## Improving the Performance and Health of All Working Dogs Through Large-Scale, Collaborative Genetics

#### Elinor K. Karlsson

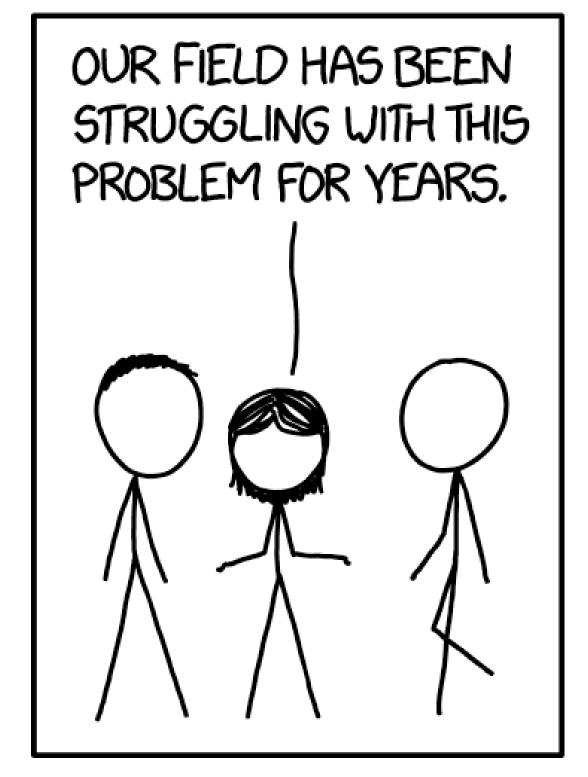
University of Massachusetts Medical School & Broad Institute of MIT and Harvard



