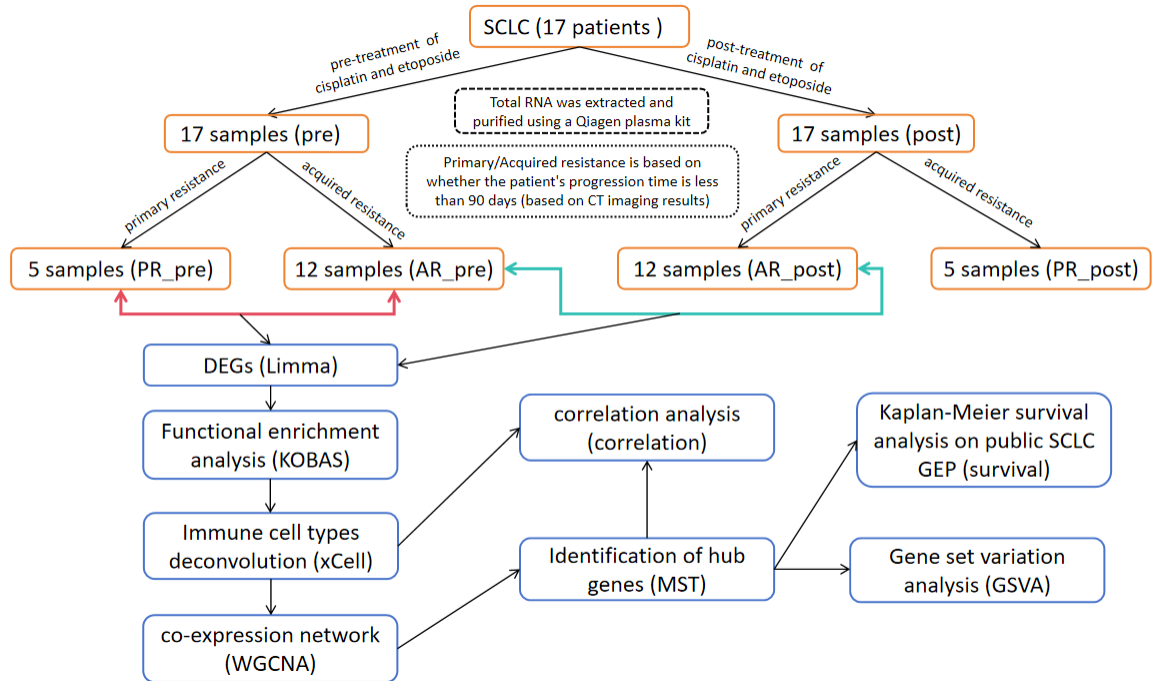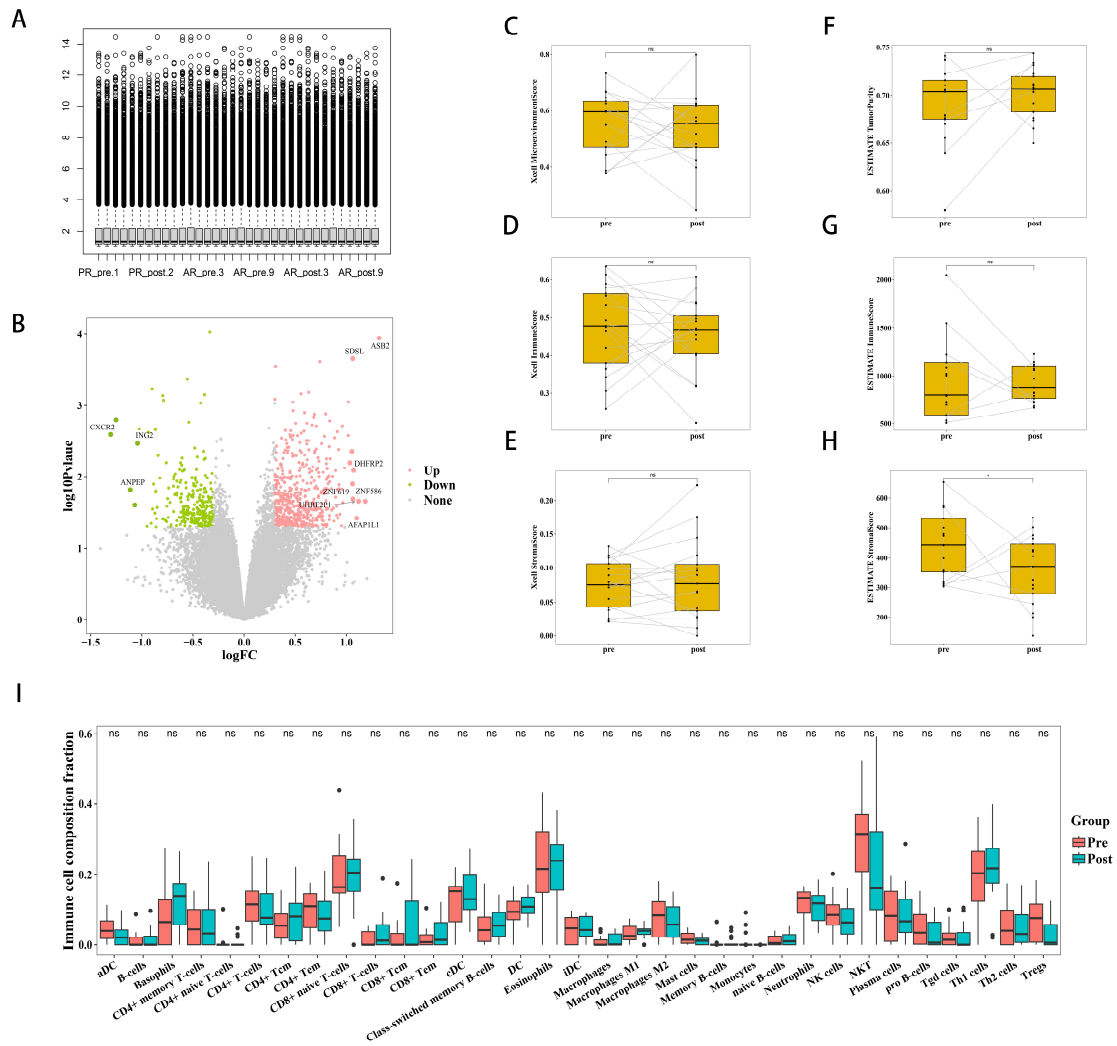Supplementary material

**Supplementary Figure S1.** The technical roadmap of the entire document.

Supplementary Figure S2. (A) Histogram of gene expression for patients after batch correction. (B) Volcano plots showing differences between pre- and post-EP treatment groups. (C-E) Boxplot showing xCell enrichment microenvironment, stromal, and immune scores between pre- and post-EP treatment groups. (F-G) Boxplot showing ESTIMATE enrichment tumor purity, immune, and stromal scores between pre- and post-EP treatment groups. (I) Boxplot showing xCell enrichment scores of 33 immune cells between pre- and post-EP treatment groups. * p-value < 0.05 and ns indicates not significant.
