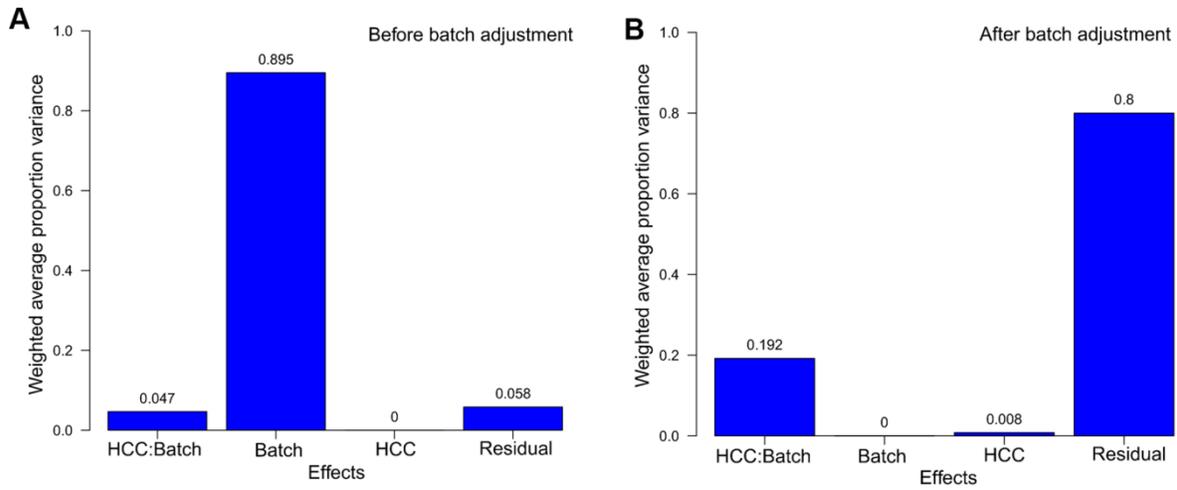
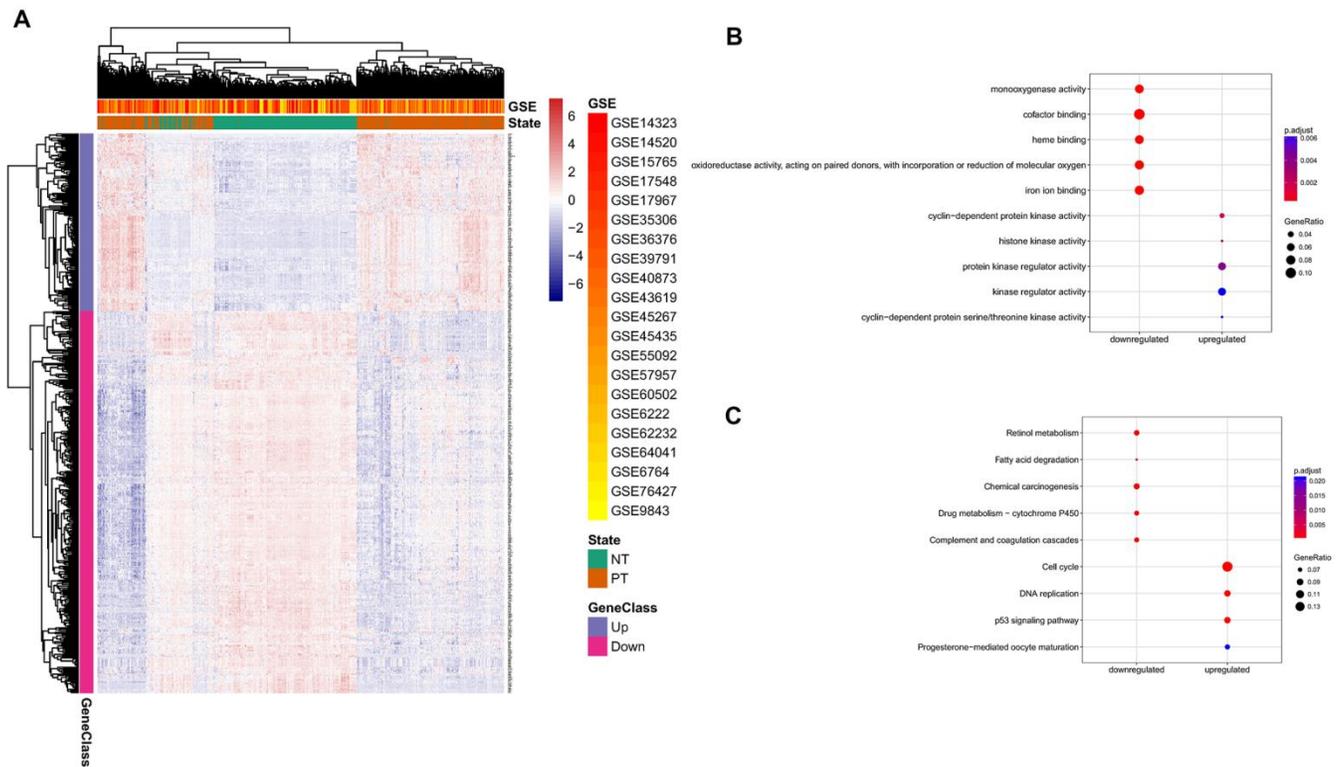


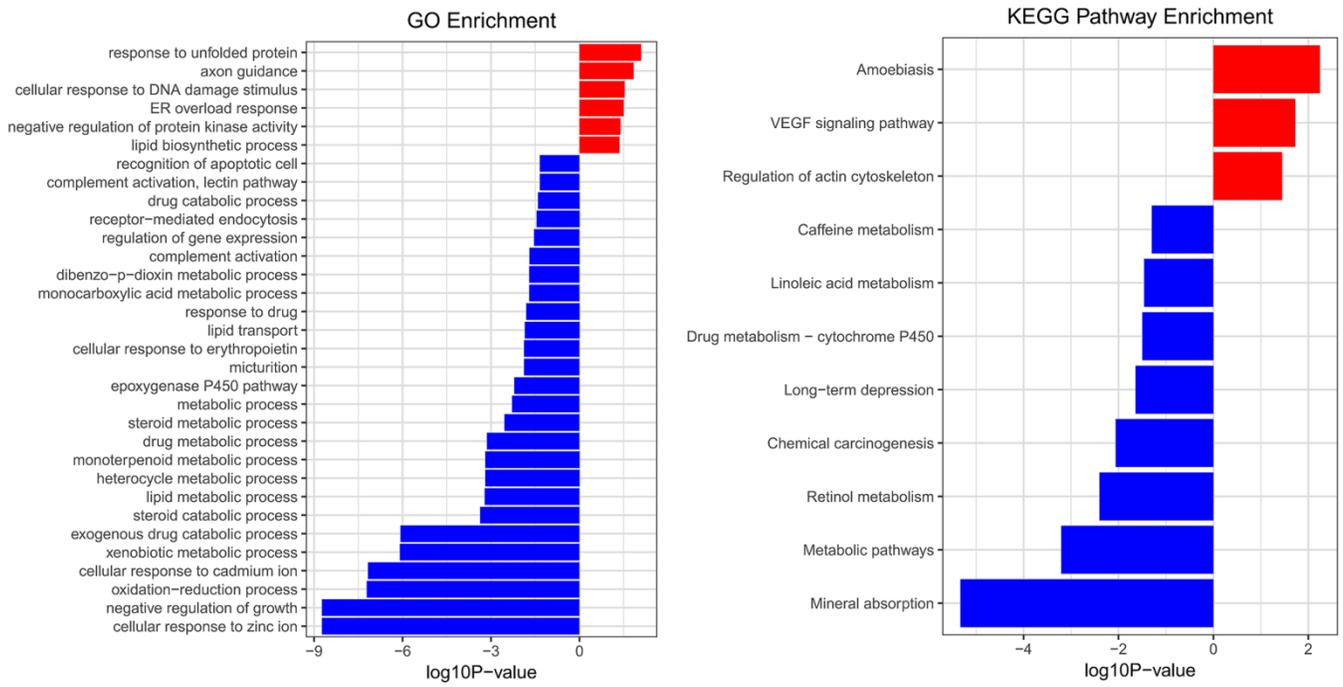
SUPPLEMENTARY FIGURES



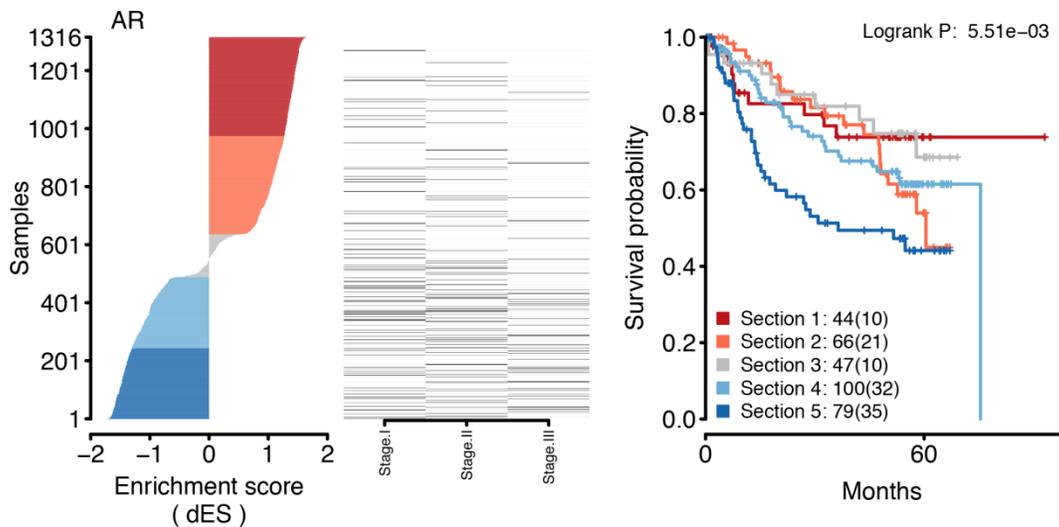
Supplementary Figure 1. Quality assessment of batch correction for microarray data merging. The bar chart shows the proportion of variation attributable to batch effects introduced from potential sources. All the effects, including batch and profile effects, interaction between batch and profile effects, and residual effects, were estimated for their contribution to the overall variation by PVCA. (A) Data before batch adjustment. (B) Data processed by ComBat as batch adjustment model.

