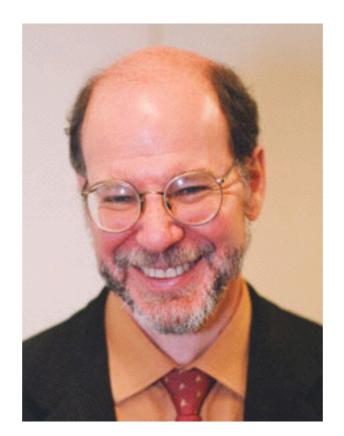
Bio393: Genetic Analysis

Step-wise genetic analysis

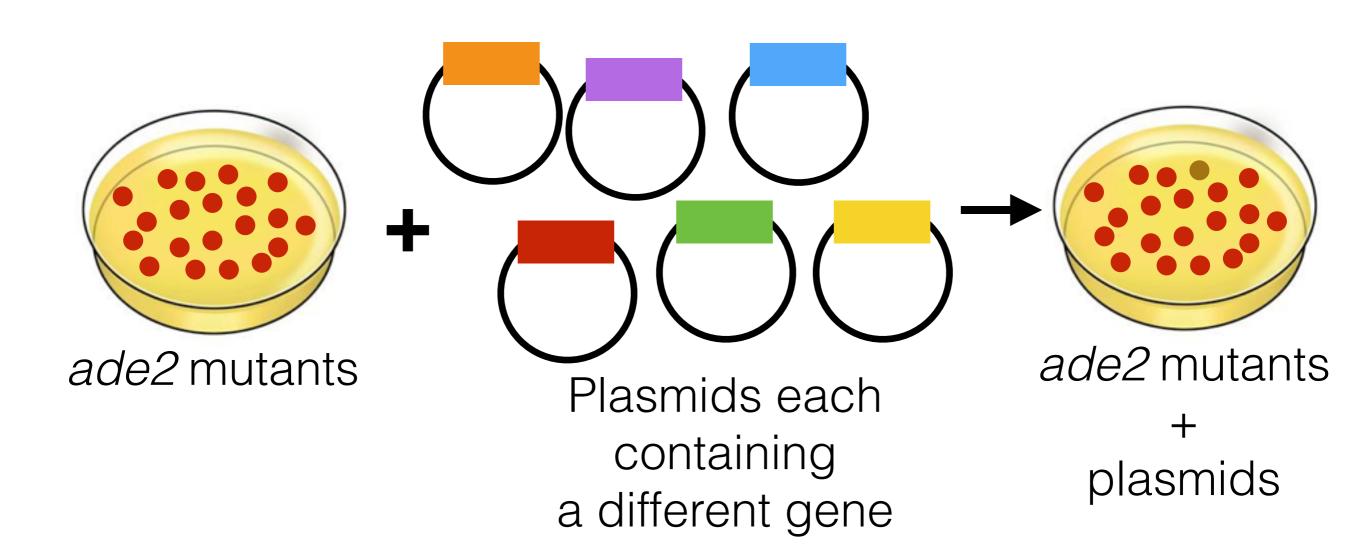


Bob Horvitz

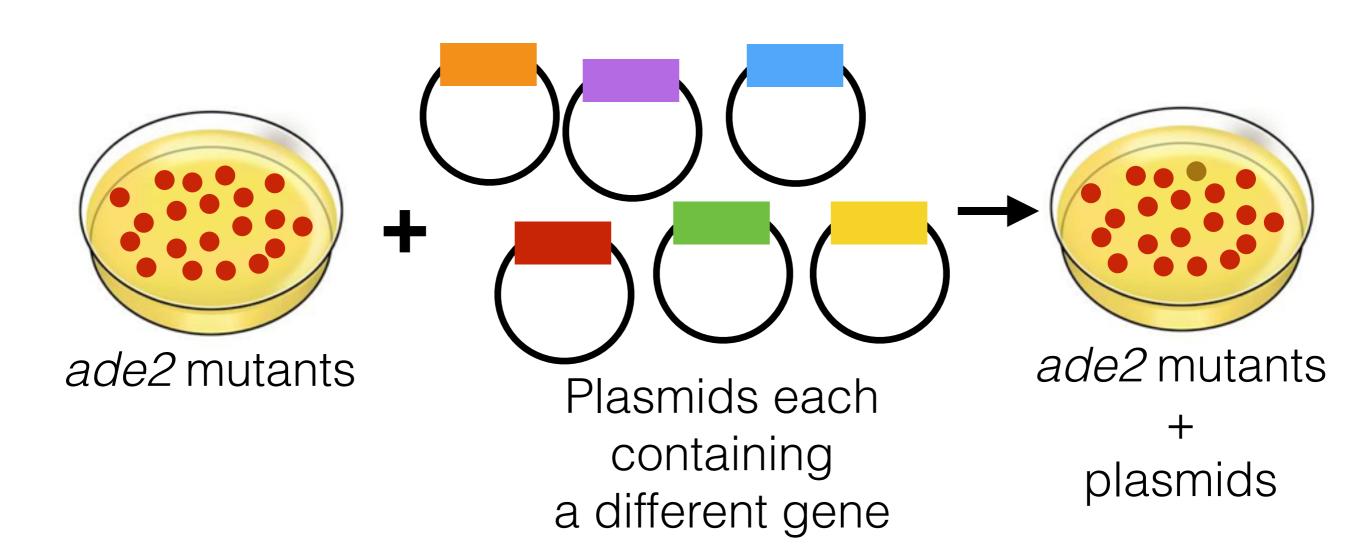
15. Clone the gene

- 1. Clone by complementation
- 2. Clone by phenocopy
- 3. Clone by sequencing

Cloning by complementation in bacteria and yeast

