miRNA and mRNA expression analysis reveals potential sex-biased miRNA expression

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Table S1: Statistical analysis based on the data in Figure 6.

miR-143	$Log_2(FC)$	t	P	miR-375	$Log_2(FC)$	t	P
Luad-all (n=41)	-1.36	-16.5429	0.0001	Luad-all (n=41)	2.56	3.1227	0.0033
Ucec-female (n=18)	-2.35	-6.4633	0.0001	Ucec- female (n=18)	3.11	2.0372	0.0575
Prad-male (n=53)	-0.54	-9.7859	0.0001	Prad-male (n=53)	1.92	10.2413	0.0001
Luad-male (n=21)	-1.49	-11.3897	0.0001	Luad-male (n=21)	2.69	2.3472	0.0293
Luad-female (n=20)	-1.27	-12.0082	0.0001	Luad-female (n=20)	2.31	2.6060	0.0174

Table S2: Functional analysis based on deregulated miRNAs and mRNAs.

Pathway	P-value
Regulation of actin cytoskeleton	9.86E-06
Wnt signaling pathway	9.10E-07
Melanogenesis	6.84E-08
MAPK signaling pathway	3.54E-04
Tight junction	7.18E-06
Focal adhesion	6.74E-04
Axon guidance	8.21E-05
Calcium signaling pathway	0.003555
Alzheimer's disease	0.003096
Purine metabolism	0.001786

The table only lists the top 10 enriched pathways.

Table S3: Selected paired tumor and normal samples in the three diseases.

Diseases	Tumor	Normal	Total
LUAD	41	41	82
UCEC	18	18	36
PRAD	53	53	106
LUAD-male	21	21	42
LUAD-female	20	20	40

A

Man-prad

5

woman-luad

1

Man-luad

1

13

0

0

0

0

0

0

1

3

1

1

0

woman-ucec

4

Figure S1 miRNA

B

Man-prad

333

woman-luad

149

Man-luad

42

11

441

38

23

468

89

6

201

103

987

19

120

woman-ucec
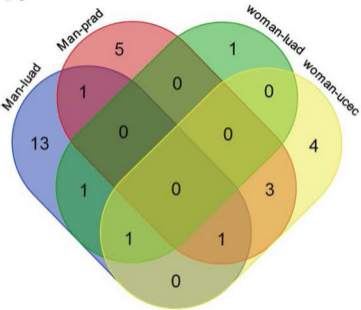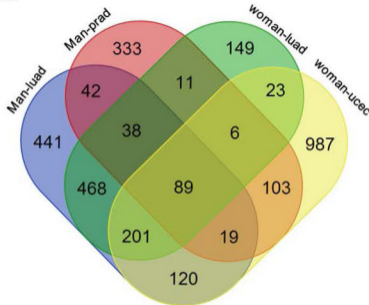
mRNA

Figure S2

TCGA database: mRNA and miRNA sequencing data

homogeneity

PRAD: man | LUAD: man & woman | UCEC: woman

Differentially expressed miRNAs and mRNAs were obtained using DESeq

Analysis at the mRNA level | Analysis at the miRNA level

Sex difference

Integrated analysis of miRNA-mRNA interaction with sex difference