

Figure S1

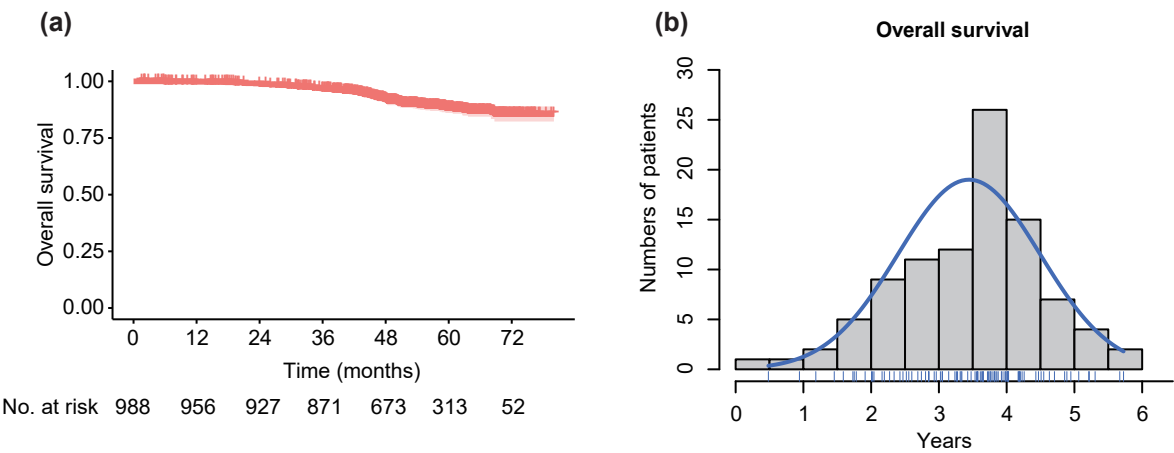


Figure S1, related to Figure 1. Survival analysis of the cohort. (a) Kaplan–Meier curve for overall survival in our cohort. (b) Distributions of overall survival in our cohort.

