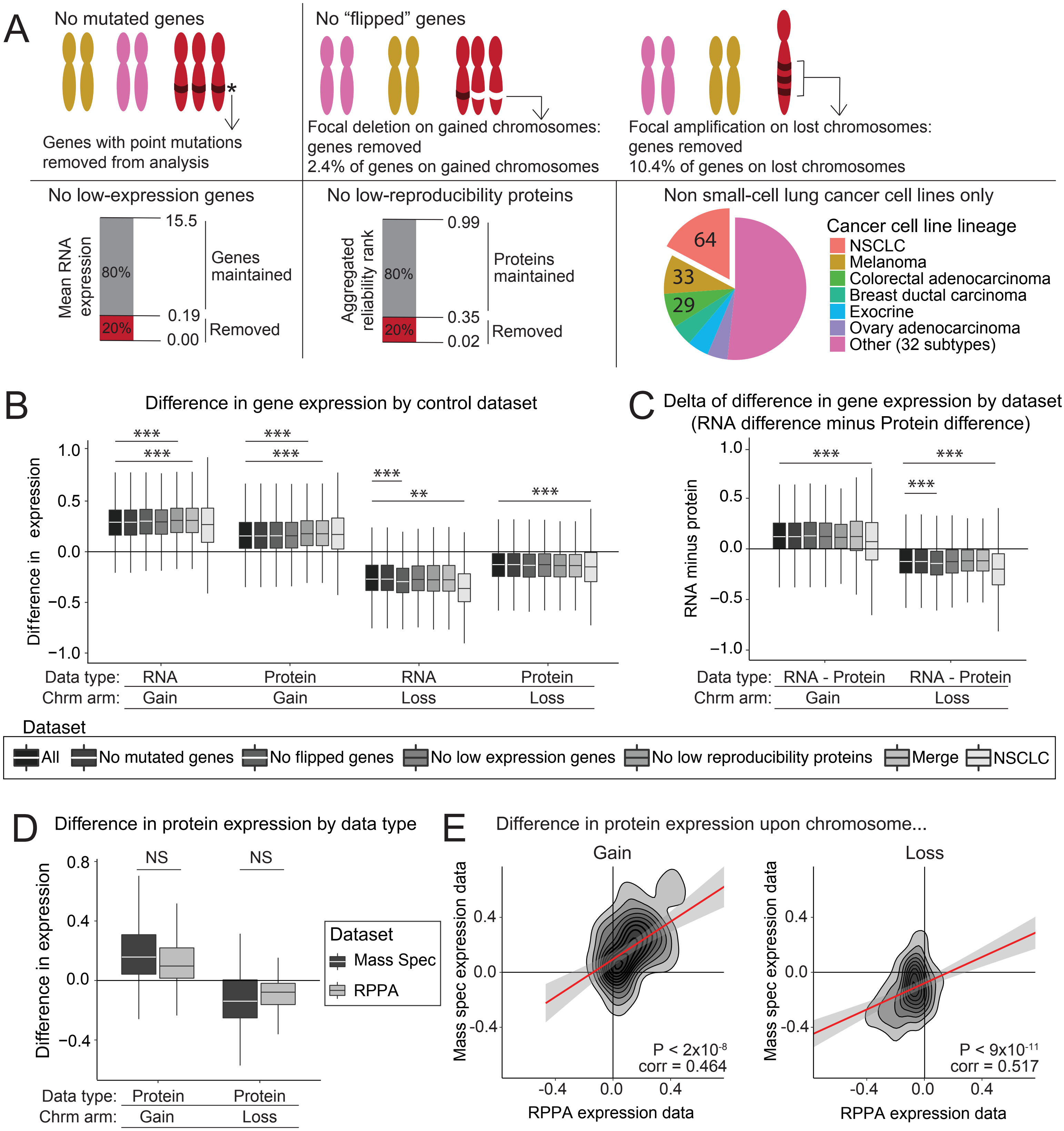
Supplemental Figure S2



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.