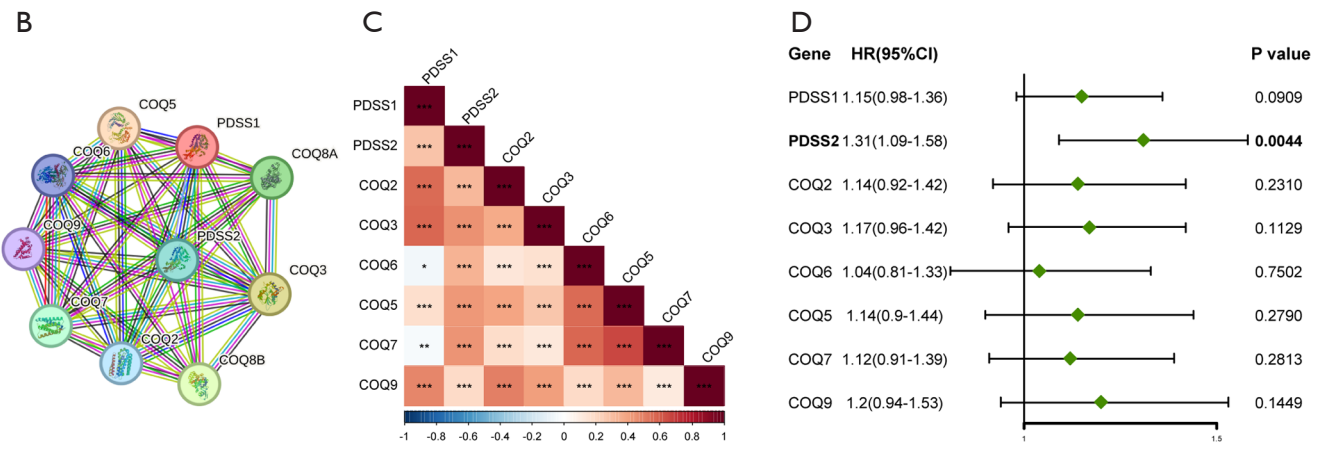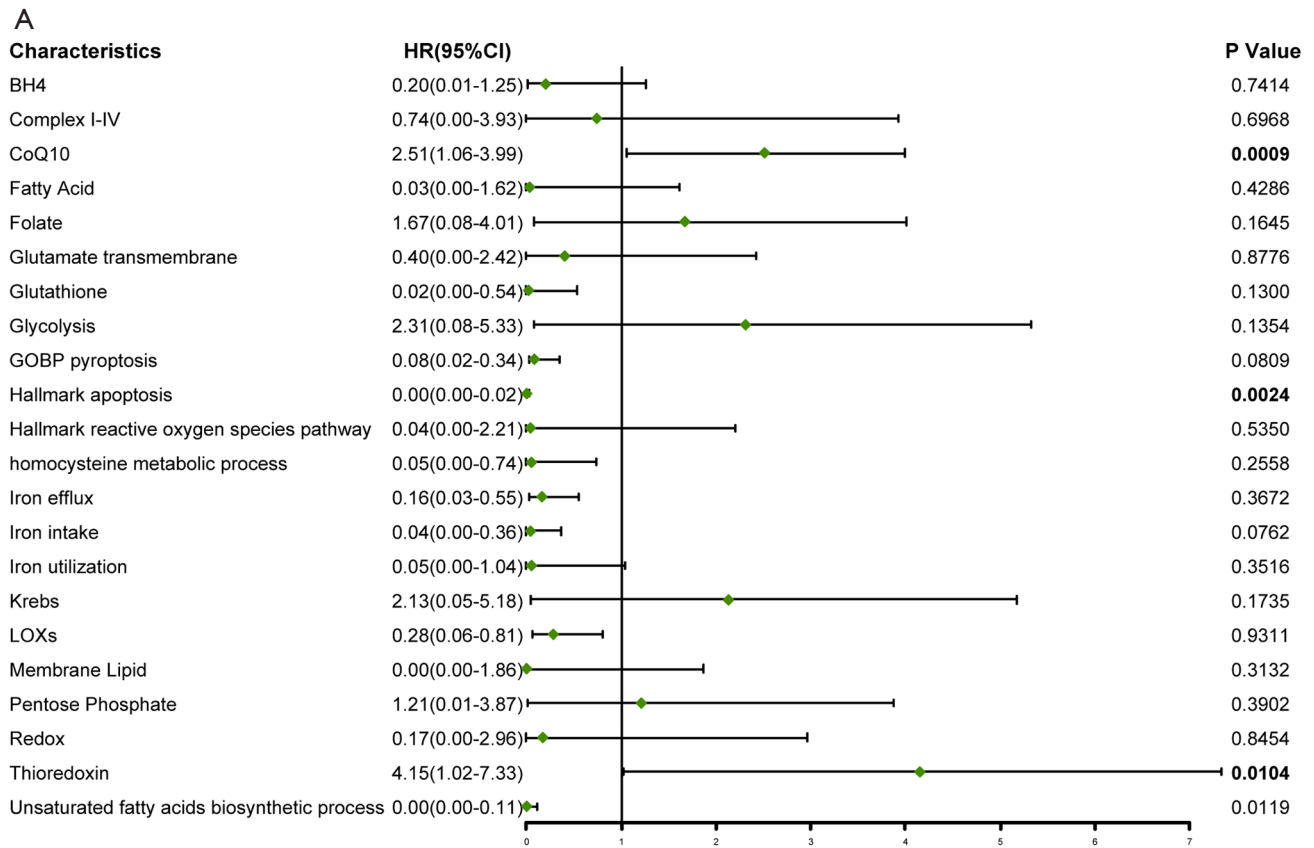**Figure S1** Heatmap displaying the expression levels of ferroptosis-related factor, along with clinical characteristic annotations for each cluster.

