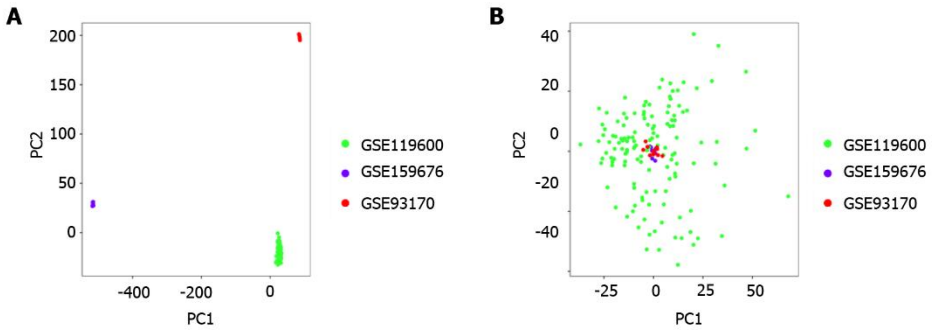
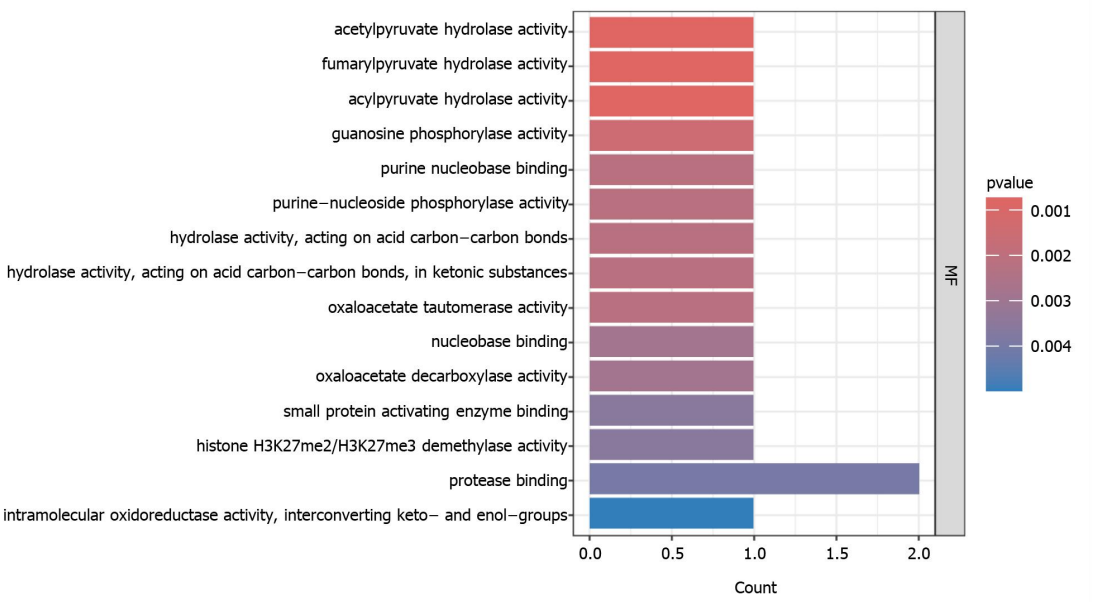
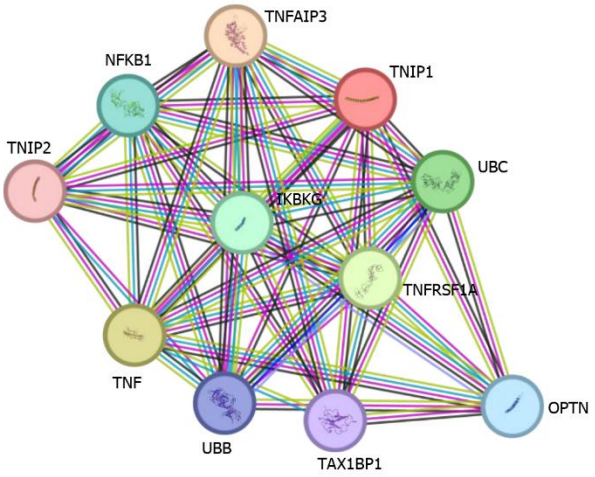


