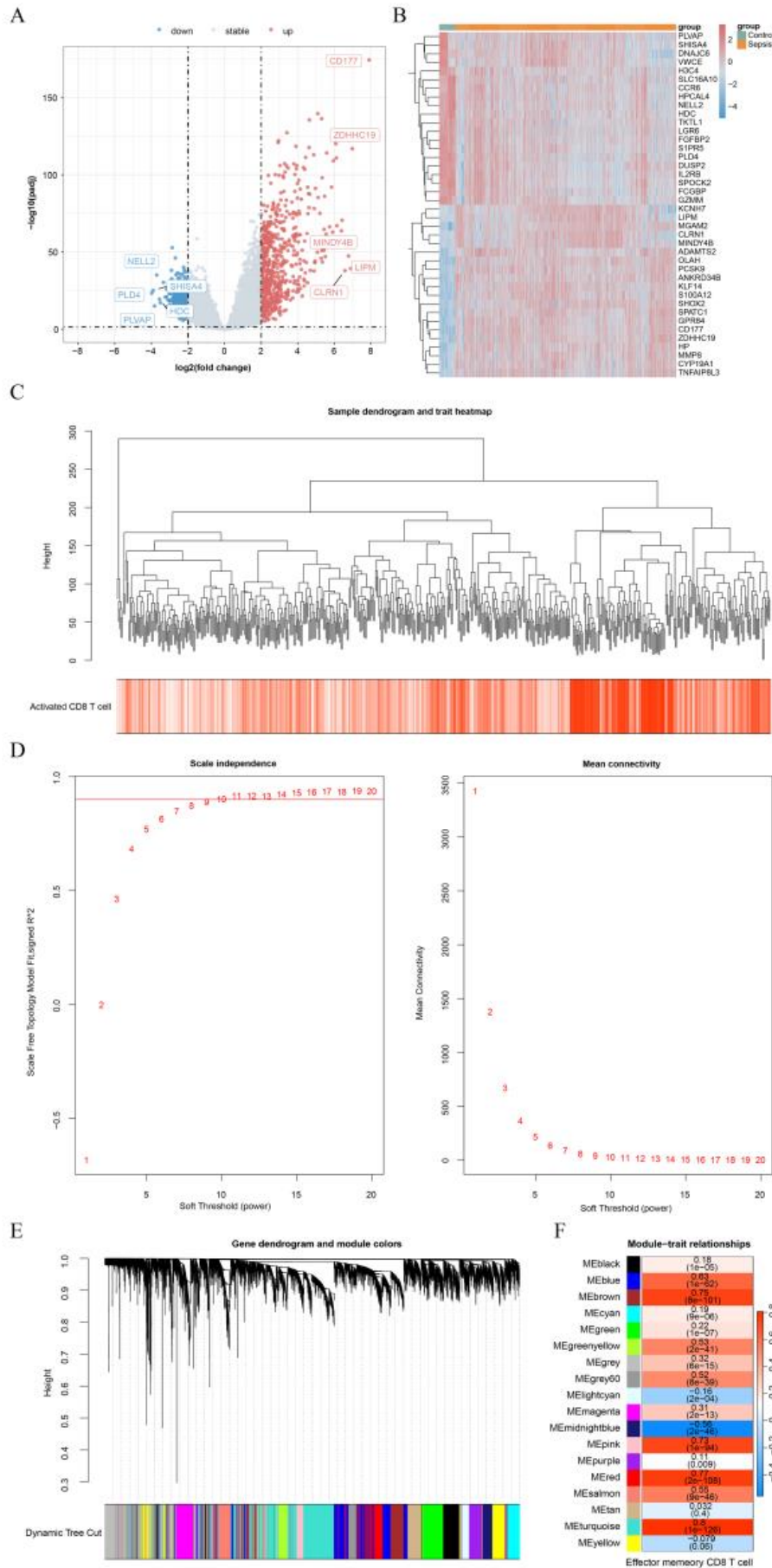