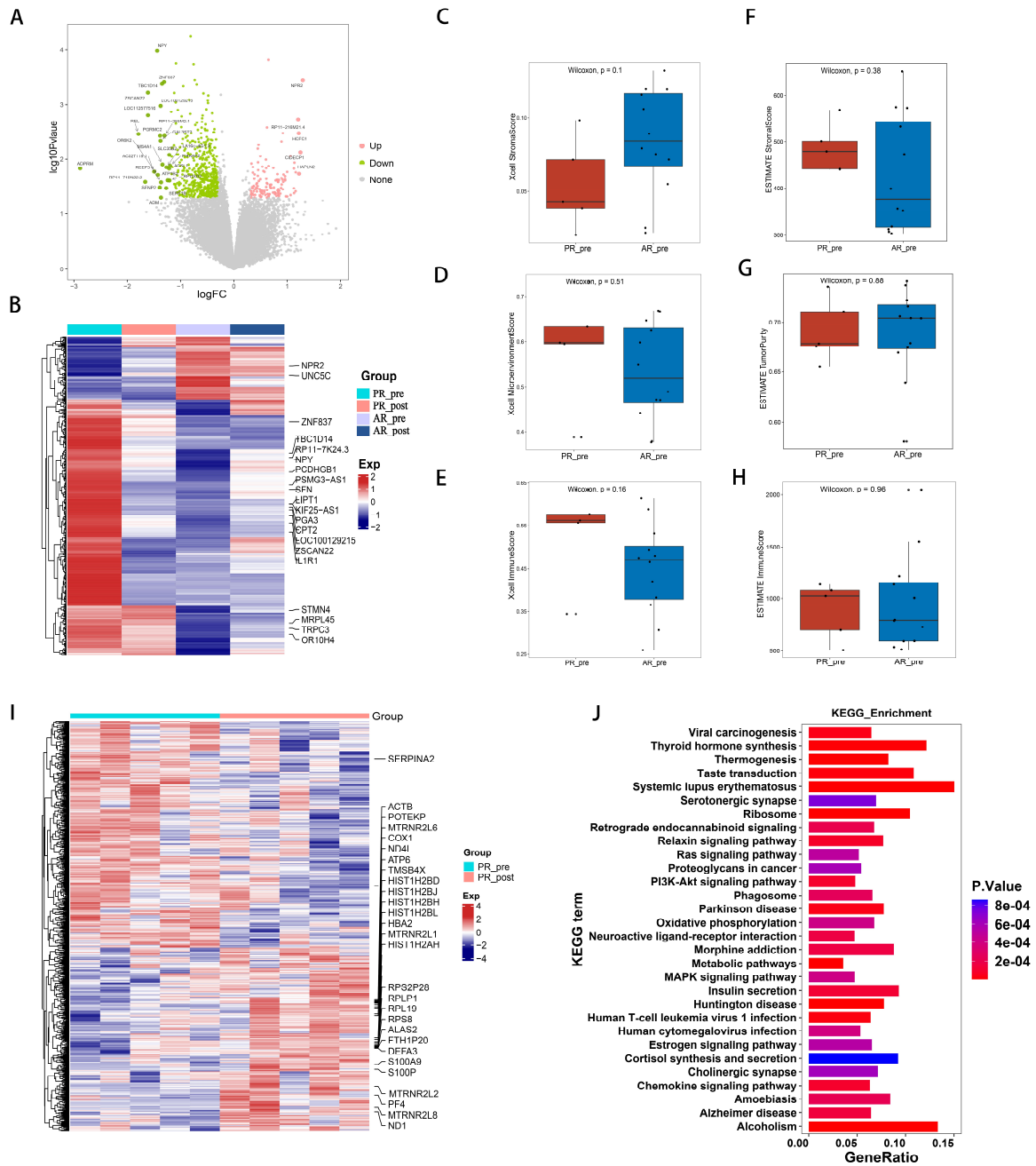
Supplementary Figure S3. (A) Volcano plots showing differences between PR_pre and AR_pre groups. (B) Heatmap analysis of mean expression of DEGs between PR_pre and AR_pre groups in four groups. (C-E) Boxplot showing xCell enrichment tumor purity, immune, and stromal scores between PR_pre and AR_pre groups. (F-H) Boxplot showing ESTIMATE enrichment scores of 14 stromal cells between PR_pre and AR_pre groups. (I) Heatmap analysis of DEGs between PR_pre and PR_post groups. (J) KEGG enrichment analysis of DEGs between PR_pre and PR_post groups.
