



Supplemental Figure 2 legend

(A) Top: Representative flow cytometry traces for each treatment schedule that C4-2 cells were subjected to as depicted in Fig. 2 and harvested just prior to when IR would have been administered, fixed and prepped for FACS analysis of DNA content as described in the material and methods section. Bottom: Quantitation of above. Data represented as relative G1 (left) and G2/M (right) enrichment averages and standard deviations of at least three independent experiments. Schedule III (adjuvant) is set to 1.

(B) C4-2 cells were treated according to the schemata depicted in Fig. 2, then 24h post treatment, cells were harvested, fixed, and prepped for FACS analysis of BrdU incorporation and DNA content as described in the material and methods section. Graphs are representative dot plots from above, x axis is DNA content, y axis is BrdU incorporation. Numbers in the bottom right corner of each graph represent average percent of the population and standard deviation of at least three independent experiments with 2N DNA content (G1) or 4N DNA content (G2/M).