Supplementary Materials

Figure S1 Webpage of each miRNA in BioXpress v3.0

Results of differential expression analysis of human whole miRNAs are shown by both table and figures in BioXpress v3.0. Each miRNA is also mapped to corresponding Ensembl, miRbase, RefSeq, and HGNC identifiers to allow users to search. Cancer types are also mapped to Disease Oncology IDs.

Figure S2 Identification of different cell types within one organ cancer by miRNA

A. Lung cancer - there are 190 significantly differentially expressed miRNAs with Δlog2FC > 1 between LUAD (Lung adenocarcinoma) and LUSC (Lung squamous cell carcinoma), including 50 having the same expression change in these two cell types. The remaining 140 miRNAs with opposite expression patterns are considered to be key factors underlying the differences between LUAD and LUSC. **B-D.** Kidney cancer - Pairwise comparisons were made between KIRP (Kidney renal papillary cell carcinoma) and KIRC (Kidney renal clear cell carcinoma) (**B**), KICH (Kidney Chromophobe) and KIRP (**C**), and KIRC and KICH (**D**). There are 330 significantly differentially expressed miRNAs with Δlog2FC > 1 between any two of the three subtypes. miRNA types and order are preserved across the three comparisons of kidney cancer. From the comparison, the development of KIRC and KIRP may be mechanistically closer with each other, compared to the development of KICH.

Figure S3 Significantly differentially expressed miRNAs that are over-expressed in at least 80 percent of patient or under-expressed per cancer

Log2FC values were used to distinguish the over- or under-expression of miRNAs per patient. Green bars with values larger than 80 percent indicate miRNAs are over-expressed in at least 80% of patient, while red bars with values larger than 80 present miRNAs (green bars lower than 20) that are under-expressed in at least 80% of patient per cancer. In the figure, some cancers have more over-expressed miRNAs than under-expressed ones, while others have the opposite trend. This suggests different cancer types can have different enrichment patterns of

differentially expressed miRNAs, which implies the potential existence of different mechanisms in their occurrence and development.

Figure S4 Survival analysis of three SDEmiRNAs specific to BRCA, hsa-mir-4784, hsa-mir-1262, and hsa-mir-320c-1 by miRpower

A. Kaplan-meier plot of hsa-mir-4784. Patients with under-expressed hsa-mir-4784 show higher survival rate than the ones with over-expressed hsa-mir-4784. Consistence with our result suggests significant over-expression of hsa-mir-4784 may be vital for BRCA development. **B.** Kaplan-meier plot of hsa-mir-1262. **C.** Kaplan-meier plot of hsa-mir-320c-1. Patients with under-expressed hsa-mir-1262 and hsa-mir-320c-1 have lower survival rate compared to those with over-expressed ones. This result also fits our study of the significant under-expression of hsa-mir-1262 and hsa-mir-320c-1.

Table S1 Unique miRNAs with significantly differential expression in one single cancer type of the 14

Table S2 Validation of a subset of 24 out of 90 significantly differentially expressed miRNAs by text mining tool DEXTER

Table S3 Significantly differential expressed miRNAs that are all over-expressed or all under-expressed in more than eight cancer types

Table S4 Tissue-specific targets of each selected miRNA per cancer type

Targets are represented by UniProt Accession Numbers.

Table S5 Significantly differential expressed miRNA in at least eight cancer types and their target counts for each cancer type

Table S6. Selected GO and PANTHER terms involved in miRNAs and their tissue-specific targets. Cancer types are represented by DOIDs (Disease Ontology ID).