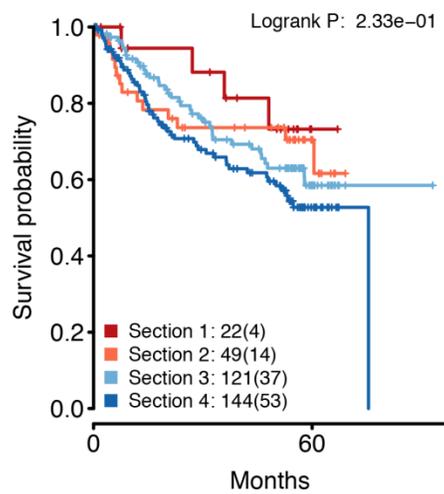
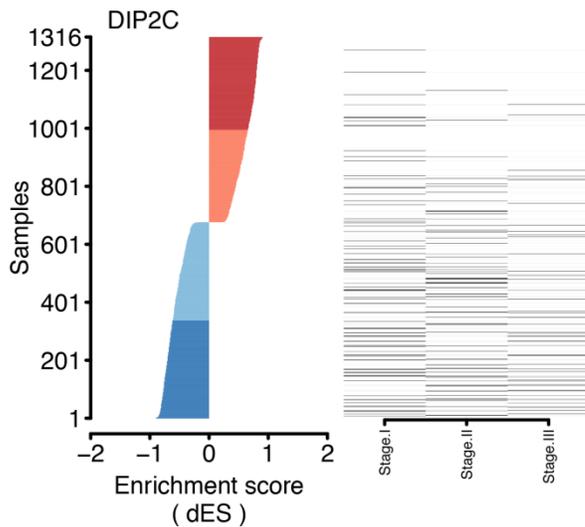
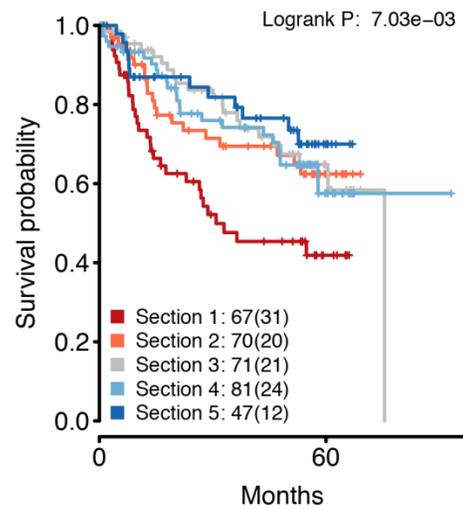
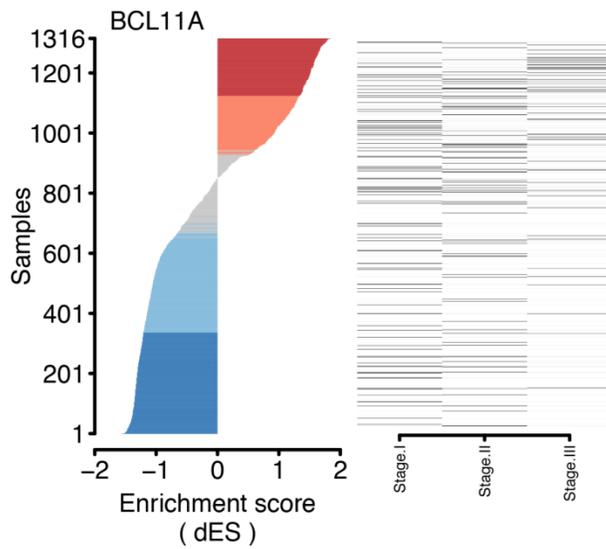
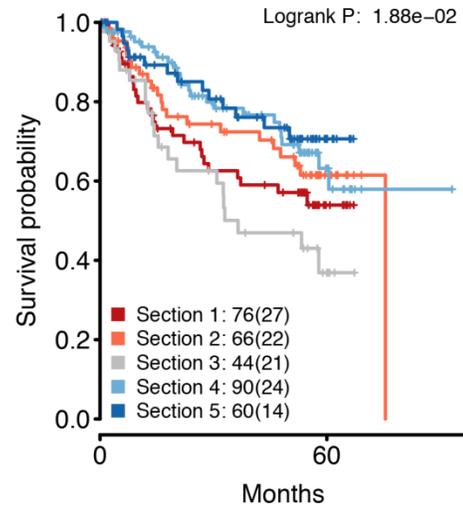
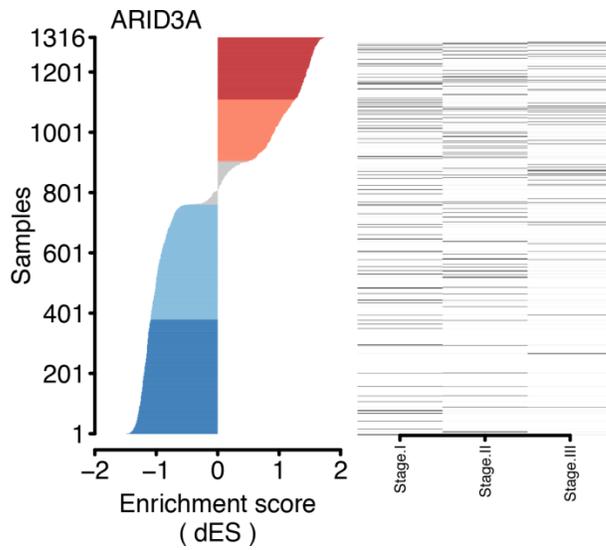


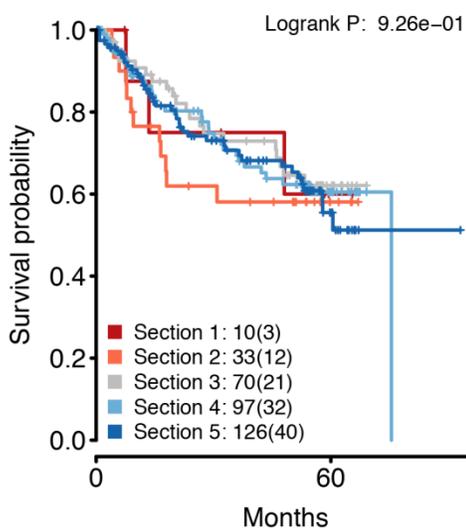
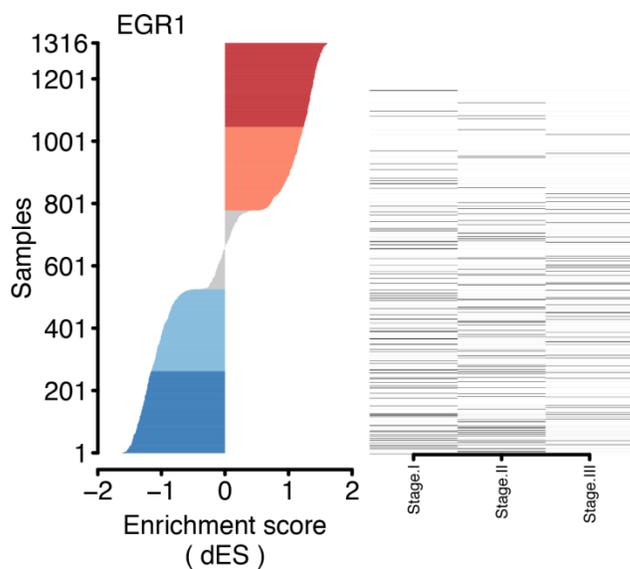
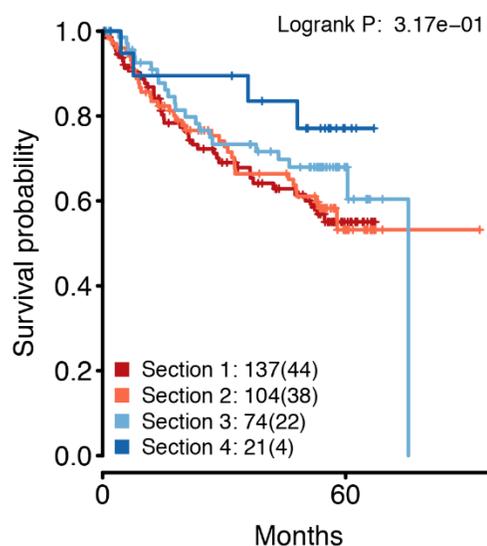
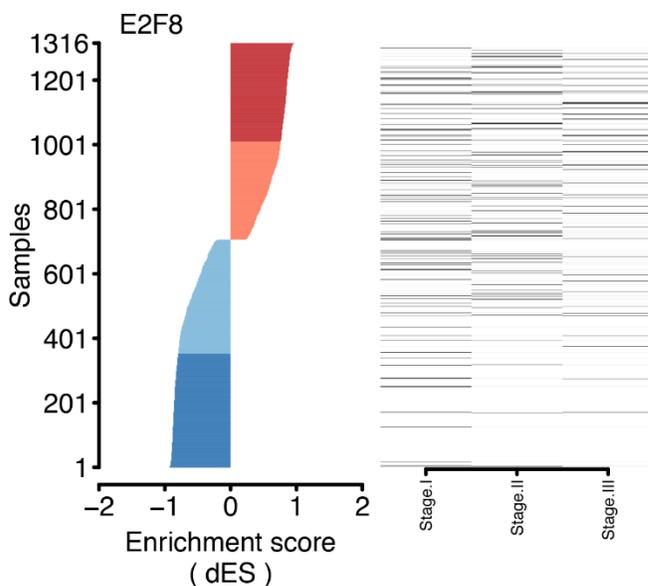
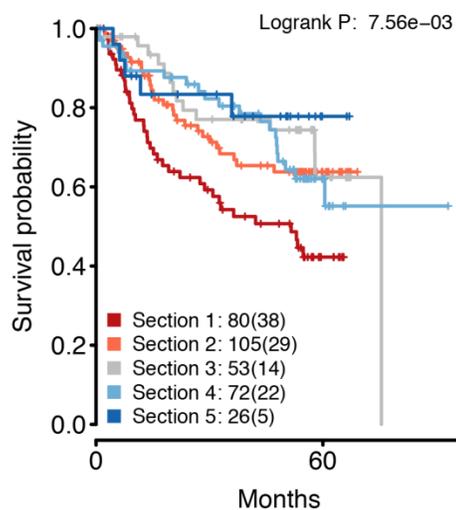
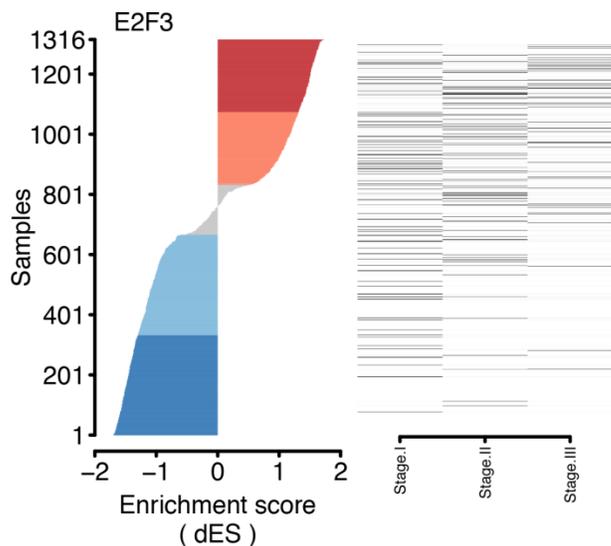
Supplementary Figure 2. HCC6 signature. (A) Clustering analysis based on expression data from 21 HCC-related datasets revealed a clear transcriptional homogeneity in the investigated samples. (B) GO and KEGG analysis of the HCC6 signature.

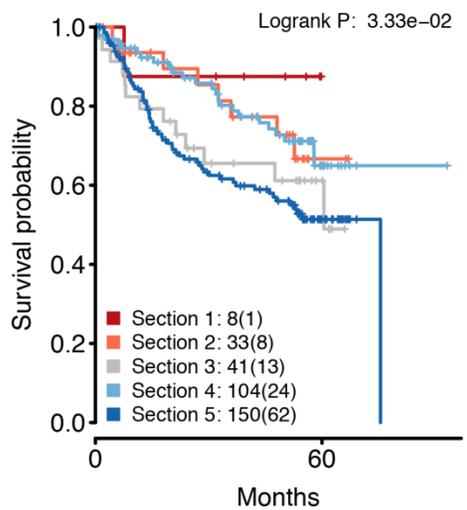
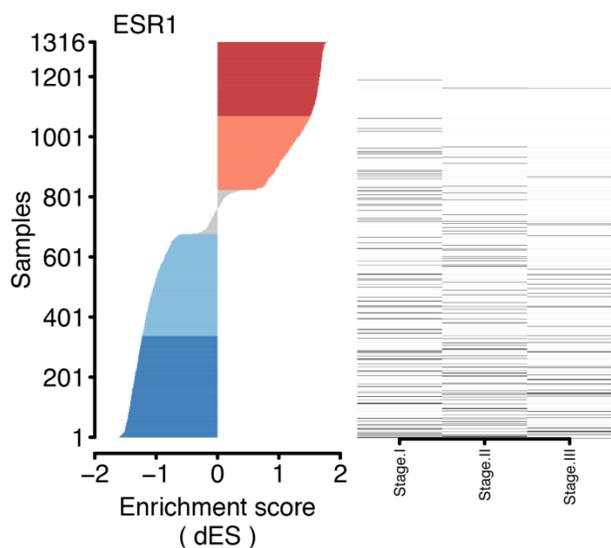
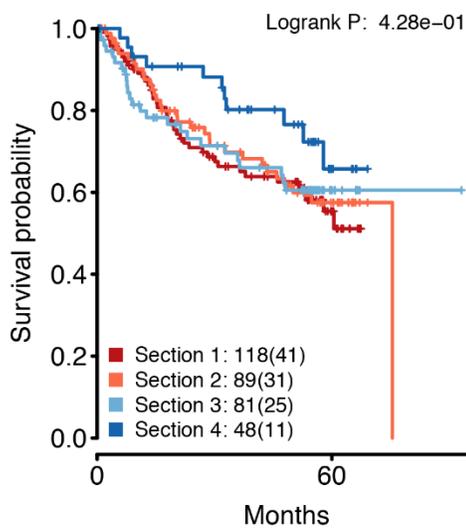
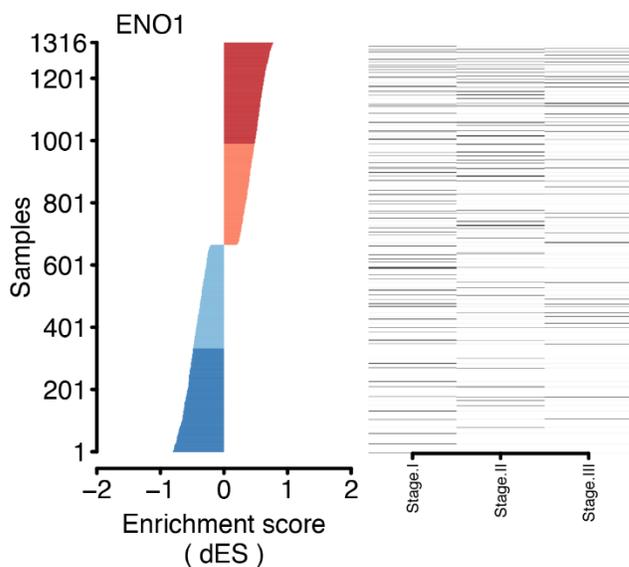
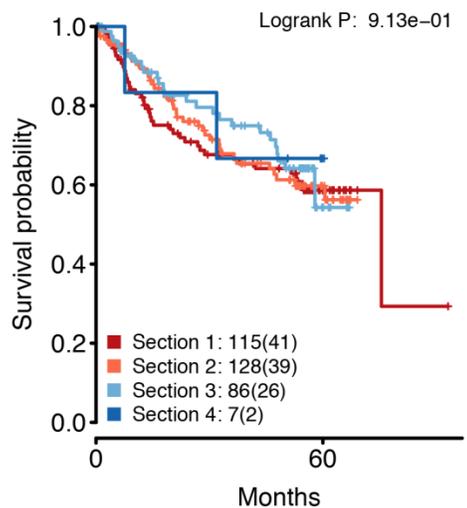
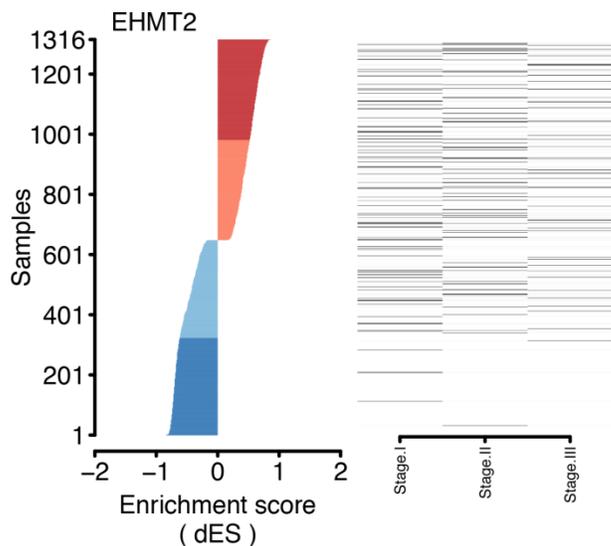