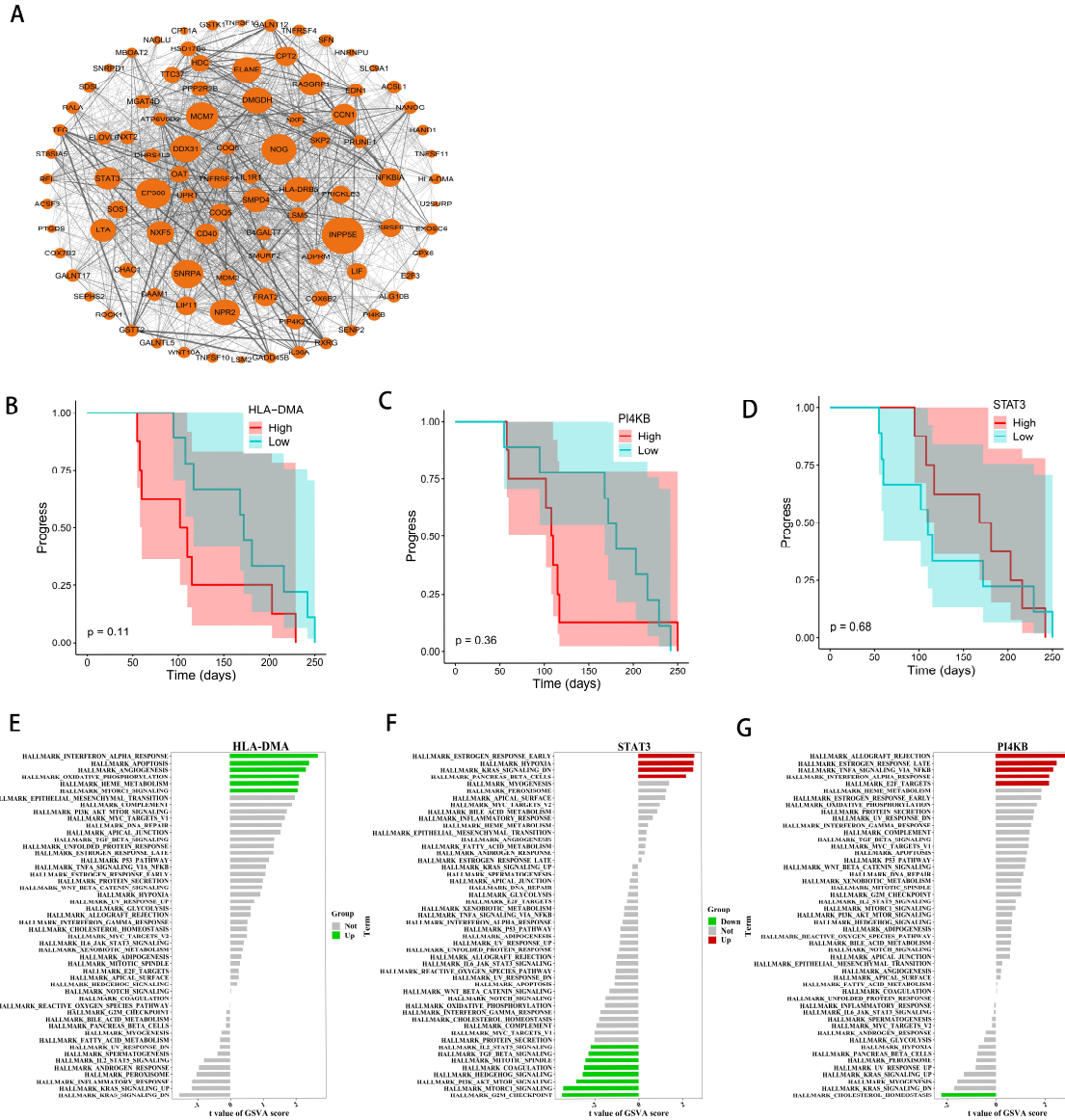
Supplementary Figure S4. (A) Network depicting co-expressed DEGs between PR_pre and AR_pre groups within cancer-associated KEGG pathways following WCGNA analysis. (B-D) Kaplan-Meier curve of *HLA-DMA*, *PI4KB* and *STAT3* with progression time. (E-G) GSVA of *HLA-DMA*, *PI4KB* and *STAT3*.
