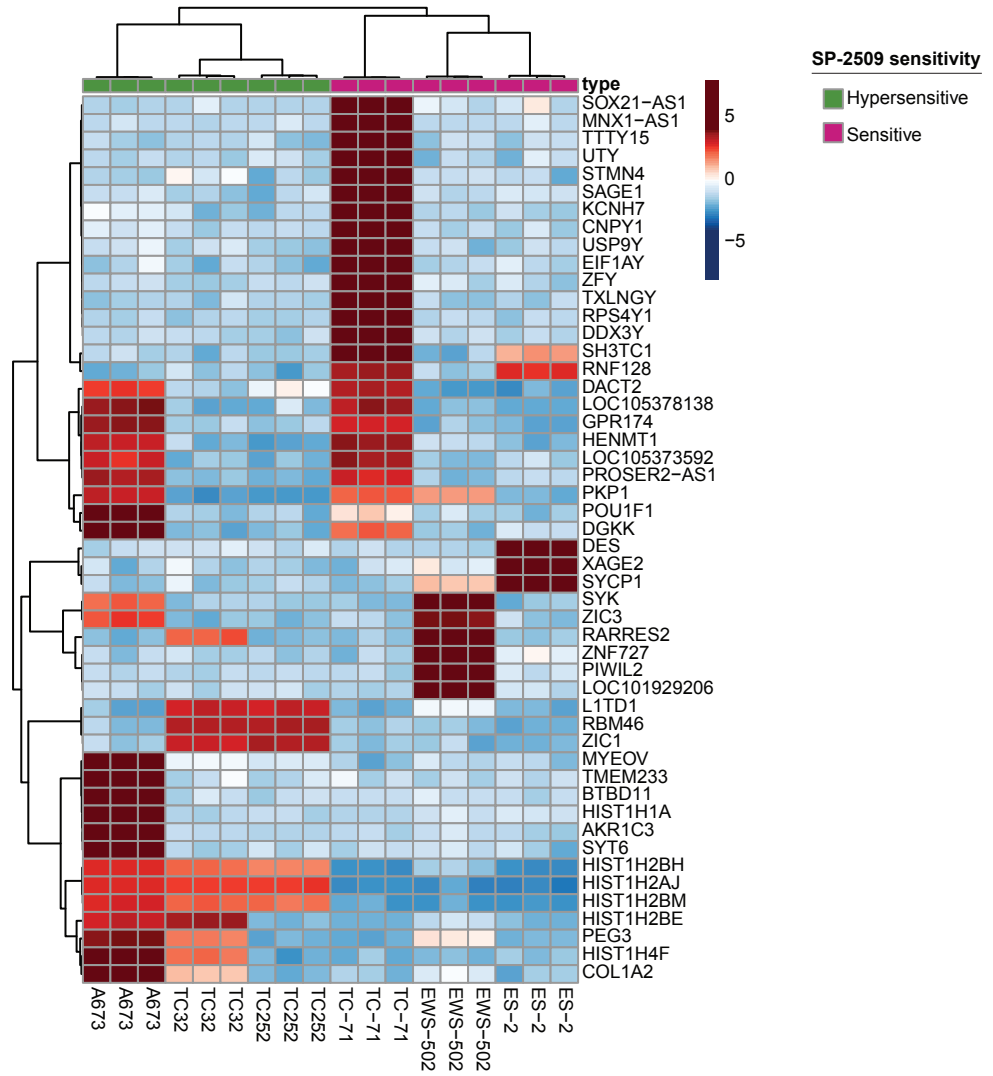
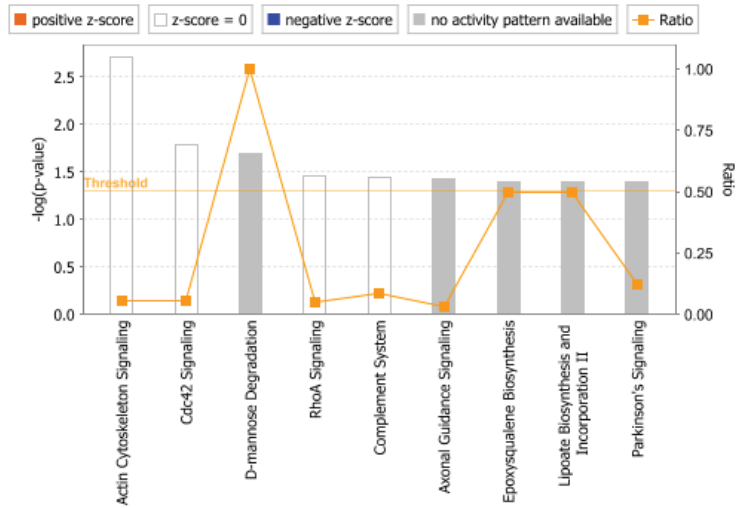


