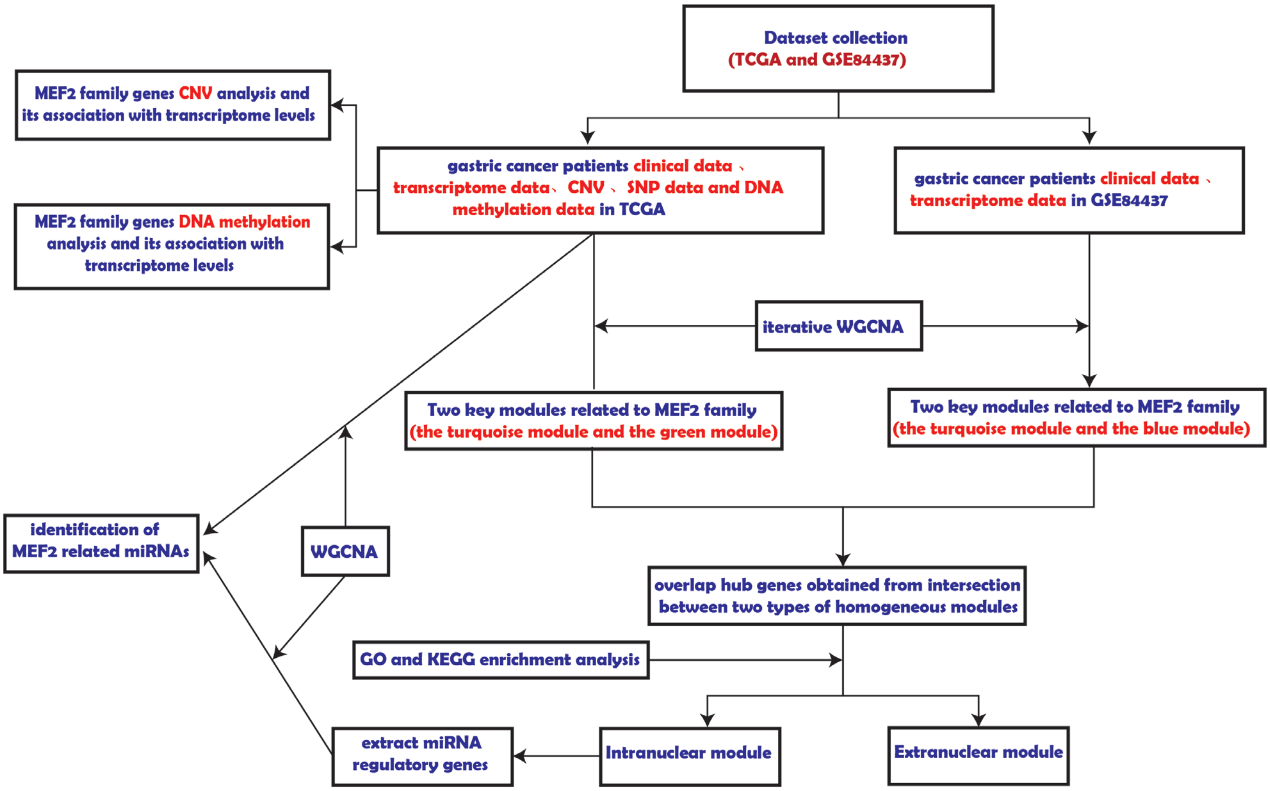

Figure S1 Flowchart.

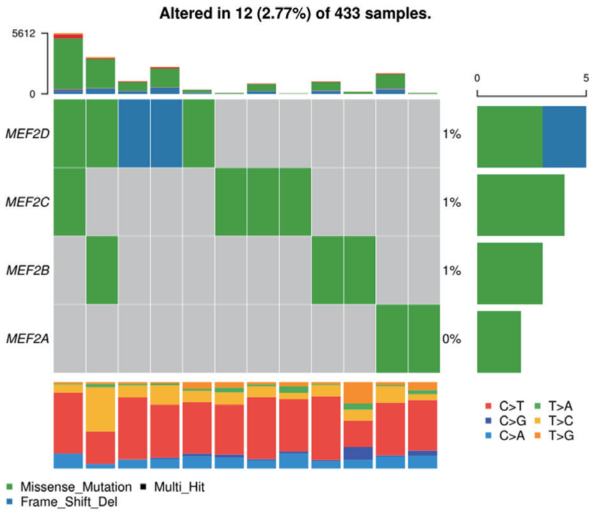

Figure S2 Waterfall showed the SNP of *MEF2* genes.

