



**Supplemental Fig. S8. Correlations Between Length of Coding Genes and Genic CCR Signal Strength.**

(A-C) Correlation between coding gene length and CCR signal strength (HP10M) in (A) mitoxantrone-, (B) pBQ-, and (C) genistein-treated samples.

(A-C) Gene categories by length are shown on X-axis. Means of all CCR signal strengths within each gene are plotted to control for tendency of longer genes to have more CCRs by virtue of increased sequence space. Boxes represent 25<sup>th</sup> to 75<sup>th</sup> percentiles; whiskers, 5<sup>th</sup> to 95<sup>th</sup> percentiles; horizontal lines, median for each length interval; chi-squared test p-values are at top right in panels. Amplified samples; same treatments merged where applicable (Supplemental Table S1). The data show that CCR signal strength correlates significantly with length of coding genes.