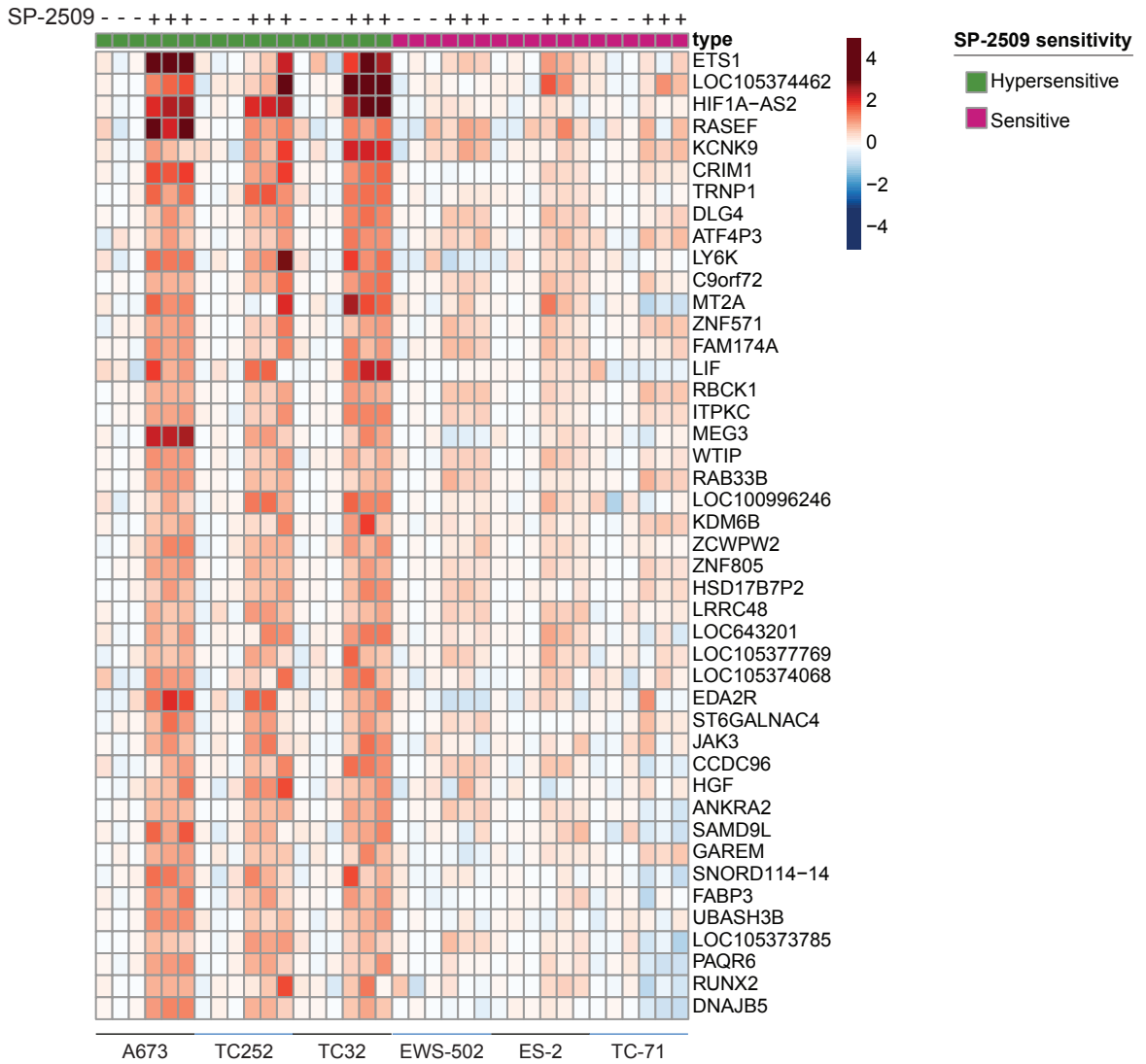
A



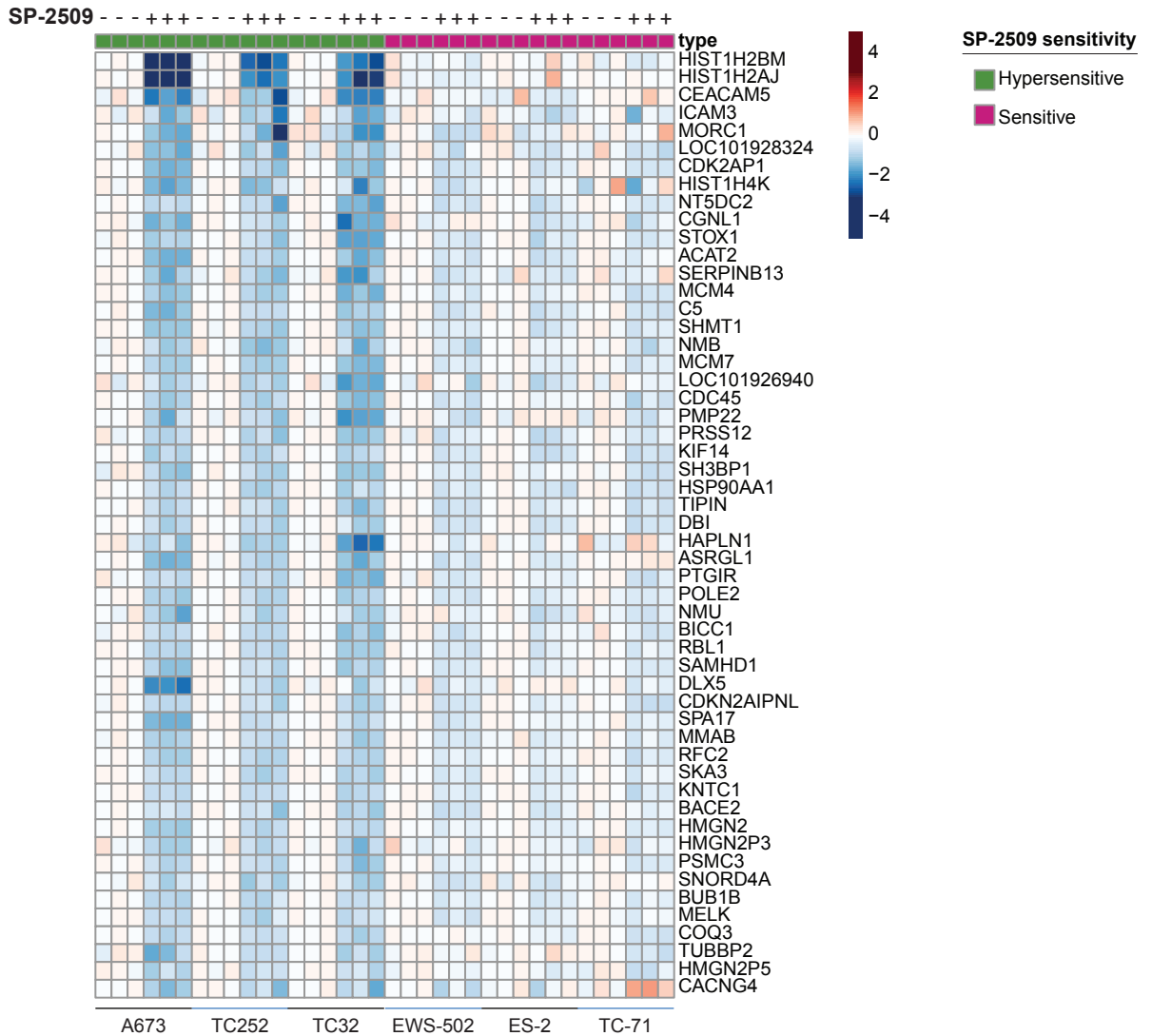
B



C



D



Supplementary Figure S5: *Hypersensitive SP-2509 Ewing sarcoma cell lines display similar transcriptomic profiles.*

(A) Unsupervised hierarchical clustering of basal transcriptomic profiles of Ewing sarcoma cell lines (triplicate samples per cell line). SP-2509 hypersensitive (A673, TC252, TC32) and sensitive (EWS-502, ES-2 and TC-71) cell lines. The top 50 most variable genes are depicted. Similarity between genes and samples were measured using Pearson correlation. This scale uses rlog-transformed expression which stabilizes the variance across the mean. (B) IPA of the 424 genes significantly differentially expressed between the two groups (SP-2509 hypersensitive versus sensitive). (C) Heatmap showing genes specifically induced (fold-change > 2 and FDR < 0.05) in all hypersensitive cell lines following SP-2509 treatment but not sensitive cell lines (n=44 genes). (D) Heatmap showing genes specifically repressed (fold-change < 2 and FDR < 0.05) in all hypersensitive cell lines following SP-2509 treatment but not sensitive cell lines (n=53 genes). For each cell line the expression (rlog transformed) is subtracted from the mean of expression after SP-2509 treatment. RNA-seq analysis was performed using triplicate DMSO (vehicle control) and matching SP-2509 treated samples for each cell line.