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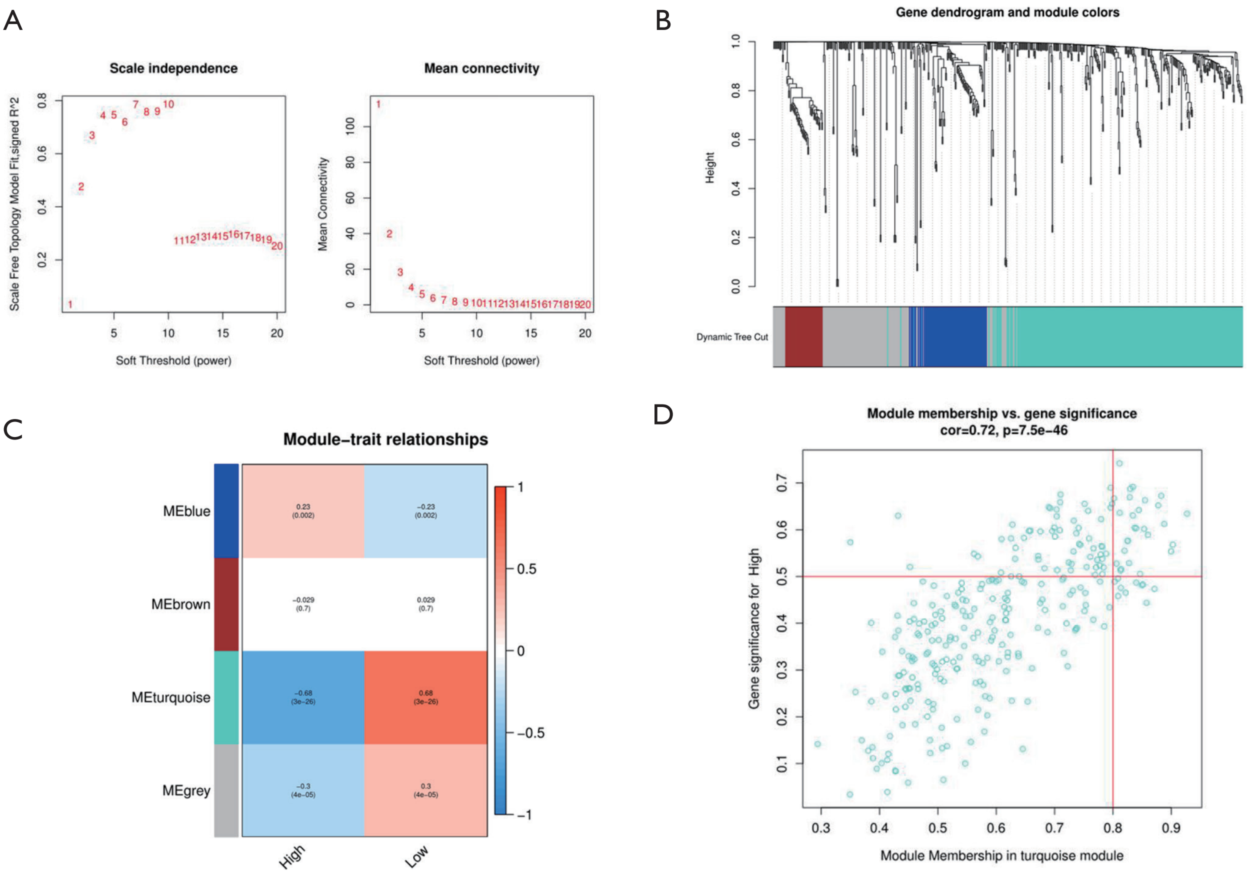

Figure S3 *MEF2* related miRNA module identification using WGCNA. (A) the abscissa is the soft threshold, and the ordinate is the natural distribution topology fitting degree and average connection degree. (B) dynamic tree cutting and module partitioning. (C) Correlation analysis between modules and *MEF2* expression. Red color corresponds to positive correlation, blue color symbol negative correlation. (D) correlation analysis of MM and GS of genes in the turquoise module.

