Supplementary Data

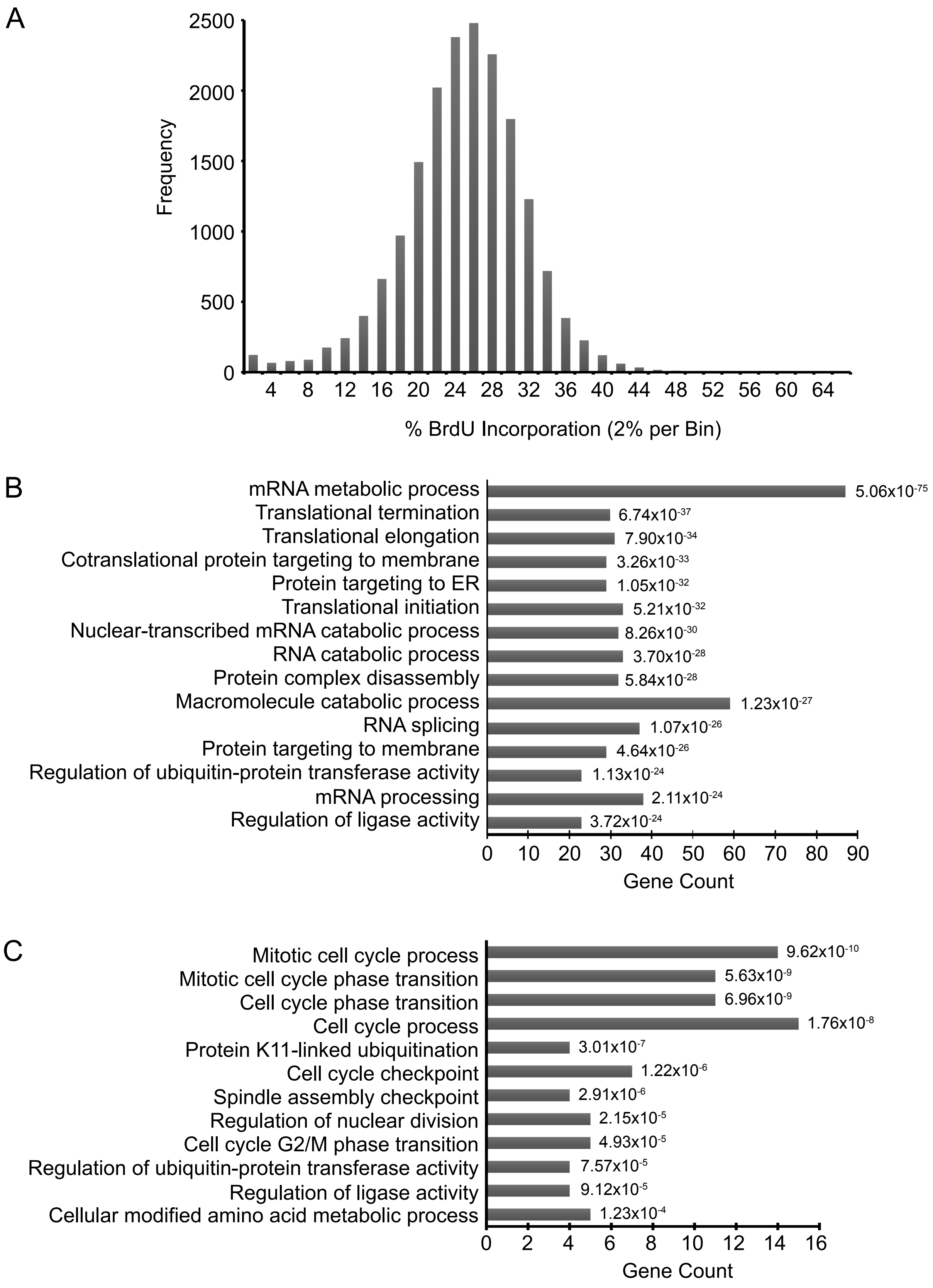
Suppl Figure 1. BrdU incorporation. (A) The percentage of BrdU incorporation for each sample was determined. The figure depicts the percentage of BrdU incorporation for all siRNAs tested. (B, C) Gene ontology analysis of genes that when knocked down resulted in BrdU incorporation three standard deviations lower (B) or higher (C) than the overall sample mean.

Suppl Figure 2. Results from validation and drug sensitivity screens for genes in which two siRNAs validated. Results for HU, ATR inhibitor and CHK inhibitor treatments are depicted. Black squares in the first column represent those siRNAs that validated in the RRS secondary screen. Black squares in the remaining columns depict siRNAs causing sensitivity to the indicated drugs. Grey squares: not determined.

