



Supplemental Figure 14. Comparison of False Positive Rate for non-targeting sgRNAs on Sanson et al. (2018)'s CRISPRn-A375 screen data. (A) Specificity comparison between CB² and MAGeCK for the six different p-value thresholds. The y-axis indicates specificity, and the x-axis indicates the level of the p-value threshold for the specificity calculation. (B) Volcano plots of the p-value of non-targeting sgRNAs. The y-axis indicates the negative logarithm value of p-value, and the x-axis indicates the \log_2 value of fold-change. All of the data points are from negative control sgRNAs. False Positive were plotted in red. Horizontal blue lines at $p = 0.01$ indicate the threshold for statistical cutoff.