Figure S2 Identify the core ferroptosis factor. (A) Univariate Cox regression analysis of levels of ferroptosis-related factor. (B) Protein interaction networks of CoQ10-related genes. (C) Correlation heatmap showing the association between CoQ10-related genes. (D) Univariate Cox regression analysis of expression of CoQ10-related genes. *, P<0.05; **, P<0.01; ***, P<0.001.
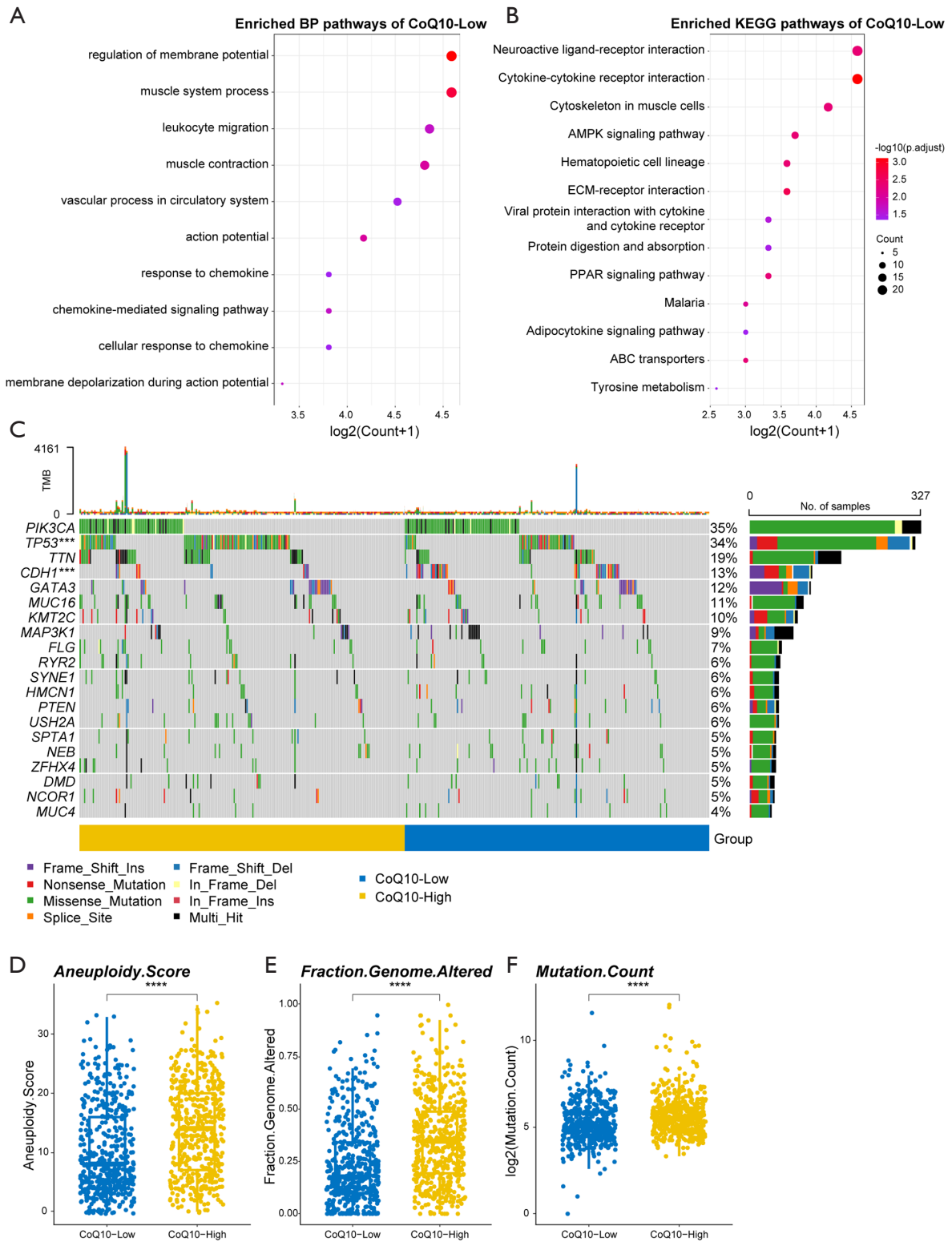
Figure S3 Differences of biological functions and mutant spectrum between CoQ10 subgroups. (A) GO analysis highlighting the biological processes (BP) enriched in CoQ10-low. (B) KEGG pathways enriched in CoQ10-low. (C) Waterfall diagram