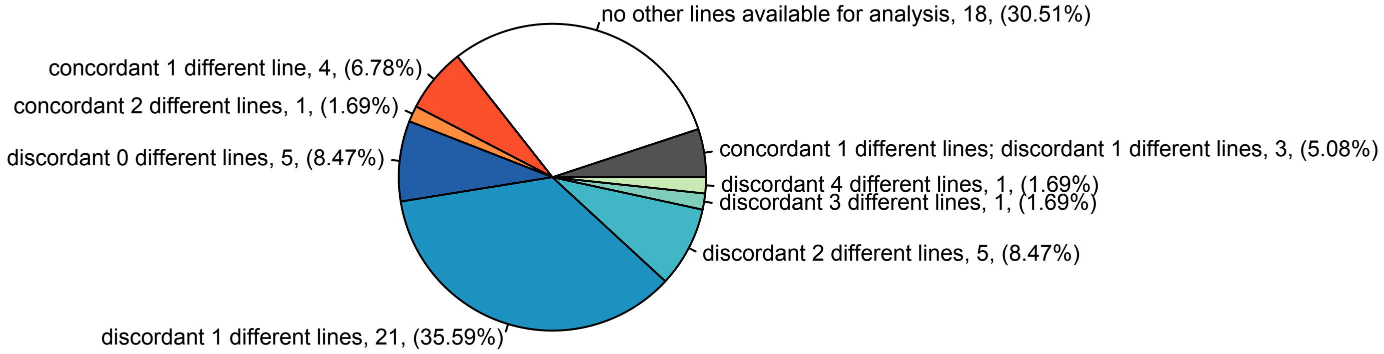
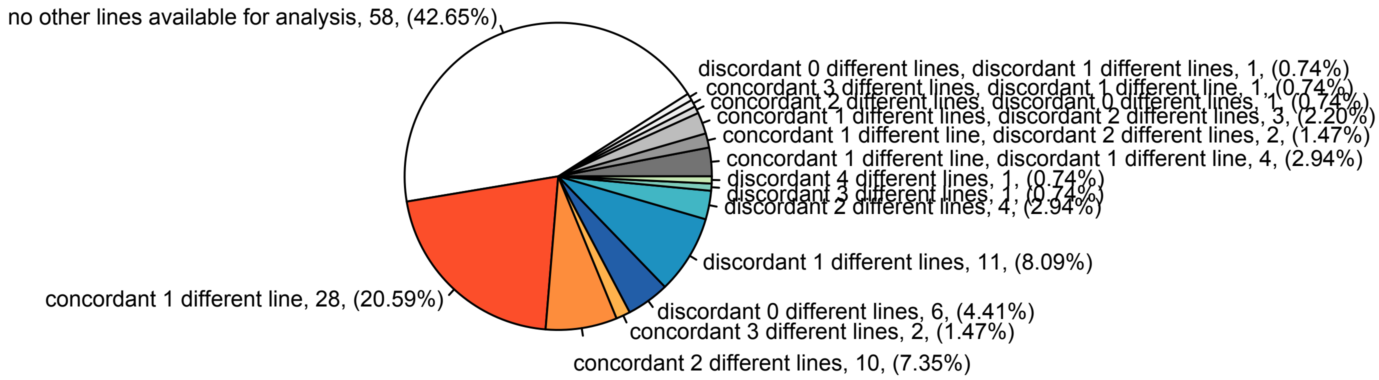
Phenotype concordance for 195 newly-evolved genes identified in Chen and Long (Science 2010) by different RNAi triggers

59 “young, essential” genes



136 “young, non-essential” genes



Legend:
Red/Orange slices : lethal or viable phenotype concordance between Chen 2010 and other studies.
Blue/Green slices : lethal or viable phenotype discordance.
Grey slices : concordant and discordant phenotypes between Chen 2010 and other studies.
White slices: no independent RNAi line data available for analysis, same phenotype reported for same line.

Notes on phenotype concordance/discordance :
discordant 0 different lines : No additional lines available for analysis, but different phenotype was reported between 2 or more different studies using the same line available.

concordant x different lines : x additional lines were found that were different from the lines(s) used in Chen and Long 2010. The phenotypes for these lines were the same when compared to the lines and results from Chen and Long 2010.
discordant x different lines : x additional lines were found that were different from the lines(s) used in Chen and Long 2010. The phenotypes were different in these lines when compared to Chen and Long 2010.

Supplementary Figure 11. Comparison of RNAi-induced lethality for recently-emerged genes using independent triggers.

We show two pie charts, representing 59 "young, essential" and 136 "young, non-essential" genes classified by Chen and Long (9). Although the vast majority of RNA-induced lethality phenotypes were originally reported to be confirmed by an additional transgene, nearly all of these validations involved insertions of the same trigger. We compiled data from actin5C-Gal4 tests using different RNAi triggers, where available.

Kondo et al,
Supplementary Figure 11