

PDF Distribution Version

May 2019

Functional Genomics Resources for Drosophila Research from the DRSC/TRiP

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Director of [DRSC/TRiP Functional Genomics Resources](#)



[@smohrfly](#)
[@DRSC_TRiP](#)

***Look out for helpful hyperlinks
throughout the presentation***



HARVARD
MEDICAL SCHOOL

PART I: in vivo fly stock production

Transgenic RNAi Project (TRiP)-KO and –OE sgRNA fly stocks

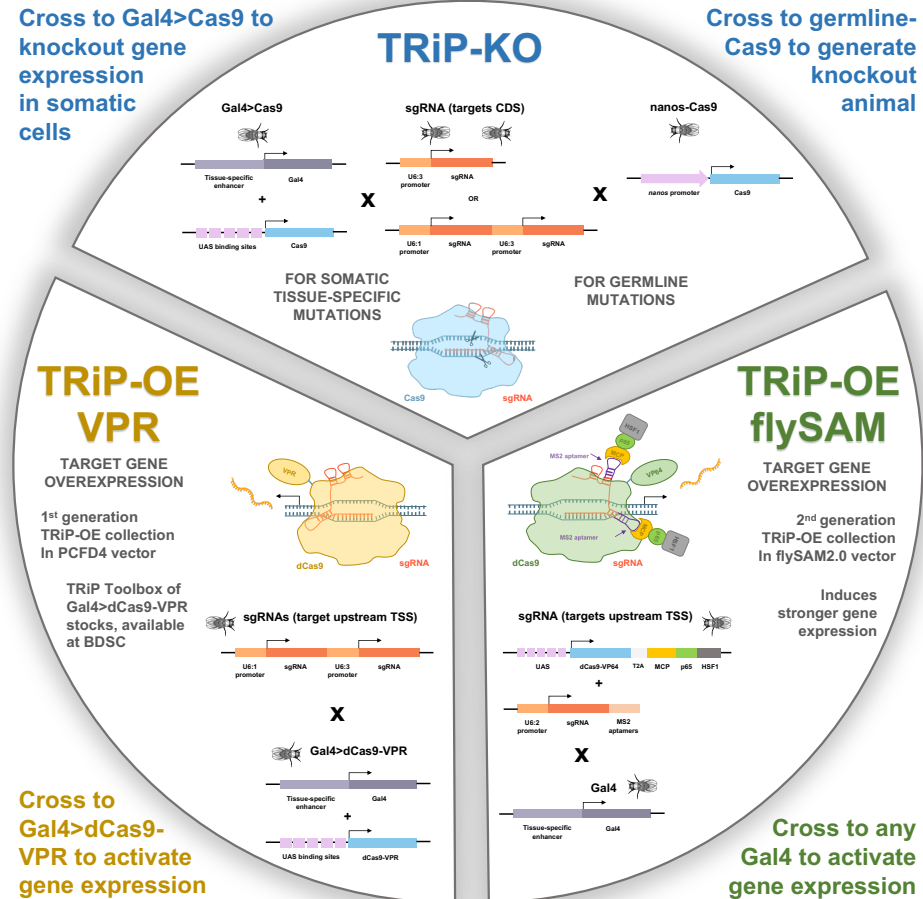
For tissue-specific CRISPR knockout or activation

<https://fgr.hms.harvard.edu/using-trip-crispr-lines>

<https://fgr.hms.harvard.edu/sgrna-vectors>

https://www.flyrnai.org/tools/grna_tracker/web/

TRiP-CRISPR overview



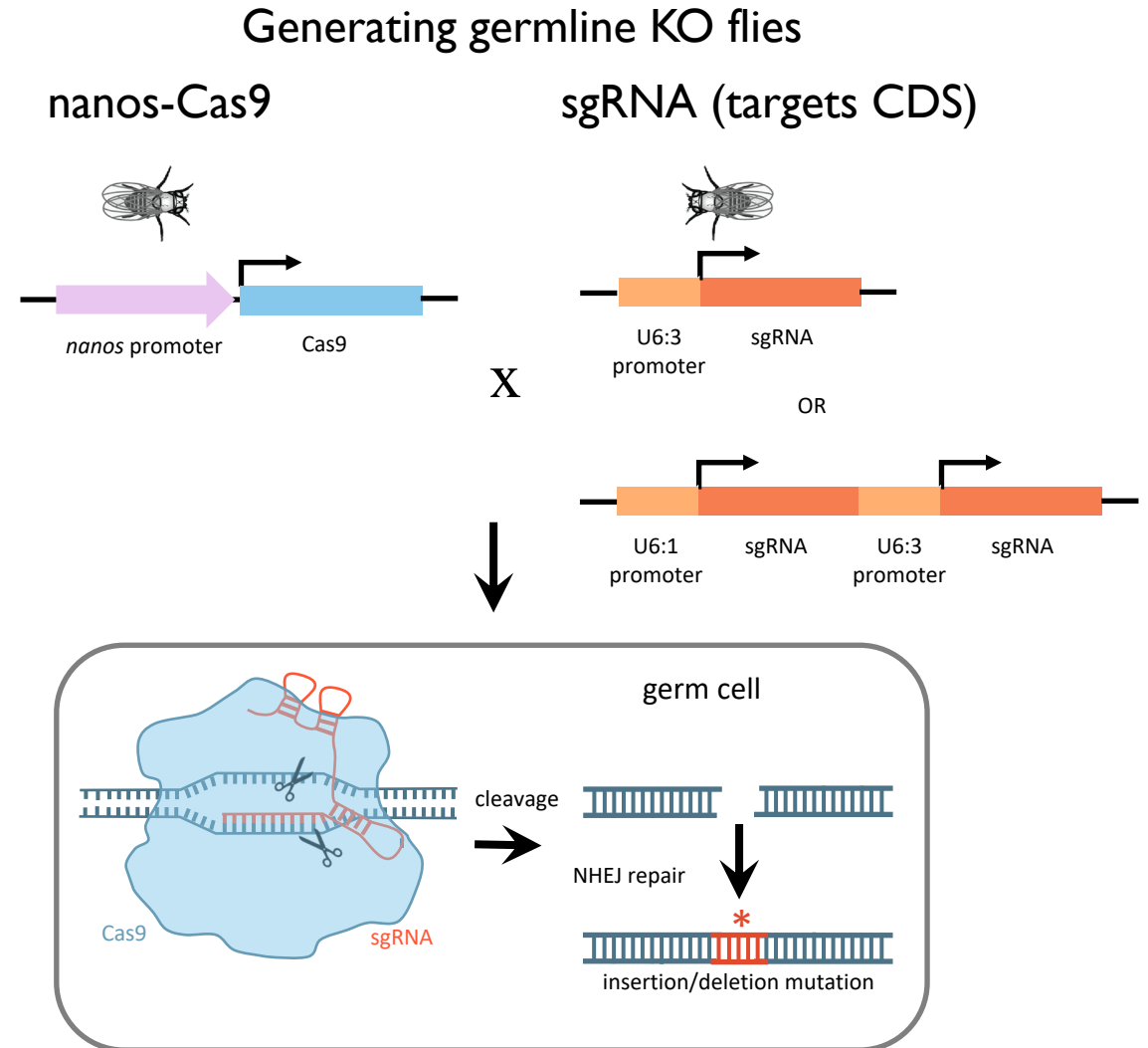
Collection	TRiP-OE			TRiP-KO
	VPR	flySAM	flySAM.dCas9	
Function	Gene Activation	Gene Activation	Gene Activation	Gene Cutting
Vectors	pCFD4	U6B-sgRNA2.0	flySAM2.0	pCFD3, pCFD4, pCFD6
Cross to	Gal4+ dCas9-VPR	Gal4+ flySAM	Gal4	Gal4+ Cas9
Notes	Use with TRiP-CRISPR Toolbox	Use with TRiP-CRISPR Toolbox	flySAM.dCas9 contain both sgRNA and activator complex	Use with TRiP-CRISPR Toolbox
Stocks	2,128	216	262	2,145

<https://fgr.hms.harvard.edu/using-trip-crispr-lines>

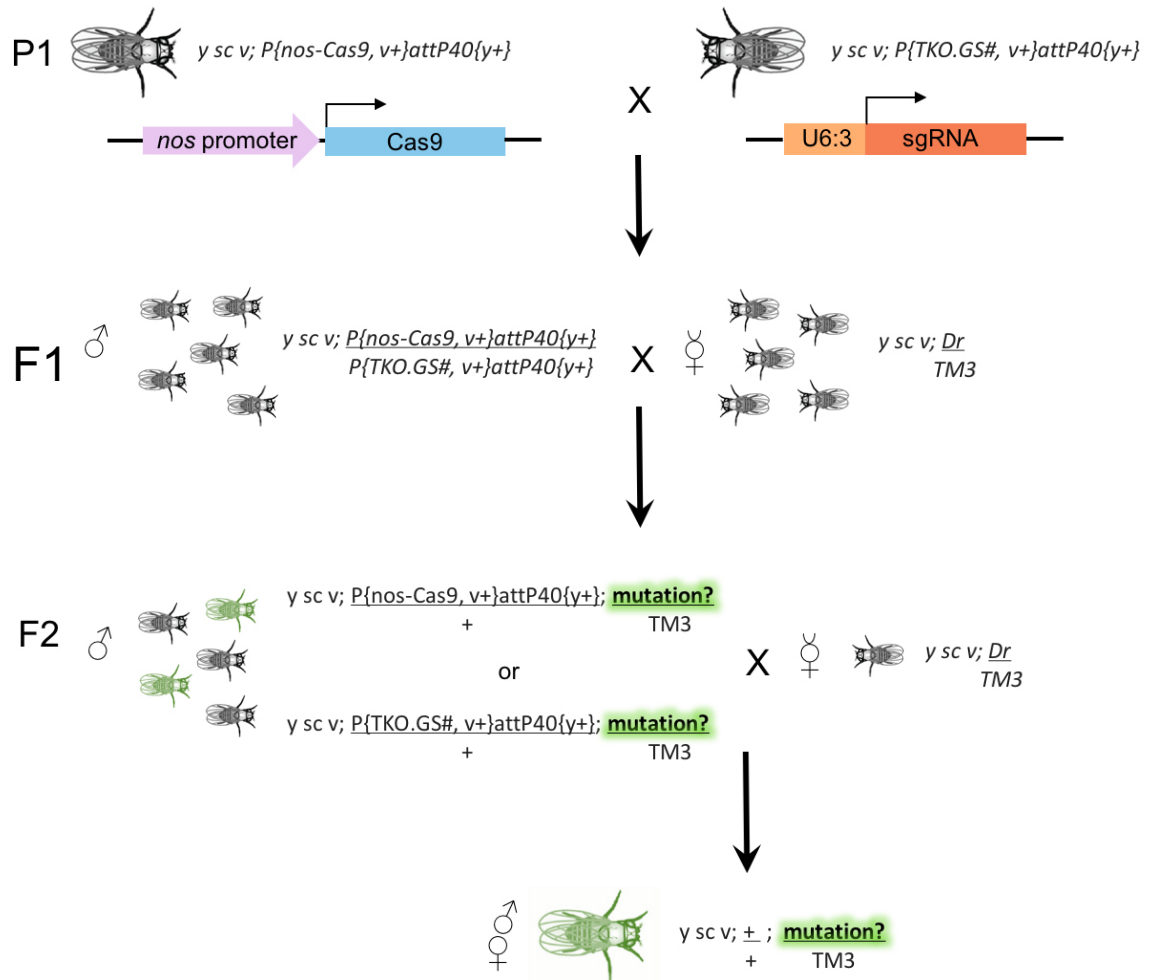
<https://fgr.hms.harvard.edu/sgrna-vectors>

TRiP-CRISPR Knockout (TRiP-KO)

- TRiP-KO flies ubiquitously express sgRNAs targeting gene coding sequence.
- Target most 5' sequence that will mutate all/most isoforms
- Mutant animals can be produced by simply crossing TRiP-KO flies to germline-specific-Cas9



Using TRiP-KO stocks to make mutants



Step 1: cross nanos-Cas9 (nos-Cas9) stock to individual TRiP-KO stock.

Step 2: collect at least 15 male F1 progeny containing both nos-Cas9 and sgRNA transgenes.

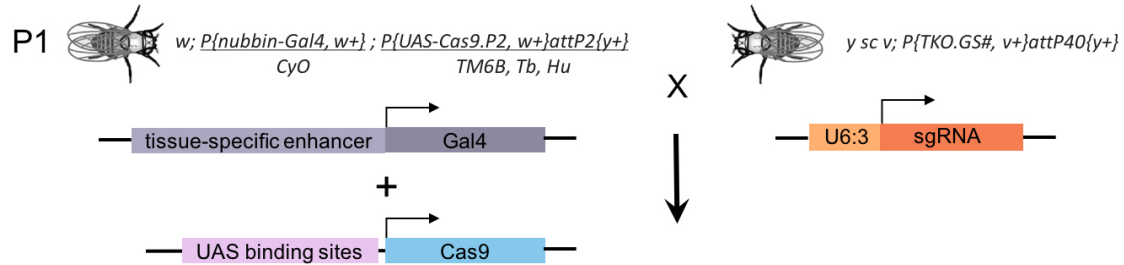
Step 3: cross male F1 progeny en masse to appropriate balancer strain for your target gene

Step 4: collect male or female F2 progeny (some will be heterozygous mutants) and cross each individually to balancer stock.