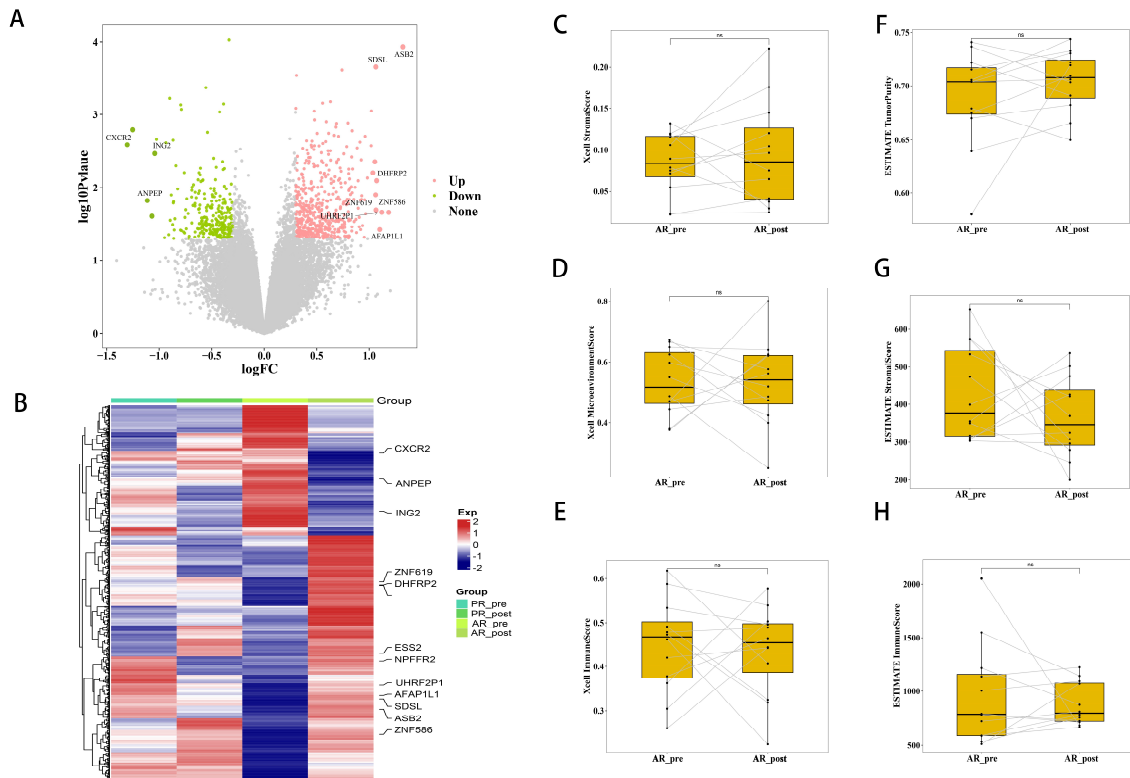
Supplementary Figure S5. (A) Volcano plots showing differences between AR_pre and AR_post groups. (B) Heatmap analysis of mean expression of DEGs between AR_pre and AR_post groups in four groups. (C-E) Boxplot showing xCell enrichment microenvironment, stromal, and immune scores between AR_pre and AR_post groups. (F-G) Boxplot showing ESTIMATE enrichment tumor purity, immune, and stromal scores between AR_pre and AR_post groups, where ns indicates not significant.
