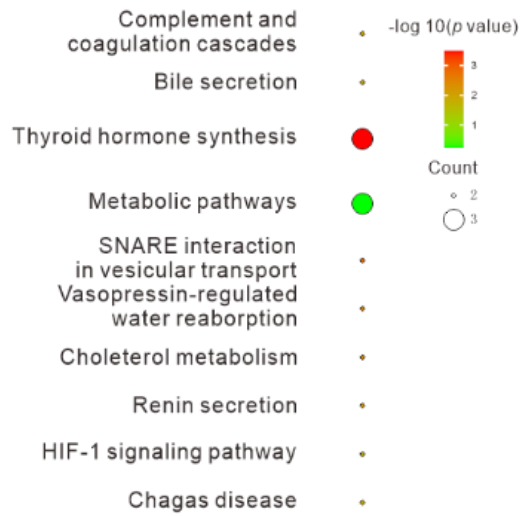


Figure S9. GO Enrichment analysis of the DE EV-proteins. (A) Enrichment analysis for GO-CC (the CAT group vs the Rest group). (B) Enrichment analysis for GO-CC (the HIIT group vs the Rest group). (C) Enrichment analysis for GO-MF (the CAT group vs the Rest group). (D) Enrichment analysis for GO-MF (the HIIT group vs the Rest group).

A



B

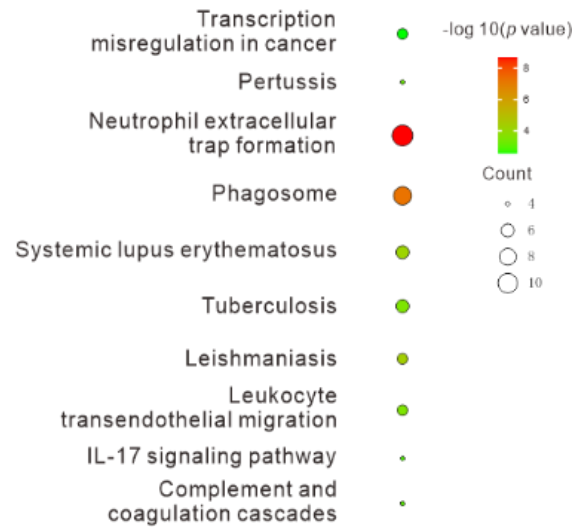


Figure S10. KEGG pathway enrichment analysis of the DE EV-proteins. (A) the CAT group vs the Rest group. (B) the HIIT group vs the Rest group.

Table S1. Clinical characteristics of exercise volunteers.

BMI: body mass index, WHR: waist hip rate, ALT: alanine aminotransferase, AST: aspartate aminotransferase, Crea: creatinine, FBG: fasting blood glucose, TG: triglyceride, HDL-C: high density lipoprotein cholesterol, LDL-C: low density lipoprotein cholesterol, BFP: body fat percentage

n	5
Sex	Male
Age (year)	29.4±1.34
BMI (kg/m ²)	24.92±2.16
WHR (%)	0.884±0.04
ALT (IU/L)	22.8±11.12
AST (IU/L)	21±7.61
Crea (umol/L)	90±6.48
FBG (mmol/L)	4.732±0.43
TG (mmol/L)	1.358±0.51
HDL-C (mmol/L)	1.238±0.13
LDL-C (mmol/L)	2.74±0.396
BFP (%)	24.04±5.18

Table S2. miRNA quantities of serum EV samples.

Samples	RNA concentration (ng/ μ L)	RNA amount (ng)
REST 1	0.39	10.92
REST 2	0.31	8.68
REST 3	0.23	6.44
REST 4	0.41	11.48
REST 5	0.49	13.72
CAT 1	0.40	11.2
CAT 2	0.15	4.2
CAT 3	0.25	7
CAT 4	0.54	15.12
CAT 5	0.44	12.32
HIIT 1	0.32	8.96
HIIT 2	0.26	7.28
HIIT 3	0.21	5.88
HIIT 4	0.50	14
HIIT 5	0.32	8.96

Table S3. The unique and overlapping GO terms of CAT group and HIIT group.

CAT	Common	HIIT
Regulation of triglyceride metabolic process		Glycerophospholipid metabolic process
Cholesterol metabolic process		Positive regulation of insulin secretion
Cardiac conduction		Positive regulation of autophagy
Renal water homeostasis		Actin cytoskeleton organization
Neural tube development		Homophilic cell adhesion via plasma membrane adhesion molecules
Cellular response to mechanical stimulus		Intracellular protein transport
Cell volume homeostasis		Actin filament organization
Cation transport		Adenylate cyclase-modulating G protein-coupled receptor signaling pathway
Protein phosphorylation		Regulation of cell shape
Transmembrane receptor protein tyrosine kinase signaling pathway	Autophagy	Protein maturation
Signal transduction	Macroautophagy	Negative regulation of transcription by RNA polymerase II
Cellular response to peptide	Negative regulation of cell population proliferation	Regulation of nucleic acid-templated transcription
Cellular ion homeostasis	Positive regulation of cell differentiation	Response to cAMP
Cell-cell junction assembly		Positive regulation of MAPK cascade
Positive regulation of calcium ion transport into cytosol		Positive regulation of transcription by RNA polymerase II
Cation transmembrane transport		Regulation of macroautophagy
Hemostasis		Negative regulation of ERK1 and ERK2 cascade
Protein autophosphorylation		Regulation of actin cytoskeleton organization
Positive regulation of cell adhesion		Wnt signaling pathway
		Positive regulation of protein kinase activity
		Regulation of ion transmembrane transport
		Response to hypoxia
		Exocytosis
		Regulation of sodium ion transport
		Intracellular signal transduction

Table S4. List for the online analysis tools.

Name of the analysis tools	Website
Ahybrid	http://bibiserv.techfak.uni-bielefeld.de/rnahybrid
Randa	http://www.microrna.org/
STRING	http://string-db.org
TAM 2.0	http://www.lirmed.com/tam2/
SignalP 5.0	https://services.healthtech.dtu.dk/services/SignalP-5.0/
Hum-mPLOC3	http://www.csbio.sjtu.edu.cn/bioinf/Hum-mPLOC3/
Tissue Atlas	https://ccb-web.cs.uni-saarland.de/tissueatlas2
Human protein atlas	https://www.proteinatlas.org
GO analysis	https://www.geneontology.org/
KEGG analysis	https://www.genome.jp/kegg/