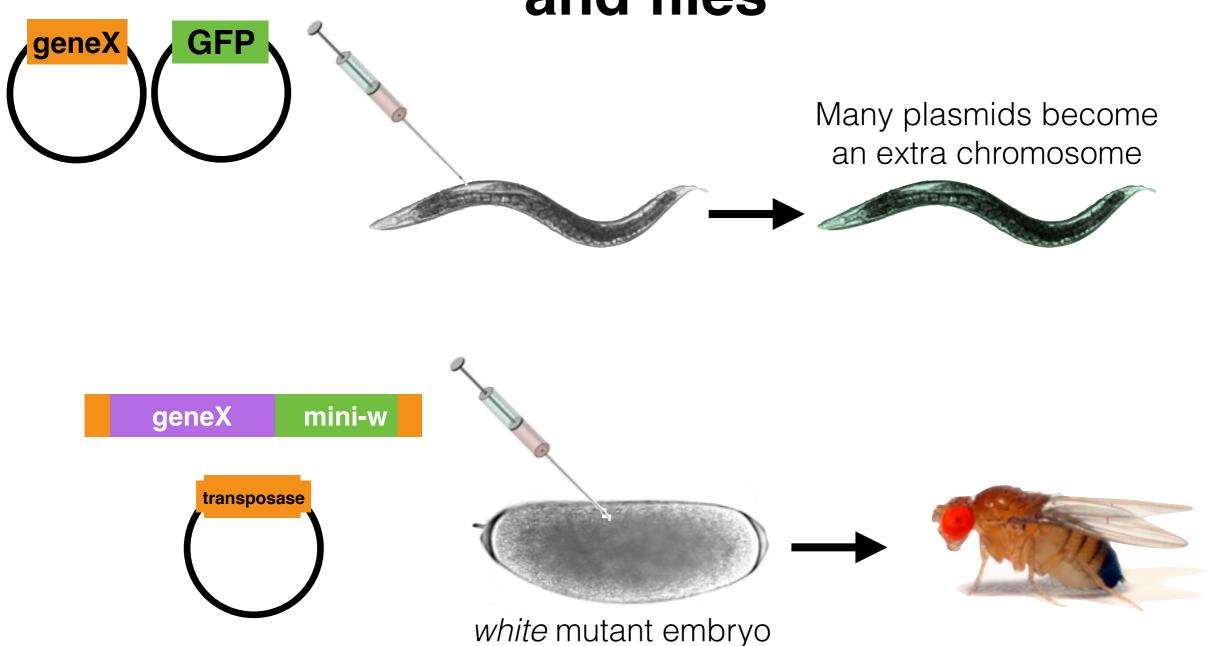


Cloning by complementation in bacteria and yeast



Caveat: overexpression bypass suppressors

Cloning by complementation in worms and flies

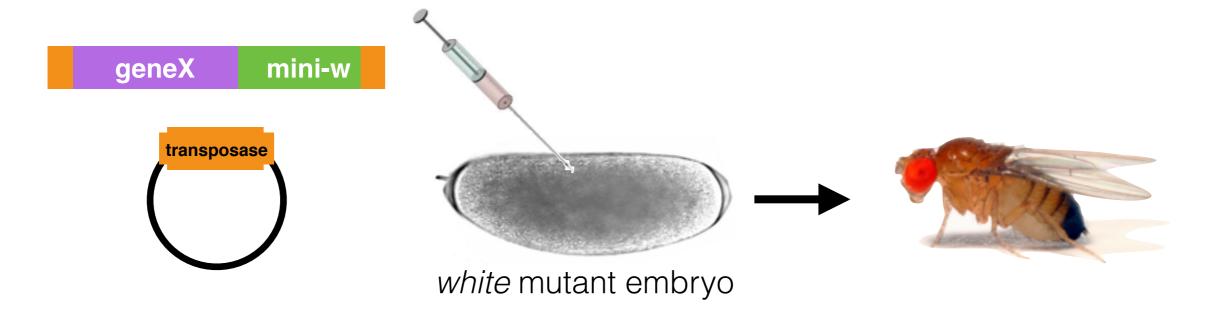


Transgenesis and rescue

Cloning by complementation in worms and flies



Caveat: overexpression bypass suppressors and not stable

