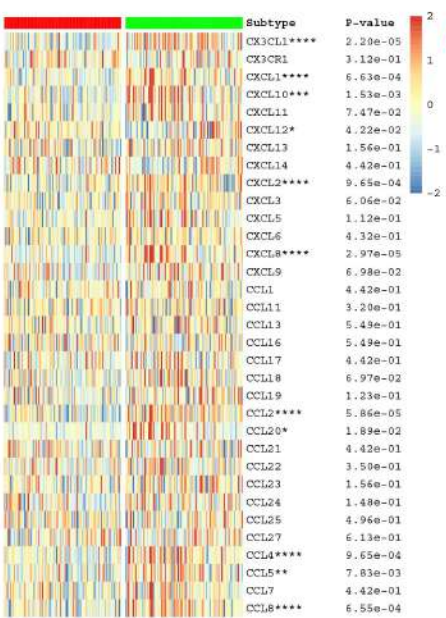
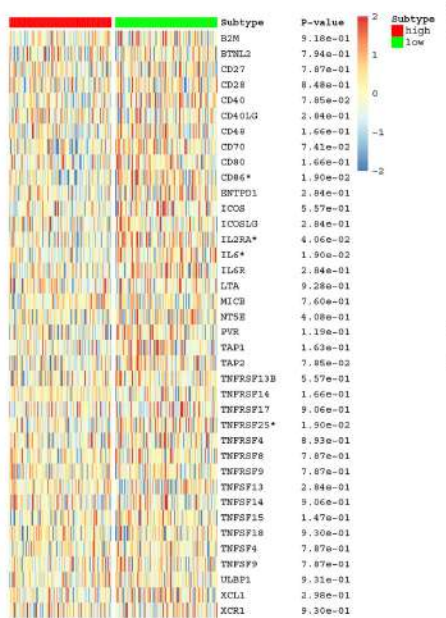


Supplement Figure 1: The effect of XBP1 on immunological status in pan-cancers. (A) The correlations of XBP1 expression and immune infiltration in pan-cancers using seven independent algorithms; (B) Correlations of XBP1 expression with immunosuppressive features of pan-cancers using TISIDB.

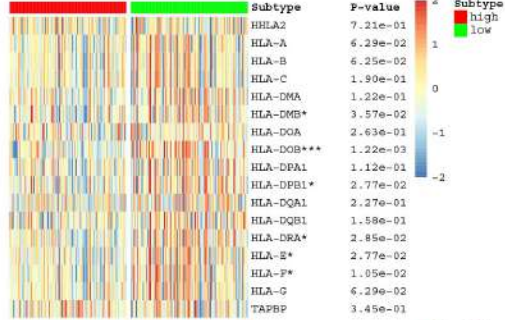
