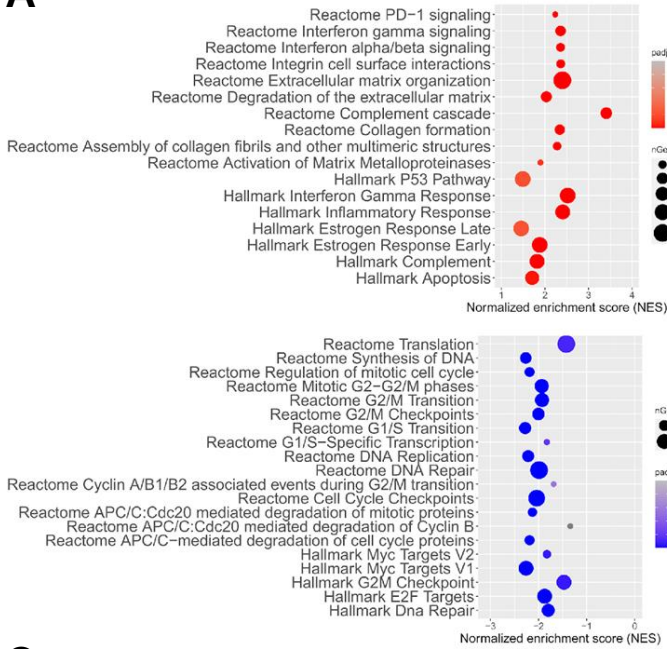
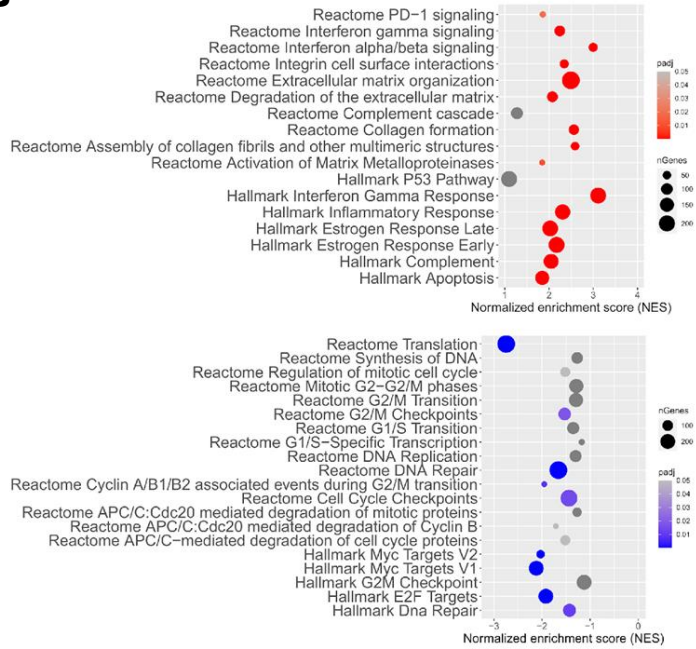


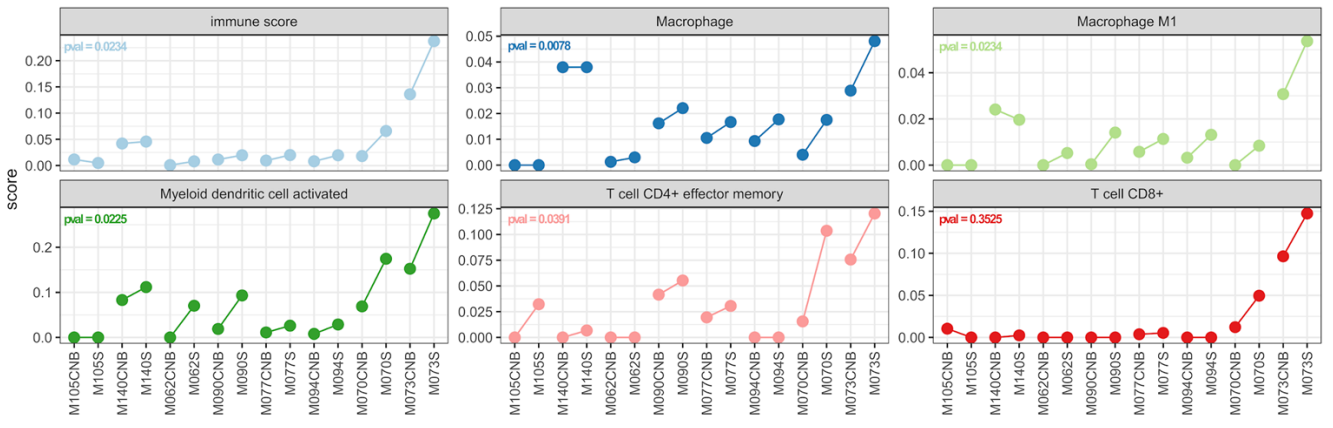
**A**



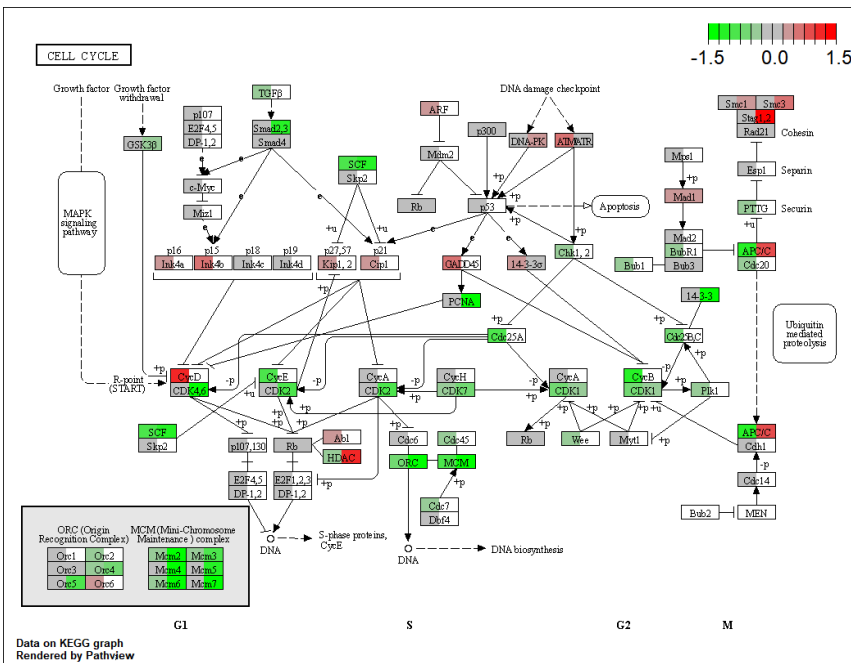
**B**



**C**



**D**



**Supplementary Figure S4. RNA-Seq and Proteomics analysis.** A and B, Dot plot of relevant enriched pathways from GSEA results (Reactome and Hallmark databases) separating responsive (A) and unresponsive tumors (B). C, Immune cell deconvolution (*xcell*) in the different tumors analyzed by RNA-Seq. Plots with significant p values analyzed by Wilcoxon test and the T cell CD8+ plot are shown. D, Kegg diagram of the *Cell cycle pathway*, that may explain mifepristone therapeutics effects. A colored code was used: the first half of the box is colored according to the RNA-Seq data (8 tumors) and the last half of the box is colored according to the proteomic data (n=10 tumors; nuclear fraction).

The same color in all the box means that both analyses yielded similar results. Absence of color in the last half means that the protein was not picked up in the Proteomic study. Grey means no change. Contrarily, RNA-Seq data from all candidates was available.