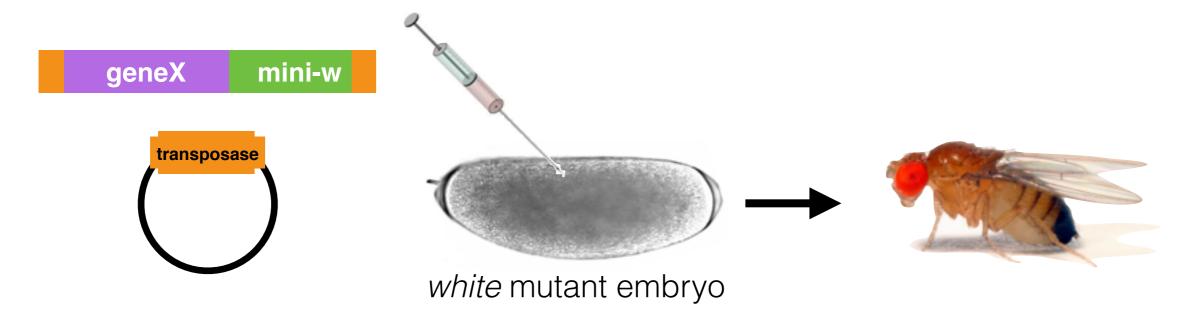


Transgenesis and rescue

Cloning by complementation in worms and flies



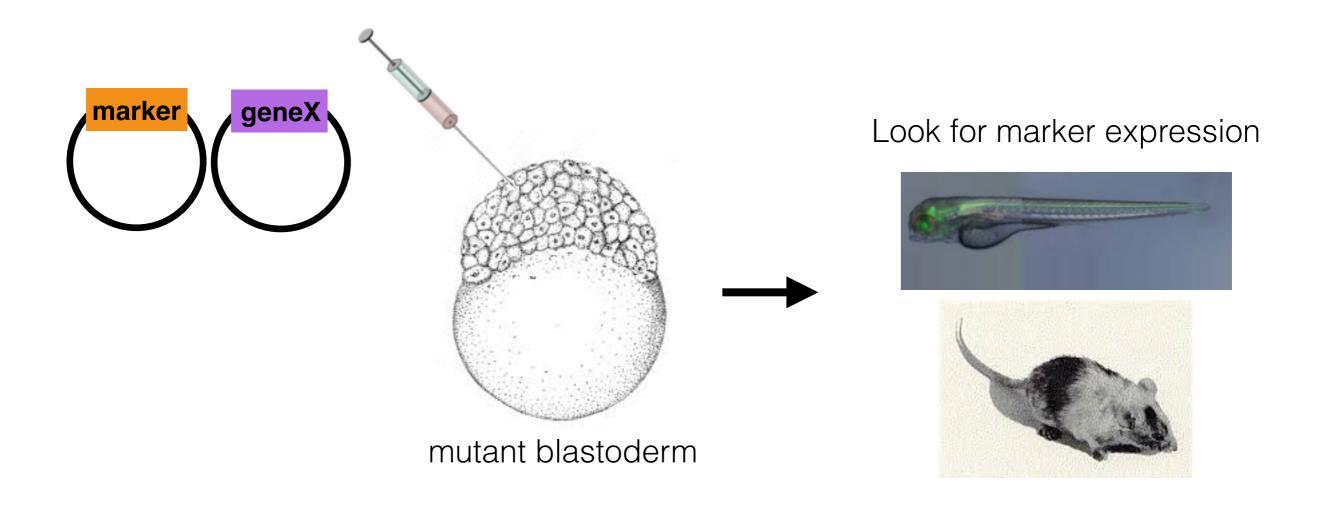
Caveat: overexpression bypass suppressors and not stable



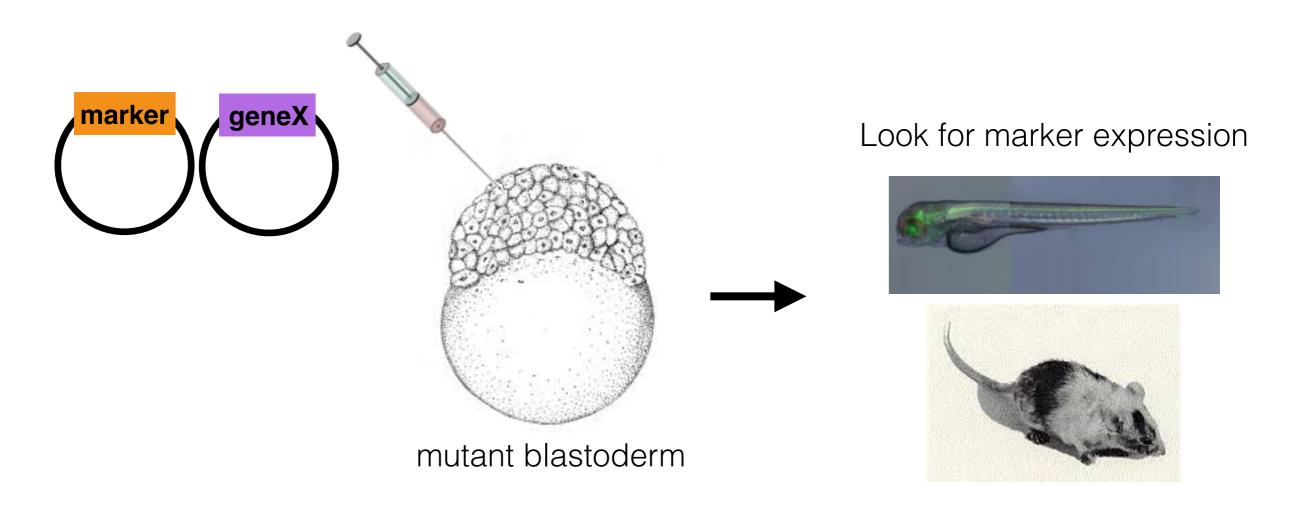
Caveat: overexpression bypass suppressor and variable expression

