

Figure S1 Visualization of dimensional reduction data with random initialization and 5000 iterations (classes 0: non-pCR, 1: pCR). pCR, pathologic complete response.

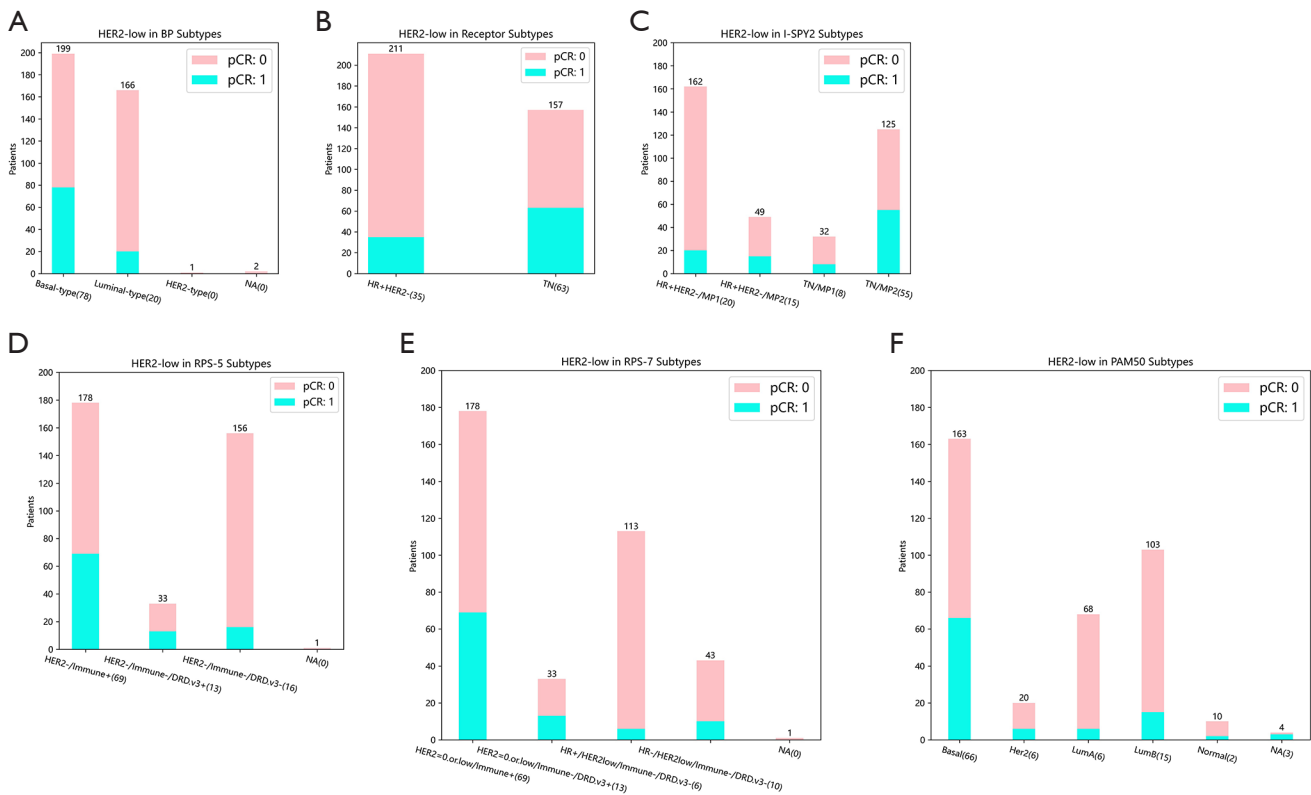


Figure S2 The pCR distribution of HER2-low BC patients in I-SPY2 trial. Subtypes divided by (A) Blueprint, (B) Hormone Receptor, (C) I-SPY2, (D) RPS-5, (E) RPS-7 and (F) PAM50. pCR, pathologic complete response; HER2, human epidermal growth factor receptor 2; BC, breast cancer.

