Advancing Authorship Library Series

Life Cycle of Launching a Publication: How the CRISPR Journal Came to Be

Ralph J. Garippa, Ph.D.
Head, Gene Editing & Screening (GES) Core Facility
Co-presentation w/ Kevin Davies, Executive Editor, Mary Ann Liebert Publishers
Memorial Sloan-Kettering Cancer Center

Wednesday, December 19, 2018 1:00-2:30 PM

Zuckerman room 105, 1st Floor

GES Core Capabilities at MSKCC

- **GeCKO v2, Brunello, Brie CRISPR KO** libraries, individual sgRNA guides (ORF, CRISPR-A)
- Extensive selection of retroviral and lentiviral **vectors**
- **Virus production** for screening
- Broad's TRC 1.0, 1.5, 2.0 mouse and human (stem loop) **shRNA** libraries (individual)
- **siRNA** (GE-Thermo) full genome arrayed libraries in 96/384
- Off-the-shelf and custom miR30 and **mirE shRNA pooled libraries and individual clones**
- Focused small molecule **compound sets** with well characterized activity for straight- or synthetic lethality screening

- Carry out arrayed and pooled CRISPR screens fee-for-service
- Assay development
- Two INCell 6000 high-content imaging platforms & automation
- BioRad S3 FACS sorter.
- PE Envision plate reader.
- Molecular biology lab (custom)
- Cell culture suite with automation
  - Agilent Bravo liquid handling
  - BioTek 406 plate washer
  - Multidrop Combi's dispensing
  - PE Janus cherry-picking
- Isolate gDNA from cell pellets, PCR amplify, prepare for Hiseq, apply analysis tools for NGS de-convolution of pooled CRISPR hits

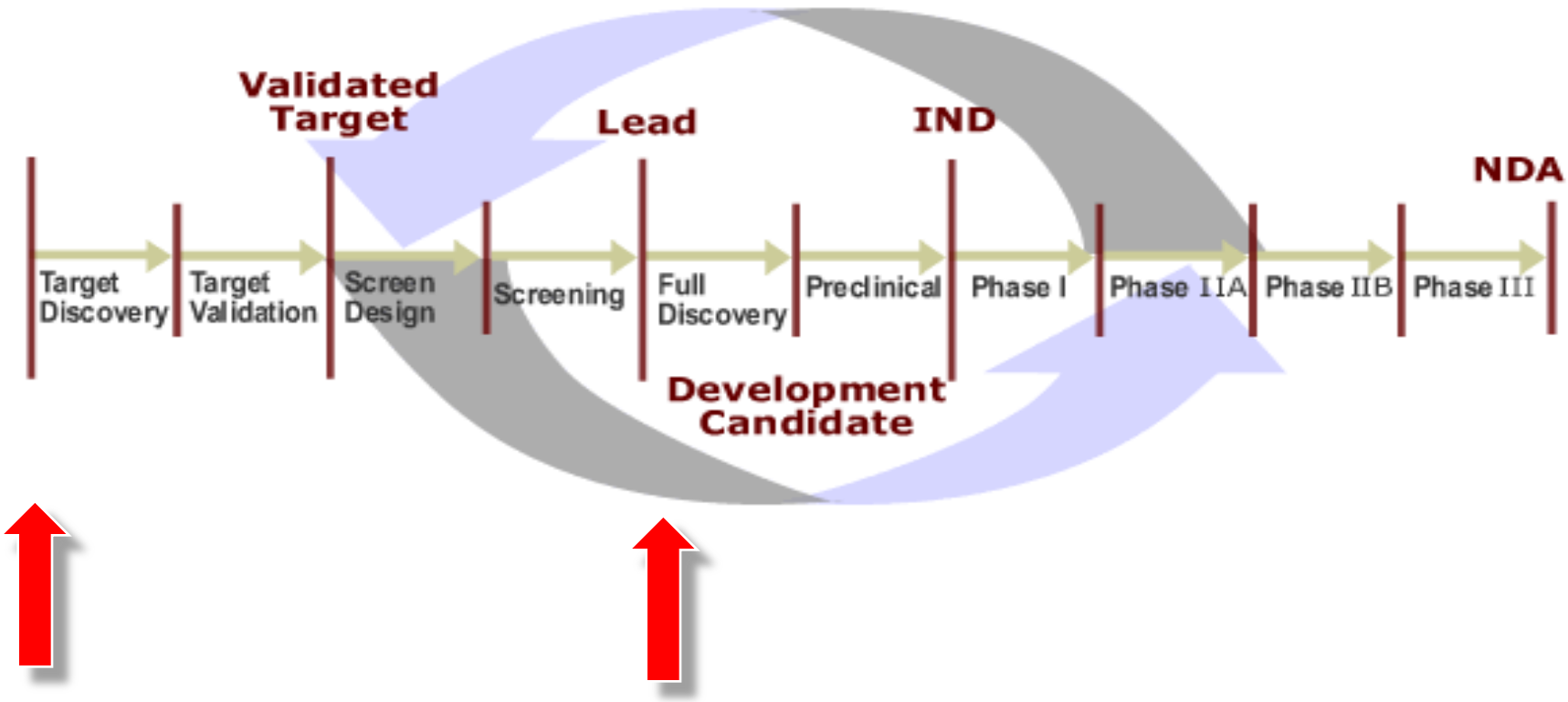
CRISPR/RNAi collections

Customized reagents

Screening services

Develop new technologies

High Level View of the Drug Development Cycle
(Framework)

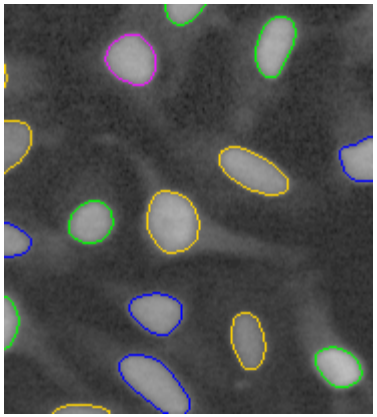


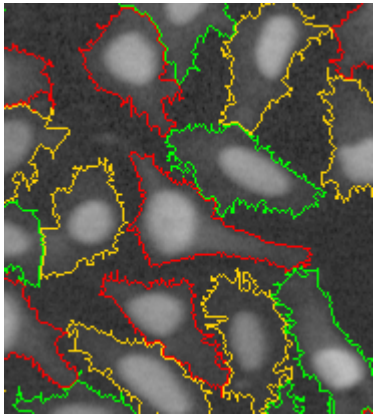
Value chain for the GES Core

IN Cell Analyzer 6000 (high content imager)

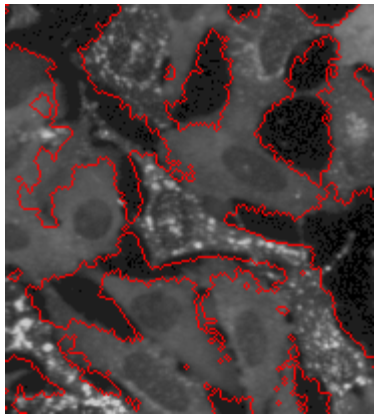
GPCR Algorithm: Graphical summary

Find nuclei and cells

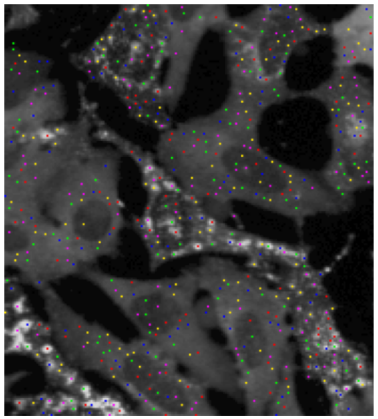


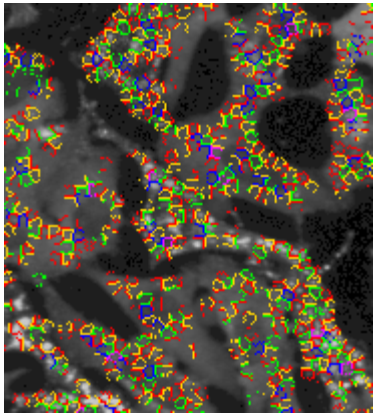


Search for spots

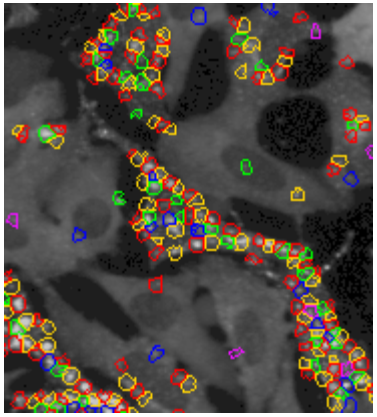


Analyze all spots found





Quantify the selected spots



GuideScan: a CRISPR sgRNA design tool

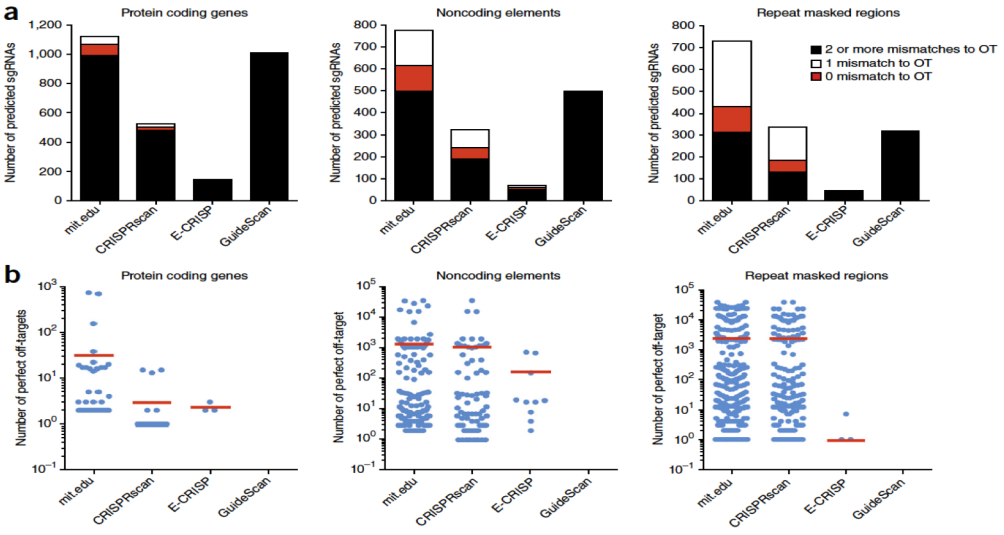
Enumerates Off-target sequences & filters out promiscuous gRNAs

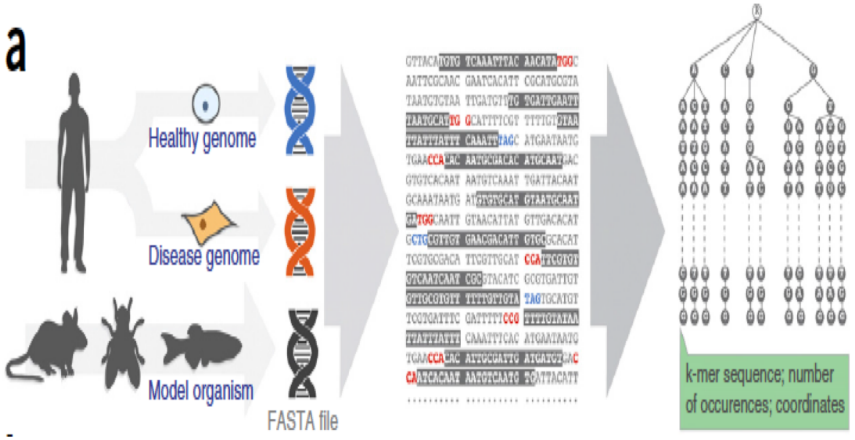
GuideScan software for improved single and paired CRISPR guide RNA design

Nature Biotech, 2017

Alexendar R Perez[1–4], Yuri Pritykin[1,4], Joana A Vidigal[2,4], Sagar Chhangawala[1,3], Lee Zamparo[1], Christina S Leslie[1] & Andrea Ventura[2]

We present GuideScan software for the design of CRISPR guide RNA libraries that can be used to edit coding and noncoding genomic regions. GuideScan produces high-density sets of guide RNAs (gRNAs) for single- and paired-gRNA genome-wide screens. We also show that the trie data structure of GuideScan enables the design of gRNAs that are more specific than those designed by existing tools.





Used 4 different tools to design 20 mer guides

Fig B. Number of OT sites; each dot = 1 sgRNA

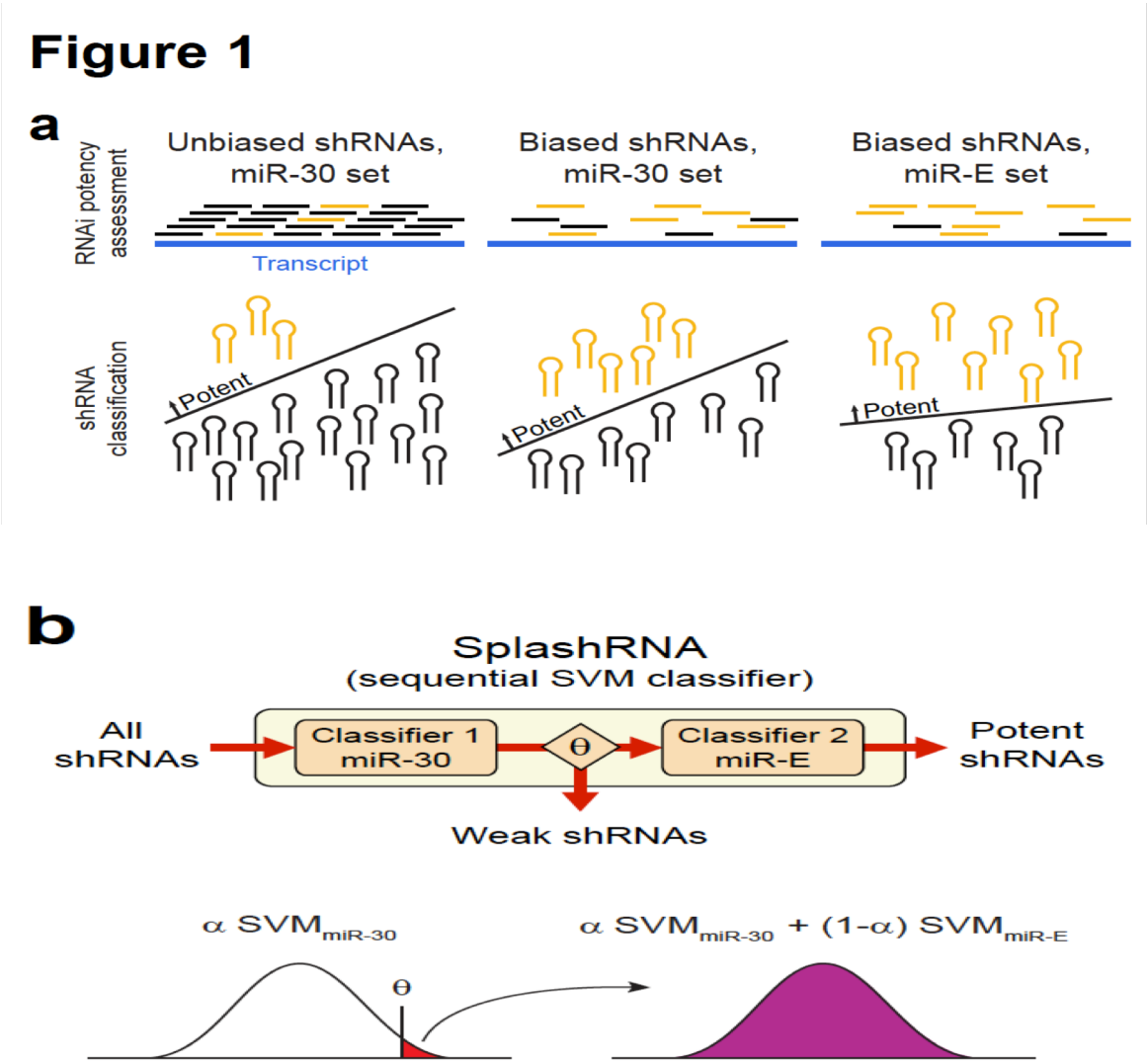
Input any genome of choice as a FASTA file

