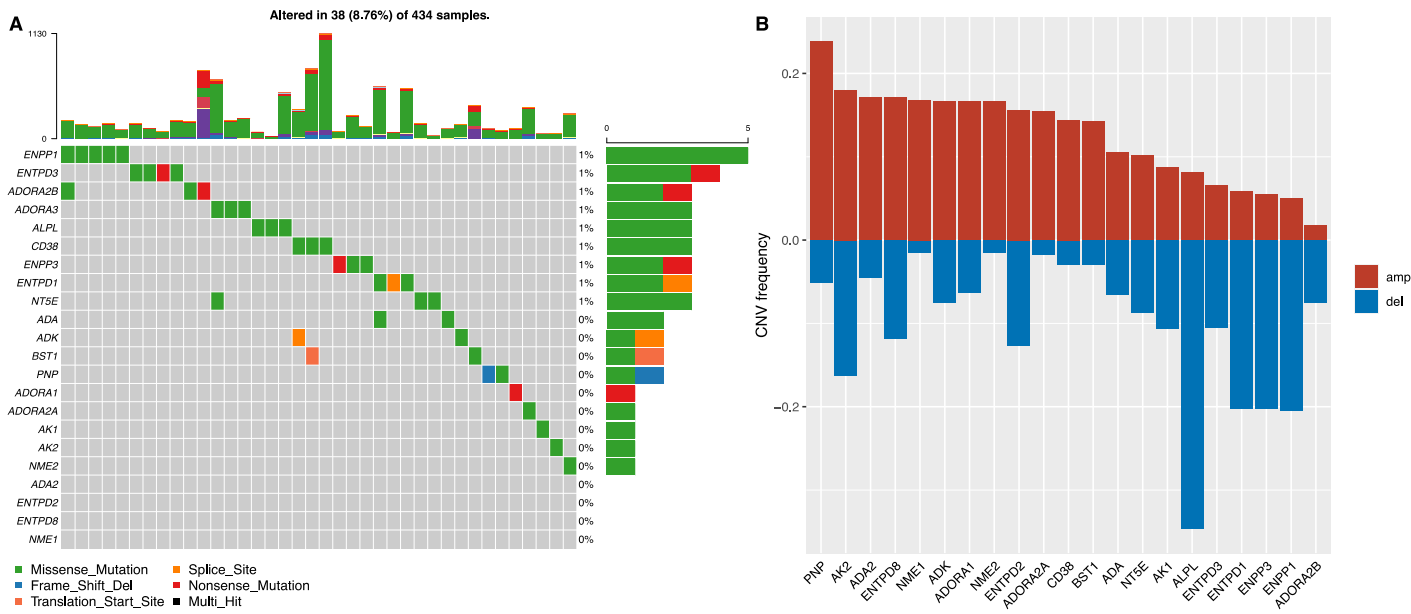
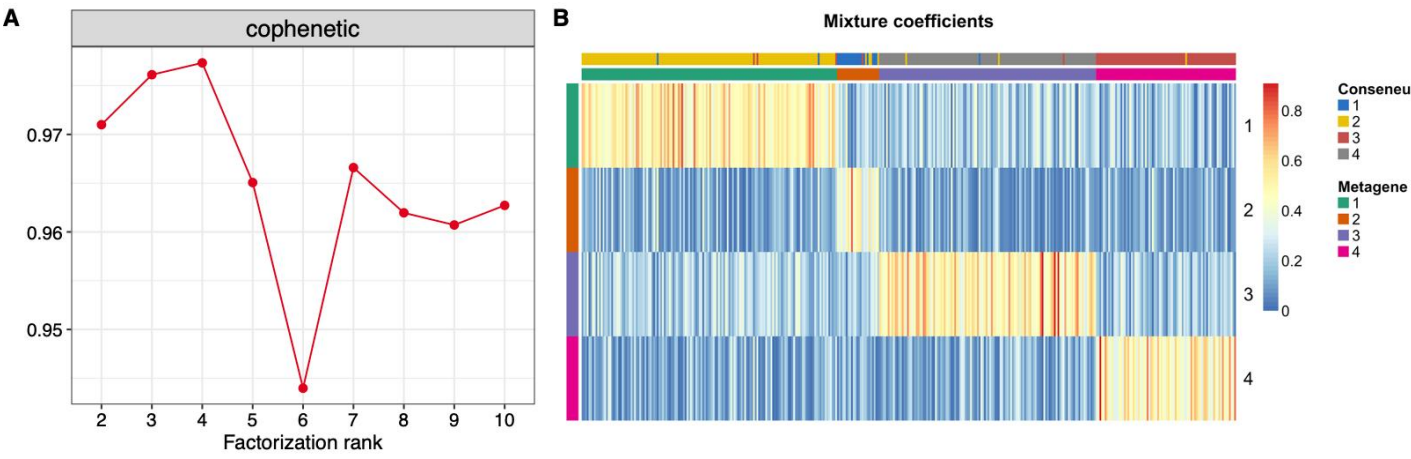
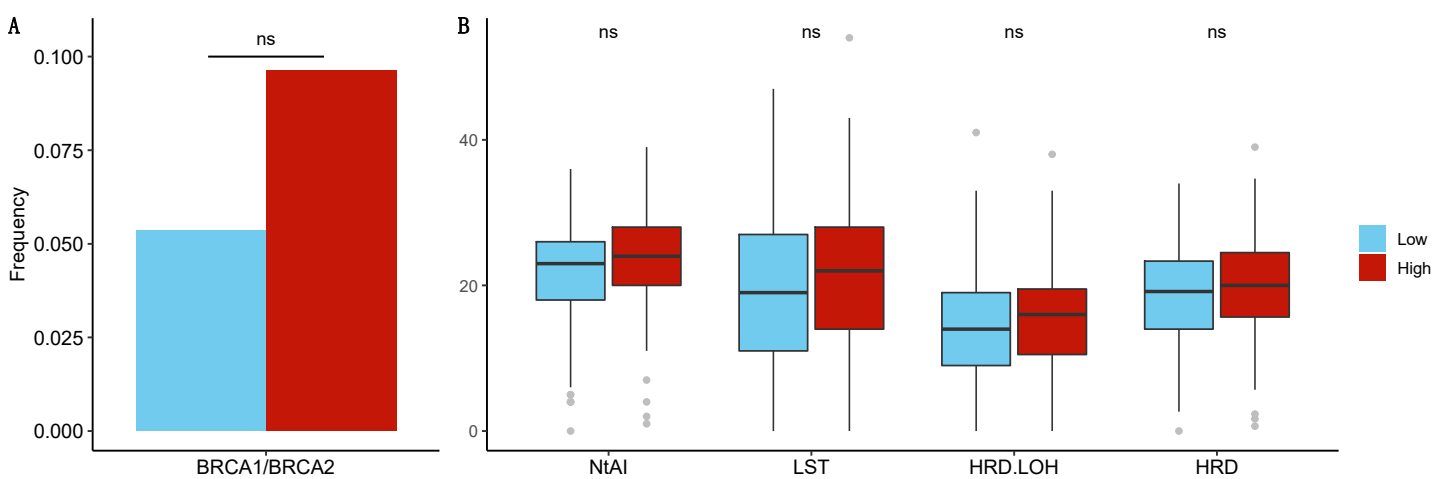