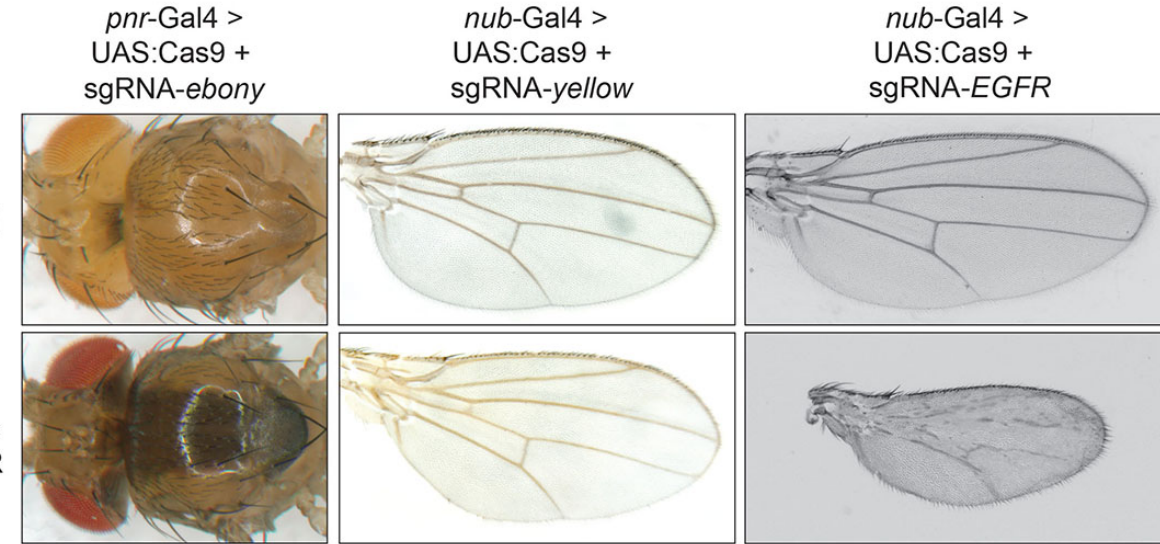
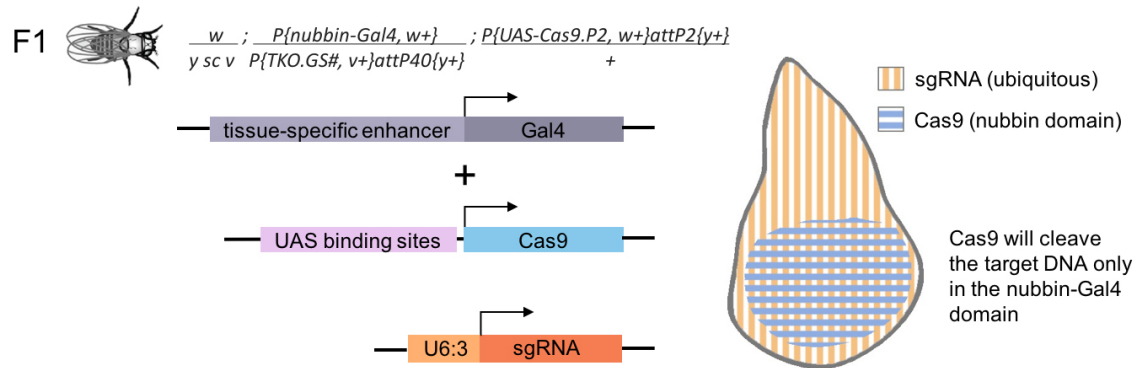
Step 5: Screen mutations by restriction profiling, endonuclease assays or high-resolution melt assays (HRMAs) and confirm by PCR and sequencing

Using TRiP-KO stocks for mosaic KO

Step 1: cross tissue specific-Gal4 + UAS-Cas9 stock to individual TRiP-KO stock.



Step 2: collect male or female F1 progeny containing tissue-specific-Gal4, UAS-Cas9 and sgRNA transgenes and analyze phenotype.

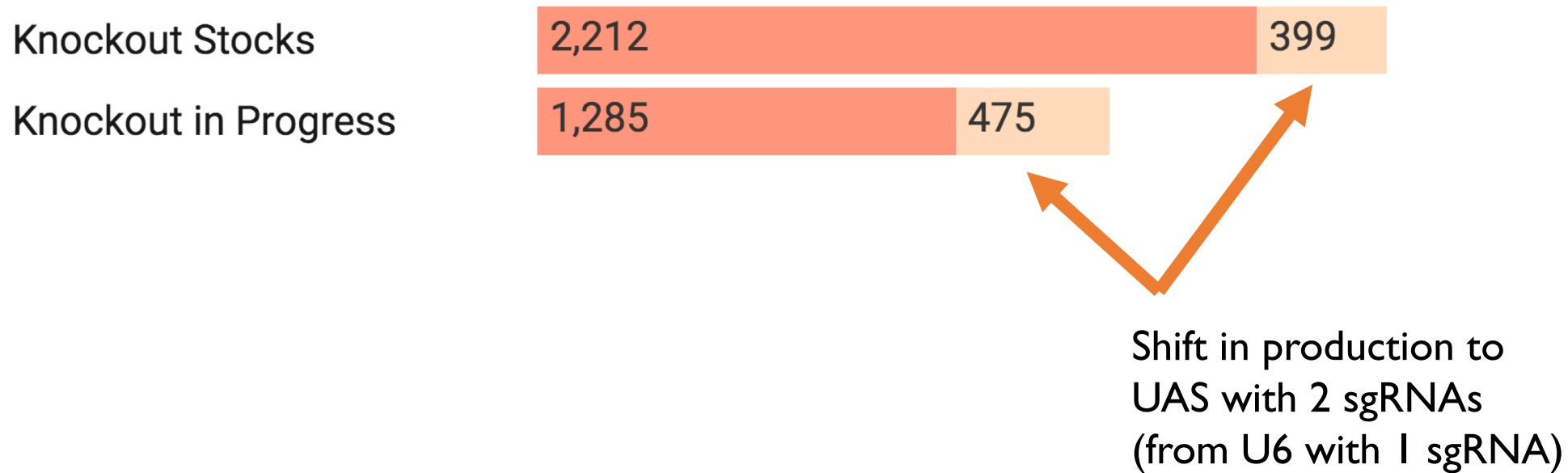


Two guides are better than one: the problem of in-frame deletions

CCATTGGCTCAGATTGACGAGGCGCCGGCAACTAAAAGA	WT
CCATTGGCTCAGATTGACG-----CCGGCAACTAAAAGA	*
CCATTGGCTCAGATTGA-----CGCCGGCAACTAAAAGA	*
CCATTGGCTCAGATTG-----GCCGGCAACTAAAAGA	*
CCATTGGCTCAGATTGACGAG-----CAACTAAAAGA	*
CCATTGGCTCAGATTGACGAa-----AACTAAAAGA	*
CCATTGGCTCAGA-----	*

TRiP-CRISPR sgRNA Production

■ single guide ■ double guide

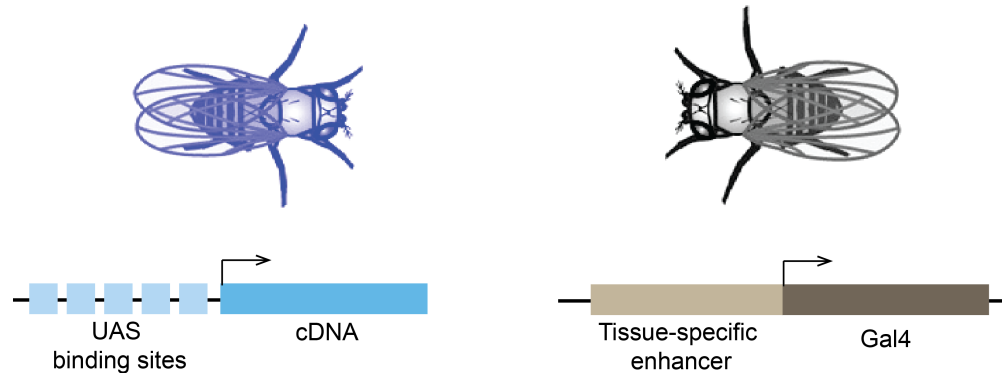


<https://fgr.hms.harvard.edu/using-trip-crispr-lines>

<https://fgr.hms.harvard.edu/sgrna-vectors>

Previous tools for over-expression in *Drosophila*

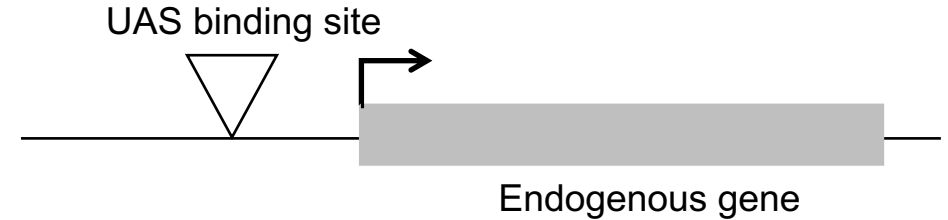
Gal4>UAS-cDNA



Limitations:

- 1) Expression is often at extremely high levels – possible toxicity
- 2) Cloning challenges – multiple isoforms, very large genes, etc.
- 3) Very hard to scale to a genome-wide resource

“EP Collection” (Rørth 1996)

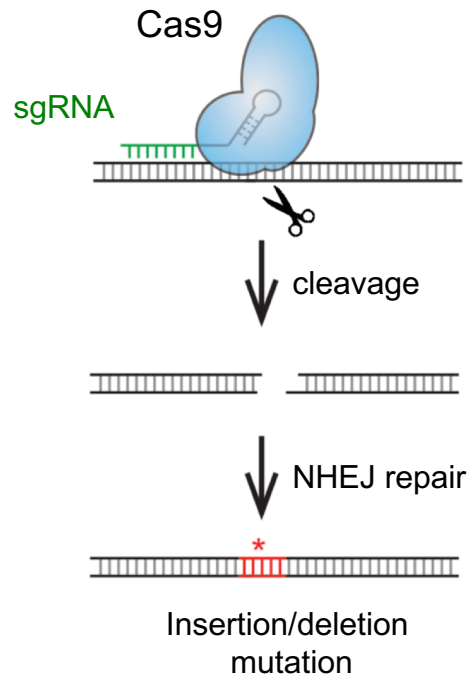


Limitations:

- 1) Expression is often very weak
- 2) Random integration
- 3) Disrupt gene

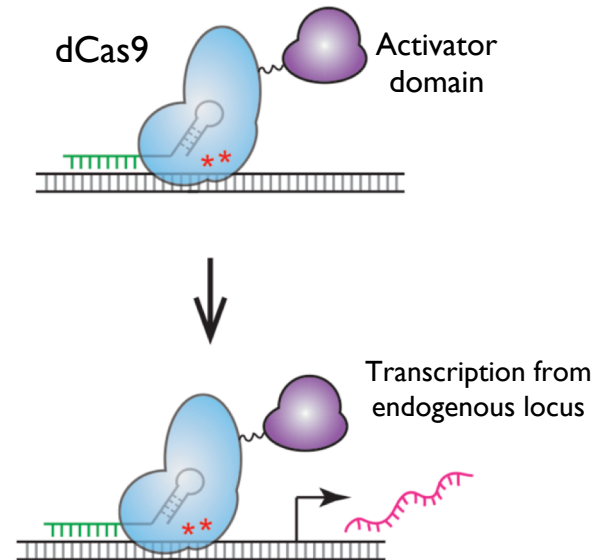
dCas9-fusions for transcriptional activation

CRISPR



CRISPRa

Transcriptional activation

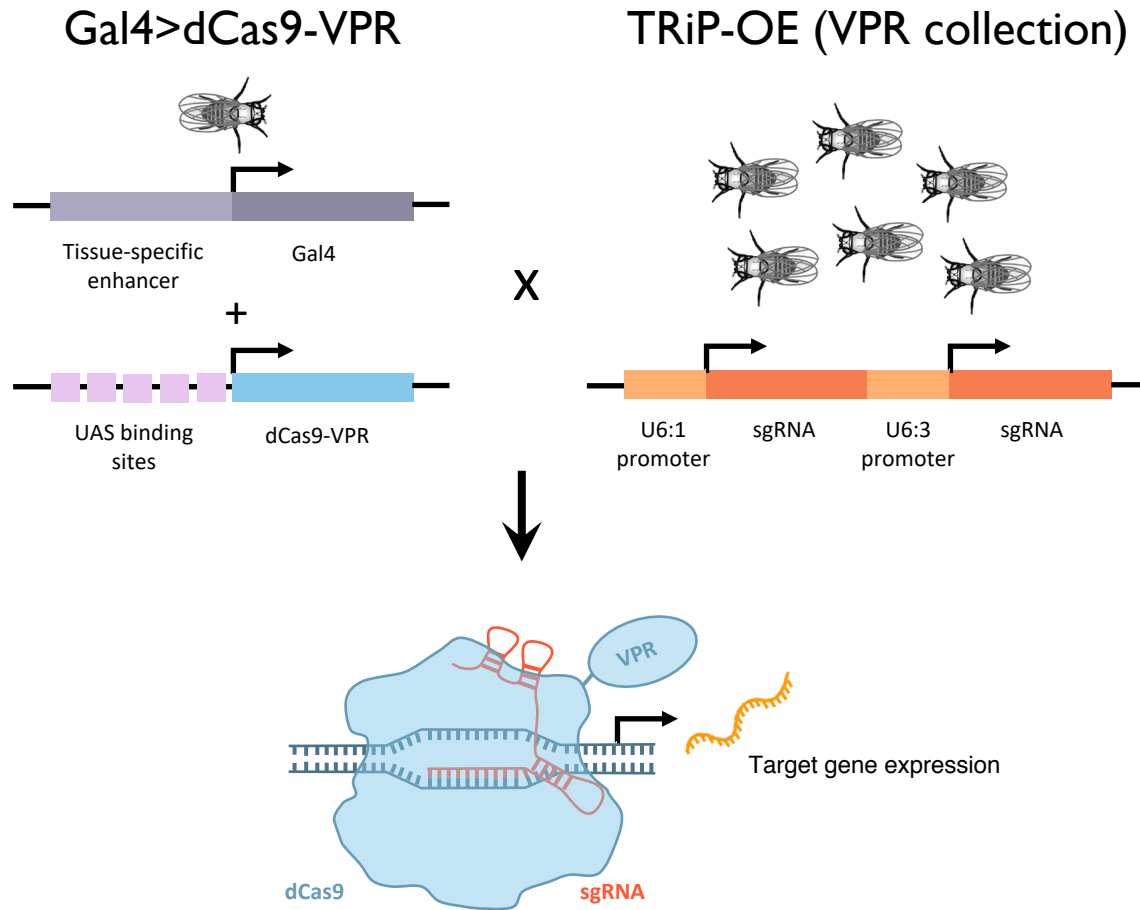


Point mutations D10A and H840A eliminate endonuclease activity (dCas9)

CRISPRa with VPR: fusion of dCas9 with VPR hybrid activation domain leads to up-regulation