Choose PAM to identify targetable sequences

Index targetable sequences in a retrieval tree

SPLASH shRNA design tool

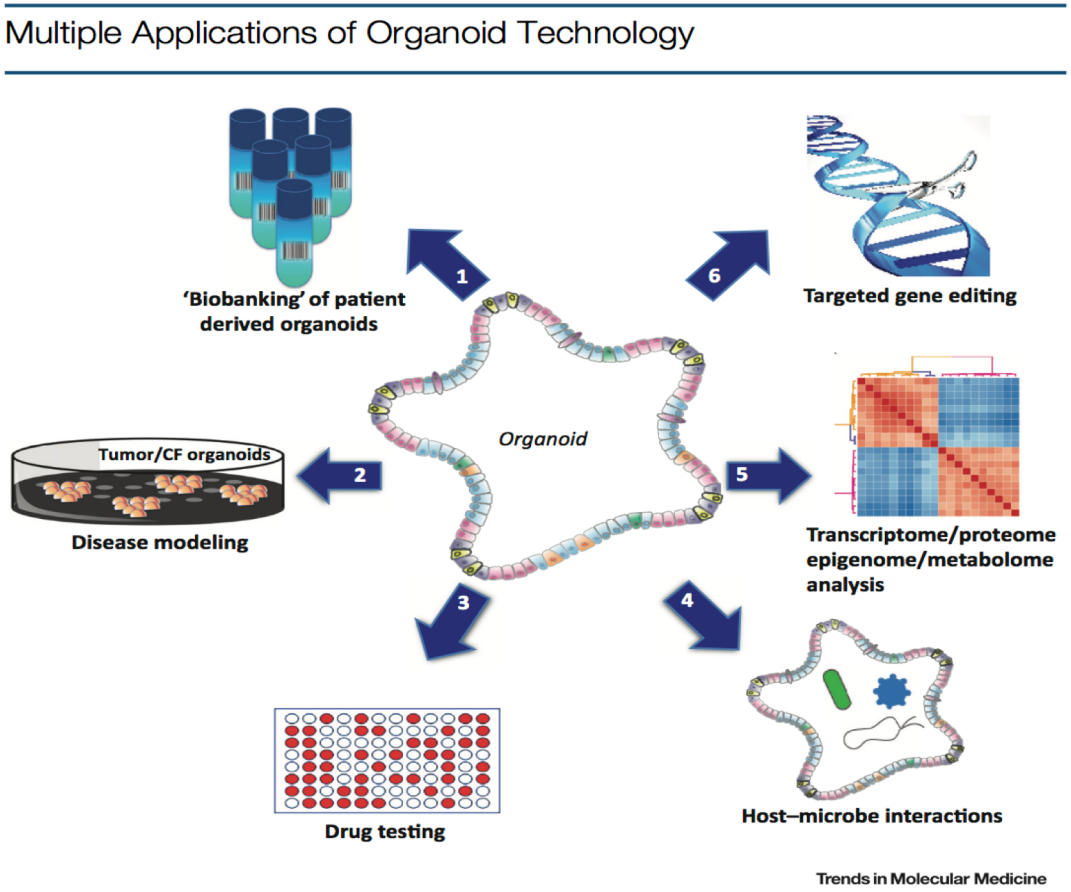
- A **sequential classifier** predicts potent microRNA-based short hairpin RNAs (shRNAs). Net result is a higher rates of positives



- **Unbiased sets** include negatives and a few positives trained on published and novel datasets; outperforms other algorithms
- >90% of predictions trigger >85% knockdown when expressed from a *single genomic integration*
- **Concept & Equation** of a sequential support vector machine classifier (SVM)
- 1st train on Mir30 to remove non-functional sequences
- 2nd train on Mir-E data to increase prediction performance

Pelossof, Leslie, Lowe, Garippa, *et al* Nat Biotech 2017

Context and spatial relevance of 3D biology: organoids



Dutta, Heo, Clevers, 2017

Why do I read The CRISPR Journal?

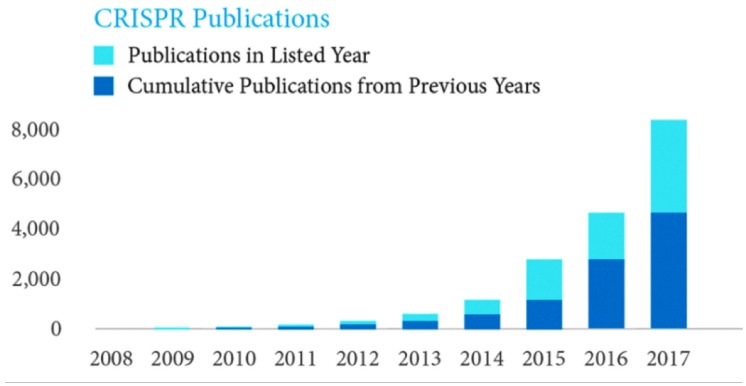
- “Dedicated to everything CRISPR”
- “aim to extensively and colorfully cover many other aspects of interest to the CRISPR community (IP, ethics, society, agriculture, reagent development, laws)”

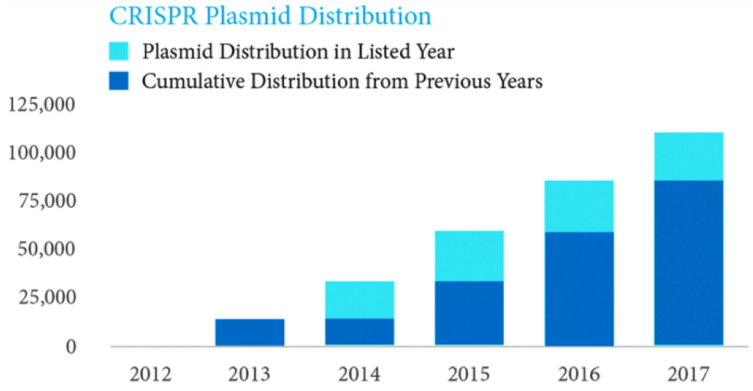
-Davies & Barrangou
CRISPR J June 2018

“*As a scientist, I am also (concurrently) a US citizen, taxpayer, food consumer, who is raising children, and entering a decade in my life where new medicines may extend or improve my quality of life”*. –R. J Garippa, Ph.D.

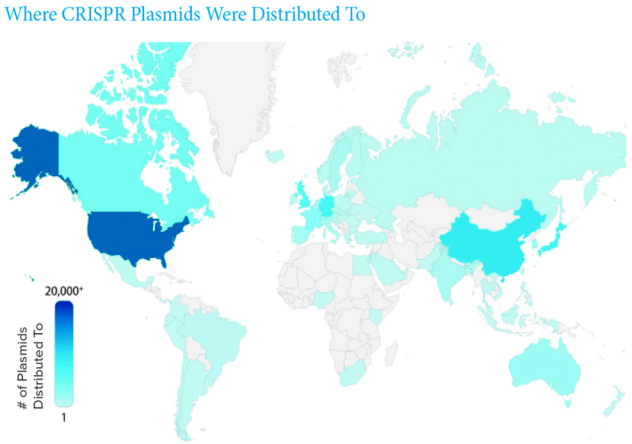
CRISPR patents: what do we know?

- 1st US Patent to mention CRISPR was issued 2004 to **Danisco** (food chemistry company) method of sequencing to detect variants of *Lactobacillus acidophilus* (**yogurt production**, phage resistance)
- Jennifer Doudna (UC Berkeley/HHMI) and Emmanuelle Charpentier (Sweden) filed May 2012 for an engineerable single guide RNA (sgRNA)
- Feng Zhang (Broad Institute) filed Dec. 2012 but was granted the first patent (fast tracking, eukaryotic use)
- **Addgene**, a non-profit repository, banks & distributes
- Broad and UC Cross-Licensing agreements with Dupont, Monsanto, Caribou, Dow, and others
- To date, US Patent & Trademark Office (**PTO**) has issued 450 CRISPR patents (note: 18 mo. kept secret)

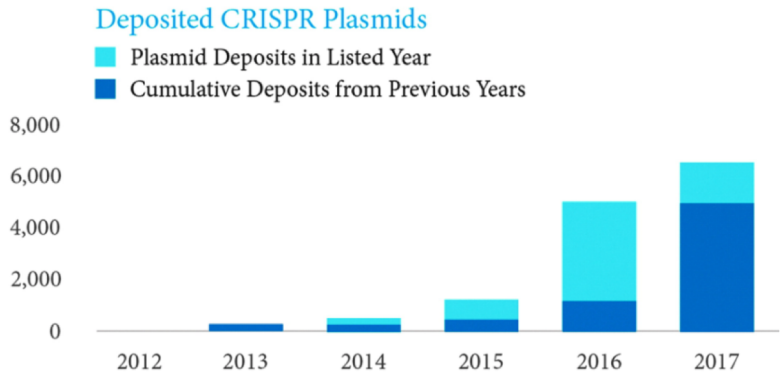


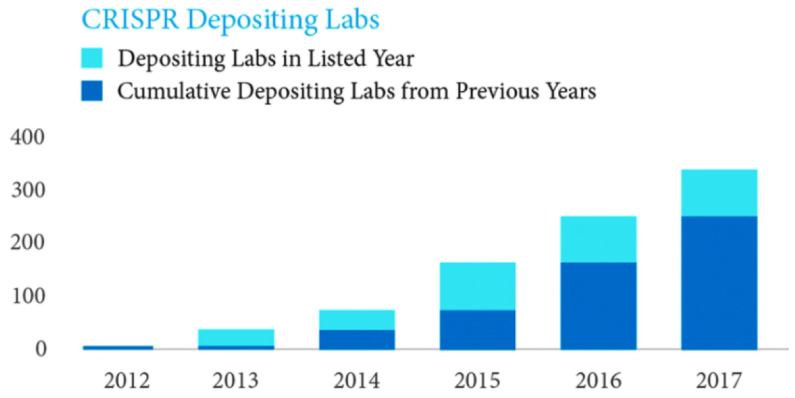


CRISPR: Rapidly conquering the world

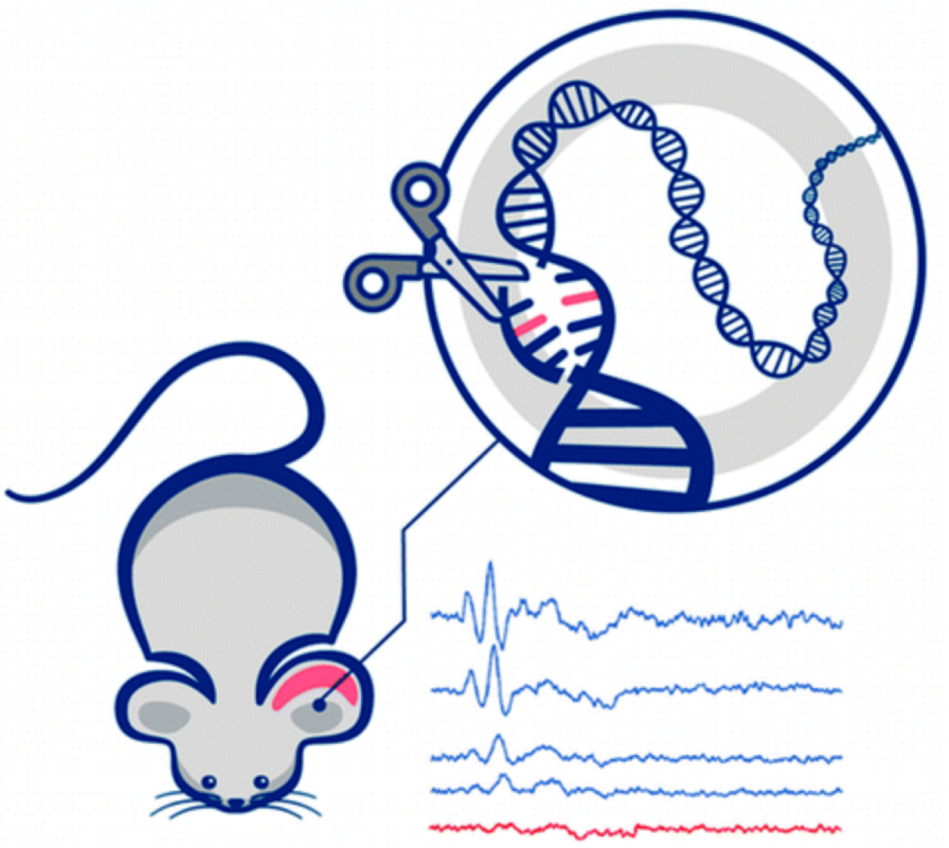


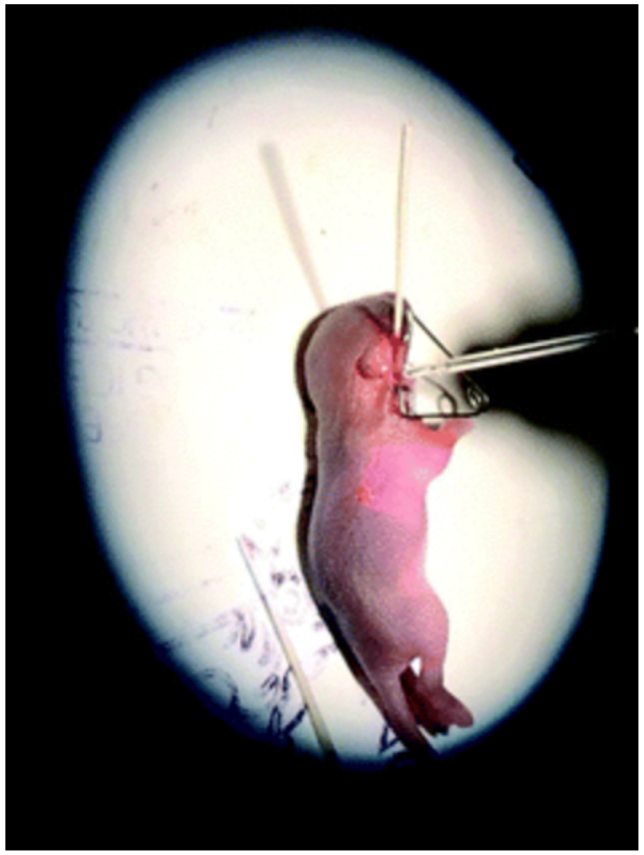
Lamanna & Barrangou
CRISPR J June 2018





CRISPR and the possibility of *treating* ***hereditary diseases (ex: deafness)***





Uses: successful treatment of a dominant TMC1 mutant mouse model of progressive hearing loss, the so called Beethoven point mutation
Risks: Lingering levels of Cas9 for days-weeks after rAAV infection could lead to off target effects or an immune response from the recipient

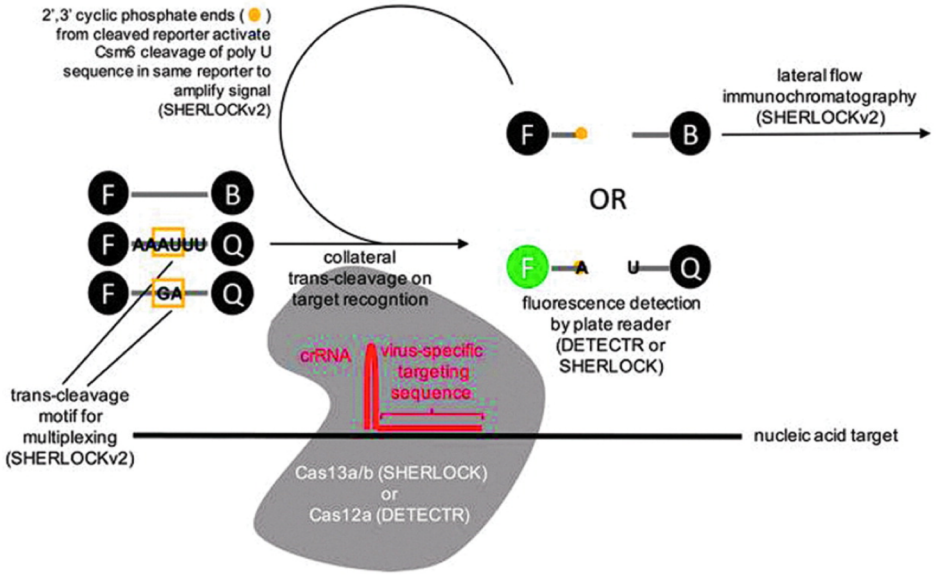
Burgio, Gaetan *CRISPR J* 2018
Gao, Tao, Lamas *Nature* 2018

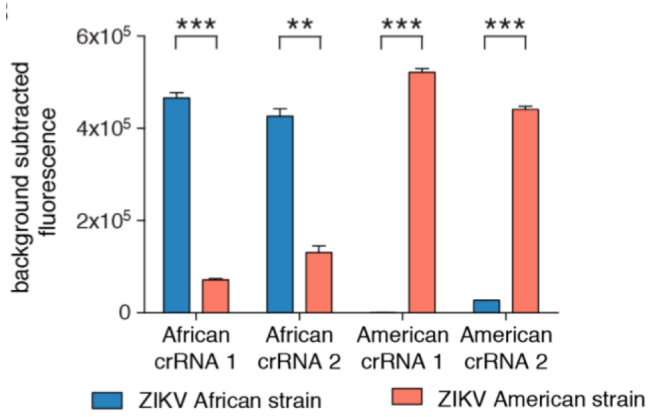
CRISPR Cas12a: A Revolution in ultra sensitive clinical diagnostics

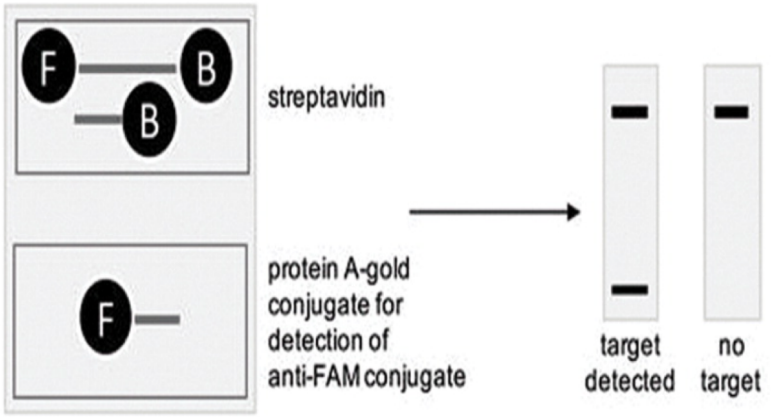
Cite as: J. S. Gootenberg *et al.*, *Science* 10.1126/science.aam9321 (2017).

