



### Supplemental Fig. S2. Characterization of TOP2A Cleavage Complexes in K562 Cells.

(A, B) Correlation in read counts in 10 kb windows between VP16, pBQ or genistein treated biological replicates +/- pre-amplification of DNA released following CIP treatment. (A) Non-amplified vs. amplified samples. (B) Amplified vs. amplified samples. The correlation coefficient for each comparison is indicated at the top left corner of the panel. The data demonstrate that there are strong correlations in read densities for 10 kb windows across the genome between the non-amplified vs. amplified and between the amplified vs. amplified individual biological replicates in our sample set. See also Fig. 1B.

(C) Percentages of TOP2A DSBs detected by high throughput sequencing in individual amplified DMSO or TOP2 poison-treated samples (Supplemental Table S1). The data demonstrate that between 2-3% of all TOP2A cleavage events are DSBs and, therefore, that the preponderance of TOP2A cleavage events are SSNs in each sample tested.