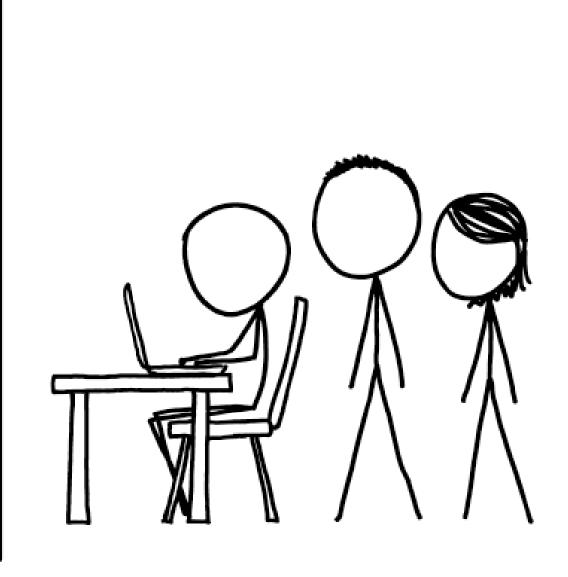


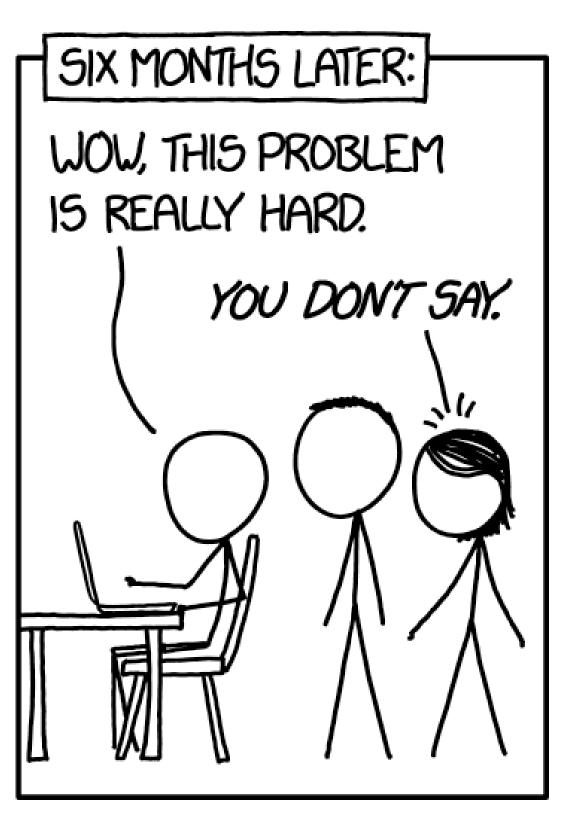










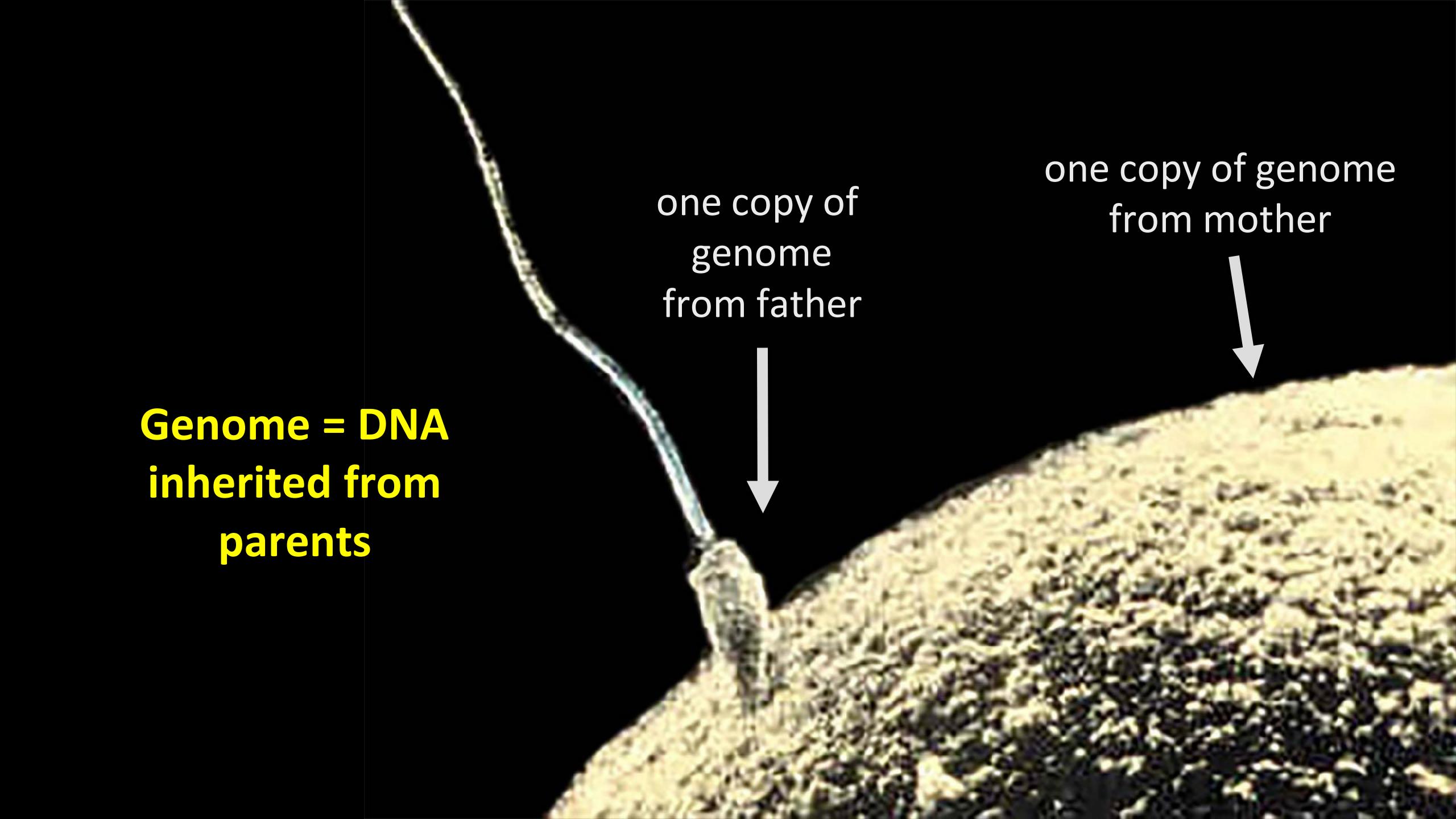


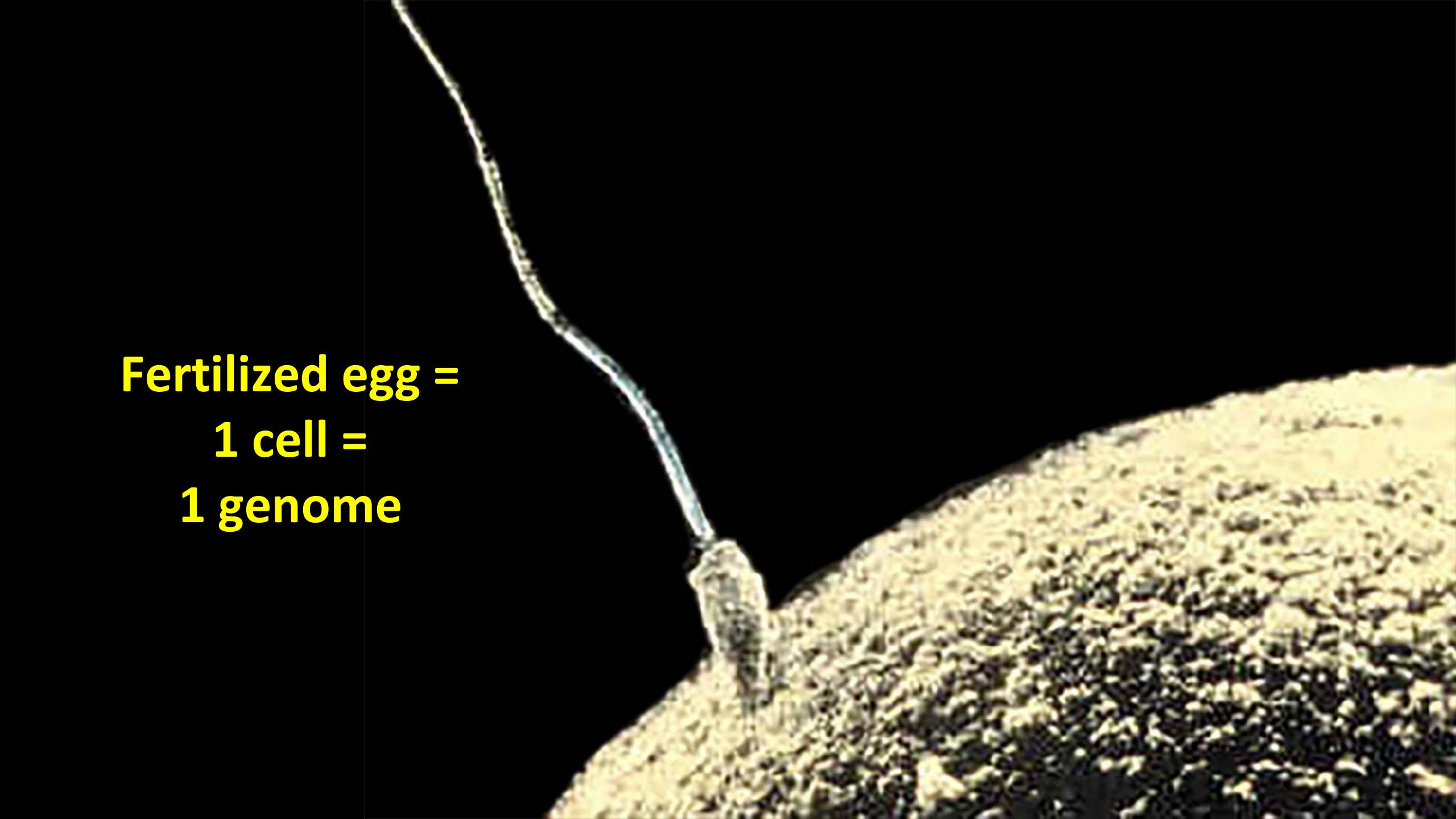


8 December 2005 | www.nature.com/nature THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE nature





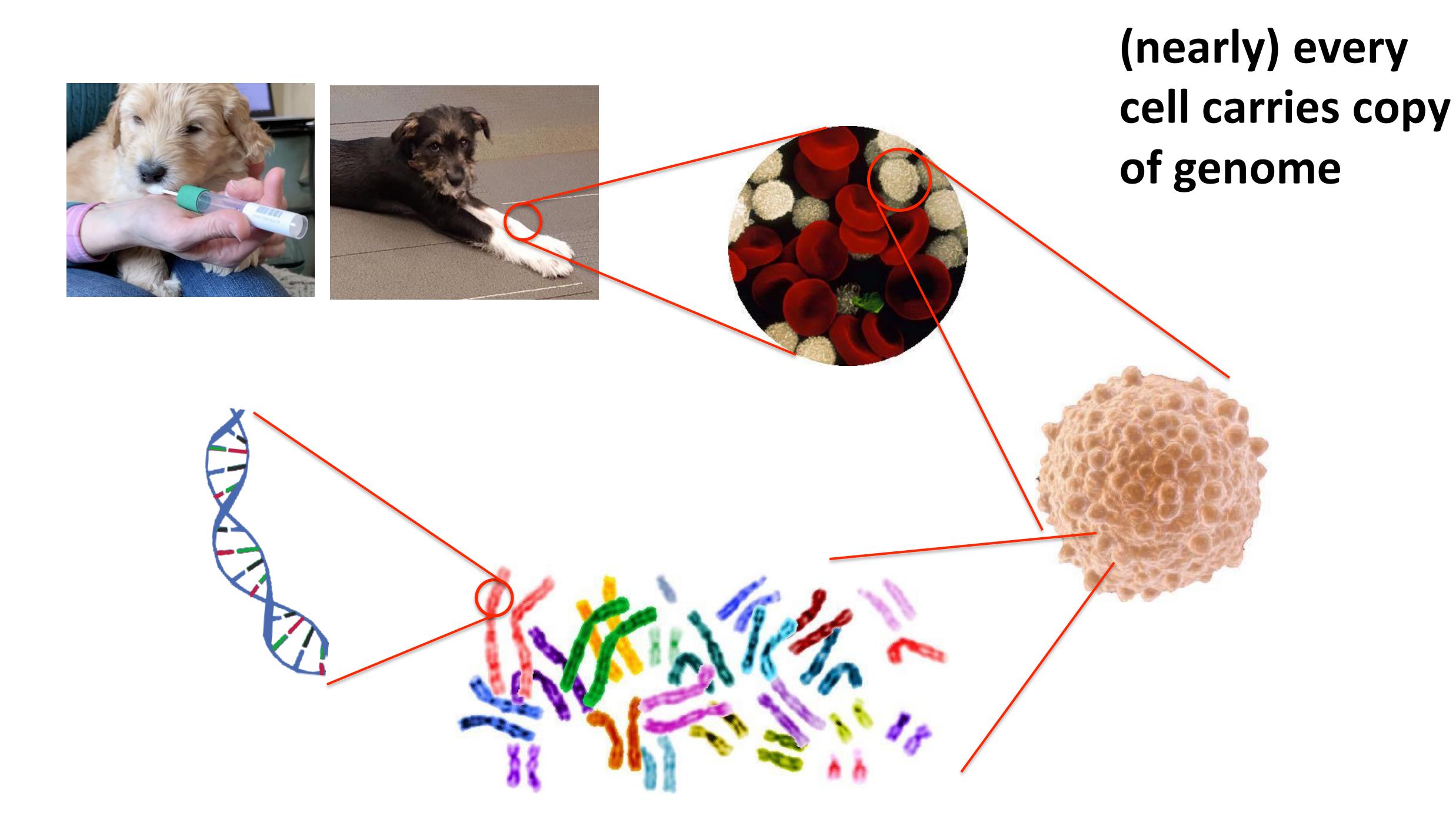


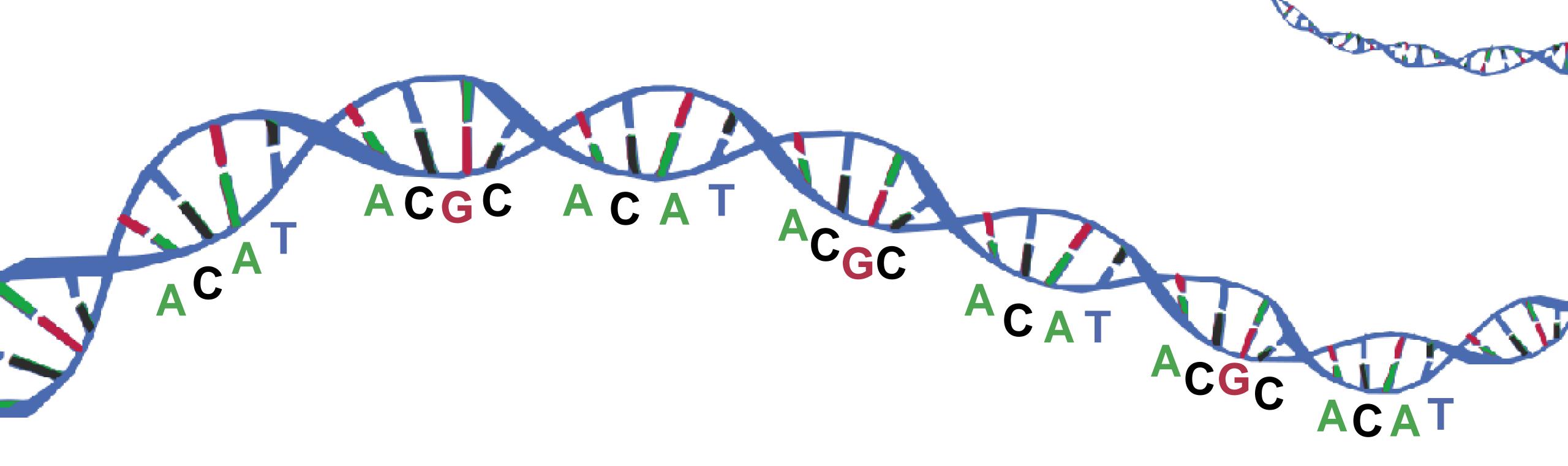


### ~40,000,000,000,000 cells\*



\* very rough estimate



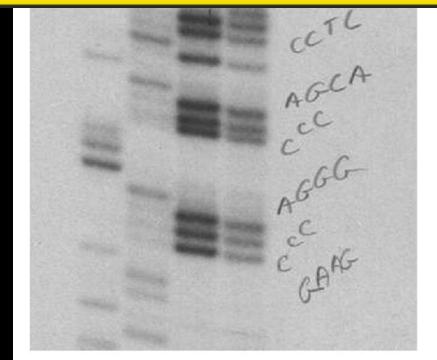


CCTTTCCCTCGCAGCTCCCTGGACGCCTGCGGCTGAGCGCCTCGAGCGGGGCGCGCGGGAGCCCCCGGGCGCCCCCGG GGGTCCCCCGCGCCCCGGGGGCTGCACCTGGGCCGGGAAGTCCCGGACCTCCTACGTGTCCCCCTCCACCCTCCGGGCGG CGGGGCTGTGTTCTCCCGCTCCTCGCCCCCGGGAGCACTCGTCGGATTTCTCCGGCACTCGTGCATTTTGTGCTCGGGAAT ACGTTGAGTCCTTGCACCCAGTTTTTGCAAAATCCTTTTCACTCGGCGCCCGGGGGCCCGTCGGGGCGGGGCGGGAGGAAGTC CGCTTCCACCCTCGGAGCAAACCCCTCTCCCCCGCGCTGACCTCCCCTCCCCCCCTCGCCGGCAGGTGTGCGGCGCCTCGGGCCA TCGAGCTGGAGATCCTGTCCATGCAGAACGTGAACGGGGAGCTGCAGAACGGGCACTGCTGCGGCGCGCGTCCGGAGCCC GGACCGCAAGTGCTCTCACGACGAGTGTGACACGTACTTCAAAGTGTGCCTCAAGGAGTACCAGTTCCGCGTCACGGCCGG