Suppl Figure 3. Results from validation and drug sensitivity screens are presented for genes in which three or four of the four siRNAs validated. Results of treatments with gemcitabine, camptothecin, and PARP inhibitor are depicted. Black squares in the first column represent those siRNAs validated in the RRS secondary screen. Black squares in the remaining columns depict siRNAs causing sensitivity to the indicated drugs. Grey squares: not determined.

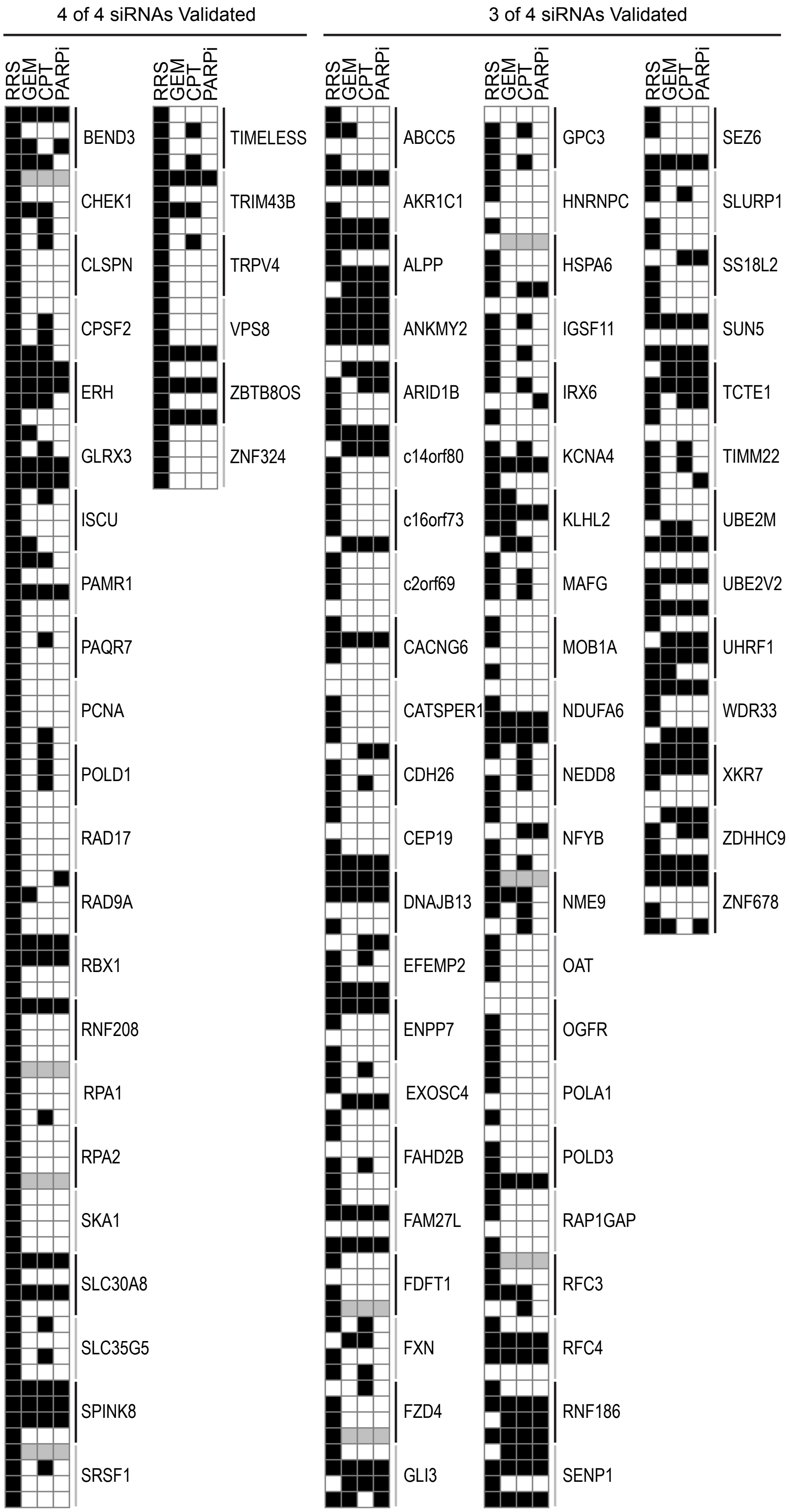
Suppl Figure 4. Results from validation and drug sensitivity screens are presented for genes in which two of the four siRNAs validated. Results of treatments with gemcitabine, camptothecin, and PARP inhibitor are depicted. Black squares in the first column represent those siRNAs validated in the RRS secondary screen. Black squares in the remaining columns depict siRNAs causing sensitivity to the indicated drugs. Grey squares: not determined.

Supplemental Figure 1



Supplemental Figure 2

Supplemental Figure 3



Supplemental Figure 4