S4 Fig. SLFN11 mRNA expression in cancer cell lines is significantly correlated between datasets. Gene expression was downloaded from CTRP v2, GDSC, and NCI60 databases as previously described. Each point represents a cell line overlapping between two databases: GDSC vs CTRP (A), CTRP vs NCI60 (B), and GDSC vs NCI60 (C). Pearson's correlations were performed. Solid line represents the best-fit linear regression line, and dotted lines represent the 95% confidence interval.