GCGCCGGCGGAGCCCCGCGGCCTCGCCAGAGGGACGGCGGGTCTGGGCTGGAGCCTGCGCGCCGGCTGGCAAAGCCTTGC GGTGCGGCGTGAGGCGGCTGCGACTCCGGTTACGGTCTCCGCGGCCTCTTGCCTAGCGCGCGACAGTGGGGAGCCCGCG GCTCGCGGGGGCTCGCGGGGCAAAGCTCCCAGGGAGGCGGGCTTATTAAACCTGCATCTAGAAGGCCCCAGAGTGACCCT CCCCCCCCCCCCCCAGCTGGGCGTCTTTATGGACGATCTCTCTTTTGCTTAACGAATTGAACCTGATGCGCCGTGGAAGGCGA GCGCAGTTCTGGCCTTCGAAGCCGTCCAAATGGTCACTCCCCCCTTTCTCGTGAGCTGCCGCGAGGGCGGGTGTGCCCTTCCT BAGGGCGTGGGGGAGCCAGTTTCCCGCCGCTGCCCGGGAGACTTTGGGGCGTGCGGGGACGCGCTCCGGGCTGGACGGG CCCTGGGAGGTGGGTGGGGTTGACTCTGGGCCGAGGCTGGAGCCGGGAGCCCGAGAGCCT Human genome: 3 billion bases long GGCCTCACTTCCAGCGGTTCCCGGGCTCTGGA GGCGGGCTCCGGCCCCCGCTAGCCTCCGGGC Dog genome: 2.4 billion bases long AGTGCCAGGGCTCGGACCCCTGCCCCGGGCC CGCTCGAGGCCCCGGGCCCGGCTGGCCCCTGCAACCACCTTTCAGTTTC

#### ancient times

G A C CT





WAL GF TGGGCCTGGGCT

Maxam-Gilbert sequencing

Cost per genome: impossible

late 1990s



Automated Sanger sequencing

\$5 billion+ to sequence the first human genome (\$50-100 million after that)