Table S1 Differential expression of 25 hub miRNAs between gastric cancer and normal

miRNA	P value	upregulated or downregulated in tumor (1 = up, 0 = down)
has-mir-106b	<1E-12	1
has-mir-1307	1.62E-12	1
hsa-mir-130b	7.07E-11	1
hsa-mir-141	9.23E-08	1
hsa-mir-15b	1.66E-12	1
hsa-mir-17	1.62E-12	1
hsa-mir-183	1.62E-12	1
hsa-mir-18a	1.62E-12	1
hsa-mir-19a	<1E-12	1
hsa-mir-19b-1	1.62E-12	1
hsa-mir-19b-2	1.19E-14	1
hsa-mir-200c	1.21E-12	1
hsa-mir-20a	1.62E-12	1
hsa-mir-210	3.72E-09	1
hsa-mir-219a-1	2.69E-07	1
hsa-mir-3127	<1E-12	1
hsa-mir-429	1.15E-02	1
hsa-mir-4746	1.62E-12	1
hsa-mir-576	2.08E-09	1
hsa-mir-7-1	3.31E-08	1
hsa-mir-92a-1	<1E-12	1
hsa-mir-92a-2	1.62E-12	1
hsa-mir-93	1.62E-12	1
hsa-mir-942	1.55E-08	1
hsa-mir-96	1.62E-12	1