Supplementary Figure 1. The mutation and CNV frequency characteristic of the ovarian cancer samples in TCGA. **(A)** The waterfall plot for the 22 adenosine metabolism related genes; **(B)** The frequency of copy number amplification and deletion for these genes.

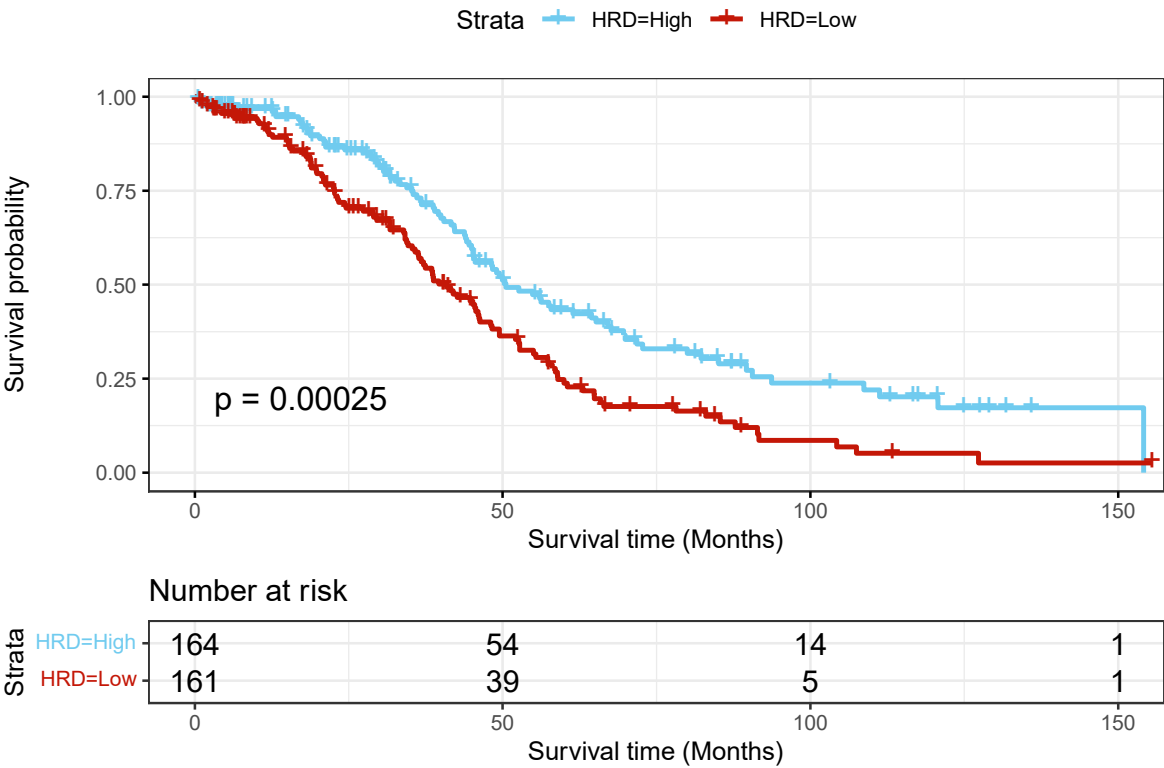


Supplementary Figure 2. Results of NMF cluster for TCGA ovarian cancer samples. **(A)** The cophenetic correlation coefficient at different factorization rank; **(B)** The heatmap of the Metagene expression for all samples.