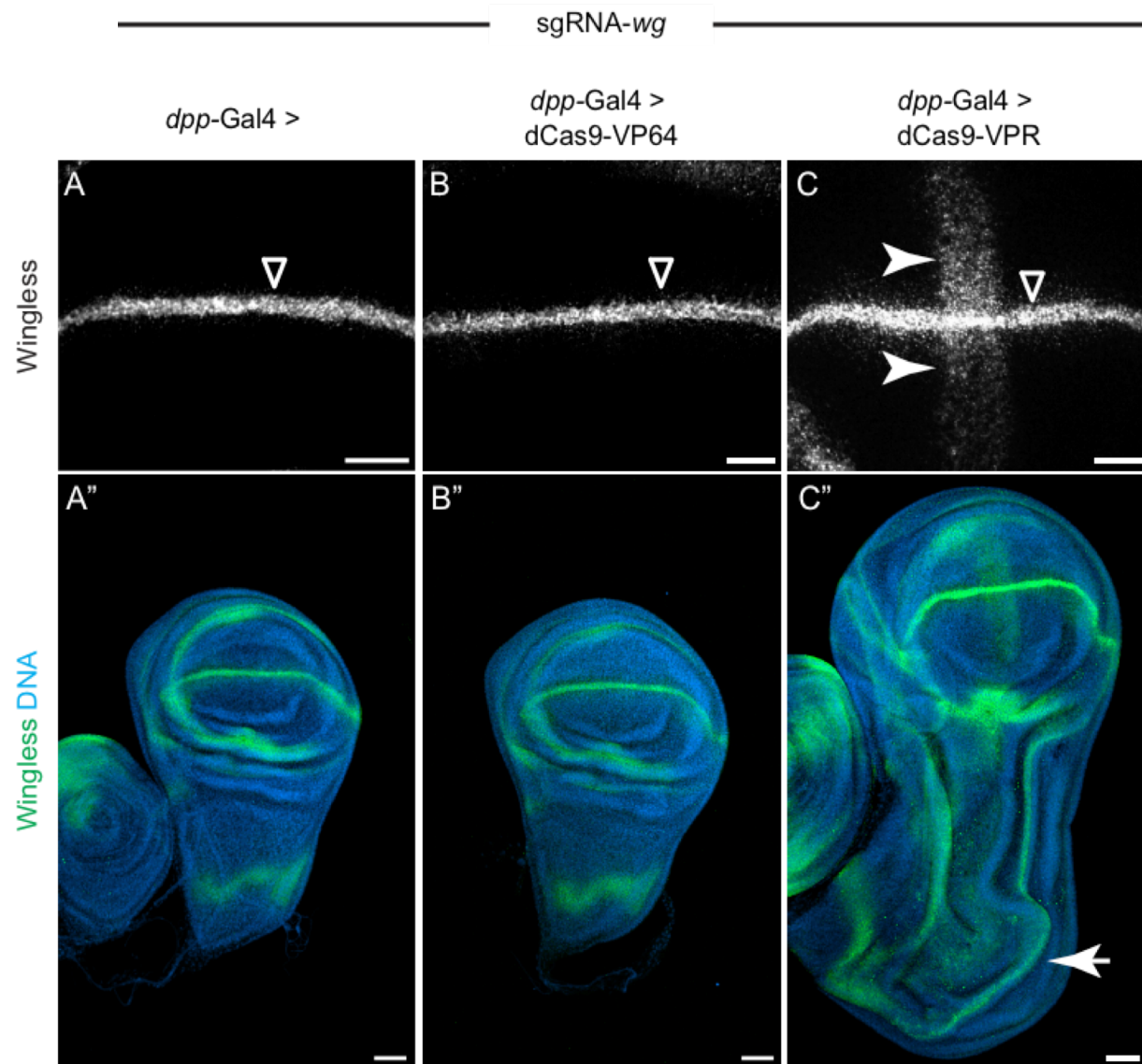
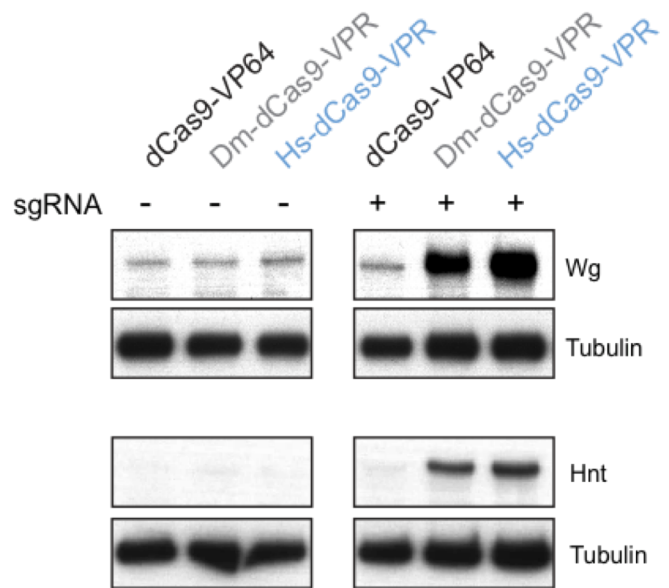
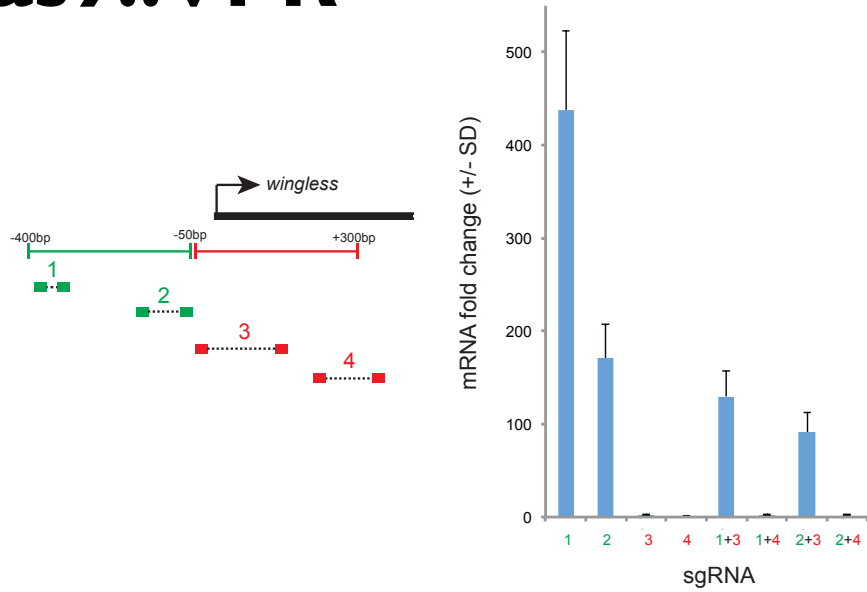
CRISPRa with FlySAM: fusion of dCas9 and modification of sgRNA backbone with MS2 loops + MS2 binding protein fused to additional activation domain

TRiP-Over-Expression (OE) stock collection—VPR

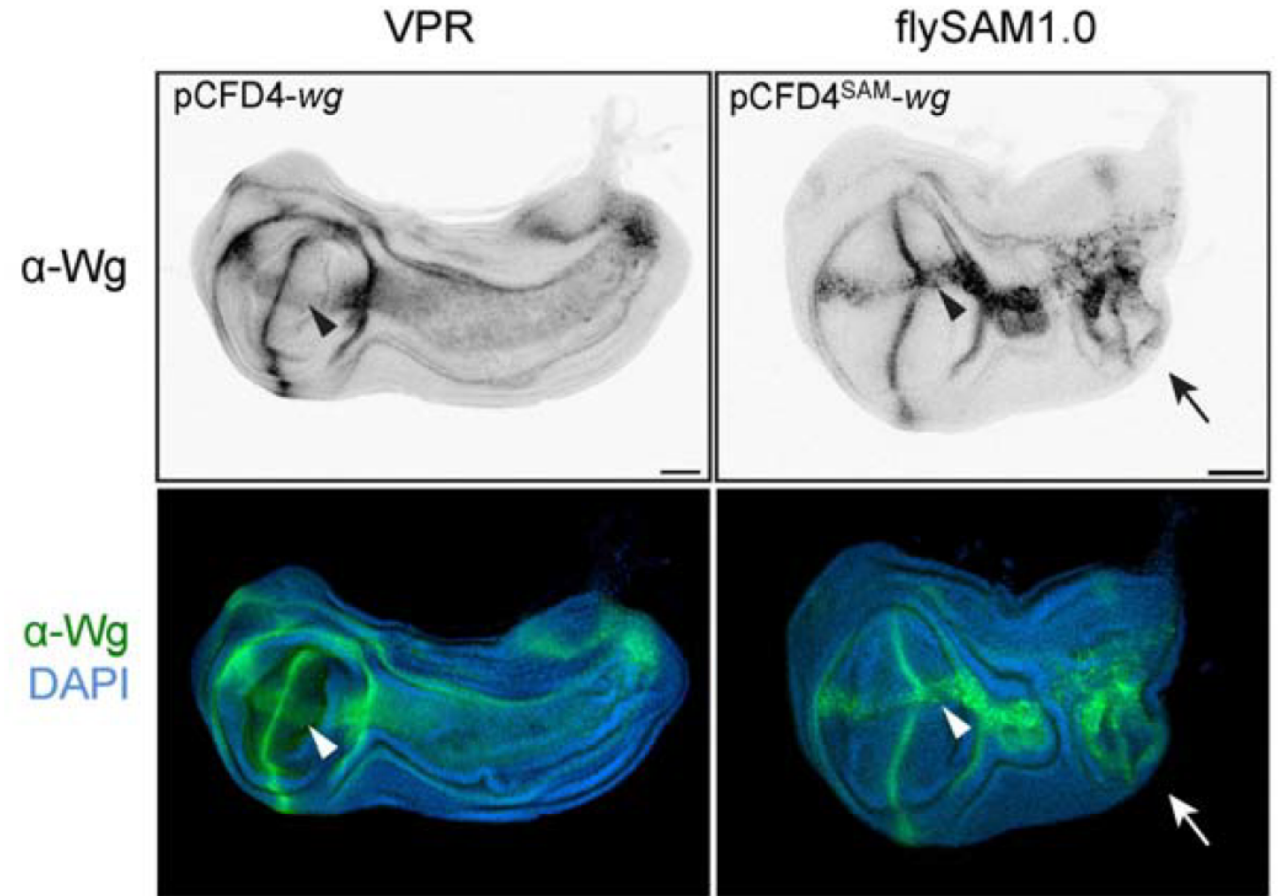
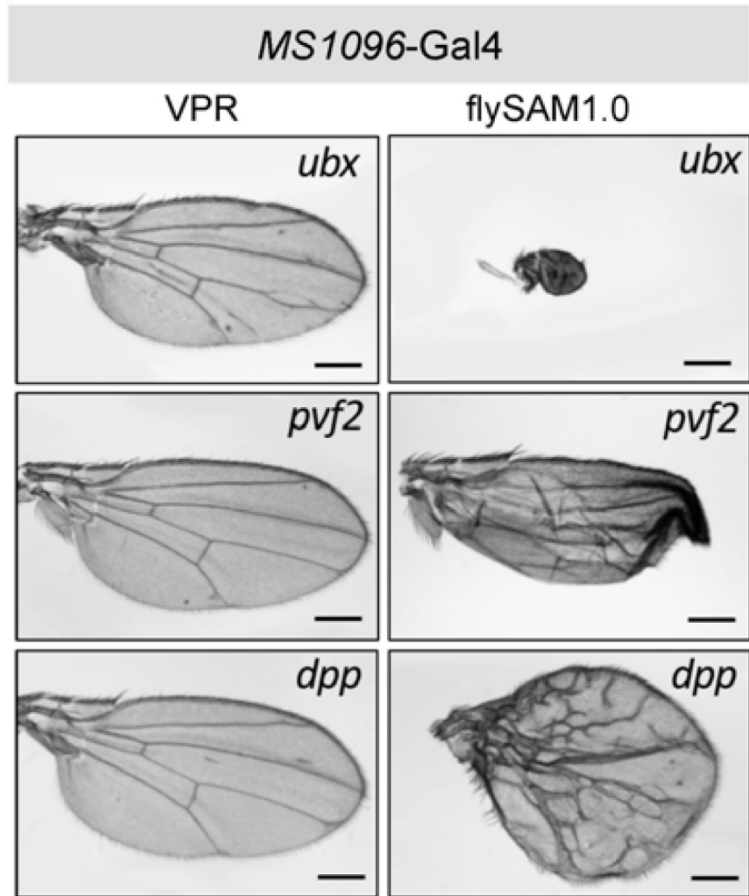


- A single gene is targeted by tandem expression of two sgRNAs from independent U6 promoters
- Stocks are made in the pCFD4 vector, developed by Phillip Port and colleagues
- Crossing TRiP-OE stocks to a Gal4 line expressing dCas9 fused to the chimeric activator domain VPR induces expression of the target gene
- Can also generate Indels and larger genomic deletions by crossing to Gal4>Cas9 flies
- Can only express wildtype proteins – no tags, no dominant negatives, etc..
- Can have off-targets if two genes are nearby.

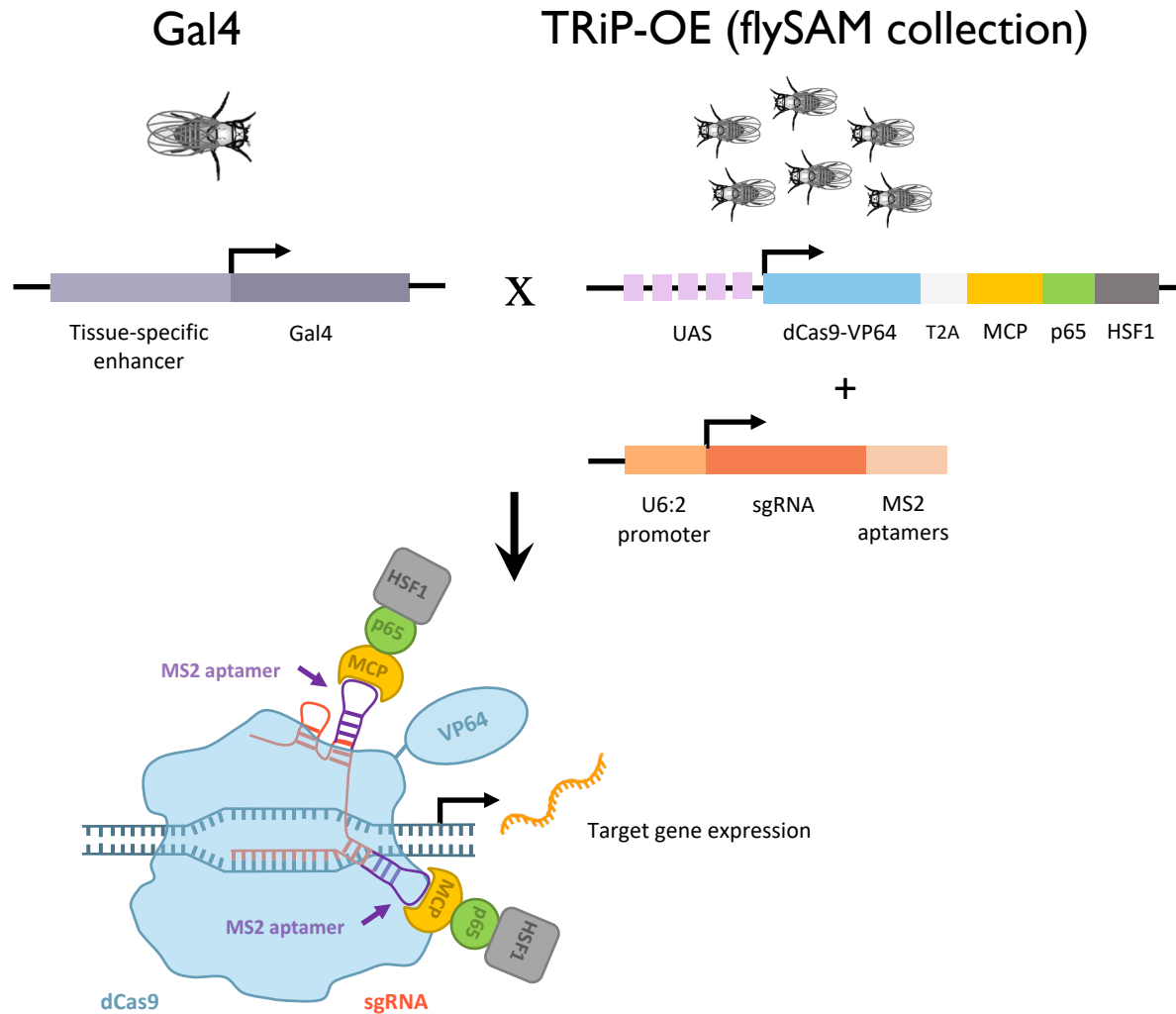
Cas9::VPR



VPR vs. FlySAM



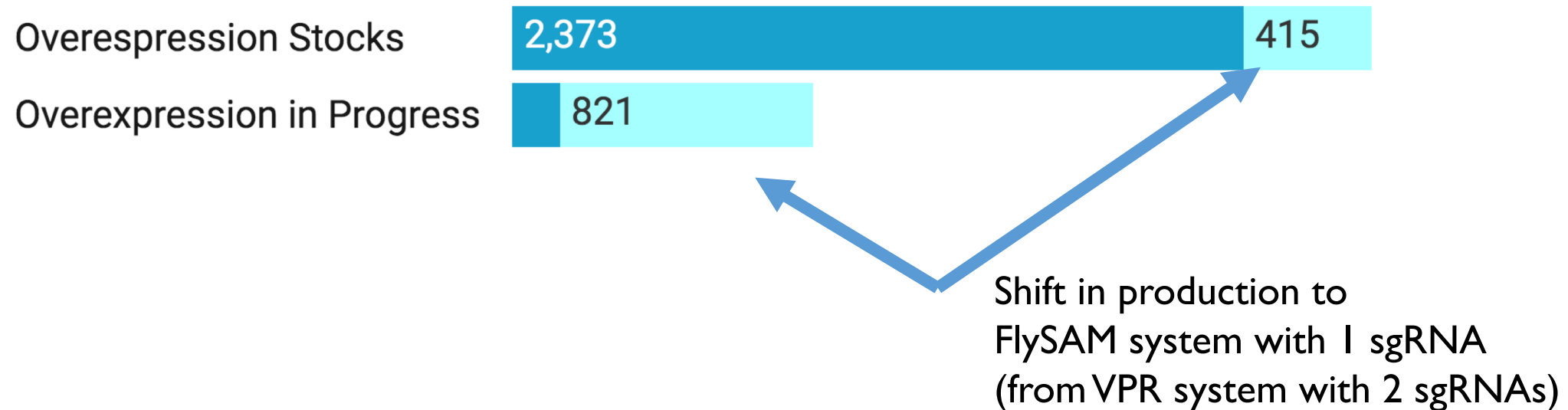
TRiP-Over-Expression (OE) stock collection—flySAM