Transgenesis and rescue

Cloning by complementation in fish and mice



Cloning by complementation in fish and mice

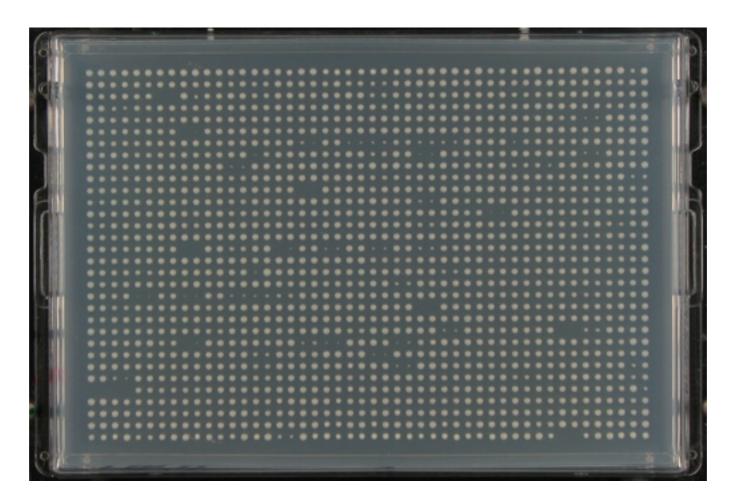


Caveat: overexpression bypass suppressors and variable expression

15. Clone the gene

- 1. Clone by complementation
- 2. Clone by phenocopy
- 3. Clone by sequencing

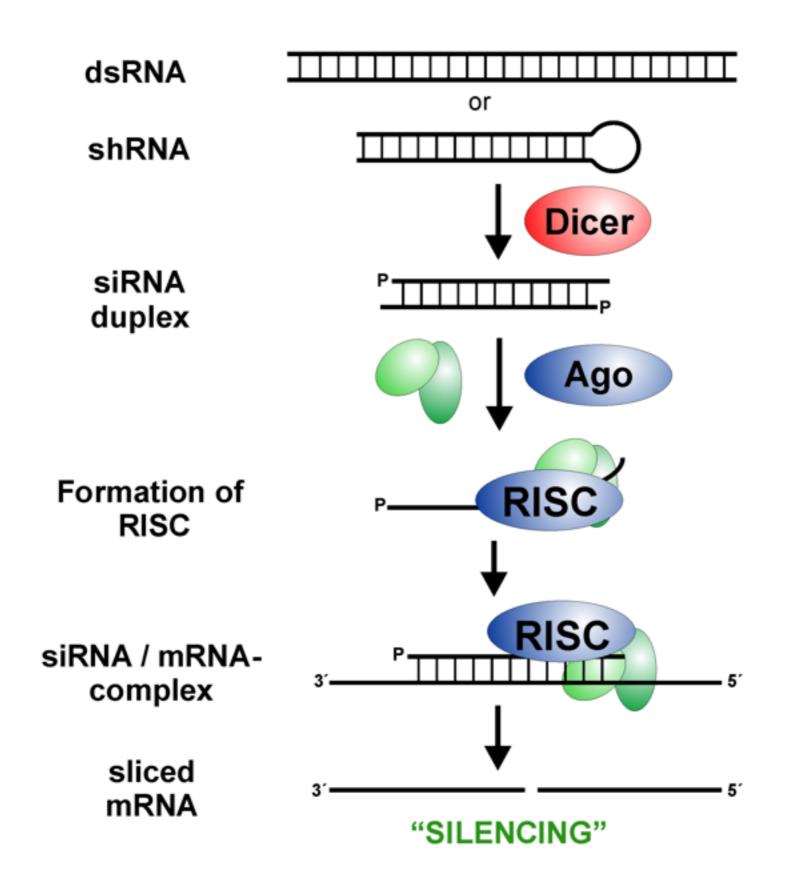
Most model organisms have libraries of strains where each strain has a unique loss-of-function mutation



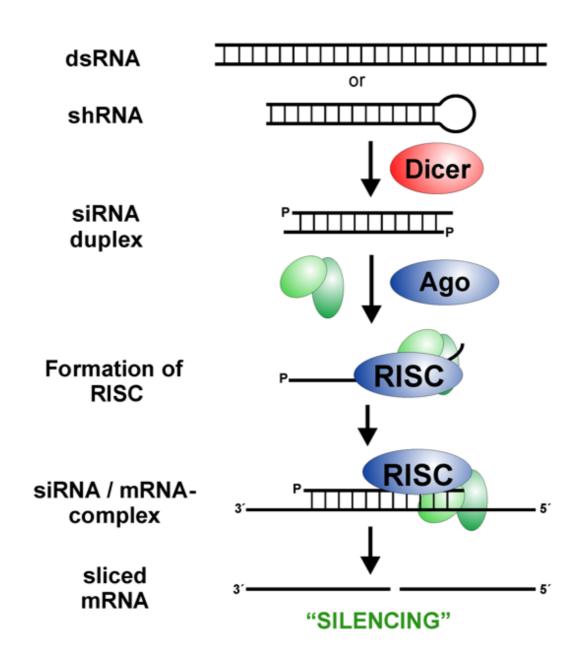
Score them all!!!

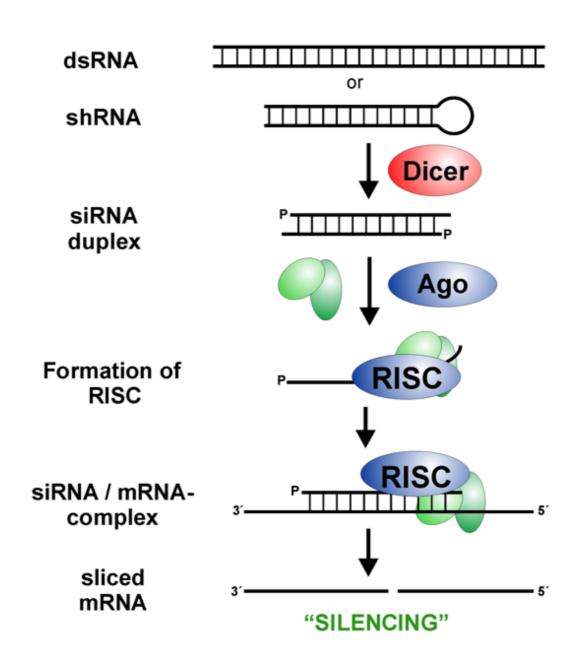
Phenotype is everything!

