

Figure S1 GO annotation (A-C) and KEGG pathway enrichment analyses (D) for the target genes of the top three most down-regulated DE-miRNAs. (A) BP, (B) CC, (C) MF, and (D) KEGG enriched pathways. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; DE-miRNAs, differentially expressed microRNAs; BP, biological process; CC, cellular component; MF, molecular function.

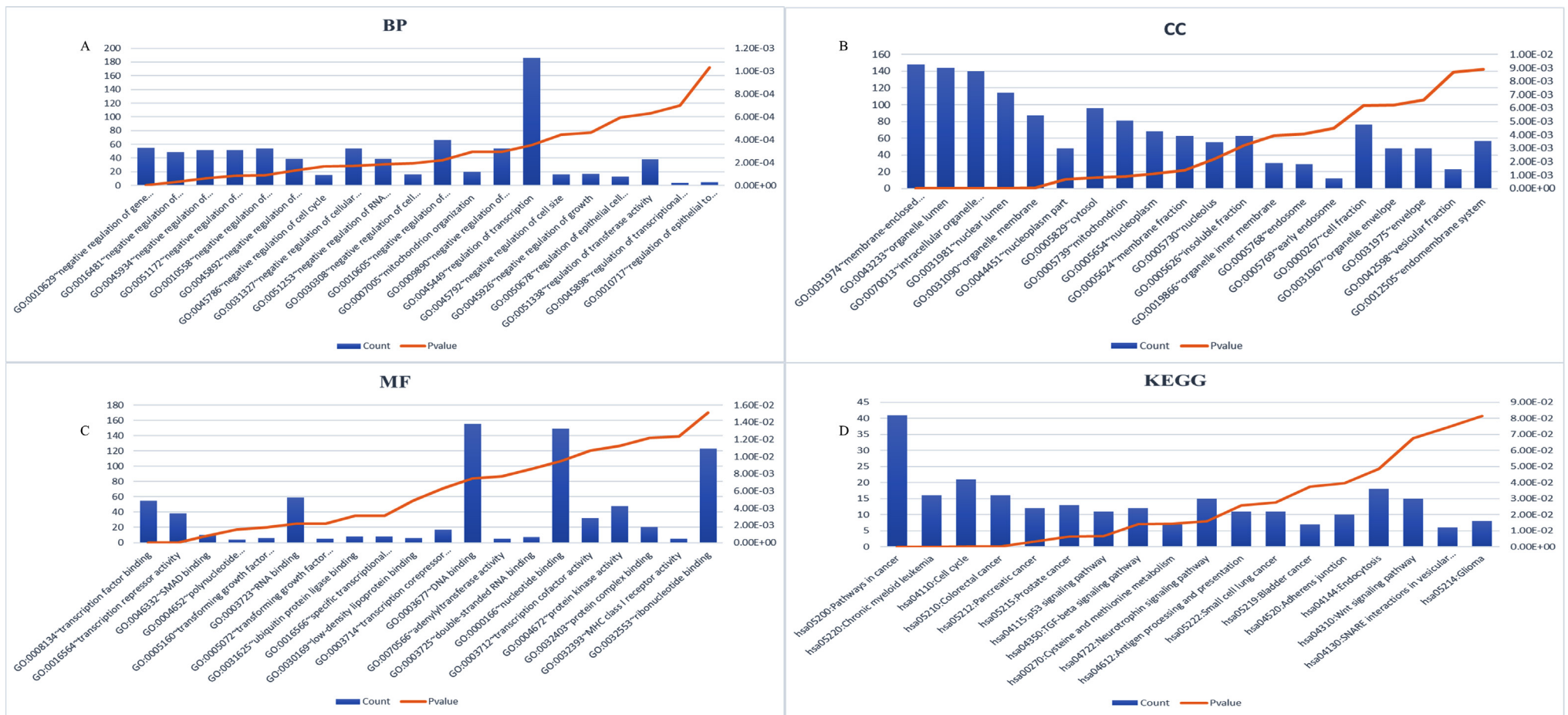


Figure S2 GO annotation (A-C) and KEGG pathway enrichment analyses (D) for the target genes of the top three most up-regulated DE-miRNAs. (A) BP, (B) CC, (C) MF, and (D) KEGG enriched pathways. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; DE-miRNAs, differentially expressed microRNAs; BP, biological process; CC, cellular component; MF, molecular function.

