

# **CRISPR and Diagnostics: Challenges and Strategies for Understanding Results from Sequencing including Variants of Unknown Significance**

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UNIVERSITY OF UTAH  
HEALTH SCIENCES

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- 3.** Crispy Zebrafish (... CRISPR and Zebrafish)
- 4.** Perils and Successes with CRISPR Modeling
  - 1.** Neuromuscular Disease
  - 2.** The nav1 problem
  - 3.** Lou Gehrig's disease

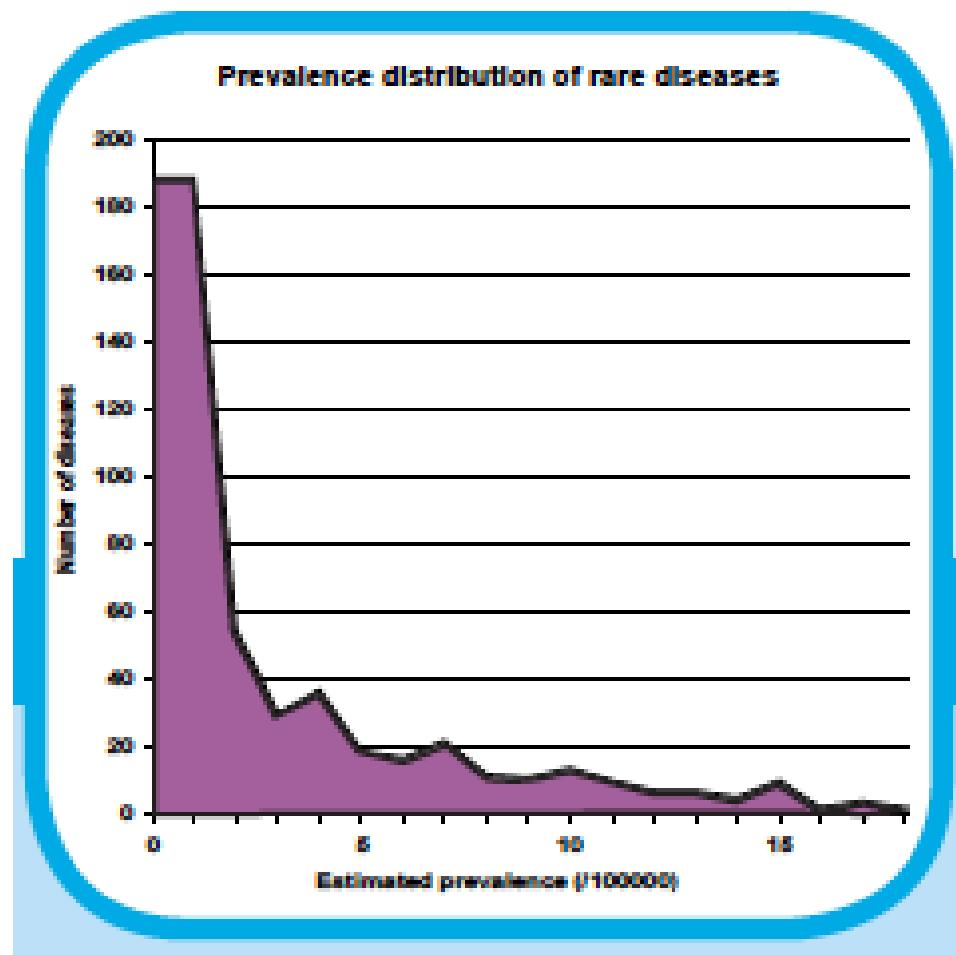
# Pediatric Neurology and the Diagnosis Problem

# Pediatric Neurological Diseases

- ~5% of all children
- Life-long morbidity; higher mortality
- Largest single group of healthcare costs for children
  - contribution to the “Diagnostic Odyssey”
    - Berry, Poduri, Bonkowsky et al., 2012, *PLoS Medicine*
- Known and unknown causes of disease
  - many rare diseases
  - for most patients the genetic cause has been unknown

# Rare and Orphan Diseases

- >2,025 rare diseases
- 25 million Americans affected
- orphan disease:  
“for which there is no reasonable expectation that the cost of developing and making available in the United States a drug for such disease or condition will [be] recovered from sales in the United States of such drug”



# Orphan Diseases and Leukodystrophies

## RARE DISEASES BY THE NUMBERS

A disease is defined as orphan in the U.S. when it affects fewer than

**200,000  
people**

There are approximately

**7,000**

**types** of rare diseases and disorders

**95%** of rare diseases have no FDA-approved drug treatment

**80%** of rare diseases are genetic in origin

Approximately **50%** of those affected by rare diseases are children

**30%** of children with a rare disease will not live to see their fifth birthday

**8:** Average number of physicians visits before diagnosis

**3:** Average number of misdiagnoses

**7+ years:** Average time until diagnosis



SOURCES: National Organization for Rare Diseases, Global Genes Project

# What is an undiagnosed disease?

- A disease that has not been diagnosed because the correct test has not yet been performed
  - rare disease
  - atypical presentation of a more common disease
- A disease that has not been diagnosed because we didn't know the disease existed
  - majority of undiagnosed diseases are neurologic

# Why does diagnosis matter?

- Cure
- Therapy/Treatment
- Clinical Trials
- Natural history studies
- Prognosis for family
- Genetic counseling
- Genetic and biochemical pathways of disease

# How good are we at diagnosis?

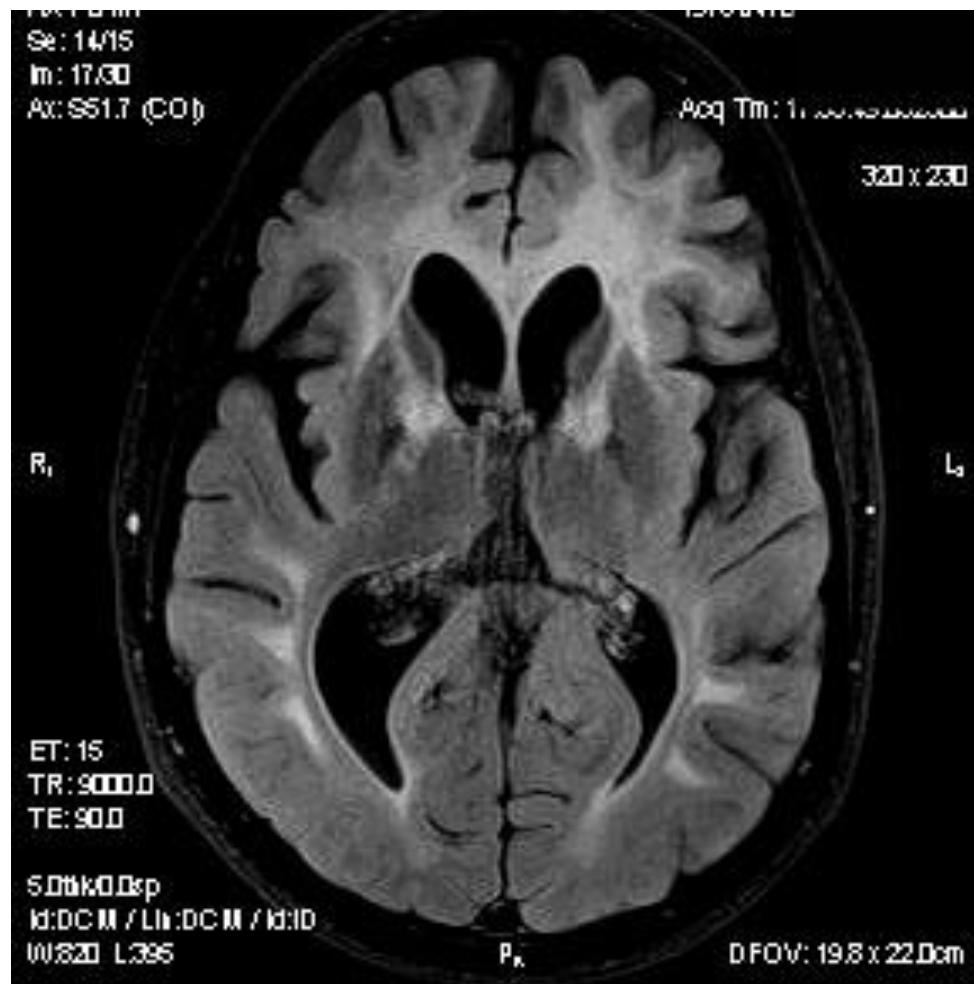
## Pediatric Neurology

- MRI: 20% diagnosis
- CGH microarray: 10%
- NGS (Next-Generation Sequencing): 40%

# Leukodystrophy

## ■ Leukodystrophy:

- Genetic
- Involvement of white matter (myelin)
  - Not secondary to a different etiology (trauma, prematurity, etc.)

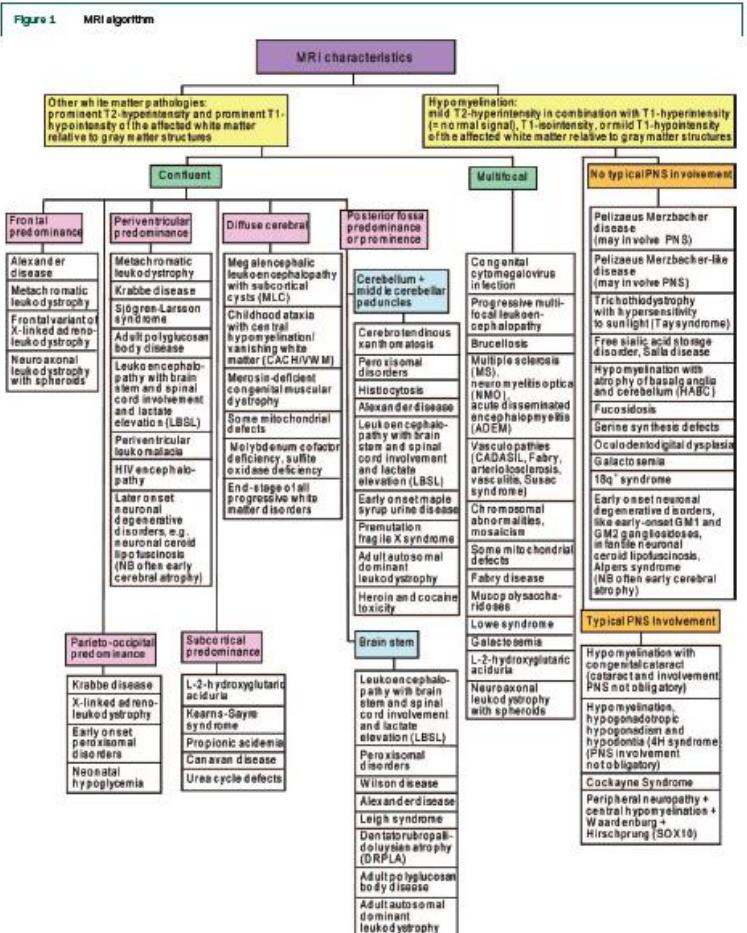


# What is a Leukodystrophy?

- Three types:
  - Hypomyelination
  - Dysmyelination
  - Demyelination
- 30 canonical genes, >700 total genes
- Diagnosis rates ~50%

# Leukodystrophy Problems

- Causes of leukodystrophies not known
  - How to diagnose unknown
  - No treatments



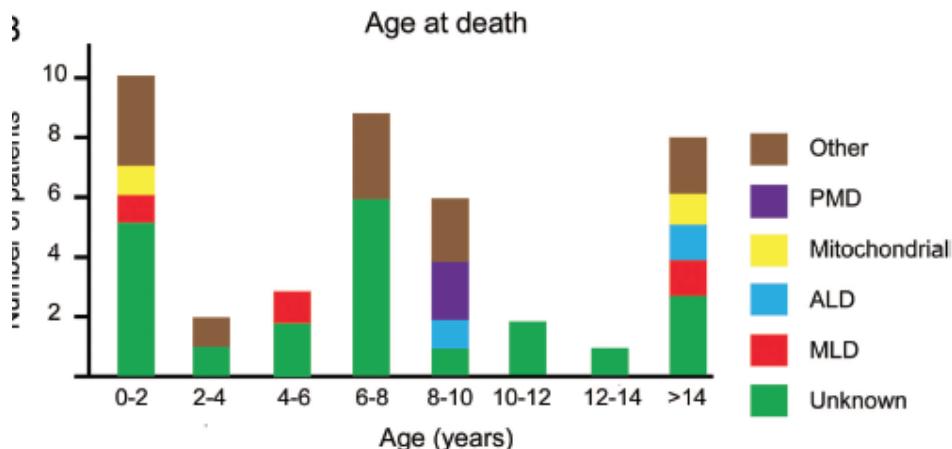


# **WESTERN LEUKODYSTROPHY PROJECT**

# The Burden of Leukodystrophies

**Table 2** Death, neurologic features, and costs in the leukodystrophy cohort<sup>a</sup>

Outcomes	Values
Death, n (%)	42 (34)
Average age at death, y	8.2
Epilepsy, n (%)	60 (49)
Average age at onset, y	4.0
Developmental regression, n (%)	39 (32)
Feeding tube, n (%)	53 (43)
Costs	
Total cohort cost	\$14,315,919
Average yearly cost/patient	\$22,579