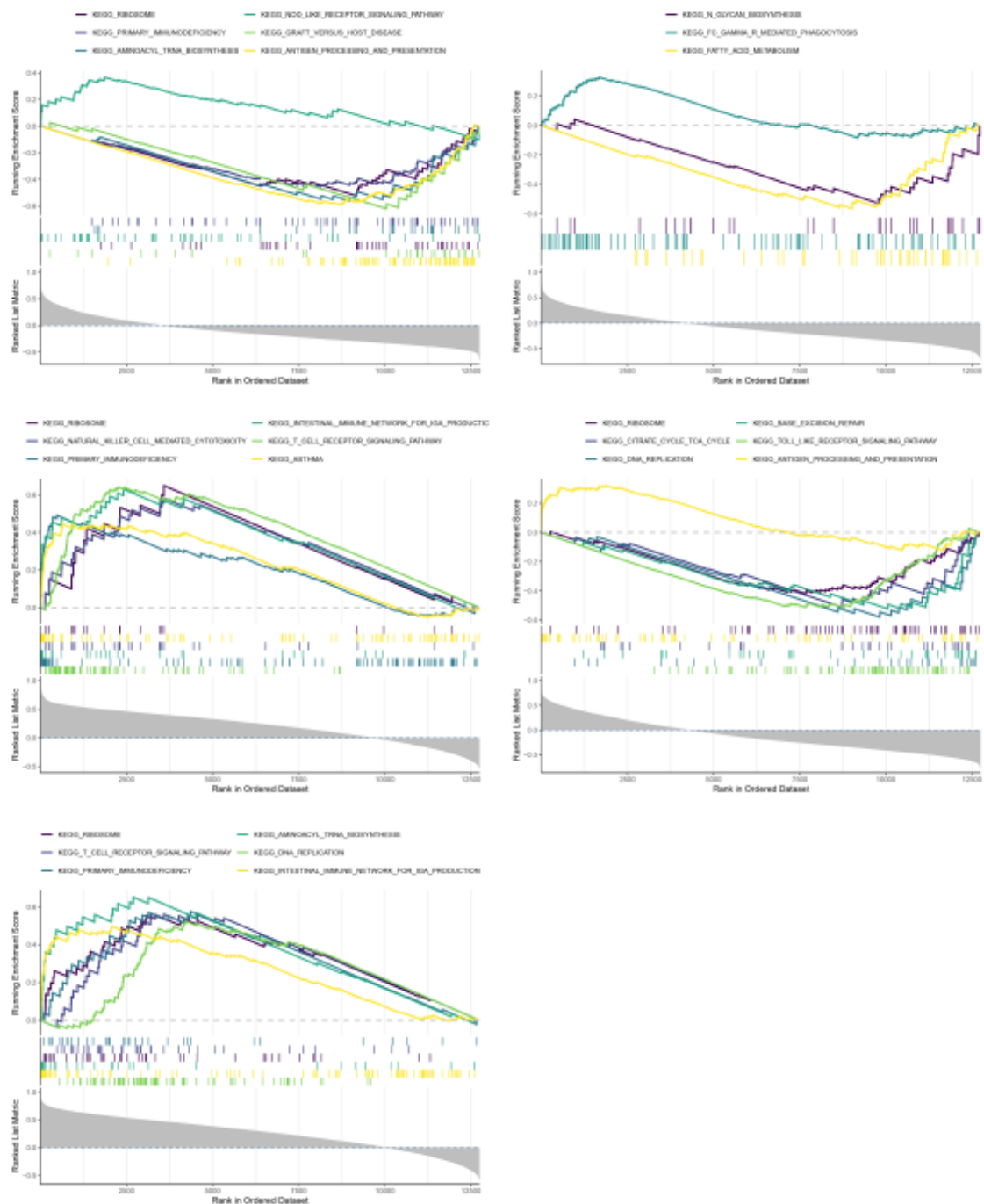