of top 20 mutated genes. (D-F) The value of several somatic cell mutations between CoQ10-low and CoQ10-high. ***, P<0.001; ****, P<0.0001.
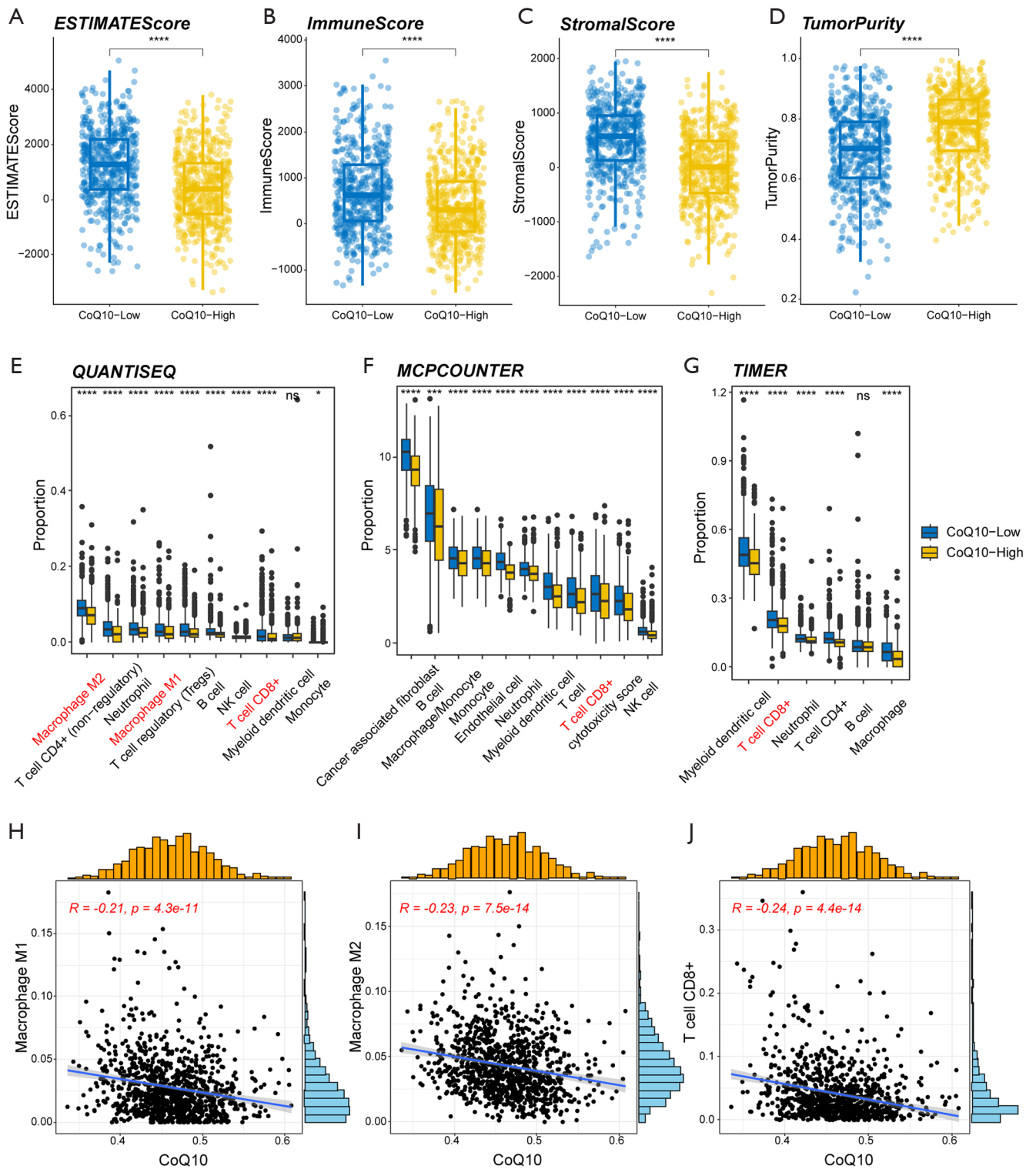
Figure S4 Immune Infiltration to immunotherapy across Clusters. (A-D) The value of ESTIMATEScore between CoQ10-low and CoQ10-high. (E-G) Boxplots showing the proportion of 22 immune cells in low/high CoQ10 groups of BRCA estimated by QUANTISEQ, MCPCOUNTER and TIMER. (H-J) Scatter plots showing the correlation between the CoQ10 score and the proportion of M1-like macrophages, M2-like macrophages and CD8+ T cells. ns, $P>0.05$; *, $P<0.05$; ***, $P<0.001$; ****, $P<0.0001$.
