Figure S1. Accuracy of tandem-mass-tag (TMT) quantitation for workflow assessing sample generation reproducibility. Box plots were generated for reported protein ratios with pooled reference channel (TMT-131) utilized for normalization.
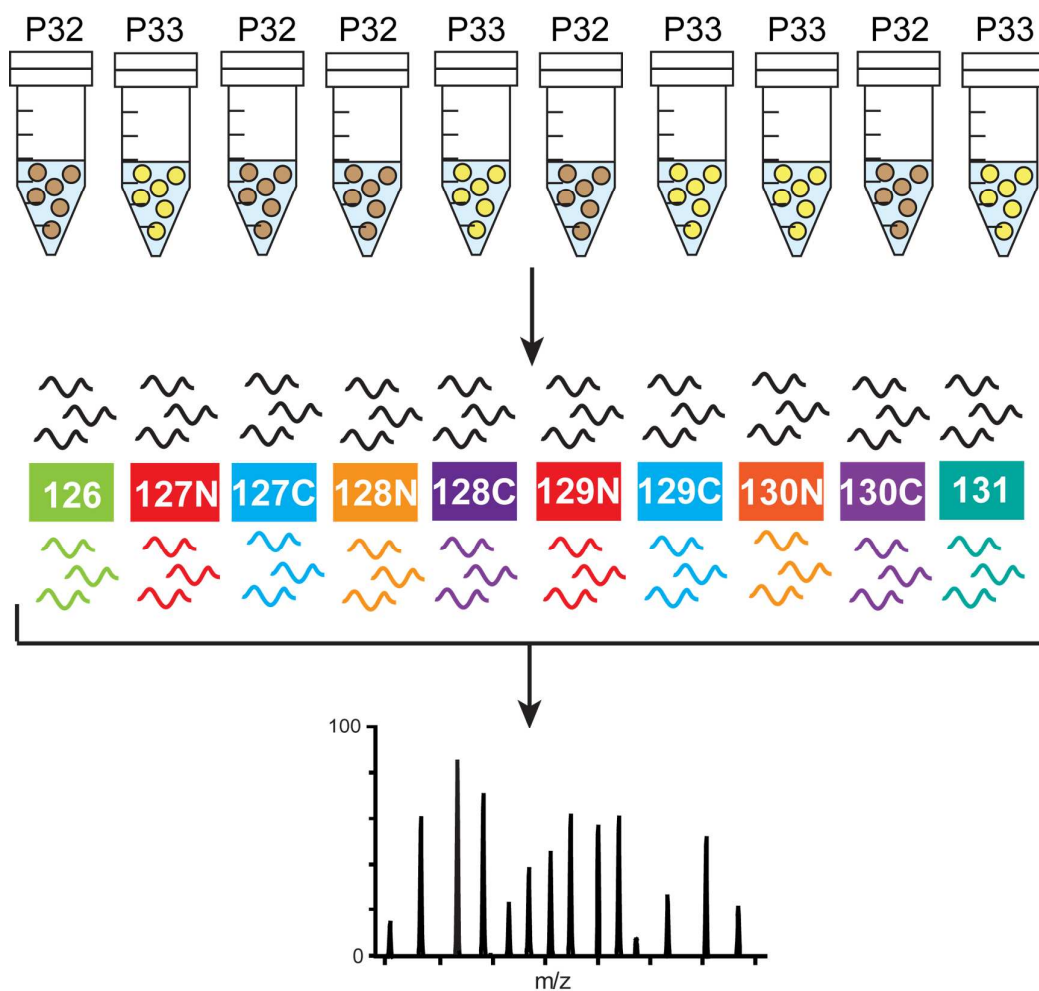
Figure S2. Schematic of PDX CompRef workflows. Equal amounts of protein from each PDX model (P32 or P33) was digested and subjected to TMT-labeling prior to LC-MS/MS analysis.