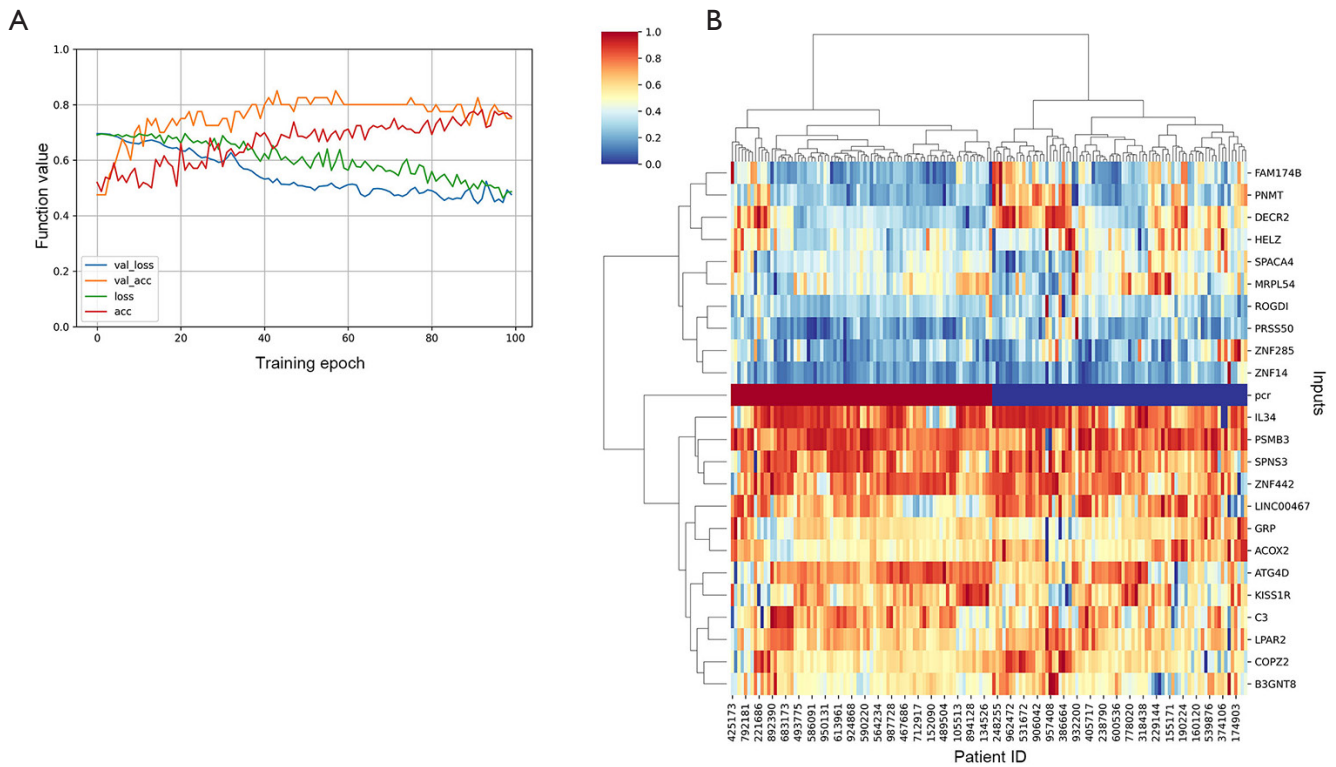


Figure S3 Visualization of training and integral gradients based on FCNN. (A) Process of FCNN model training (stop training when the val_loss no longer descent. Lines color meaning: red-training_accuracy, green-training_loss, orange-validation_accuracy, blue-validation_loss). (B) Heatmap of the normalized attribution values with Ward's unsupervised hierarchical clustering (bottom: patient ID, right column: selective significant features for modeling). FCCN, fully connected neural network.

Table S1 Inputs of the multi-omics model

Type	Number	Inputs
Biomarkers (pathological)	23	ICS5_score, Chemokine12_score, Module5_TcellBcell_score, STAT1_sig, Module3_IFN_score, Dendritic_cells, B_cells, Mast_cells, Module11_Prolif_score, MP_index_adj*(-1), Basal_Index, PARPi7_score, PARPi7_plus_MP2, VCpred_TN, STMN1_dat, HER2_Index, Mod7_ERBB2, IGF1R_dat, Mod10_ECM, RPL24_dat, LYMPHS_PCA_16704732, Luminal_Index, ER_PGR_avg
Clinical information	4	HR, MP2, Immune+, DRD+
mRNA	23	FAM174B, DECR2, IL34, ROGD1, PSMB3, PNMT, HELZ, SPNS3, COP22, GRP, ZNF285, ATG4D, B3GNT8, LINC00467, C3, ZNF442, SPACA4, PRSS50, MRPL54, KISS1R, ZNF14, ACOX2, LPAR2

mRNA, messenger RNA.