Nucleic acid detection with CRISPR-Cas13a/C2c2

Jonathan S. Gootenberg,[1,2,3,4,5*] Omar O. Abudayyeh,[1,2,3,4,6*] Jeong Wook Lee,[7] Patrick Essletzbichler,[1,2,3,4] Aaron J. Dy,[1,4,8] Julia Joung,[1,2,3,4] Vanessa Verdine,[1,2,3,4] Nina Donghia,[7] Nichole M. Daringer,[8] Catherine A. Freije,[1,11] Cameron Myhrvold,[1,11] Roby P. Bhattacharyya,[1] Jonathan Livny,[1] Aviv Regev,[1,9] Eugene V. Koonin,[10] Deborah T. Hung,[1] Pardis C. Sabeti,[1,11,12,13] James J. Collins,[1,4,6,7,8†] Feng Zhang[1,2,3,4†]





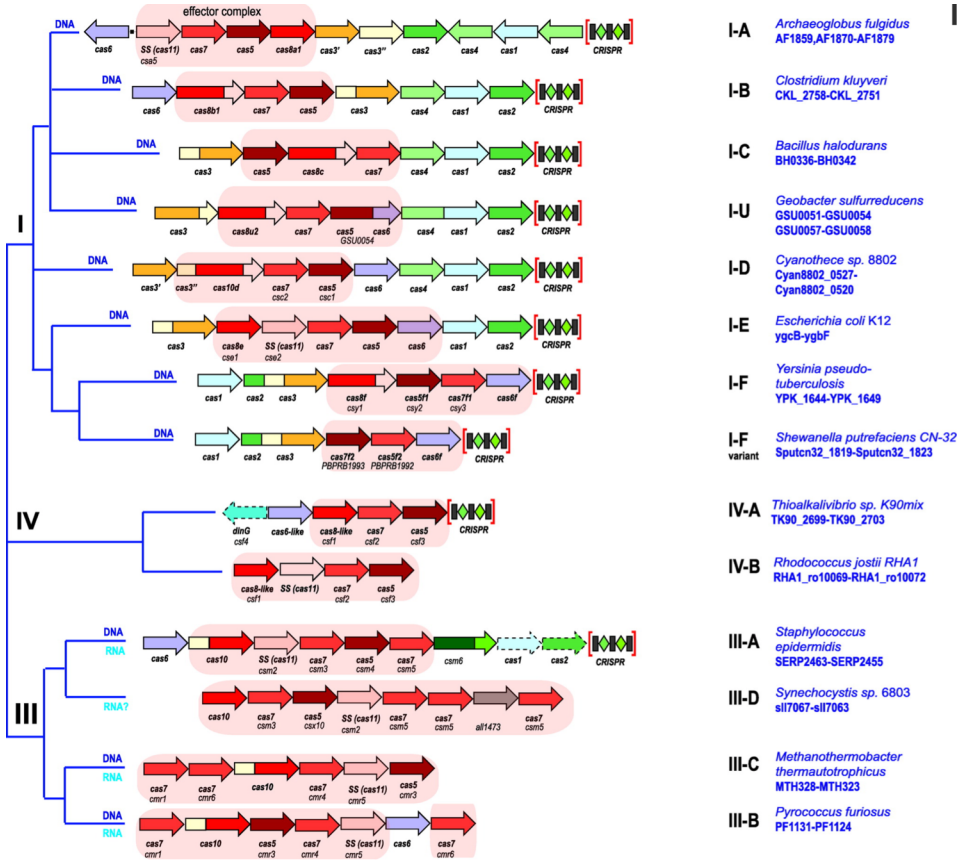


Cas12a will cleave quenched reporter molecules only in the presence of a specified nucleic acid target sequence (HPV, Lyme)

Petri & Pattanayak, CRISPR J 2018

Classification and nomenclature of CRISPR-Cas9 systems and tracking *anti-CRISPR* names

- Now 36 families of distinct anti-CRISPRs



I-A *Archaeoglobus fulgidus* AF1859,AF1870-AF1879

I-B *Clostridium kluyveri* CKL_2758-CKL_2751

I-C *Bacillus halodurans* BH0336-BH0342

I-U *Geobacter sulfurreducens* GSU0051-GSU0054 GSU0057-GSU0058

I-D *Cyanothece sp. 8802* Cyan8802_0527-Cyan8802_0520

I-E *Escherichia coli K12* ygcB-ygbF

I-F *Yersinia pseudo-tuberculosis* YPK_1644-YPK_1649

I-F variant *Shewanella putrefaciens CN-32* Sputcn32_1819-Sputcn32_1823

IV-A *Thioalkalivibrio sp. K90mix* TK90_2699-TK90_2703

IV-B *Rhodococcus jostii RHA1* RHA1_ro10069-RHA1_ro10072

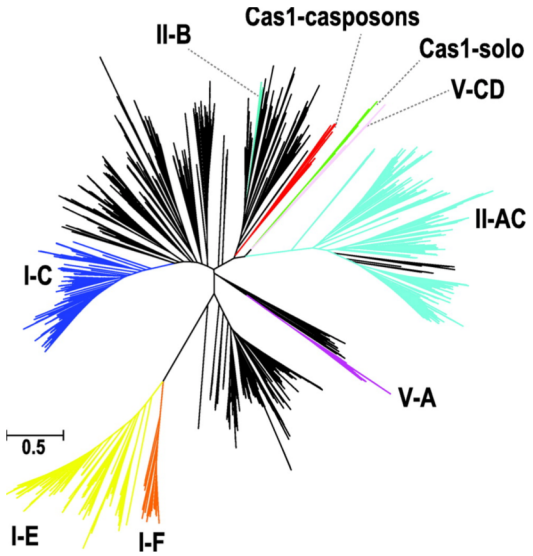
III-A *Staphylococcus epidermidis* SERP2463-SERP2455

III-D *Synechocystis sp. 6803* sll7067-sll7063

III-C *Methanothermobacter thermautotrophicus* MTH328-MTH323

III-B *Pyrococcus furiosus* PF1131-PF1124

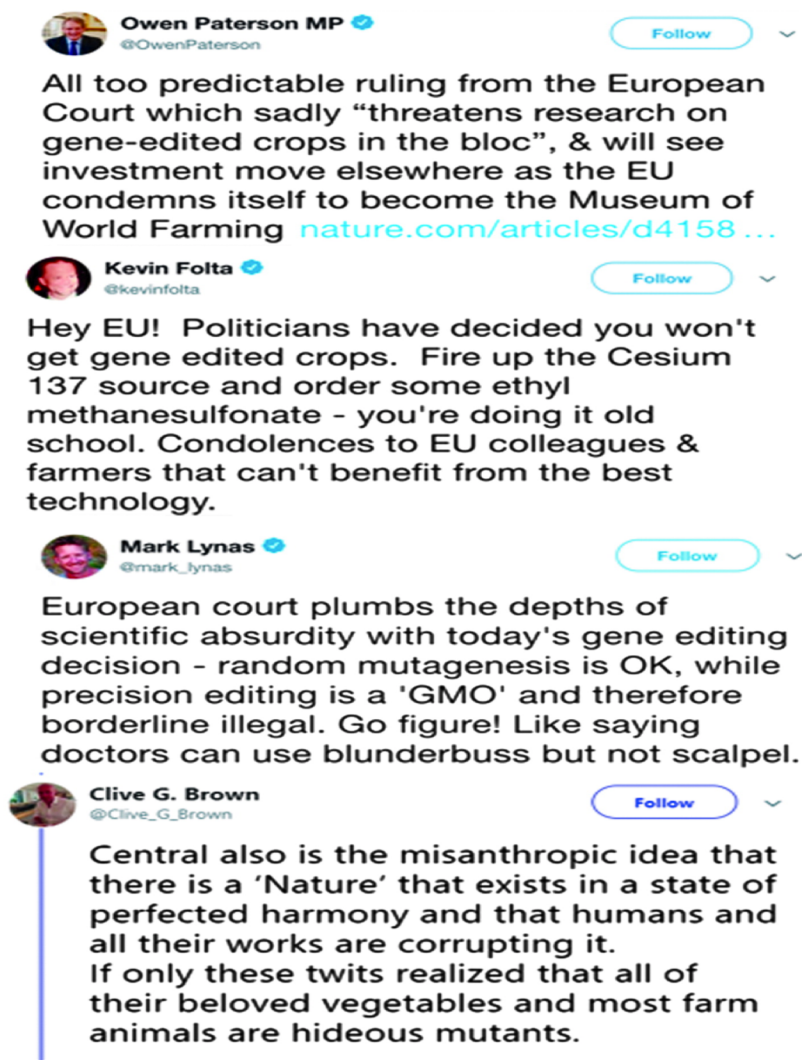
Alignment of 2,512 representative Cas1 protein sequences via iterative clustering



Recently updated Class 1 CRISPR-Cas systems

Makarova & Koonin
CRISPR J Oct 2018

Plant Breeding: Is a GE plant really a GMO? European Court of Justice (EJC) says “yes”



Barrangou, CRISPR J 2018

CRISPR and the possibility of ***Genetic Rescue***

Black footed ferret
(threatened by sylvatic plague,
a non—native bacterial infection)

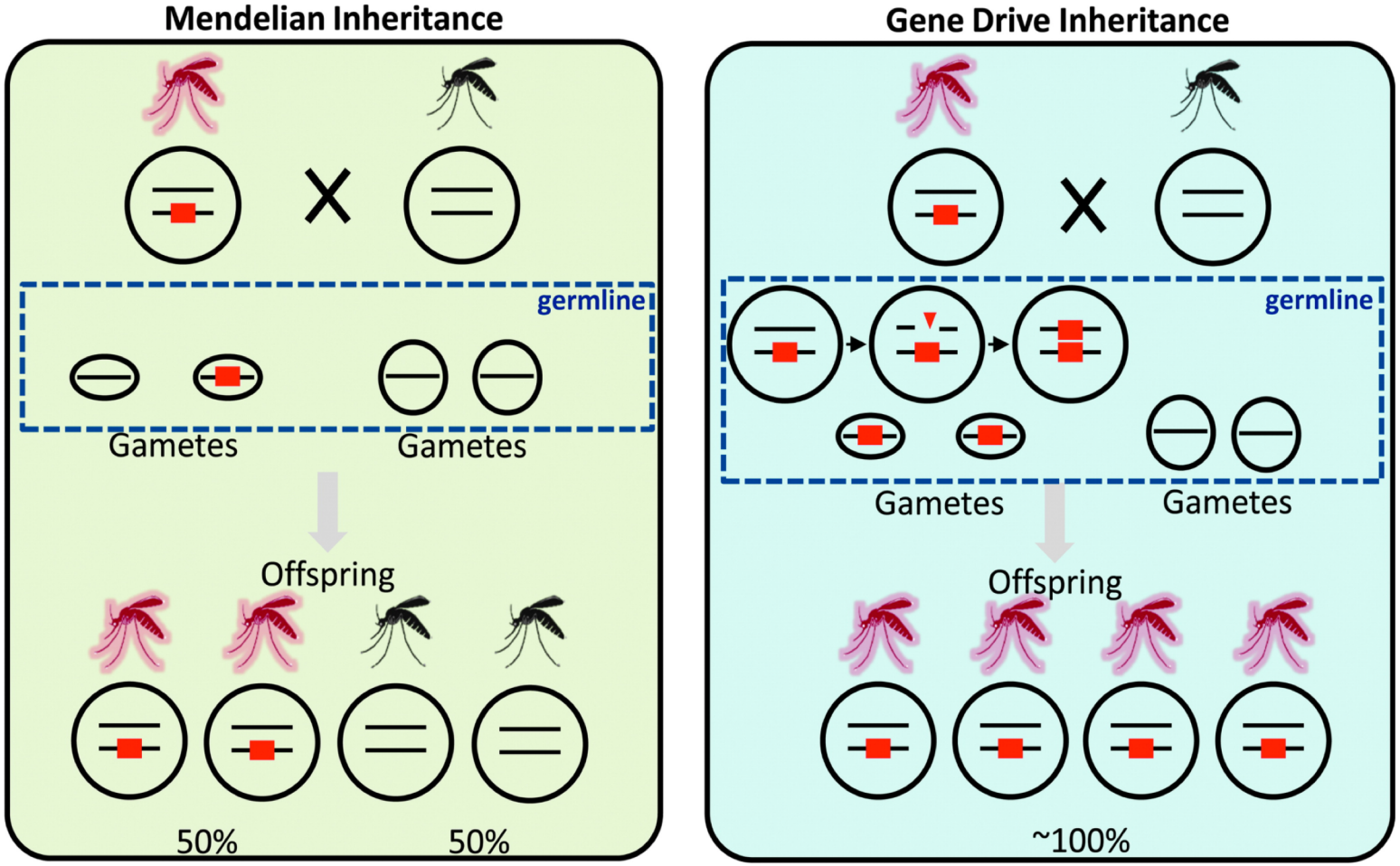
American Chestnut
(threatened by fungal blight)

<u>Other applications include:</u>
- Woolly Mammoth Revival project (de-extinction)
- Remove island rodents (w/o rodenticides)
- Hawaiian trees

<u>Successes for far with Gene Edit breeding:</u>
- Hornless Holstein dairy cattle
- Taming wild mice
- Sheep with increased musculature

Novak, Maloney Phelan *CRISPR J* 2018
Steiner, K.C., et al *New Forests* 2017

CRISPR and the possibility of ***Gene Drives***



Uses: population suppression (ex: reduce the # of viable females) or trait replacement (ex: makes the population less harmful)
Risks: Spread to unintended populations or resistance

Nolan, Tony *CRISPR J* 2018
Gantz & Bier *Science* 2015

CRISPR: Friend or Foe?

RUTGERS
New Jersey Medical School

Rutgers and the Federal Bureau of Investigation presents:

EVOLVING TECHNOLOGIES and BIOSECURITY

When: Thursday, December 1, 2016, 1pm-4pm
Where: New Jersey Medical School,
Medical Science Building, Lecture Hall B-610
185 South Orange Avenue, Newark, NJ

Featured Presentations

- **CRISPR and Gene Editing: Therapeutic Use and Potential Misuse**
  Ralph Garippa, PhD, RNAi Core Head
  Memorial Sloan Kettering Cancer Center
- **Big Data and Improved Therapeutics**
  Brian L. Strom, MD, MPH,
  Chancellor, Rutgers Biomedical & Health Sciences
- **Biosecurity and Big Data**
  Edward You, FBI - Weapons of Mass Destruction Directorate
- **BioCrimes**
  Cases presented by FBI and US Attorneys:
  Douglas Beecher PhD, FBI Laboratory (Anthrax)
  Scott Nawrocki, FBI WMD Coordinator for New Jersey (Ricin)
  Francisco J. Navarro, Assistant US Attorney
- **Panel discussion and Q&A**
  Conference Chairs:
  Steven Schutzer MD, Rutgers, NJMS-Department of Medicine
  Scott Nawrocki, FBI- Weapons of Mass Destruction Directorate

Rewriting Life

Top U.S. Intelligence Official Calls Gene Editing a WMD Threat

Easy to use. Hard to control. The intelligence community now sees CRISPR as a threat to national safety.

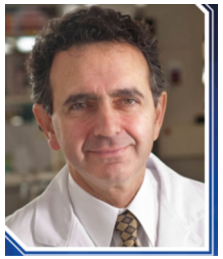
by Antonio Regalado February 9, 2016

Genome editing is a weapon of mass destruction.

