* Compare\_samples.R: This function takes in a variant caller output of a sat mut screen before and after timepoint, compares them (i.e. calculates net growth rates for mutants present in both samples, and adds pseudo-counts for the after condition, if specified)
  + Example Inputs: dataframes with BCRABL D0 and D2 data, net growth rate without drug of the cell line, and the mutant count before and after
  + Output: dataframe with netgrowth rates and enrichment scores of the BCRABL D2 vs D0 comparison
* Compare\_screens.R: This function compares two sets of compare\_samples.R outputs.
  + Example Inputs: BCRABL D0 and D2 data for replicate 1, BCRABL D0 and D2 data for replicate 2
  + Example Outputs: BCRABL D0 and D2 data for both replicates, with a mean net growth rate indicating the mean across both replicates