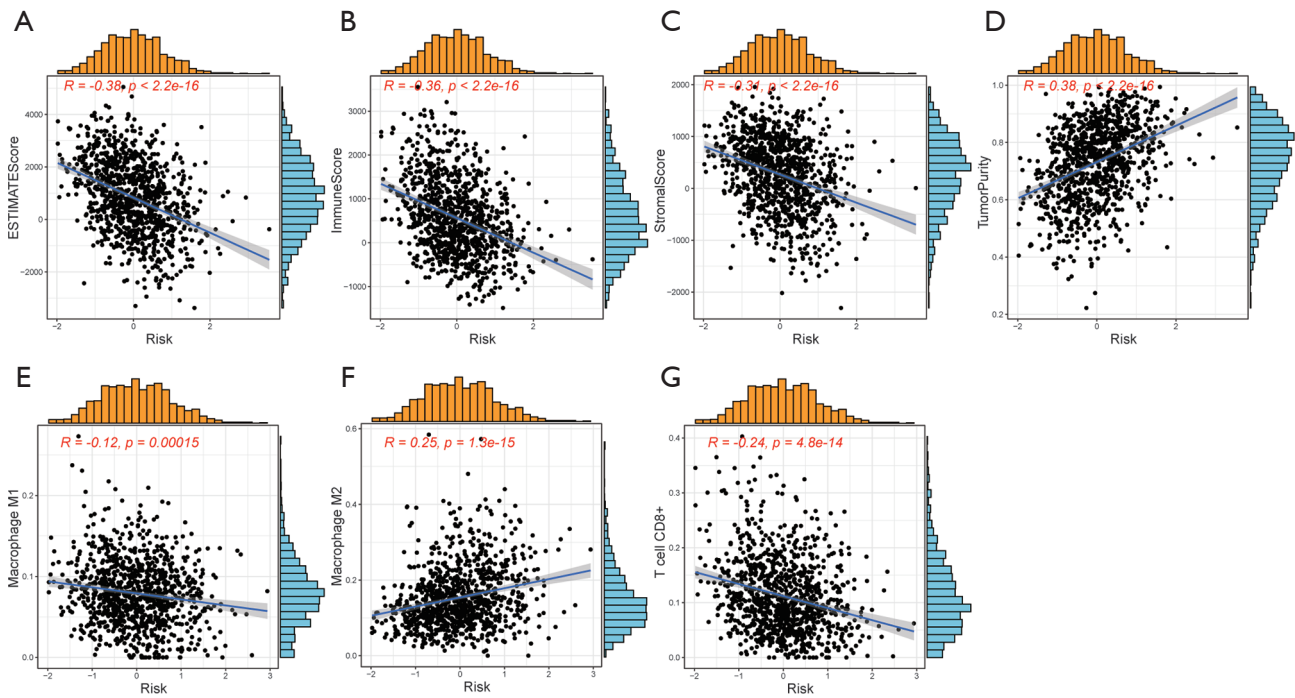
Figure S5 Immune Infiltration to immunotherapy across risk group. (A-D) Scatter plots showing the correlation between risk score and ESTIMATEScore. (E-G) Scatter plots showing the correlation between risk score and the proportion of M1-like macrophages, M2-like macrophages and CD8+ T cells.