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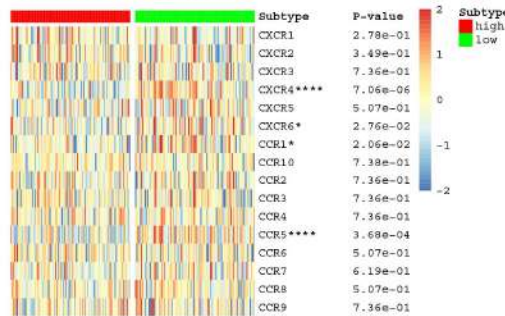
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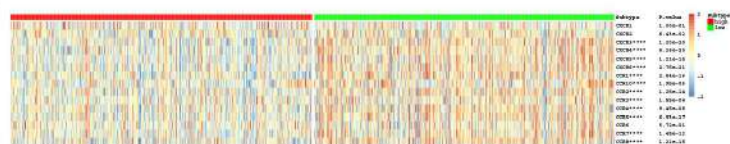
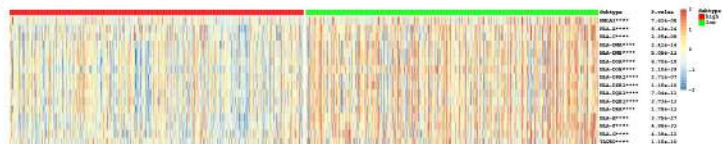
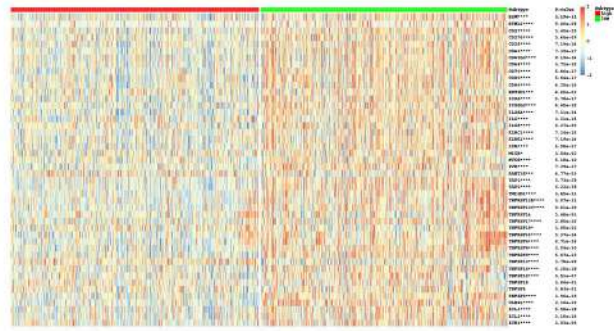
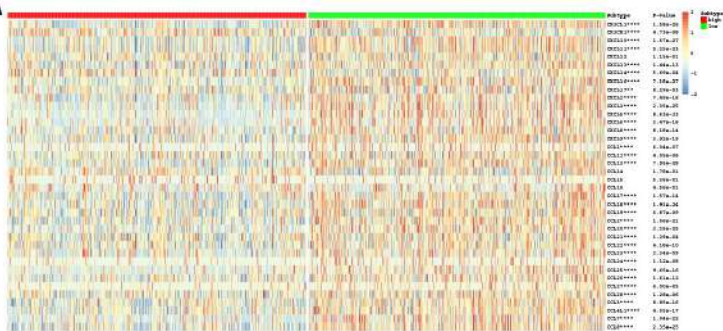
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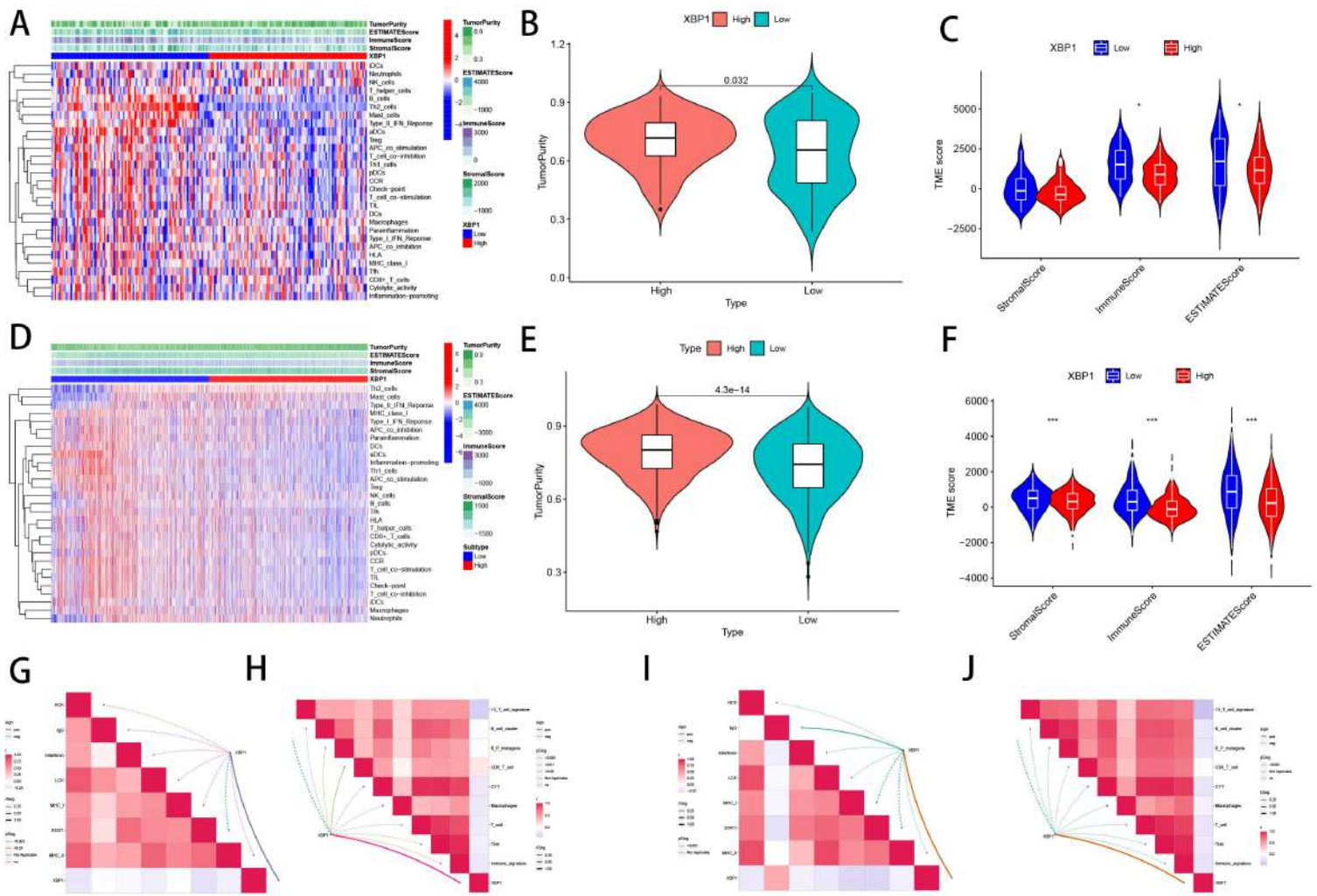
