# Supplemental Files

**#1 Supplemental Tables**

There were three supplemental tables containing in this file.

**File name:** Supplemental Table 1.

**Title of data:** Primers Sequence of two miRNAs.

**Description of data:** The primer sequence of the validated miRNA, i.e., mmu-miR-190a-3p, was used for real-time PCR assay.

**File name:** Supplemental Table 2.

**Title of data:** Prediction binding sites for mmu-miR-190a-3p from miRwalk 3.0.

**Description of data:** The data were predicted by using miRwalk 3.0 for obtaining reliable targets for mmu-miR-190a-3p. The parameters for target prediction in the miRwalk3.0 used as following: 1) Binding over than 0.9; 2) Energy less than -16; and 3) Accessibility less than 0.05.

**File name:** Supplemental Table 3.

**Title of data:** Genes and miRNAs involved in red module.

**Description of data:** In order to provide a comprehensive expression pattern among the mRNAs and miRNAs and detect the interaction of the transcripts, we performed our co-expression analysis by combined the mRNA and miRNA dataset together. First, we constructed a weighted network according to the gene pair correlations among all the mRNAs and miRNAs; second, by using the default parameters to assess the network interconnection, 25 specific modules were hierarchically clustered. These module sizes were from 50 to 17,500 genes. A total of 314 genes and 5 miRNAs were grouped in the red module as shown in Supplemental Table 3.

**#2 Supplemental Figures**

There were four supplemental figures containing in this file.

**File name:** Supplemental Figure 1.

**Title of data:** The detailed time line of the euthanization of study animals.

**Description of data:** According to the protocol of our research work, all mice were euthanized before we were prepared to obtain hippocampal tissue. When those mice scheduled for obtaining the hippocampal tissue, one by one, they were put into an anesthetic introduction chamber and were anesthetized with isoflurane into a deeper level. The introduction chamber was kept clean to minimize the odor that might distress animals subsequently anesthetized. A rodent anesthesia machine were used (Model: ABM09-002, Reward, Shenzhen) and the anesthetic used was isoflurane. The concentration of the vaporizer was set at 3% and the oxygen flow rate was set at 3L/min during anesthesia. All mice were deeply anesthetized based on following signs: the slowed rising and falling of chest, no respond to toe pinch, and corneal reflex disappeared. Then, the mice were decapitated by using a guillotine in a uniformly instantaneous manner. The brain was instantly dissected on ice, and the hippocampal tissue was obtained and put into liquid nitrogen. All the mice were decapitated 24h after operation.

**File name:** Supplemental Figure 2.

**Title of data:** Volcano plot of miRNA expression in replication cohort.

**Description of data:** This dataset (GSE95070) was downloaded from the NCBI GEO database. For replication the findings of our own data, we performed a replication analysis with the same procedure by using this miRNA microarray dataset. In this miRNAs expression profile, we detected 85 significantly up-regulation miRNAs and 103 significantly down-regulation miRNAs ($p< 0.05$).

**File name:** Supplemental Figure 3.

**Title of data:** The results of qRT-PCR for technical replication.

**Description of data:** Expression level of the most significantly aberrant miRNA, mmu-miR-190a-3p, was validated by using real-time PCR assay. Reverse transcription reaction was performed with M-MLV Reverse Transcriptase kit (Takara Code: D2639A) based on the manufacturers' protocol. Real-time PCR was performed with SYBR Premix Ex Taq kit (Takara Code: DRR041A). The miRNA expression level was evaluated relative to the expression of U6 of the $2^{-\Delta\Delta Ct}$.

**File name:** Supplemental Figure 4.

**Title of data:** WGCNA module-based analysis for genes and miRNAs expression data of GSE73507.

**Description of data:** The genes and miRNAs expression data of GSE73507 were acquired from

GEO database (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE73507). By excluding the expression data from other brain regions and mutant mice, we only downloaded the mRNAs and miRNAs expression data from hippocampus tissue of wild type mice for our analysis (n = 24). A total of 16,425 mRNAs and 1,057 miRNAs were correctly mapped onto the mouse genome. Threshold for filtering out genes expressed at low levels was set to greater than 1 of the average fpkm. After the filtering process, 13,241 mRNAs and 546 miRNAs were included for WGCNA analysis.

**File name:** Supplemental Figure 5.

**Title of data:** KEGG pathway enrichment analyses for mmu-miR-190a-3p highly related genes in red module.

**Description of data:** ClueGO (v. 2.3.4), a plug-in software of Cytoscape, was used to decipher the pathways network and determine their biological functions for the candidate genes. The potential biological functions of each gene set were annotated using the pathway profiles of Kyoto Encyclopedia of Genes and Genomes (KEGG). We refined 169 genes from red module with a highly connected with mmu-miR-190a-3p (Figure 2b). To determine whether these highly correlated genes have critical roles in psychiatric disorders, we performed similar pathway-based enrichment analysis of these 169 genes and found several significant enriched pathways, which was in line with the results based on all genes in red module.