

Figure S1. Top 10,000 miRNA-mRNA interactions. The red circles represent the miRNAs and the blue circles represent the mRNAs. miRNAs with >100 nodes were labeled. miRNA/miR, microRNA.

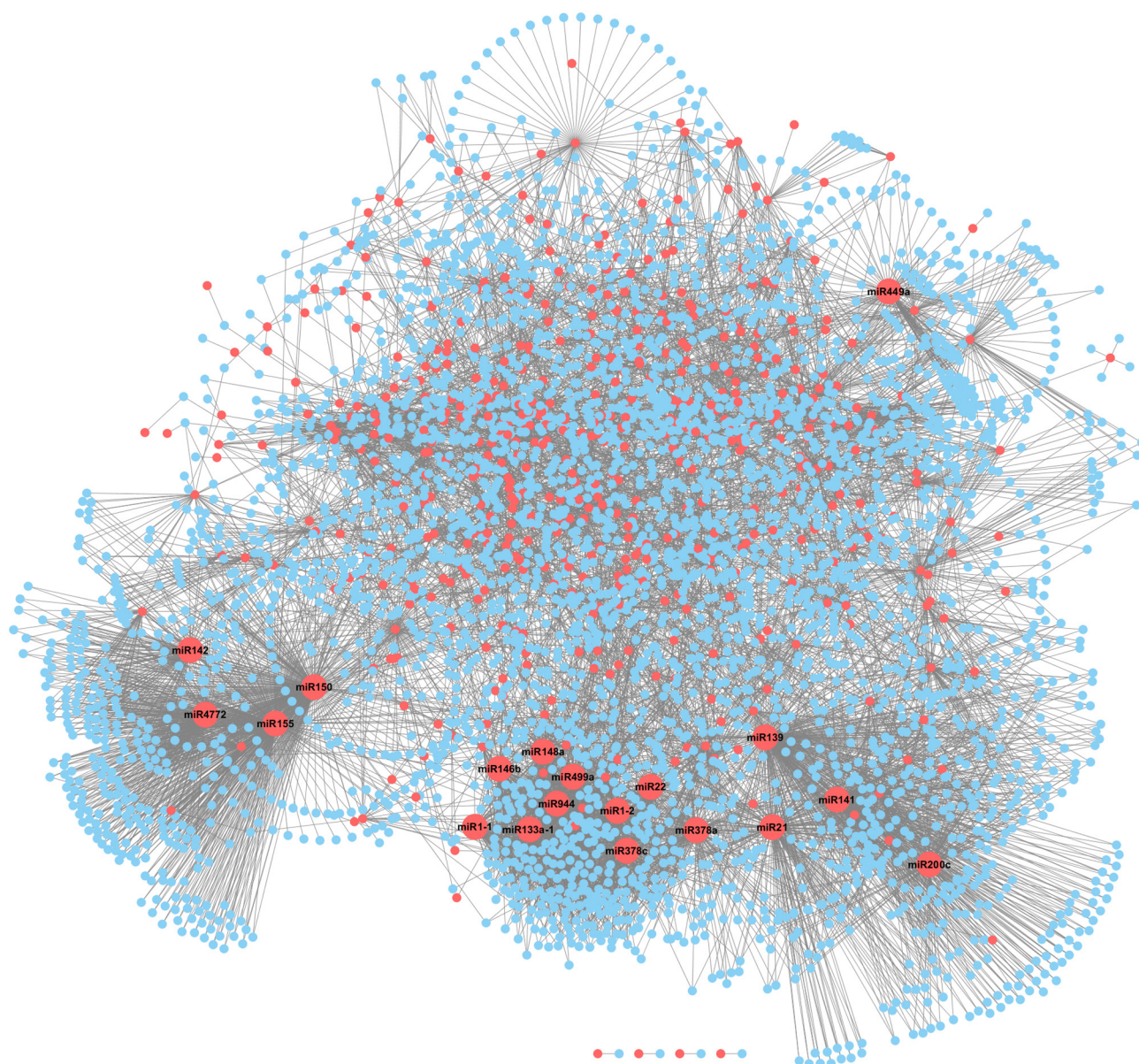


Figure S2. Linear correlation between miR150 and its target genes in the validation dataset of GSE22220. The figure presents the 5 predicted target genes (BTLA, EGR2, EREG, LTBP2 and MYB). The correlation coefficients and P-values were calculated by unary linear model. miR, microRNA.