- Simplified strategy for *in vivo* CRISPR activation
- Stronger overexpression phenotypes
- A single gene is targeted by expression of one sgRNA from U6:2 promoter
- Stocks are made in the flySAM2.0 vector, developed by [Jian-quan Ni and colleagues](#)
- TRiP-OE/flySAM stocks contain UAS-Cas9, so simply crossing to a Gal4 induces expression of the target gene

TRiP-CRISPR sgRNA Production

■ VPR ■ flySAM



<https://fgr.hms.harvard.edu/using-trip-crispr-lines>

<https://fgr.hms.harvard.edu/sgrna-vectors>

gRNA Fly Stock Database

Online portal for community nomination, production tracking, information

The screenshot shows the website's header with the text "gRNA FLY STOCK DATABASE". Below this is the main title "DRSC/TRiP gRNA Fly Stock Database" and a search instruction: "Search for **TRiP-CRISPR Overexpression (TRiP-OE)** and **TRiP-CRISPR Knockout (TRiP-KO)** fly stocks by gene or stock ID to obtain detailed information on sgRNA sequence, vector, and availability." The interface includes a search section with radio buttons for "Search stocks by:" (FBgn, gene symbol, or CG annotation; GP or GS number) and a text input field for "Enter Search Terms:". To the right, there are links for "Nominate genes for TRiP-OE or TRiP-KO production", "Download list of all finished stocks (Last updated: 2018-11-04)", and "Other links:" which includes "Vector maps and cloning protocols", "Quick link to CRISPR sgRNA design tool", and "Internal tracking site (login required)". A "NEWS" section on the right contains updates for April 2018 and December 2017. A large white box with a black border is overlaid on the bottom right of the screenshot, containing two bullet points.

gRNA FLY STOCK DATABASE

DRSC/TRiP gRNA Fly Stock Database

Search for **TRiP-CRISPR Overexpression (TRiP-OE)** and **TRiP-CRISPR Knockout (TRiP-KO)** fly stocks by gene or stock ID to obtain detailed information on sgRNA sequence, vector, and availability.

» Search stocks by:

- FBgn, gene symbol, or CG annotation
- GP or GS number

Enter Search Terms:

Search

» **Nominate genes** for TRiP-OE or TRiP-KO production

» **Download** list of all finished stocks (Last updated: 2018-11-04)

» Other links:

- **Vector maps and cloning protocols** to build your own constructs and flies for custom applications, time-sensitive studies, or isoform-specific targets
- Quick link to **CRISPR sgRNA design tool**
- **Internal tracking site** (login required)

— NEWS —

Apr 2018: issue with submitting new nominations has been resolved. Nominations can be submitted as normal.

Dec 2017: TRiP-OE stocks are now being made in the flySAM2.0 (VTPHG) vector instead of pCFD4. flySAM2.0 induces higher levels of gene overexpression and only requires a single gRNA design.

- Nominate your gene(s) of interest for CRISPR KO and/or CRISPR OE guide RNA fly stock production by the TRiP team
- Track progress and view completed fly stocks

https://www.flyrnai.org/tools/grna_tracker/web/

PART 2:

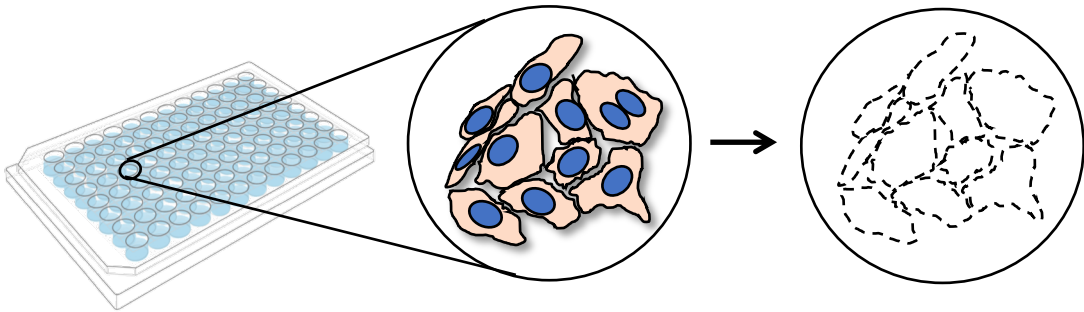
cell-based screens and cell lines

Drosophila RNAi Screening Center (DRSC) RNAi and CRISPR screening

And knock-in of GFP for live-cell visualization of organelles and compartments

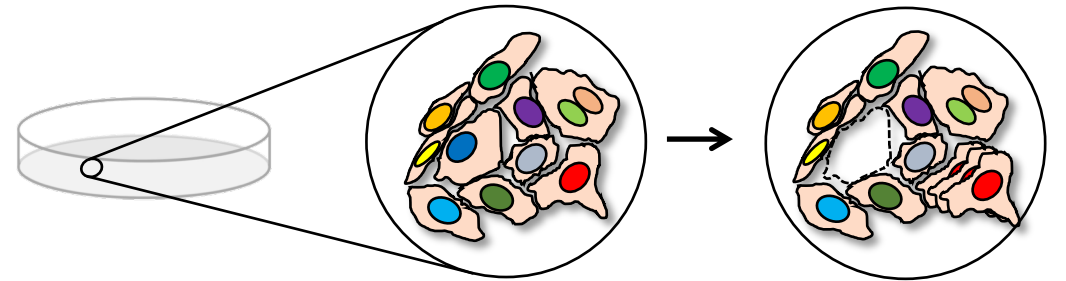
Arrayed Screens

- Micro-well plates
- Liquid handling automation
- Assay period of days
- Automated high-content assays
- Look up 'hits' in a database

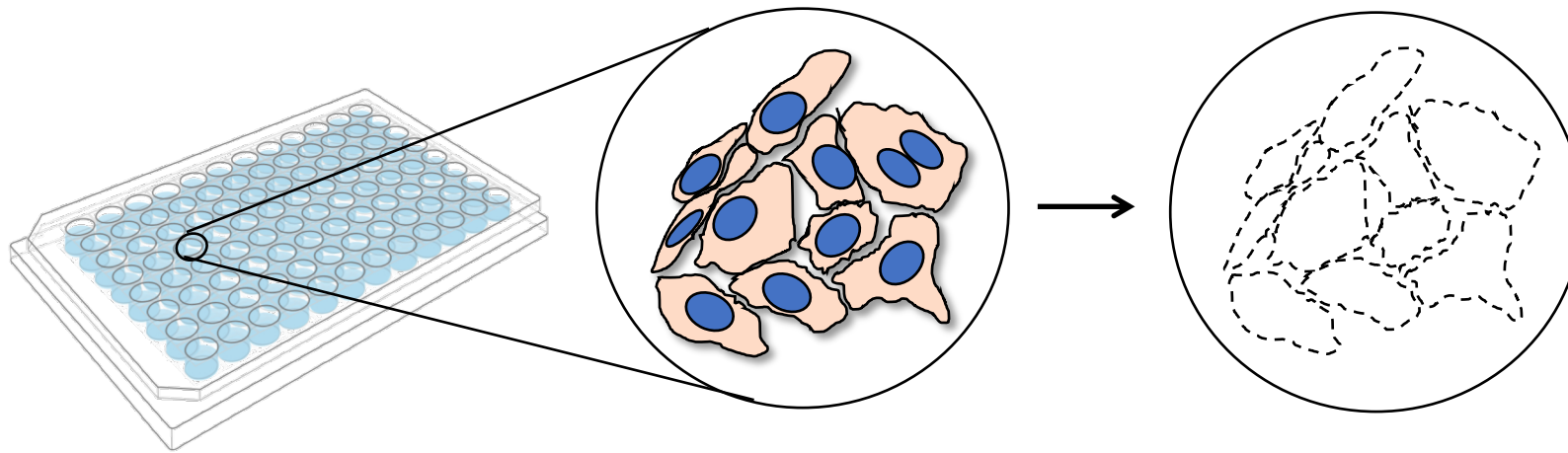


Pooled Screens

- In bulk culture
- No automation needed
- Assay period of weeks
- Drop-out or selection assays
- NGS readout to identify 'hits'



Since 2003:
Arrayed Format Screening
Double-stranded RNAs (dsRNAs)



DRSC dsRNA library production

- Automated, fully in vitro process (no bacterial transformation steps)
- T7 primer used to re-amplify PCR amplicons (2-3 designs/gene, all genes)
- PCR amplicons used as template for in vitro transcription
- dsRNAs are normalized and re-arrayed
- Concentrated dsRNAs are diluted to assay-ready concentration
- dsRNAs are aliquoted to 384-well plates for cell-based assays

Library info:

<https://fgr.hms.harvard.edu/fly-cell-rnai-libraries>

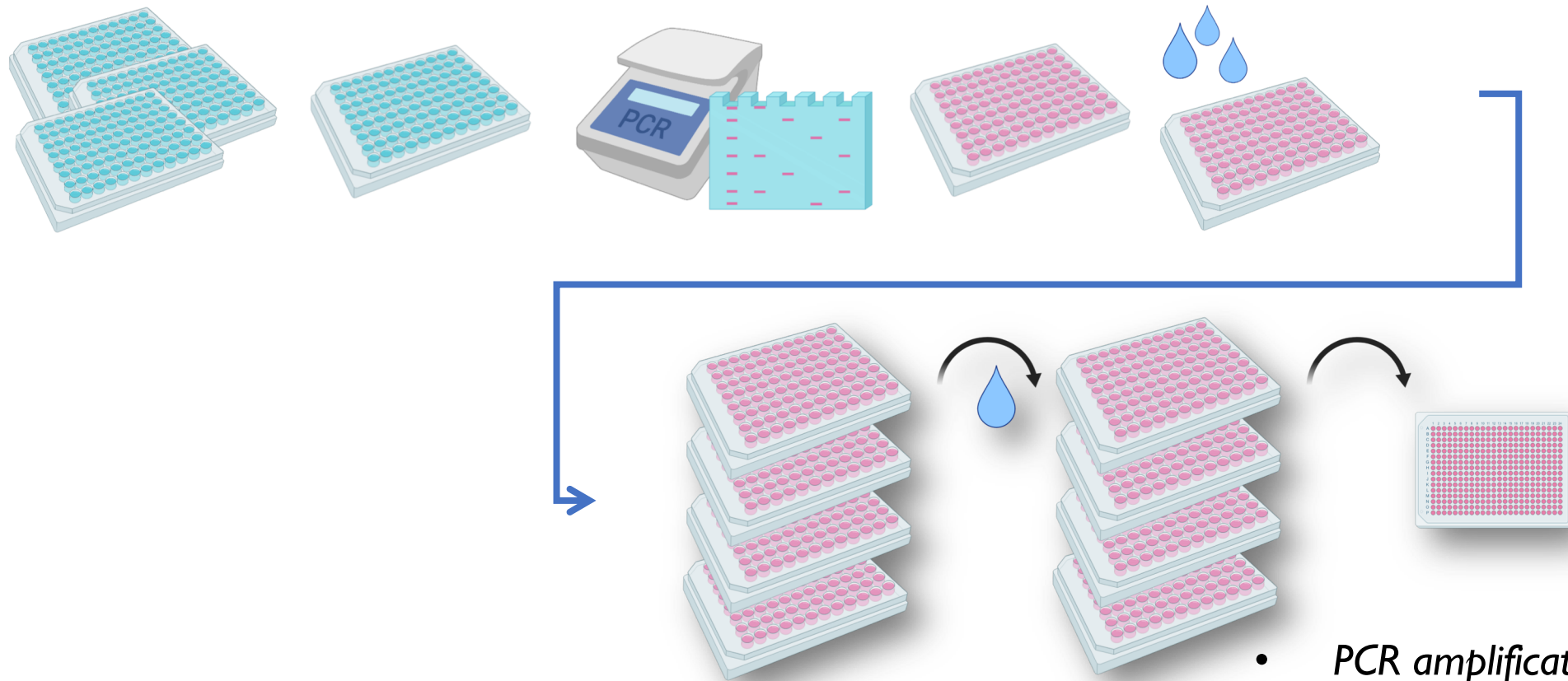
<https://fgr.hms.harvard.edu/drsc-20-genome-wide-screening-library>

<https://fgr.hms.harvard.edu/drsc-focused-sub-libraries>

Protocols:

<https://fgr.hms.harvard.edu/drsc-cell-rnai>

dsRNA production workflow



Library info:

<https://fgr.hms.harvard.edu/fly-cell-rnai-libraries>

<https://fgr.hms.harvard.edu/drsc-20-genome-wide-screening-library>

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Protocols:

<https://fgr.hms.harvard.edu/drsc-cell-rnai>

- *PCR amplification of templates*
- *In vitro transcription to make dsRNA*
- *Normalization of concentrations*
- *Dilution to 1x concentration*
- *Assay-ready 384-well plate production*
- *Quality control & analysis throughout*

Cell-based RNAi libraries and services

- **>200 RNAi screen projects since 2003**

- View public datasets:
 - <https://www.flyrnai.org/screensummary>

- **Full-genome dsRNA library**

- **Focused sub-libraries** (kinases, transcription factors, etc.)

