



**SUPPLEMENTARY FIG. S4.** Scheme summarizing work overflow for phosphoproteomics analysis. Five independent batches of K562 or K562-STI-R cells were revived, cultured until they reached logarithmic growth phase, harvested, and lysed; then samples were subjected to tryptic digestion and enriched for phosphopeptides. Phosphopeptides were identified using LC-MS/MS analysis and the resulting SIC peak areas were quantified.