

Figure S1. Normalized data of GSE67882 and GSE69580. GSE67882 data (A) before and (B) following normalization. GSE69580 data (C) before and (D) following normalization.

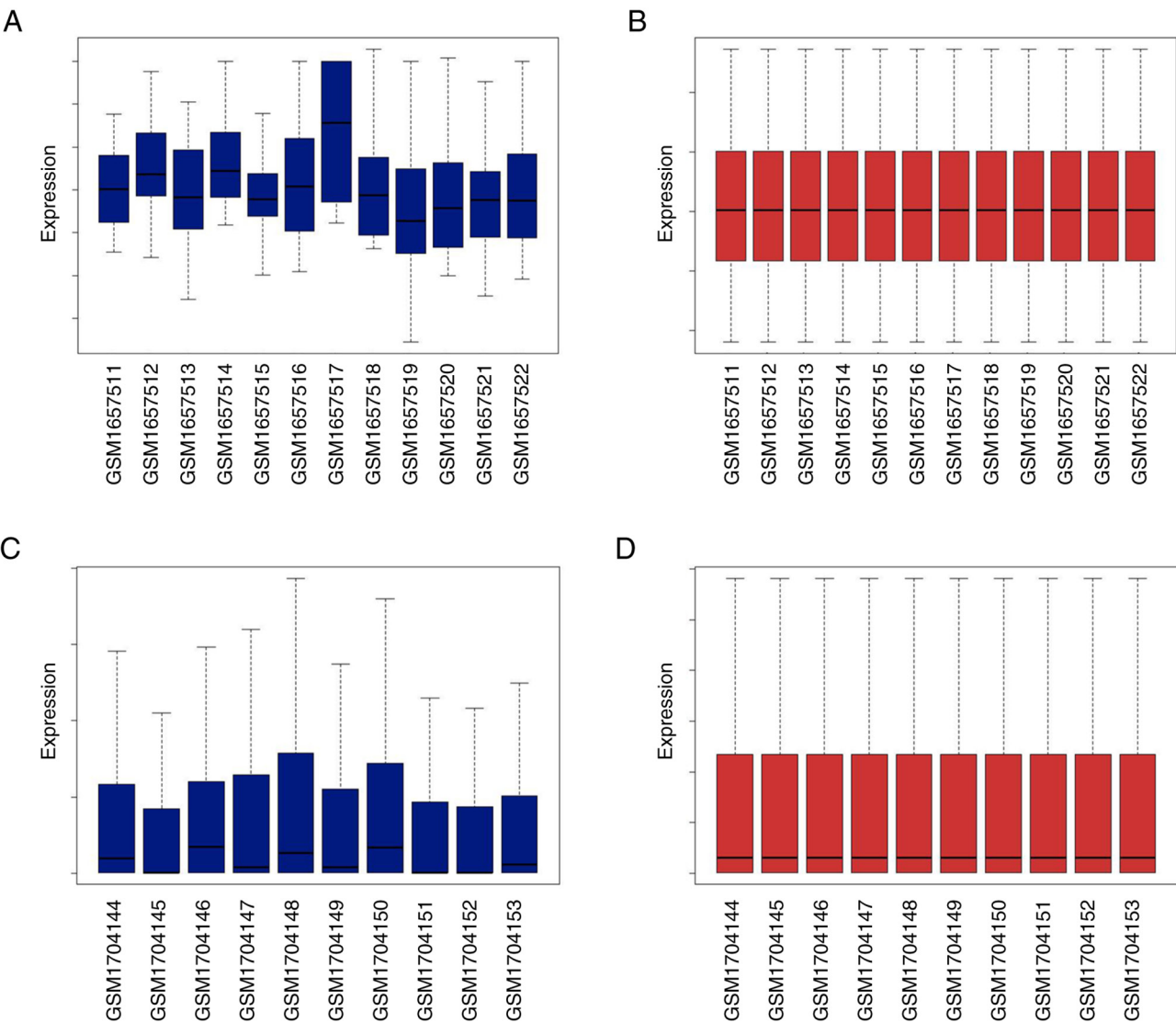


Figure S2. Volcano plots of GSE67882 and GSE69580 data. Volcano plot of (A) GSE67882 and (B) GSE69580 data. The candidate differentially expressed microRNAs were defined as fold-change >2 and $P < 0.05$.

