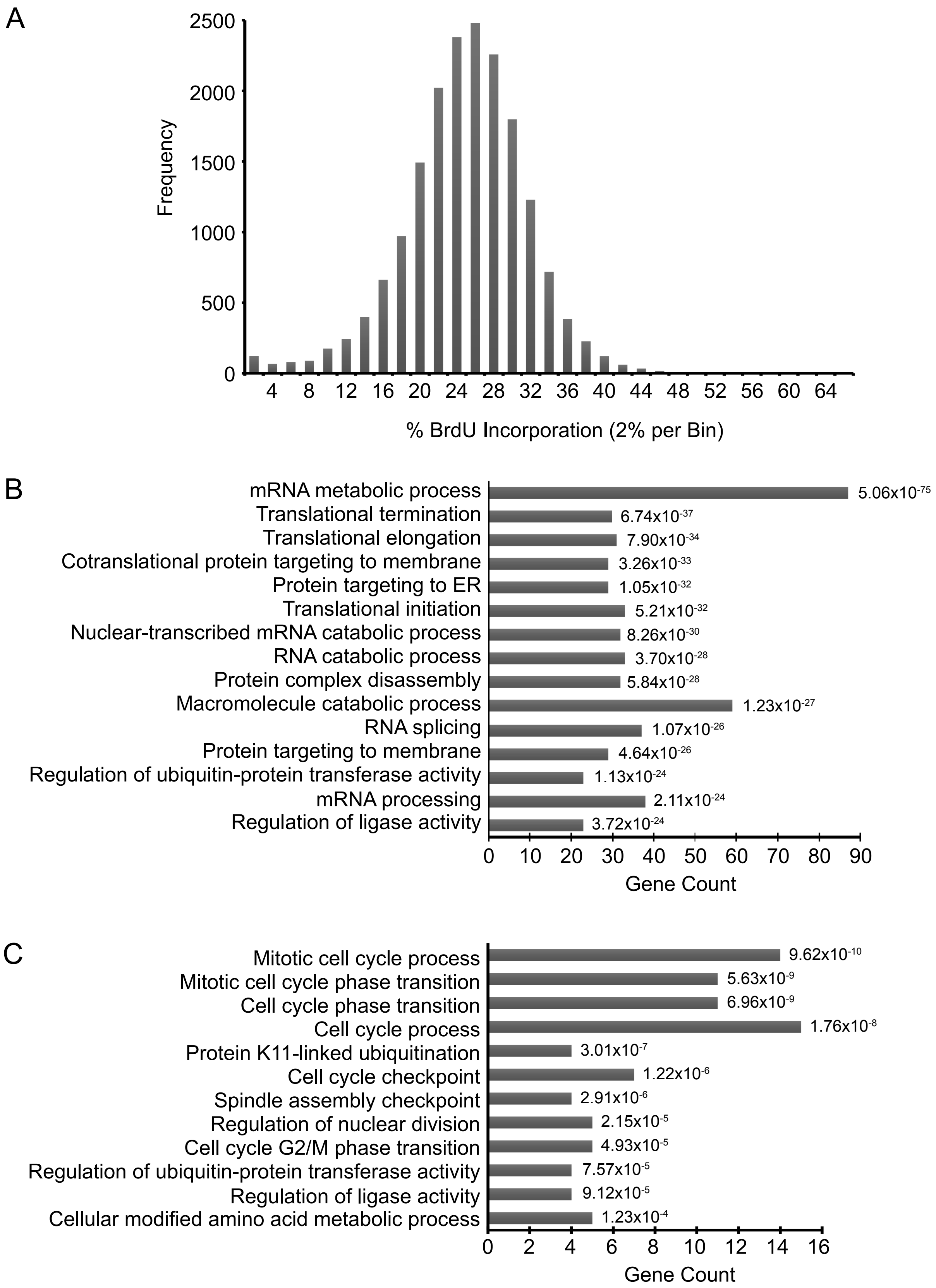
## SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. (A) Frequency distribution of BrdU incorporation percentage for all samples in the whole genome screen. The mean BrdU incorporation of the dataset was 23.9 percent with a standard deviation of 6.6 percent. (B, C) Gene ontology analysis of biological processes for samples with BrdU incorporation with three standard deviations below (B) and above (C) the mean.

Supplemental Figure 2. Heatmaps depicting results from validation and drug sensitivity screen for genes with 2 validated siRNAs. Black squares in first column (RRS average) depict those siRNAs that validated the phenotype of the original screen. Black squares in the remaining columns depict siRNAs sensitive to the drugs indicated. White squares: not validated or sensitive to drug. Grey squares: not determined.

Supplemental Figure 1



Supplemental Figure 2