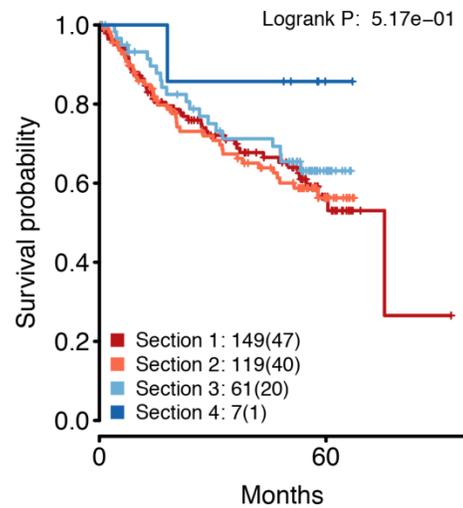
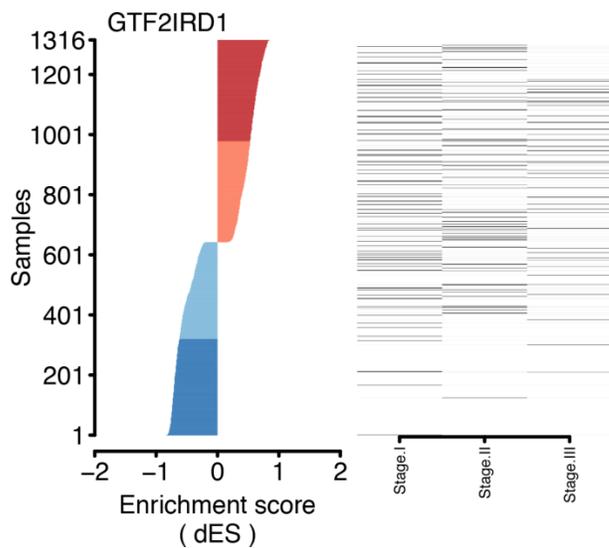
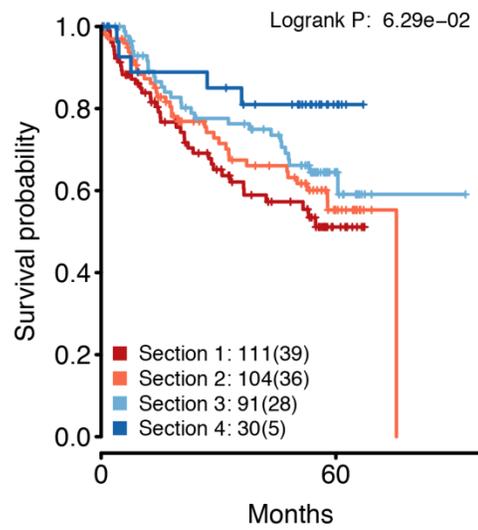
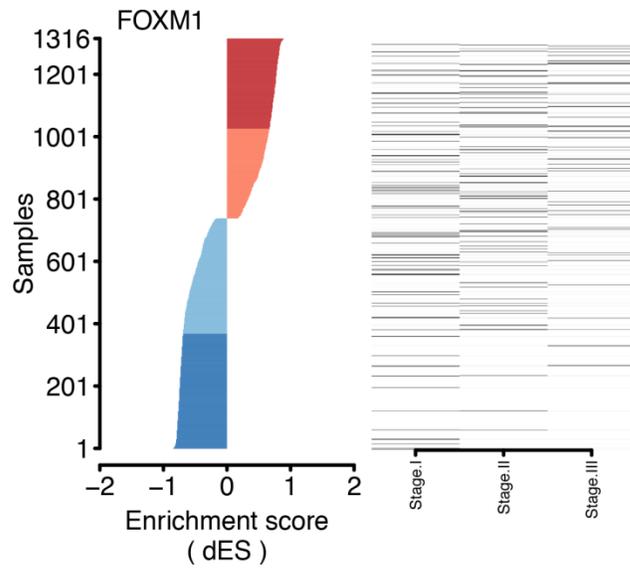
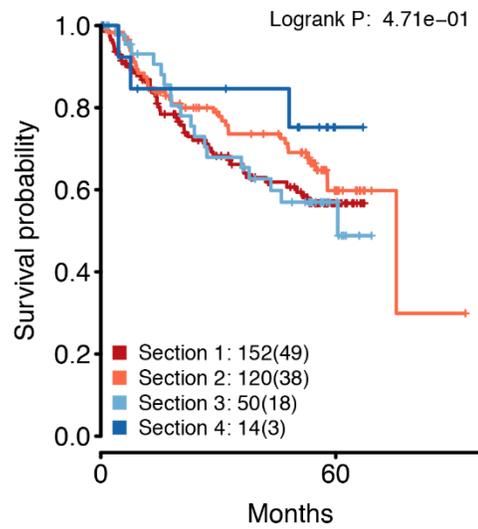
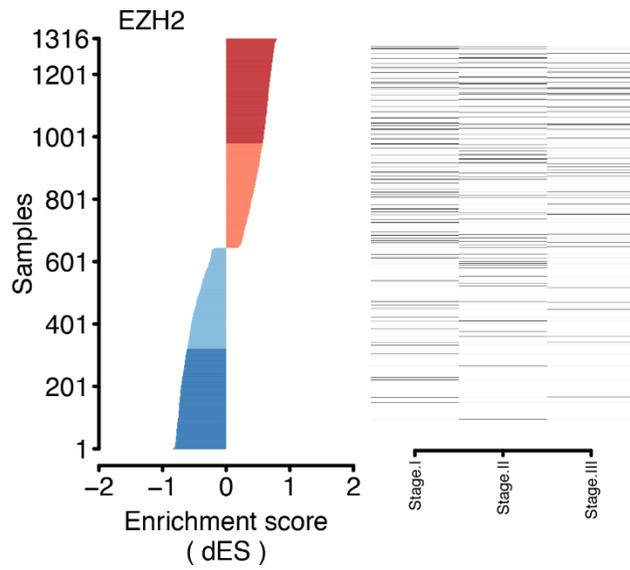
Supplementary Figure 3. Functional annotation of the ESR1 regulon. Red indicates the activated functions by ESR1 regulon. Blue indicates the repressed functions by ESR1 regulon.

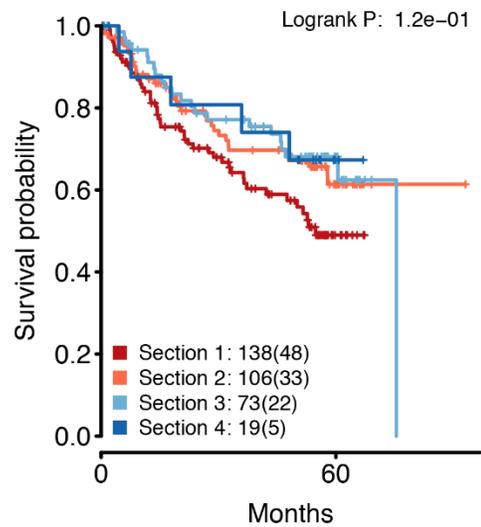
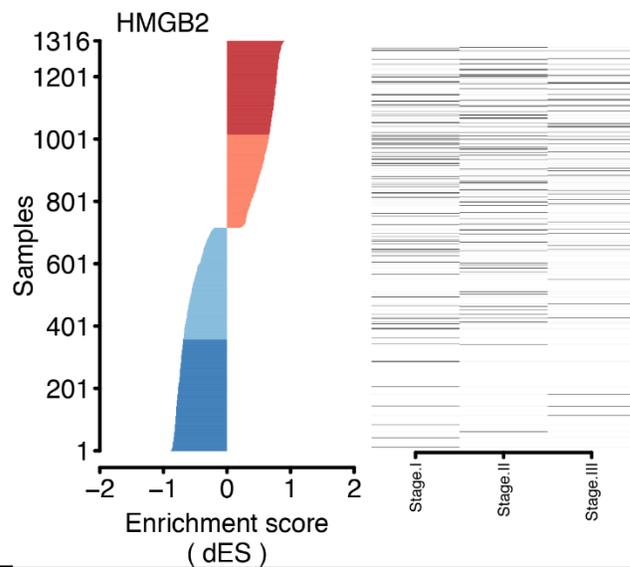
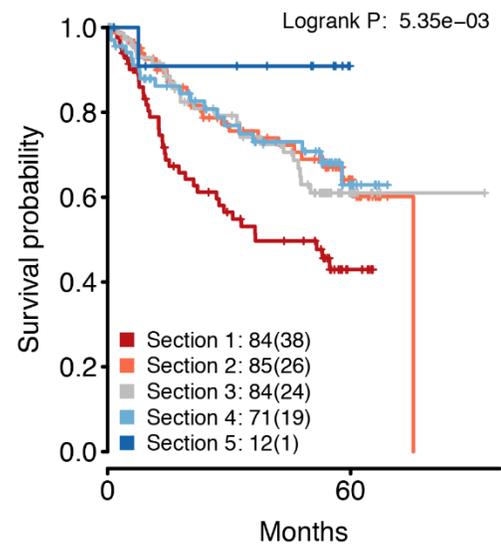
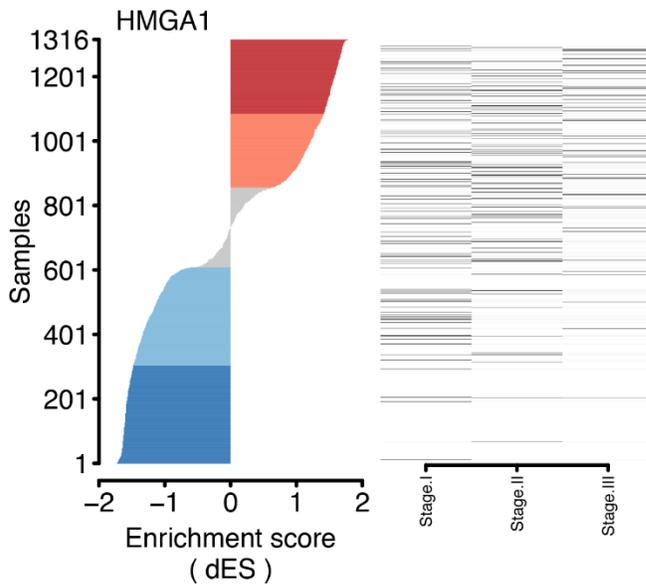
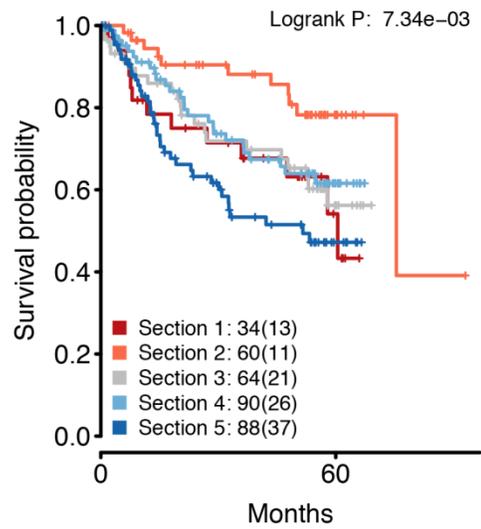
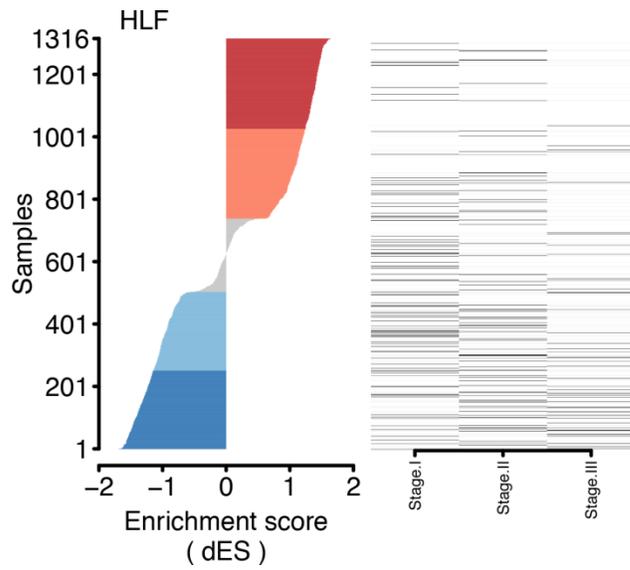