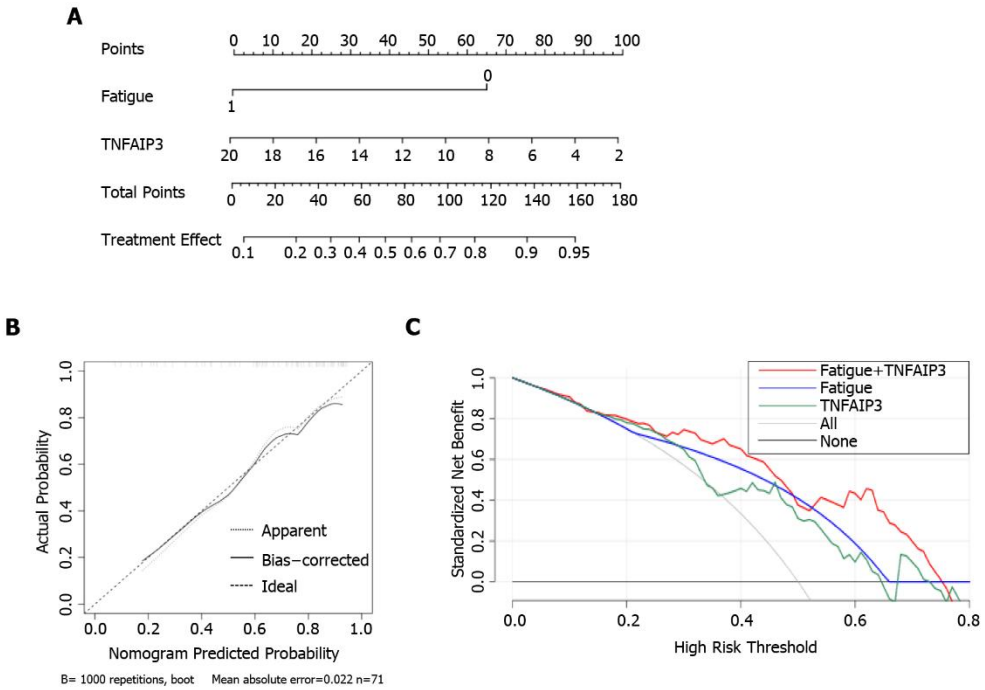
Supplementary Figure 1 Principal visualized component analysis of the three datasets batch correction. A: Principal visualized component analysis of the three datasets before batch correction; B: Principal visualized component analysis of the three datasets after batch correction.



Supplementary Figure 2 Gene Ontology enrichment analysis of molecular functions for the 13 shared DEGs. Significantly enriched molecular functions are displayed, with protease binding highlighted as the most relevant activity. TNFAIP3 and SUMO1 were specifically enriched in protease binding, supporting their potential role in protease interaction pathways.



Supplementary Figure 3 Protein-protein interaction network of TNFAIP3.



Supplementary Figure 4 Construction and validation of the nomogram predictive model. A: Nomogram for predicting the probability of non-response to UDCA in patients with PBC; B: Calibration curve for the model; C: Decision curve analysis evaluating the clinical utility of the nomogram model.

Supplementary Table 1 Top 5 enriched biological processes associated with TNFAIP3

GO-term	Description	Count in network	Strength	Signal	False discovery rate
GO:0043122	Regulation of I-kappaB kinase/NF-kappaB signaling	9 of 255	1.8	3.91	1.02e-11
GO:0033209	Tumor necrosis factor-mediated signaling pathway	5 of 56	2.2	3.01	8.58e-07
GO:0002221	Pattern recognition receptor signaling pathway	5 of 101	1.95	2.45	5.78e-06
GO:0043123	Positive regulation of I-kappaB kinase/NF-kappaB signaling	6 of 191	1.75	2.38	2.14e-06
GO:0002224	Toll-like receptor signaling pathway	4 of 61	2.07	2.22	3.42e-05