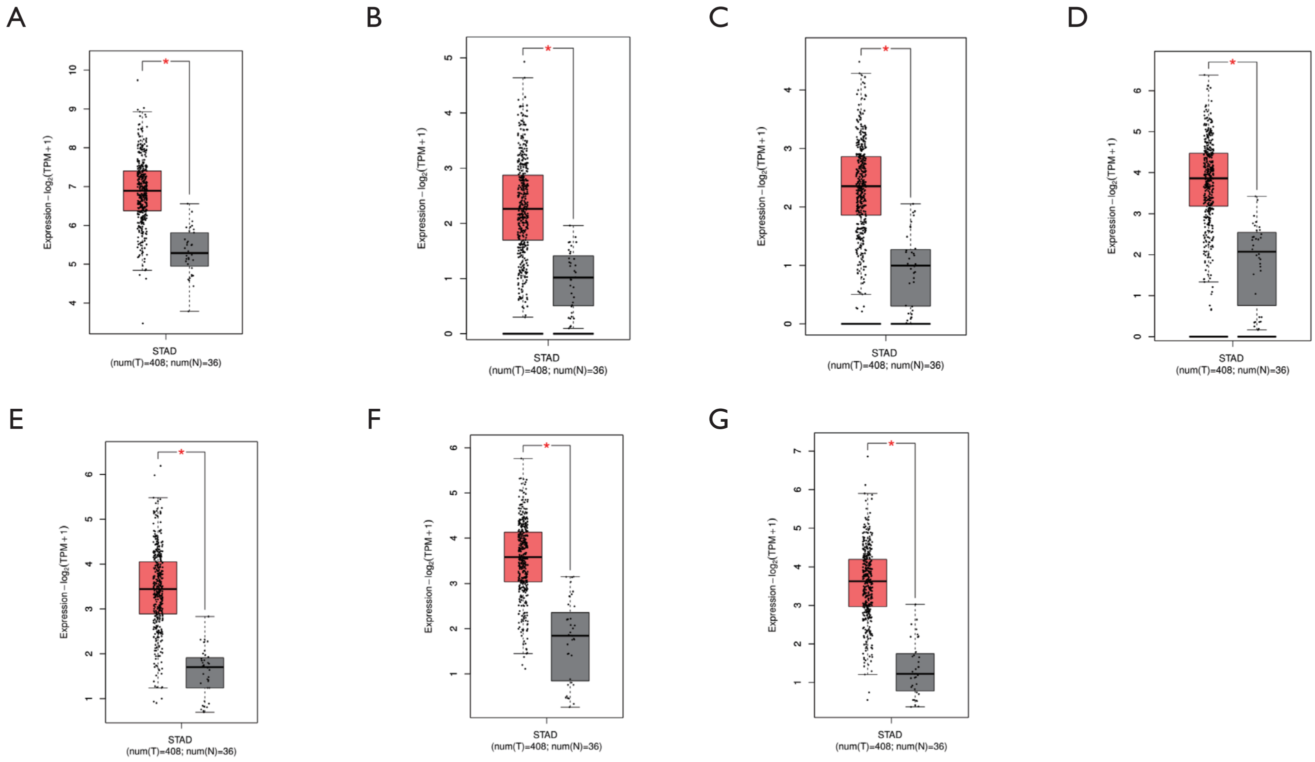

Figure S4 Distribution of expression of 7 miRNA regulatory genes in STAD and normal gastric tissues. (A-G) showed *STMN1*, *CDC25A*, *CDC25C*, *CDCA5*, *E2F1*, *EZH2* and *KIF23*, respectively. P value <0.05 was considered significant. *, P<0.05.

