**Calibration curve for dark kinase peptides.**

The calibration reverse curve plot with linear robust regression analysis is shown (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2855883/>). The observed concentrations of the stable isotopically labeled peptide surrogate was obtained for each peptide using LC-MS in parallel reaction mode with a constant quantity of natural isotope abundance peptide as the internal standard (25 fmol/µL) (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3494192/>). The analyte matrix was a tryptic digest of pooled patient derived xenografts (1 µg/µL) that was prepared according to CPTAC-SOP. Each of the three most intense peptide fragment ions is depicted as a different symbol. The measurements from replicate LC-MS analyses are depicted as the same symbol (<https://proteomics.cancer.gov/sites/default/files/assay-characterization-guidance-document.pdf>). The LOD was determined using a non-parametric method with eight LC-MS analyses without added analyte ((<http://clinchem.aaccjnls.org/content/50/4/732>). The LOQ was generated from the LOD (“Algorithms, Routines and S Functions for Robust Statistics” (CRC Press, Boca Raton, Florida, USA, 1993)). The plots are dimensioned such that the theoretical line is at a 45° angle to facilitate assessment of peptide recovery and performance. The LOD, LOQ, and regression parameters are summarize in the Table.