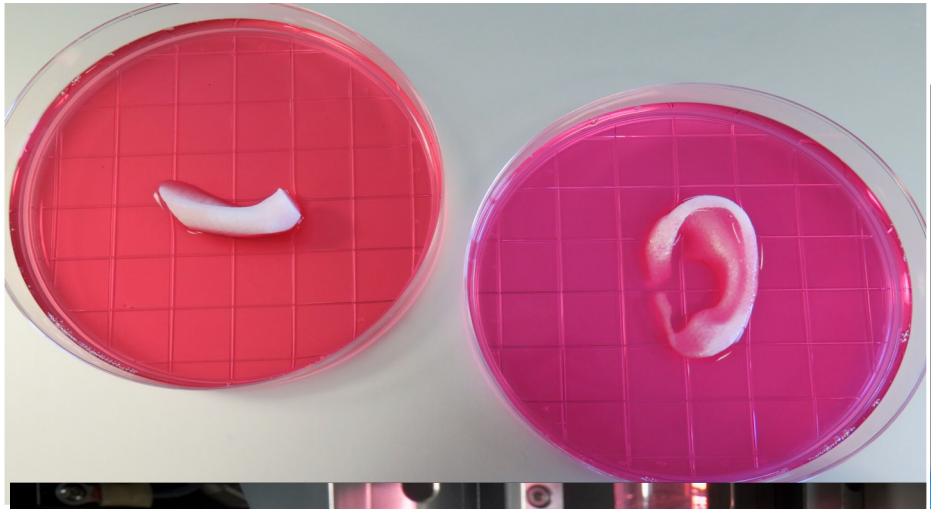
MEGAN MOLTENI SCIENCE 11.16.17 04:31 PM

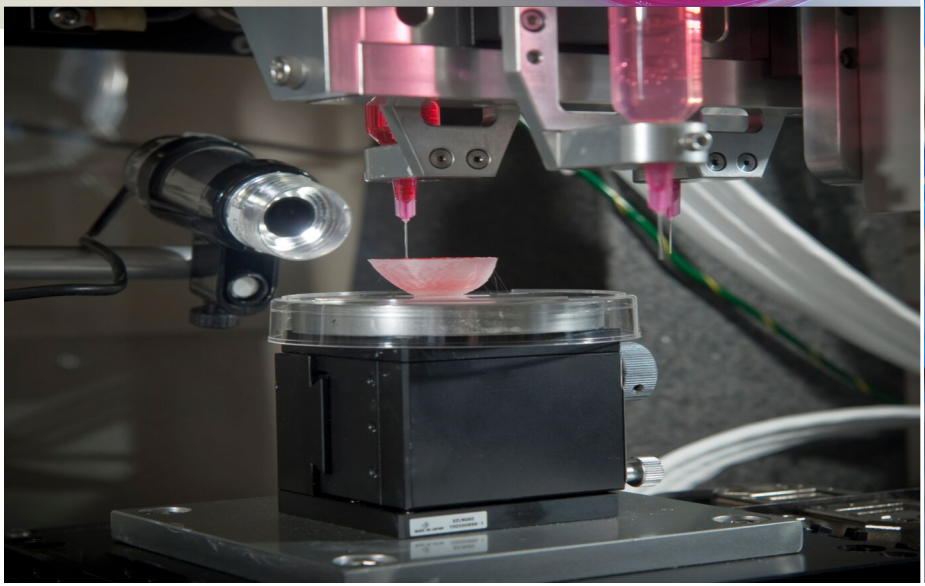
THIS GENE-EDITING TECH MIGHT BE TOO DANGEROUS TO UNLEASH

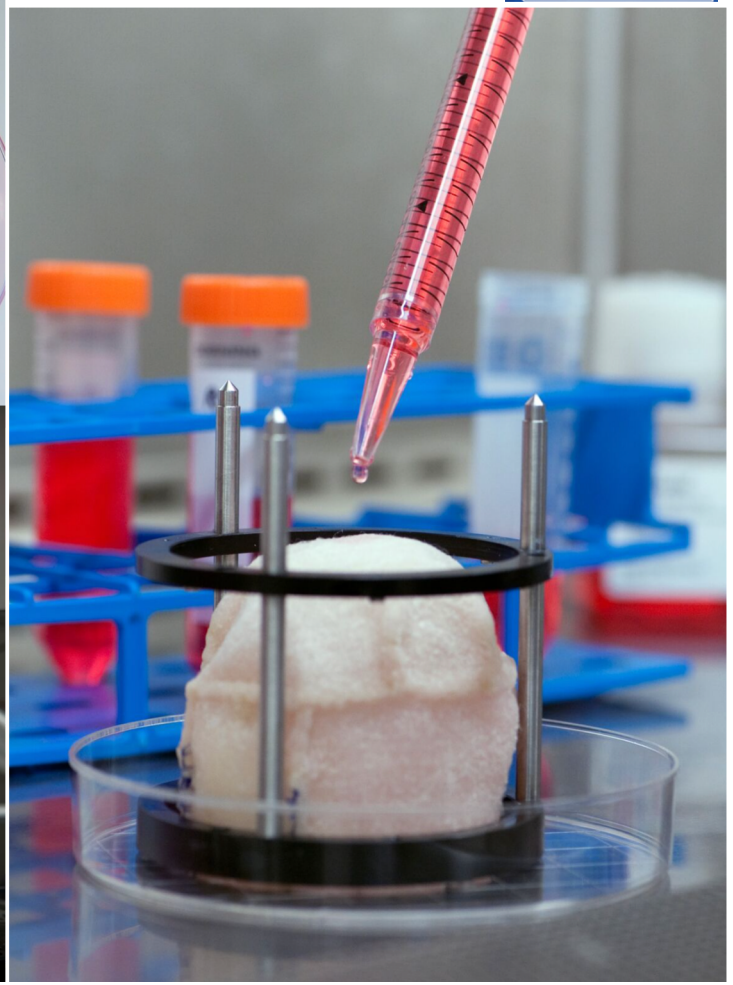
Using stems cells to combat disease, replace cancerous organs, and blunt diseases such as Parkinsons and ALS



Dr. Anthony Atala,
Wake Forest Univ.







The Danwei Huangfu Lab MSKCC

The ability to program naïve cells or to reprogram differentiated cells into particular fates will open the door to the discovery of novel therapeutics for diseases such as diabetes. The goal of my lab is to understand the fundamental principles that govern the identity of a cell, and to use these principles to manipulate cell fates for regenerative medicine. In pursuit of this goal, we employ a variety of approaches including cellular programming and reprogramming through gene transduction, directed differentiation of embryonic stem (ES) cells, chemical screening, mouse genetics, adult tissue injury and regeneration, and tissue/cell transplantation.

Learn more ›

In search of stem cell derived pancreatic beta cells to treat Type I and Type II diabetes

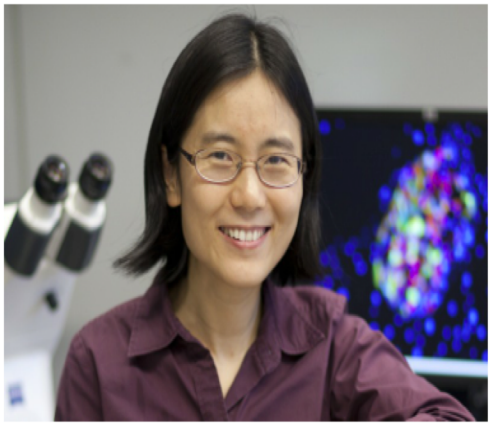
Danwei Huangfu, PhD

Research Focus

Developmental biologist Danwei Huangfu investigates the fundamental mechanisms that govern cell identity and how they could be exploited therapeutically to manipulate cell fates in regenerative medicine.

Education

PhD, Cornell University



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212-639-5239

Lab Phone:
212-639-5240

Stem Cell Therapies for Treating Diabetes: Progress and Remaining Challenges

Cell Stem Cell, 2018

Julie B. Sneddon,[1,2,3] Qizhi Tang,[4] Peter Stock,[4] Jeffrey A. Bluestone,[1,5] Shuvo Roy,[6,7] Tejal Desai,[6,7] and Matthias Hebrok[1,3,*]

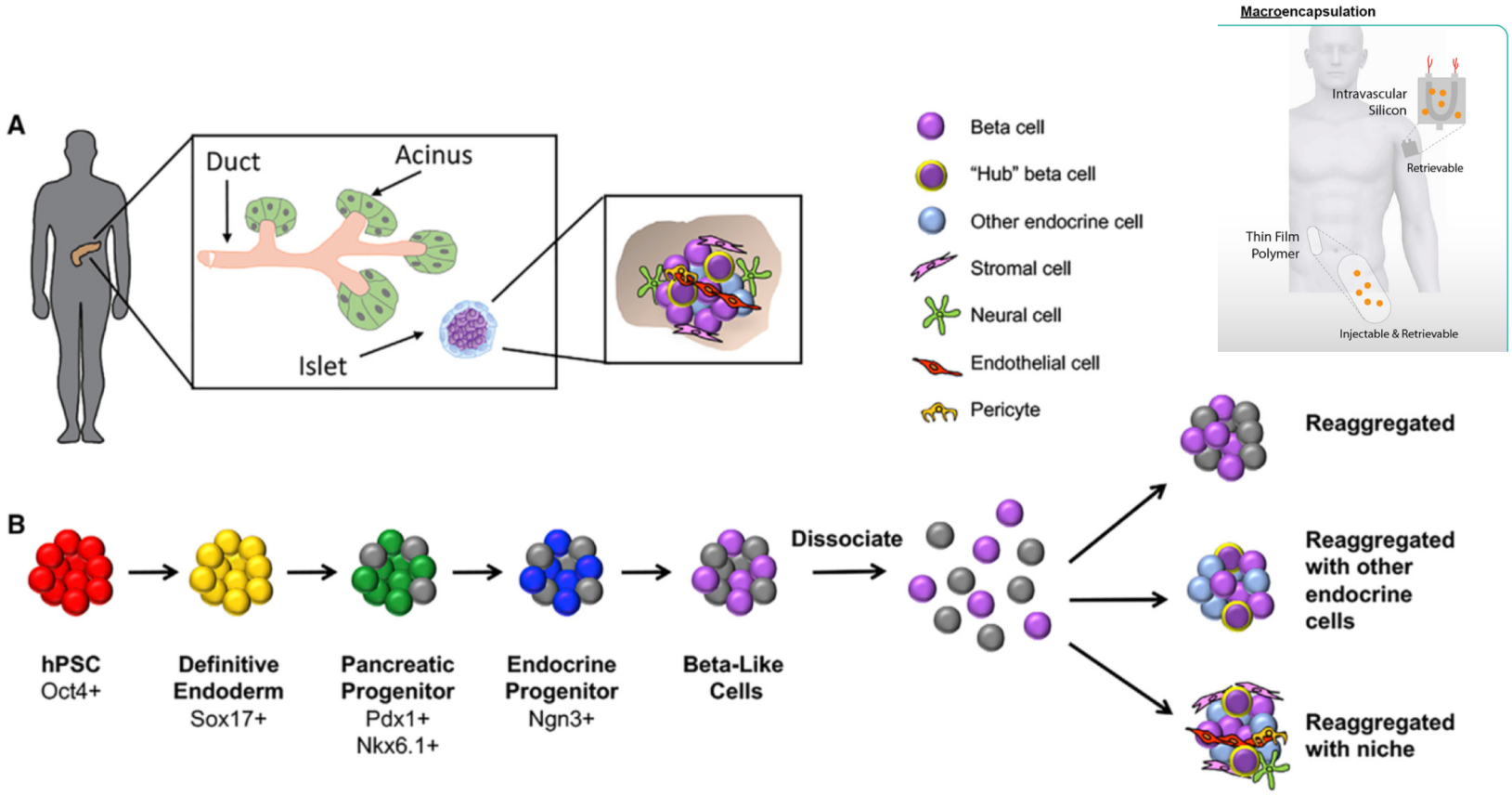
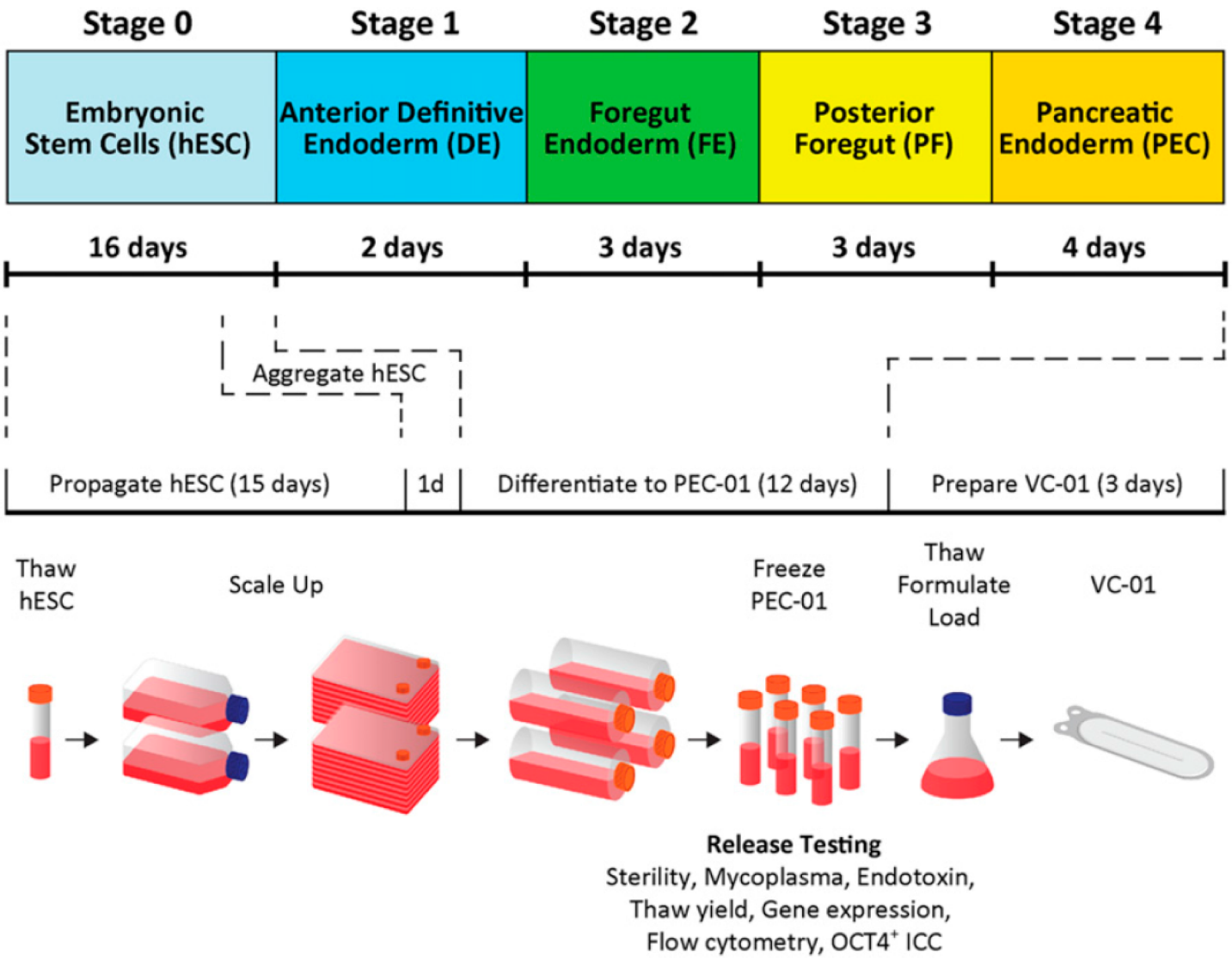
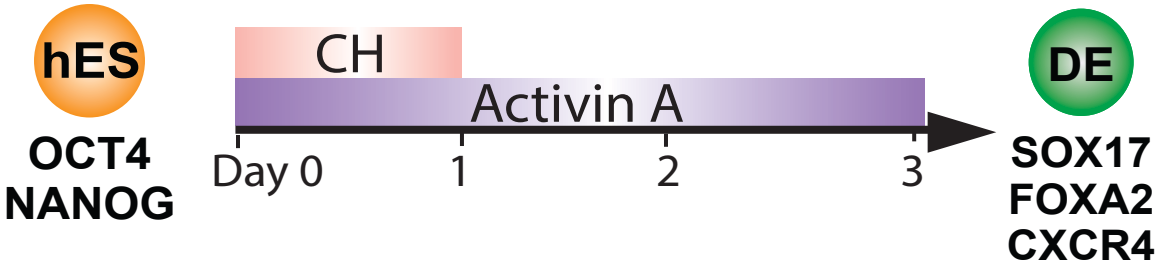