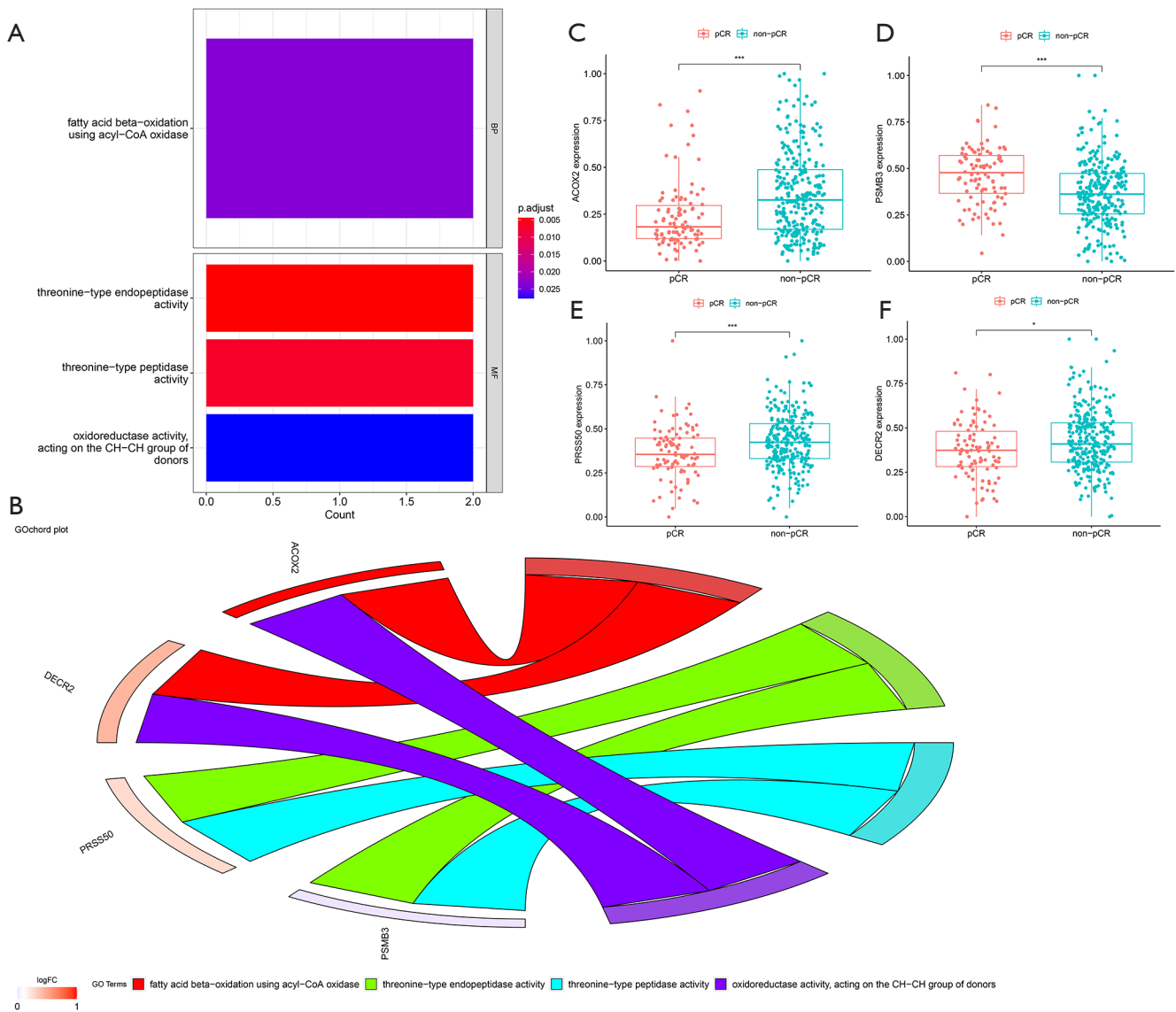


Figure S4 GO enrichment analysis of differential genes. (A) Bar plot showing four significant function pathways (BP, MF). (B) Chord plot connected the significant function pathways and genes (the logFC of ACO2 was -0.98 , DECR2 was -0.37 , PRSS50 was -0.19 , PSMB3 was 0.11). (C-F) Box plot showed the expression of four genes between pCR (Red) and non-pCR (Blue) (***, $P < 0.001$; *, $P < 0.05$). GO, Gene Ontology; BP, biological process; MF, molecular function; pCR, pathological complete response.