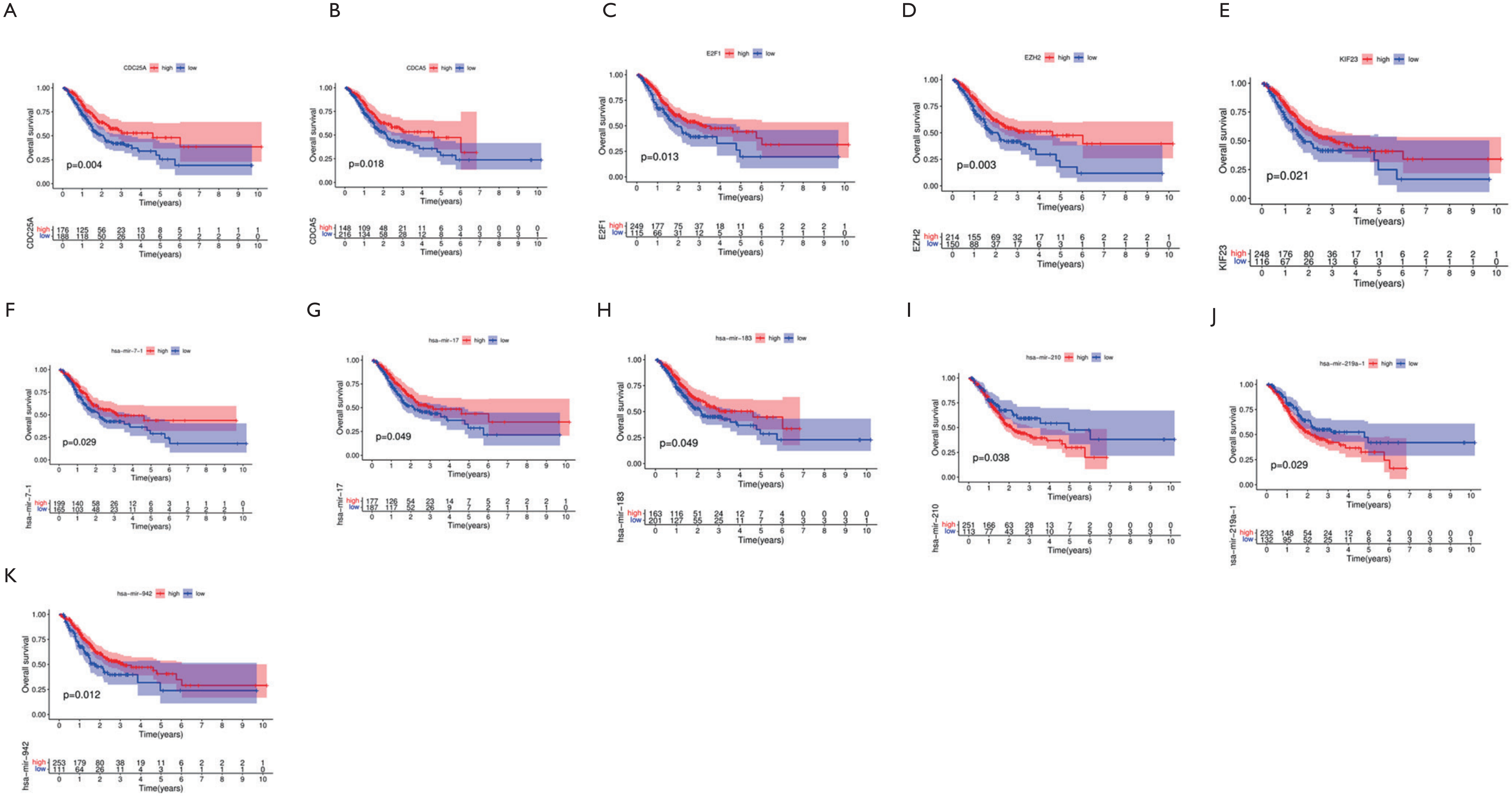

Figure S5 Overall survival analysis of miRNA and miRNA regulatory genes (A-E) KM overall survival curve showed the correlation between prognosis and expression of *CDC25A*, *CDCA5*, *E2F1*, *EZH2*, and *KIF23*, respectively. (F-K) KM overall survival curve showed the correlation between prognosis and expression *has-mir-7-1*, *has-mir-17*, *has-mir-183*, *has-mir-210*, *has-mir-219a-1*, and *has-mir-942*, respectively.

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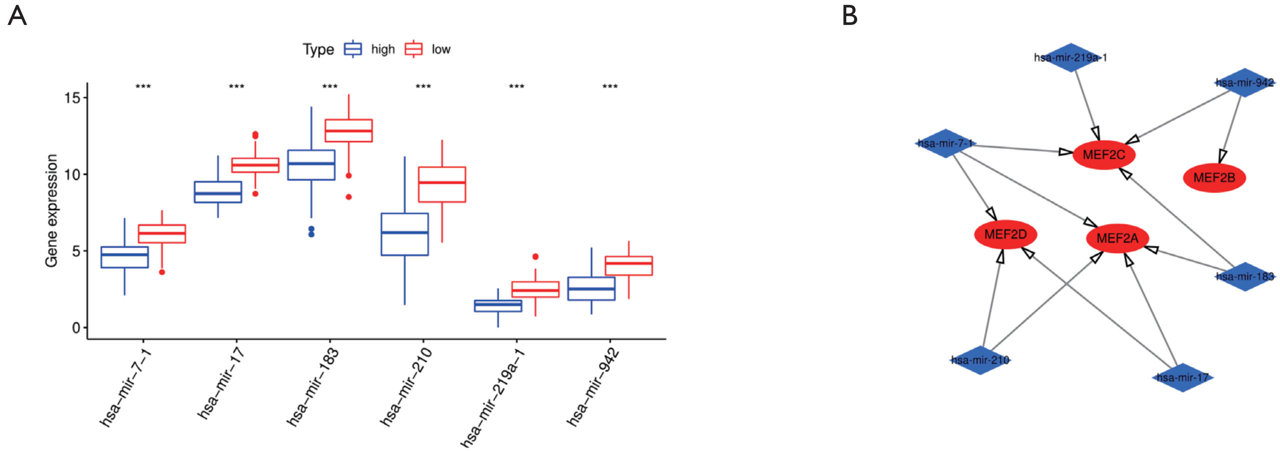

Figure S6 Interaction between *MEF2* family genes and 6 miRNAs. (A) miRNA expression distribution in *MEF2* high and low group. (B) The diagram representing the interaction between *MEF2* genes and its miRNA. P value <0.05 was considered significant. ***, P<0.001.

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