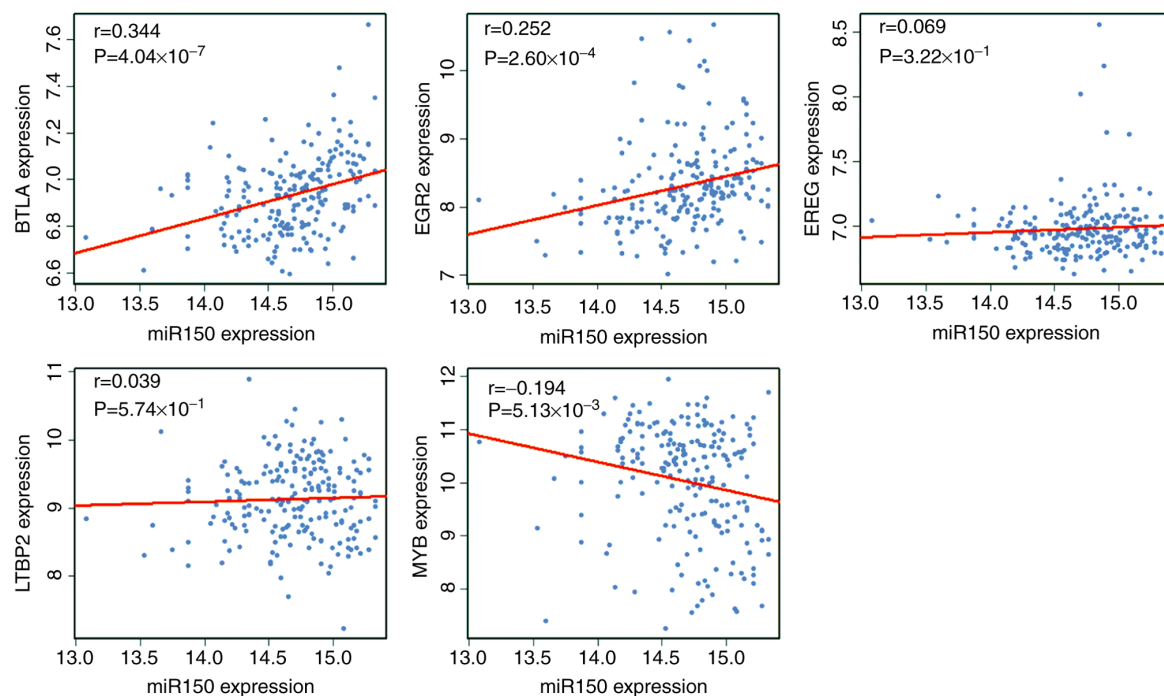


Figure S3. Enriched Kyoto Encyclopedia of Genes and Genomes pathways in the validation dataset of GSE22220. Since there were no controls in GSE22220, the enriched pathways were analyzed in the low-miR150 group compared with the high-miR150 group. miR, microRNA.