Illumina HiSeq 2000 \$5000-\$10,000 per genome





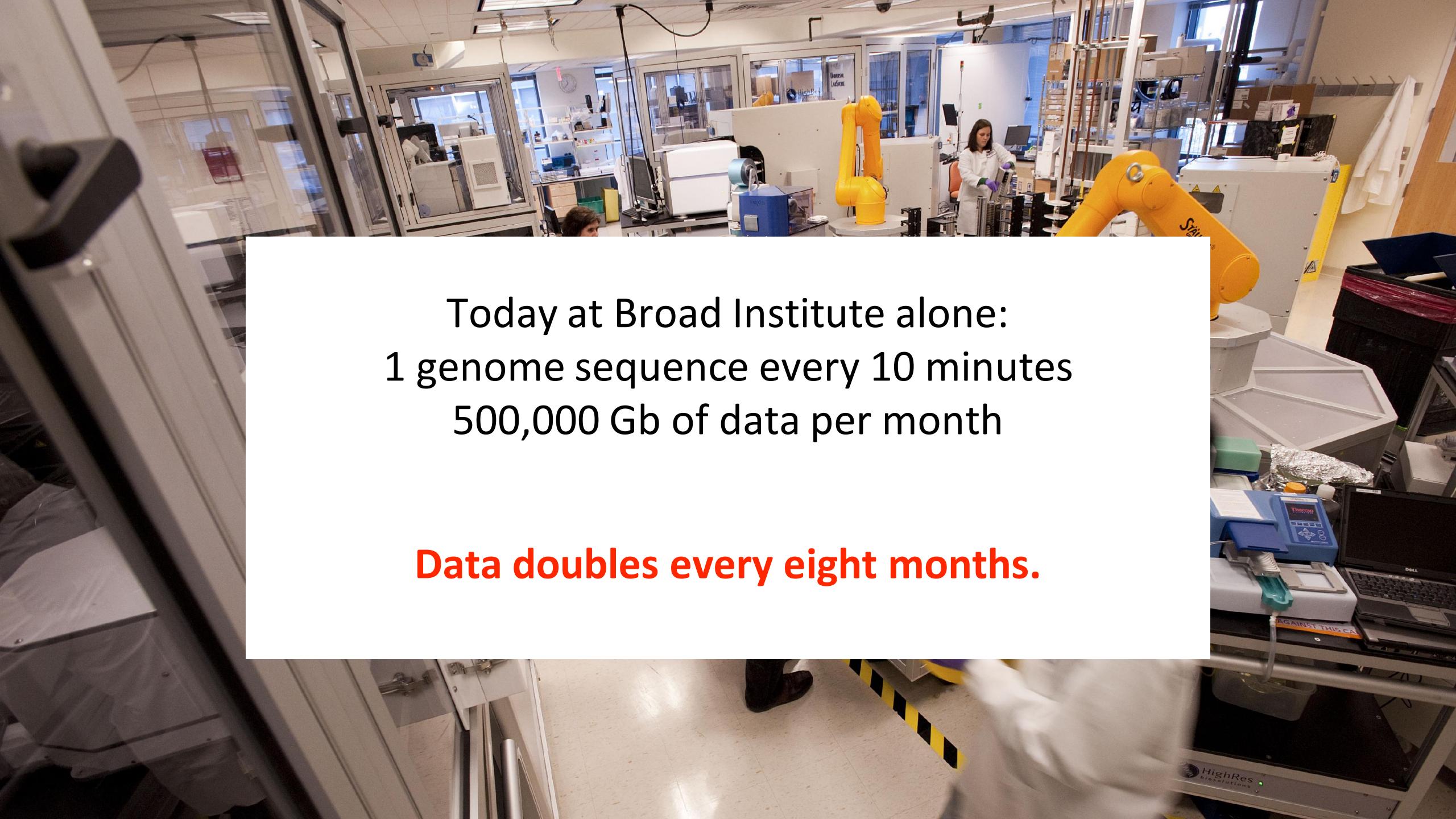


Illumina HiSeq X \$750 / genome \$100 -> most info

NEXT GENERATION
SEQUENCING

2007

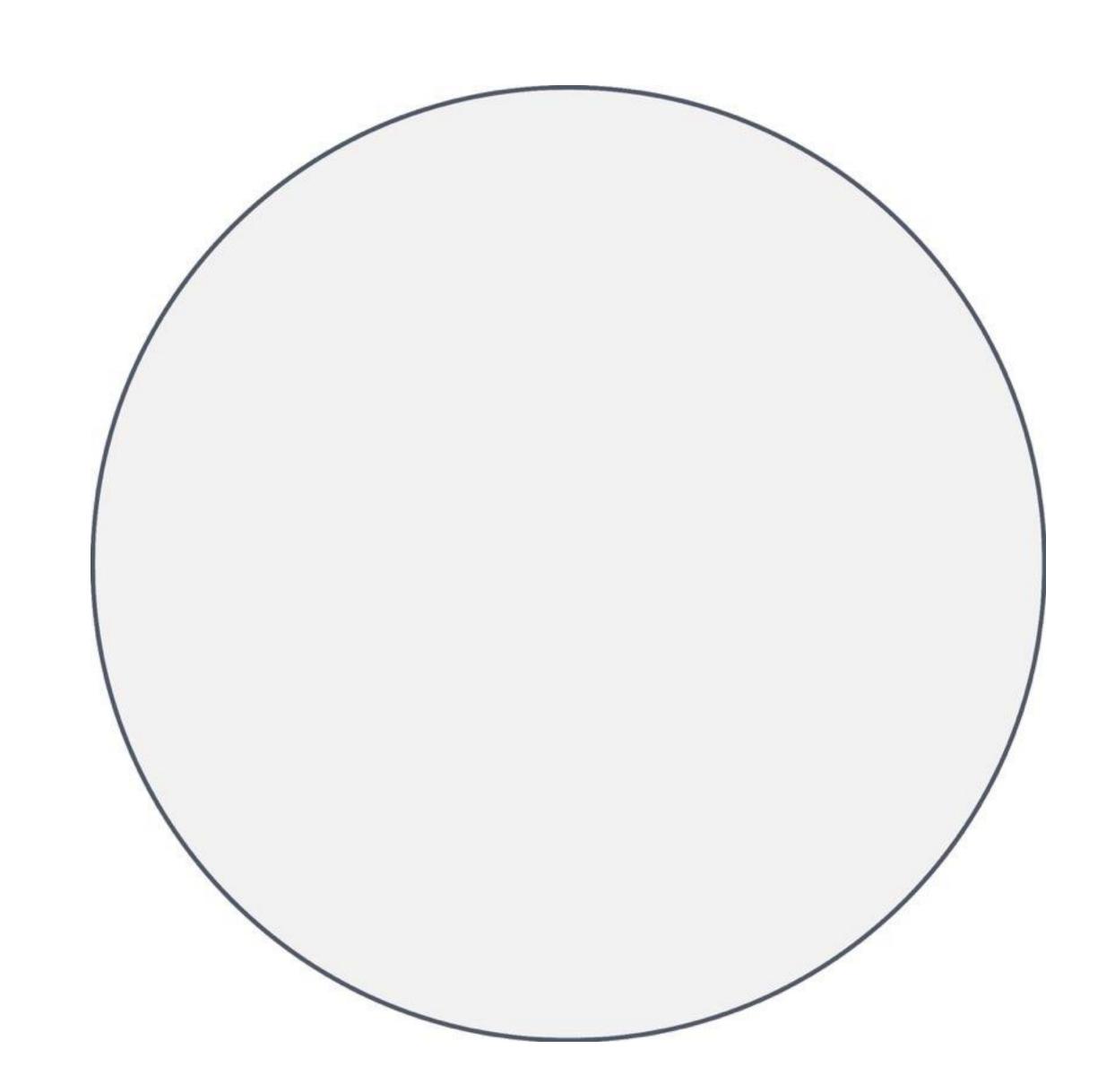


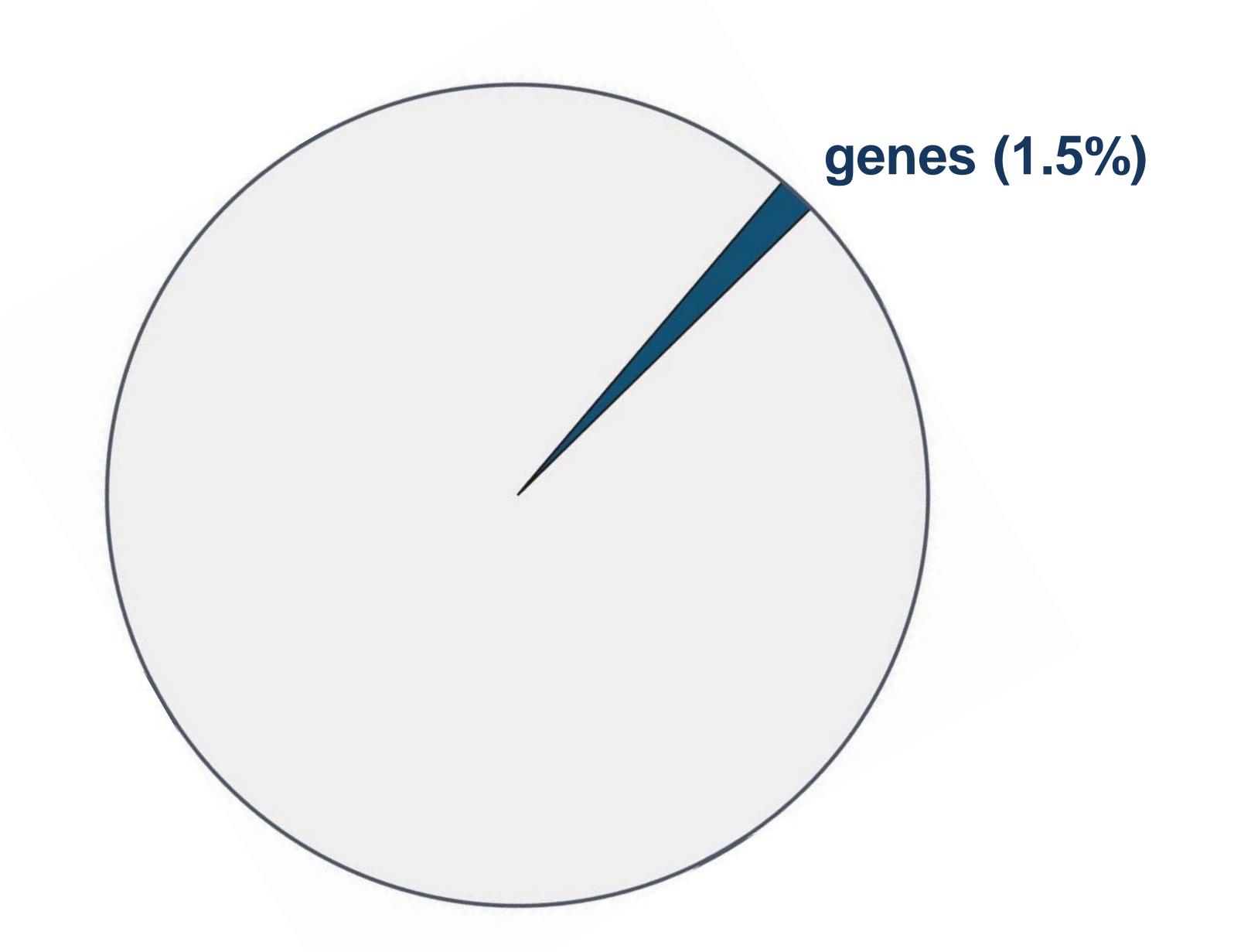


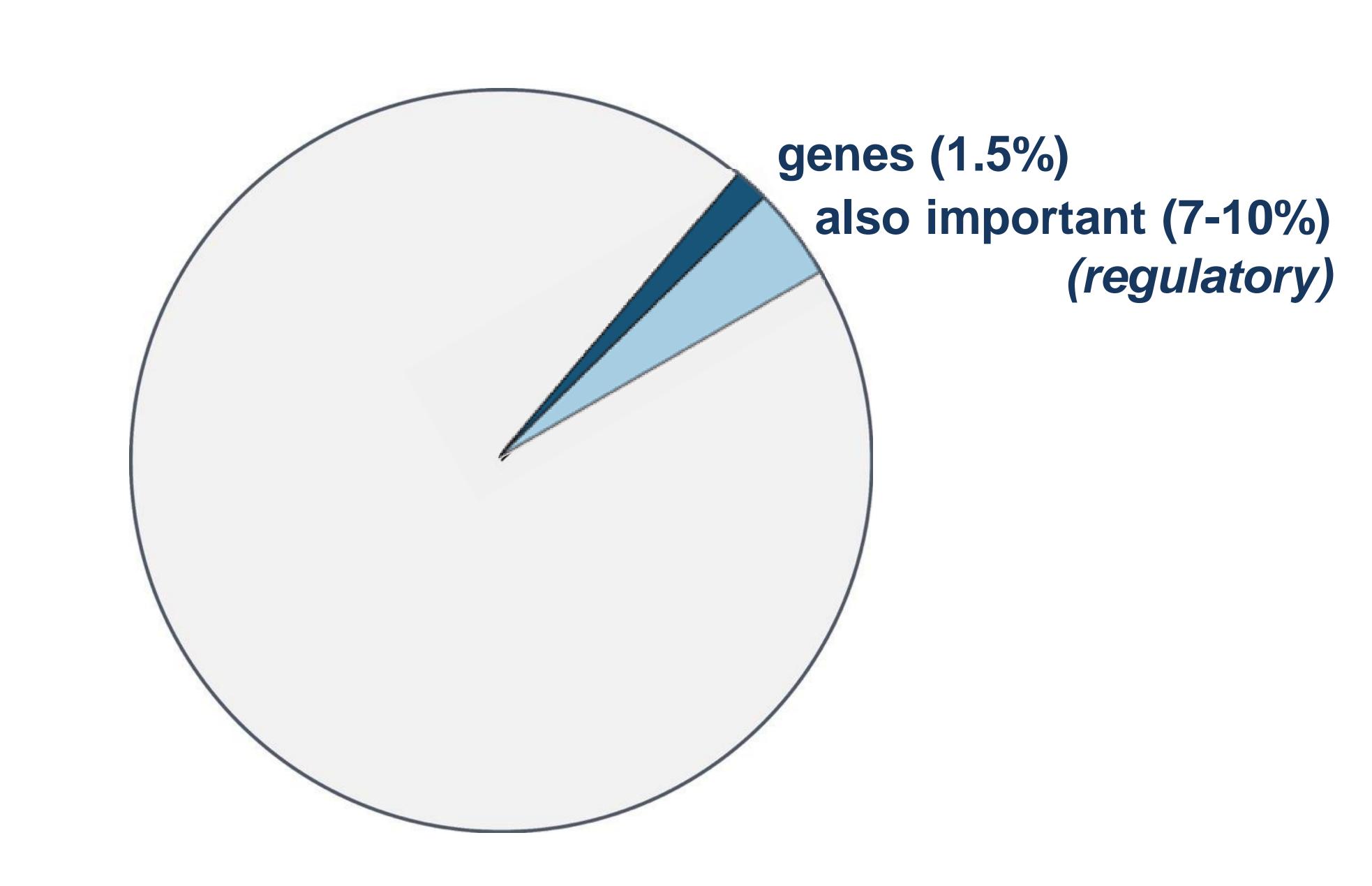


< 1000 dogs - but that is starting to change

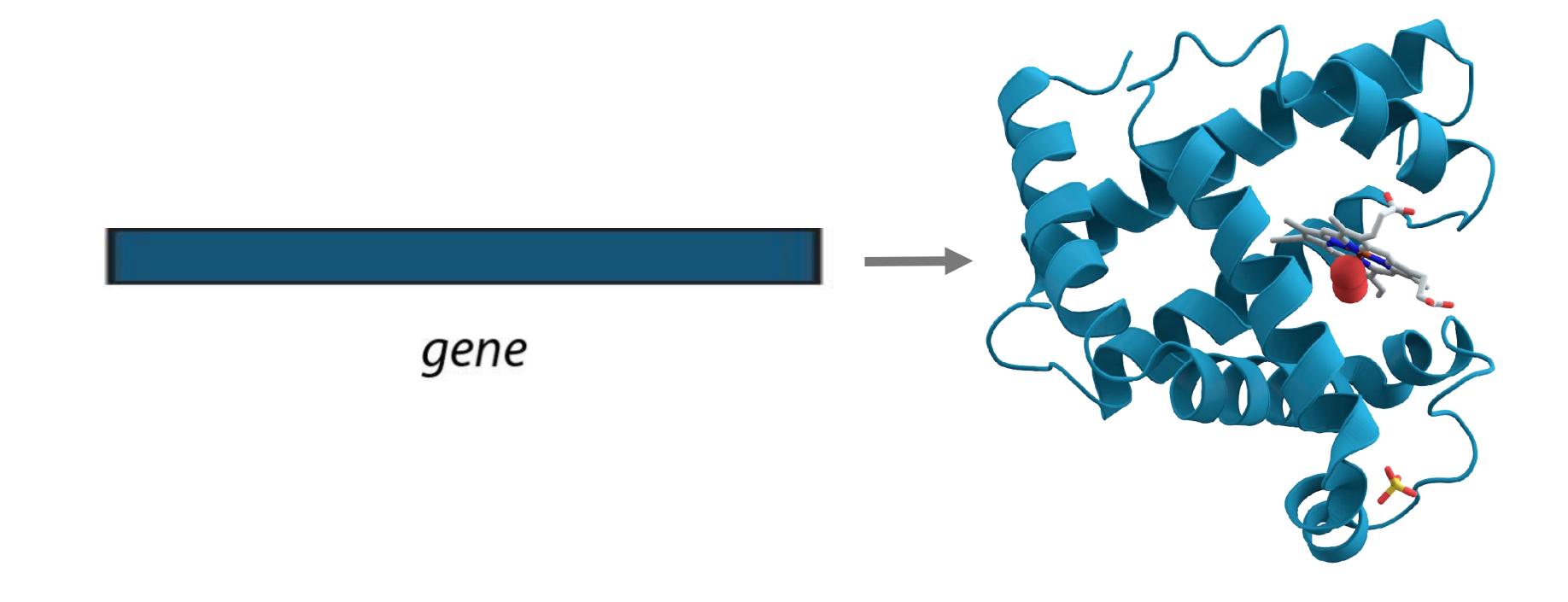






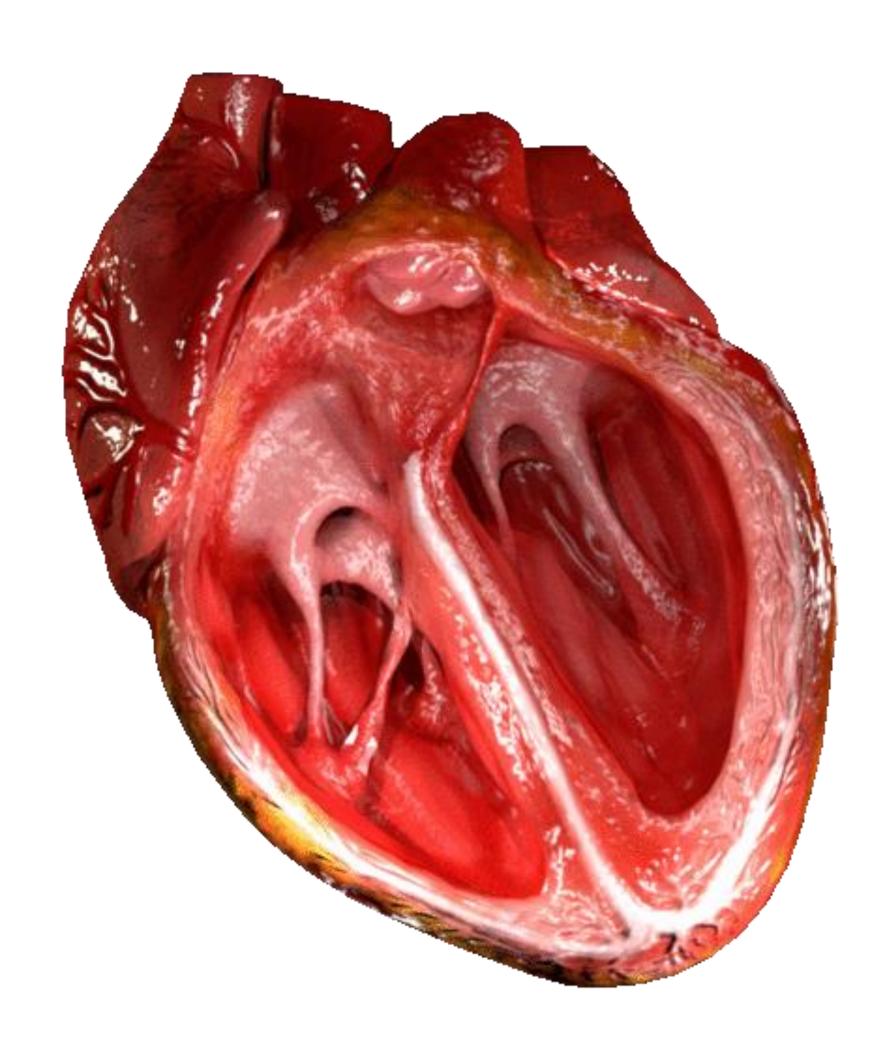