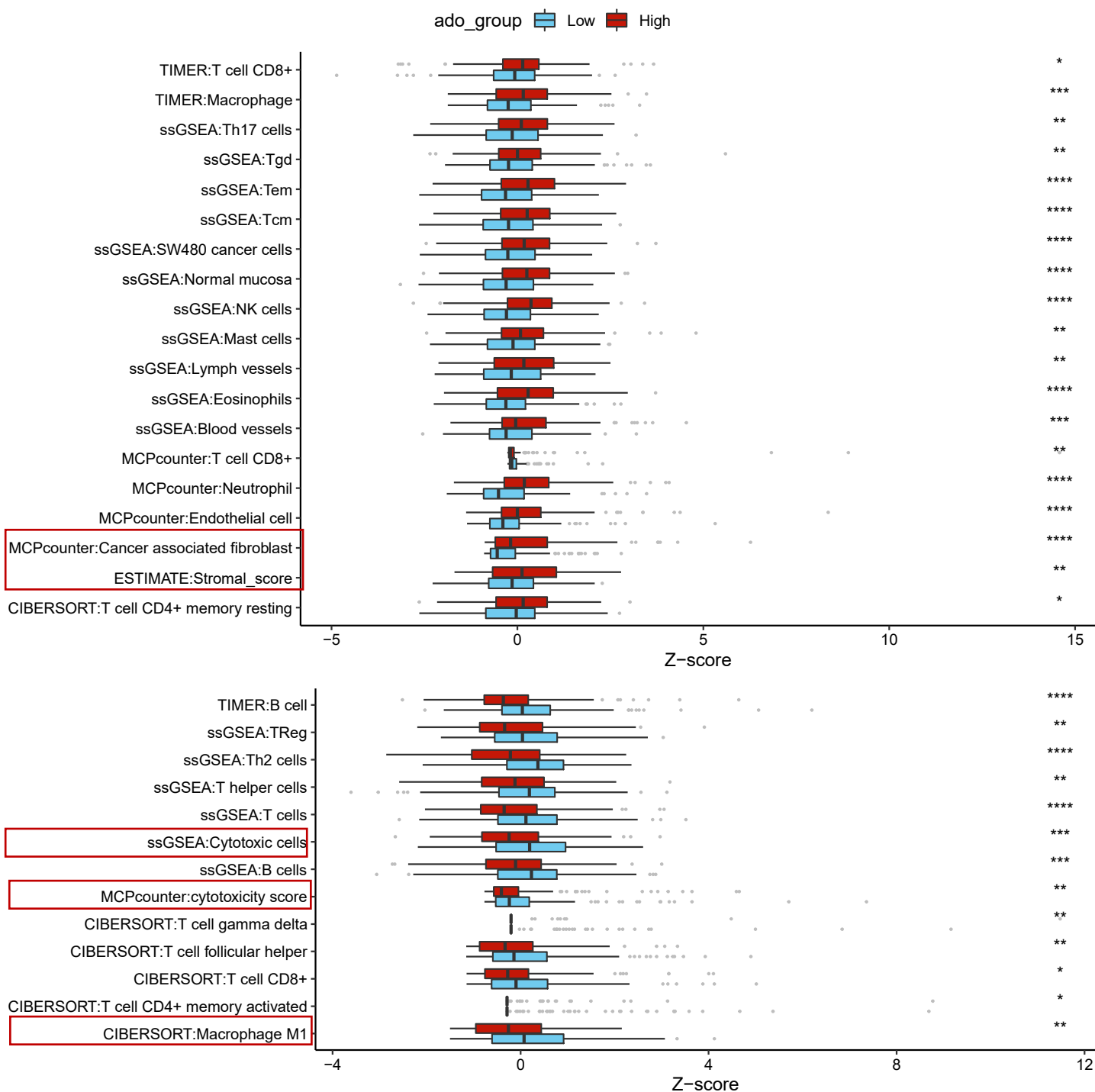


Supplementary Figure 3. Comparison of BRCA1/2 mutation frequency and genome instability between two ADO groups. (A) Barplot of BRCA1/2 mutation frequency; (B) Boxplots of Number of Telomeric Allelic Imbalances (NtAI) count, Large-scale State Transitions (LST) count, Homologous Recombination Deficiency (HRD-LOH) score, and the HRD score. (ns: $P > 0.05$, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, $****P < 0.0001$)

HRD prognostic analysis with all samples



Supplementary Figure 4. Kaplan-Meier survival curve between HRD groups in TCGA dataset.



Supplementary Figure 5. Boxplots of ADO score and immune cell signatures (*P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001)