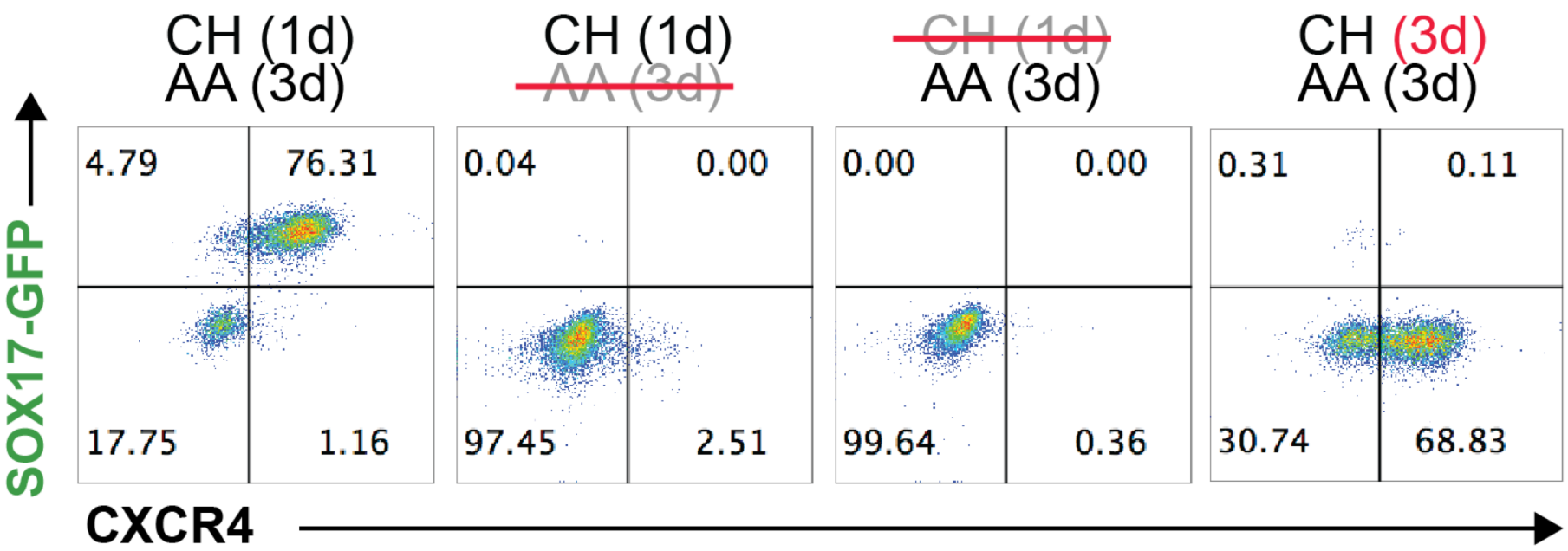
Figure 1. Strategies for Generating Human Pluripotent Stem Cell (hPSC)-Derived Pancreatic Islets for Transplantation

Schultz, 2015 Viacyte ™



Endoderm differentiation relies on TGFβ and WNT activation



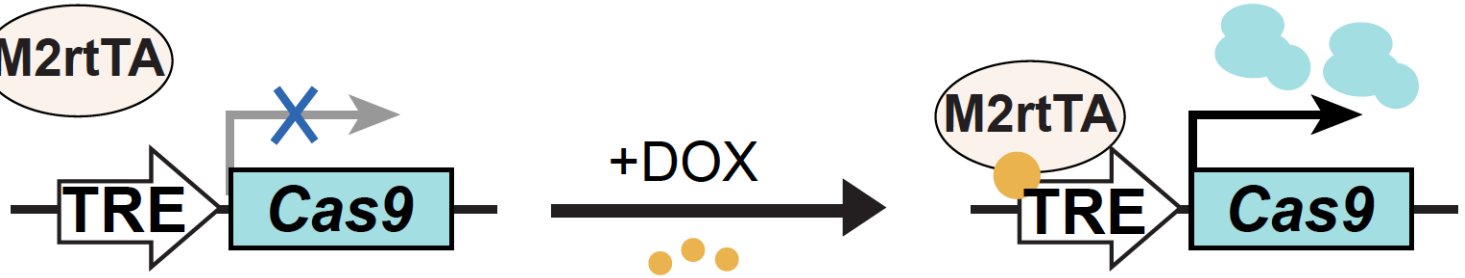


GSK beta 3 inhibitor CHir99021

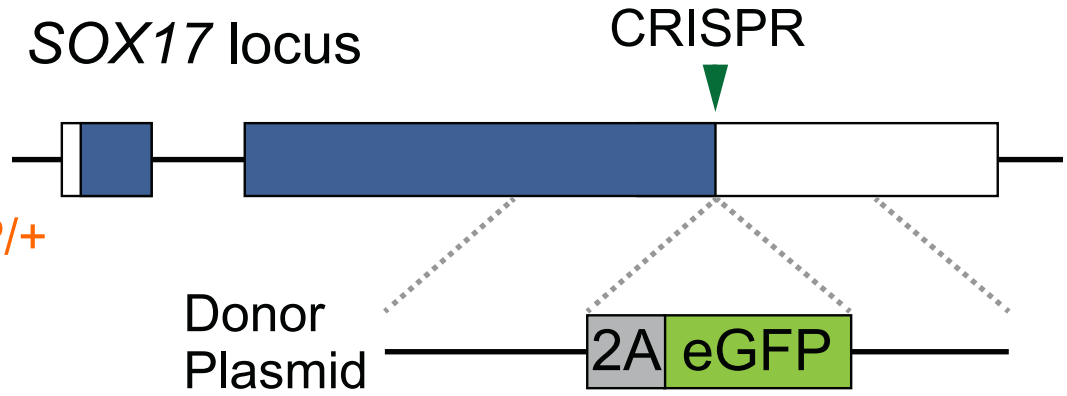
Qing Li, Danwei Huangfu, et al., unpublished

Generate *inducible* Cas9 SOX17$^{GFP/+}$ cells for the screen

Cas9

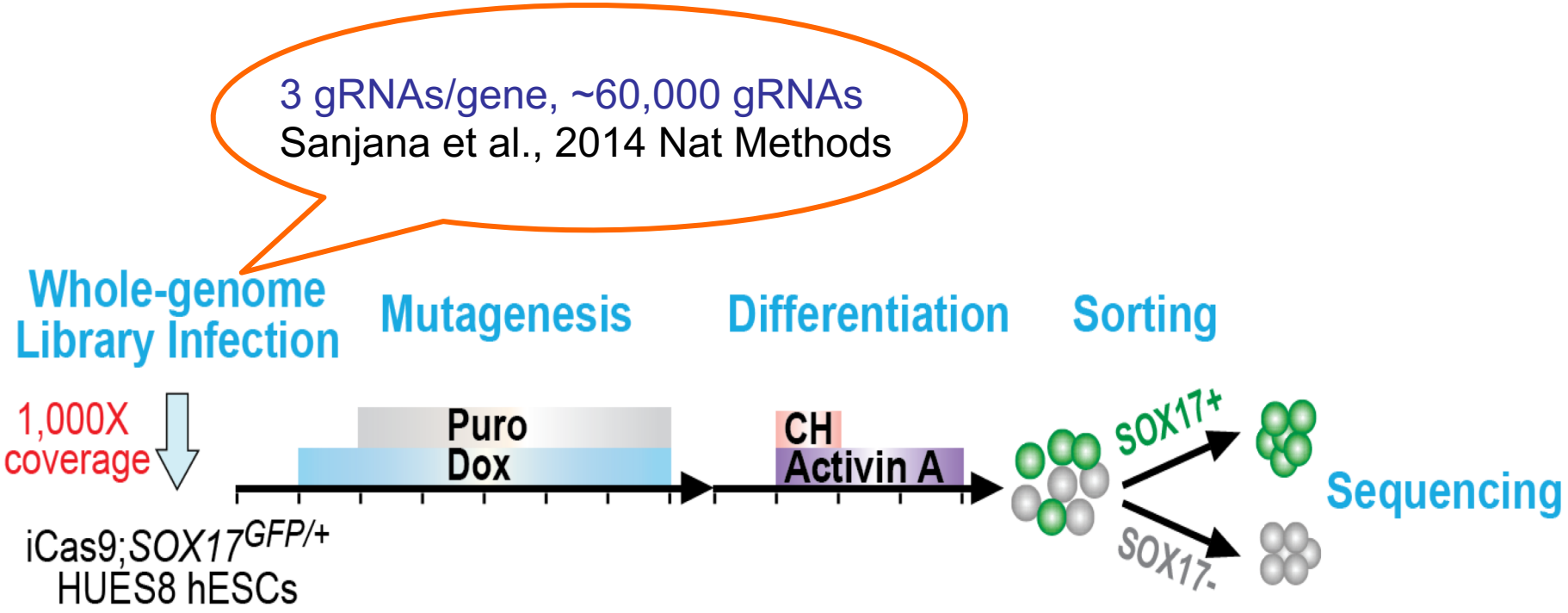


Cas9
SOX17$^{GFP/+}$



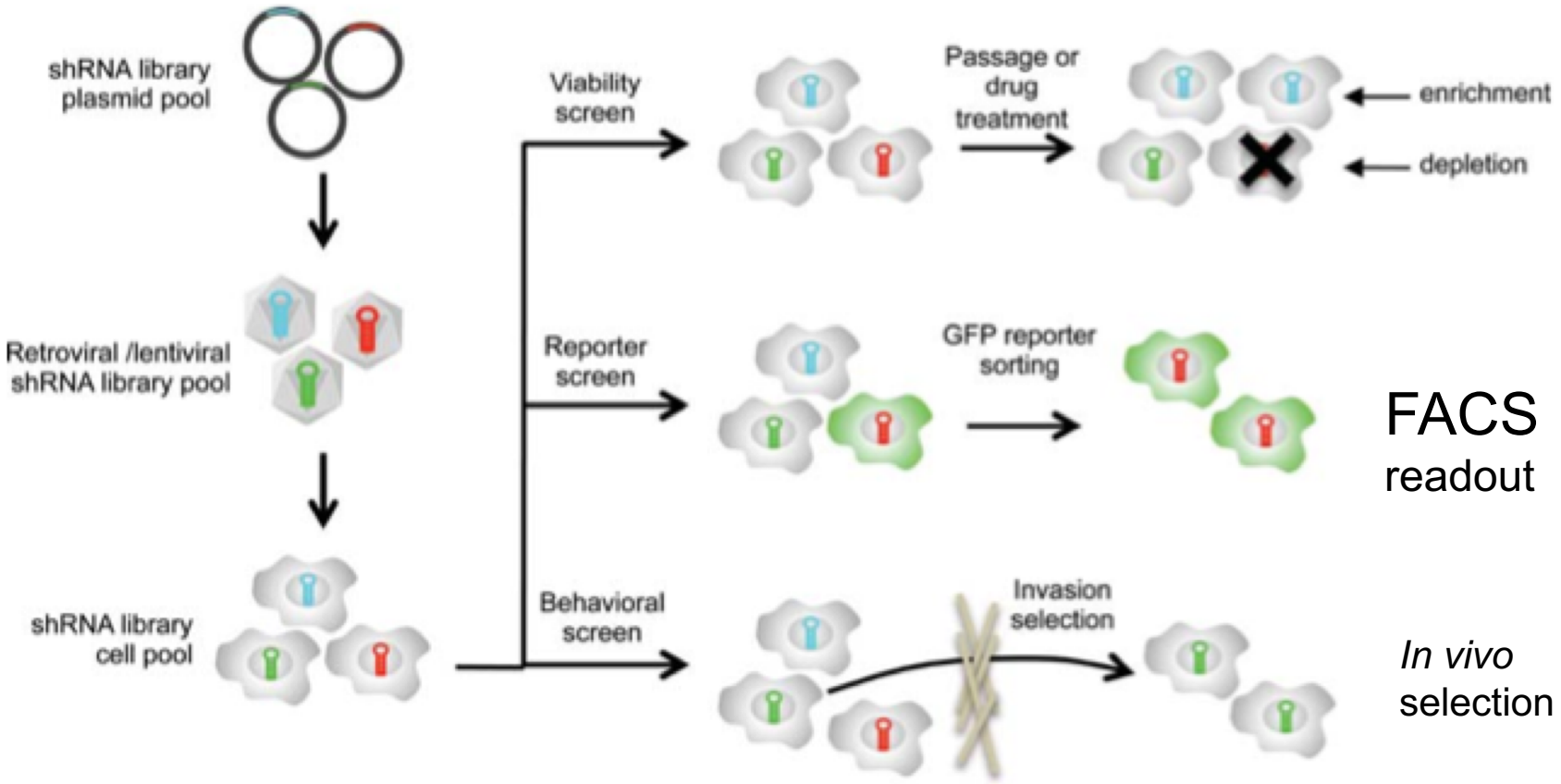
Gonzalez, Zhu, Shi et al. 2014 Cell Stem Cell
Qing Li, Danwei Huangfu, et al., unpublished

Genome wide CRISPR Cas9 knockout screen using pooled gRNA library



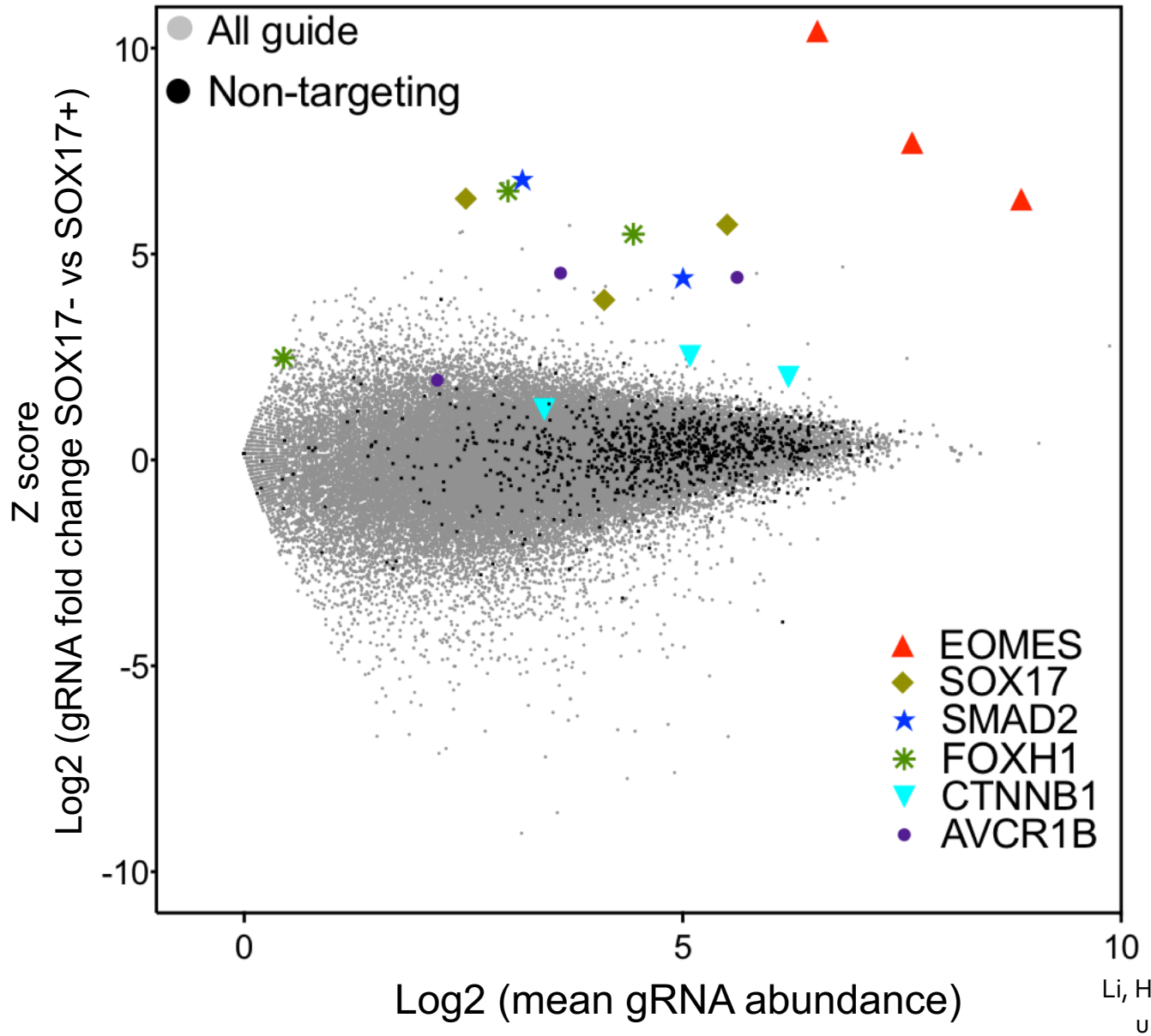
Qing Li, Danwei Huangfu, et al., unpublished