# Diagnosis: Costs and NGS (Next-Generation Sequencing)

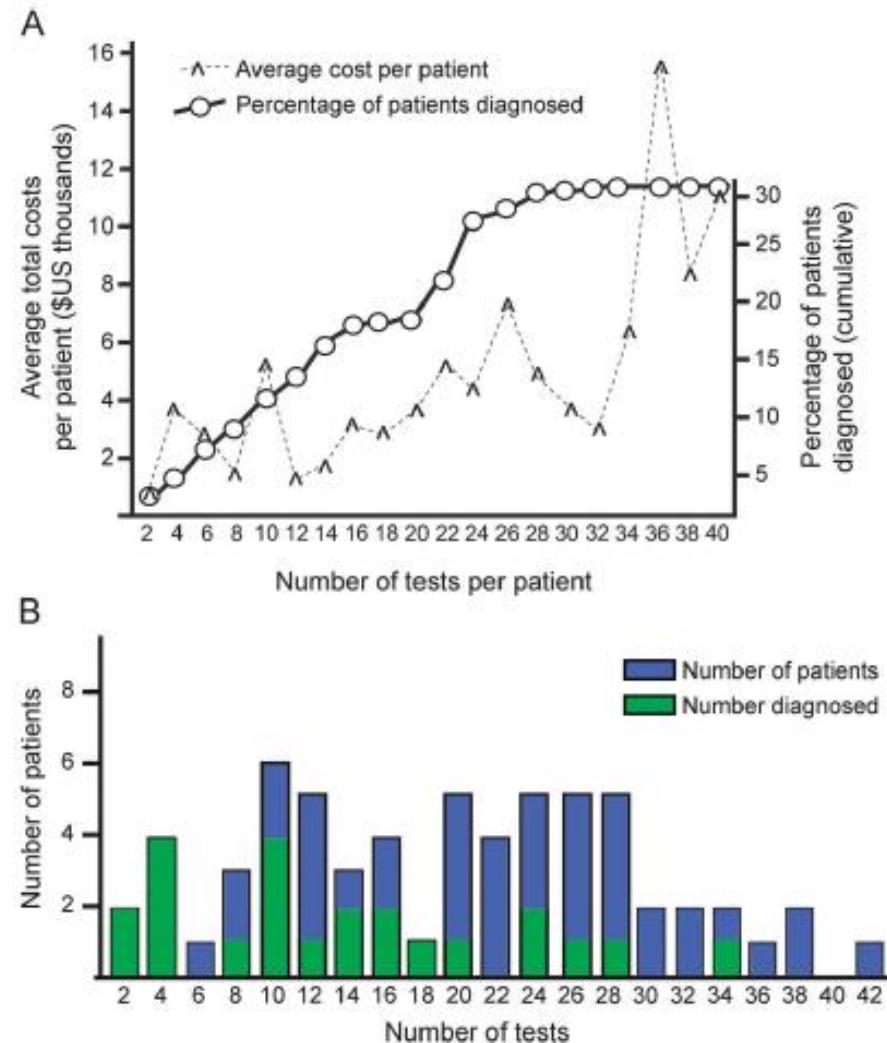
# The Diagnostic Odyssey

Hypotheses:

1. costs are substantial.
2. NGS will help.

# 1. Costs are substantial

- False
- Average costs of \$4209/patient
  - Compared to average healthcare costs of \$107,000/patient
- Conclusion: *reaching a diagnosis is not the primary driver of costs*



## 2. NGS will help

- True
- Charges for the entire cohort= \$538,053
- If NGS had been performed instead=  
\$371,200
  - and equal or better diagnosis rate
- Conclusion: *Use NGS early*

Richards et al., 2015, Neurology

Richards et al., 2015, Am J Med Genetics

# Next Generation Sequencing: NGS

- NGS has revolutionized diagnosis
  - Sequencing technology is on the time-scale of hours/days
    - Interpretation is weeks to months
- But accompanying limitations:
  - sequencing informatics bottleneck
  - ***biology bottleneck of variants***
    - each individual has ~74 germline de novo mutations
  - the spectre of non-coding variants
  - the role of somatic mutations

# **Diagnosis: Today!**

Two Steps:

**1. Test treatable disorders**

Either:

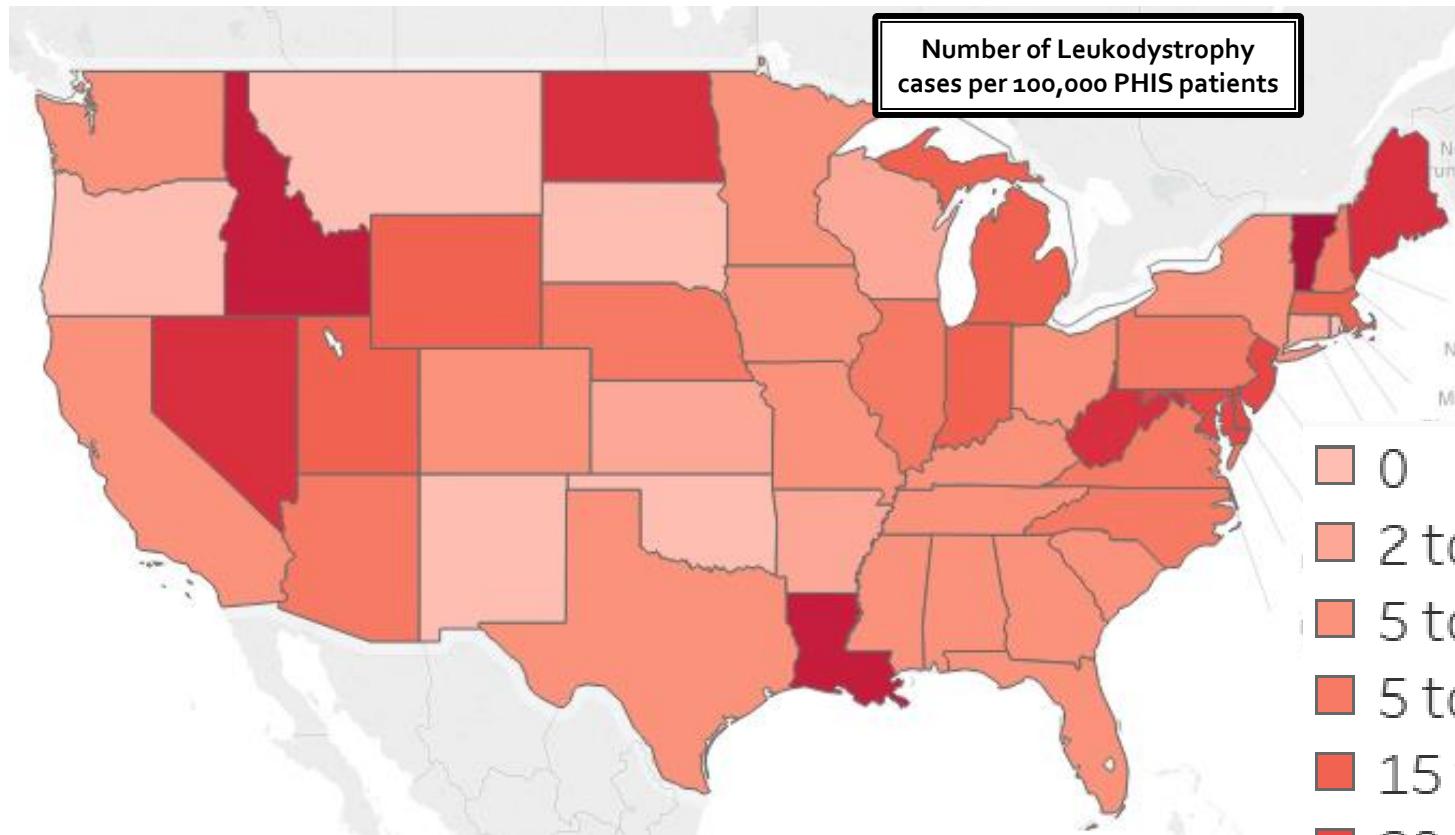
Leukocyte Lysosomal Enzymes and  
Serum Very Long Chain Fatty Acids

*or*

Rapid Whole Exome

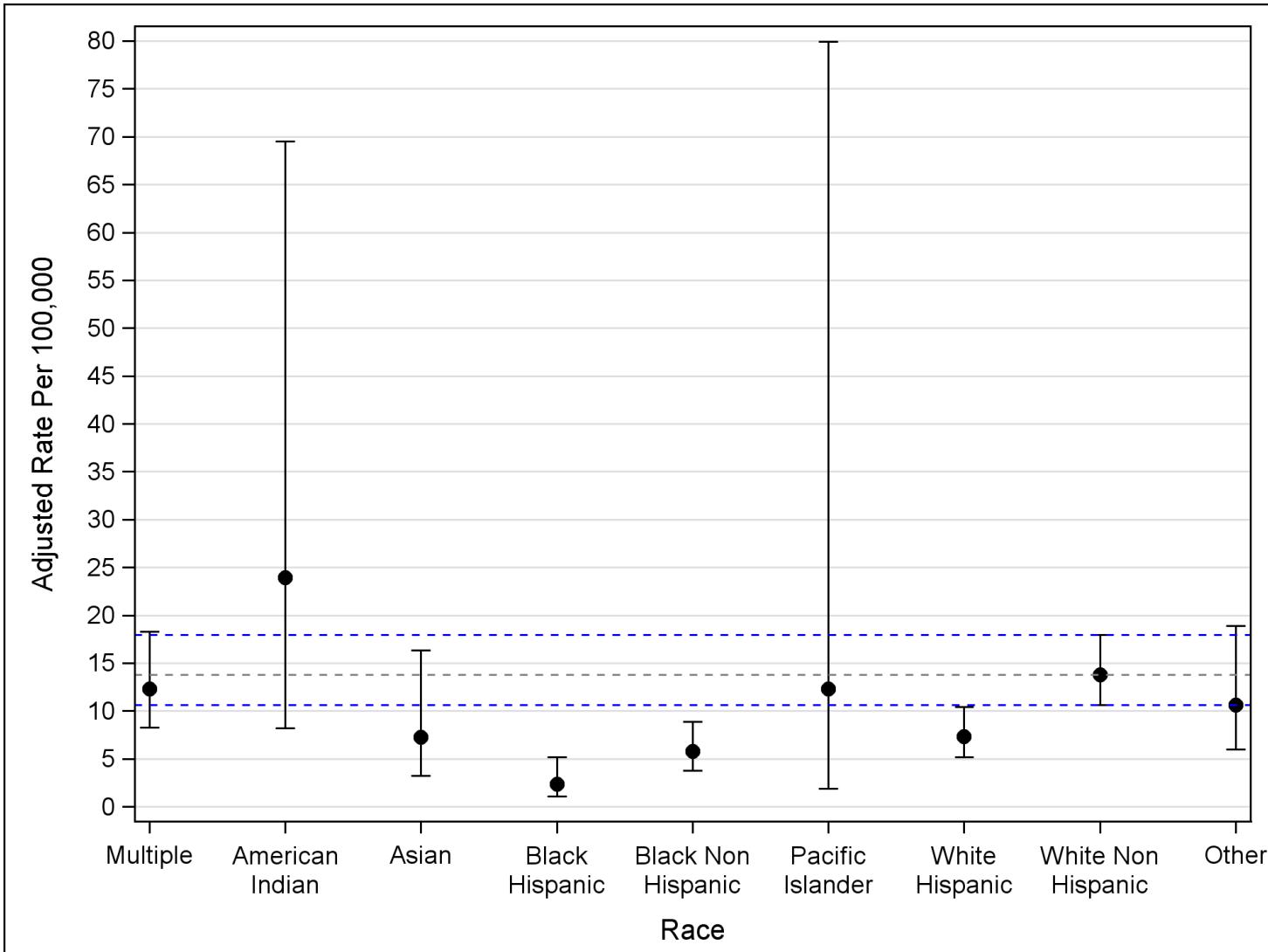
**2. Whole exome/genome or  
leukodystrophy gene panel**

