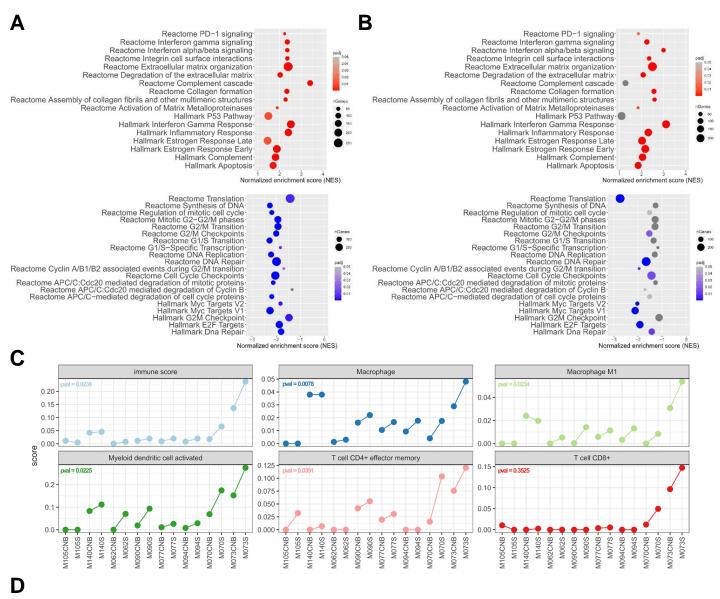
Elia et al., Supplementary Fig. S4



CELL CYCLE -1.5 0.0 Growth facto withdrawal Smc1 Smc3 ARF Rad21 Cohesin w200 GSK38 M Mrsl Esp1 Separin Skn2 c-Iviye Rh Apoptosis PTTG Securit Mizt MAPk signaling pathway Chk1, 2 p16 p15 p18 p19 p27,57 p21 Ink4a Ink4o Ink4c Ink4d Kip1, 2 Cip1 14-3-30 14 Ubiquitin mediated renteolysis R-point (START) Cdc6 Cdc45 SCF Skp2 Abl Rb Wee Myti / p107,130 Rb Cdc14 Bub2 MEN MCM (Mini-C ORC (Origin O DNA G1 G2 Data on KEGG graph Rendered by Pathvie

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.