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Supplement Figure 2: Correlation between XBP1 and immunomodulators based on GSE25065. (A) chemokines; (B) immunostimulators; (C) MHC; (D) receptors.

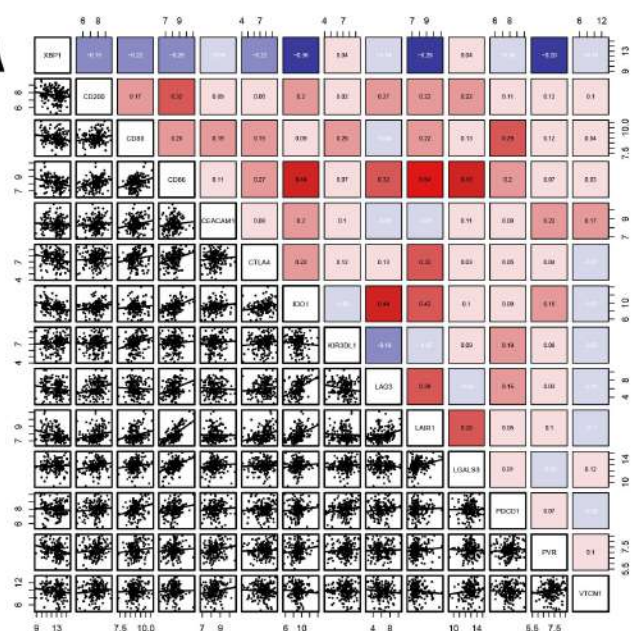


Supplement Figure 3: Correlation between XBP1 and immunomodulators based on TCGA dataset. (A) chemokines; (B) immunostimulators; (C) MHC; (D) receptors.

