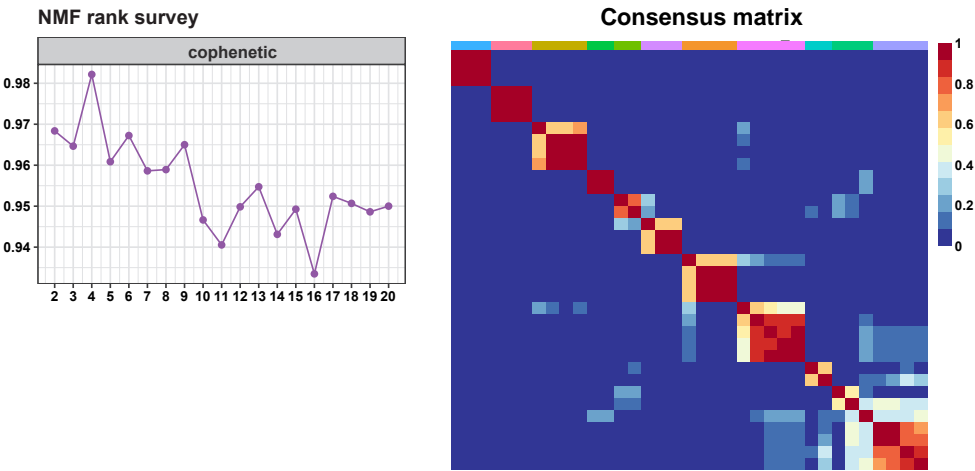
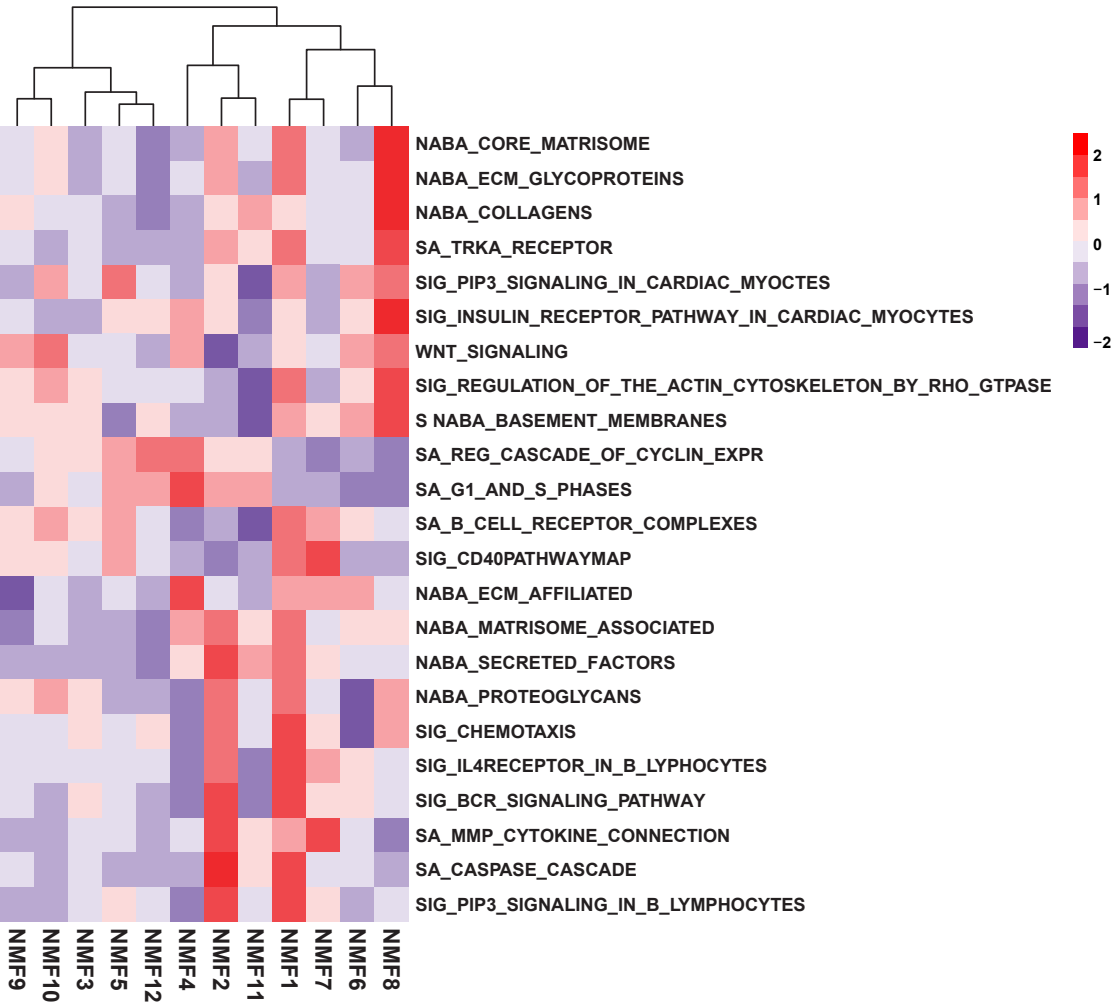