# Diagnosis Disparities- a role for NGS?

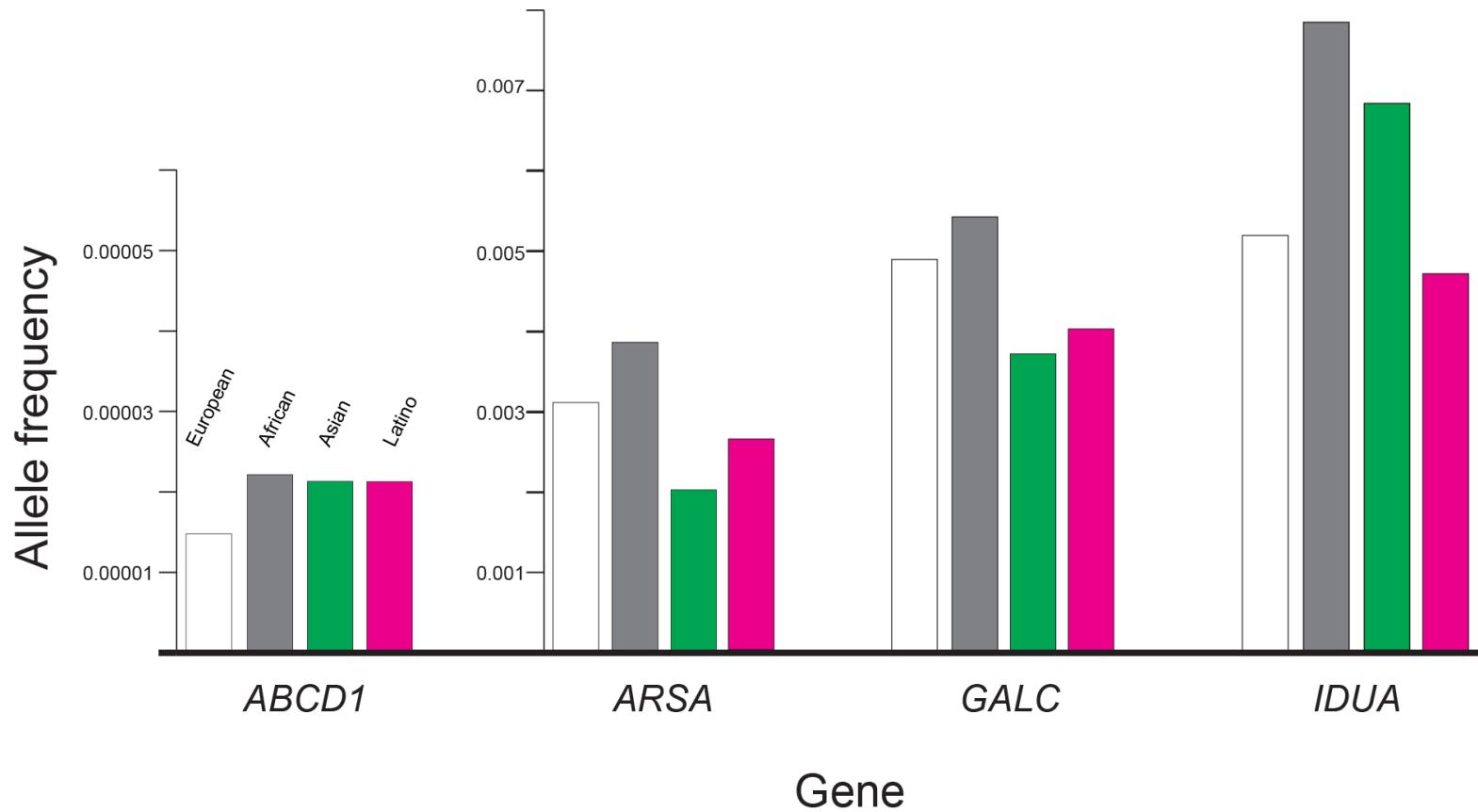


- 0
- 2 to 5
- 5 to 10
- 5 to 15
- 15 to 20
- 20 to 30
- 50 to 100
- 100+
- 300+

# Diagnosis rates are >50% lower in some racial groups



# No evidence for genetic



# Conclusions

- NGS diagnosis is less expensive
  - Than traditional diagnosis
  - Than clinical care
    - The Diagnostic Odyssey can be finite
- NGS algorithms for diagnosis should be developed
- Consider NGS to reduce diagnosis disparities

# **Crispy Zebrafish**

## **(CRISPR and Zebrafish)**

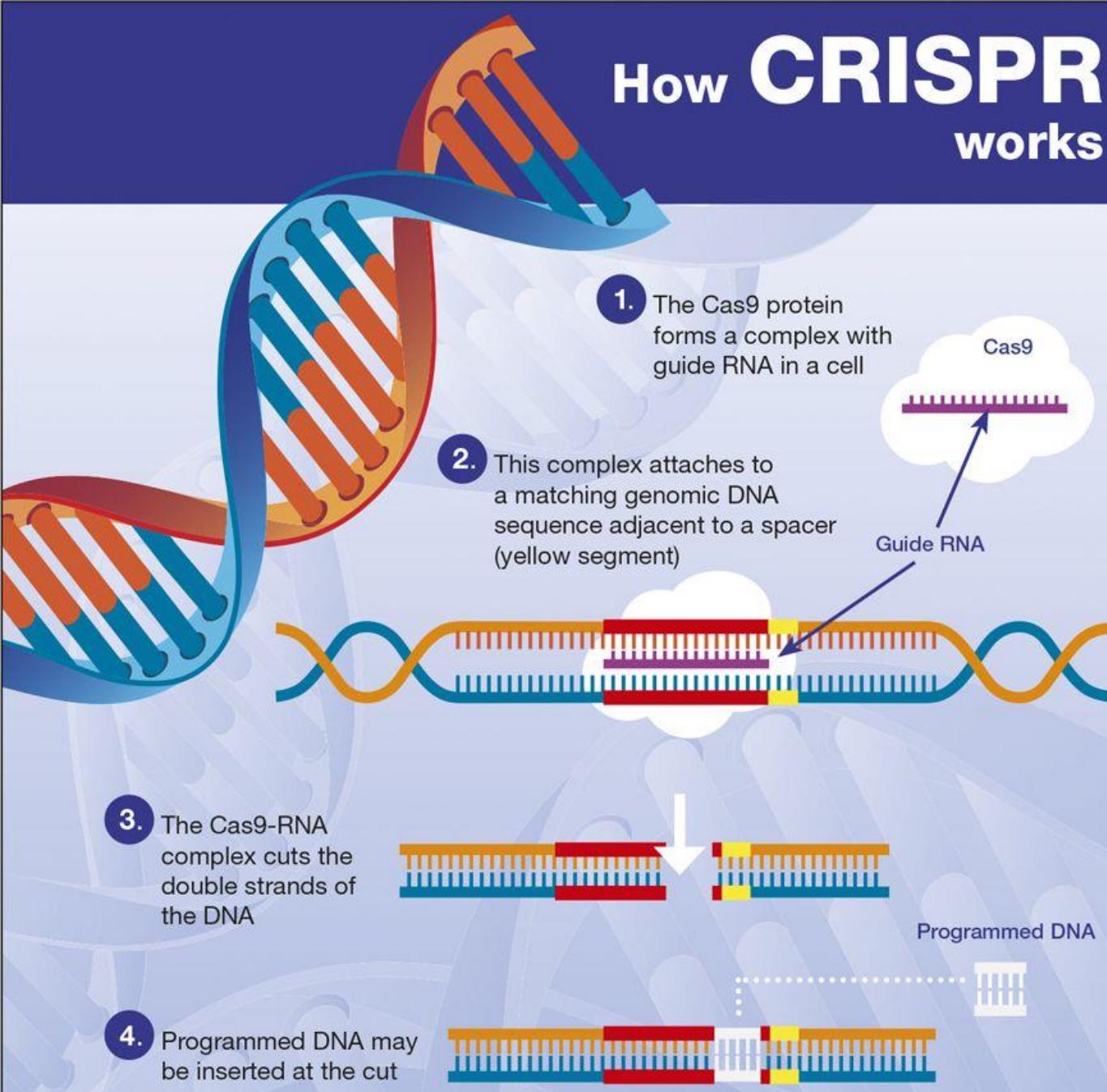
# CRISPR

- CRISPR is the most recent and most successful of genome editing techniques
  - ZFN (zinc-finger nucleases)
  - TALENs (transcription activator-like effector nucleases)
- ZFNs and TALENs require customization to efficiently target a sequence, and are more costly and difficult to develop for each target

# CRISPR mechanics

- CRISPR/Cas system is a prokaryotic (bacterial) “immune” system to attack foreign DNA
  - CRISPR:  
Clustered Regularly Interspaced Short Palindromic Repeats
  - Cas: CRISPR-associated system
    - Cas9: an RNA-guided DNA endonuclease
- Synthetic gRNA (guide RNA) matches a sequence in the target, and then guides the Cas9 system over to cut at that locus