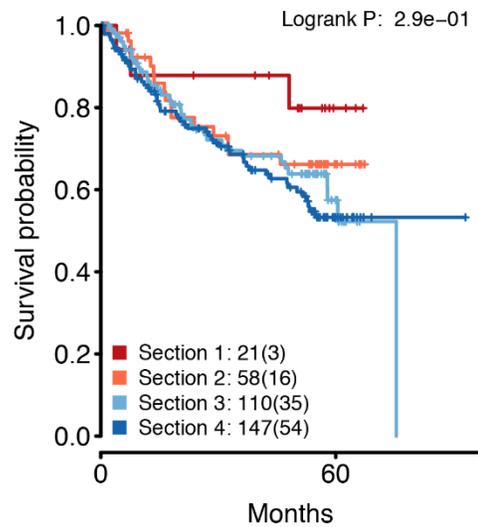
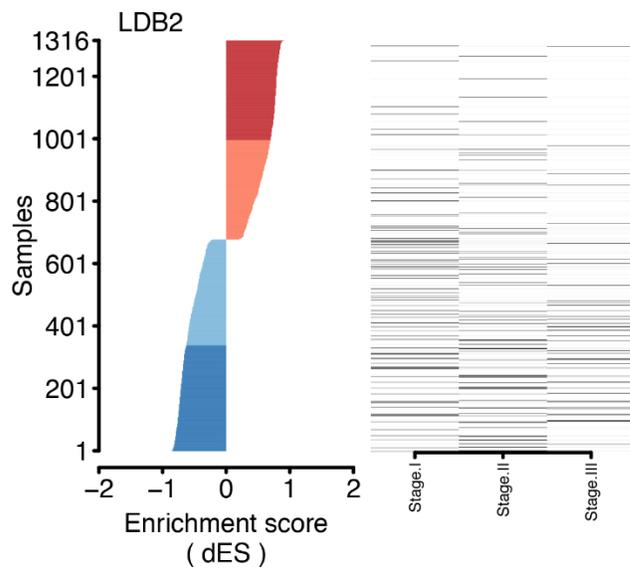
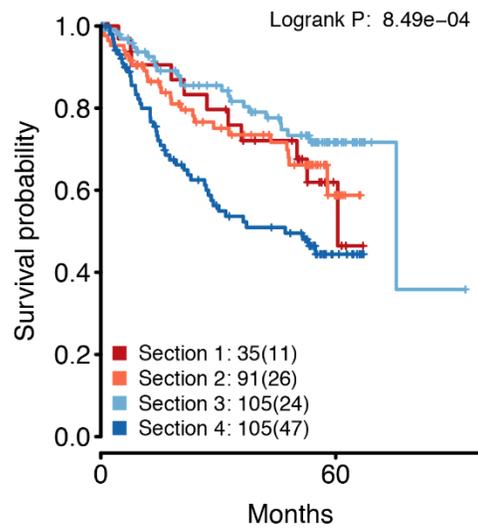
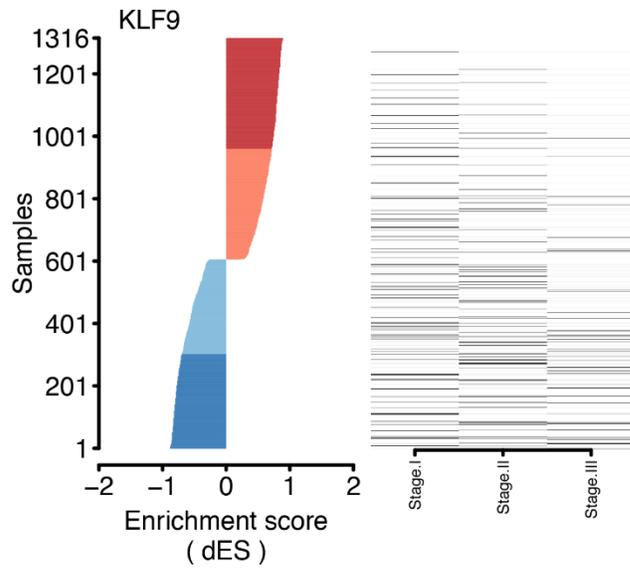
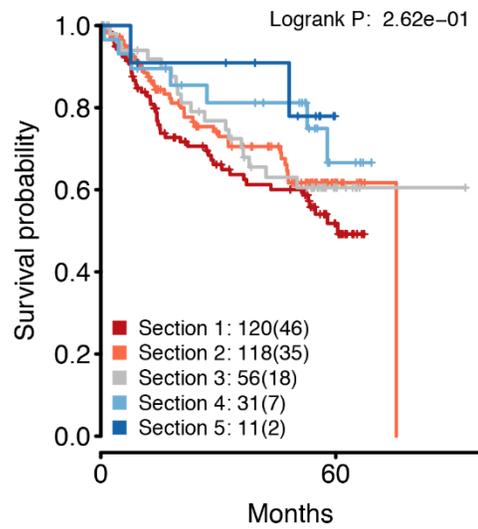
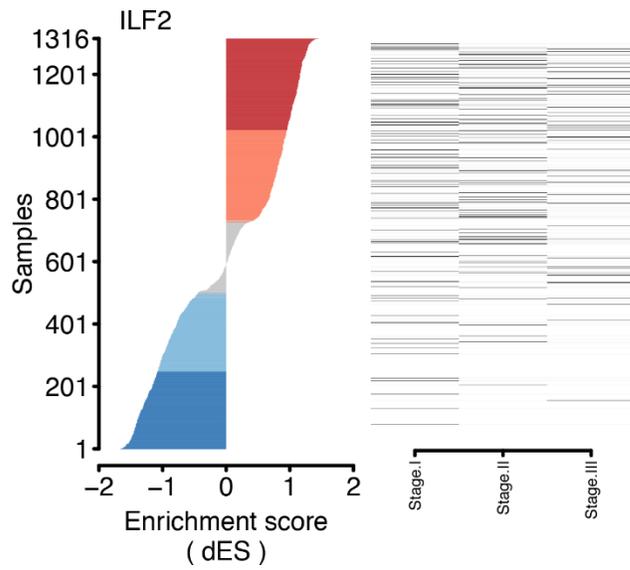


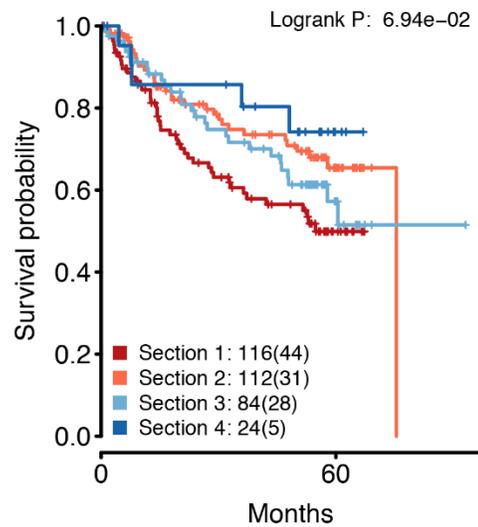
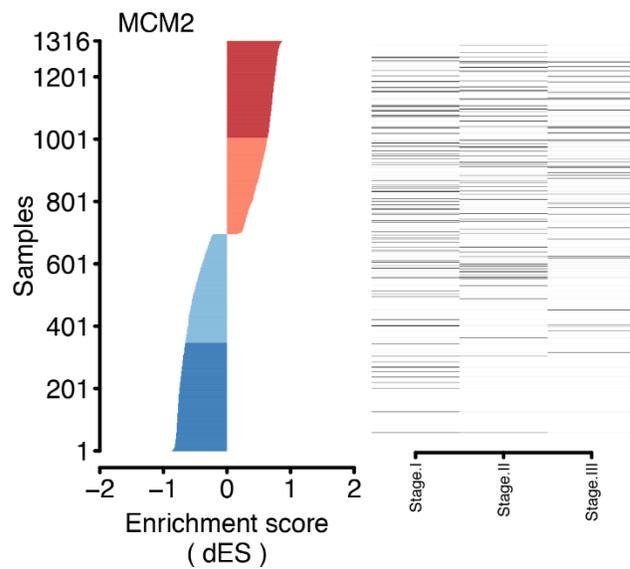
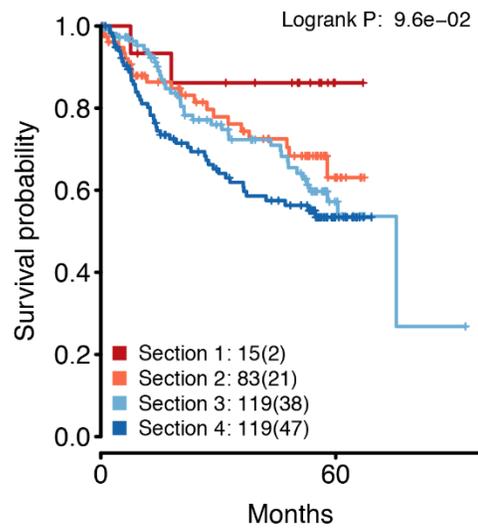
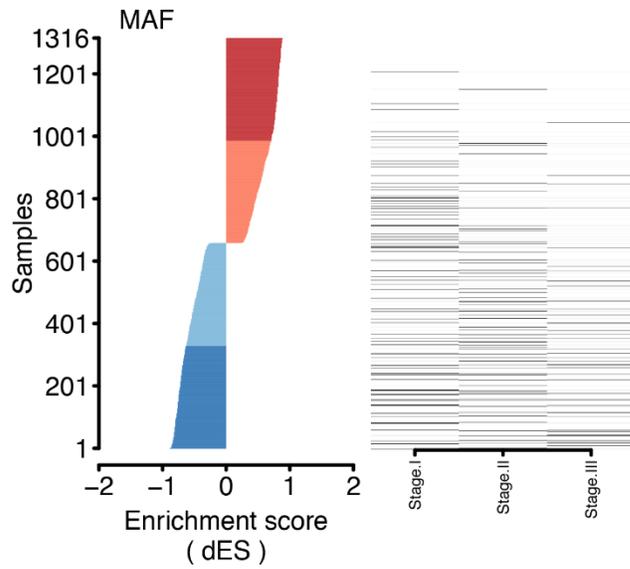
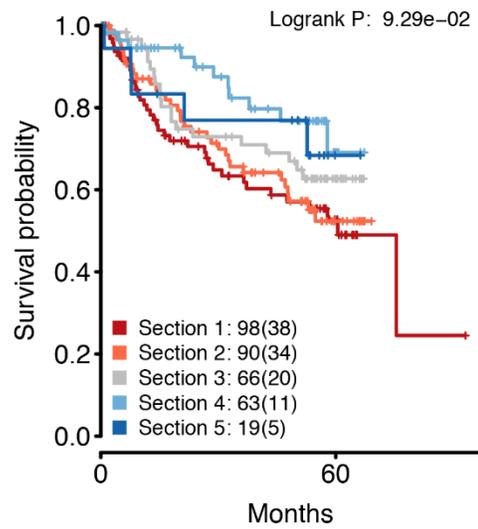
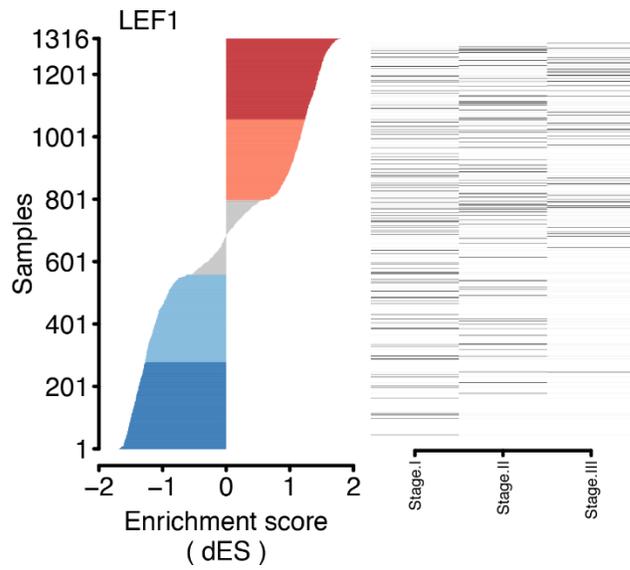