#### If every cell in your body has the same DNA (your genome) ...

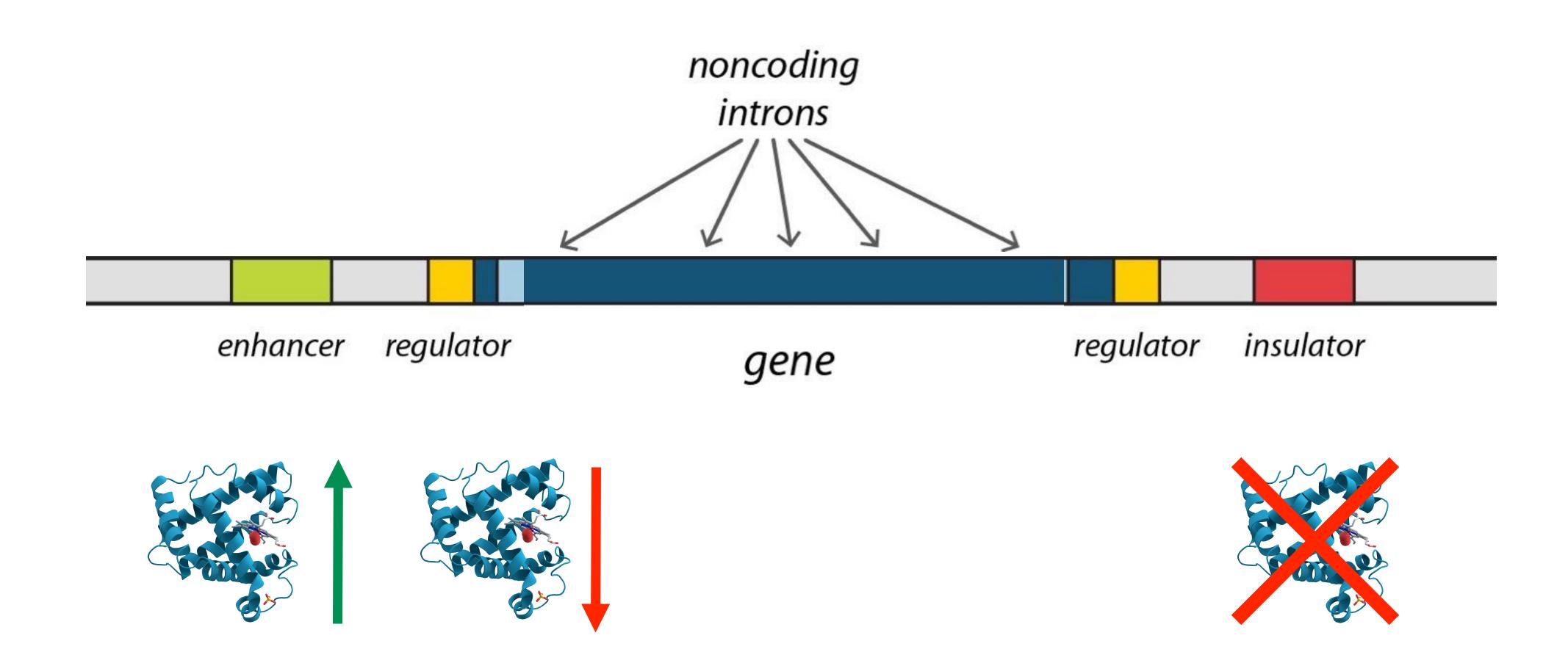


#### Why isn't every cell the same?

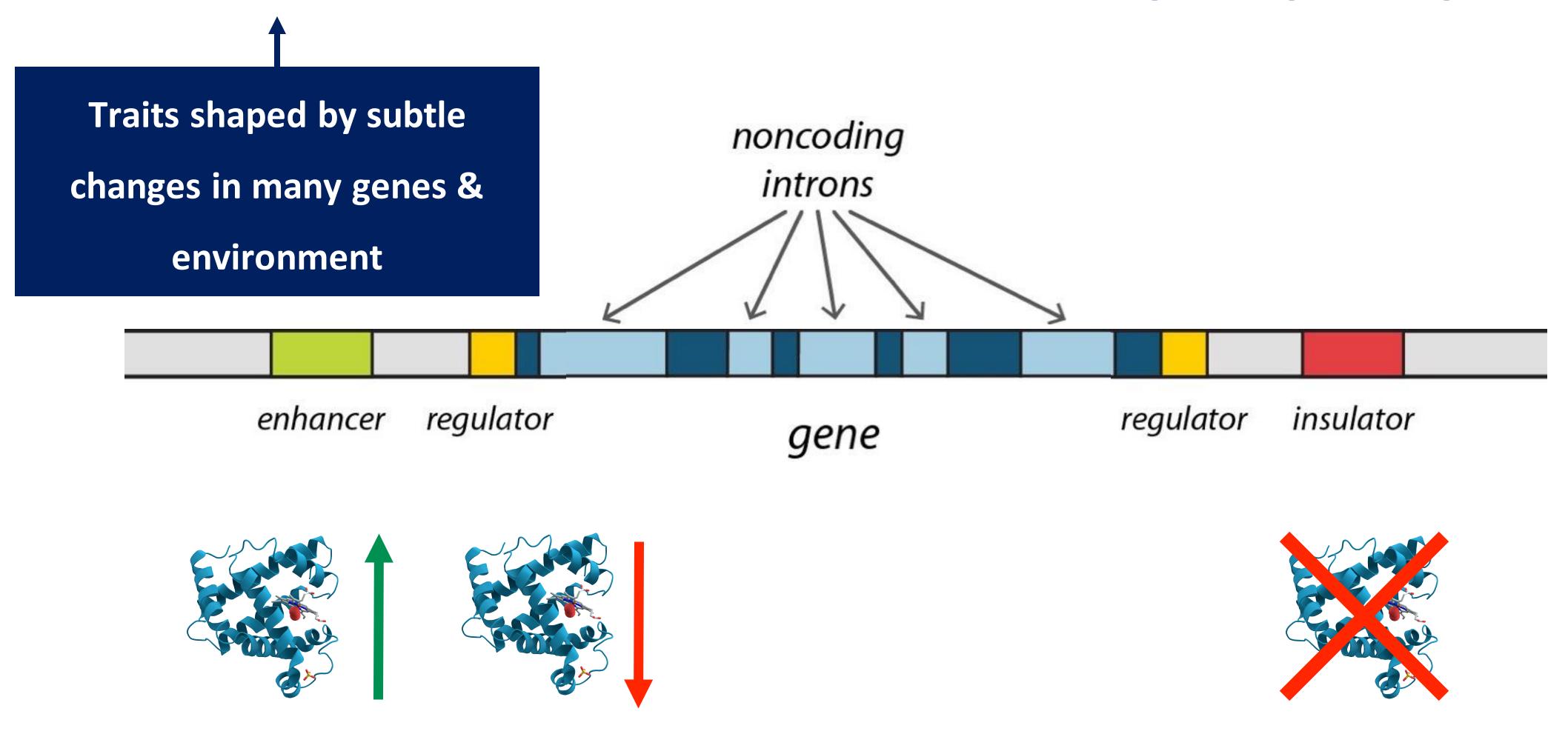




#### Regulatory sequence controls how the DNA is used



#### Complex traits, like behavior, result from changes in gene regulation



# How do we find important parts of the genome?

How do we figure out what they do?

