Supplemental Figure S2 No mutated genes No "flipped" genes Focal deletion on gained chromosomes: Focal amplification on lost chromosomes: Genes with point mutations genes removed genes removed removed from analysis 2.4% of genes on gained chromosomes 10.4% of genes on lost chromosomes No low-expression genes No low-reproducibility proteins Non small-cell lung cancer cell lines only 15.5 0.99 Cancer cell line lineage Aggregated reliability rank 64 Mean RNA expression **NSCLC** Genes **Proteins** Melanoma 80% 80% maintained maintained 33 Colorectal adenocarcinoma Breast ductal carcinoma 29 Exocrine 0.19 0.35 Ovary adenocarcinoma Removed Removed 0.00 0.02 Other (32 subtypes) B Delta of difference in gene expression by dataset Difference in gene expression by control dataset (RNA difference minus Protein difference) 1.0 Difference in expression RNA minus protein *** 0.5 0.5 0.0 0.0 -0.5-0.5 -1.0-1.0RNA Protein RNA Protein Data type: RNA - Protein RNA - Protein Data type: Gain Gain Chrm arm: Gain Loss Loss Chrm arm: Loss Dataset No mutated genes No flipped genes Rolow expression genes No low reproducibility proteins Merge E Difference in protein expression by data type Difference in protein expression upon chromosome... Loss NS NS 8.0 Mass spec expression data Mass spec expression data Difference in expression 0.4 0.4 Dataset Mass Spec 0.0 0.0 -0.4 0.4 P < 2x10⁻⁸ P < 9x10⁻¹¹ corr = 0.464corr = 0.517

0.4

-0.4

Data type: _Protein

Gain

Chrm arm:

Protein

Loss

0.0

RPPA expression data

0.4

0.0

RPPA expression data

-0.4

Supplemental Figure S2. RNA and protein expression differences within individual cancer cell lines and expression differences split based on cell line ploidy.

- A) Diagram displaying different methods of dataset filtering to produce control datasets. The merged-control dataset is a combination of no mutated genes, no flipped genes, no low expression genes and no low reproducibility genes.
- B) Boxplots displaying mean difference in RNA and protein expression upon chromosome gain or loss by control datasets. Boxplots display the 25th, 50th, and 75th percentile of the data, while the whiskers indicate a 1.5 interquartile range. P-values are from two-sided t-tests relative to bulk analysis, with *< 0.01, **<0.001, ***<0.0001, corrected for number of tests.
- C) Boxplots displaying mean difference in RNA expression minus the mean difference in protein expression upon chromosome gain and loss by control dataset. Boxplots display the 25th, 50th, and 75th percentile of the data, while the whiskers indicate a 1.5 interquartile range. P-values are from two-sided *t*-tests relative to bulk analysis, where *< 0.01, **<0.001, ***<0.0001, corrected for number of tests.
- D) Boxplots displaying mean difference in RNA and protein expression upon chromosome gain or loss, with data originating from the mass spectrometry dataset and the RPPA dataset. Boxplots display the 25th, 50th, and 75th percentile of the data, while the whiskers indicate a 1.5 interquartile range, while p-values in the boxplots were calculated from two-sided *t*-tests.
- E) A density plot comparing the difference in mass spectrometry and RPPA protein expression originating upon the gain (left) or loss (right) of the chromosome arm the gene is located on. Pearson correlation coefficient and p-value are displayed. Linear regressions (red) with 95% confidence intervals are displayed.