It has to be scalable, quantitative, reproducible, and accurate



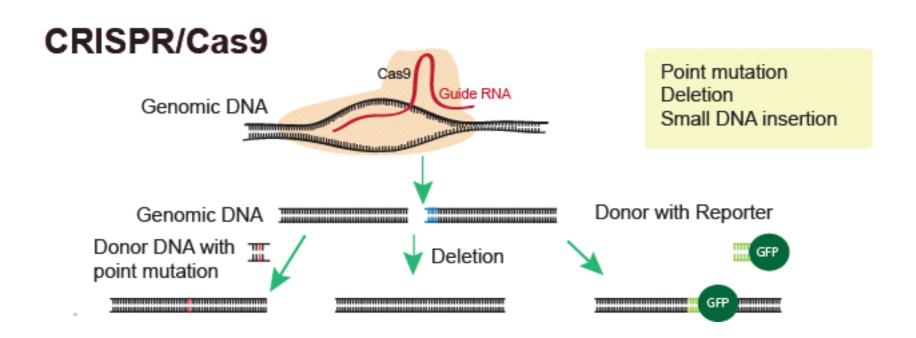
You have to dsRNA or get these RNAs shRNA into the organism siRNA duplex Formation of RISC **RISC** RISC siRNA / mRNAcomplex sliced **mRNA** "SILENCING"



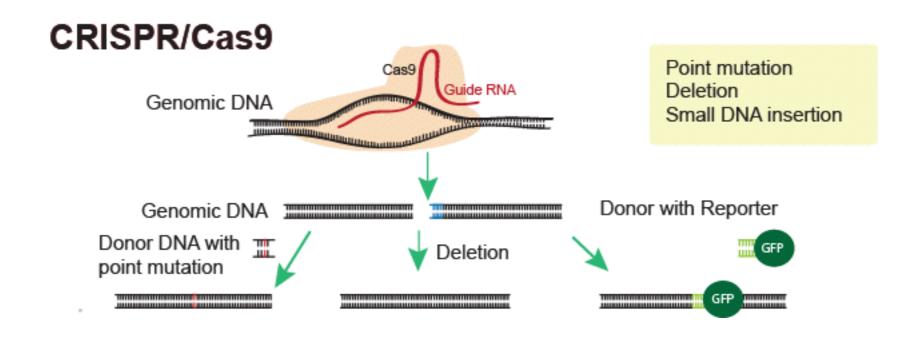


Caveat: Delivery is problematic, highly variable effects, not heritable, not loss-of-function, not specific

CRISPR/cas9 can be used to create heritable loss-of-function mutations in a variety of organisms



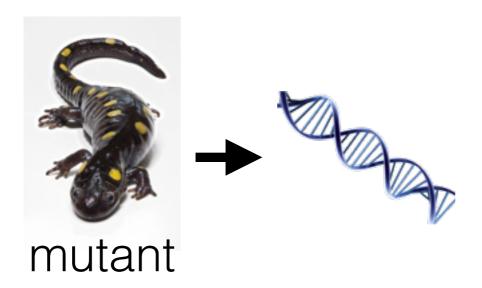
CRISPR/cas9 can be used to create heritable loss-of-function mutations in a variety of organisms