3 Examples of pooled sgRNA CRISPR Cas9 (or shRNA) screen designs



Hu and Luo, 2012

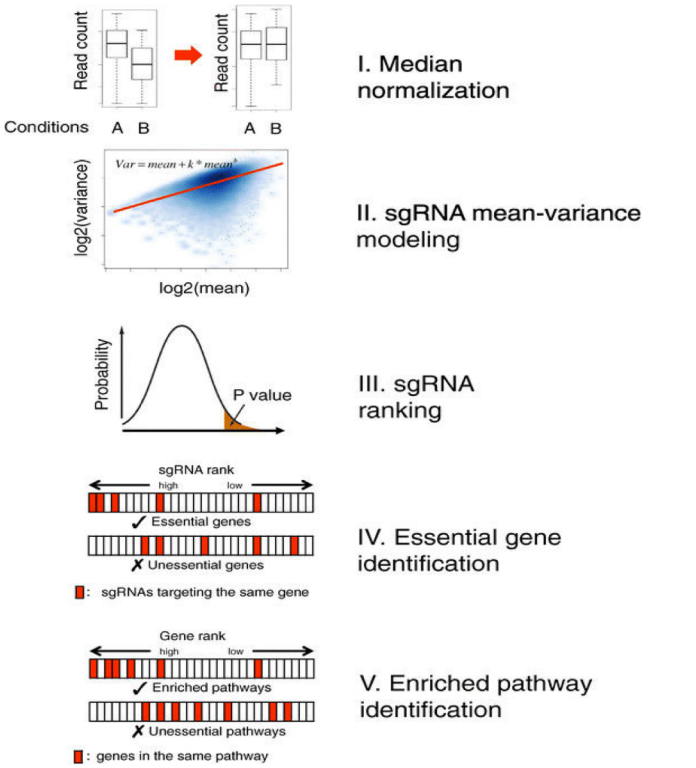
100 plates (150 mm) later…the screen outcome…

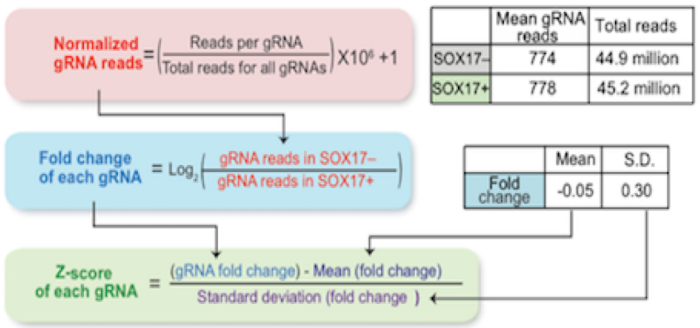


Li, Huangfu, et al., unpublished

MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens

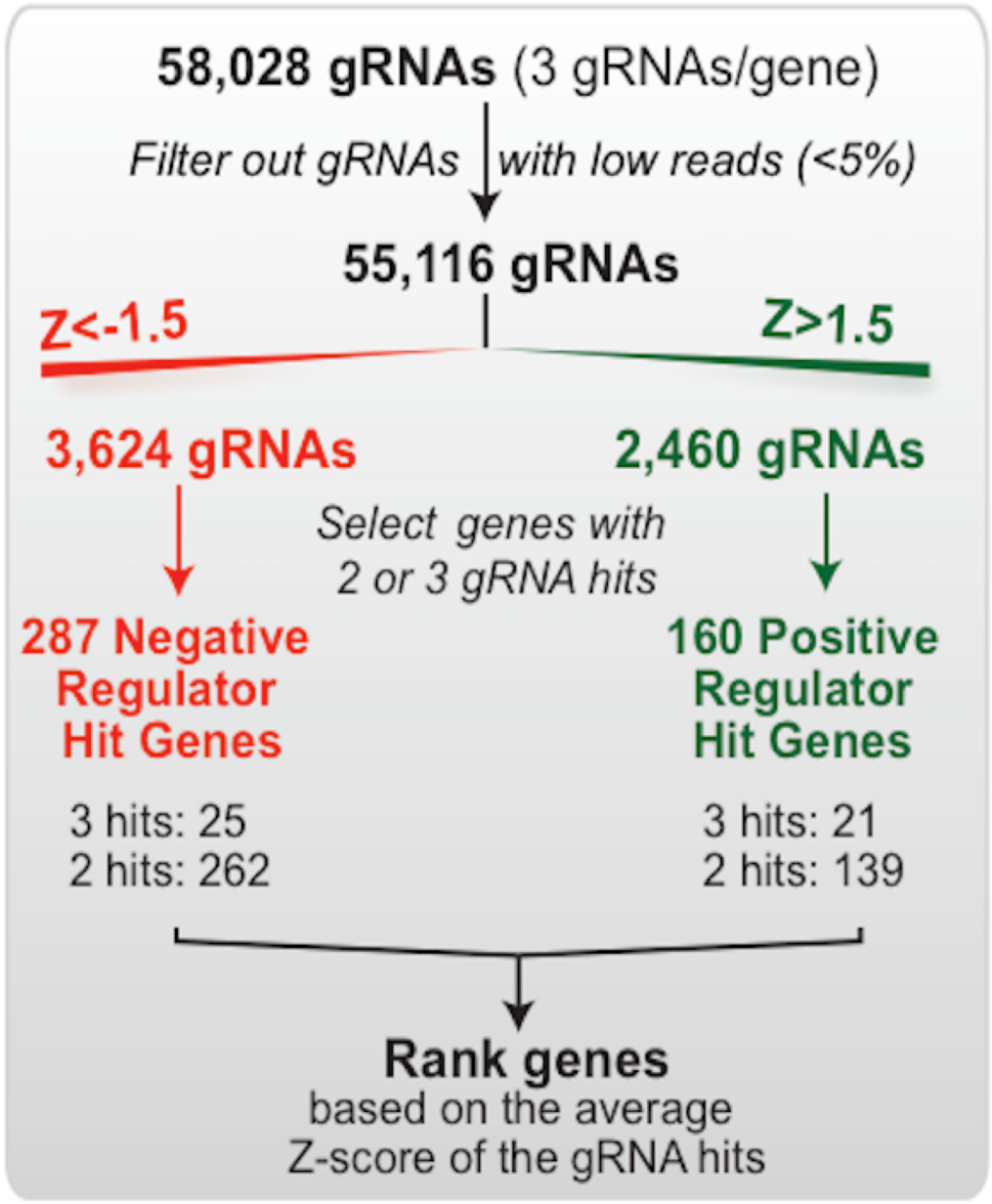
Wei Li, Han Xu, Tengfei Xiao, Le Cong, Michael I Love, Feng Zhang, Rafael A Irizarry, Jun S Liu, Myles Brown and X Shirley Liu





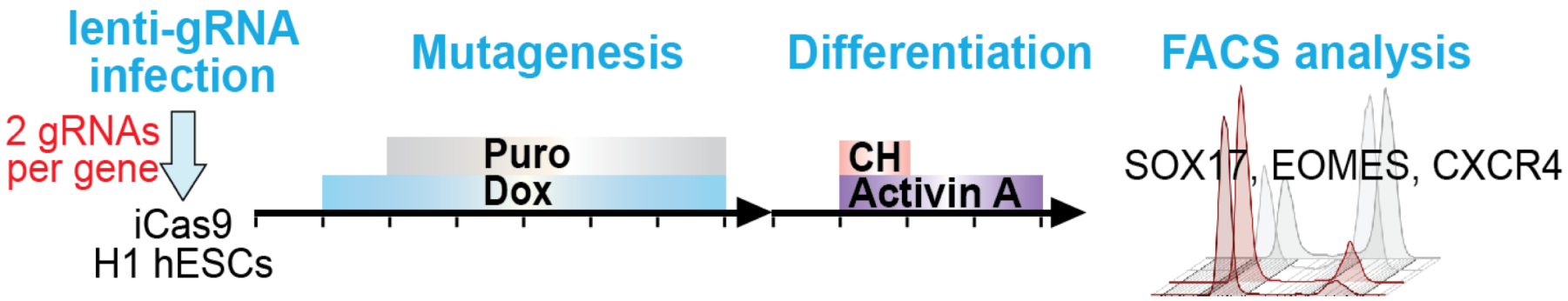
	Mean gRNA reads	Total reads
SOX17–	774	44.9 million
SOX17+	778	45.2 million

	Mean	S.D.
Fold change	-0.05	0.30



Z score and Robust Ranking Aggregation (RRA)

Hit validation (on genes with 2-3 gRNA hits)



- Tested 22 of the top 50 positive regulators (Z >= 2.22)

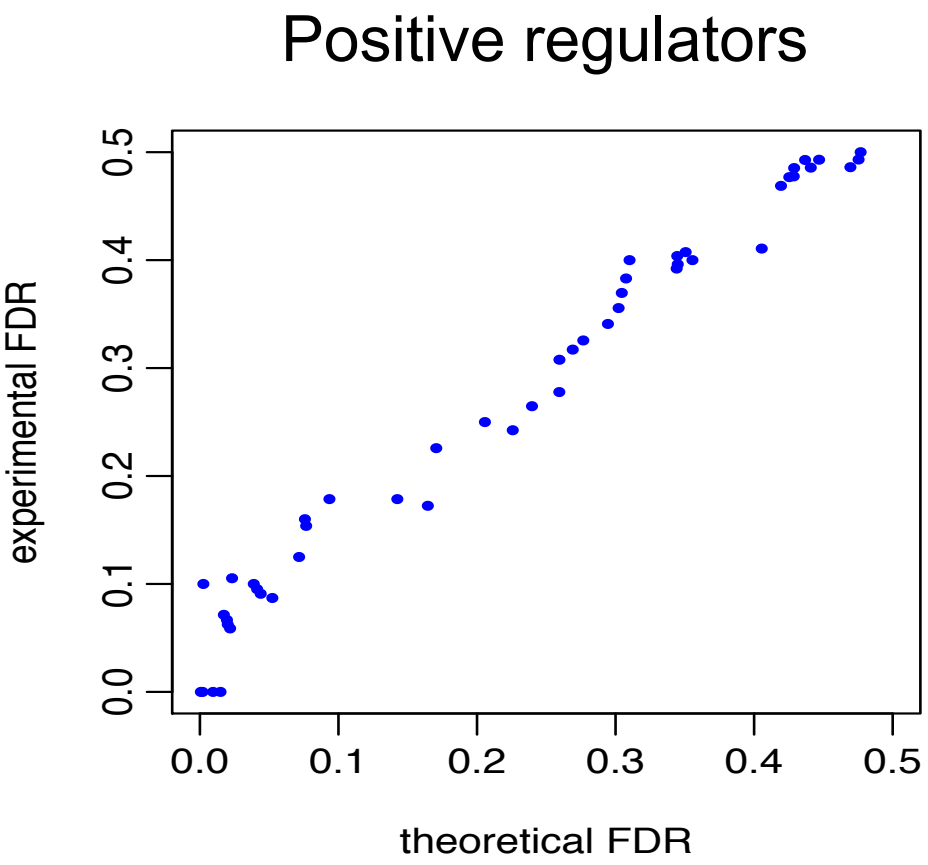
  2 CRISPRs were used per gene

- Validated 16 of the 22 tested

  (9 of the 16 are novel)

Li et al., unpublished

Using Brunello Library to validate the pooled lenti CRISPR Gecko library



Use the Brunello library screen as *experimental* FDR in order to validate the GeCKO *theoretical* FDR (false discovery rate)

Conclusions/Take-home messages

- Use of a CRISPR-Cas9 full genome lenti Gecko pooled screen allowed us to discover previously unknown ***positive and negative modulators*** of endodermal differentiation in addition to confirming several known players in this pathway
- Discovery of such targets will not only increase our understanding of the ***regulation of organogenesis*** but also create opportunities for intellectual property (IP) and potentially impact development and commercialization strategies in bringing forward new **cellular therapies** (which could be secretory or structural, re: tissue and organ repair)
- Gene knockout (KO) led to ***strong phenotypes*** which facilitated our detection and confirmation of hits

Key **Oncolytic Viruses** in Clinical Trials

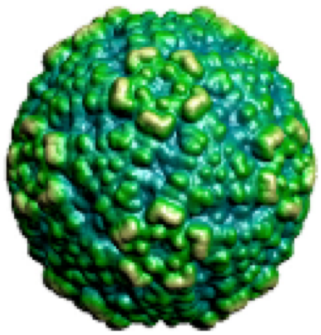
Table 3 | **Key oncolytic viruses in clinical trials**

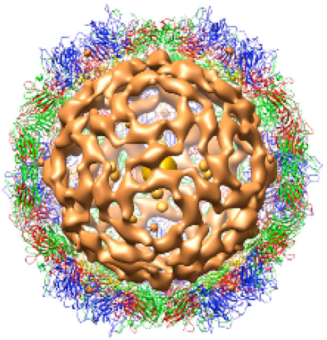
Virus	Manufacturer	Modification	Number of clinical trials			Cancers
			Phase I	Phase II	Phase III	
Adenovirus						
Onyx-015	Onyx Pharmaceuticals	Type 2/5 chimaera, E1B deletion	6	6	0	Head and neck cancer, pancreatic cancer, ovarian cancer, colorectal cancer, gliomas, lung metastases, and liver metastases
H101	Shanghai Sunwaybio	E1B deletion, partial E3 deletion	1	2	1	Squamous cell carcinoma and head and neck cancer
DNX-2401	DNAtrix	Δ24-RGD insertion	4	0	0	Glioblastoma, ovarian cancer
VCN-01	VCN Biosciences	PH20 hyaluronidase insertion	2	0	0	Pancreatic cancer
Colo-Ad1	PsiOxus Therapeutics	Chimeric Ad11/3 group B	1	2	0	Colon cancer, NSCLC, renal cancer, bladder cancer, and ovarian cancer
ProstAtak	Advantagene	TK insertion	4	1	1	Pancreatic cancer, lung cancer, breast cancer, mesothelioma, and prostate cancer
Oncos-102	Oncos Therapeutics	Δ24-RGD-GM-CSF insertion	1	0	0	Solid cancers
CG0070	Cold Genesys	GM-CSF and E3 deletion	1	1	1	Bladder cancer
Vaccinia virus						
Pexa-vac (JX-594)	Jennerex Biotherapeutics	GM-CSF insertion, TK disruption	7	6	0	Melanoma, liver cancer, colorectal cancer, breast cancer, and hepatocellular carcinoma
GL-ONC1	Genelux	TK disruption, haemagglutin disruption, F14.5L disruption	4	1	0	Lung cancer, head and neck cancer, and mesothelioma