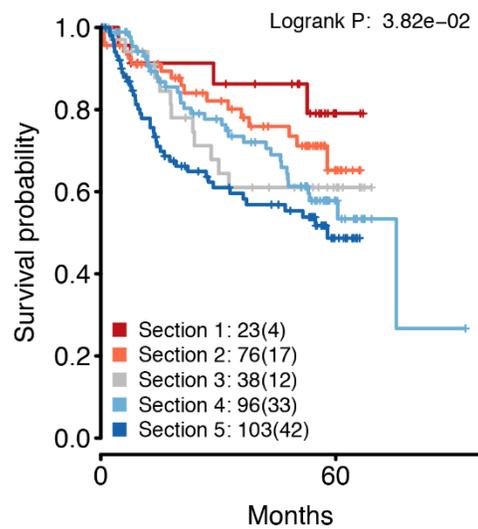
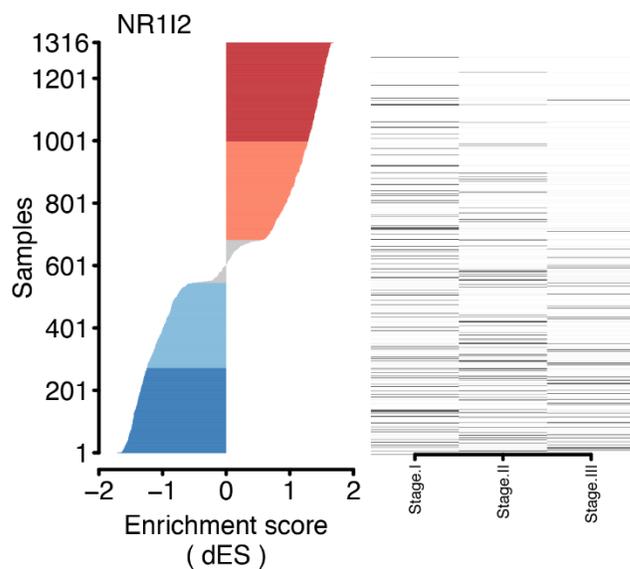
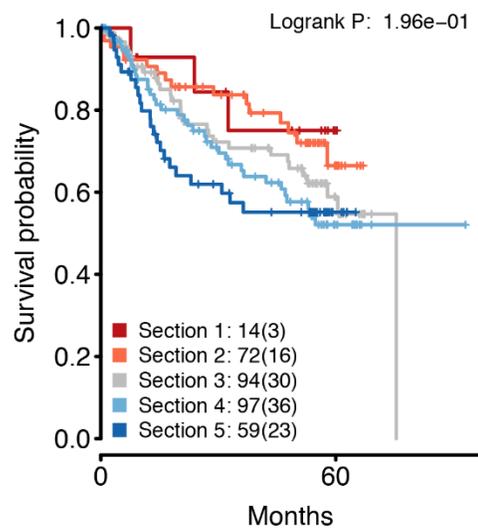
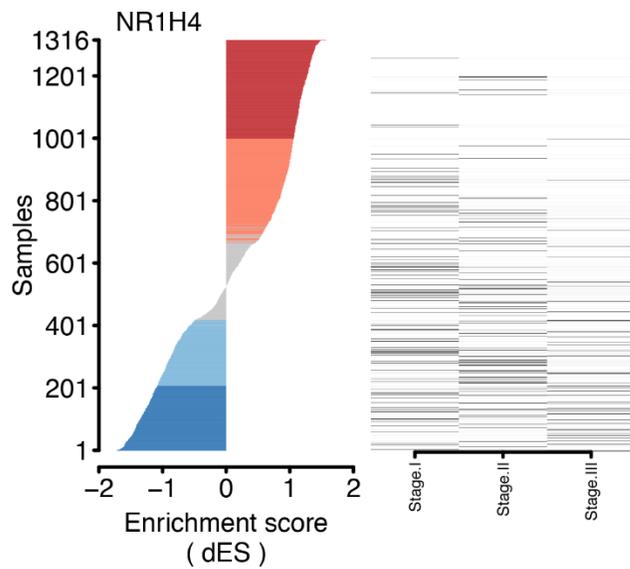
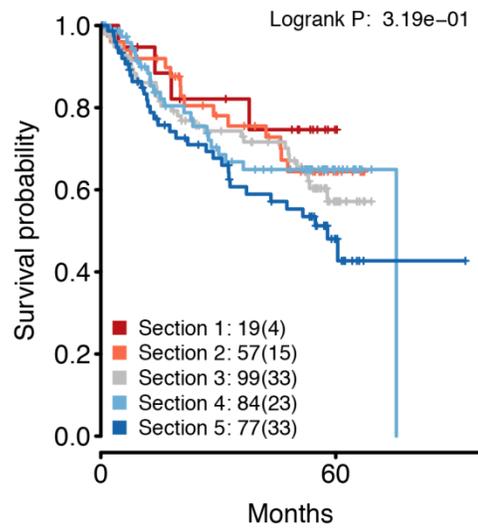
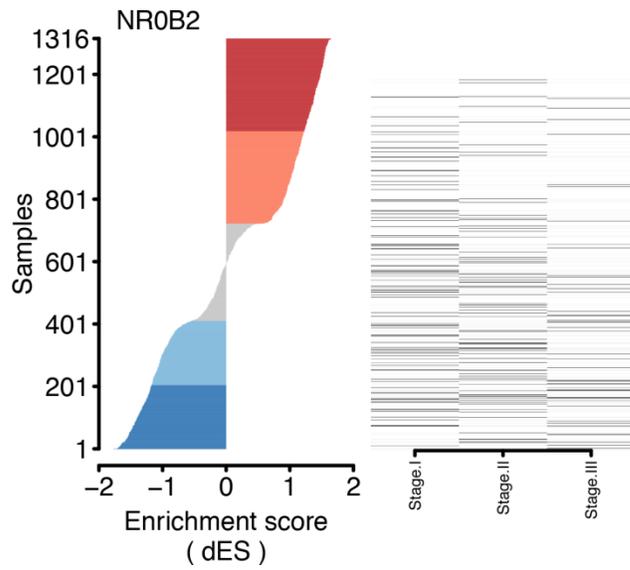


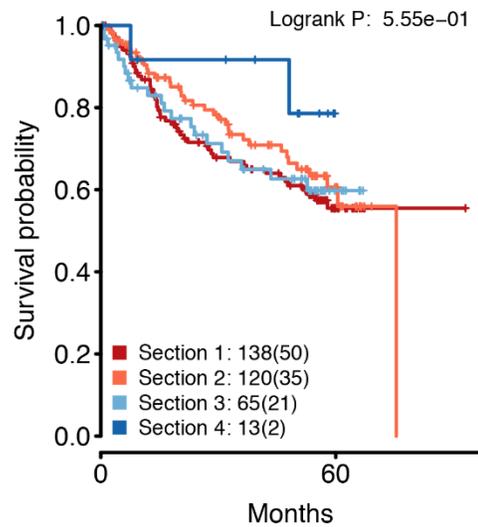
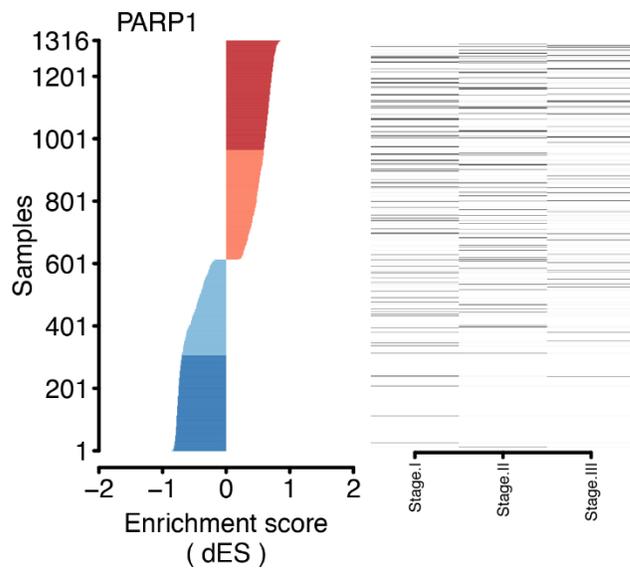
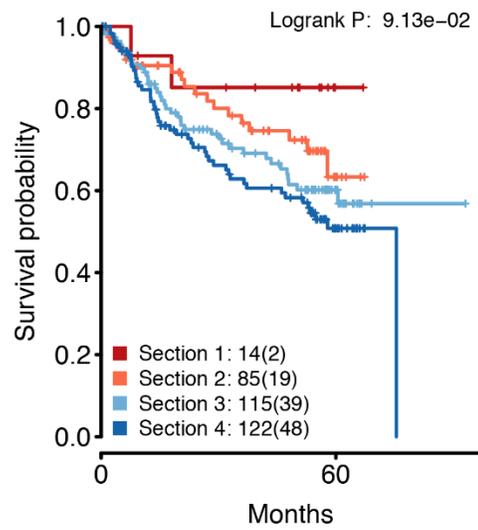
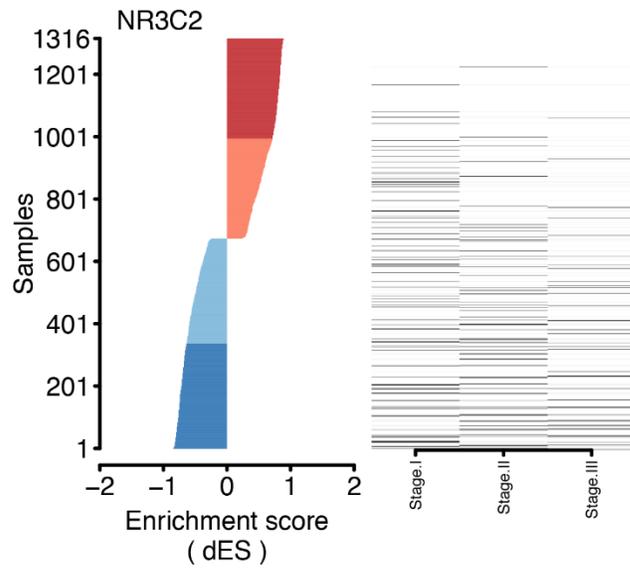
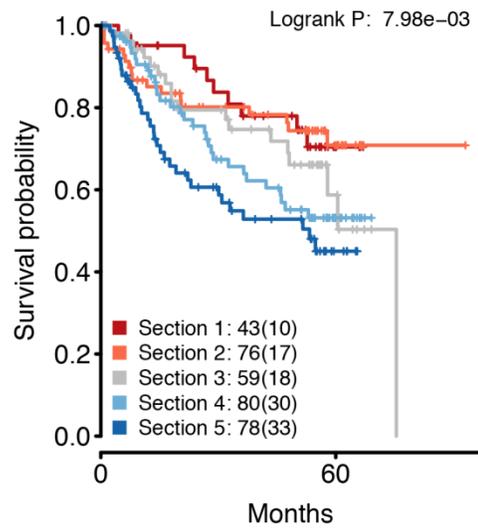
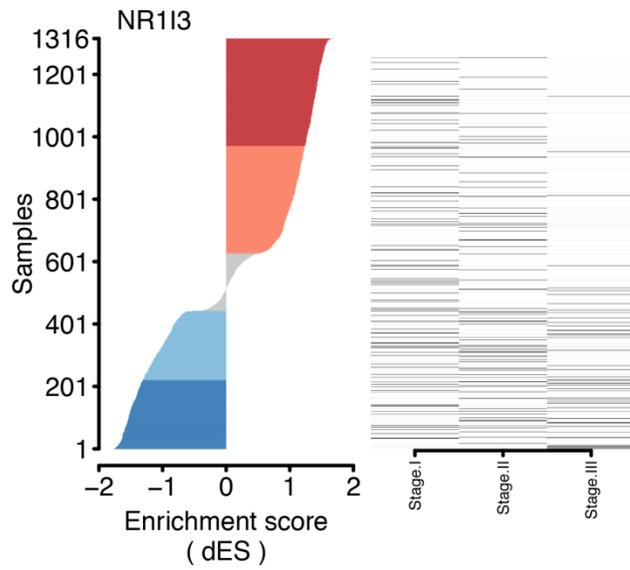


