

Figure S1. Efficacy for the intent-to-treat (IIT) population and exploratory subgroup pCR rates analysis.

- (A) Longitudinal change in target-lesion size by treatment cycle; each line represents one patient, colored by best overall response (PR/SD/PD). Dashed lines indicate standard RECIST thresholds.
- (B) Waterfall plot of best percentage change from baseline, color-coded by best overall response; PD-L1 status (CPS strata) is annotated beneath each bar.
- (C) Exploratory subgroup pCR rate analysis.

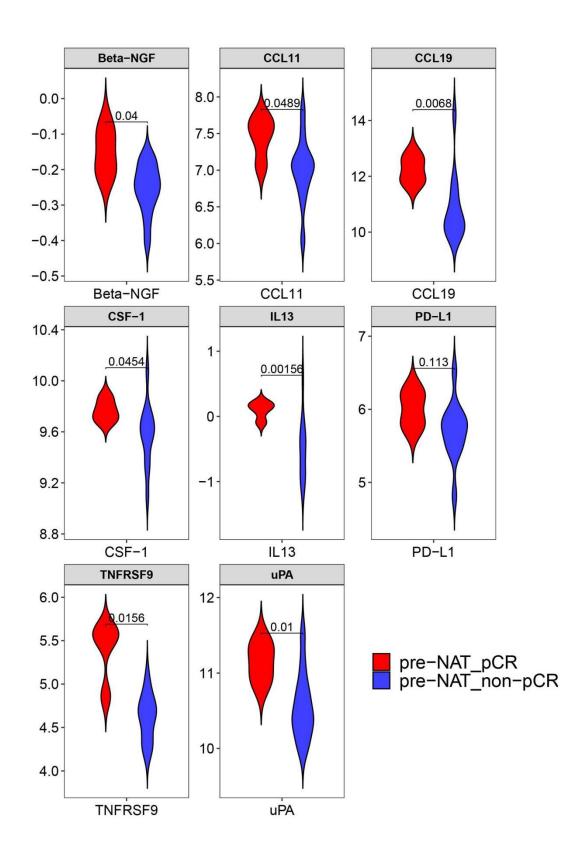


Figure S2. Differential proteins between pCR and non-pCR patients at baseline (pre-NAT). Violin plots show baseline expression of selected proteins in patients who achieved pCR (red) versus those with non-pCR (blue).

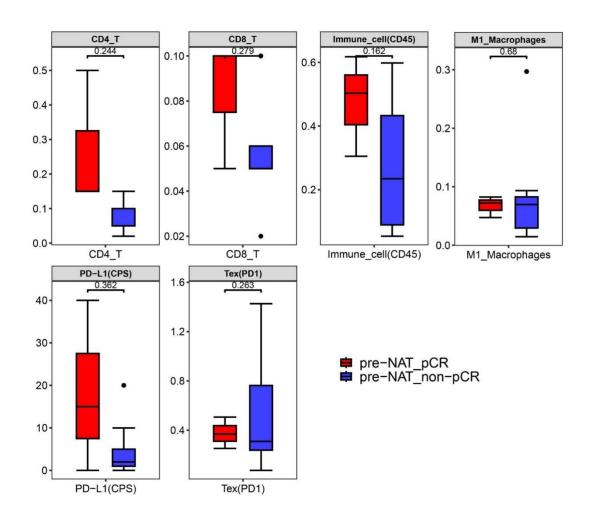


Figure S3. Immune cell profiles at baseline (pre-NAT) in pCR and non-pCR patients. Box plots show selected immune cell populations mIF and IHC in patients who achieved pCR (red) versus non-pCR (blue).

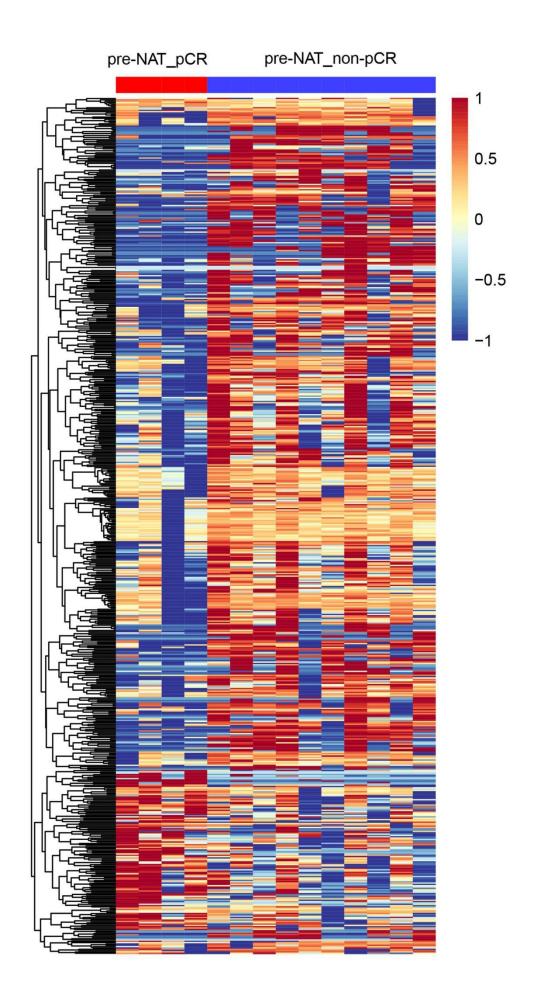


Figure S4. Heat map of RNA comparison between pCR and non-pCR patients at baseline. Unsupervised hierarchical clustering of differentially expressed genes (DEGs) at baseline, comparing patients who achieved pCR (red) versus those with non-pCR (blue).