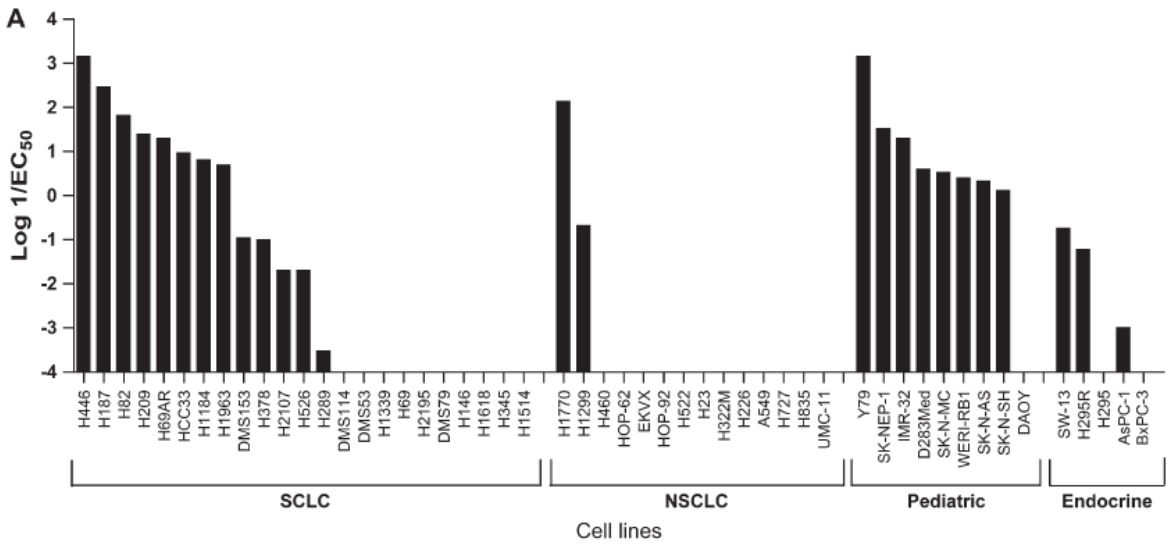
Kaufman, et al Nature Reviews 2015

Seneca Valley Virus (SVV) Infects Cancers with Neuroendocrine Features

Memorial Sloan-Kettering Cancer Center





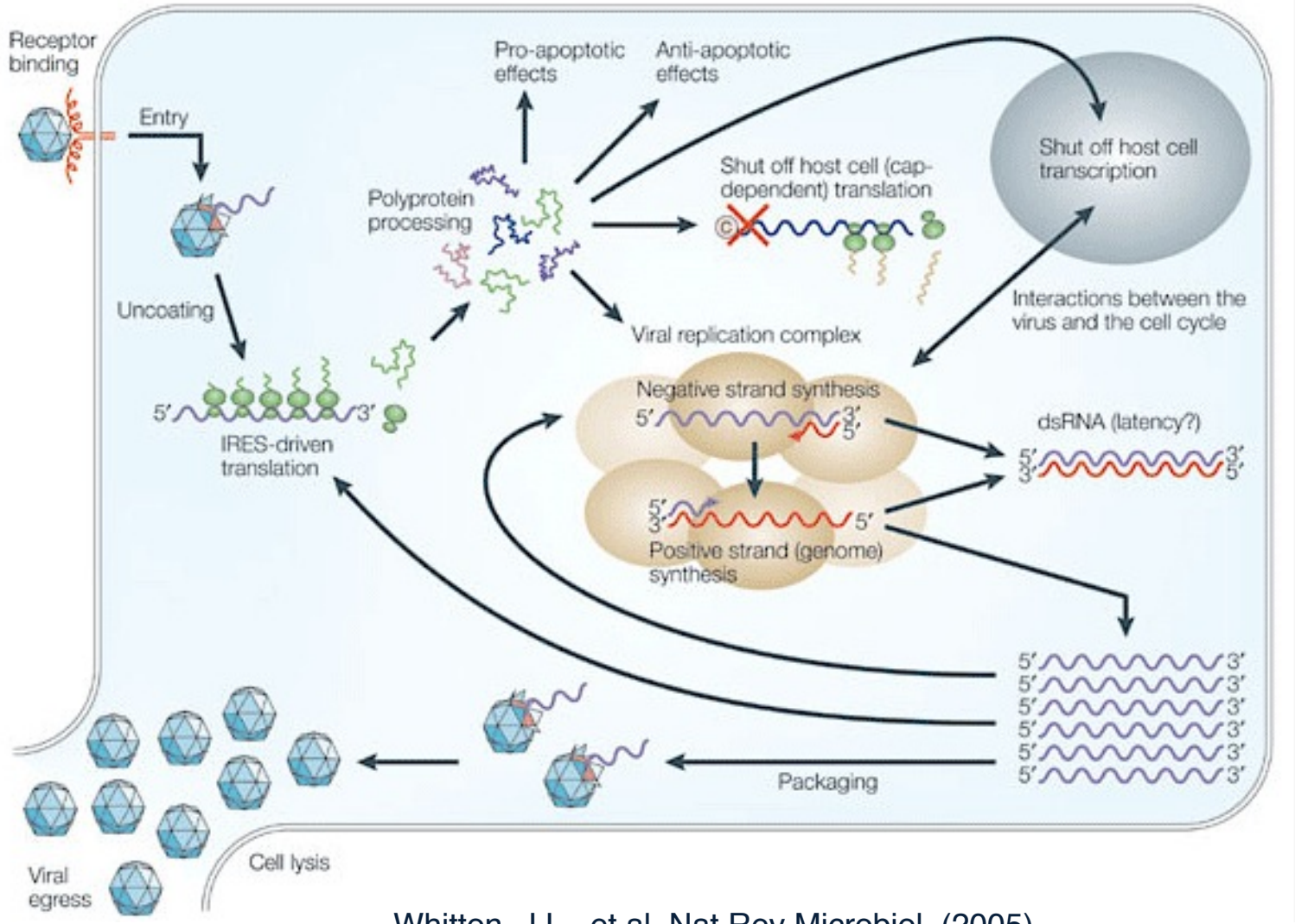


Family	Picornaviridae
Genus	*Senecavirus*
Nucleic Acid	+RNA
Genome Size	7.3 kb
Proteins	P1, 2C, 3C, 3D
Capsid Type	Icosahedral
Capsid	325 Å
Subunits	60
Protomers	VP1, VP2, VP3, VP4

Venkataraman et al., Structure (2008); Hales et al., Journal Gen Virology (2008); Reddy, P.S. et al. JNCI (2007)

Understanding Seneca Valley *oncolytic* virus (SVV) Biology

Memorial Sloan-Kettering Cancer Center



Whitton, J.L., et al. Nat Rev Microbiol. (2005)

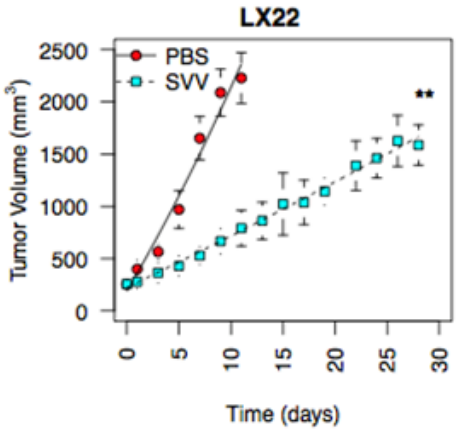
Seneca Valley Virus (SVV) Features

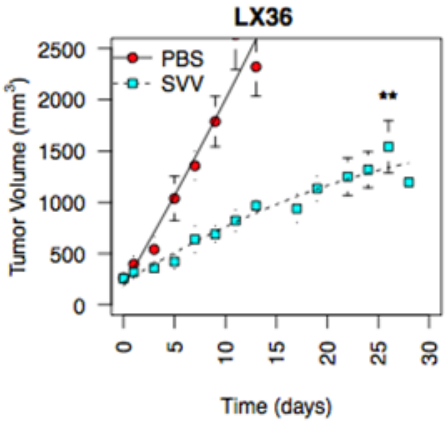
Memorial Sloan-Kettering Cancer Center

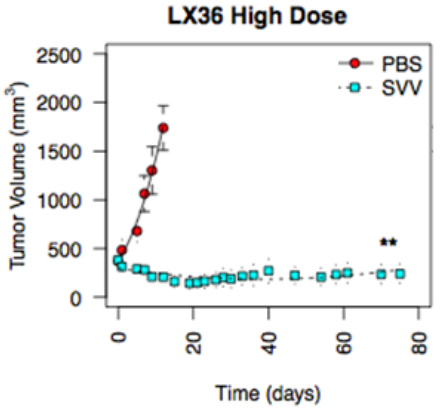
- Administer intravenously; does not integrate w/ host genome
- Replication competent (6-8 h life cycle), persists ~1 month
- No DNA stage; immunologically stable
- Systemically available
  - Not inactivated by blood components
  - Does not cause hemagglutination
  - Homes to the tumor through vasculature
  - Pre-existing antibodies are rare (low antigenicity risk)
- Selective
  - Greater than 10,000 fold higher potency in tumor compared to normal human tissues
  - Not known to cause disease in humans or animals

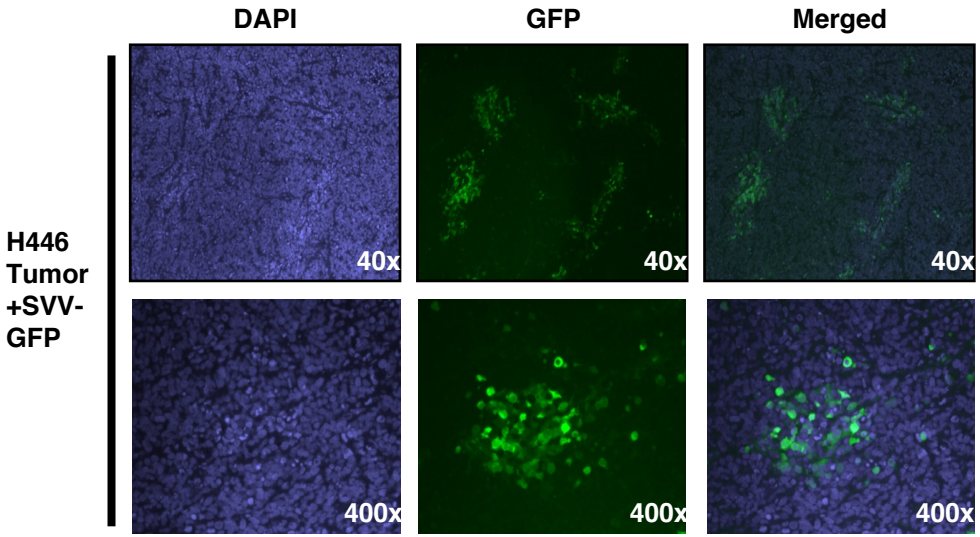
Selectivity and Efficacy of SVV *In Vivo*

Memorial Sloan-Kettering Cancer Center









Using patient-derived SCLC xenographs in immuno-compromised mouse hindflank (pockets of viral infection are evident)

Poirier, J.T. et al. J Gen Virol. (2012); Poirier J.T. et al JNCI (2013).

Neotropix -> Perceiver Pharma
Phase I Clinical Trial Results @ Johns Hopkins

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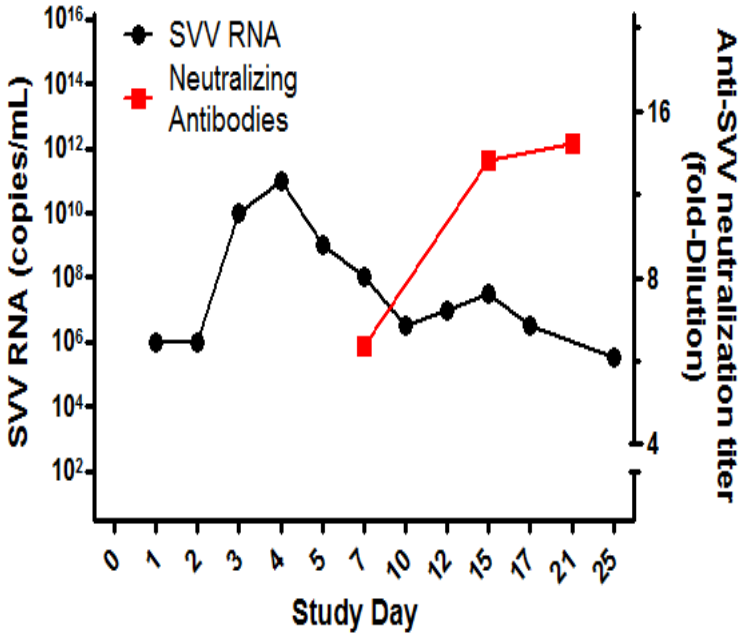
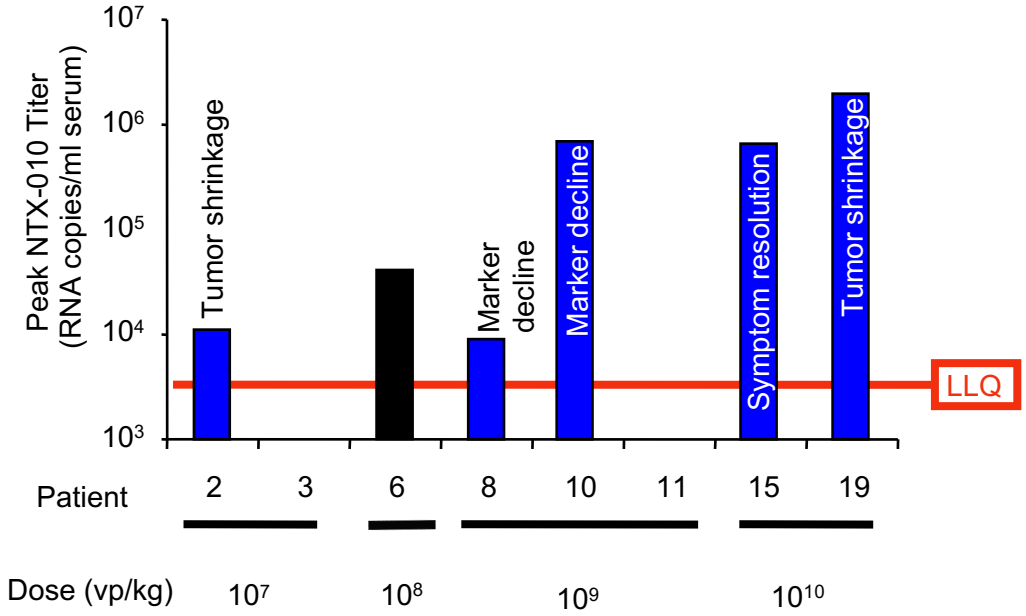
A.



The immune response is an important component of the antitumor effect but also a "double-edged sword".

Oncolytic viruses have increased specificity for cancer cells and environments where IFN responses are limited (less viral clearing)



Rudin, C.M., et al. Clin Cancer Res (2011)

Pooled CRISPR screen provides a breakthrough

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Note: All previous efforts to identify essential SVV host proteins, especially the surface receptor, failed!
These include:

- RNAi screens
- cDNA libraries from H446 (which is hypertriploid)
- Cell Surface Glycopeptide Capture

Possible Reasons for Failure:

- Low abundance receptor protein
- Incomplete knockdown of protein
- Multiple receptors/complex
- More than 1 factor may be needed for permissivity

Genome wide CRISPR Knockout (GeCKO) sgRNA Library

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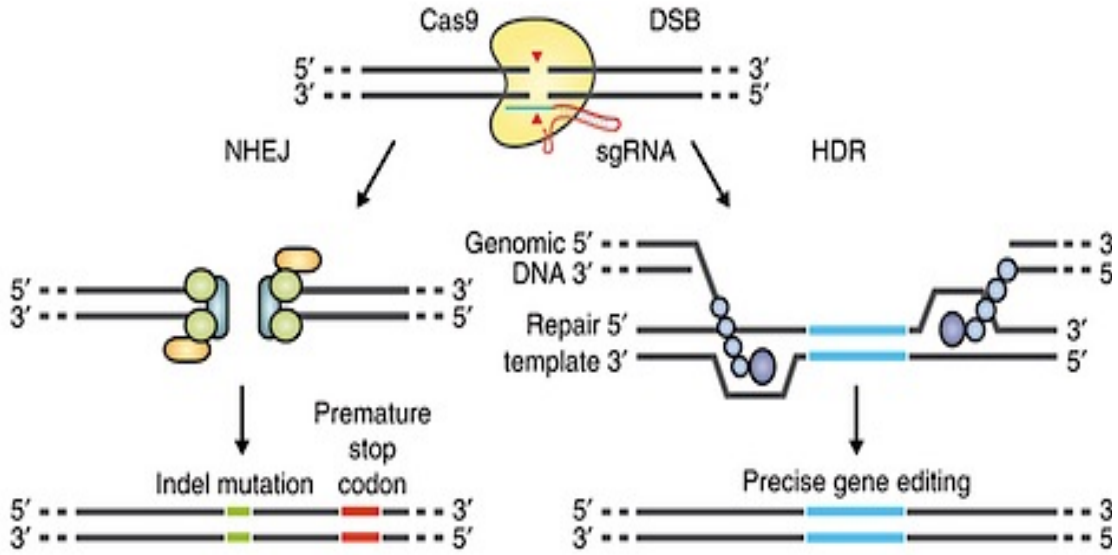


GeCKO v2.0 library specifications

	GeCKO v2 human library
Species	human
Number of genes targeted	19,050
Targeting constructs per gene	6 per gene (3 in Library A, 3 in Library B)
Number of miRNA targeted	1,864
Targeting constructs per miRNA	4 per miRNA
Control (non-targeting) sgRNAs	1,000
Total sgRNA constructs	122,411 (65,383 in Library A, 58,028 in Library B)
Viral plasmid vector	Single and dual vector: lentiCRISPR v2 and lentiGuide-Puro

PCR-amplified, maxi-prepped and HiSeq QC'd in the RNAi/ CRIPSR Core at Memorial Sloan Kettering

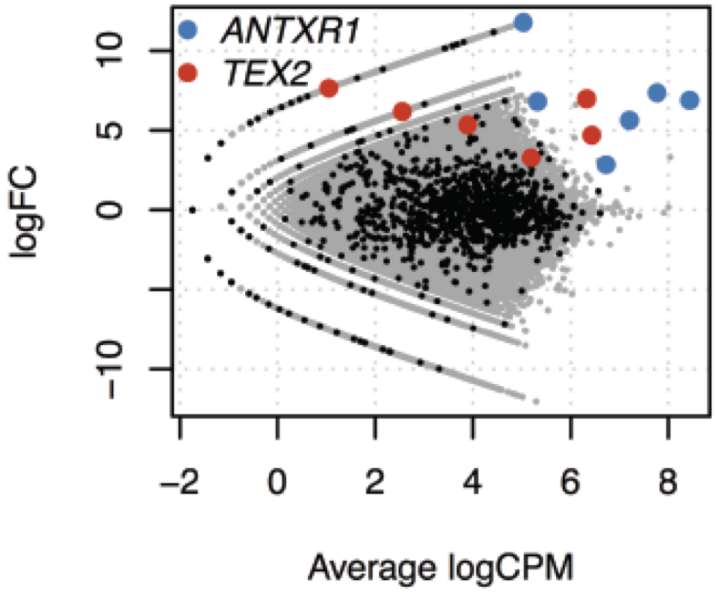
Ran, F.A. et al (2013) Nat Protoc.; Sanjana, N. et al. (2014) Nature Methods

GeCKO Screen HiSeq Results

Memorial Sloan-Kettering Cancer Center

HAP1

B



Black = non-targeting sgRNAs

H446

D

Gene Target	# of Unique sgRNAs	# of Clones	% Total Colonies
ANTXR1	3	23	92%
PPBP	1	6	24%
hsa-mir-548ah	1	6	24%
PLXNB2	1	5	20%
KCNJ1	1	3	12%
ZNF101	1	2	8%
LSMEM2	1	1	4%
TACO1	1	1	4%
ZDHHC7	1	1	4%

Lower scoring hits are likely to be passenger sgRNAs

What is ANTXR1?