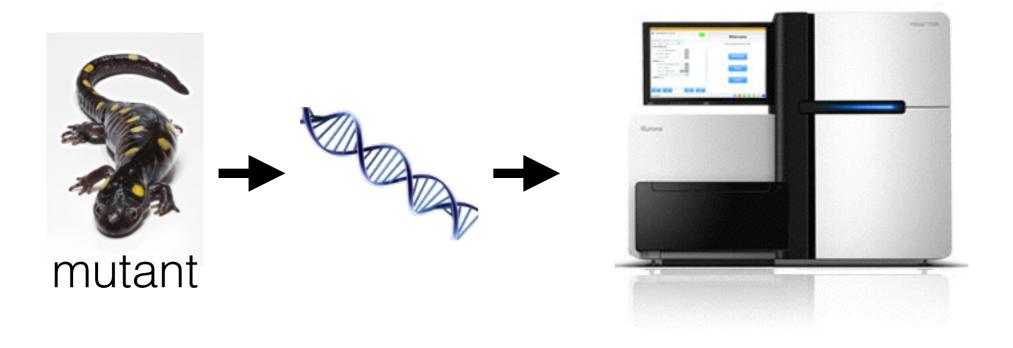


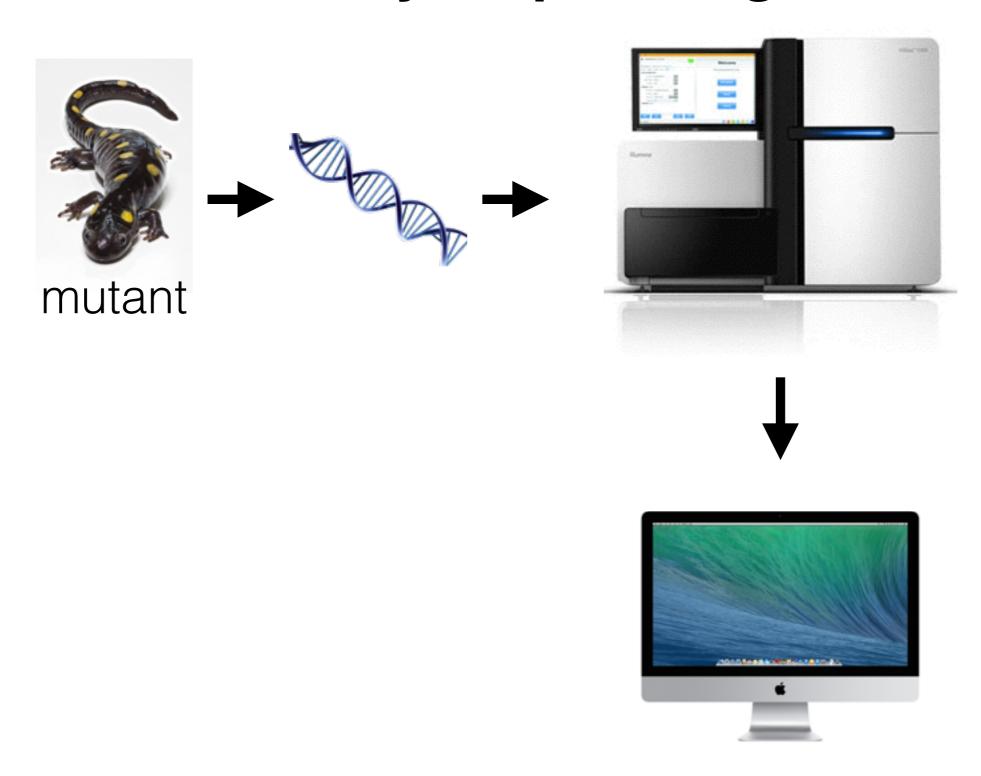
Caveat: Sometimes not specific (off-target effects)

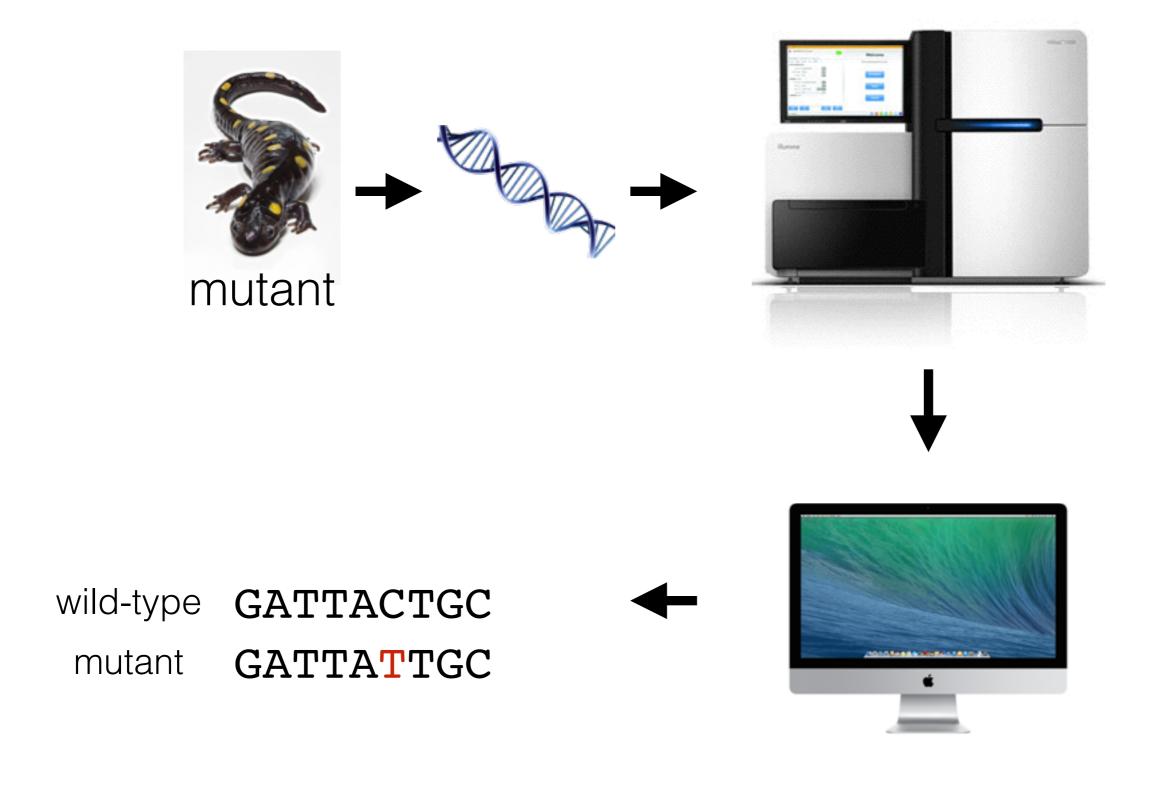
Generate "mutations" by reverse genetic RNAi or CRISPR for "all" genes in an organism