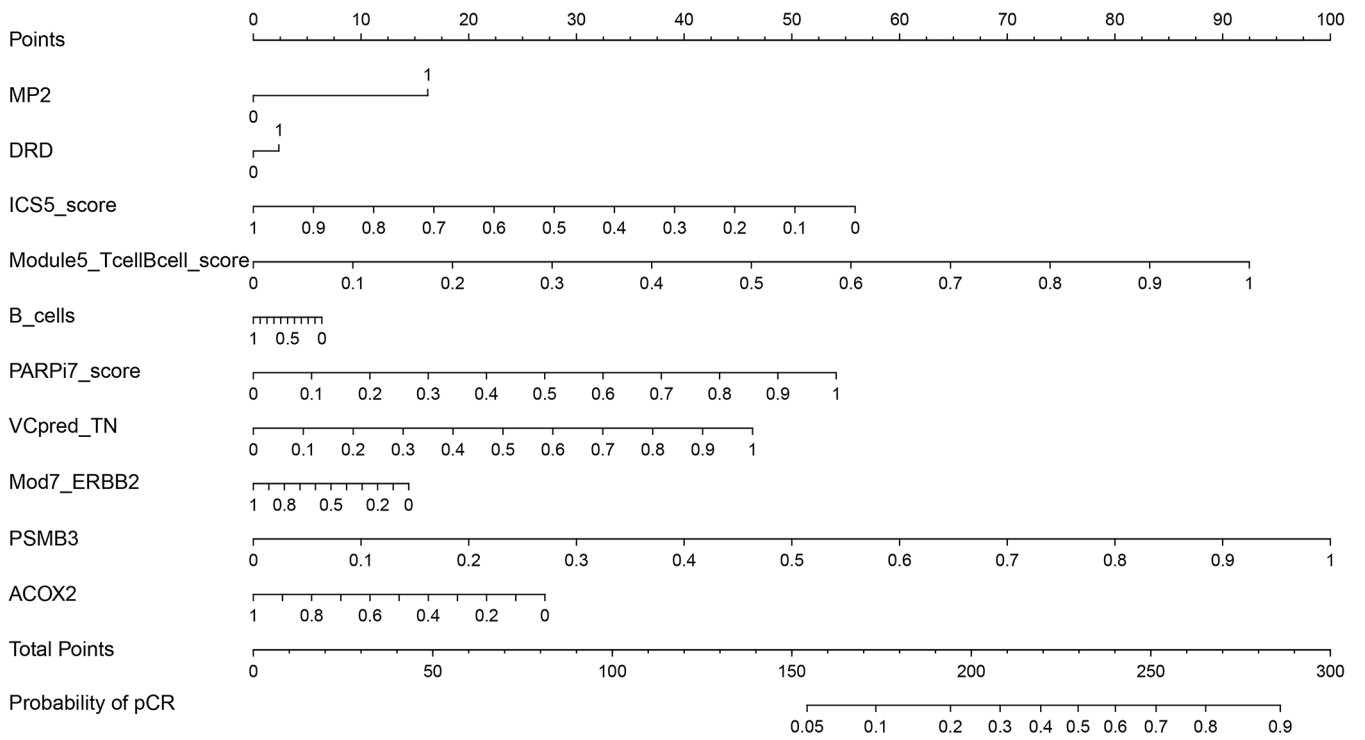


Figure S5 A nomogram based on the top 10 strong-related features, with an AUC value of 0.803. AUC, area under the curve; MP2, MammaPrint (MP) status 2; DRD, DNA repair deficiency; ICS, Integrated Cytokine Score; PARP, Poly(ADP-ribose) polymerase; VC, Veliparib + Carboplatin; TN, triple negative; pCR, pathologic complete response.