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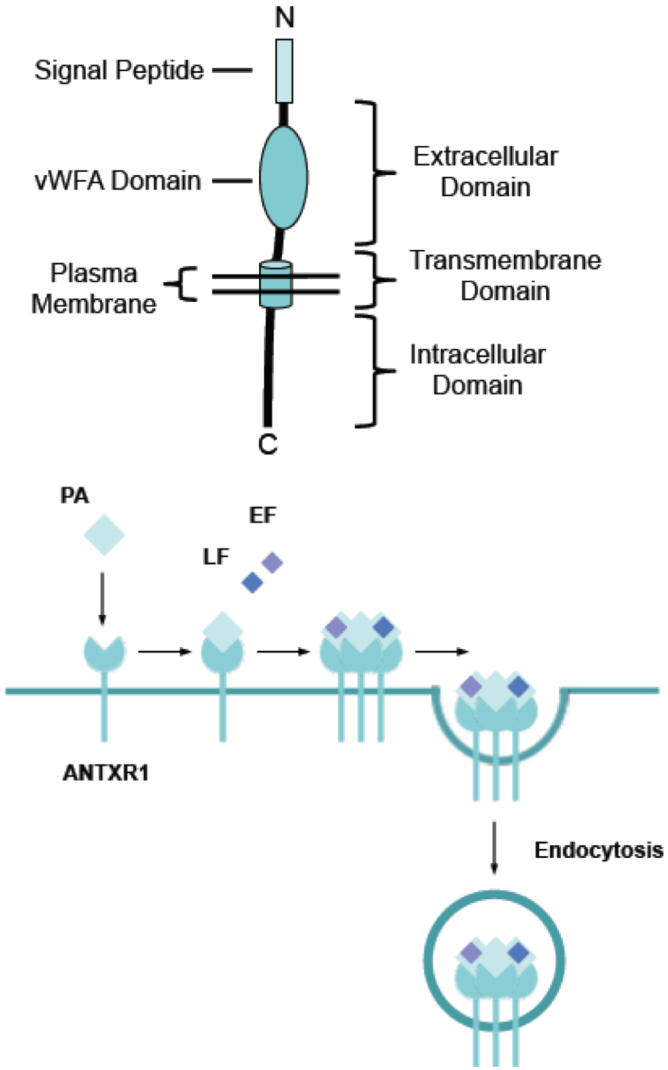

- *ANTXR1* encodes the Anthrax Toxin Receptor 1
- 1 of 2 cellular receptors for the anthrax toxin of *Bacillus anthracis*
- Single trans-membrane receptor
- Has been separately identified as **tumor endothelial marker 8** (TEM8), a protein over-expressed in tumor endothelial cells

Knockout of the *ANTXR1* gene leads to the *loss of* SVV permissivity

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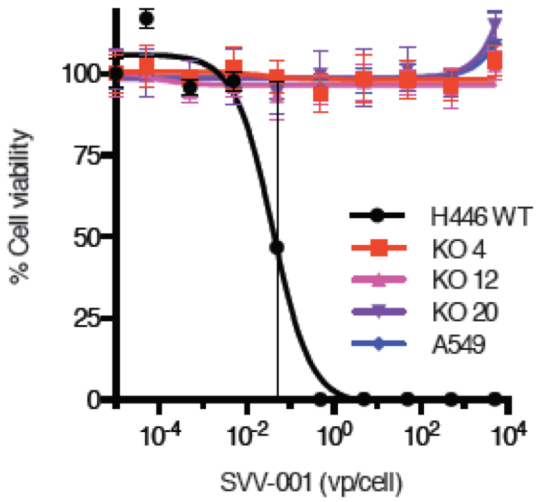
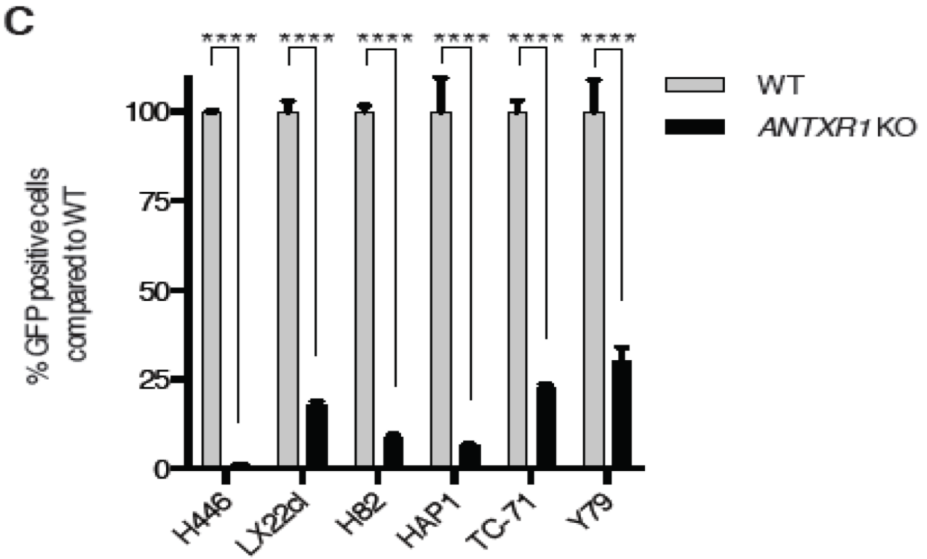
A

ANTXR1 KO	Mutation (Exon/Change)
4	Ex 2/ 1bp insertion Ex 2/ 4 bp insertion
12	Ex 2/ 1 bp insertion Ex 2/ 5 bp insertion
17	Ex 2/ 11 bp deletion
20	Ex 2/ 11 bp deletion Ex 2/ 4 bp insertion
24	Ex 2/ 11 bp deletion

B



C



- Examples of indels created ANTXR1 KO lines
- ANTXR1 KO leads to *loss of SVV permissivity* in:
  - SCLC lines
  - HAP1
  - Ewing's Sarcoma line (TC71)
  - Retinoblastoma line (Y79)

Re-expression of ANTXR1 protein
reconstitutes SVV permissivity in H446 KO cells

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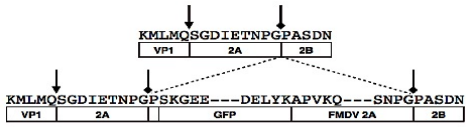
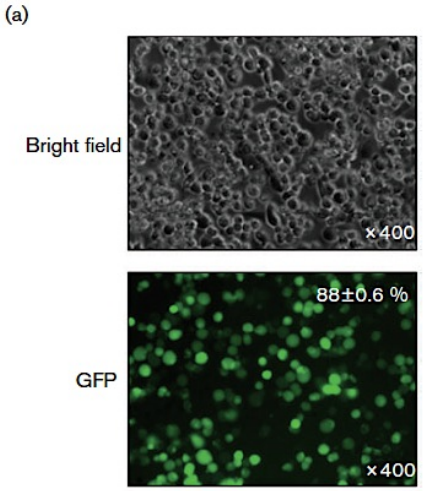
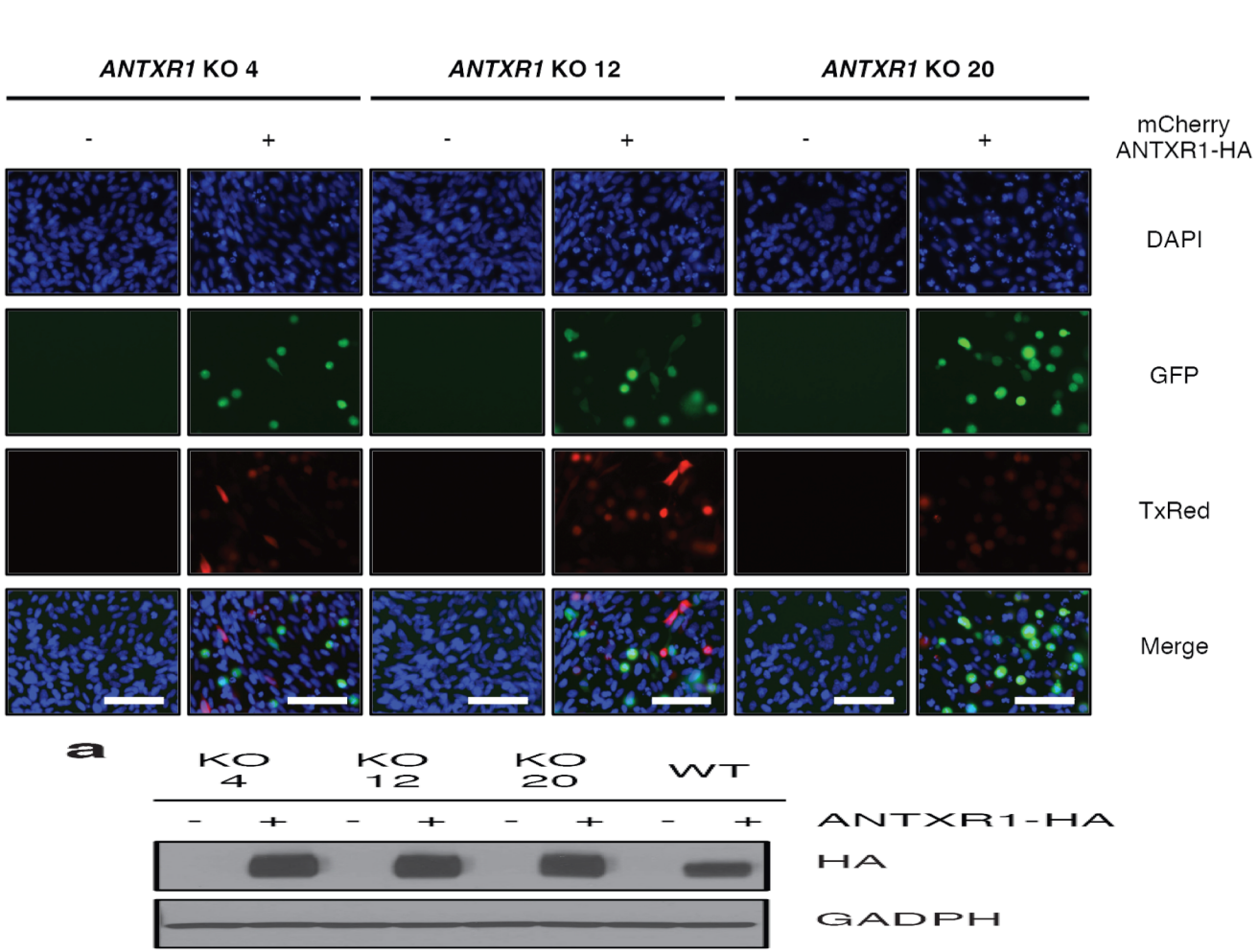
SVV-GFP







SVV Oncolytic Virus Permissivity is Dictated by Two Factors…

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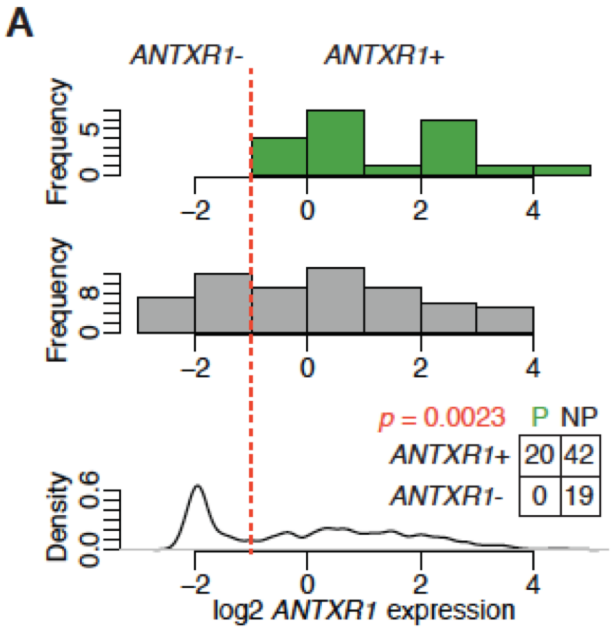

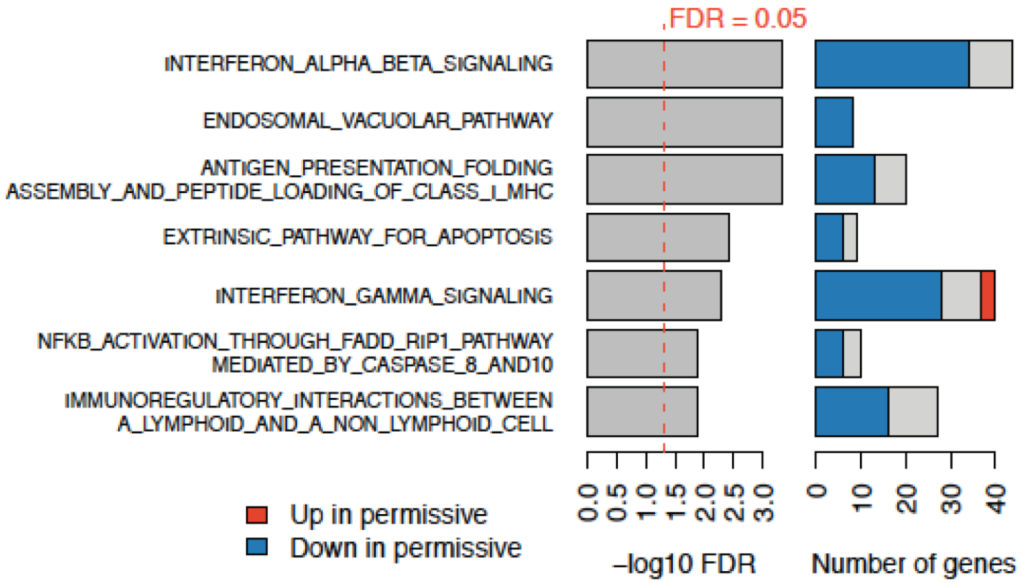

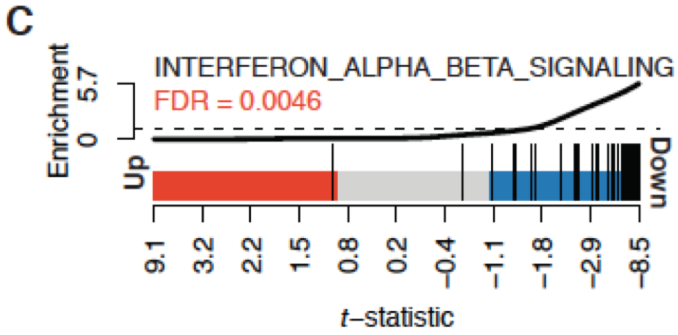

- All permissive cells express ANTXR1
- Permissive cells also have defects in innate immune response (IFN signaling)

Pooled CRISPR screen conclusions

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- The GES Core-generated GeCKO sgRNA library was utilized to perform two genome wide CRISPR Cas9 loss-of-function screens
- *ANTXR1* (TEM8) knockout was found to cause SVV resistance in both screens and was confirmed by secondary screens
- ANTXR1 expression was confirmed by LOF and GOF experiments to be *the major deteminant* for SVV permissivity
- Binding experiments confirmed SVV interacts directly with ANTXR1

The Journal of Clinical Investigation RESEARCH ARTICLE

Anthrax toxin receptor 1 is the cellular receptor for Seneca Valley virus

Linde A. Miles,[1] Laura N. Burga,[2] Eric E. Gardner,[1] Mihnea Bostina,[2,3] John T. Poirier,[1,4] and Charles M. Rudin[1,4,5]

2016

The CRISPR Gene Editing & Screening Core Facility is…

- Ralph Garippa, Ph.D. (Head)
- Alice Refermat, Ph.D.
- Yana Zorina, Ph.D.
- Sanjay Mehta
- Hsiu-Yu Liu
- Daniel Zakheim

- Samia Williams (admin)

- Scott Lowe, Ph.D. Founder, Director

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- Diane Tabarini, Robert Benezra
- Donna Gibson (MSK Medical Library)

Collaborators

- Danwei Huangfu, Qing Li
- John Poirier, Linde Miles

Granting mechanisms

- Beene Foundation, Agilent Thought Leader Award, Breast P01, CCSG