

## **Prioritizing candidate disease miRNAs by integrating phenotype associations of multiple diseases with matched miRNA and mRNA expression profiles**

**Chaohan Xu,<sup>a</sup> Yanyan Ping,<sup>a</sup> Xiang Li,<sup>a</sup> Hongying Zhao,<sup>a</sup> Li Wang,<sup>a</sup> Huihui Fan,<sup>a</sup> Yun Xiao,<sup>\*a</sup> and Xia Li<sup>\*a</sup>**

Affiliations:

<sup>a</sup> College of Bioinformatics Science and Technology, Harbin Medical University, Harbin, China.

\*To whom correspondence should be addressed. Yun Xiao, xiaoyun@ems.hrbmu.edu.cn; Xia Li, lixia@hrbmu.edu.cn

Supplementary information

Supplementary Figure S1. The functional enrichment results of the top 50 candidate miRNAs for all cancer types.

Supplementary Figure S2. Evaluation of the importance of disease phenotype similarity.

Supplementary Figure S3. These non-cancer-related miRNAs in the top 20 candidate lists are associated with metabolic diseases in the miR2Disease and HMDD databases.

Supplementary Figure S4. The results of functional enrichment analysis of six miR-17 family members.

Supplementary Table S1. The matched miRNA and mRNA expression data of eleven cancer types.

Supplementary Table S2. The known disease-related miRNAs stored in miR2Disease and HMDD databases.

Supplementary Table S2. The miRNA members in the miR-17 family that occurred in the top 20 miRNAs .