# How CRISPR works

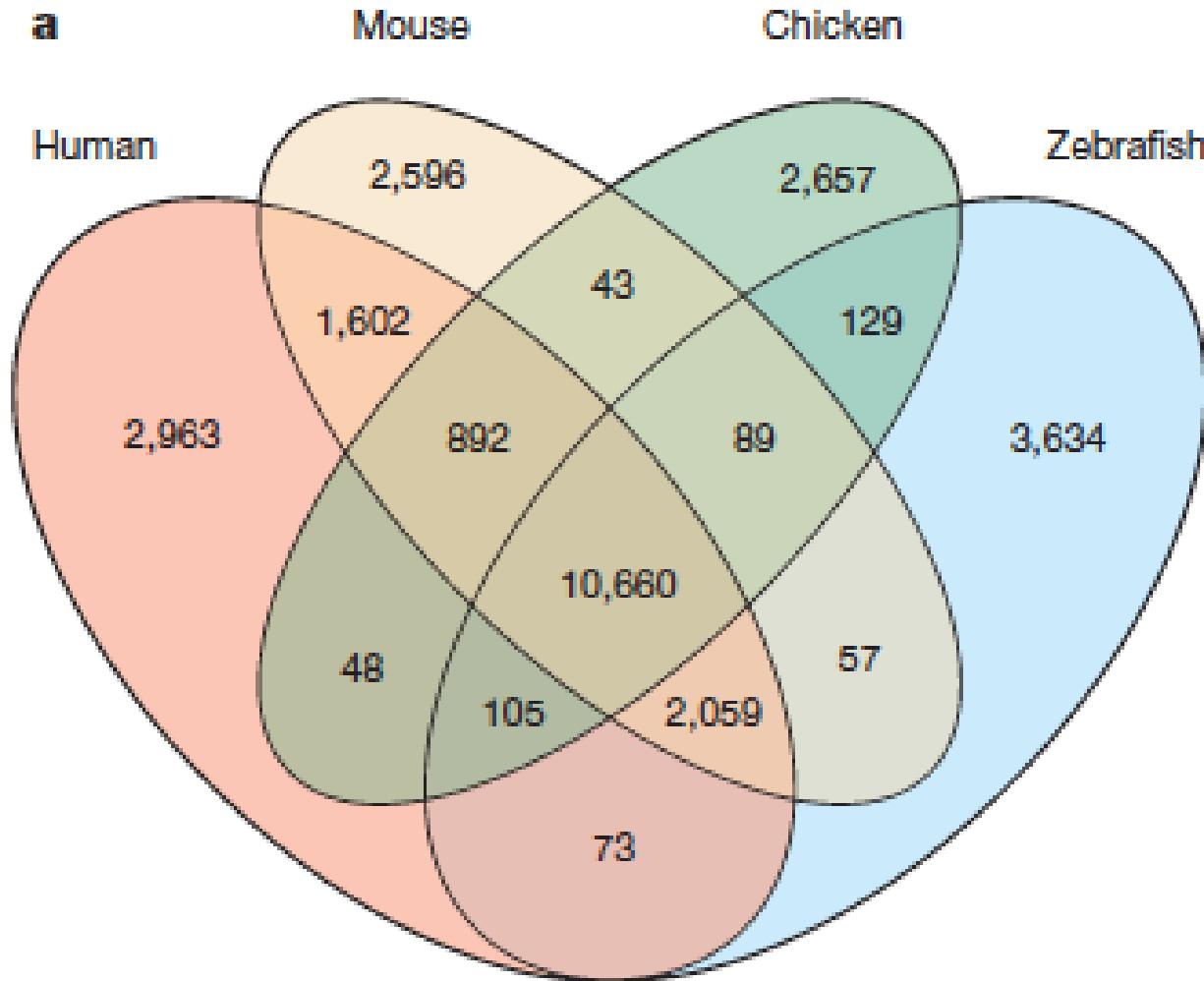


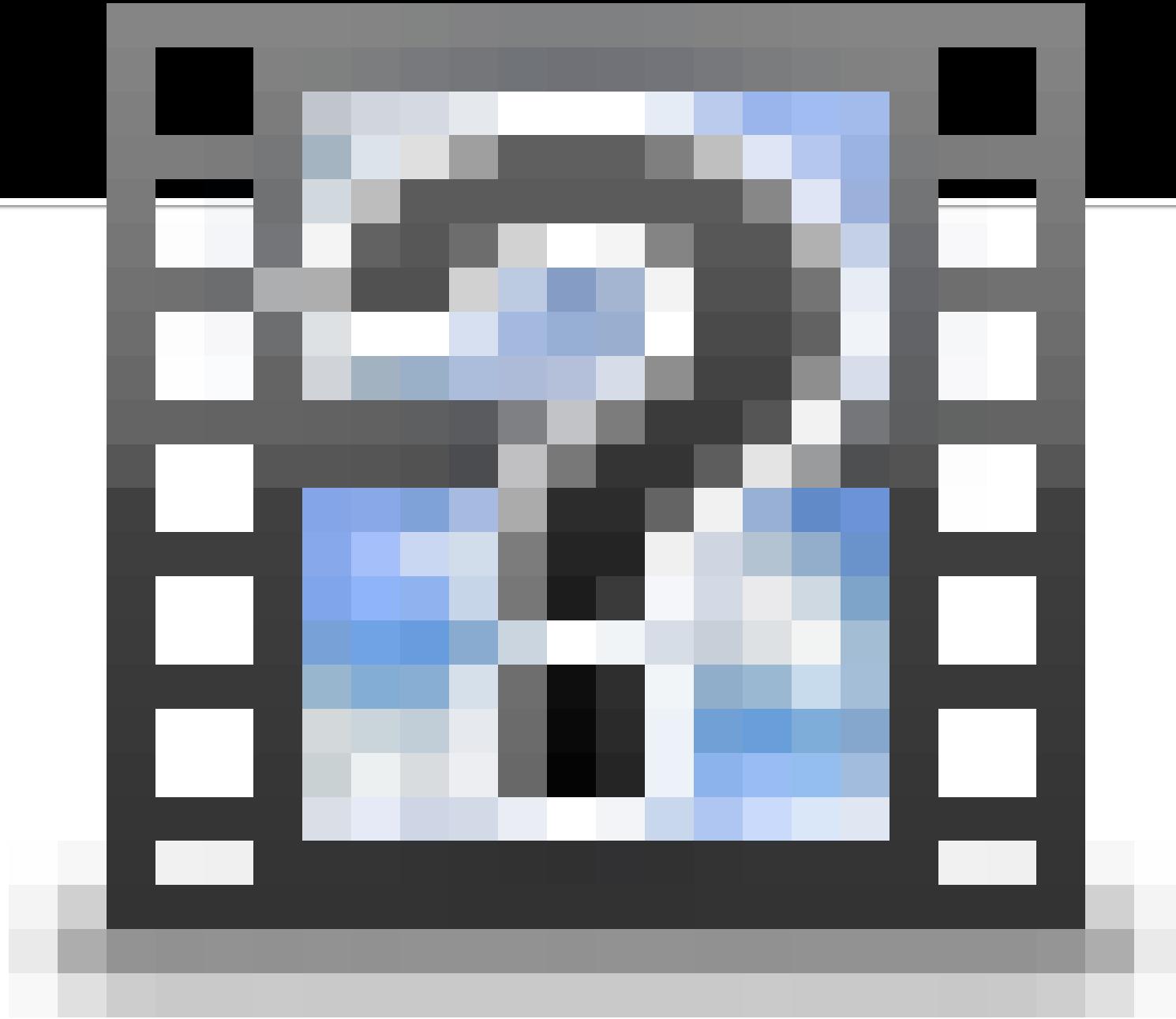
# Zebrafish as a Model Organism



1. Vertebrate
2. Conserved genes
3. Rapid development
4. Inexpensive

# Zebrafish and Human Genes are Conserved





# Using Model Systems

## Genomic responses in mouse models poorly mimic human inflammatory diseases

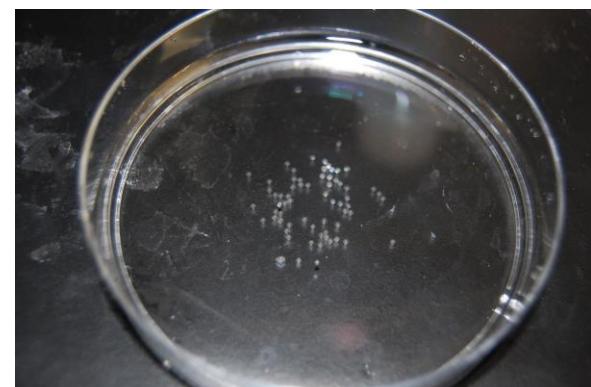
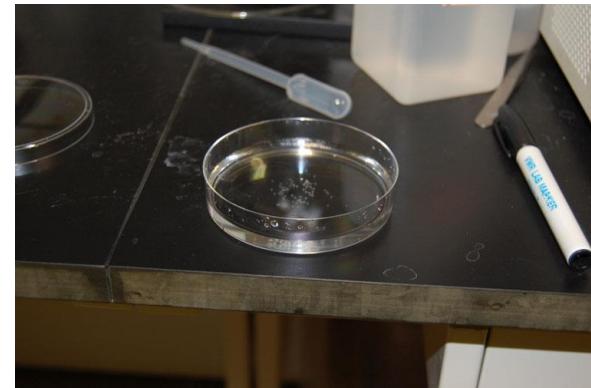
Junhee Seok<sup>a,1</sup>, H. Shaw Warren<sup>b,1</sup>, Alex G. Cuenca<sup>c,1</sup>, Michael N. Mindrinos<sup>a</sup>, Henry V. Baker<sup>c</sup>, Weihong Xu<sup>a</sup>, Daniel R. Richards<sup>d</sup>, Grace P. McDonald-Smith<sup>e</sup>, Hong Gao<sup>a</sup>, Laura Hennessy<sup>f</sup>, Celeste C. Finnerty<sup>g</sup>, Cecilia M. López<sup>c</sup>, Shari Honari<sup>f</sup>, Ernest E. Moore<sup>h</sup>, Joseph P. Minei<sup>i</sup>, Joseph Cuschieri<sup>j</sup>, Paul E. Bankey<sup>k</sup>, Jeffrey L. Johnson<sup>h</sup>, Jason Sperry<sup>l</sup>, Avery B. Nathens<sup>m</sup>, Timothy R. Billiar<sup>l</sup>, Michael A. West<sup>n</sup>, Marc G. Jeschke<sup>o</sup>, Matthew B. Klein<sup>j</sup>, Richard L. Gamelli<sup>p</sup>, Nicole S. Gibran<sup>j</sup>, Bernard H. Brownstein<sup>q</sup>, Carol Miller-Graziano<sup>k</sup>, Steve E. Calvano<sup>r</sup>, Philip H. Mason<sup>e</sup>, J. Perren Cobb<sup>s</sup>, Laurence G. Rahme<sup>t</sup>, Stephen F. Lowry<sup>r,2</sup>, Ronald V. Maier<sup>j</sup>, Lyle L. Moldawer<sup>c</sup>, David N. Herndon<sup>g</sup>, Ronald W. Davis<sup>a,3</sup>, Wenzhong Xiao<sup>a,t,3</sup>, Ronald G. Tompkins<sup>t,3</sup>, and the Inflammation and Host Response to Injury, Large Scale Collaborative Research Program<sup>4</sup>



Among genes changed significantly in humans, the murine orthologs are close to random in matching their human counterparts (e.g.,  $R^2$  between 0.0 and 0.1)

# Economy of scale

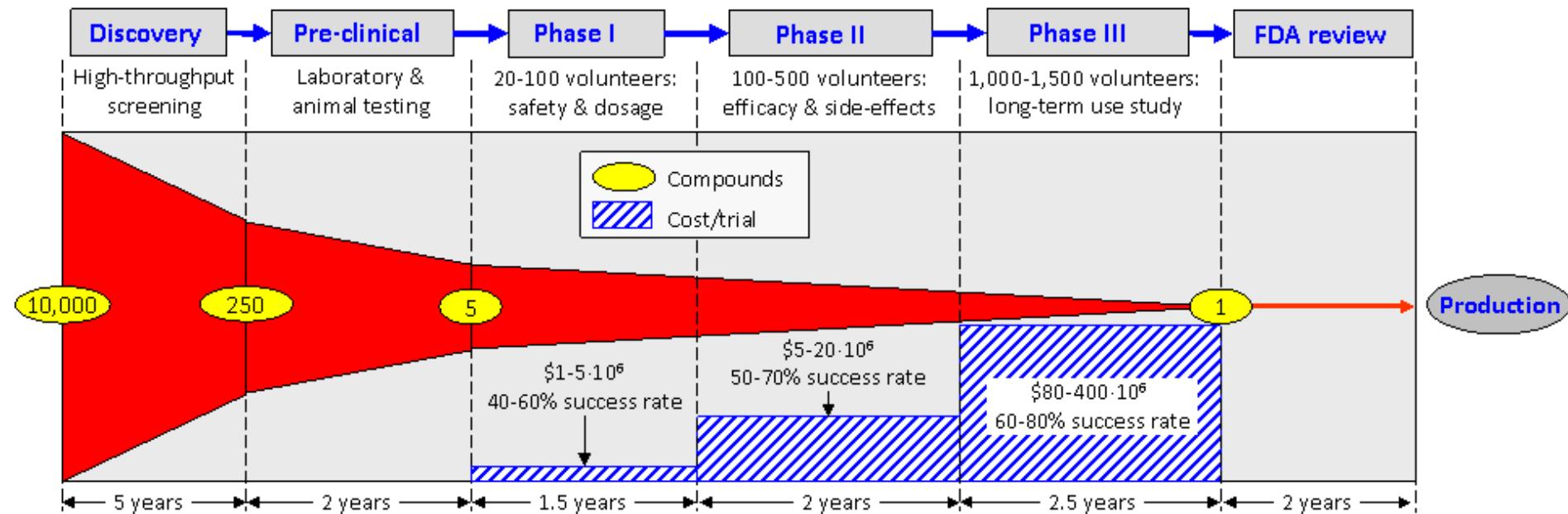
- Analyze 1000s of animals per day
- 1000s of tanks in a facility
- Generation time: 8 weeks



