



S2 Fig. Survival analysis for top 12 selected COAC-inferred gene co-expression subnetworks from scRNA-seq data in Melanoma patients. The top selected subnetwork for each survival analysis was highlighted in each subfigure. The bulk RNA-seq data and clinical profiles for each melanoma patients were collected from TCGA website [2]. Survival analysis was conducted for these two groups using the R survival package [3].