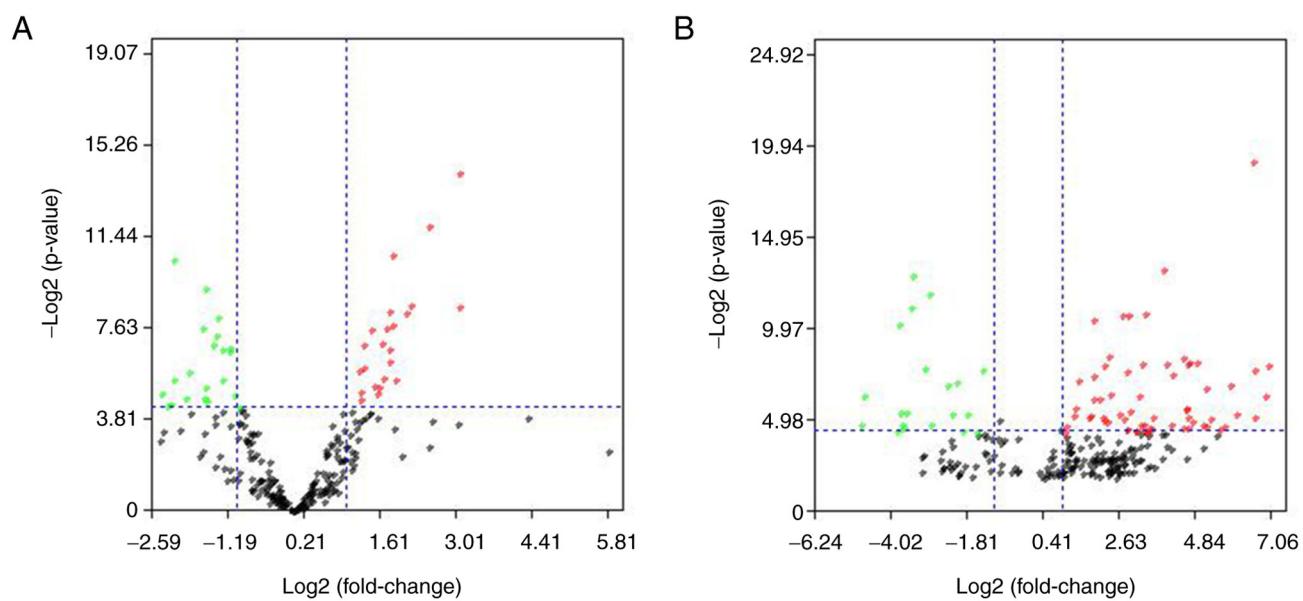
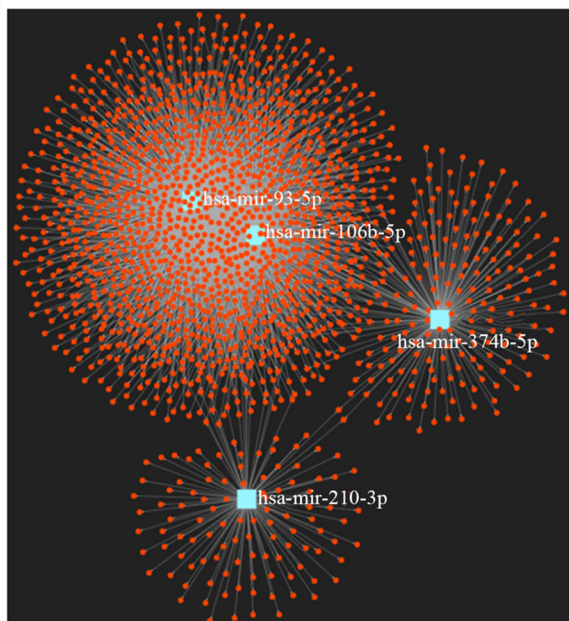


Figure S3. miRNet prediction of potential target genes of DE-miRNAs in HBV-related HCC. (A) Four up- and (B) one downregulated DE-miRNAs and corresponding predicted target genes. Certain genes were simultaneously regulated by several miRNAs.

A



B

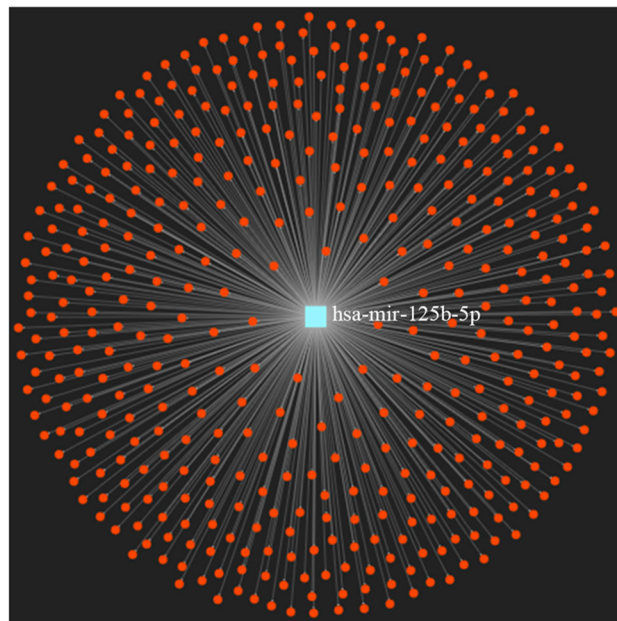


Figure S4. Expression levels of seven differentially expressed microRNA target genes were dysregulated in UALCAN database. Differential expression levels of (A) Cyclin D1, (B) MYC, (C) E2F1 (E2F Transcription Factor 1), (D) E2F2 (E2F Transcription Factor 2), (E) E2F3 (E2F Transcription Factor 3), (F) GRB2 (Growth Factor Receptor Bound Protein 2) and (G) CCNE1 (Cyclin E1) in tumor and normal tissue according to ethnicity. ns, not significant.

