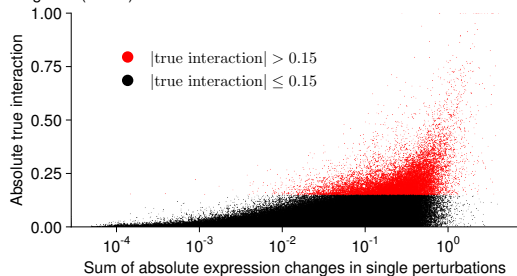
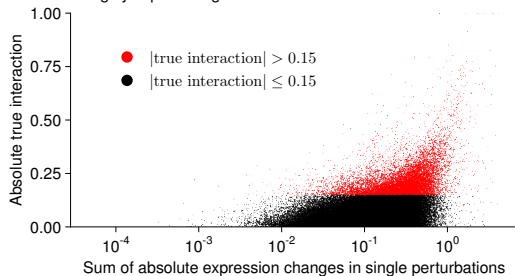


(A) Size of true interaction effects vs. size of single effects

All genes (19 264)

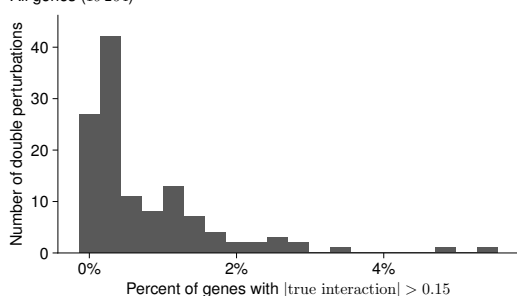


1 000 most highly expressed genes

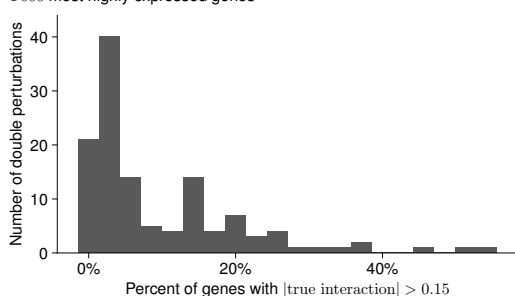


(B) Fraction of genes with non-linear interaction effect per double perturbation

All genes (19 264)

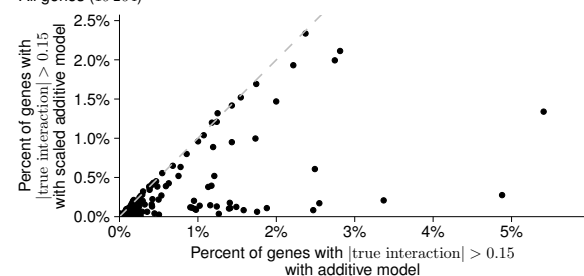


1 000 most highly expressed genes



(C) Additive model ($\delta AB = \delta A + \delta B$) vs. scaled additive model ($\delta AB = \alpha(\delta A + \delta B)$)

All genes (19 264)



1 000 most highly expressed genes