注: A 为脓毒症与对照组间的差异表达基因(Differentially expressed genes1, DEGs1) 的火山图; B 为 DEGs1 的热图; C 为样本聚类; D 为软阈值筛选; E 为模块聚类树; F 为模块与效应记忆 CD8⁺ T 细胞的相关性热图。

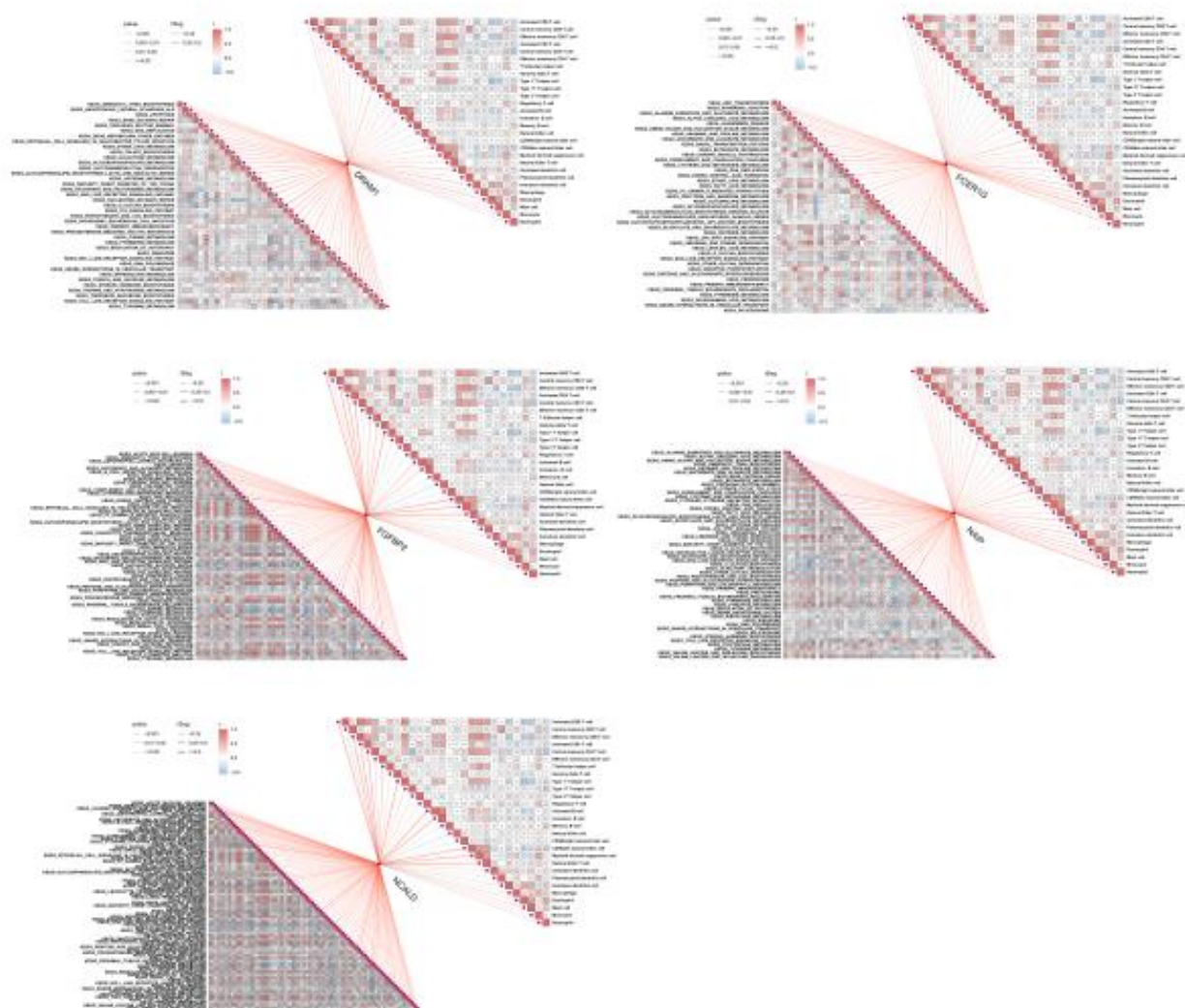
附图 1 差异表达和加权基因共表达网络分析 (Weighted gene co-expression network analysis, WGCNA)