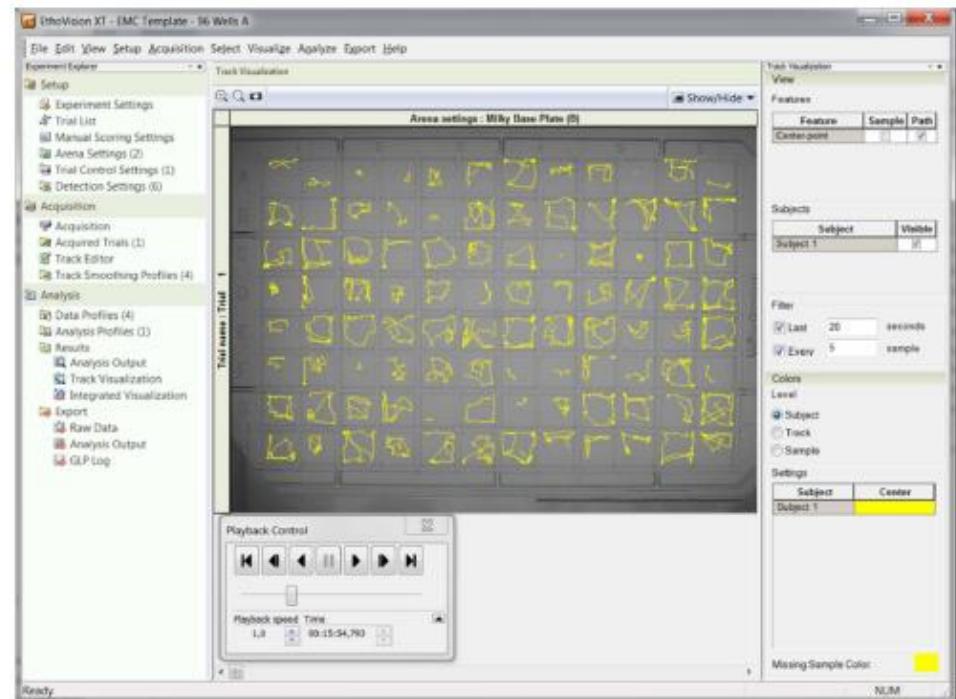
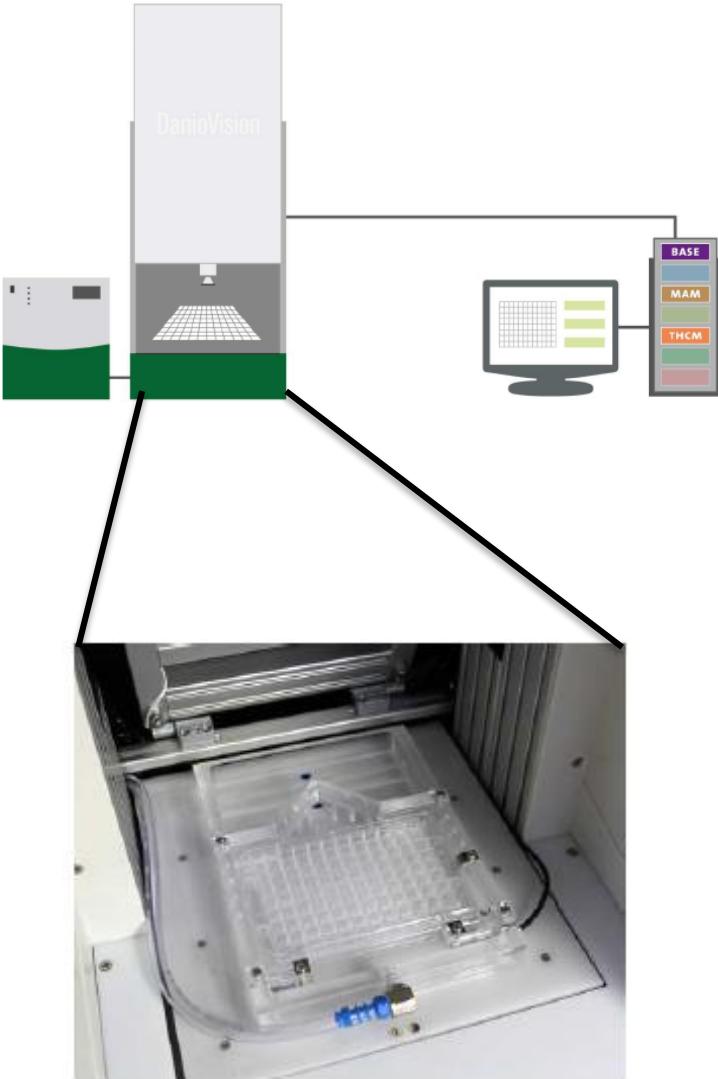
# Power of Drug Discovery in Zebrafish

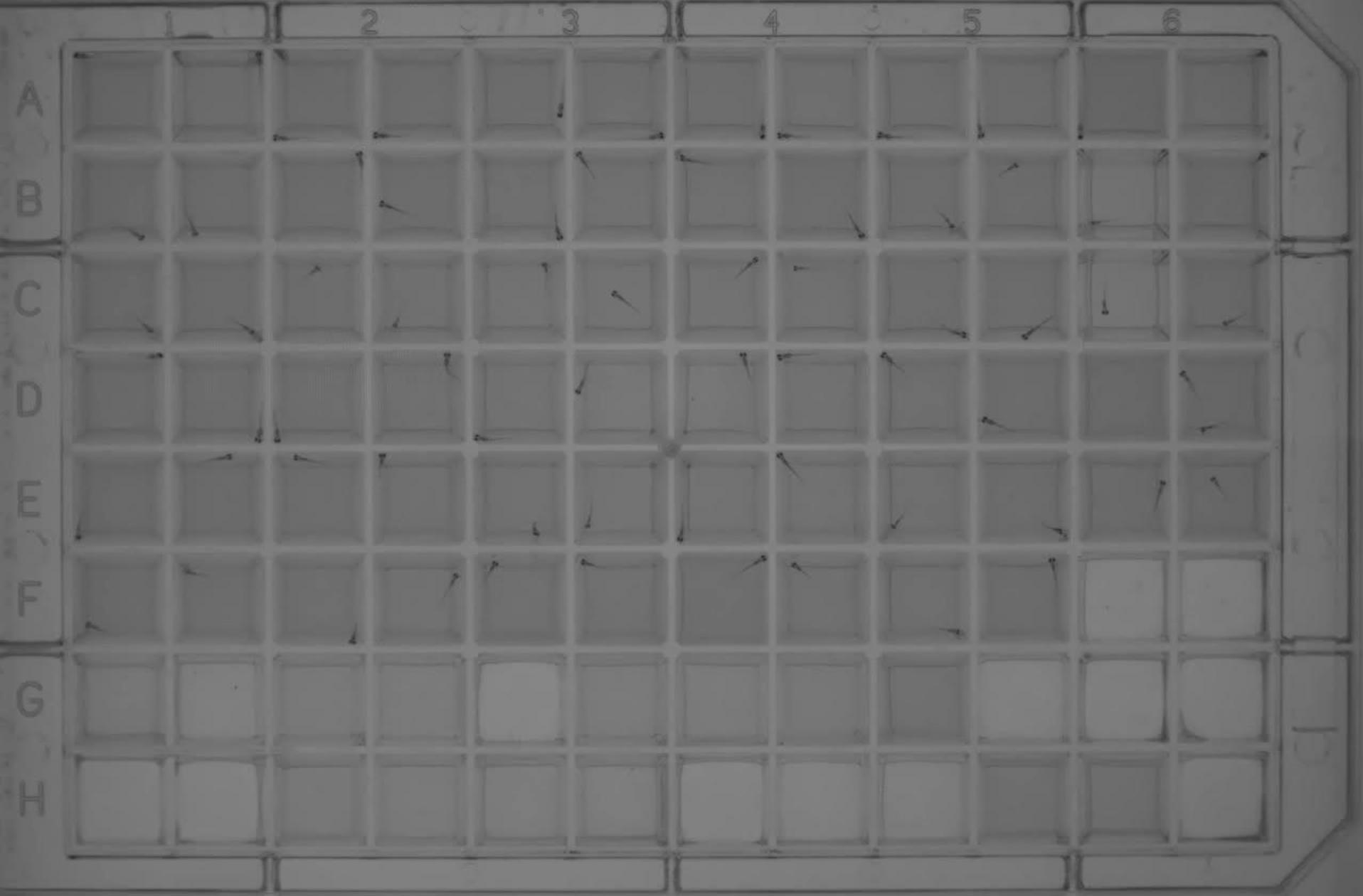
- whole animal biological complexity
- rapid development
- high-throughput screening
  - 62% of new drugs discovered using phenotypic screening

# Drug Pipeline



# Automated screening





# CRISPR in Zebrafish

- Bi-allelic knockdown using CRISPR >80%
  - Both copies of a gene are mutated
  - From the 1-2 cell stage of life
- CRISPR construct is easy to make and can be ready in <1 week and <\$400
- Multiple genes can be targeted simultaneously
- >1000 animals can be generated in a week and tested by an undergraduate
- Results can be known in 1-2 weeks for developmental disorders
  - Because embryogenesis occurs in first 3 – 7 days

# Zebrafish CRISPR limits

- *Limits*
  - Some genes in the zebrafish genome are duplicated
  - A stable mutant for long-term studies takes 1 year to generate
  - Some disorders are not amenable for zebrafish (for example, thumb development, or disorders of the placenta, etc.)
  - Some “rescue” may occur by orthologs

# Conclusions

Zebrafish have unique benefits as a vertebrate model organism

- rapid generation time, high numbers, and inexpensiveness

CRISPR is fast and efficient in zebrafish

Zebrafish have emerged as a powerful tool for testing NGS results

# Perils and Successes with CRISPR Modeling

Three tales (tails?)

# Guidelines for Demonstrating Variant Pathogenicity

1. specific gene variant enriched/specifically associated with a disease
2. a mutant phenotype in a model system matches a phenotype from human
3. Rescue of the mutant phenotype with wild-type allele
4. Inability of mutant allele to rescue phenotype

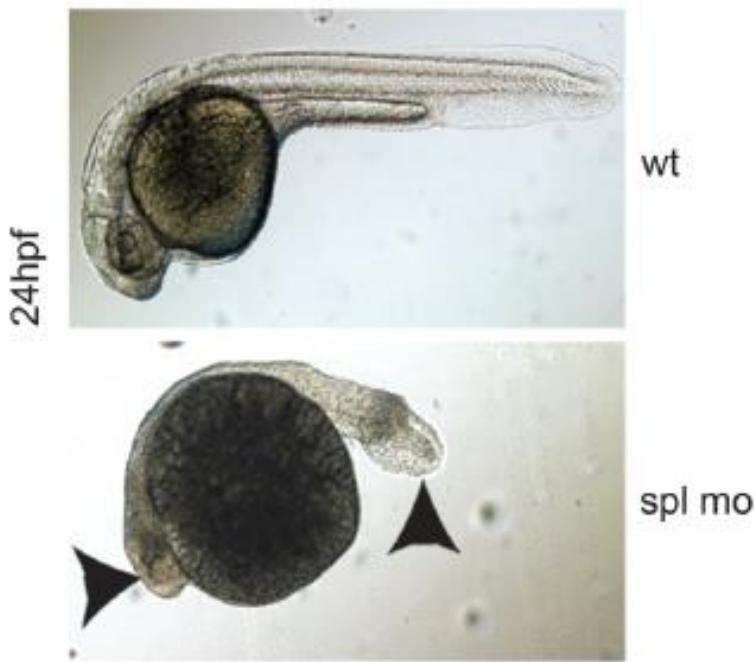
adapted from Chakravarti et al., 2013, Cell

# Two congenital motor neuron diseases: ...a New Gene... and the Wrong Gene

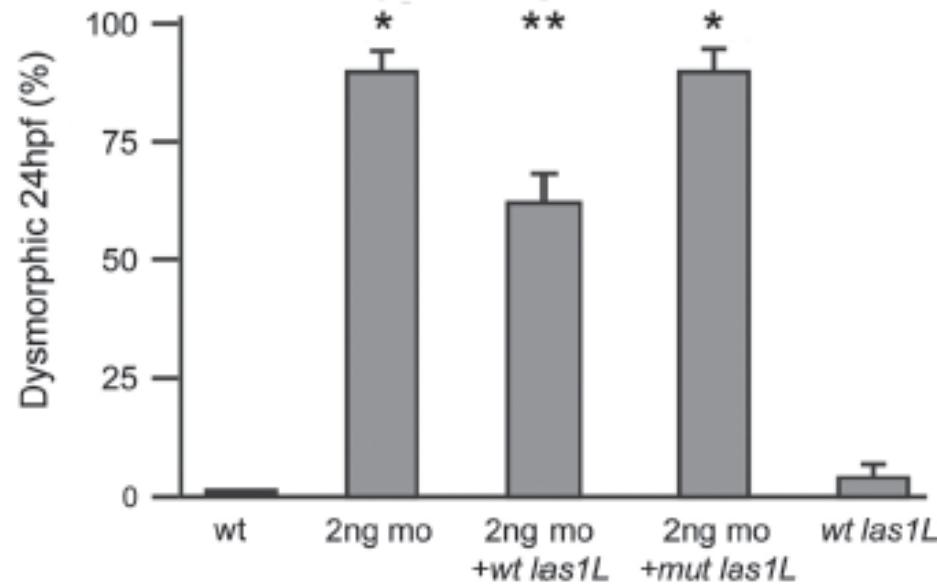
- Case 1:
  - Newborn infant requiring artificial ventilation
  - Genetic testing showed that it was not SMA
  - Guidance needed for parents and physicians