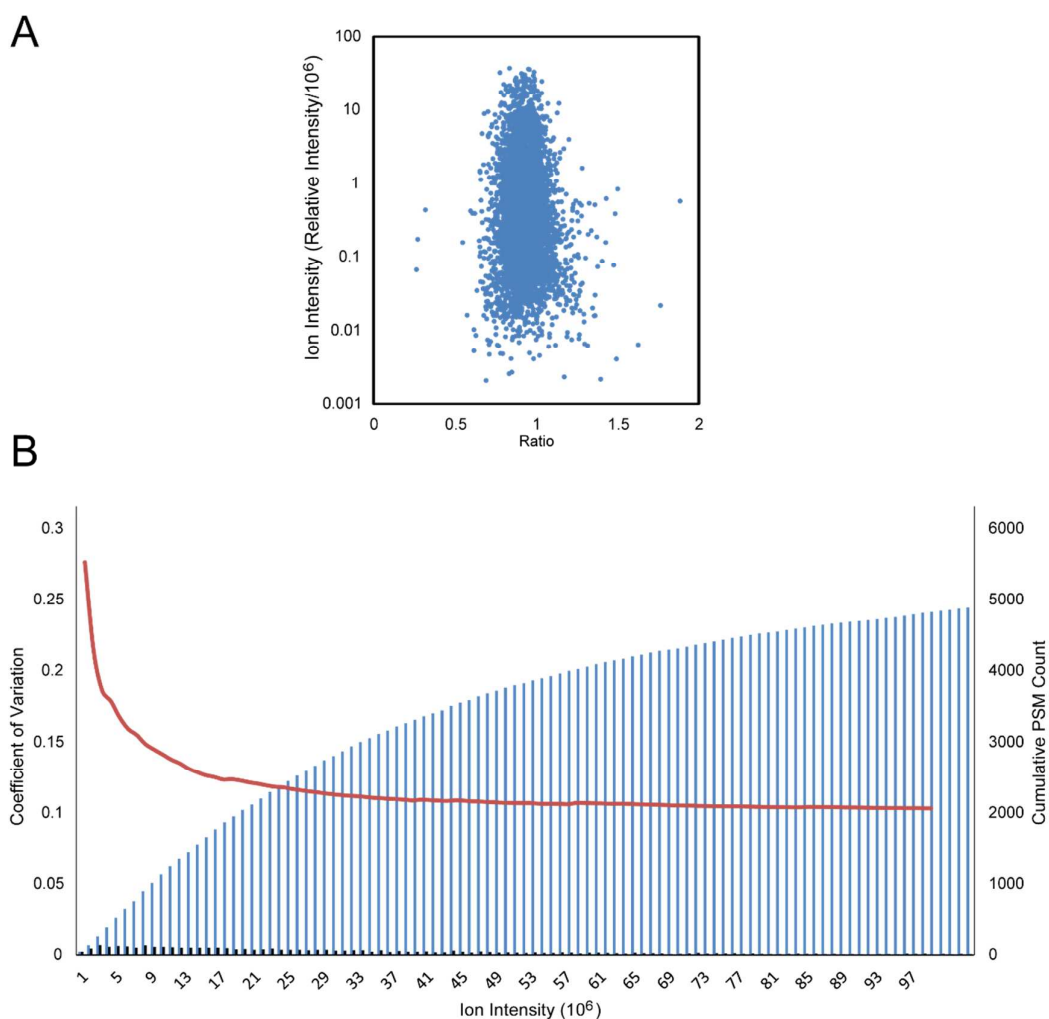
Figure S3. Accuracy of tandem-mass-tag (TMT) quantitation influenced by ion intensity on reporter tag accuracy. (A) Ion intensity was plotted against reported TMT ratio. (B) Coefficient of Variation and Cumulative PSM Count is plotted against Ion Intensity. Cumulative PSM Count (Blue), PSM Count (Black), and Cumulative CV (Red). Data plotted is from workflow for assessing sample digestion reproducibility Technical Replicate #1, Fraction #1.