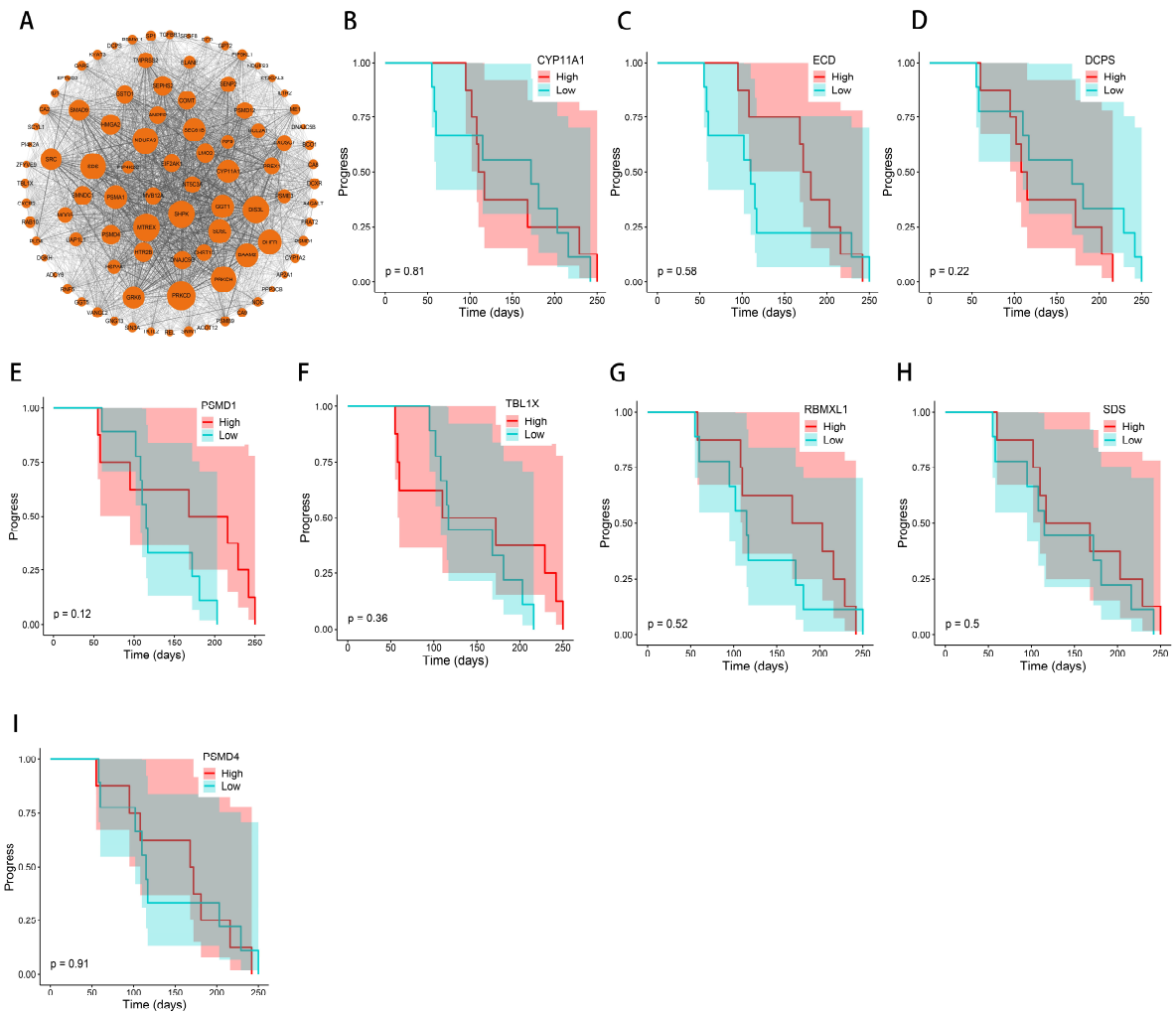
Supplementary Figure S6. (A) Network depicting co-expressed DEGs between AR_pre and AR_post groups within cancer-associated KEGG pathways following WCGNA analysis. (B-I) Kaplan-Meier curve of *CYP11A1*, *ECD*, *DCPS*, PSMD1, *TBL1X*, *PBMXL1*, *SDS*, and *PSMD4* with progression time.