# LAS1L gene identified and had phenotype in zebrafish

C



A

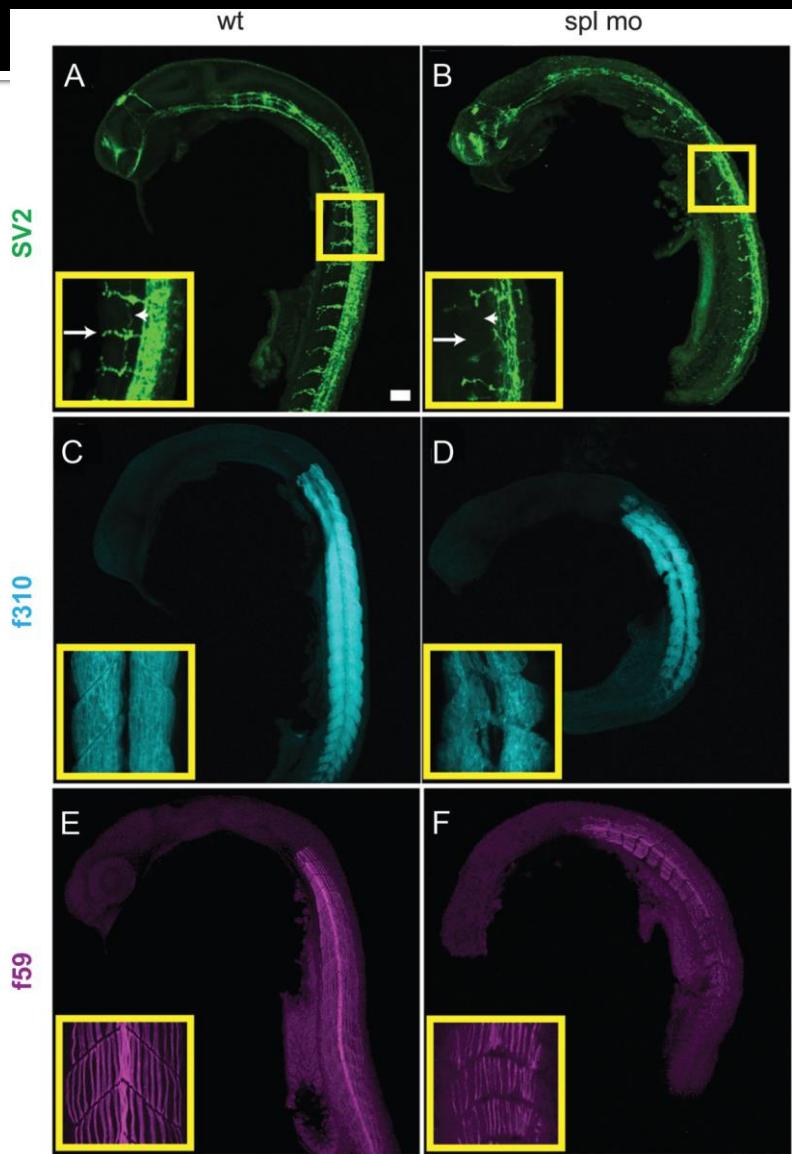


# LAS1L Pathogenicity

- Sequencing showed p.S477N mutation in a ribosomal biogenesis protein: LAS1-like
- Confirmed in zebrafish
- New biochemical pathway in neurological disease

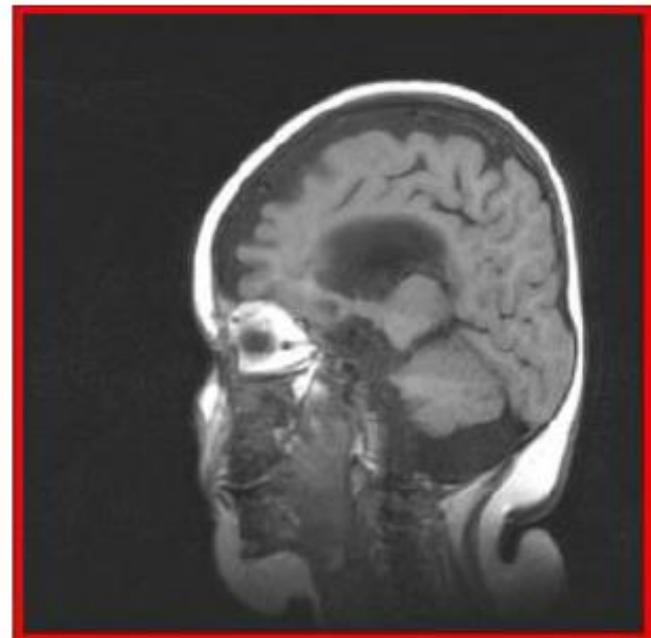
Congenital lethal motor neuron disease with a novel defect in ribosome biogenesis

Butterfield et al., Neurology, 2014

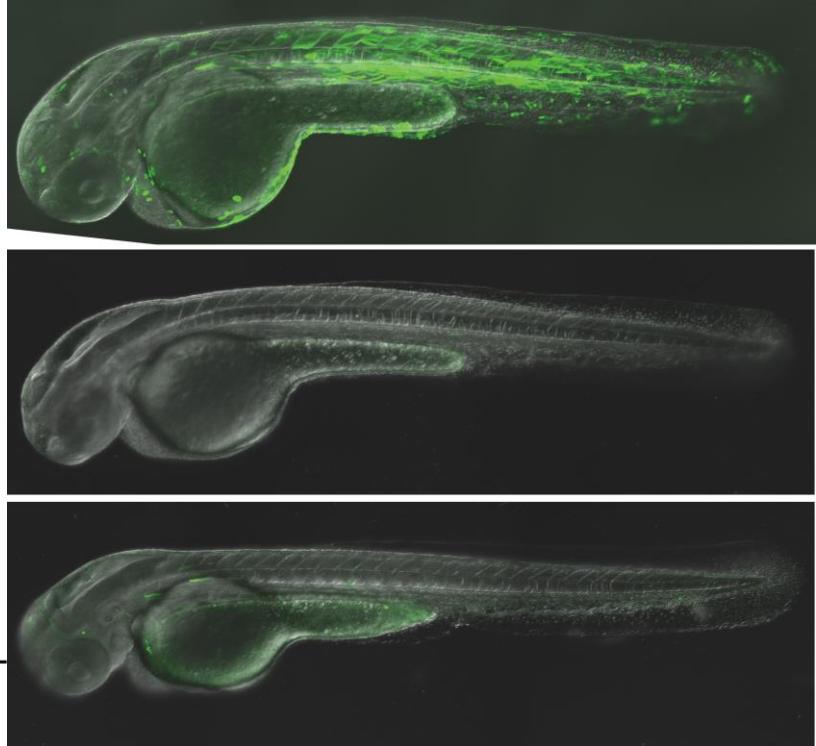
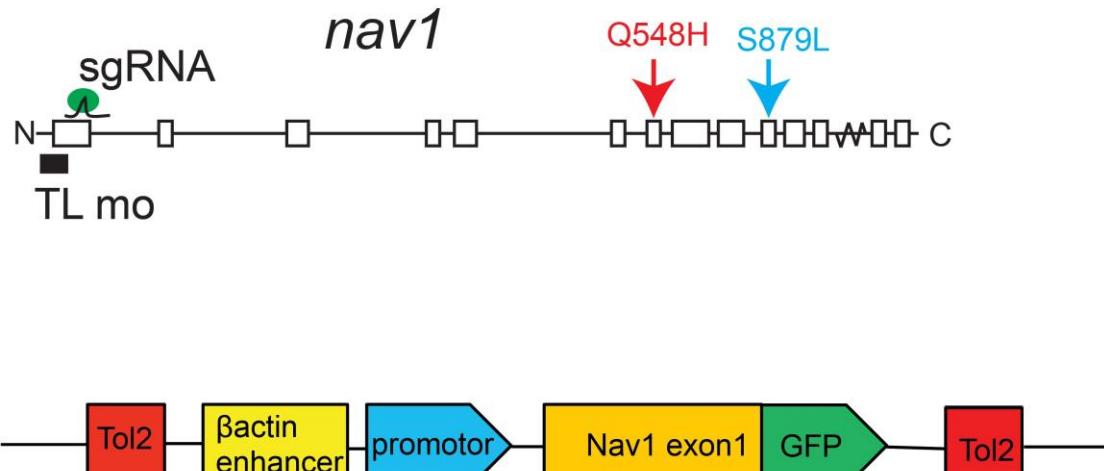


# Case 2

- Stevenson and Carey, AJMG, 2007
- Siblings with muscular contractures, seizures, and brain structural abnormalities
- NGS suggested NAV1 gene