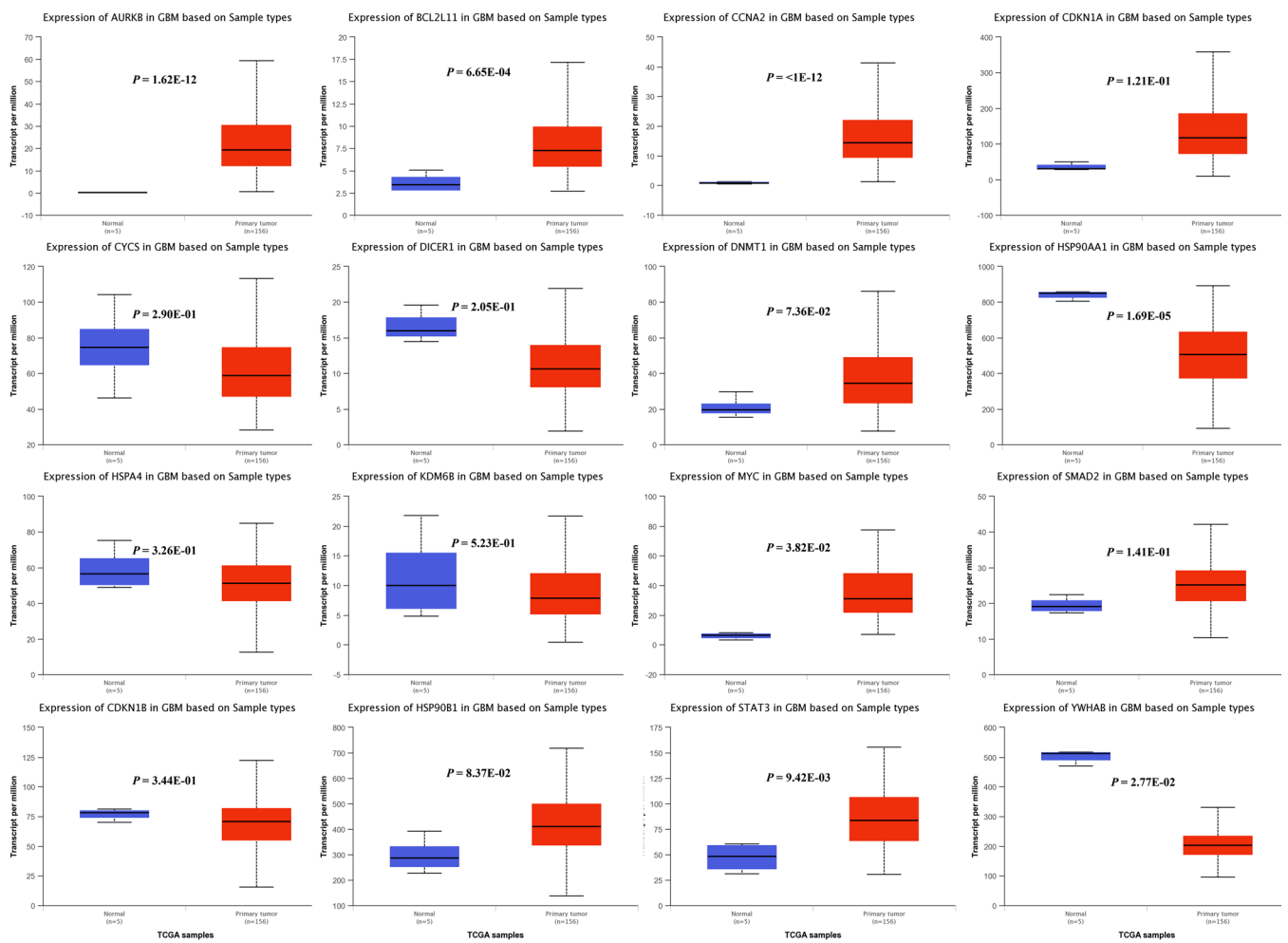


Figure S3 The expression levels of hub genes of miR-148a-3p in the UALCAN database. UALCAN, University of Alabama Cancer.