- Recently developed: “FDA” library targeting fly orthologs of human genes that encode proteins that are known drug targets
- Recently updated: Ubiquitin-related library
- View library list and info:
 - <https://fgr.hms.harvard.edu/drsc-focused-sub-libraries>

- **Custom ‘cherry-pick’ of templates**

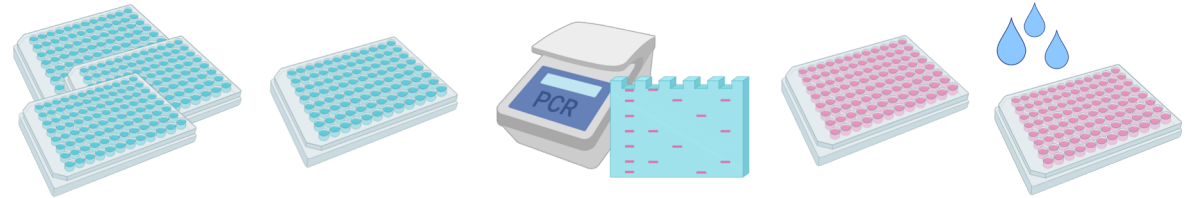
- one, a few, or many—for small-scale studies, establishing controls, etc.

- **Custom dsRNA synthesis based on our existing templates**

- billed by the 96-well plate—e.g. for a cell-based functional assay of candidates identified using another ‘omics approach, enough dsRNA for many assays

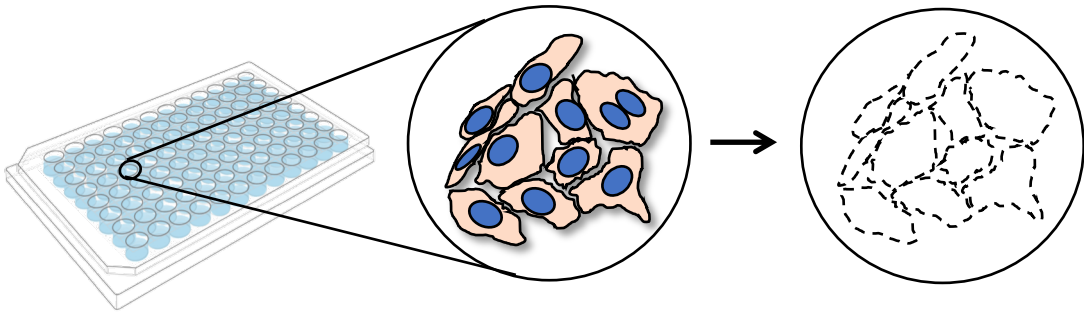
- **Screen on-site at DRSC, e.g. with GE IN Cell automated confocal microscope**

- **-or- Screen at a screening center local to your area (libraries shipped to you)**



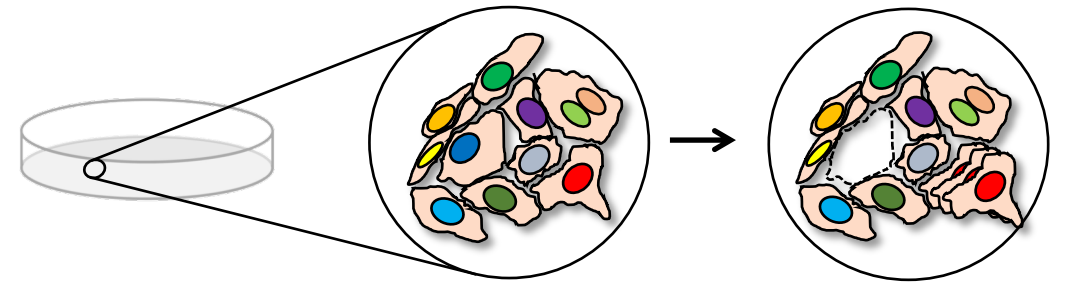
Arrayed Screens

- Micro-well plates
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- Automated high-content assays
- Look up 'hits' in a database



Pooled Screens

- In bulk culture
- No automation needed
- Assay period of weeks
- Drop-out or selection assays
- NGS readout to identify 'hits'



Pooled screens in *Drosophila* culture cells

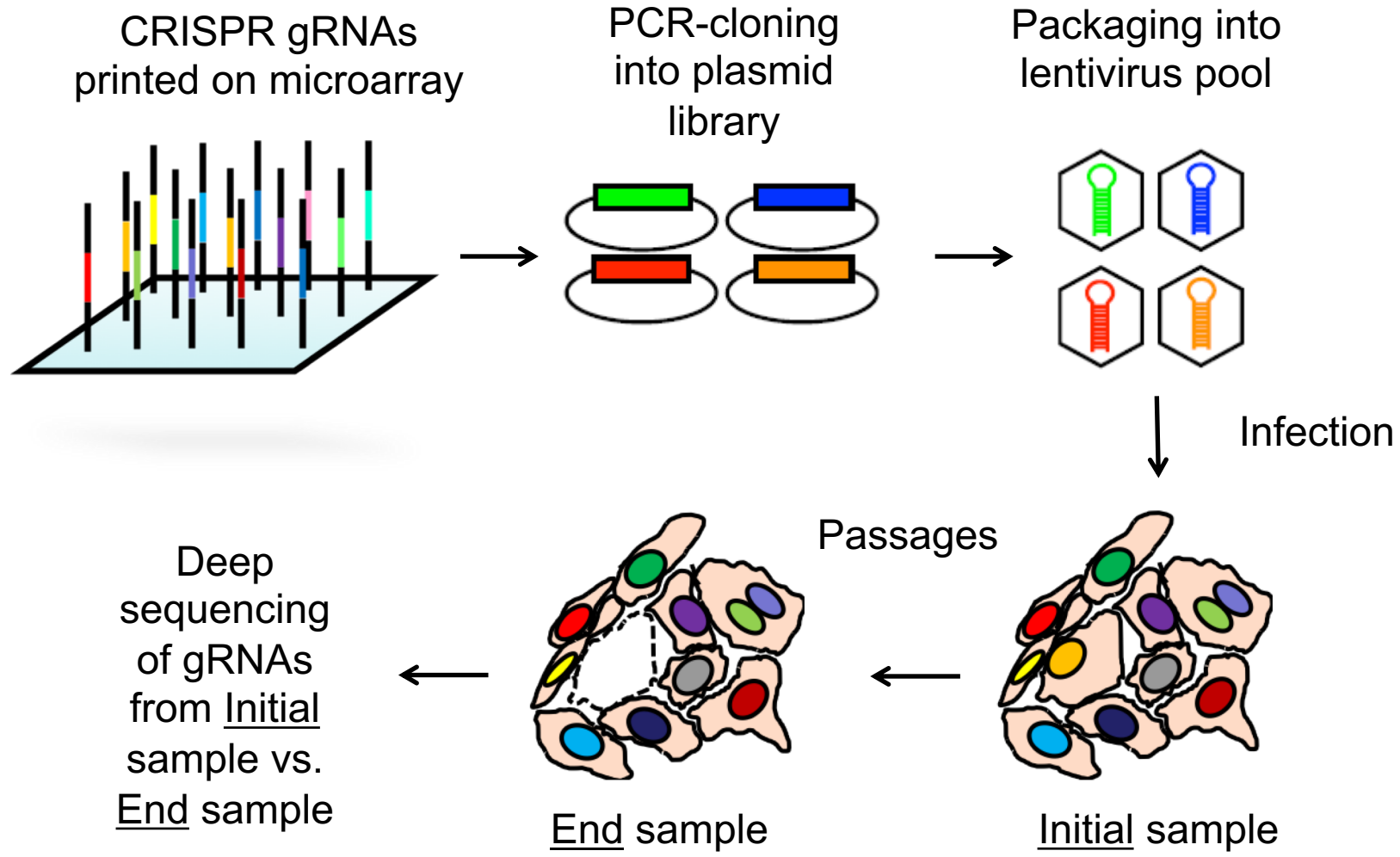
Why?

- Low gene redundancy vs. humans
- Relevance to humans, insect disease vectors, insect pests
- Different types of assays vs. arrayed-format RNAi assays

How?

- Reagent delivery method—transfection
- Reagent library design—DRSC bioinformatics
- Reagent library production—on-chip, 6 sgRNAs per gene
- Reagent integration into genome? Had been a barrier—no longer!

Mammalian genome-scale CRISPR knockout screen workflow



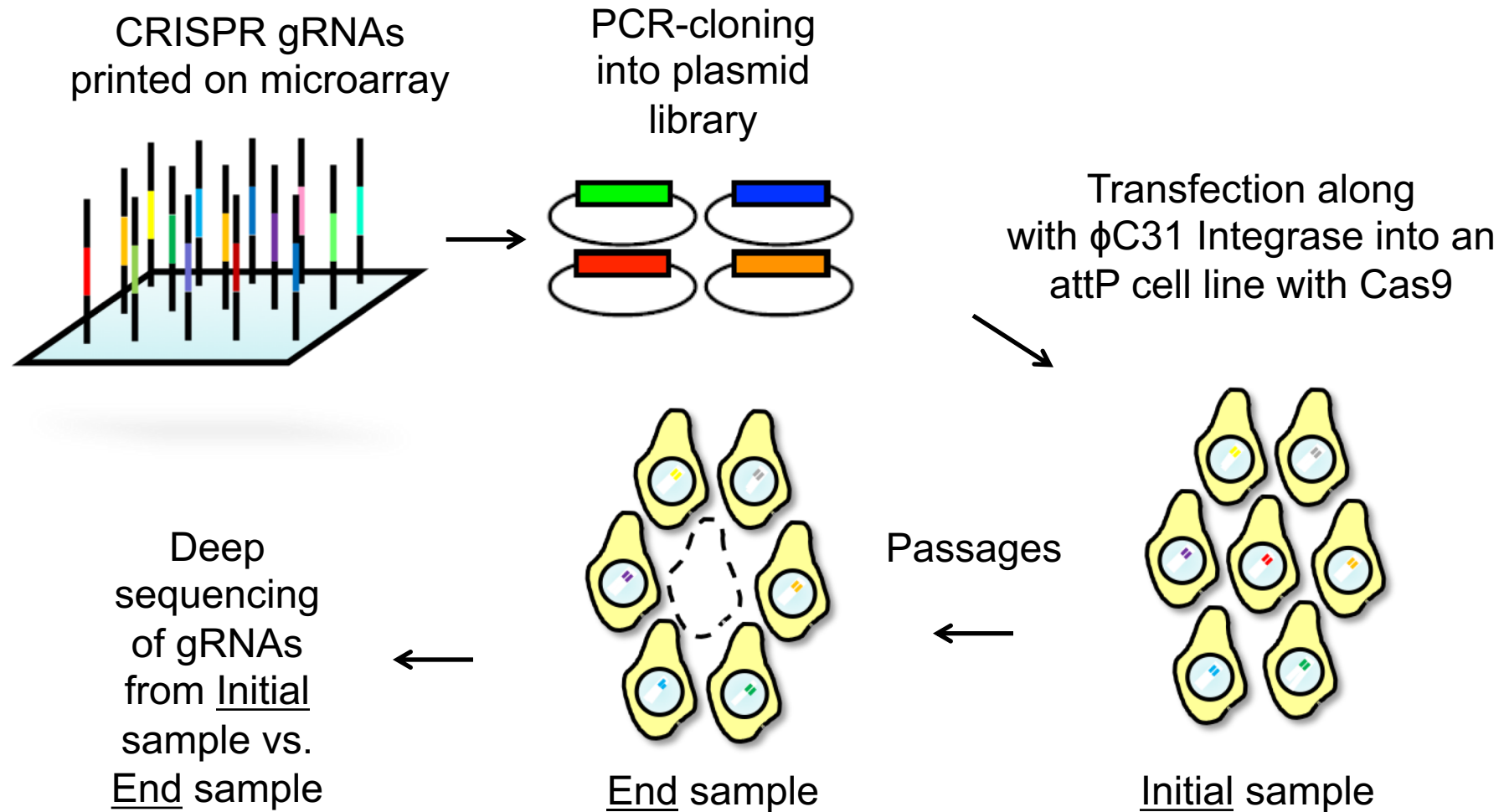
- **Lentiviral delivery results in integration into genome**
- **Amplification of integrated sgRNAs allows for identification of hits**

But:
lenti system doesn't work in fly cells—so,

How integrate sgRNAs into fly cells?

Answer: attP landing sites

Drosophila genome-scale CRISPR knockout screen workflow



CRISPR pooled-format screens in fly cells:

Relevant publications and data sets

Proof-of-principle screens:

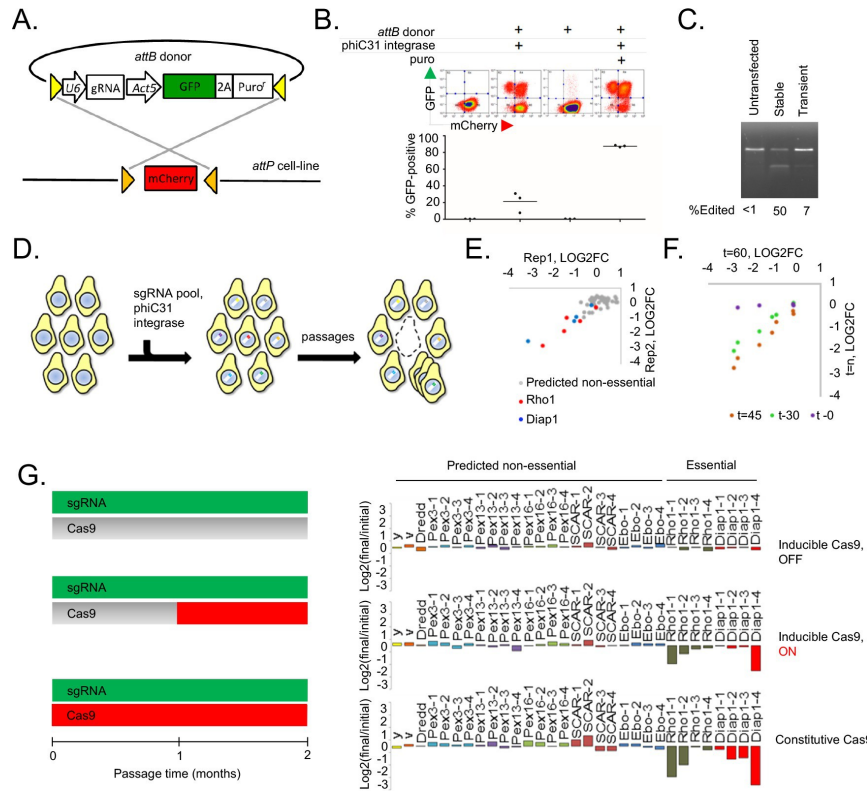
Viswanatha R, Li Z, Hu Y, Perrimon N. **Pooled genome-wide CRISPR screening for basal and context-specific fitness gene essentiality in Drosophila cells.** *Elife*. 2018 Jul 27;7. pii: e36333. PMID: [30051818](#)

Example use to identify new gene functions:

Okamoto N, Viswanatha R, Bittar R, Li Z, Haga-Yamanaka S, Perrimon N, Yamanaka N. **A Membrane Transporter Is Required for Steroid Hormone Uptake in Drosophila.** *Dev Cell*. 2018 Nov 5;47(3):294-305.e7. PMID: [30293839](#)

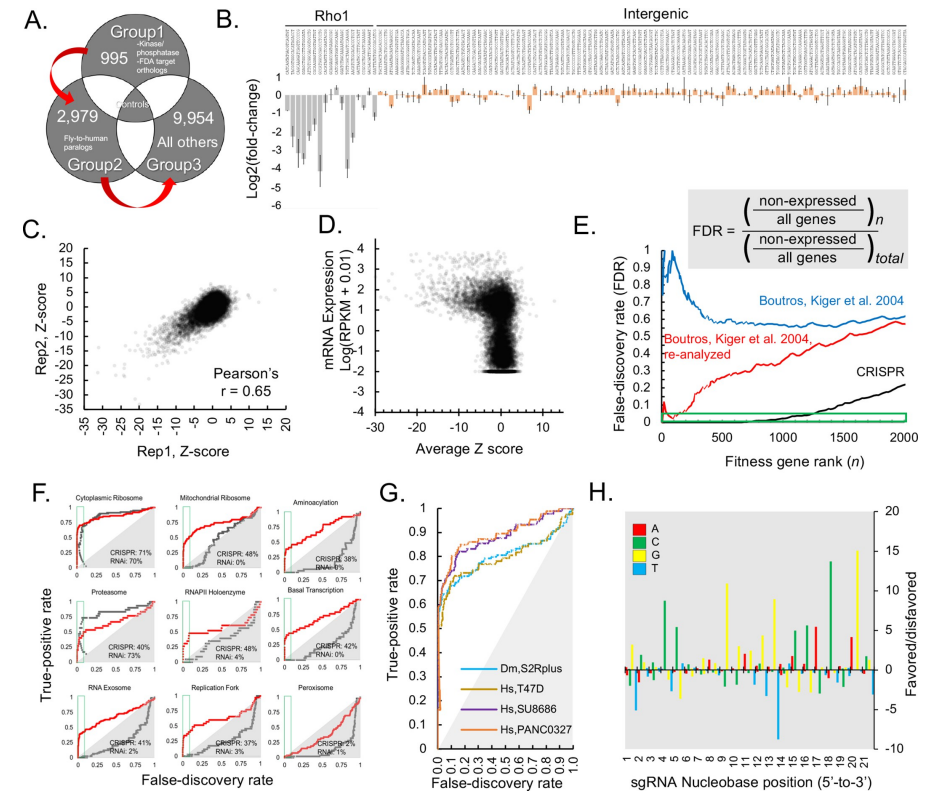
Note: [Raw data download](#) is available for Viswanatha et al. (2018)

CRISPR pooled-format screens in fly cells: proof-of-concept screens



Optimization

- Delivery
- Timing



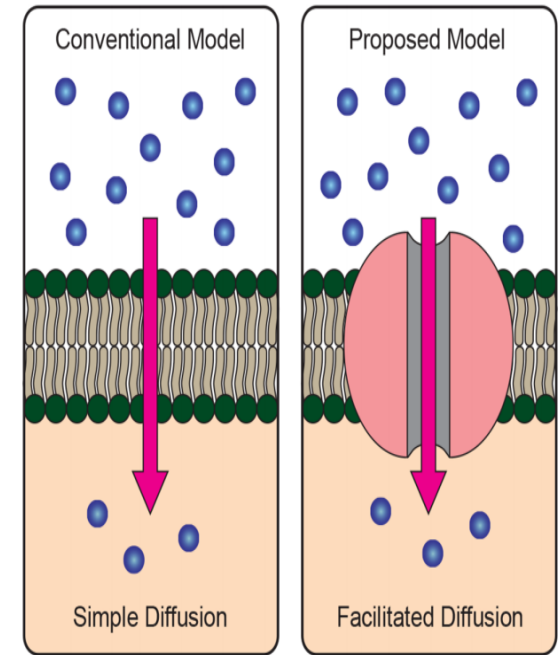
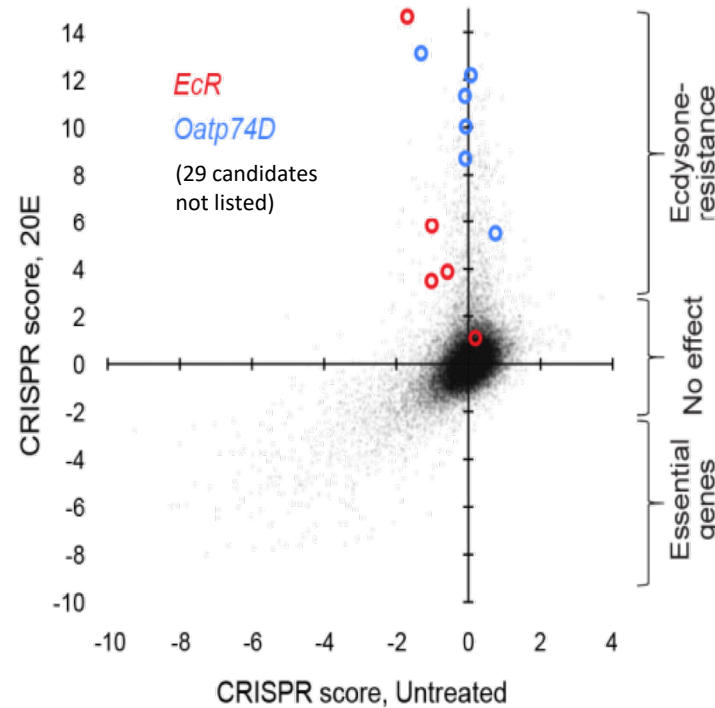
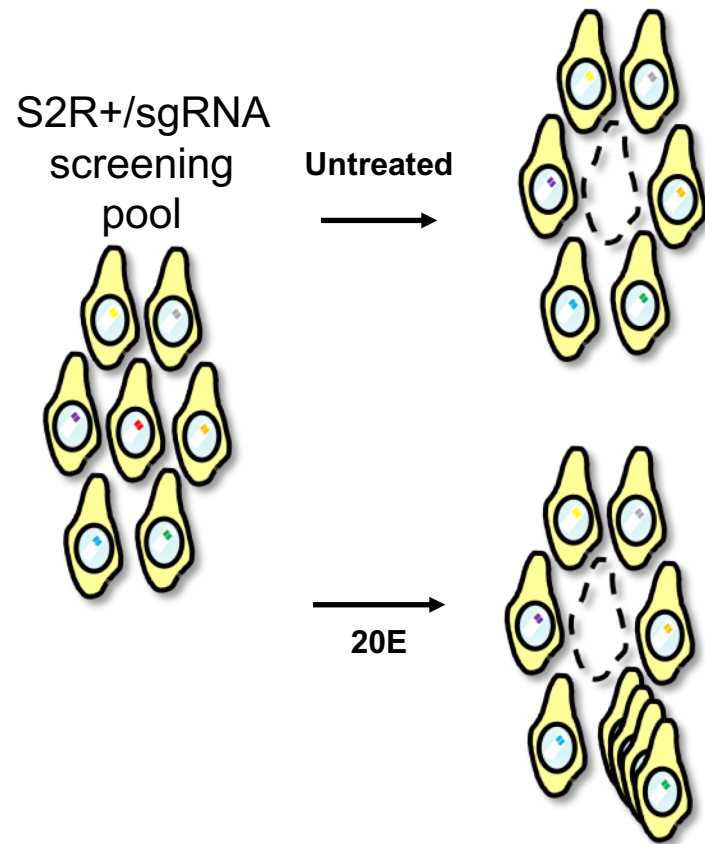
Application

- Large-scale library
- Identify essential genes

CRISPR pooled-format screen—example selection assay

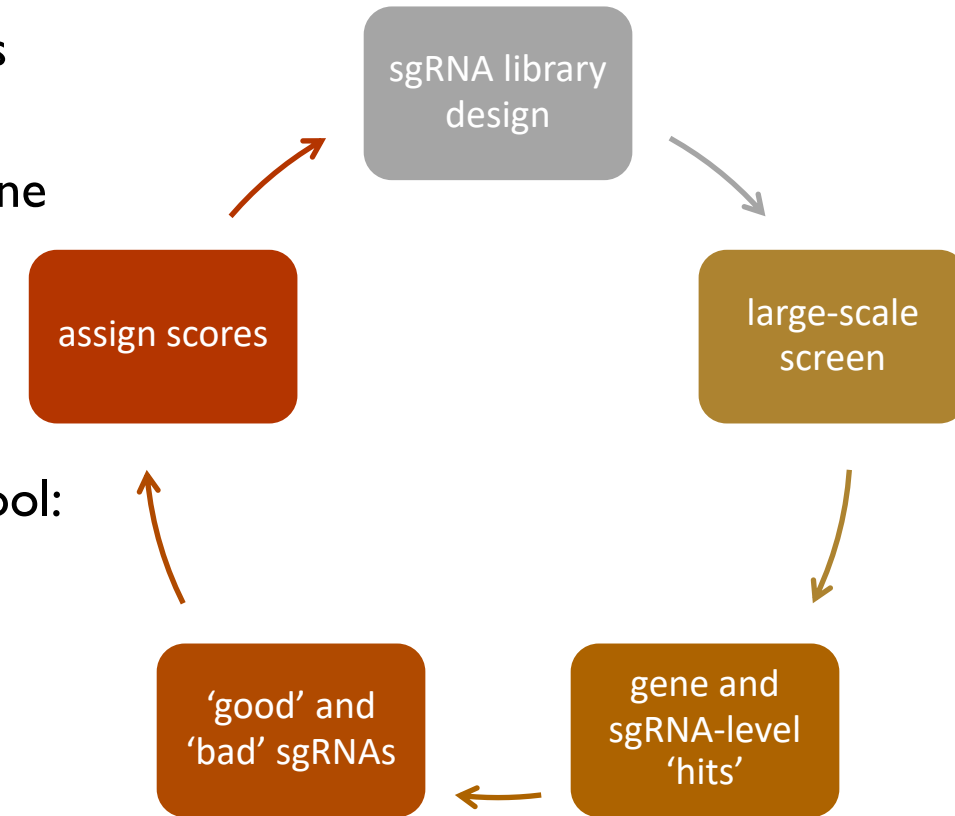
Screen assay approach: Identify resistance to proliferative block caused by 20E treatment

Results led to revised model for entry of ecdysone into cells



Machine Learning approach to sgRNA design

- Genome-wide library in the Viswanatha et al. pooled CRISPR studies includes ~6 sgRNAs per gene
- Data sets generated in the study provides opportunity to use machine learning to identify new rules, assign scores
- Define hits at gene level, then identify 'good' and 'bad' designs
- ML approach applied using 'good' and 'bad' as training set
- ML-based scores to be added to our Find CRISPRs sgRNA design tool:
 - <https://www.flyrnai.org/crispr/>
- Follow-up on ML results currently in progress
 - *Testing if ML-assigned scores are predictive of performance*
 - *Expanding the screen library to ~8 sgRNAs per gene coverage*



Virtuous cycle of ML-informed design, experimental testing, and new library development

CRISPR pooled-format screens

How might they be useful to your studies?

Example assays

- Drop-out screen for essential genes (e.g. in new cell lines)
- Drop-out screens in a knockout cell vs. parental cell to identify synthetic lethal genes
 - To uncover genetic networks (e.g. for poorly understood genes)
 - To find potential new drug targets (e.g. starting with tumor suppressor KO cells)
- Select for drug or other cytotoxin resistance
 - To identify transporters or entry factors
 - To study relevant biological process(es)
- Select by transwell migration assay or other physical separation
- Select by flow cytometry (e.g. loss or gain of a fluorescence marker)

Additional applications of the approach

- In other *Drosophila* cell lines (add attP, add Cas9)
- With other Cas9 derivatives/types (e.g. CRISPR activation—pilot screen in progress)
- In other insect cell lines (add attP, add Cas9, design library)
 - e.g. mosquito vectors of disease—assay development in progress

... also in cell lines ...

New GFP-tagged cell line resource for:

- Small-scale live or fixed-cell studies
- High-throughput screens, e.g. arrayed-format image-based screens
- Proteomics, e.g. using reagents directed against GFP

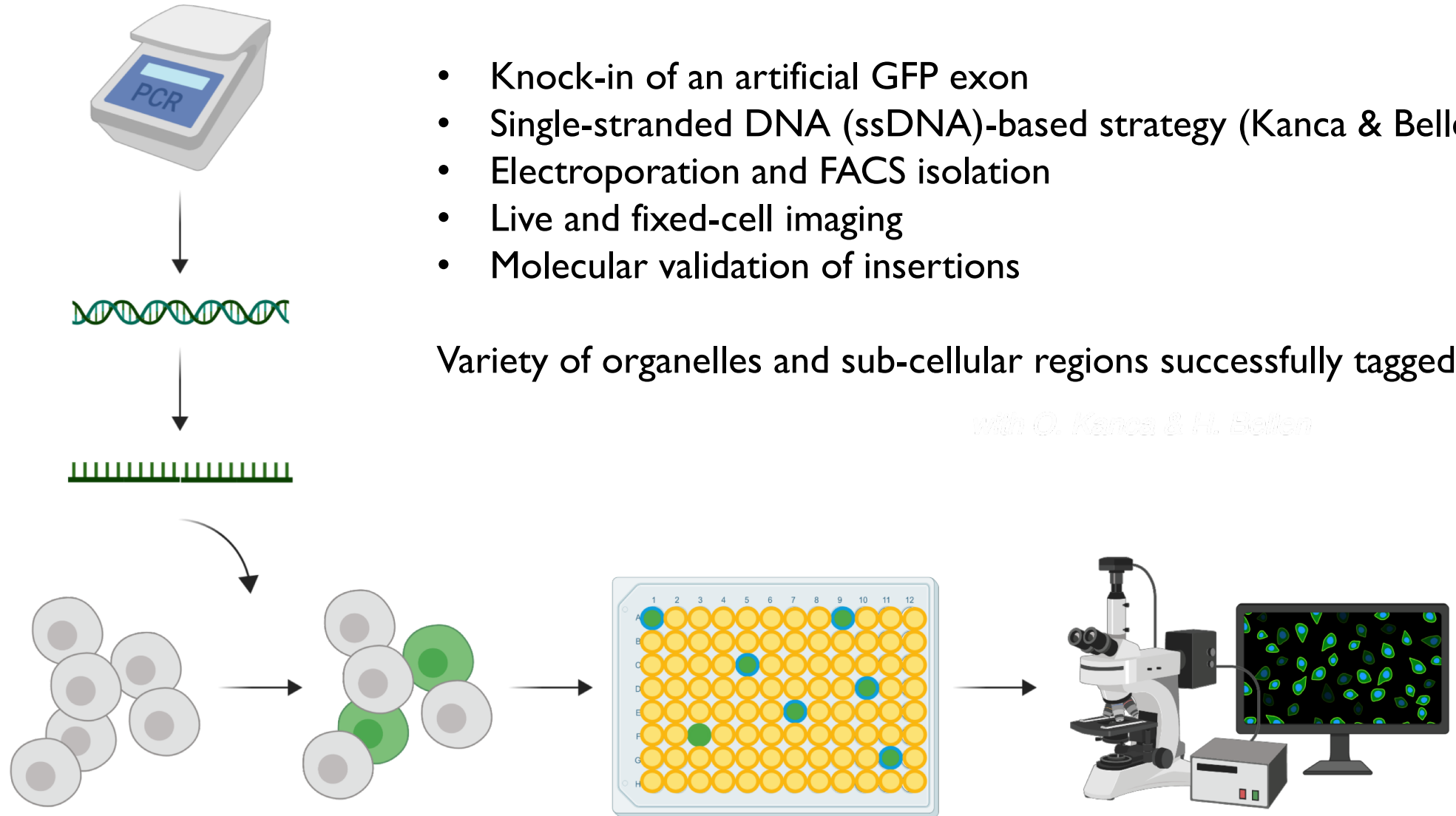
New Resource of GFP-tagged cell lines

- GFP tagging of organelles and sub-cellular compartments
 - Targets based on yeast, mammalian literature
 - ~two dozen candidate proteins identified to ‘paint’ various cell regions
- Overall workflow improved by switching from plasmid-based donors with long homology arms to single-stranded DNA donors with shorter homology arms (collaboration with Kanca & Bellen)
- GFP-tagged cell line workflow:
 - Parental cell lines is a DRSC S2R+ cell line (mCherry+ Cas9+) ([available at DGRC](#))
 - Electroporated, FACS single-cell isolated, then validated by live imaging, fixed imaging (Ab co-stain), molecular characterization of insertion site
 - Validated cell lines being deposited at DGRC (Bloomington) for distribution, see “S2R+” section on cell lines catalog