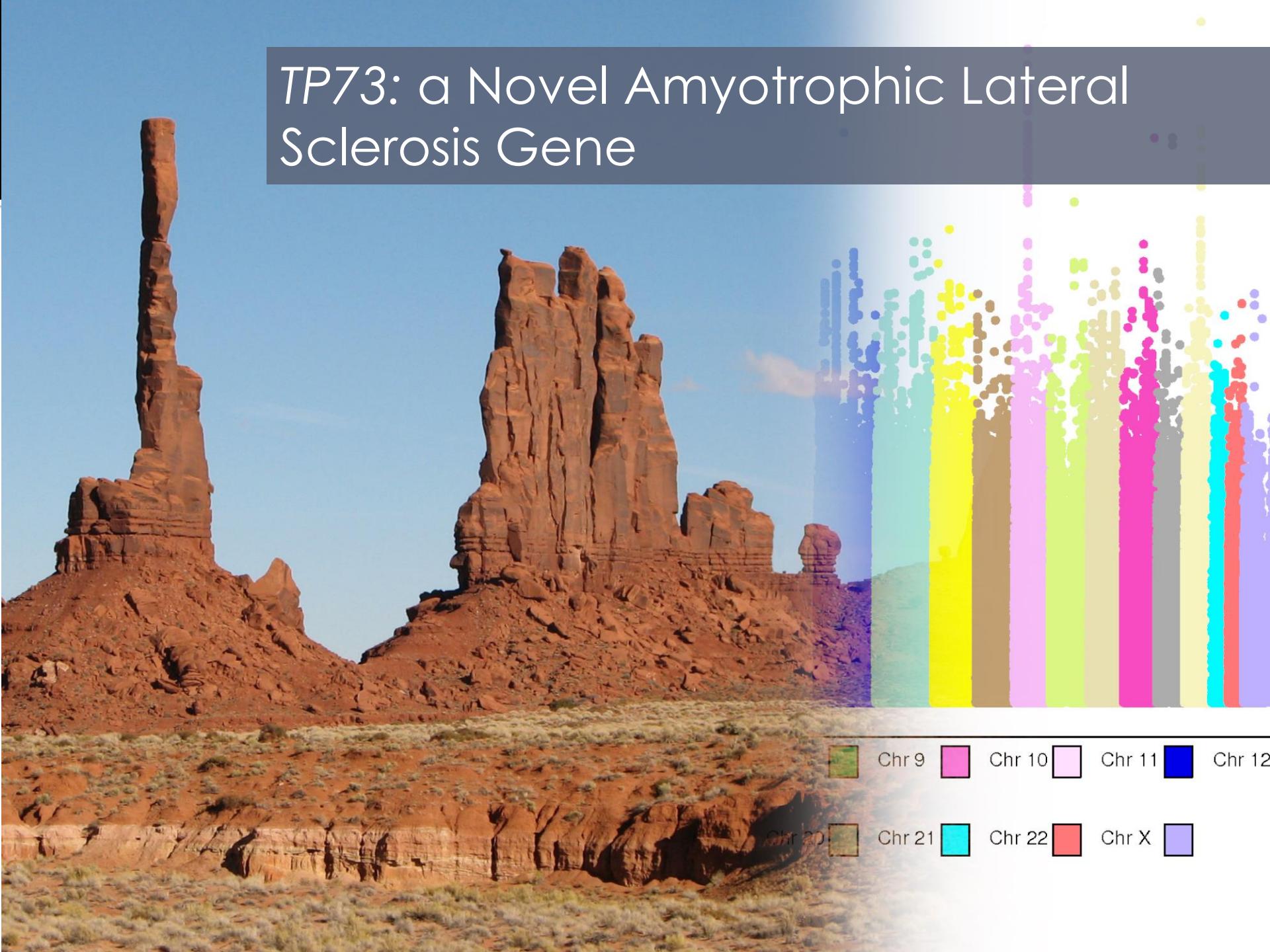


# NAV1 gene incorrect



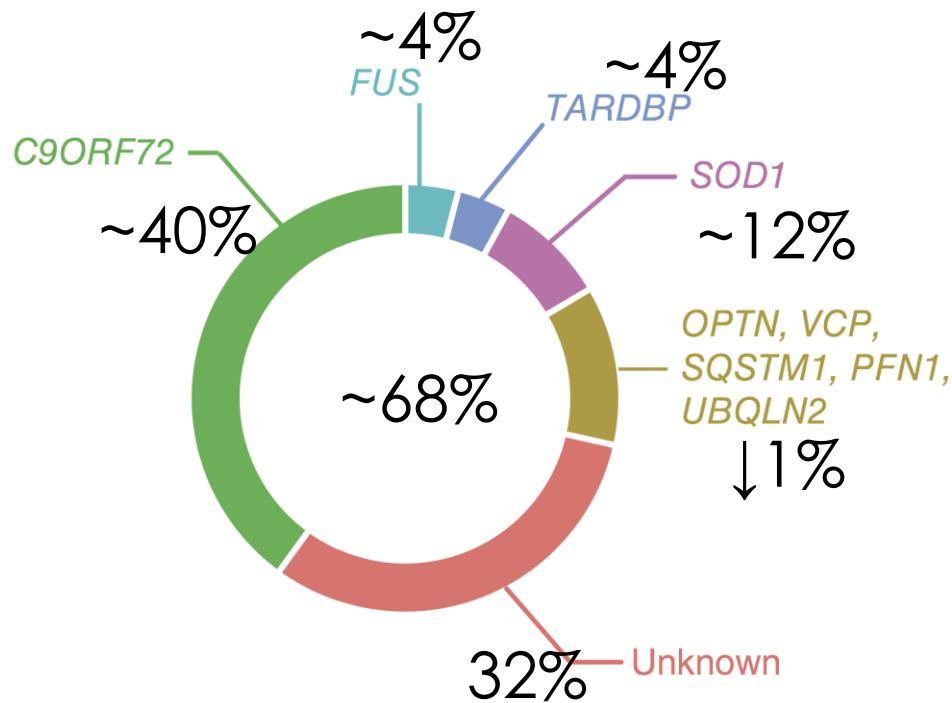
- zebrafish morphants and CRISPR are normal
  - *sequence re-analysis did not confirm NAV1 (and did not identify other better candidates)!*

# *TP73*: a Novel Amyotrophic Lateral Sclerosis Gene



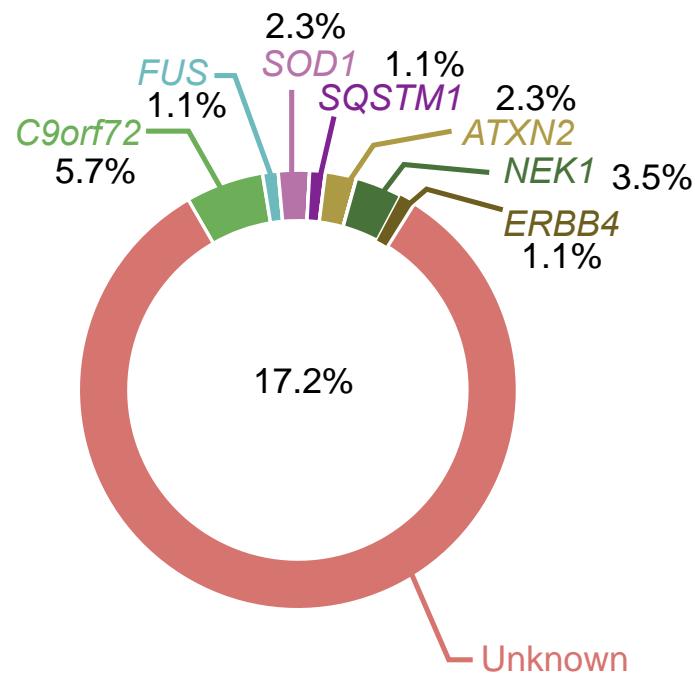
# Most ALS cases have an unknown genetic cause for disease

## Familial ALS (10%)



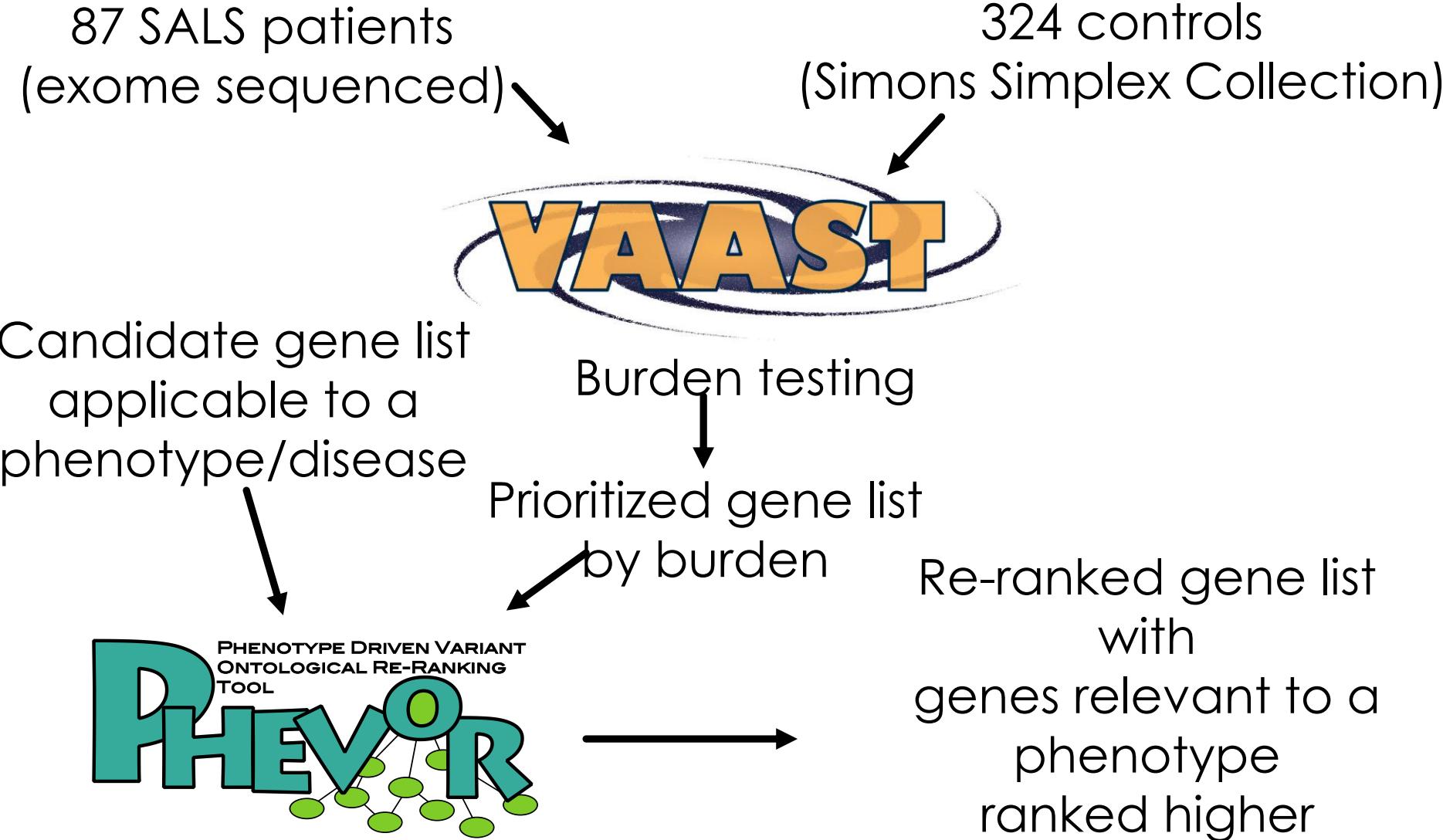
Renton et al. (2014),  
Nat. Neurosci

## Sporadic ALS (90%)



Gibson, Downie et al. (2017),  
Neurology

# Determine whether novel loci ALS loci can be identified using next-generation sequencing



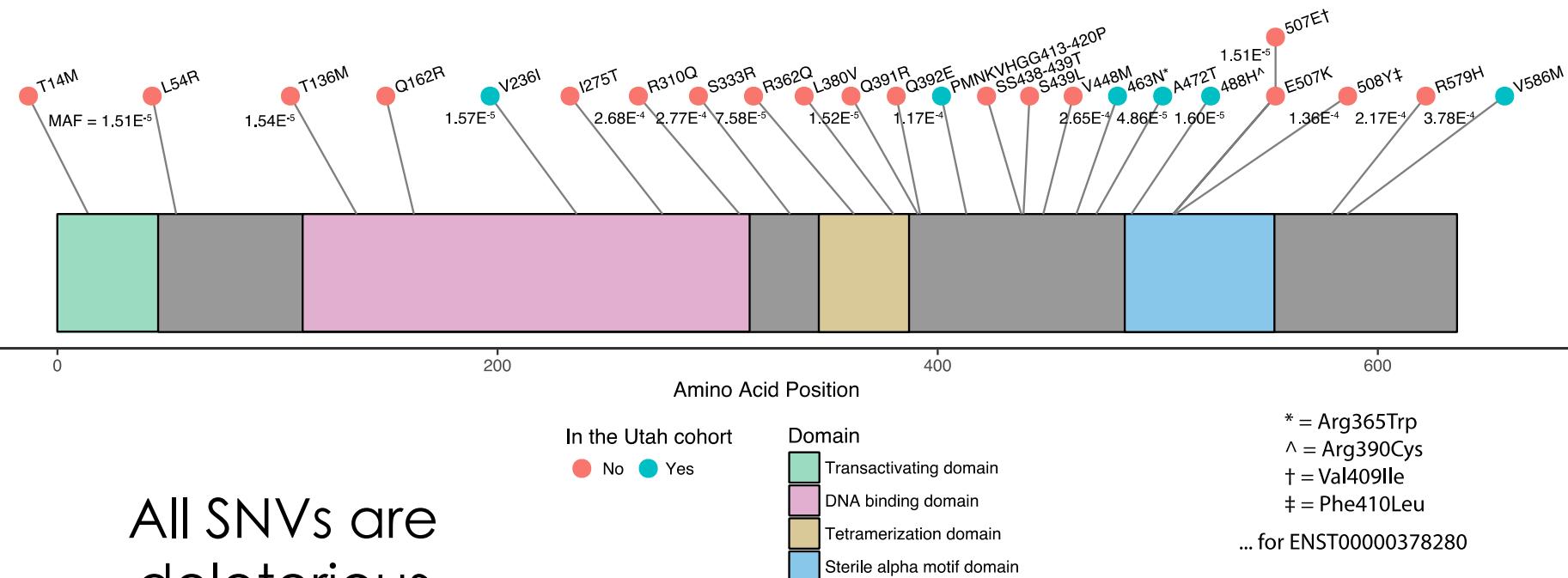
# **TP73 has multiple qualities that make it an attractive ALS gene candidate**

- Two known ALS genes in top 5 ranked genes from VAAST/PHEVOR
  - *MAPT* (rank: 3)
  - *SOD1* (rank: 5)
- *TP73* (rank 2)
  - One of two genes that possessed a VAAST burden level approaching genome-wide significance
  - Four different rare missense SNVs in five patients
    - 1 in-frame indel upon screening for indels
  - Part of the p53 family of tumor suppressor proteins
  - Neuronal survival factor