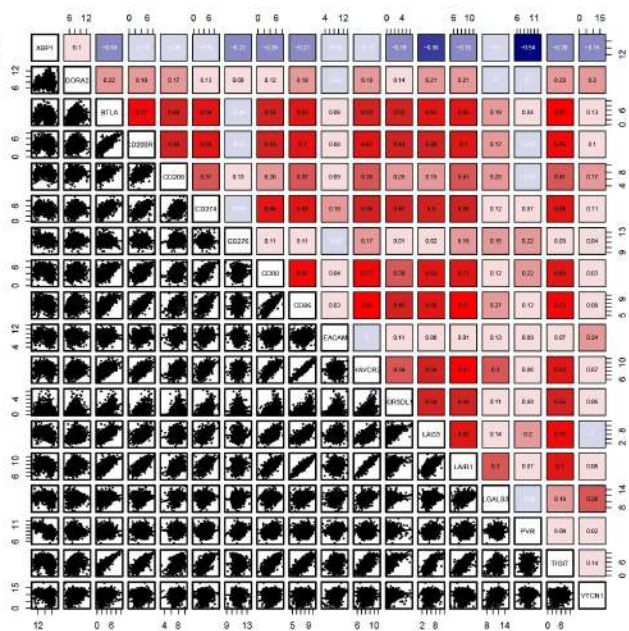


Supplement Figure 4: XBP1 shapes a non-inflamed TME in breast cancer based on GSE25056 and TGCA dataset. Scores of the 29 immune-related gene sets between high and low XBP1 group based on (A) GSE25055 and (D) TGCA dataset; Difference in TumorPurity between high and low XBP1 group based on (B) GSE25055 and (E) TGCA dataset; Difference in TME score between high and low XBP1 group based on (C) GSE25055 and (F) TGCA dataset; Correlations between XBP1 and enrichment scores of inflammatory activation functions based on (G) GSE25055 and (I) TGCA dataset; Correlations between XBP1 and enrichment scores of immunocytes based on (H) GSE25055 and (J) TGCA dataset.