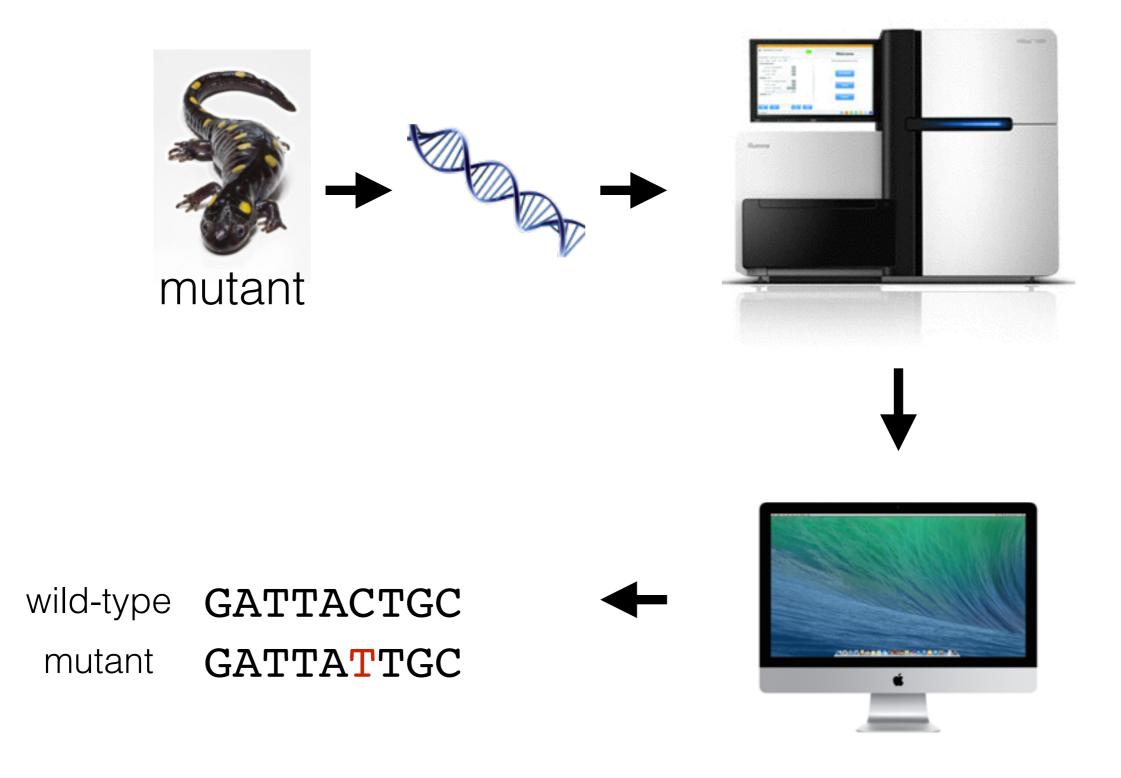
Organism	Approx. # of genes
Yeast (S. cerevisiae)	6,000
Fly (D. melanogaster)	15,000
Worm (C. elegans)	21,000
Zebrafish (<i>D. rerio</i>)	26,000
Chicken (G. gattus)	17,000
Mouse (M. musculus)	23,000
Mustard plant (A. thaliana)	28,000
Human (H. sapiens)	30,000







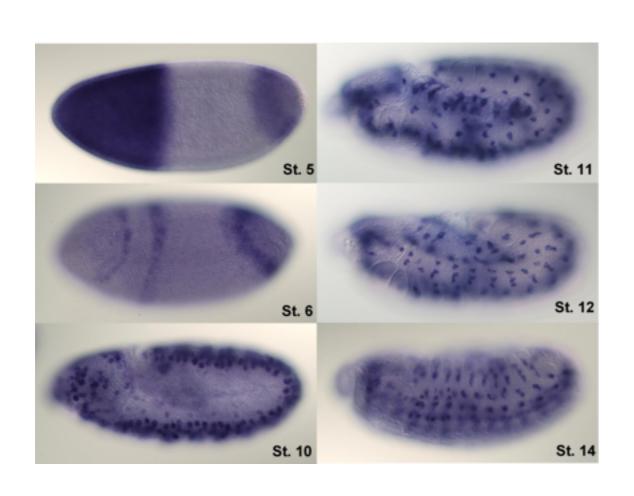


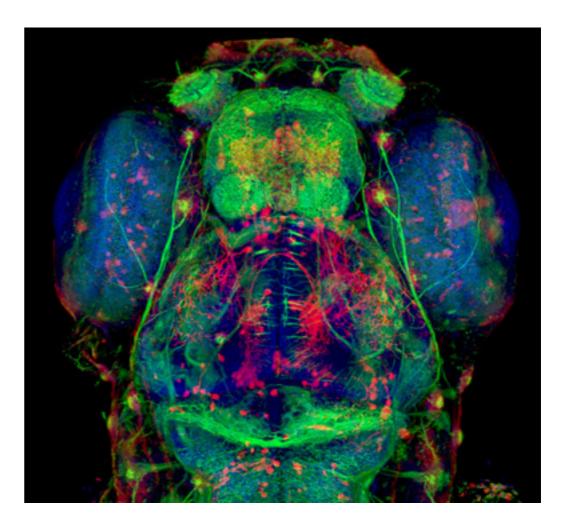


Need multiple non-complementing alleles and mapping

With no transgenesis:

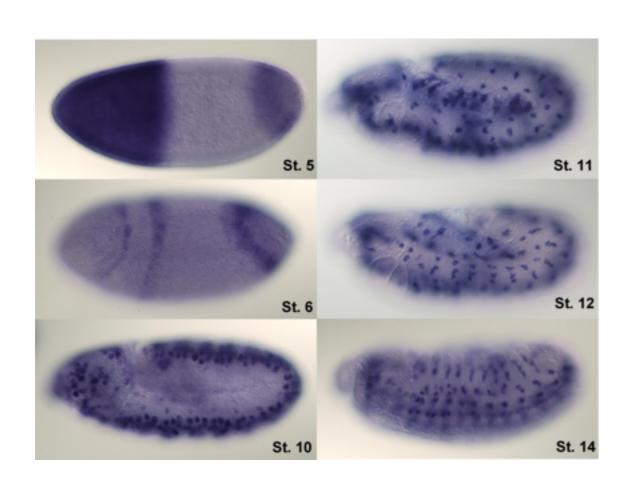
- 1. *in situ* hybridization (RNA localization)
- 2. Antibody immunofluorescence (protein localization)