Figure S2

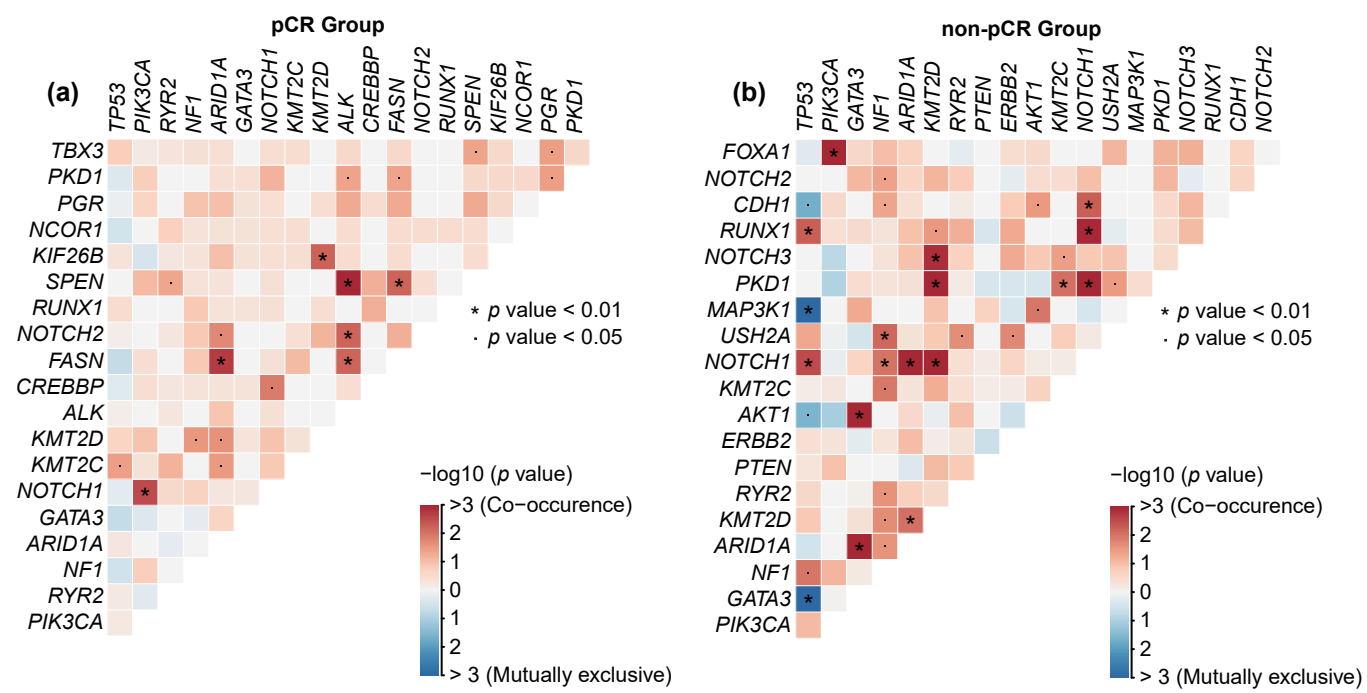
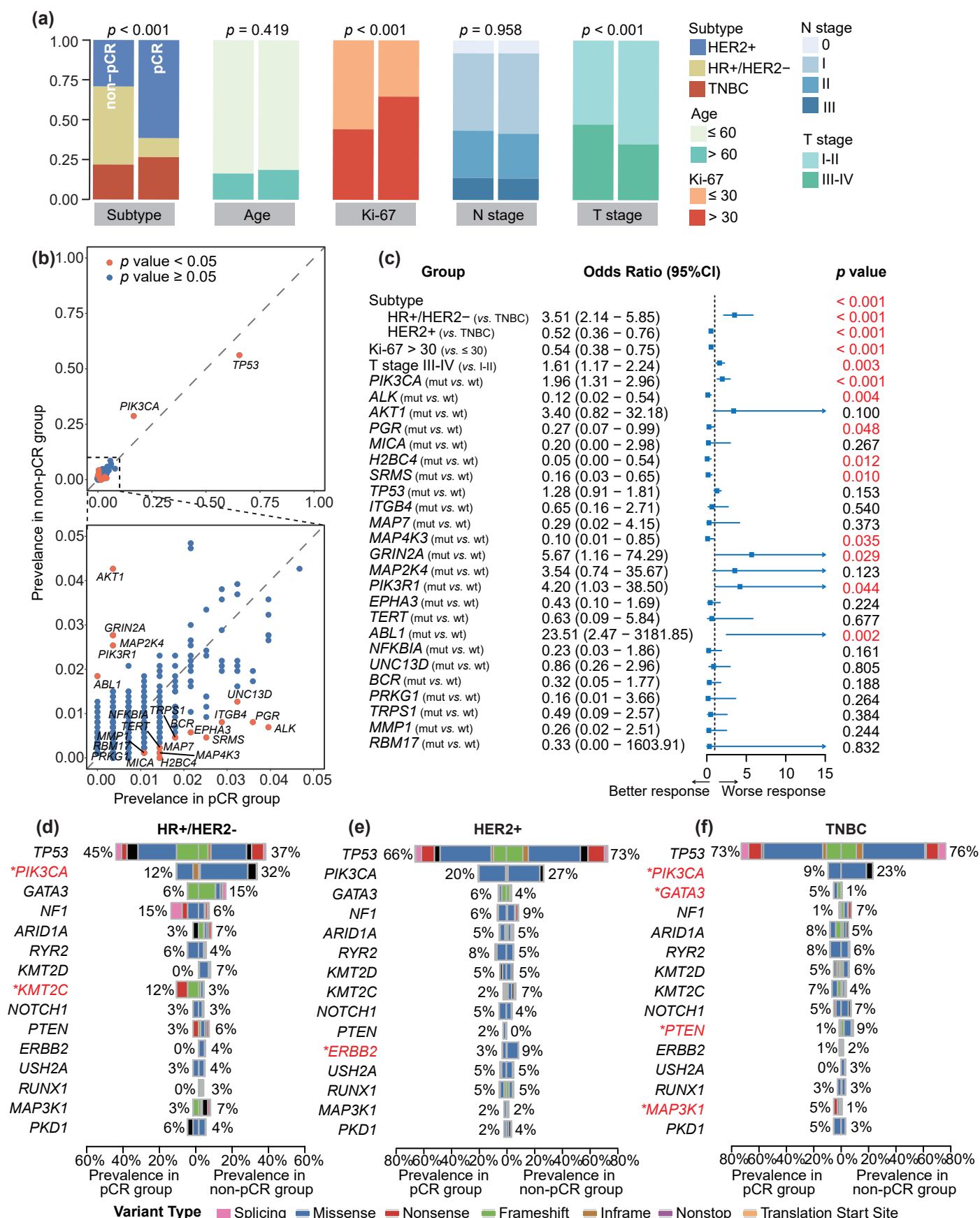