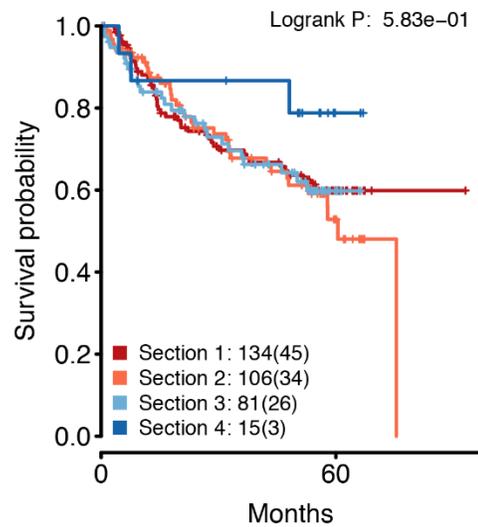
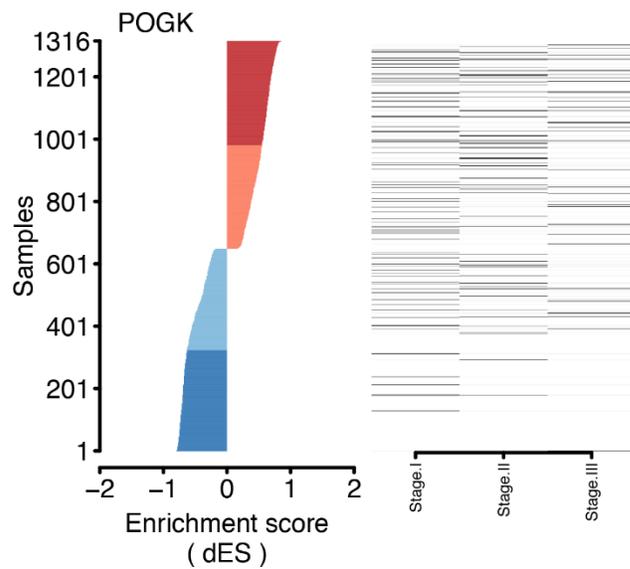
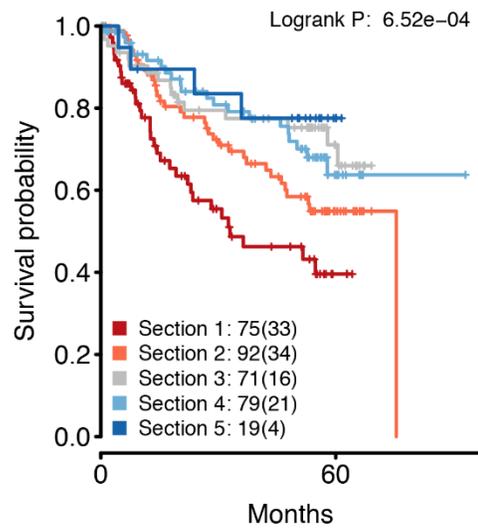
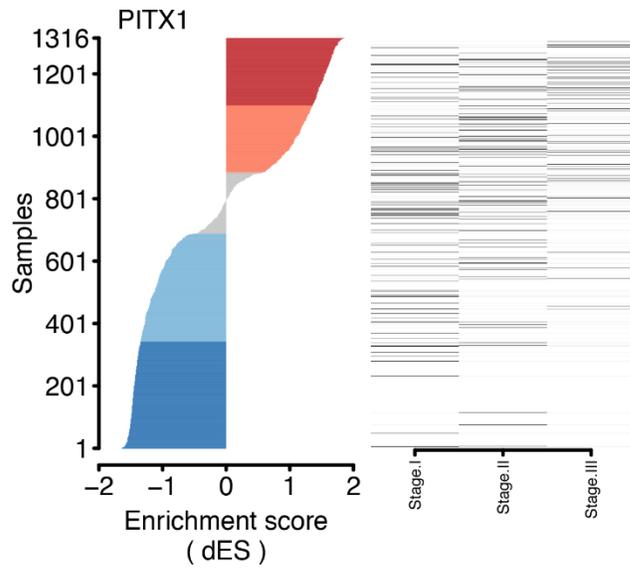
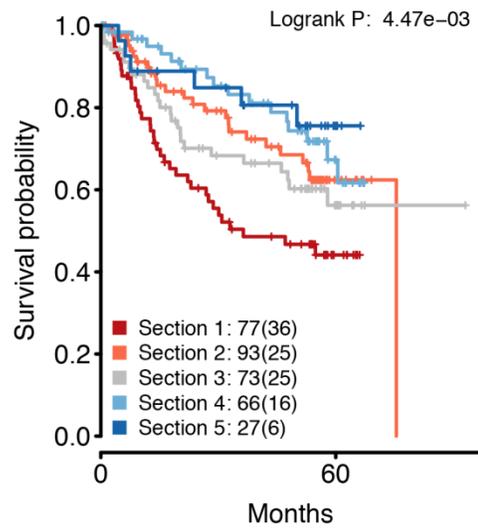
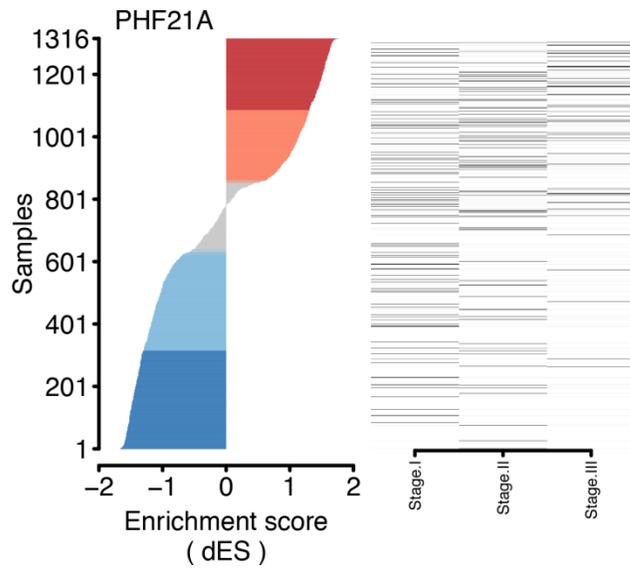


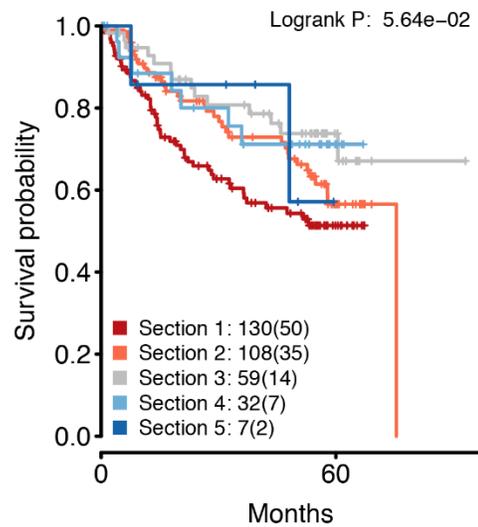
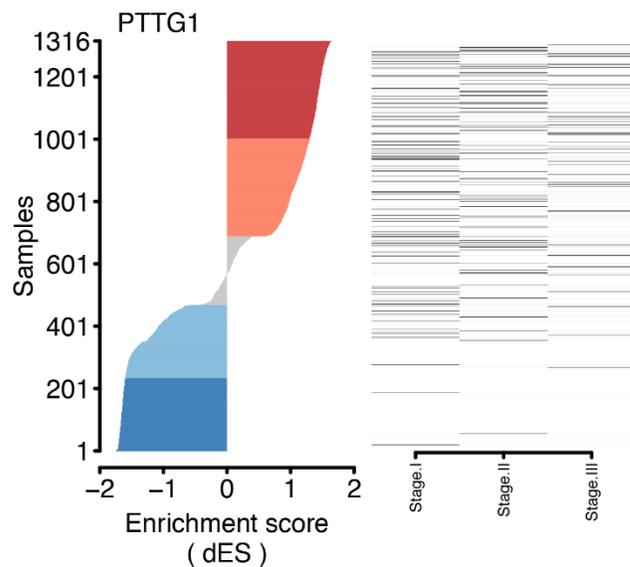
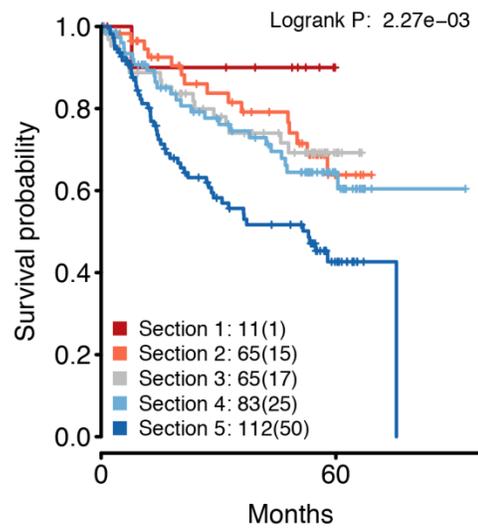
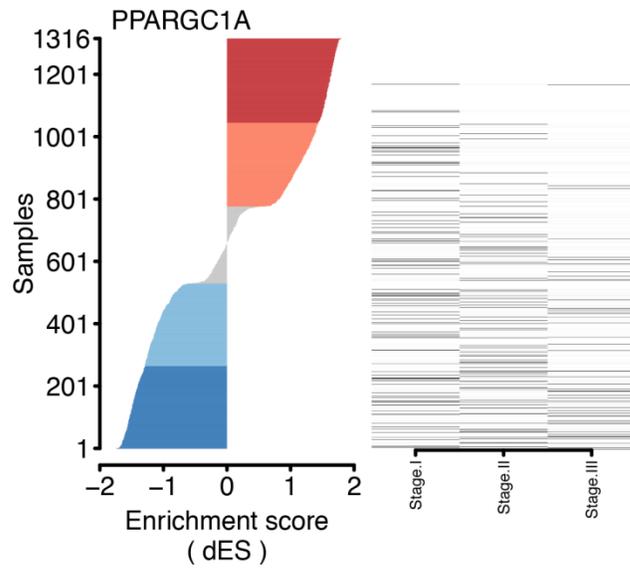
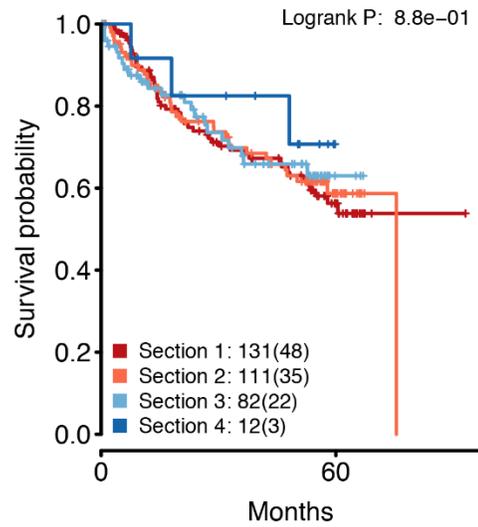
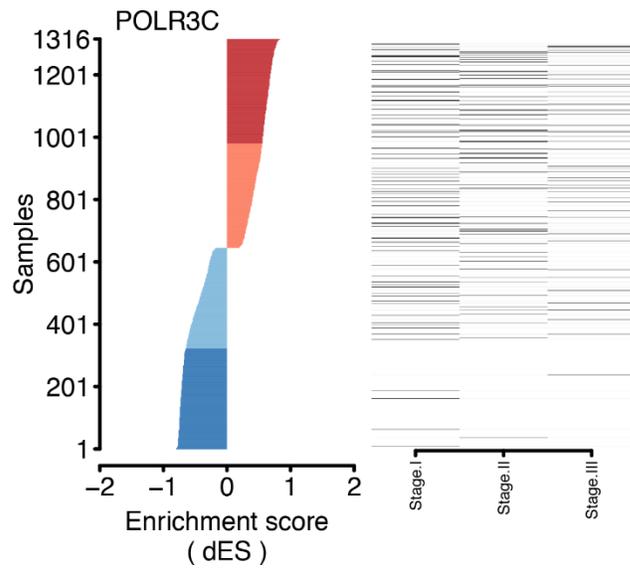