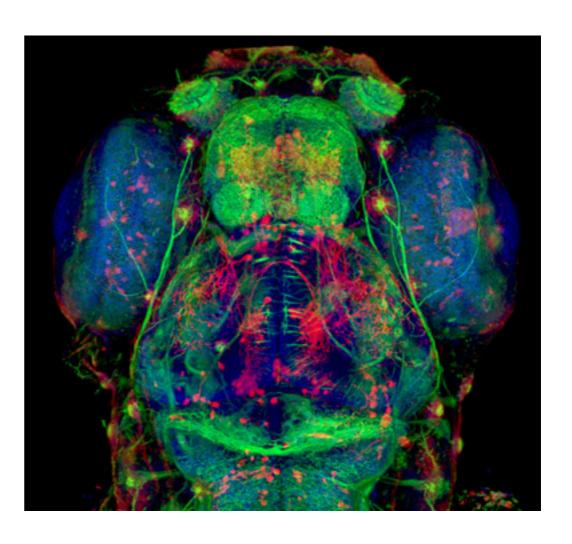




With no transgenesis:

- 1. *in situ* hybridization (RNA localization)
- 2. Antibody immunofluorescence (protein localization)





How do we know we have the right expression pattern?

With transgenesis:

1. Fluorescent reporters (GFP, mCherry)





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1. Fluorescent reporters (GFP, mCherry)



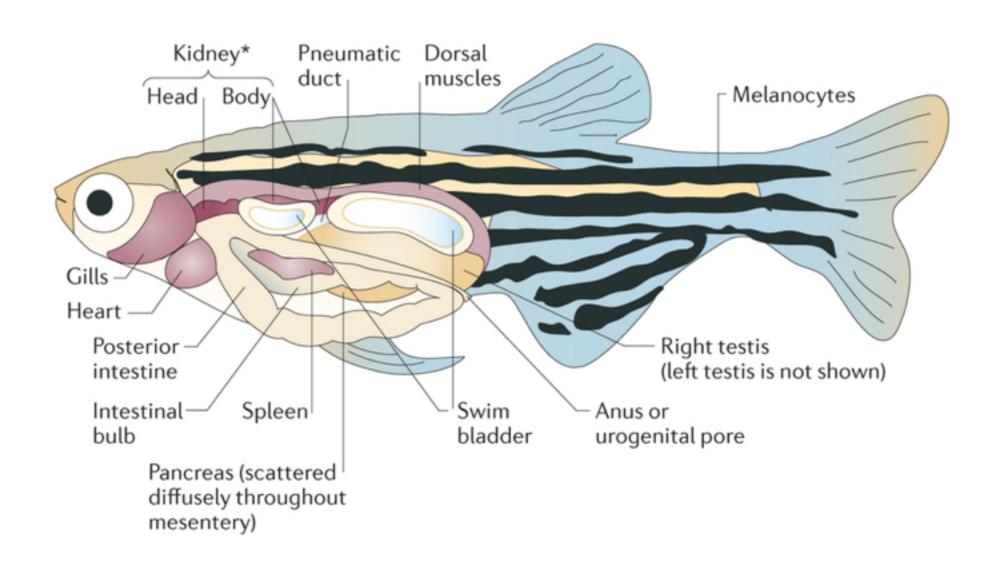


How do we know we have the right expression pattern?

17. Determine site of gene action

What is the cell, organ, and/or tissue where the gene functions?

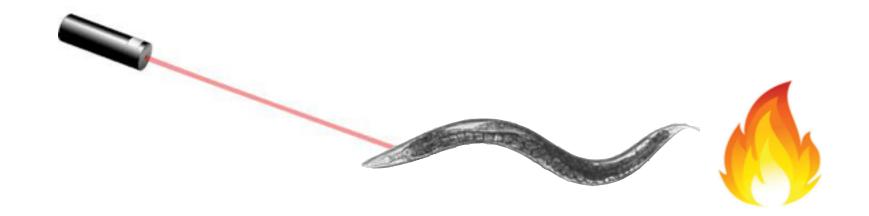
- 1. Rescue a mutant phenotype in a specific cell, organ, or tissue
- 2. Mosaic analysis (cell autonomy experiments)



18. Determine time of gene action

When does the gene function?

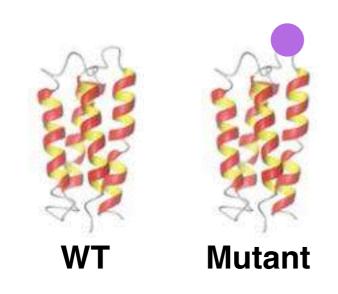
1. Induce expression to rescue a mutant phenotype at a specific time



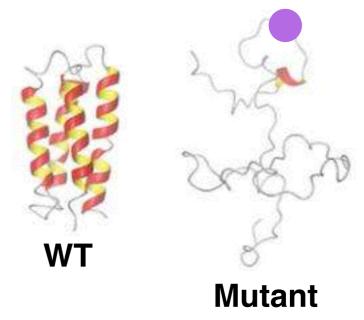
18. Determine time of gene action

When does the gene function?

- 1. Induce expression to rescue a mutant phenotype at a specific time
- Use temperature-labile mutants to define the temperature-sensitive period



Permissive temperature



Restrictive temperature

18. Determine time of gene action

Temperature-sensitive period