

Figure 1

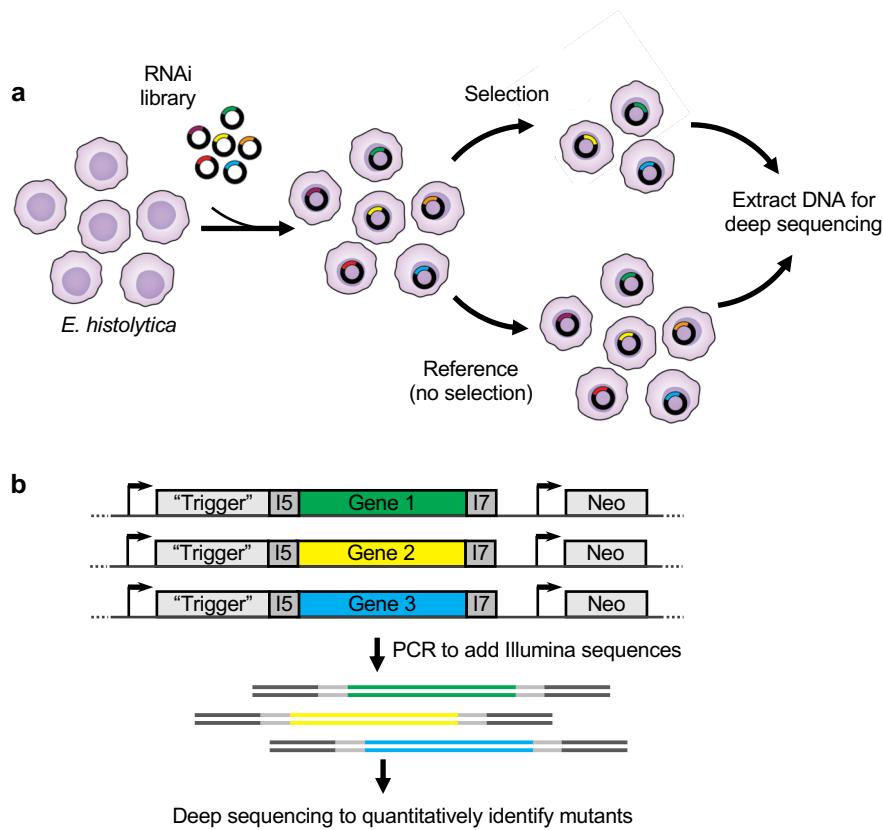


Figure 2

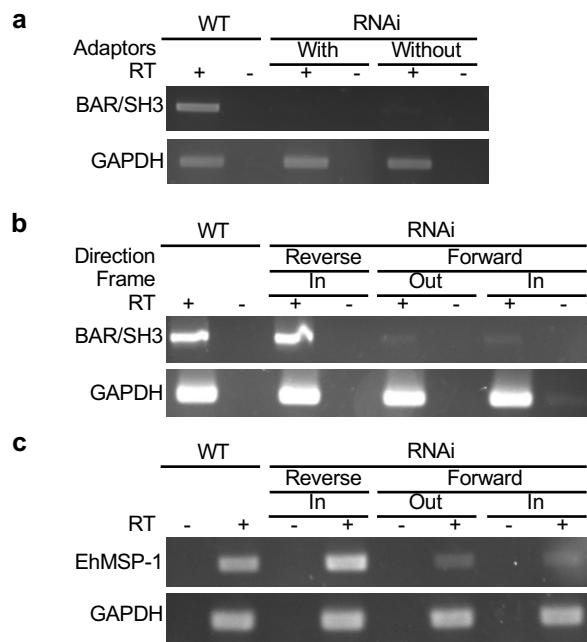


Figure 3

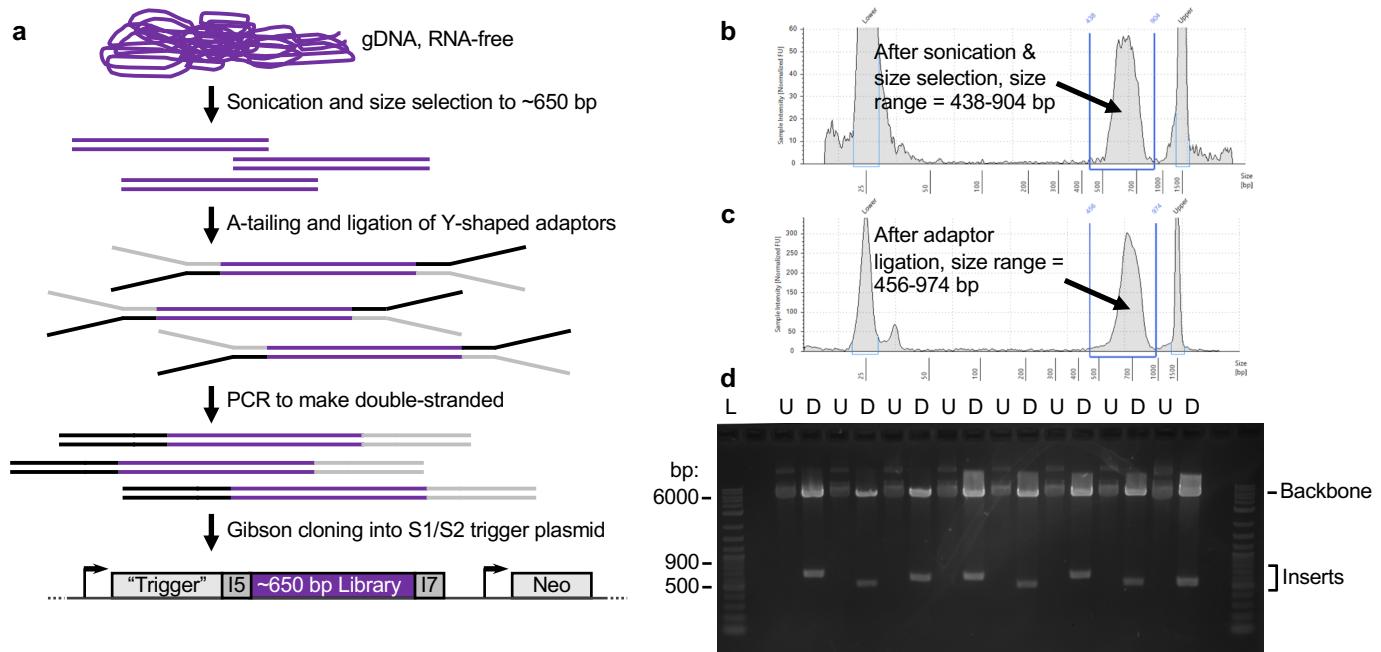
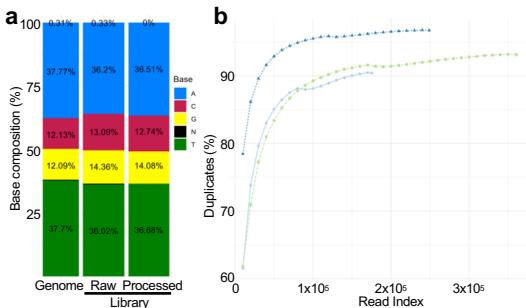


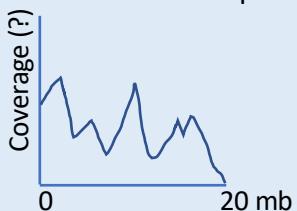
Figure 4 (Sequence analysis of plasmid library)



These data above are from our initial, least complex, plasmid library that has only about 400 unique genomic fragments. Since we probably have a better library now, we'd like the figures/tables shown in the paper to focus on characterizing our best library, instead. We do need to include at least some analysis on the ~400 fragment library (probably just a table) to show characterization/details, since Akhila did transfet amoebae & obtain mutants using this library as a pilot.

Data that we would like to be able to show in figures:

- A visual representation of the genome (or at least a stretch of genome) to show representation of genomic fragments. Potentially a way to show if there is any bias (i.e., regions of the genome that are not represented or that are overrepresented?). Maybe one way to show bias would be like this?:



- Histogram showing range of sizes of genomic fragments in plasmid library (could also compare/contrast with the size range of the fragmented DNA)
- Base composition of genome vs. fragmented DNA vs. plasmid library
- Something to show consistency of technical sequencing replicates (to get at PCR bias)?