Figure S2, related to Figure 2. Somatic interaction landscape of the cohort. (a-b) co-occurrence and mutually exclusive genes in pCR (a) and non-pCR group (b). p values were calculated using pair-wise Fisher's Exact test.

Figure S3

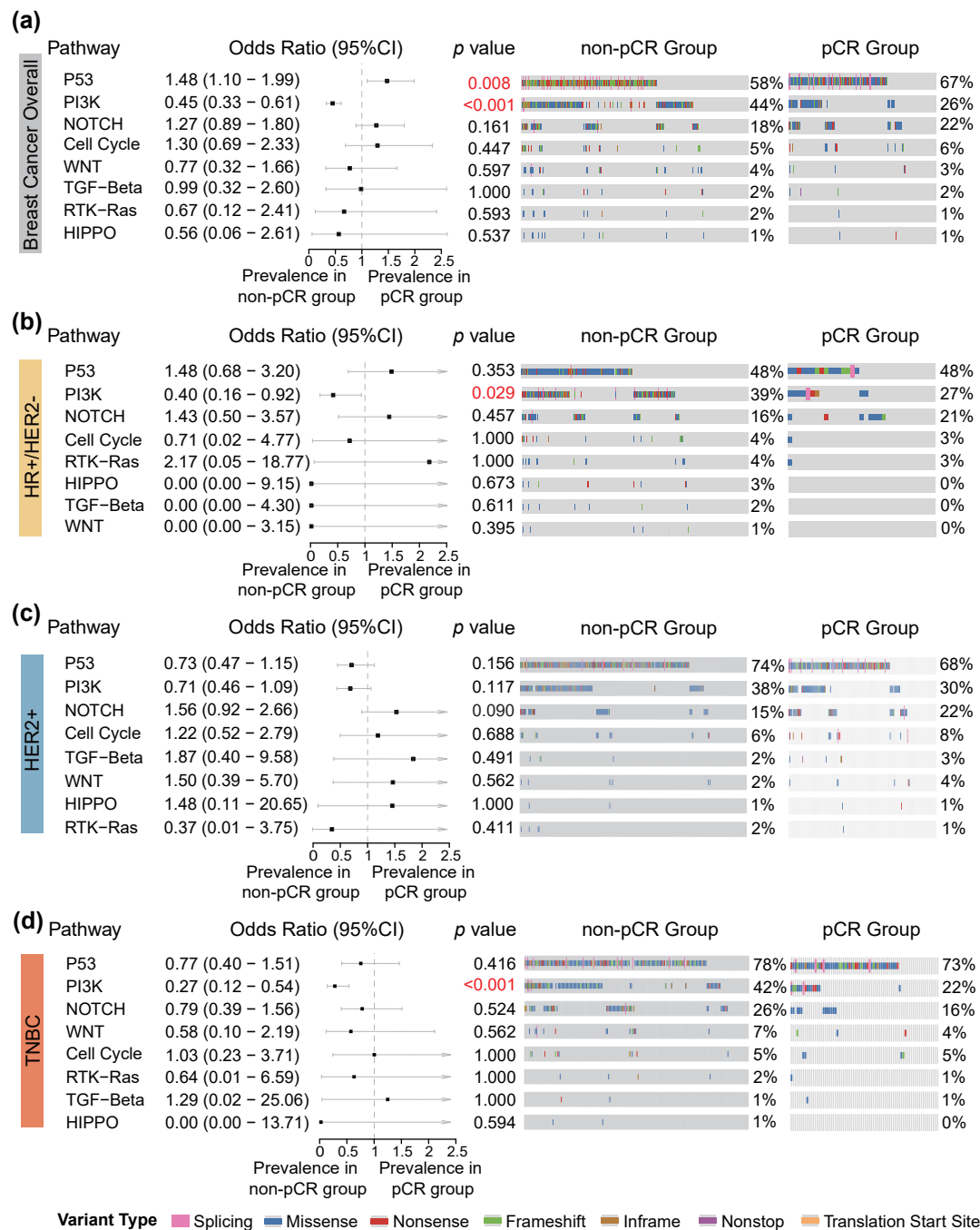


Figure S4. Pathway-level mutational characteristics associated with treatment response. (a-d) Comparison of mutations in oncogenic signaling pathways between non-pCR and pCR groups across entire cohort (a) and subtype-specific analyses in HR+/HER2- (b), HER2+ (c), and TNBC (d) subgroups. Odds ratios are shown with 