Fig S1 Differential expression analysis and WGCNA



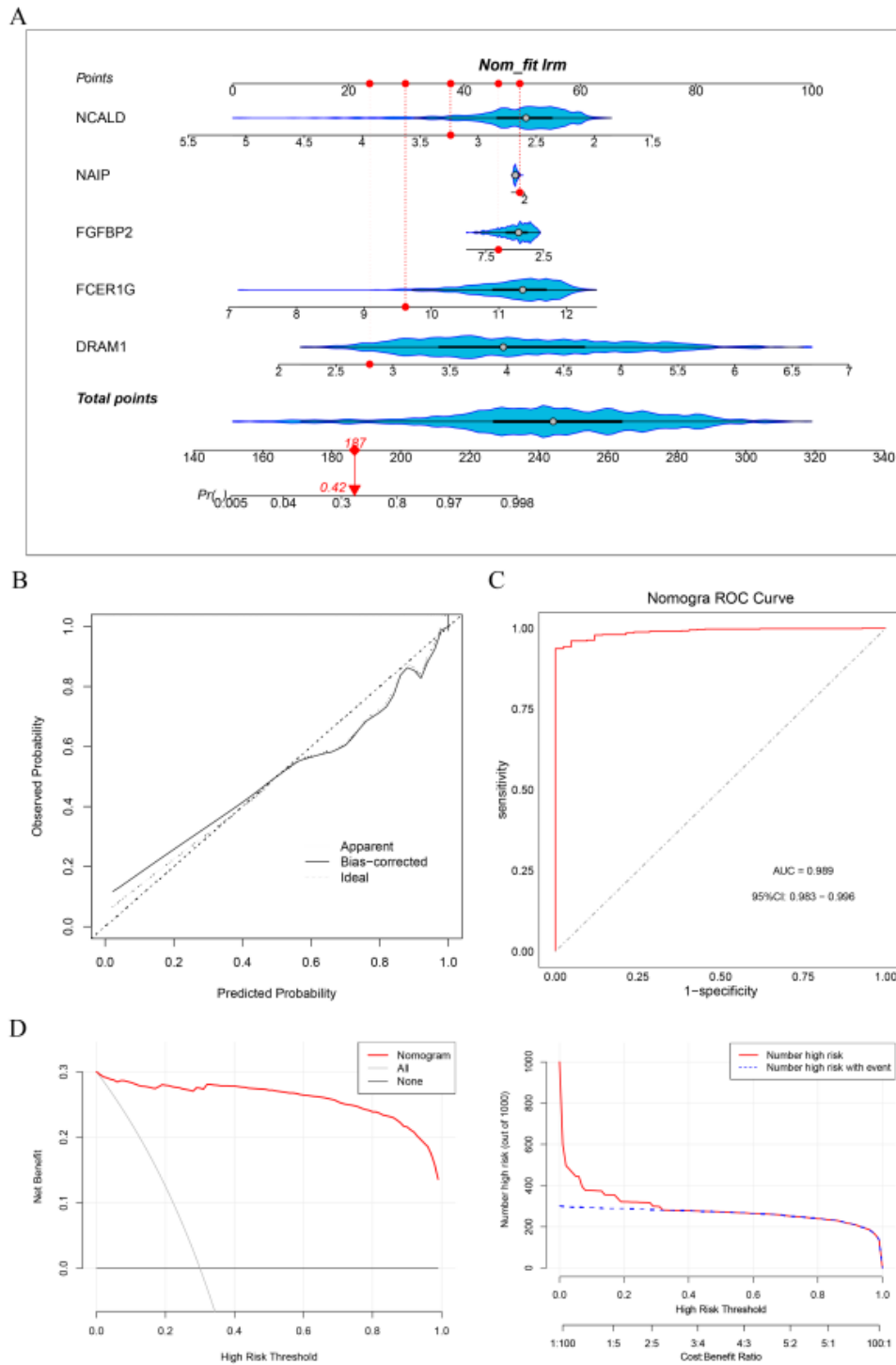
附图 2 DRAM1、FCER1G、FGFBP2、NAIP 和 NCALD 的基因集富集分析
(Gene set enrichment analysis, GSEA)

Fig S2 GSEA of DRAM1, FCER1G, FGFBP2, NAIP, and NCALD, respectively



附图 3 生物标志物与通路和免疫细胞的相关性

Fig S3 The correlations of biomarkers with pathways and immune cells were analyzed



注：A 为列线图；B 为校准曲线；C 为 ROC 曲线；D 为决策曲线和临床影响曲线。

附图 4 列线图的构建（验证集）

Fig S4 Construction of the nomogram (Validation set)