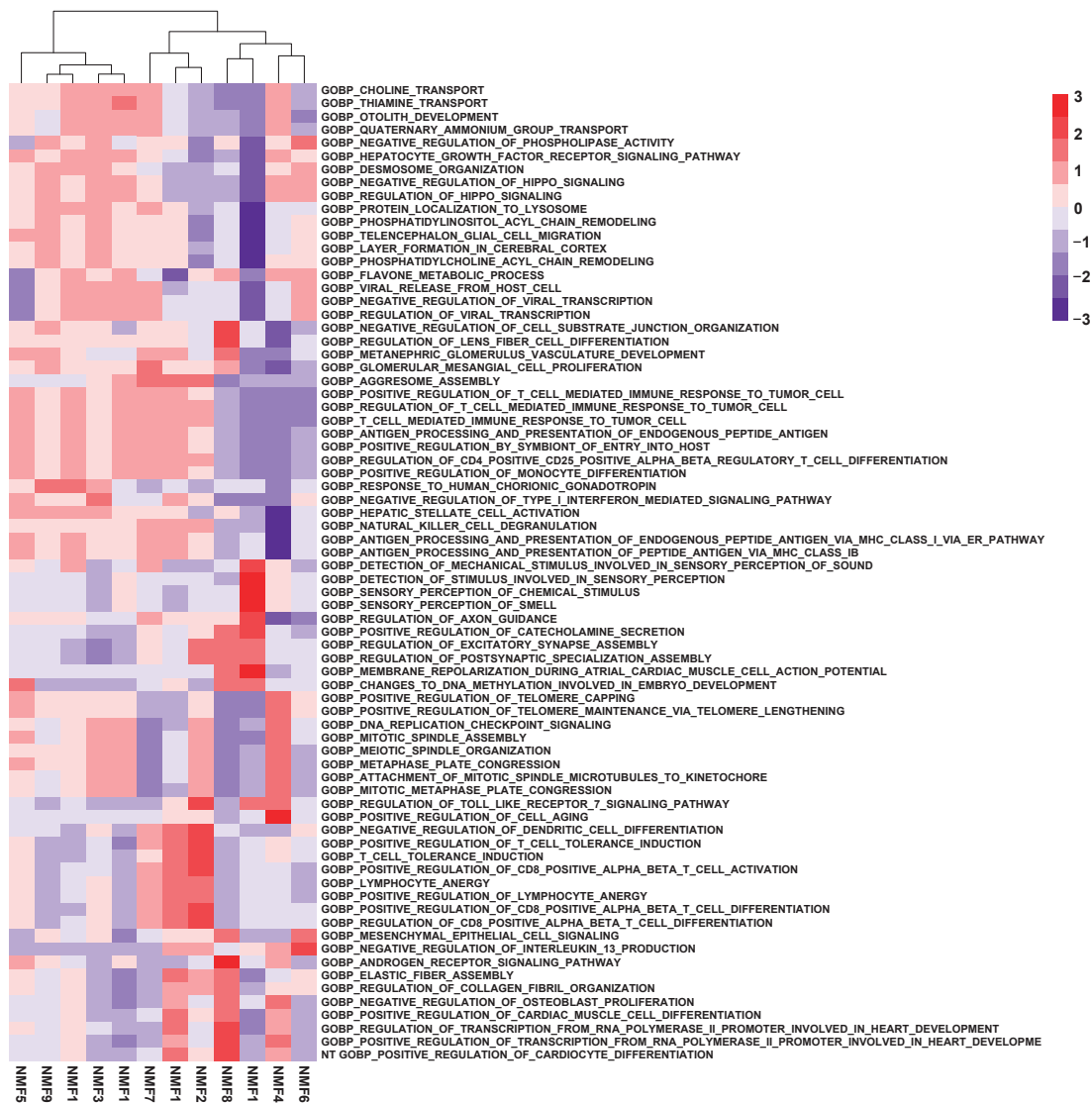
A



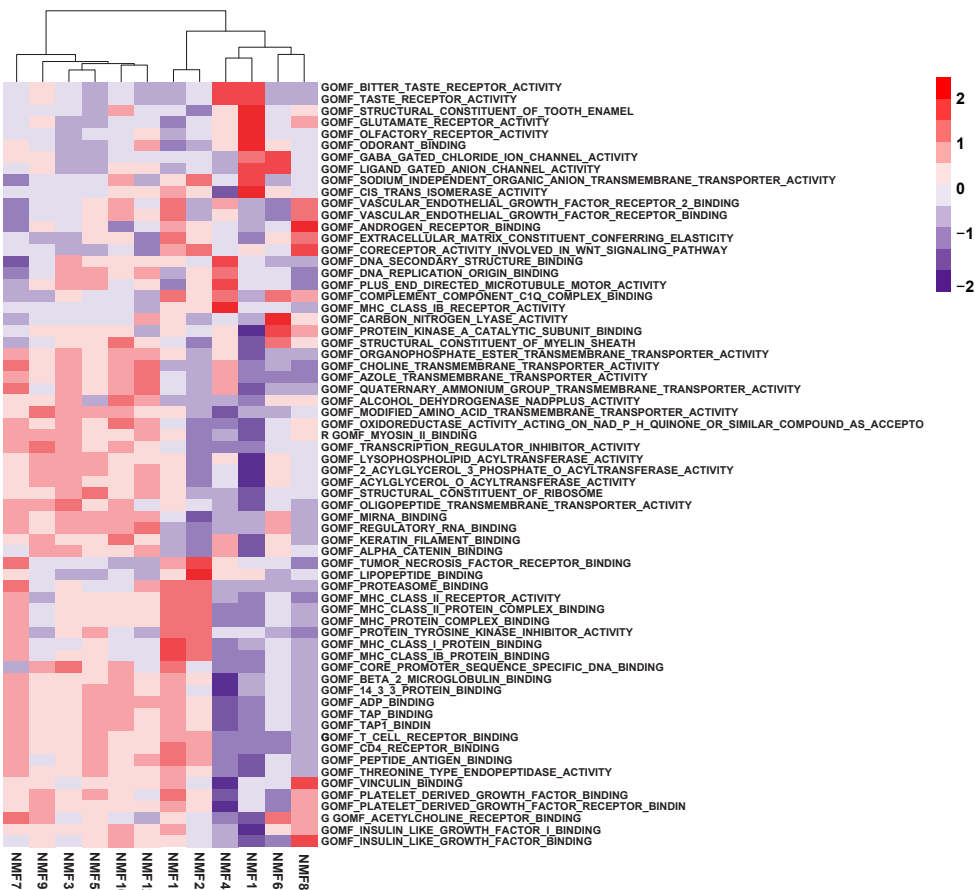
B



C



D



E



Figure S1. Analysis of pre- and post-treatment datasets using NMF. A, Cophenetic distribution was calculated in 2-20 runs. We selected K=12 as optimal and visualized the consensus matrix to calculate the robustness. B, Heatmap of the Curated gene sets pathway result. C, Heatmap of the Ontology gene sets (BP) pathway result. D, Heatmap of the Ontology gene sets (MF) pathway result. E, Heatmap of the Hallmark gene sets pathway result.