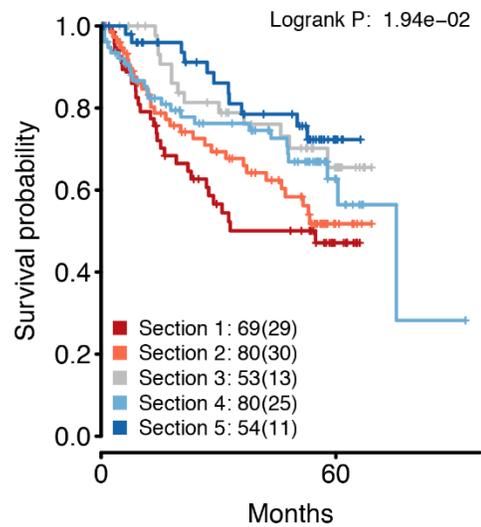
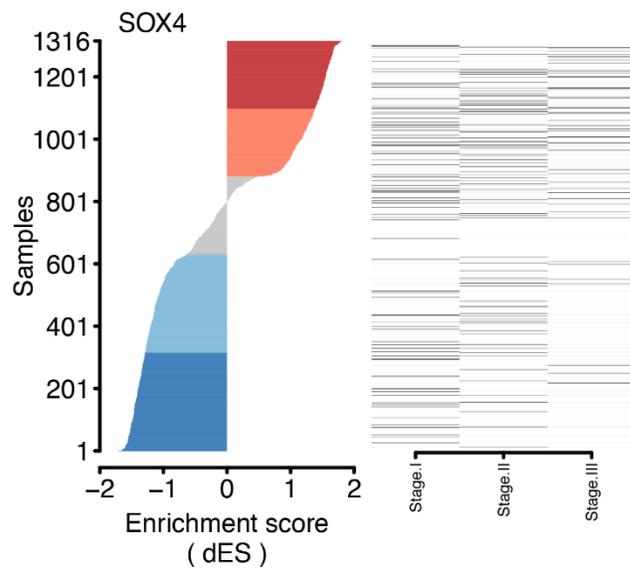
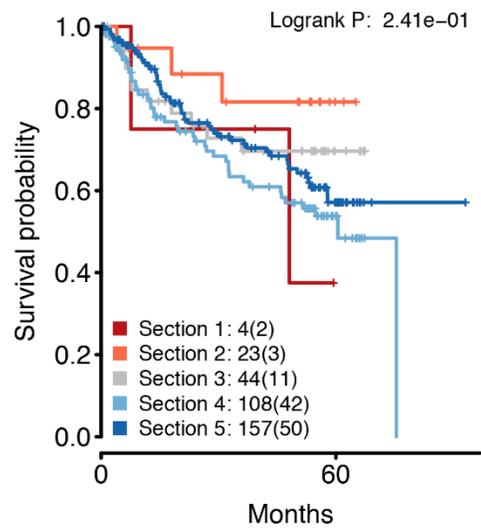
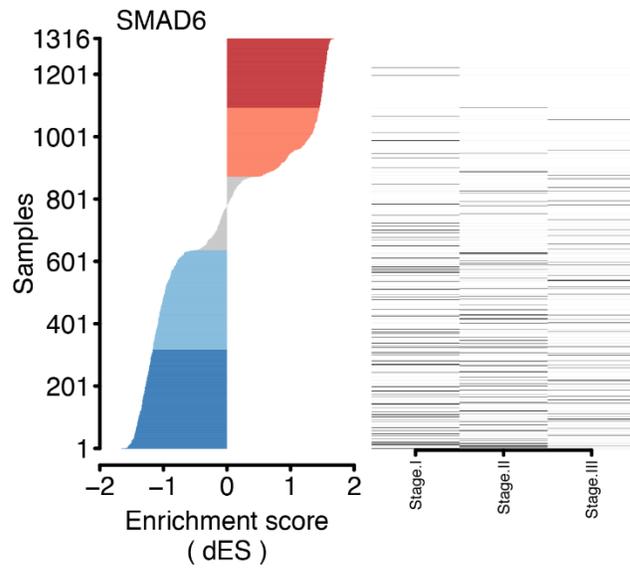
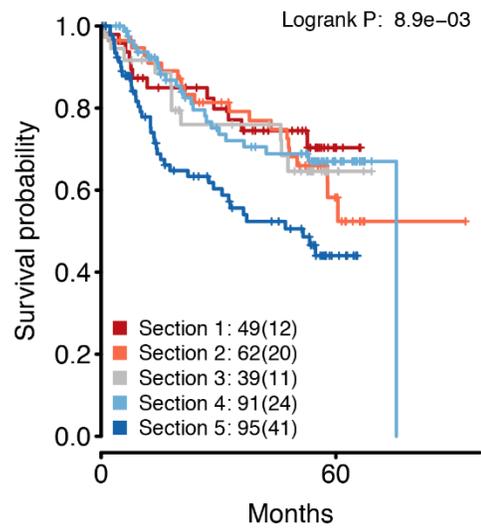
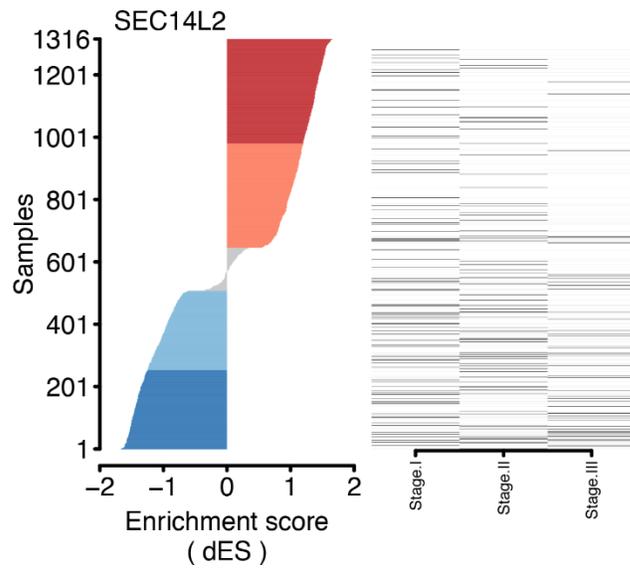


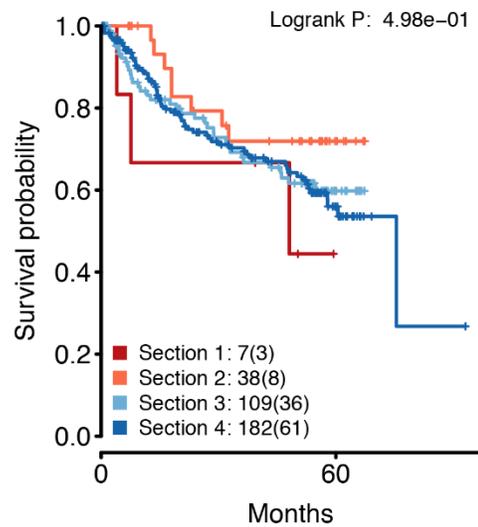
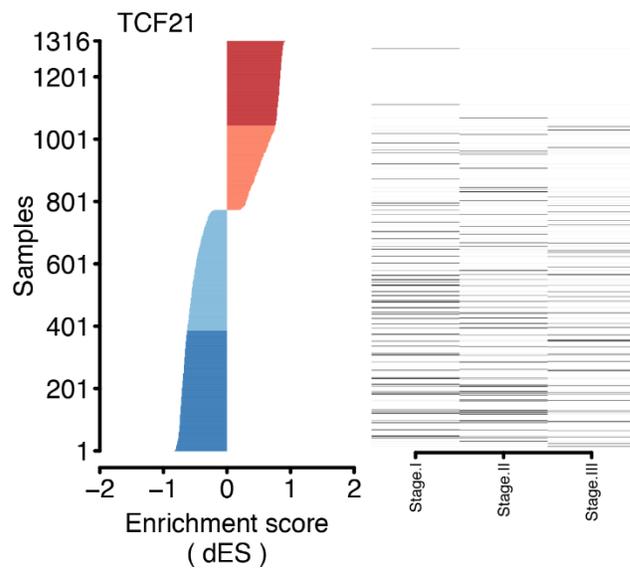
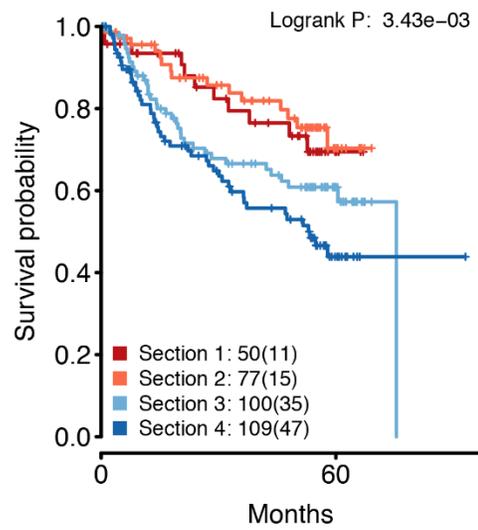
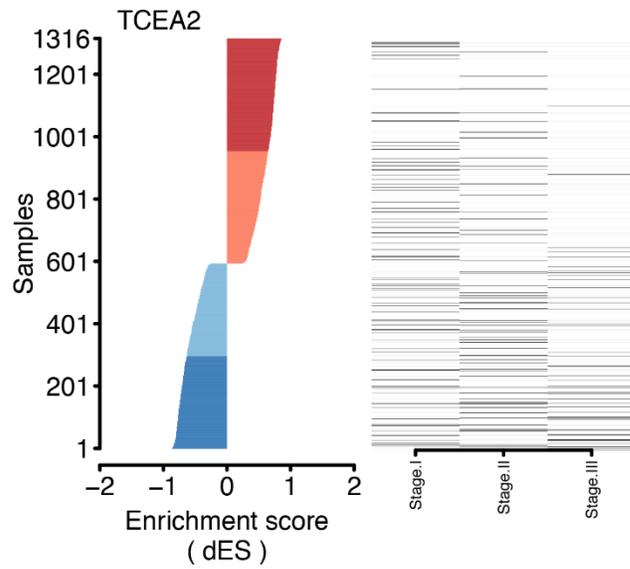
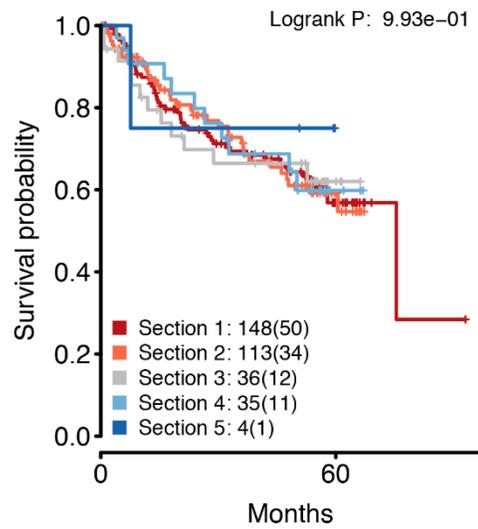
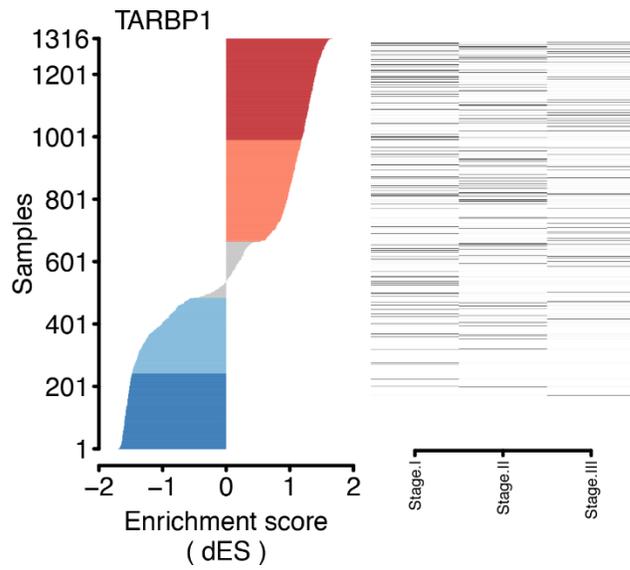