Data that we would like to be able to show in tables:

- For fragmented DNA vs plasmids – what % of the genome is represented? What % of genes are represented? How many unique fragments are there? (Also, more for our own use – comparing the plasmid library that was made from 18 cycles of PCR vs standard 5 cycle PCR of the other libraries – to see if this created bias/changed representation of sequences).
- Something to get at density of coverage or redundancy of representation of genomic fragments that are in genes – i.e. is there just one fragment represented per gene, or multiple unique fragments? Maybe a histogram, like this?:

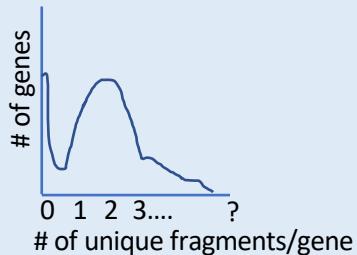


Figure 5

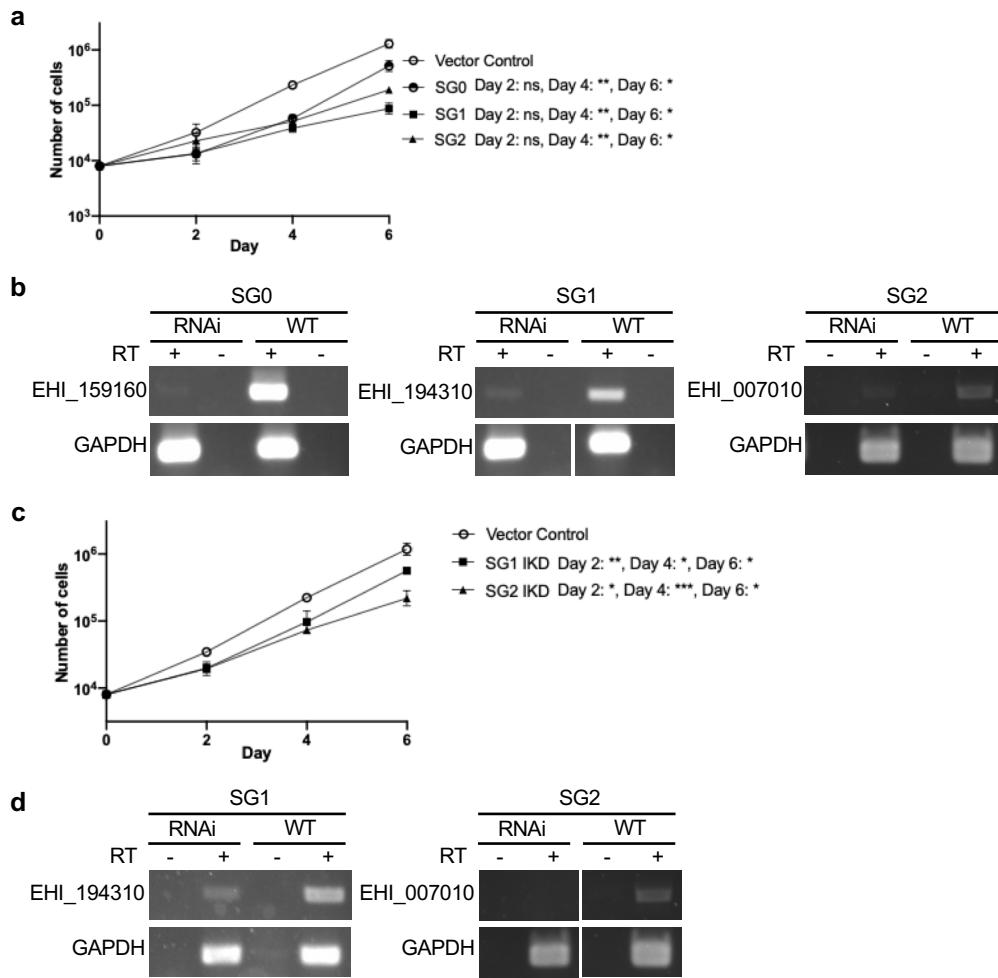
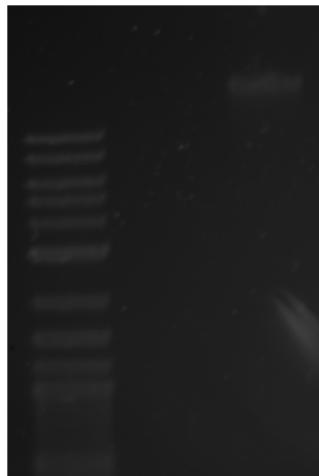


Table 1

Add table with info on the mutants – gene ID/insert size & position/annotation or domains/any published studies?