Summary info & links to distribution:

<https://fgr.hms.harvard.edu/crispr-modified-cell-lines>

GFP-tagged cell line resource—workflow summary




- Knock-in of an artificial GFP exon
- Single-stranded DNA (ssDNA)-based strategy (Kanca & Bellen)
- Electroporation and FACS isolation
- Live and fixed-cell imaging
- Molecular validation of insertions

Variety of organelles and sub-cellular regions successfully tagged

with O. Kanca & H. Bellen

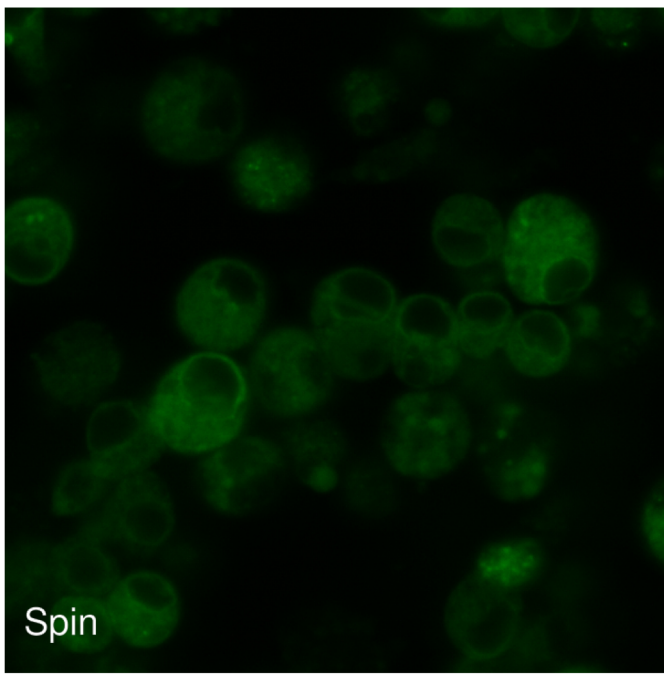
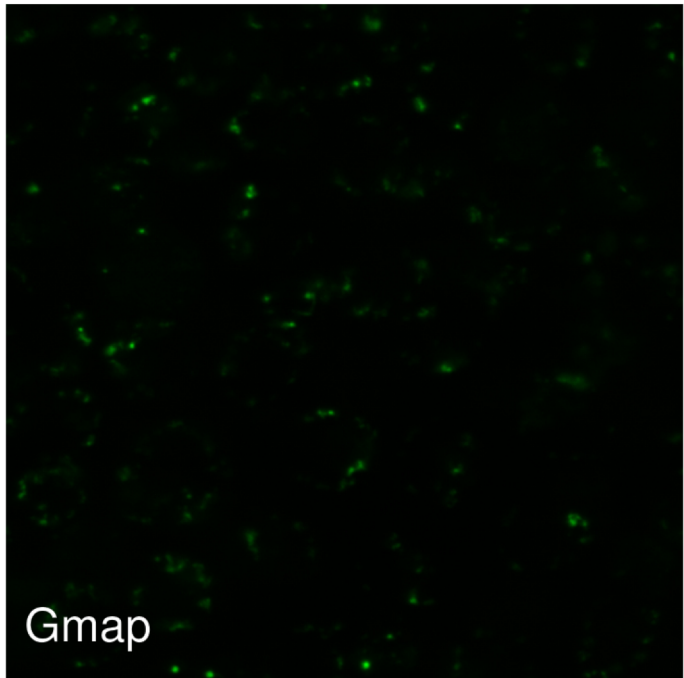
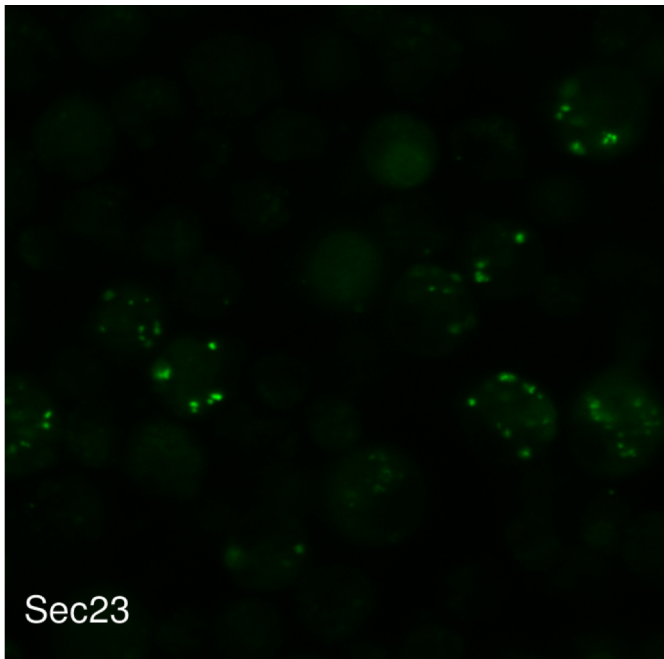
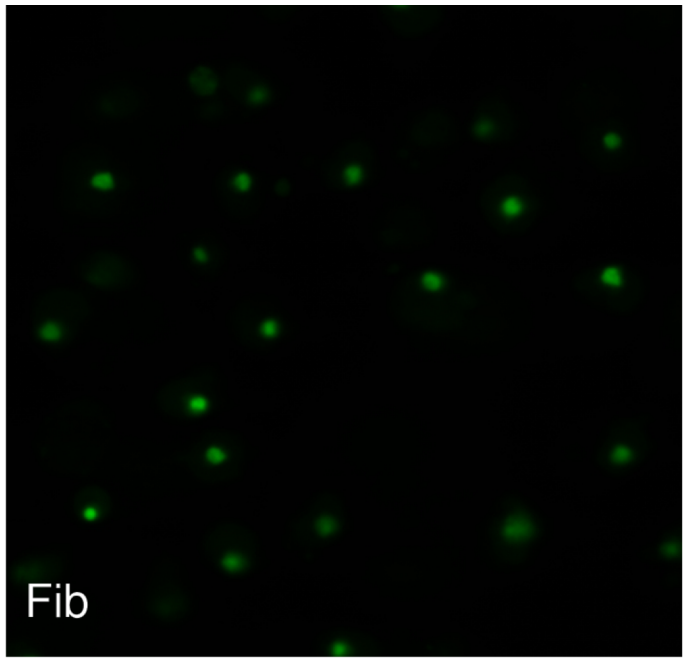
GFP-tagged cell lines—summary

Links to DGRC's cell line catalog (more tagged cell lines are on the way from DRSC to DGRC)



Organelle	GFP Fusion With	clones obtained	population imaged	clones imaged	insertion sequence verified	Immuno-staining	Correct GFP localization	DGRC product ID
Endoplasmic reticulum (ER)	Calnexin99A	16			Y	a-Cnx99a	Y	273
Endoplasmic reticulum (ER), transitional	Sec23	30			Y	--	?	sent
Endosomes, recycling	Rab11	23			Y	--	?	274
Golgi (cis-Golgi)	Gmap	10			Y	a-GMAP	Y	276 , 277
Golgi (trans-Golgi)	Golgin245	1			Y	a-Golgin245	Y	280
Kinetochores	Polo	2			Y	a-aTub	Y	275
Lysosomes	spin	2			Y	--	?	sent
Lysosomes	Arl8	9			Y	a-Arl8	Y	sent
Nuclear membrane, inner	Lamin	53			Y	a-Lamin	Y	sent
Nucleolus	Fibrillarin	14			Y	a-Fib	Y	278 & 279

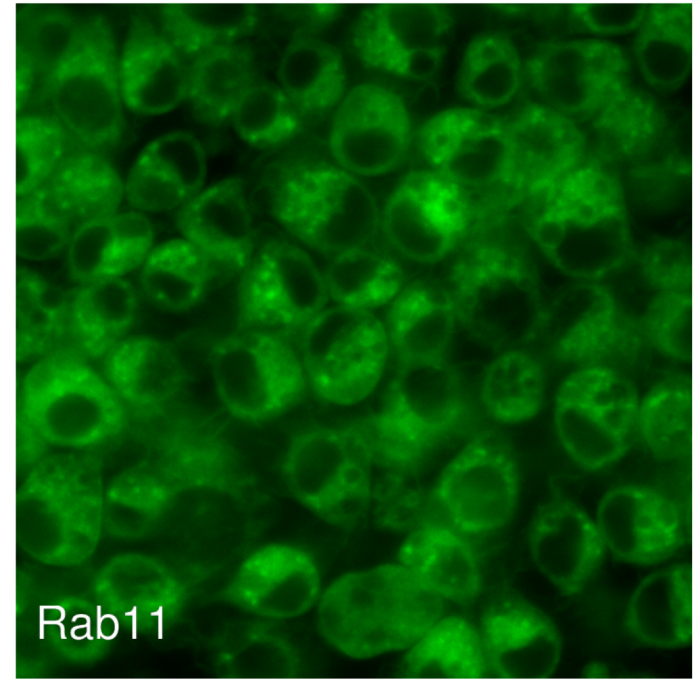
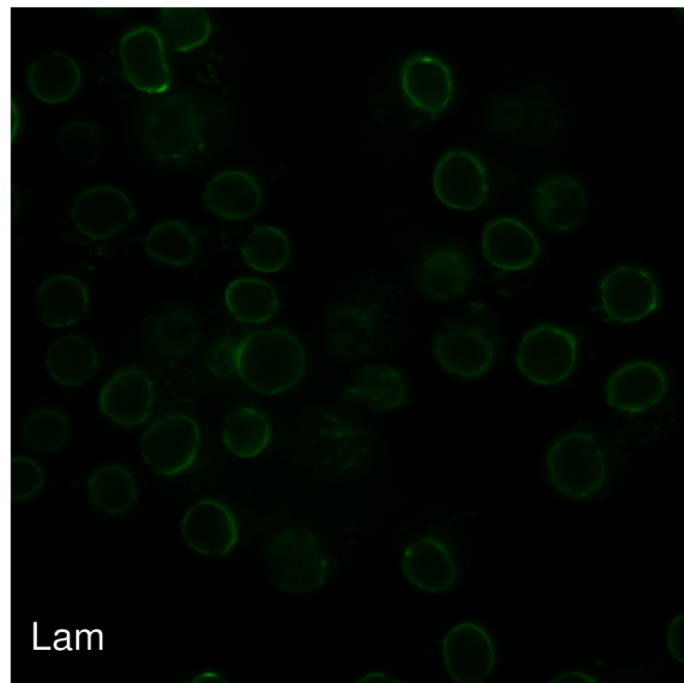
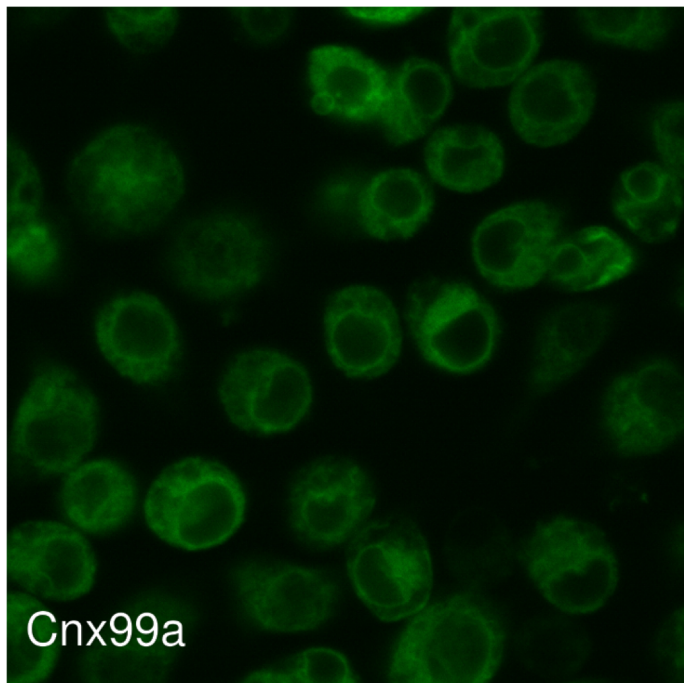
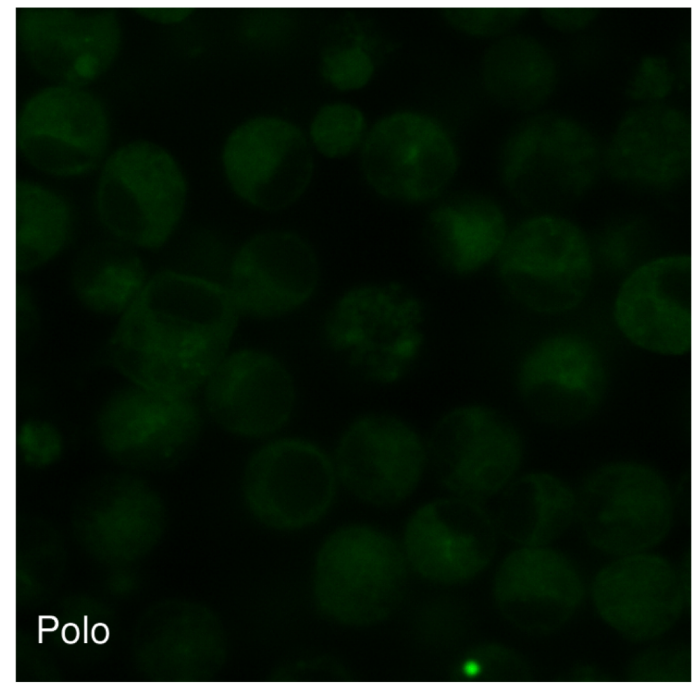
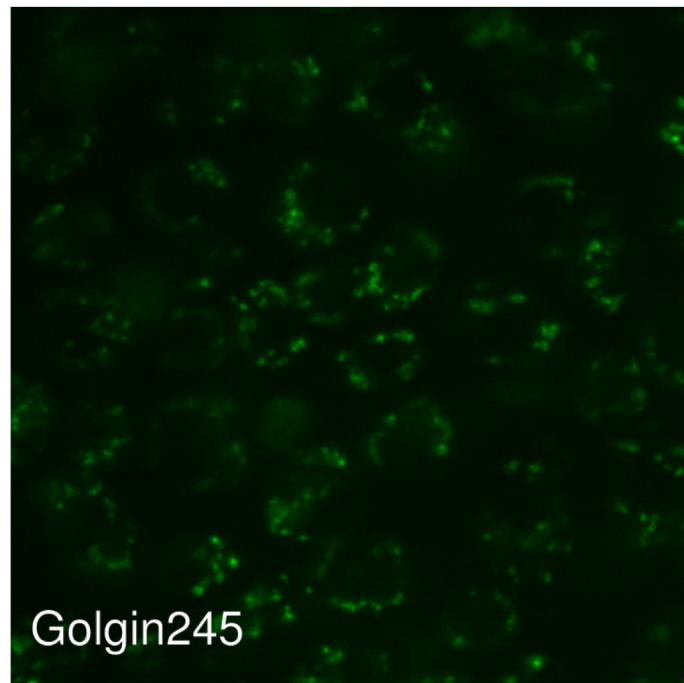
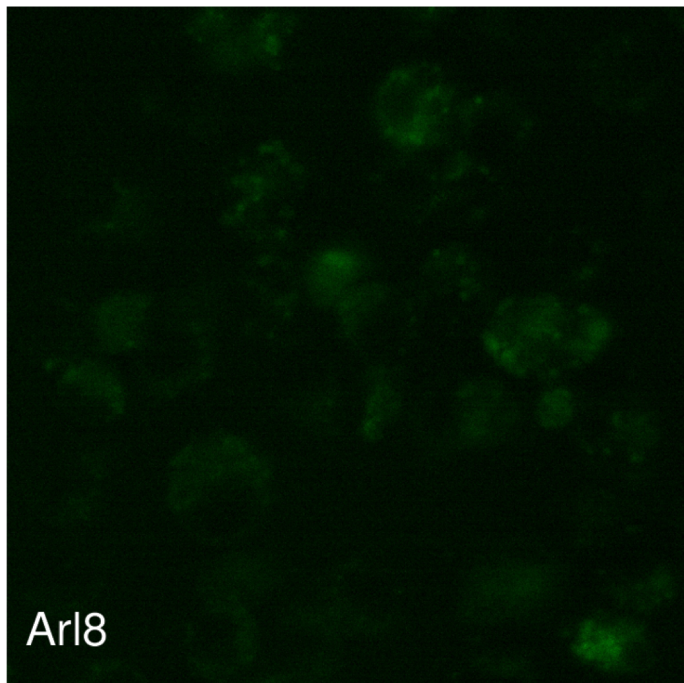
<https://fgr.hms.harvard.edu/crispr-modified-cell-lines>