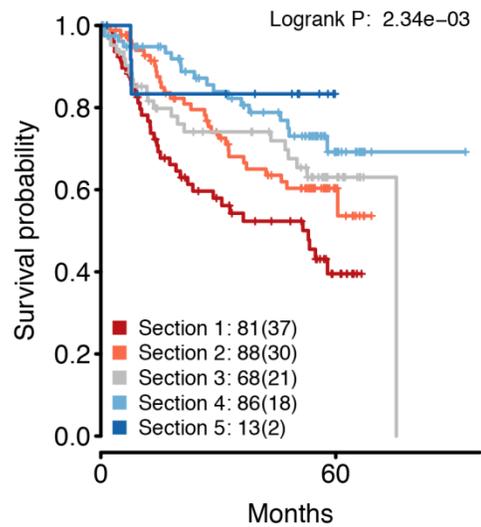
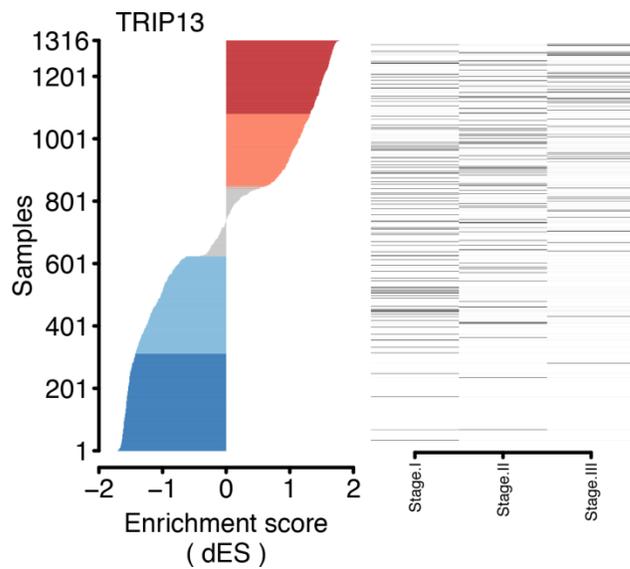
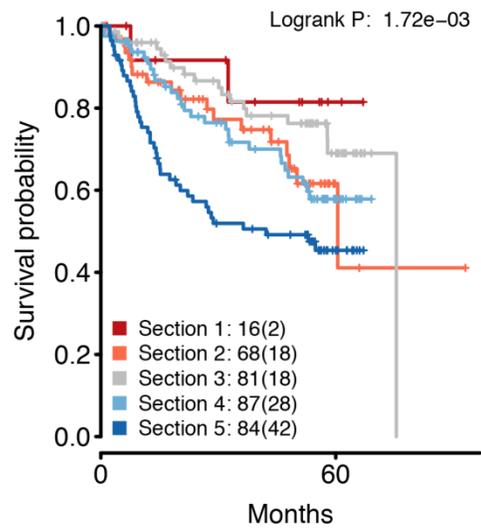
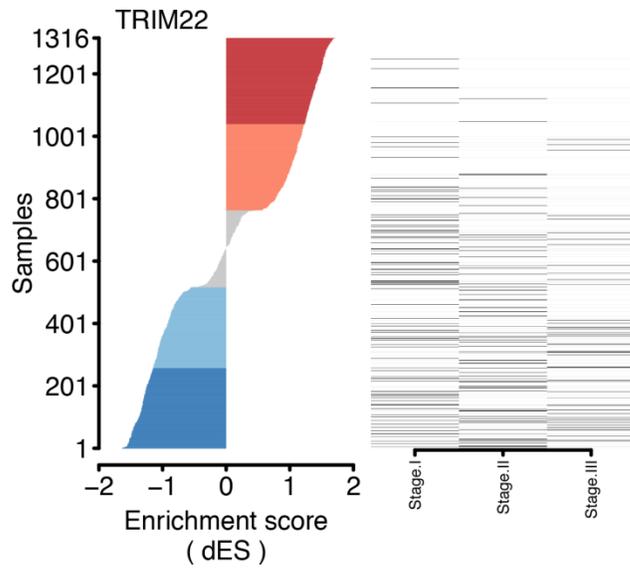
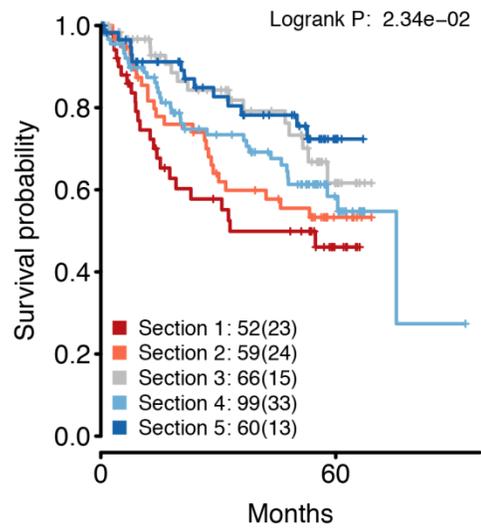
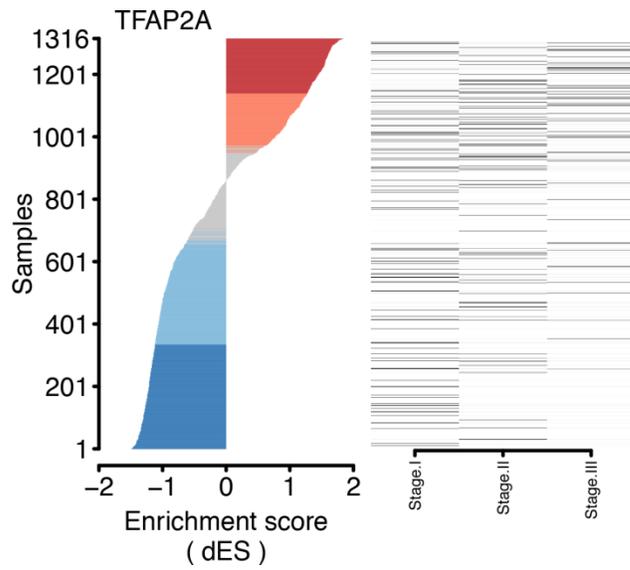


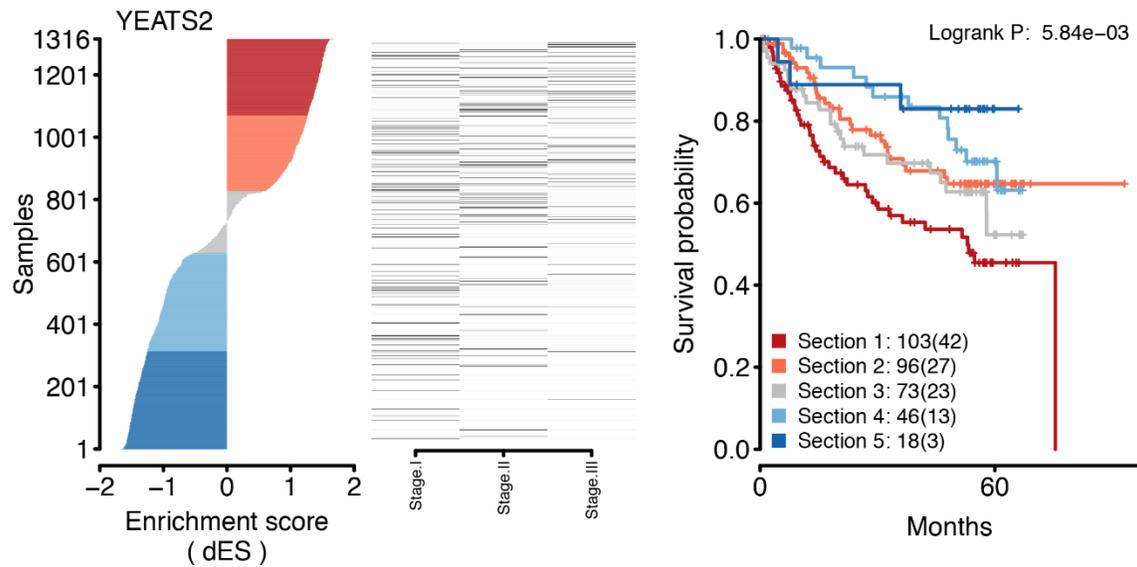




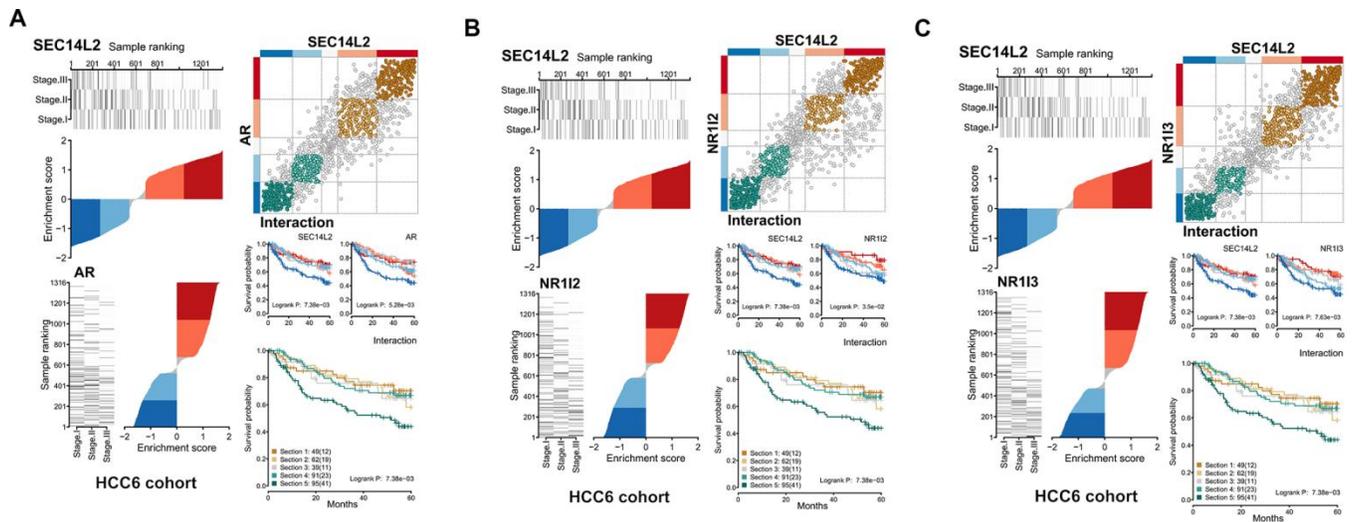




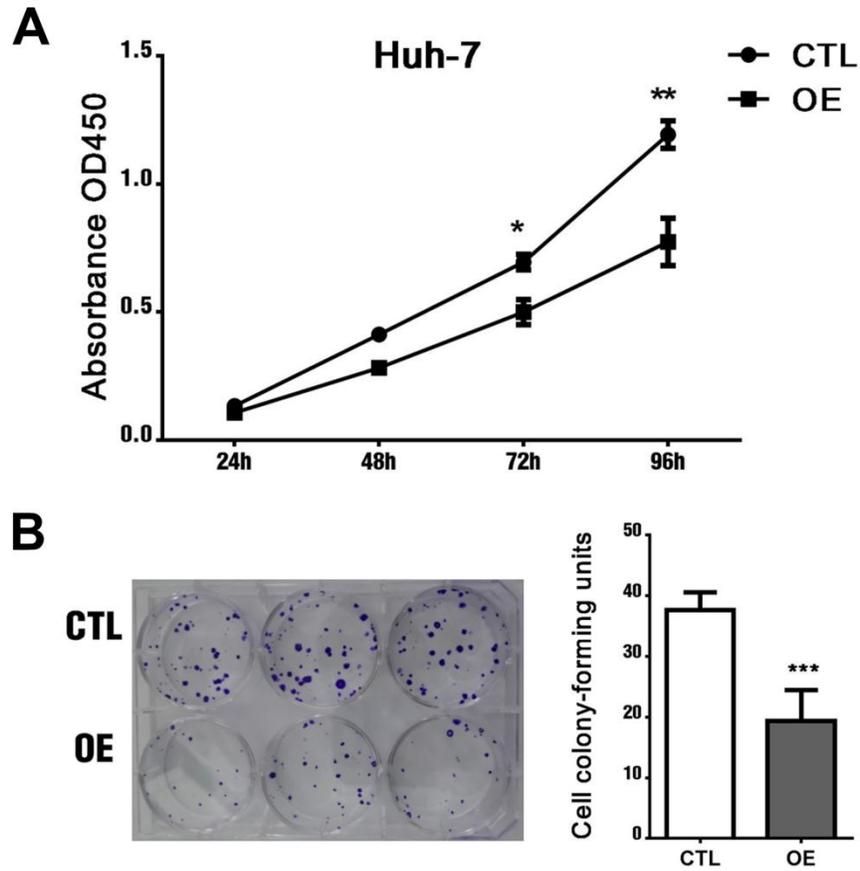




Supplementary Figure 4. Prognosis relevance for identified MRs.



Supplementary Figure 5. Regulon activity of SEC14L2: interaction with multiple NRs. (A) SEC14L2-AR interaction. (B) SEC14L2-NR12 interaction. (C) SEC14L2-NR113 interaction.



Supplementary Figure 6. SEC14L2 overexpression significantly inhibited cell proliferation in Huh7 cells. (A) Proliferation (CCK-8) assay in Huh7 cells. (B) Colony formation assay and quantitative analysis.