# Rare, deleterious variants in *TP73* are found at appreciable frequency in ALS patients

24 rare (MAF<0.0005) *TP73* coding variants were found in ~2,900 ALS patients

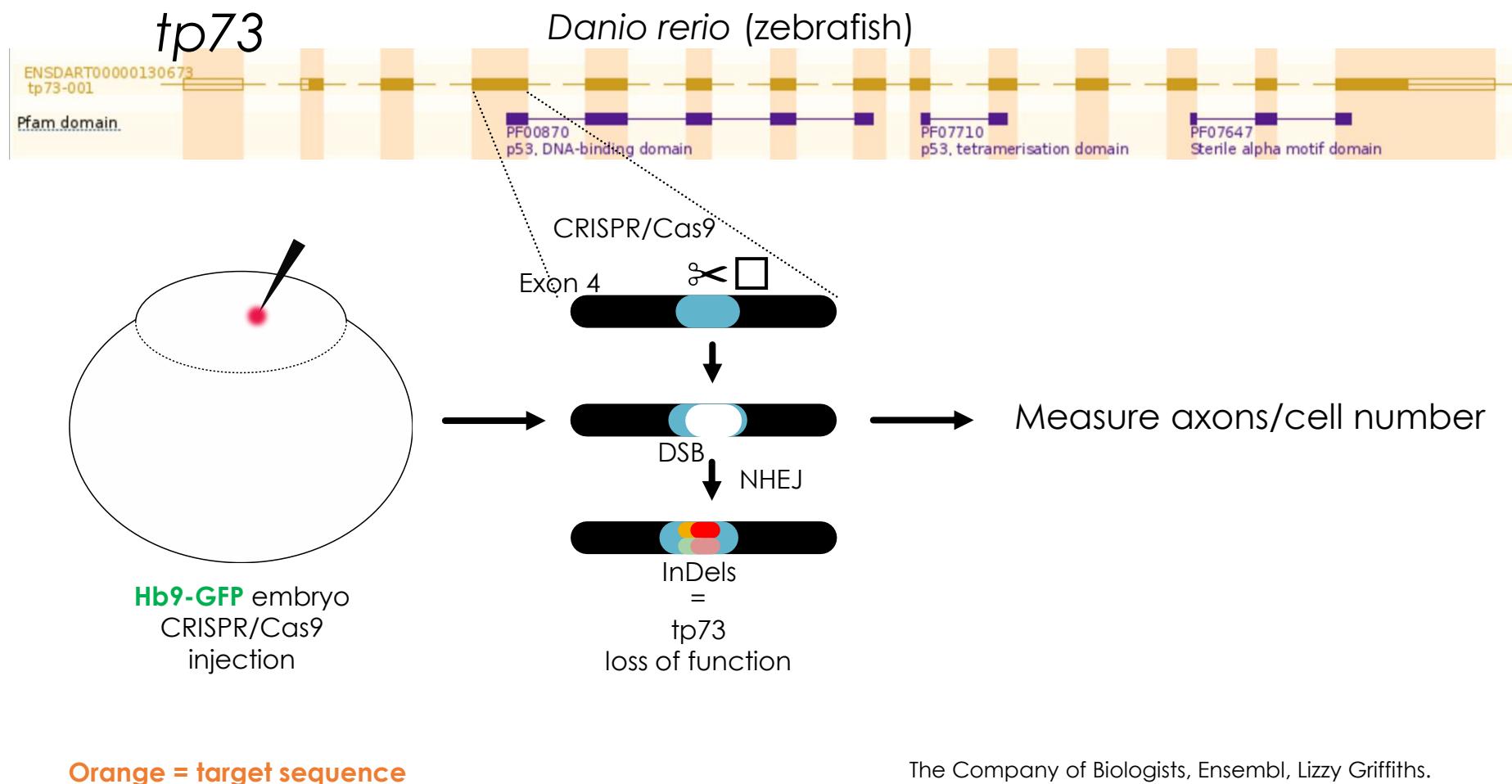
TP73; ENST00000378295



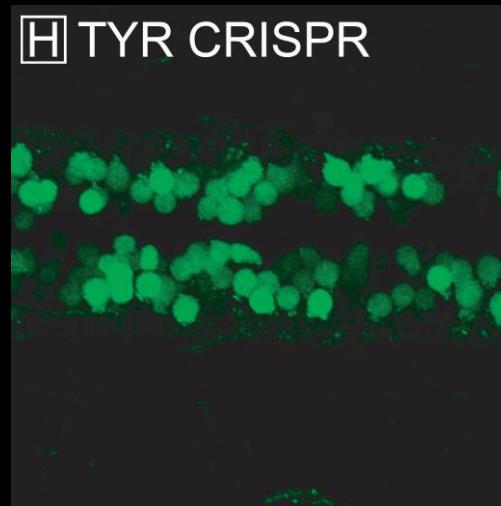
All SNVs are deleterious according to MetaSVM

~2,800 patients from Cirulli et al. (2015) Science

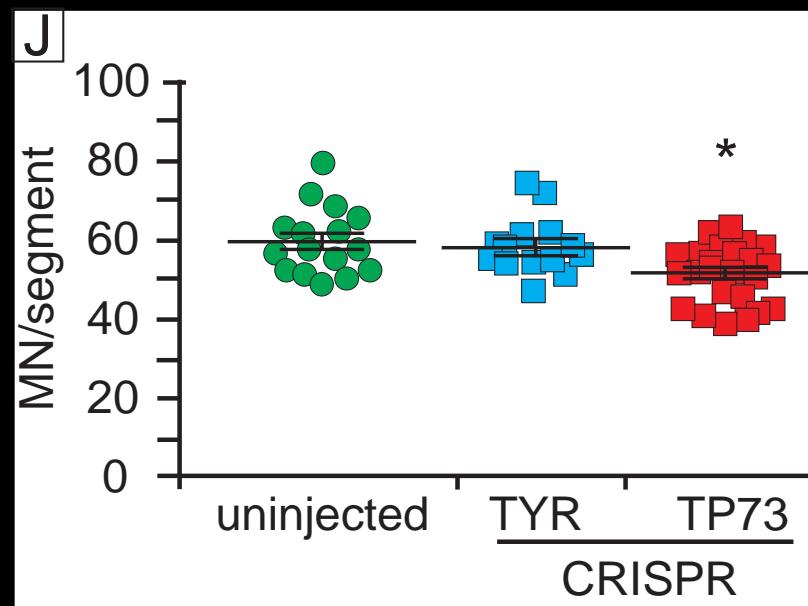
# A CRISPR/Cas9 zebrafish system was developed to test how loss of p73 affects spinal motor neurons



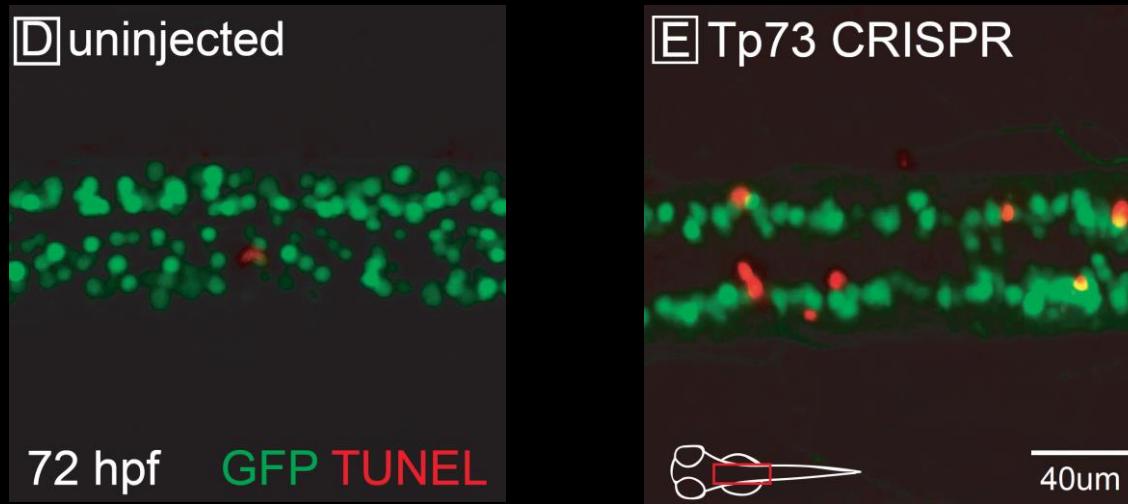
# The number of spinal motor neurons is significantly reduced in *tp73* zebrafish mutants



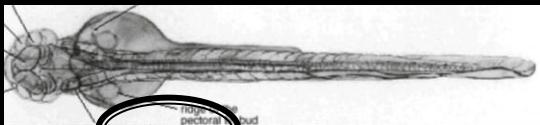
*Hb9* = motor neuron promoter  
hpf = hours post fertilization  
MN = motor neuron  
\* =  $p < 0.01$



# p73 CRISPR zebrafish have increased apoptosis of spinal motor neurons



Tg[Hb9:Gal4-UAS:GFP]



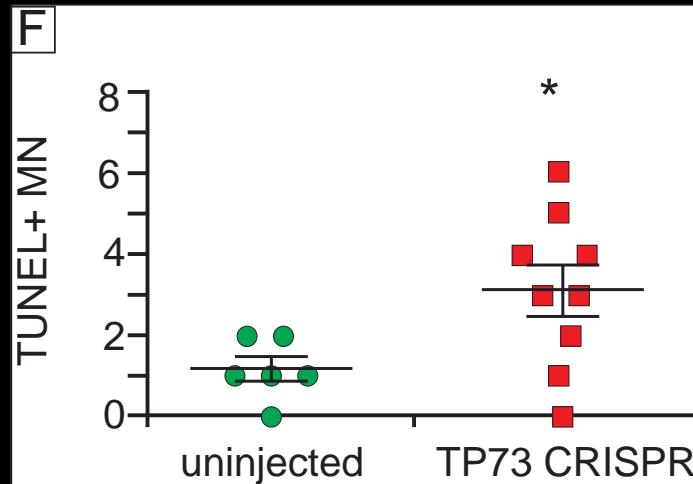
Confocal: 10x; 5μm/step, 21 steps

Hb9 = motor neuron promoter

hpf = hours post fertilization

MN = motor neuron

\* = p < 0.05



# Conclusions

- May have identified a new ALS risk gene.
  - Rare and deleterious variants *TP73* are found in ALS patients
  - These variants impair *TP73* function
    - Loss of C2C12 myoblast ability to escape differentiation
  - Development and survival of motor neurons are negatively affected in *Tp73* mutant zebrafish
- Expands the list of cellular processes involved in ALS pathogenesis.

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(GM118335)



Chr 9 Chr 10 Chr 11 Chr 12

Chr 20 Chr 21 Chr 22 Chr X

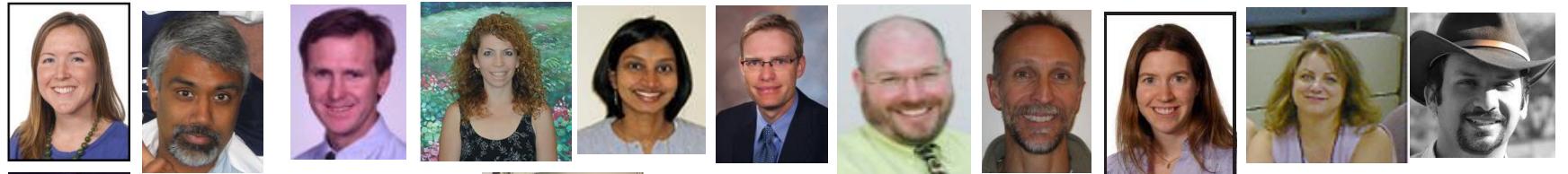
# Conclusions

- NGS is changing the landscape not only of diagnosis, but redefining what diseases exist
- NGS results can be challenging to interpret, as often the results are the first of their kind
- CRISPR genome editing is a powerful, efficient, and inexpensive method for testing gene function
- The zebrafish is a uniquely powerful vertebrate model system for testing certain diseases and NGS results

# Funding



# People





University Health Care  
Pediatrics