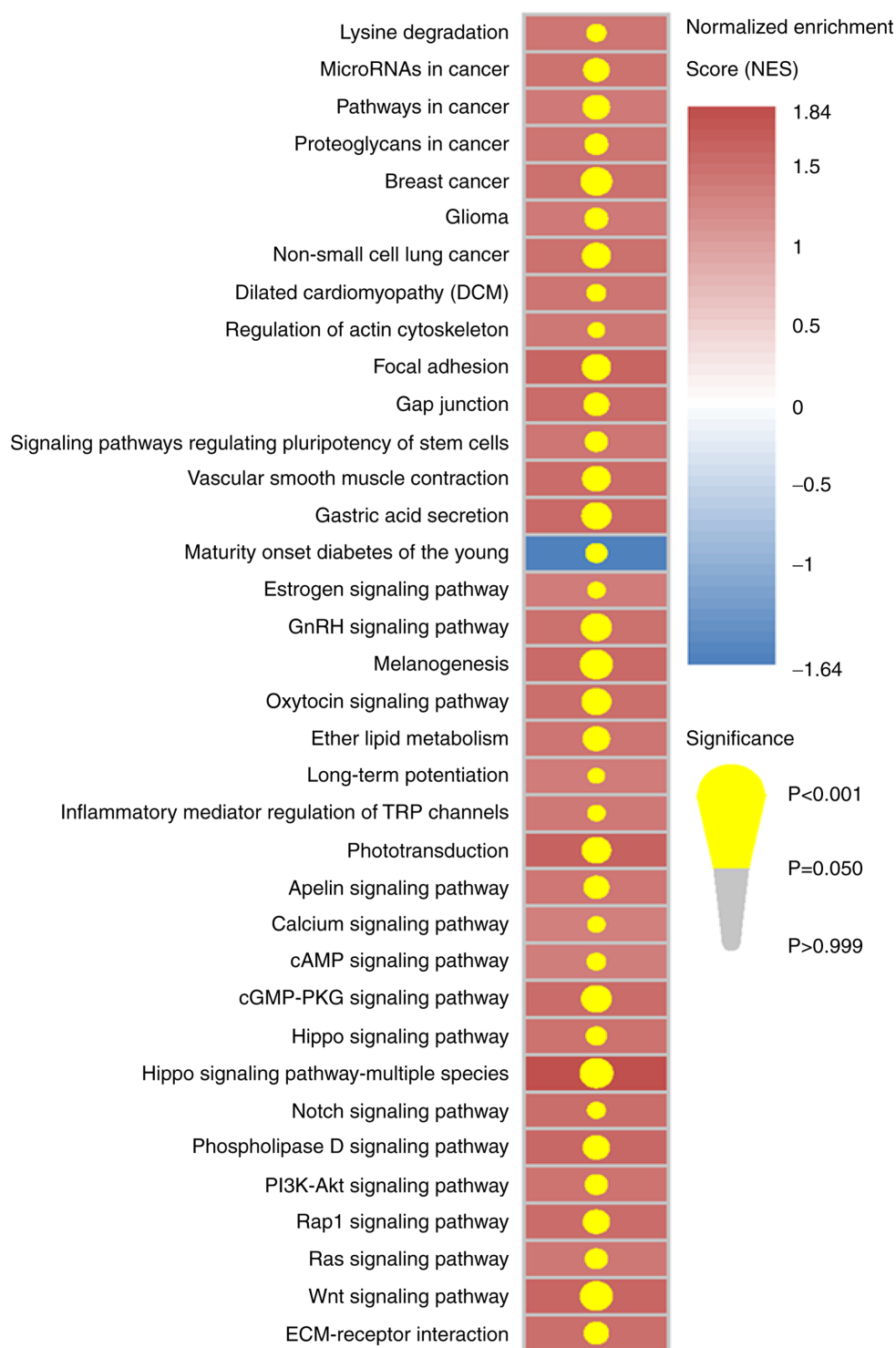


Figure S4. Validation of miR150 on patient prognosis. Overall survival was analyzed using the dataset of GSE40267, while disease-free survival using the dataset of GSE22220. (A) Effect of miR150 on patient overall survival. Effect of miR150 on patient overall survival in (B) high-miR150 group and (C) low-miR150 group. (D) Effect of miR150 on patient disease-free survival. Effect of miR150 on patient disease-free survival in (E) high-miR150 group and (F) low-miR150 group. miR, microRNA; HR, hazard ratio.