### Why IS dog genetics a thing?







Aggression
Anxiety
Cognitive disfunction
Compulsive disorders
Noise & storm phobia
Impulsivity

Allergies
Cancer
Others

### How do changes in DNA lead to changes in dog behavior & health?

Can this help us find better treatments for diseases?













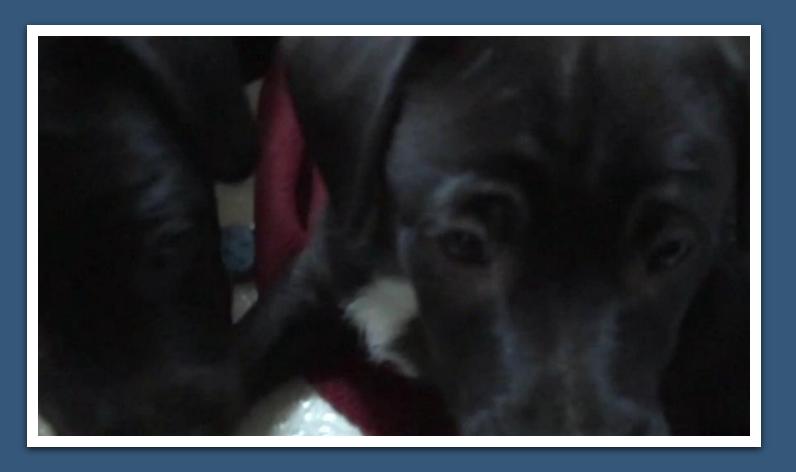
#### Can we use genomics to:

Help predict whether a puppy will be successful

