SUPPLEMENTAL MATERIAL

Data S1: The list of identified target genes

The possible target genes of significantly changed miRNAs were predicted by

TargetScan and Miranda software. The gene symbol, align score, energy, miRNA

start, miRNA end, gene start, gene end, miRNA aglin, alignment and gene align are

shown in the excel file.

Data S2: The biological functions indicated by the target genes of differentially

expressed miRNAs

The GO categories were analyzed. GO id, GO name, enrichment, p-value, FDR, gene

id and gene name were shown in the file.

Data S3: The pathway analysis on the miRNAs target genes

The pathways were also analyzed. Path id, path name, path gene count, enrichment,

p-value and FDR were shown in the file.

Data S4: MicroRNA-gene relationship

MicroRNA-gene relationship was described in the file. The enrichment degree of

microRNAs and genes were shown in the file, respectively.