Figure S1. Singular value decomposition of the raw shRNA fold change matrix.

(a) Fraction of total variance explained by the top 10 singular values by SVD of the first half of the fold change matrix. Signal is concentrated in the first vector, which accounts for ~42% of total variance.

(b) The distribution of all hairpin projections onto the first left singular vector (black). Strong positive projections indicate dropout across informative samples. Green, example of hairpins targeting a given gene. Value of the projection of the median hairpin (starred) is used for calculating P-value, as described in the main text and methods.

(c) Projection of individual samples onto first right singular vector. Strong negative projections indicate more informative screens.

(d) Sample projection onto first right singular vector is correlated with the number of cell doublings at which the sample is measured; more cell doublings yields more informative screens.