Increase the rate of selection in breeding programs

Put dogs into the right jobs





PLUS: Can be done at young age

CAUTION: Will never be perfect (environment matters)



#### We're building a shared data resource to accelerate research

No one owns the data We'll share share any genetic tests we develop



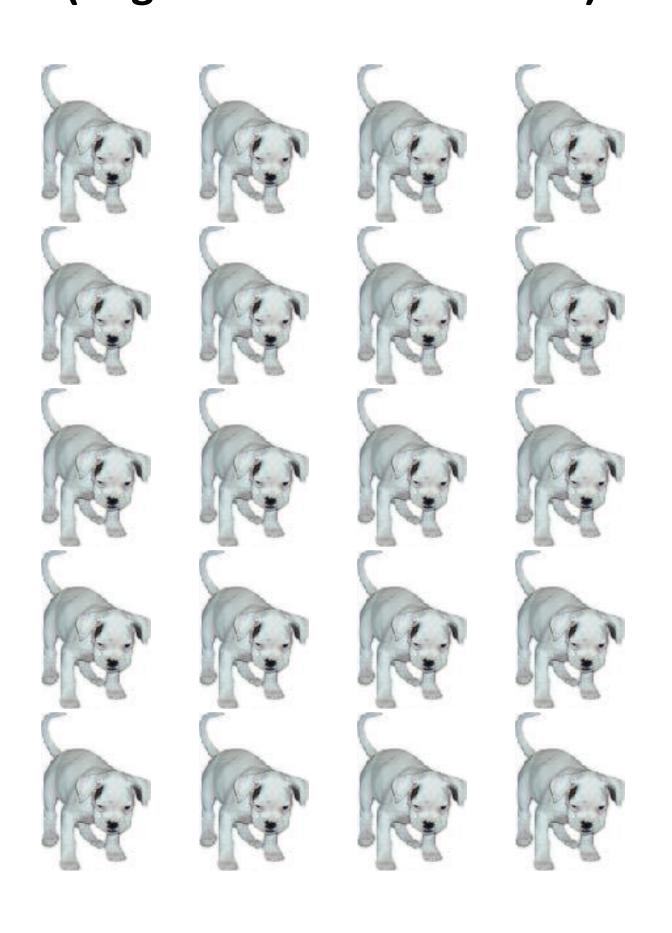


# Mapping genes in dogs: the science

controls (healthy dogs)

Where are they different?