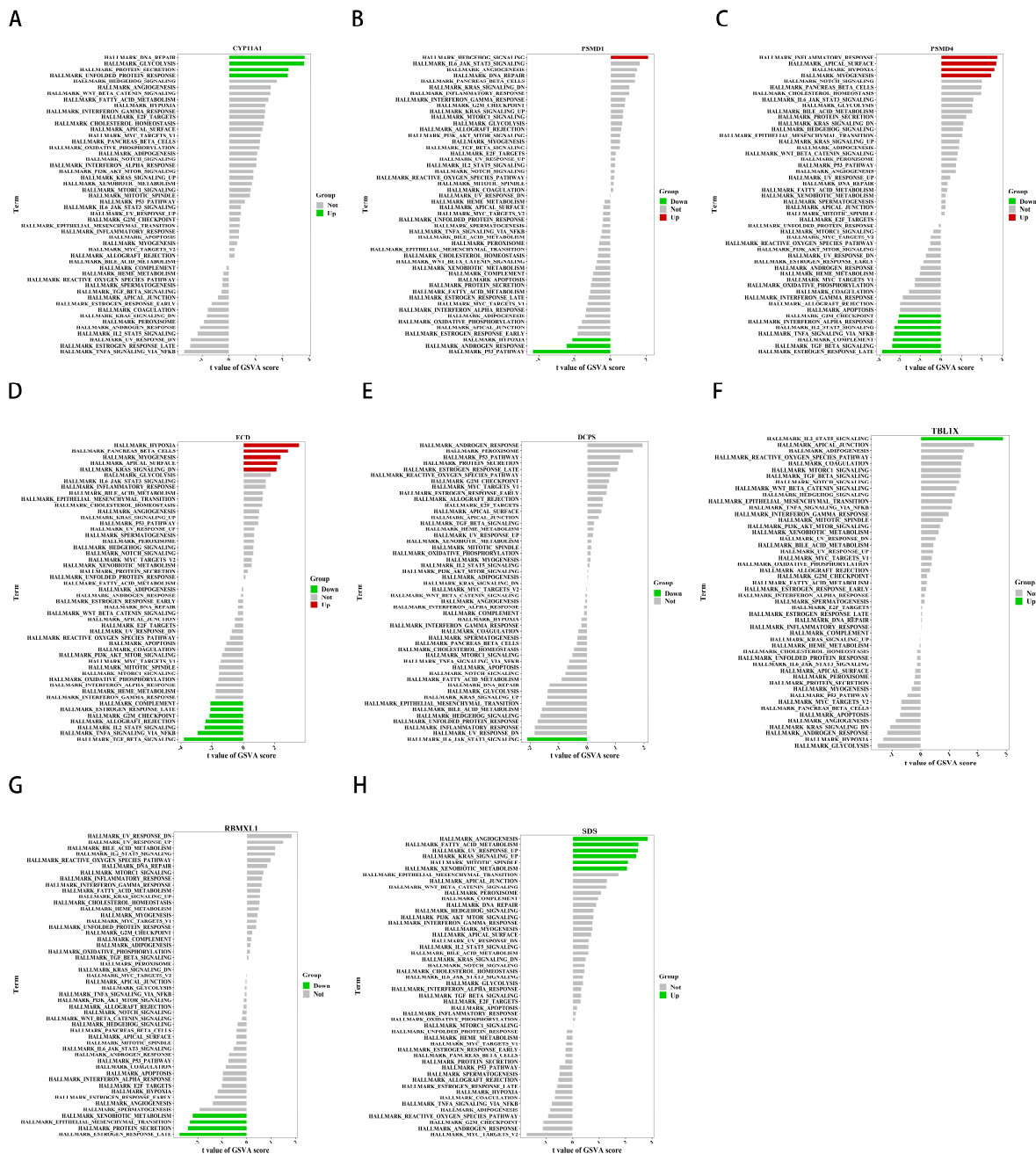
Supplementary Figure S7. (A-H) GSVA of *CYP11A1*, *ECD*, *DCPS*, PSMD1, *TBL1X*, *PBMXL1*, *SDS*, and *PSMD4*.