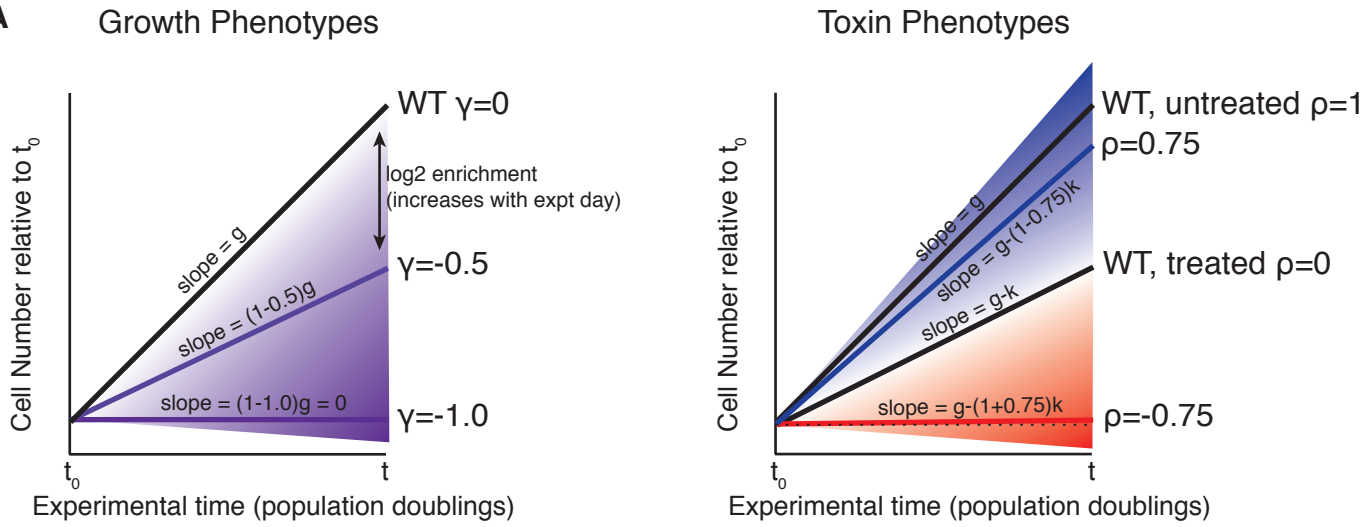
Figure S1

A



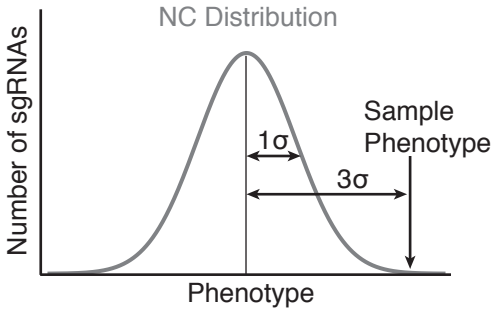
$\log_2$enrichment = $\log_2$(Cell Fraction$_t$/Cell Fraction$_{t0}$)
Normalized $\log_2$e = Sample $\log_2$e - Median NC $\log_2$e

γ = Normalized $\log_2$e / t

$\log_2$enrichment = $\log_2$(Cell Fraction$_{treated}$/Cell Fraction$_{untreated}$)
Normalized $\log_2$e = Sample $\log_2$e - Median NC $\log_2$e\

ρ = Normalized $\log_2$e / t

B



z-score:
sgRNA phenotype / NC σ

Phenotype-signed z-score:
positive if sgRNA phenotype = known gene knockdown phenotype; negative otherwise