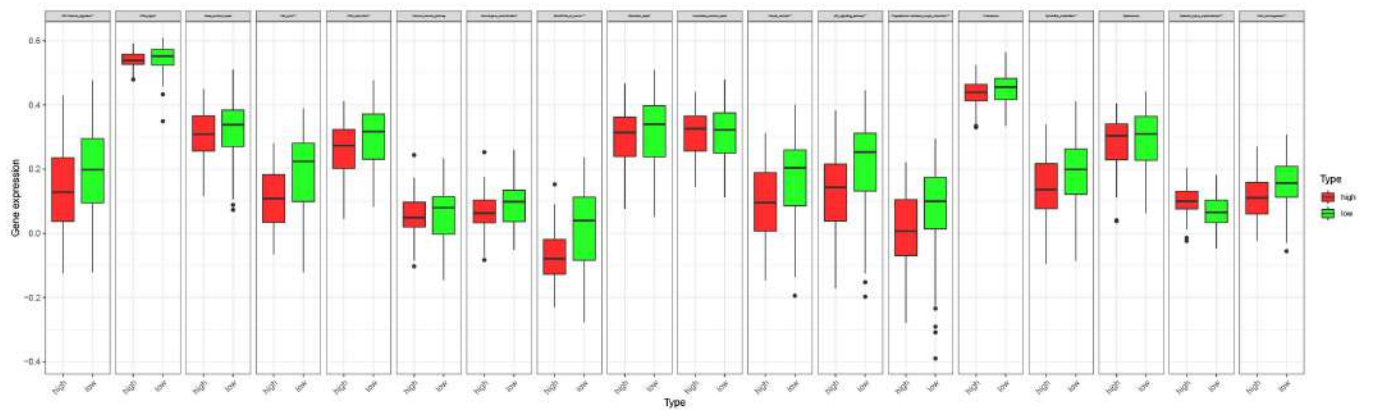
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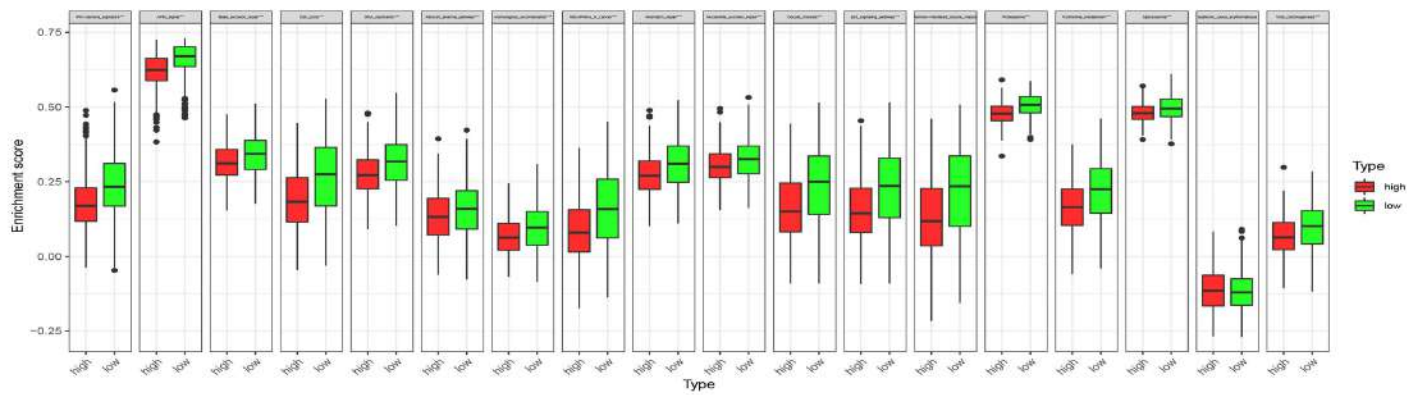
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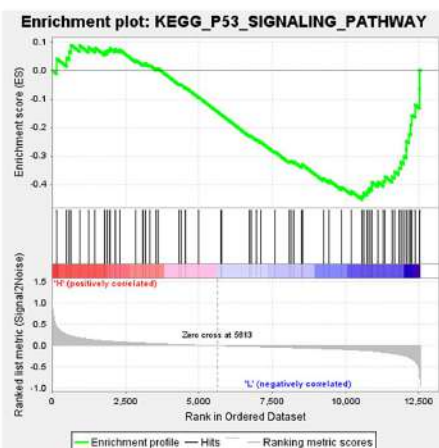
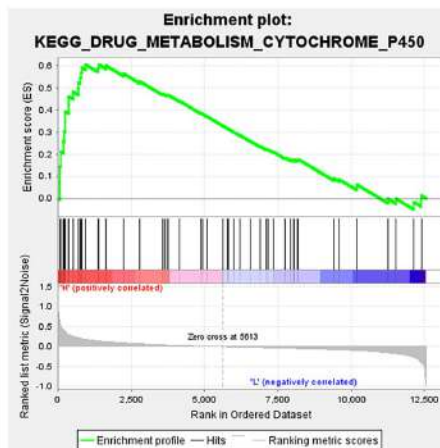
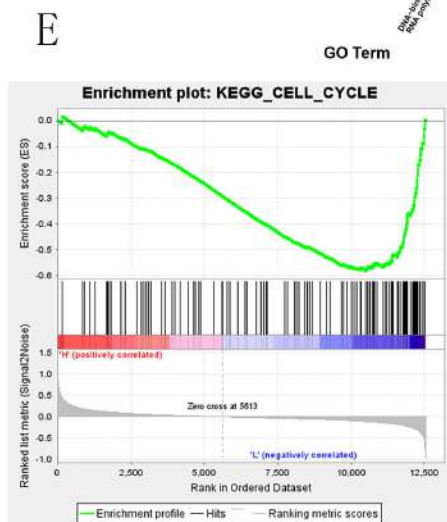
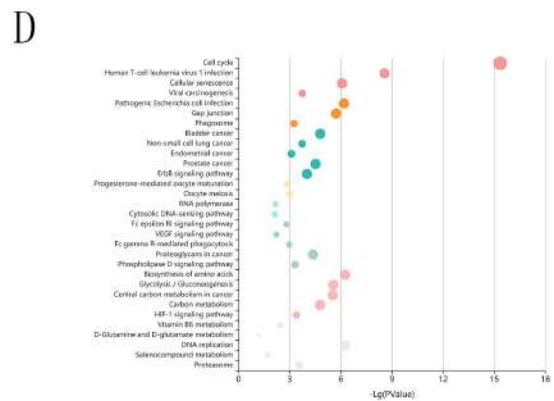
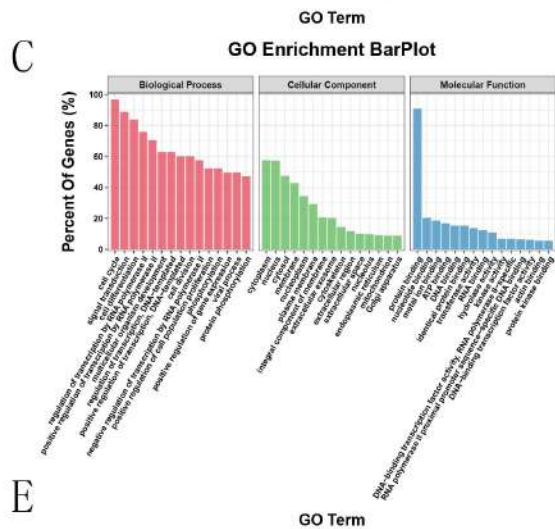
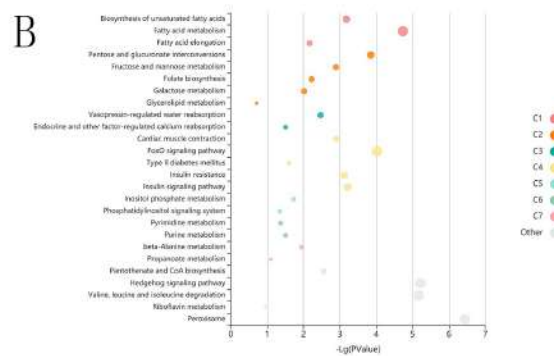
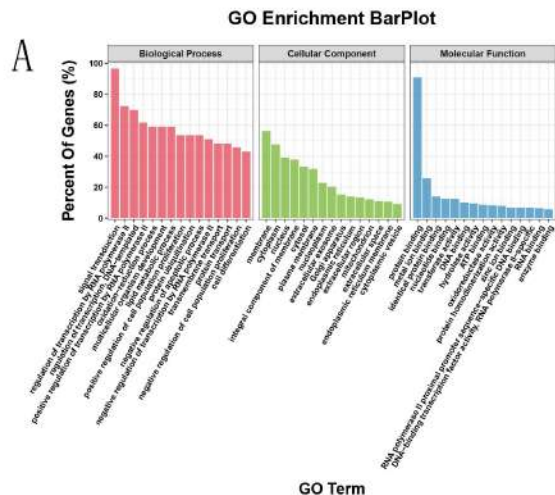
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D



Supplement Figure 5: Correlation between XBP1 and inhibitory immune checkpoints based on GSE25055 and TGCA dataset. Correlation between XBP1 and inhibitory immune checkpoints based on (A) GSE25055 and (B) TGCA dataset; Differences in the enrichment scores of immunotherapy-predicted pathways between high and low XBP1 groups based on (C) GSE25055 and (D) TGCA dataset.



Supplement Figure 6: Functional enrichment analysis based on breast cancer patients received neoadjuvant chemotherapy. (A) Go enrichment of positively correlated significant genes of XBP1 using OmicStudio tool; (B) KEGG enrichment of positively correlated significant genes of XBP1 using KOBAS tool; (C) Go enrichment of negatively correlated significant genes of XBP1; (D) KEGG enrichment of negatively correlated significant genes of XBP1; (E) Gene set enrichment analysis revealed KEGG signaling pathways.