This slide and next—live
imaging of GFP-tagged
cell lines

To view a time-lapse movie
of Polo::GFP

[CLICK HERE](#)



PART 3:

bioinformatics resources

New online tool overview page—view our suite of online resources

Brief introduction to newest online resources iProteinDB and BioLitMine

HARVARD MEDICAL SCHOOL

DRSC/TRiP Functional Genom Resources

Home Technologies **Online Tools** Protocols

DRSC/TRIP sgRNA Fly Stock Database

Search for [TRIP-CRISPR Overexpression \(TRIP-OE\)](#) and [TRIP-CRISPR Knockout \(TRIP-KO\)](#) fly stocks by gene or stock ID to obtain detailed information on sgRNA sequence, vector, and availability.

Search stocks by:

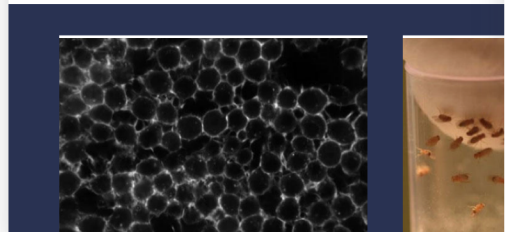
- Gene Identifiers (CG, FBgn, gene symbol)
- Gene IDs
- Gene Symbols
- Gene Names
- Gene Aliases
- Gene IDs (FlyBase)
- Gene Symbols (FlyBase)
- Gene Names (FlyBase)
- Gene Aliases (FlyBase)

nominate for in vivo CRISPR flies

nominate & track CRISPR-KO and -OE sgRNA fly stocks

Search

Navigation: < > < >



Multi-Species				
 DIOPT DRSC integrated ortholog search tool	 Gene2Function	 BioLitMine	 MARRVEL	 DIOPT-DIST
DIOPT ortholog search 10 species, 18 algorithms [Demo Video]	Gene2Function orthologs & gene info summaries (orthologs, GO, publications, & more)	BioLitMine literature mining tool (genes, pathways, people, MeSH terms)	MIST protein-protein & genetic interactions (multi-source) [Demo Video]	MARRVEL Connect human gene variants to ortholog info (multi-source)
DIOPT-DIST Connect disease genes to ortholog info or vice versa (OMIM & GWAS)				
Fly CRISPR		Fly PTMs		
 fly sgRNA database/LIMS	 Find CRISPRs	 CRIMIC CRISPR MIMIC Gene Trap	 RSVP Plus	 iProteinDB
TRIP sgRNA LIMS nominate or track TRIP-KO & -OE fly stock production	Find CRISPRs fly sgRNA design with genome view	CRIMIC nominate for GDP gene trap fly stocks	RSVP Plus in vivo CRISPR & RNAi phenotype data	iProteinDB fly post-translational modifications (multi-source)
Fly RNAi				
 UP-TORR	 SnapDragon	 RSVP Plus	 Screen Summary	 GeneLookup
UP-TORR cell and in vivo RNAi reagent search	SnapDragon design dsRNAs for fly cell RNAi	RSVP Plus in vivo CRISPR & RNAi phenotype data	Screen Summary browse DRSC cell RNAi screen data sets	GeneLookup (search DRSC & TRIP reagents by gene)
More fly resources			Fly Protocols	
 DGET	 GLAD	 FlyPrimerBank	 Fly Protocols	
DGET mine bulk RNAseq data for fly	GLAD view grouped gene lists for fly	FlyPrimerBank find qPCR primers for fly studies	More fly resource and utility tools Cell Line Expression HRMA online tool List of Utility Tools	
Network & Complex			Contact Us	
COMPLEAT protein complex enrichment analysis (fly, human, yeast) [Demo Video]	SignedPPI fly PPIs with activate/inhibit relationships [Demo Video]	fly PPI fly PPIs	Contact Us	
Data Sets				
List of Data Sets (DRSC & Perrimon) with links	Single-cell RNAseq for fly gut data set Hung et al.	Inst RNAi Vir		
Pooled CRISPR fly cell screen raw data sets Viswanatha et al.	Nucleolar fly cell RNAi image-based screen data set Neumuller et al.	DRS RNAi sc Mohr et al.	Summary	

Tip: Scroll down on the overview grid page to view relevant publications

Shown to the left:
[New online grid view of DRSC online resources](#)

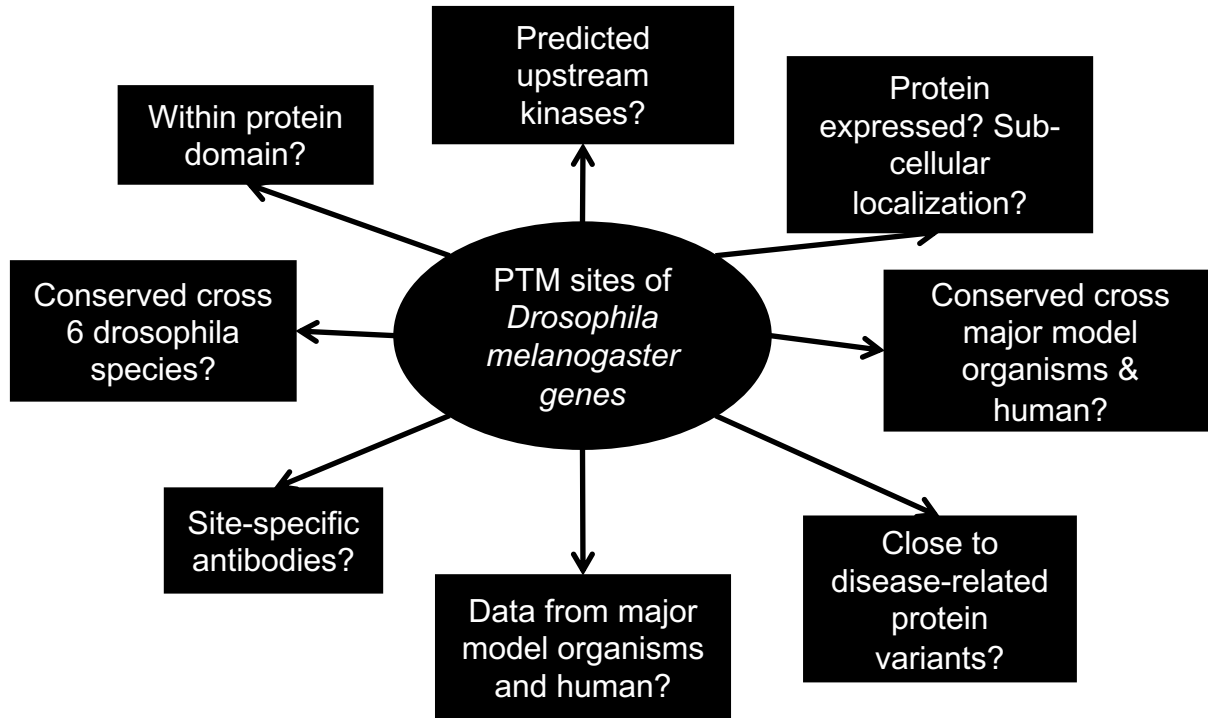
Resources include:
Multi-species resources
Fly-specific resources
Reagent design and info
Data mining and navigation
Large-scale data sets

Most popular resource:
[DIOPT integrated ortholog search tool](#)

Newest resources:
[iProteinDB](#)
[BioLitMine](#)

Have you seen?
[FlyPrimerBank--qPCR primer designs](#)
[DGET RNAseq search & visualize](#)
[Fly Protocols Portal](#)
[Gene2Function](#)

iProteinDB: Database of fly post-translational modifications



HOME ABOUT CONTACT

iProteinDB

INTEGRATED PROTEIN DATABASE OF PTM FOR DROSOPHILA GENES

iProteinDB is an online integrated protein database and resource tool for providing information on post-translational modifications (PTMs) in *Drosophila* species. It currently contains phosphoproteomics data for *D. melanogaster*, *D. ananassae*, *D. pseudoobscura*, *D. simulans*, *D. virilis*, and *D. yakuba*. Comparative analysis is available between these species, as well as human and other major model organisms.

SEARCH

- Enter genes or proteins
Enter one search term per line.
Accepted entries (case-insensitive) are FBgn/FBpp IDs, gene symbols, and gene annotations.
[Use sample terms](#)
- Upload from file

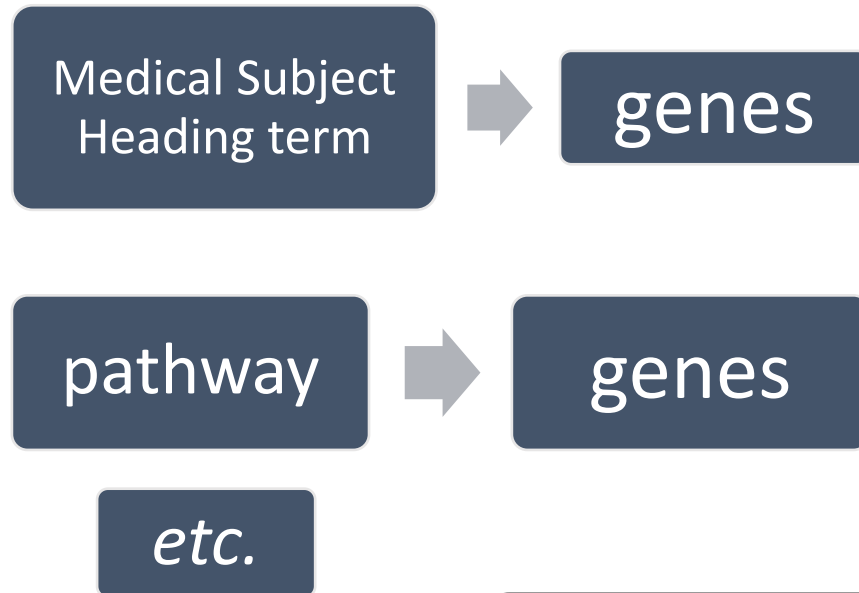
YTS
iProteinDB

© 2017-2018 iProteinDB, v1.0.0
Perrimon Lab, Harvard Medical School |

[iProteinDB](http://iProteinDB.org)

BioLitMine: text mining of PubMed literature

Connect:



Tip: Looking for experts to review a paper, give a talk, advise on a project? Doing a Gene or Pathway to People query can help you identify experts who've published relevant work.

Home About News/Updates Contact FGR Tools

Biological Literature Mining Tool for Human and Model Organisms

BioLitMine

Find relationships between genes, MeSH terms, pathways, and people from PubMed literature

Single Term Search

Step 1 - what do you want to find?

Step 2 - select organism

Step 3 - enter search term (case-insensitive)

[+] Filter Options

Enrichment Analysis

Step 1 - enter gene names, symbols or Entrez ids (one per line)

Step 2 - select organism

Step 3 - choose MESH category to search in

- All
- Anatomy
- Organisms
- Diseases

[BioLitMine](https://biolitmine.org)

Keep up-to-date with new resources, technologies, etc.

- Visit the [News section of our website](#)
- Follow us on Twitter [@DRSC_TRiP](#)

Future directions:

- New emphasis on technology development in partnership with specific projects
- CRISPR activation pooled screening—proof-of-concept studies in process
- Application of CRISPR screen technologies to mosquito cell lines
- New technologies related to proteomics and protein detection
- Updates to the website on these and other topics
- *Your ideas and input are always welcome*

Interested in outreach within and beyond our community?

So are we. Check out for example these resources:

drosophilaresearch.org

flydiseasemodels.blogspot.com

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Howard Hughes Medical Institute

dsRNA and GFP cell line workflow illustrations
drawn using BioRender



fgr.hms.harvard.edu
drosophilaresearch.org
flydiseasemodels.blogspot.com
[perrimon lab website](#)

We are here to help!

For screen consultation,
new collaborations,
& new projects,
contact:

stephanie_mohr@hms.harvard.edu