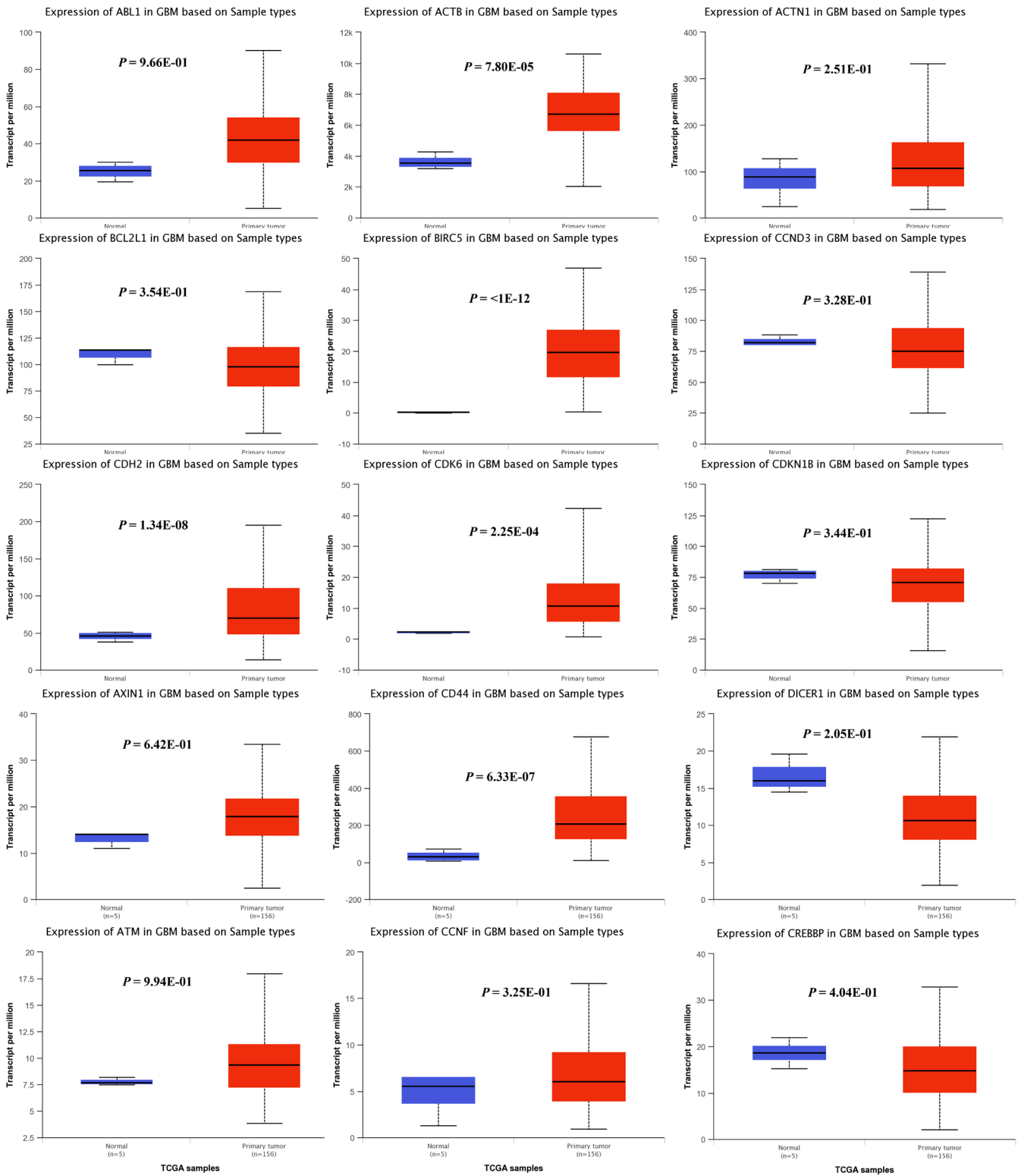


Figure S4 The expression levels of hub genes of miR-218-5p in the UALCAN database. UALCAN, University of Alabama Cancer.