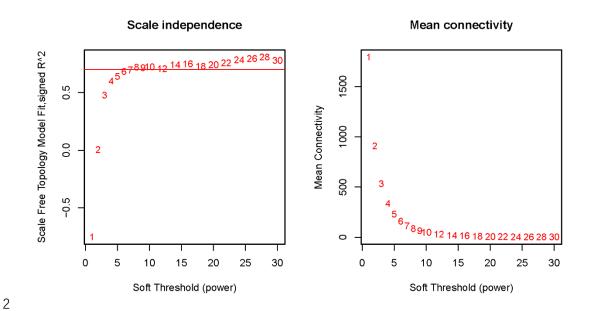
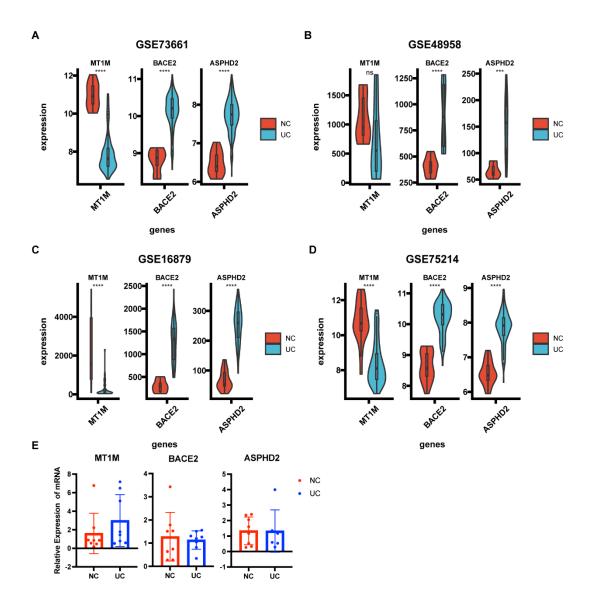
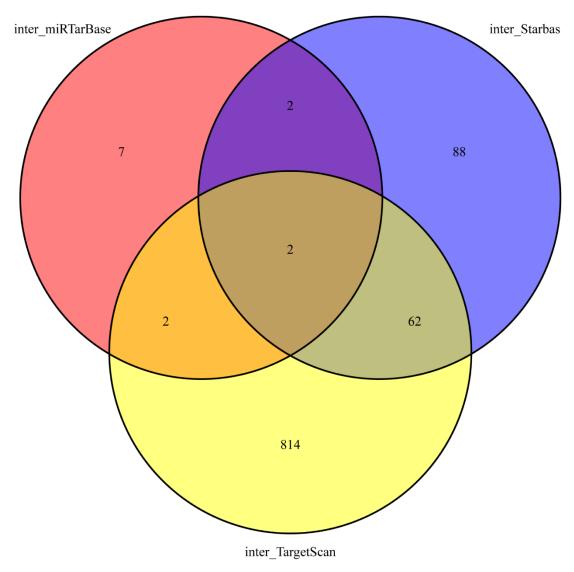
## 1 Supplementary Information



Additional file 1: Figure S1. network topology analysis. Left panel shows scale-free fit index as a function of soft threshold power, while right panel shows mean connectivity.



**Additional file 2: Figure S2.** Identification of the expressions of candidate hub genes. The expressions of MT1M, BACE2, and ASPHD2 in GSE73661 **(A)**, GSE48958 **(B)**, GSE16879 **(C)**, and GSE75214 **(D)**. **(E)** qRT-PCR validation of the MT1M, BACE2, and ASPHD2. ns, no significance; \*\*\* means P < 0.001; \*\*\*\* means P < 0.0001.



**Additional file 3: Figure S3** The Venn diagram depicts the overlap between miRNAs predicted by Starbase, miRTarBase, and TargetScan.