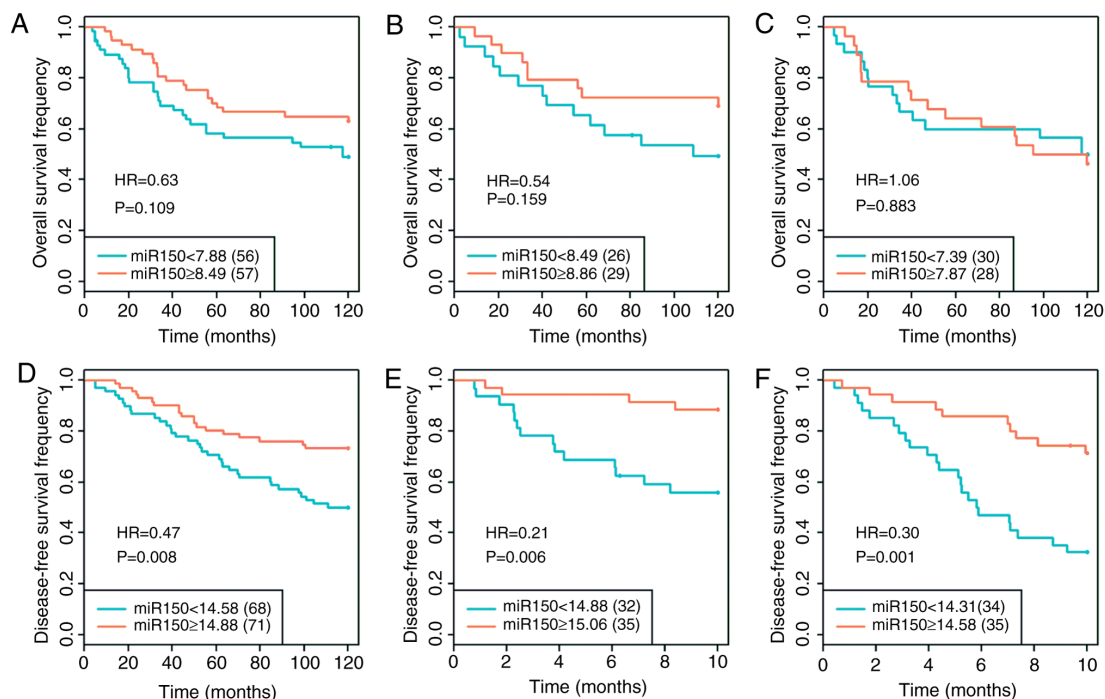


Figure S5. Reverse transcription-quantitative PCR results to analyze the mRNA expression levels of BTLA when miR150 was overexpressed or knocked down. (A) BTLA expression was increased when miR150 was overexpressed. (B) BTLA expression was decreased when miR150 expression was knocked down. *** $P \leq 0.001$. BTLA, B and T lymphocyte attenuator; NC, negative control; miR, microRNA.

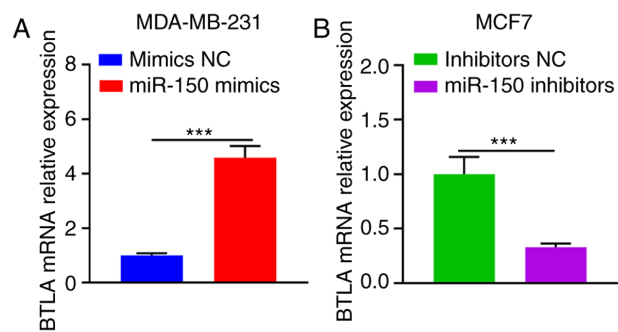


Figure S6. MCF7 cells were transfected with si-NC or si-BTLA, and the expression levels of BTLA were detected via reverse transcription-quantitative PCR. ^{**} $P \leq 0.01$. BTLA, B and T lymphocyte attenuator; si, small interfering; NC, negative control.