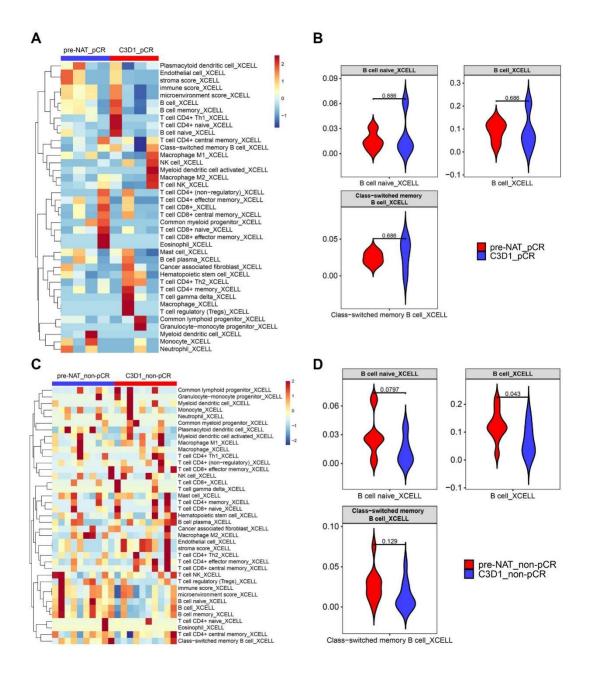


Figure S5. xCell deconvolution results in patients amd selected B-cell subsets in patients (C3D1 v.s. pre-NAT).

- (A) Deconvolution results in pCR patients.
- (B) Selected B-cell subsets in pCR patients at C3D1 versus pre-NAT.
- (C) Deconvolution results in non-pCR patients.
- (D) Selected B-cell subsets in non-pCR patients at C3D1 versus pre-NAT.

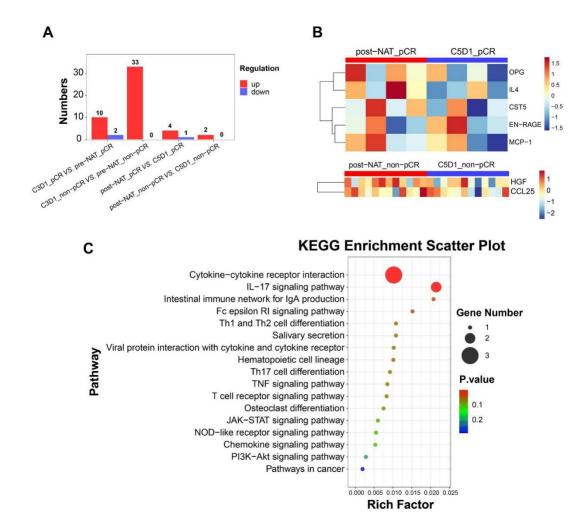


Figure S6 Proteomic dynamics during the rapid response phase (C3D1).

- (A) Differential protein statistics of pCR and non-pCR patients in the rapid response stage (pre-C3D1) and late response stage (C5D1-post) respectively.
- (B) Differential protein heatmap of pCR and non-pCR patients in the late response stage (C5D1-post) respectively.,
- (C) KEGG enrichment of differentially expressed proteins in C5D1-post of pCR patients.

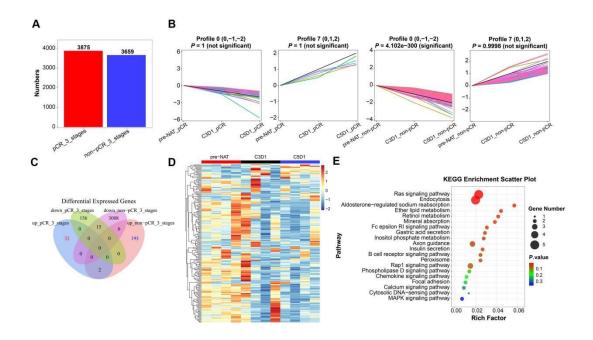


Figure S7 Longitudinal RNA changes across three treatment periods in pCR and non-pCR patients.

- (A) Numbers of significantly altered DEGs identified by repeated-measures ANOVA.
- (B) Temporal trends of RNA changes based on STEM analysis in both groups.
- (C) Venn diagram shows the intersection of DEGs in different group.
- (D) Heatmap of selected DEGs which are within the regions represented by red and blue numbers in the C plot.
- (E) KEGG pathways enriched among selected DEGs pCR and non-pCR patients.

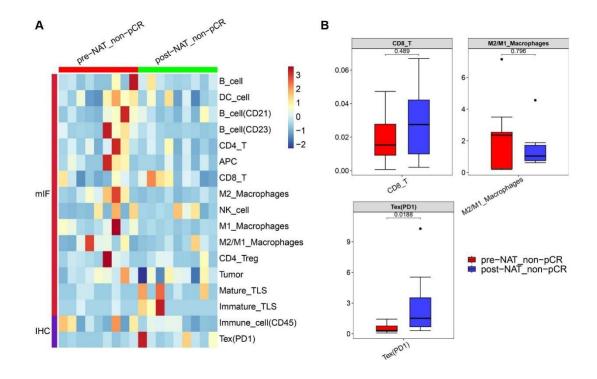


Figure S8 Immune-related cellular changes in non-pcr patients at baseline and after neoadjuvant therapy.

- (A) Heatmap of immune-related cells in non-pCR patients at baseline and after neoadjuvant therapy.
- (B) Boxplots showing representative immune cell subsets, highlighting an increase in exhausted CD8⁺ T cells (TexPD-1) after treatment.