95% confidence intervals. *p* values were calculated using the Fisher's exact test. Abbreviations: TNBC, triple-negative breast cancer; CI, confidence interval.

Figure S5

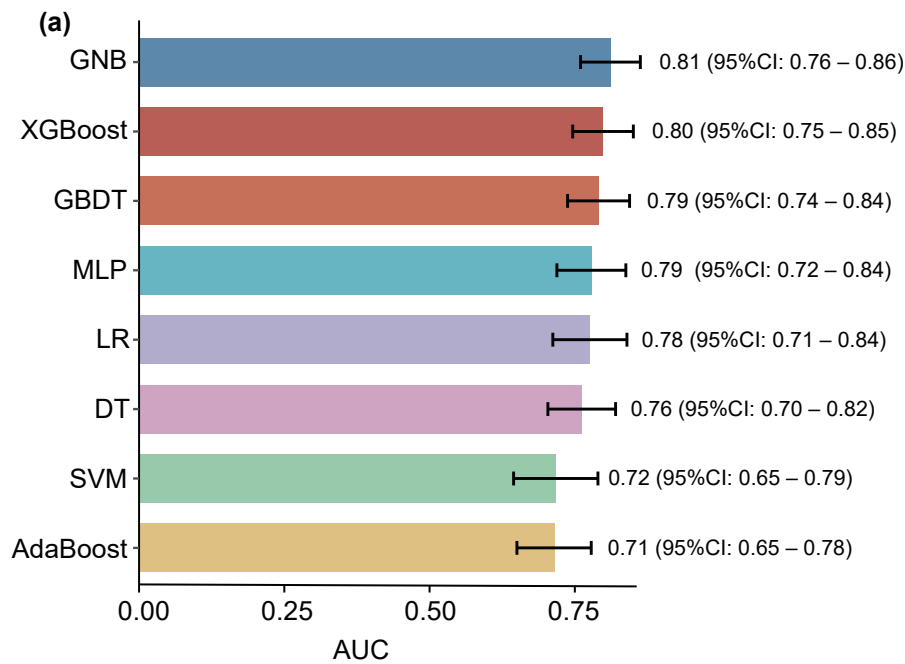


Figure S5, related to Figure 6. Test AUC scores across different machine learning models. Abbreviations: GNB, Gaussian naïve Bayes; XGBoost, gradient boosting; AdaBoost, adaptive boosting; DT, decision tree; GBDT, gradient boosting decision tree; LR, logistic regression; MLP, multilayer perceptron; SVM, support vector machine; AUC, area under curve; CI, confidence interval.