Figure S1

a

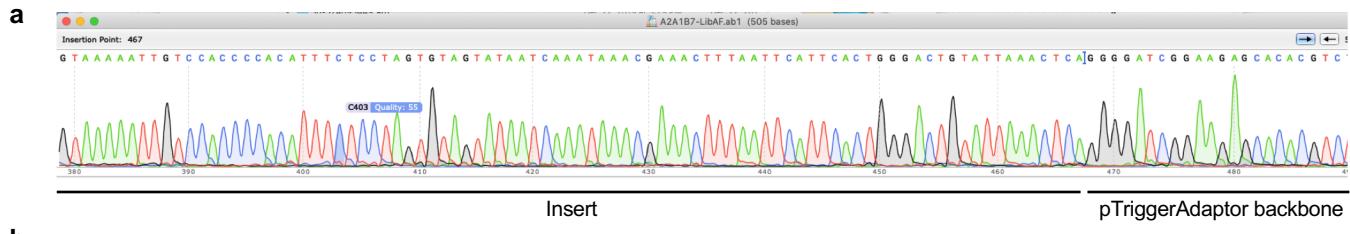


b

Add gels from
different
vendors/protocols

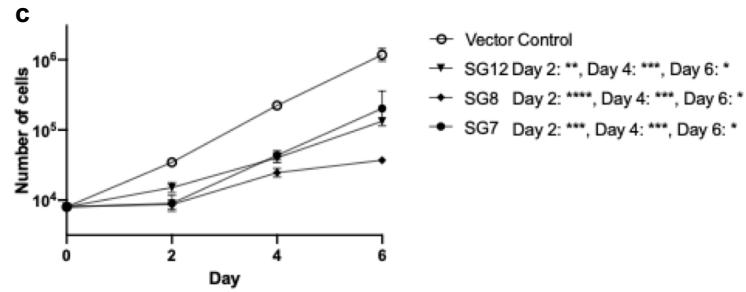
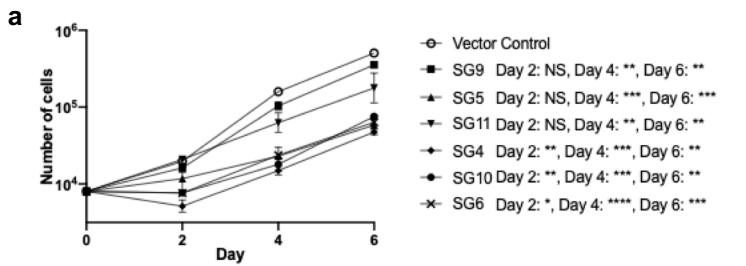
Improve appearance if possible with Fiji
Add labels to the lanes (is it Ladder, empty, gDNA?)
Label a few marker bands

Figure S2

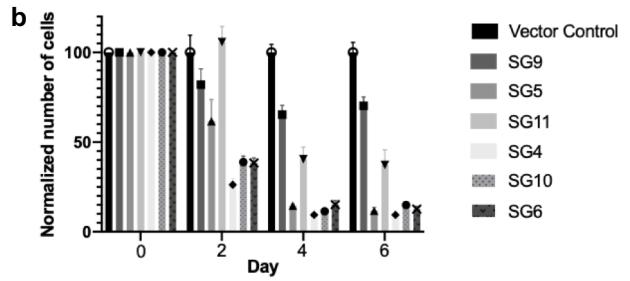


Add more info from experiments that support 1 plasmid/clonal line – e.g. sequencing of 2nd round clones (I believe I remember this experiment) – make into a chart that shows clone # and gene ID recovered from sequencing

Figure S3



Reformat to remove symbols
Add stats



Make a plot like panel b

Table S1

Add table with info on the sequences used in knockdown plasmids & the primers used for RT-PCR