**Cases** (dogs with disease or trait)



## **Coat Color in Boxers**



9 SolidBoxers

SS



Ssw



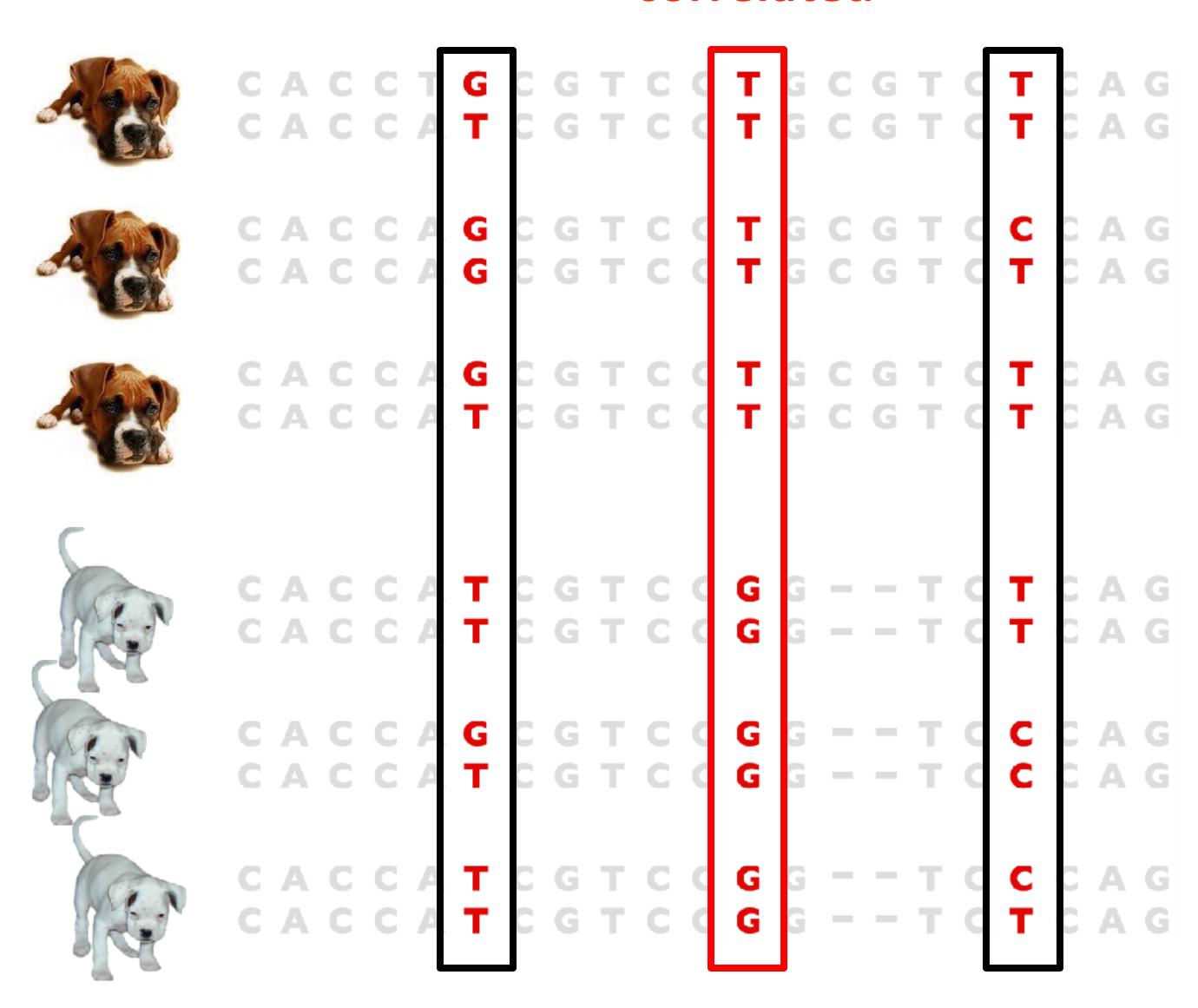
10 White Boxers

**S<sup>W</sup>S<sup>W</sup>** 

~2% deaf

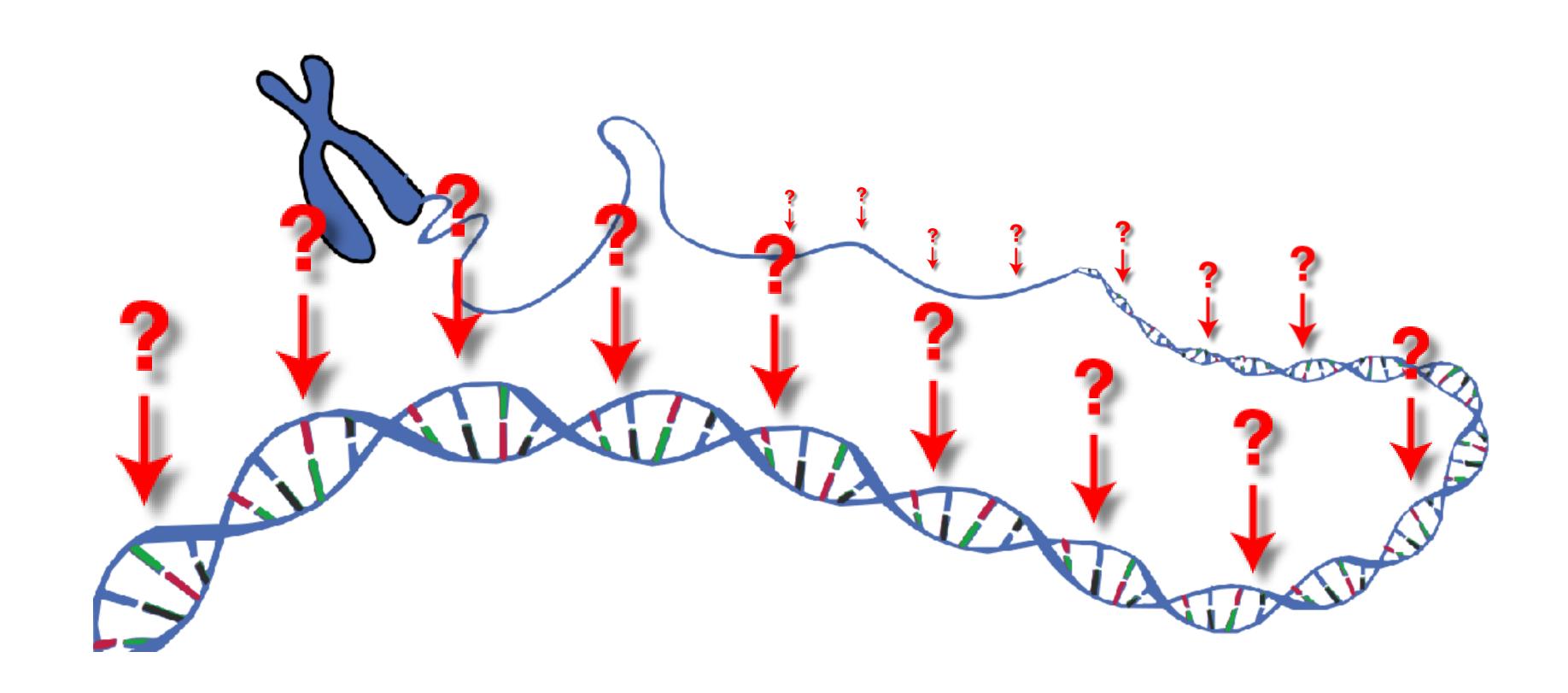
# "Is this marker correlated with my trait?"

### correlated

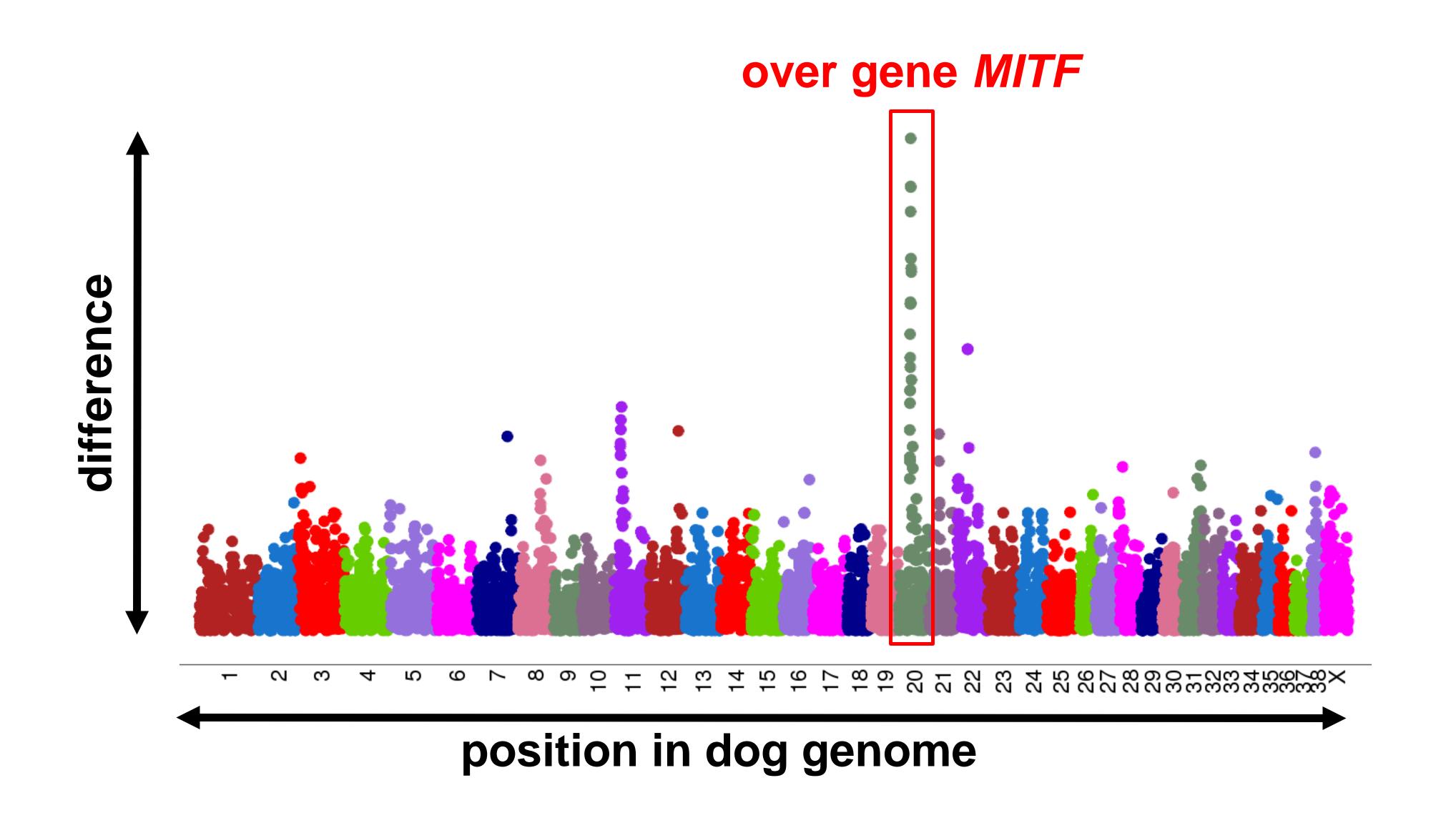


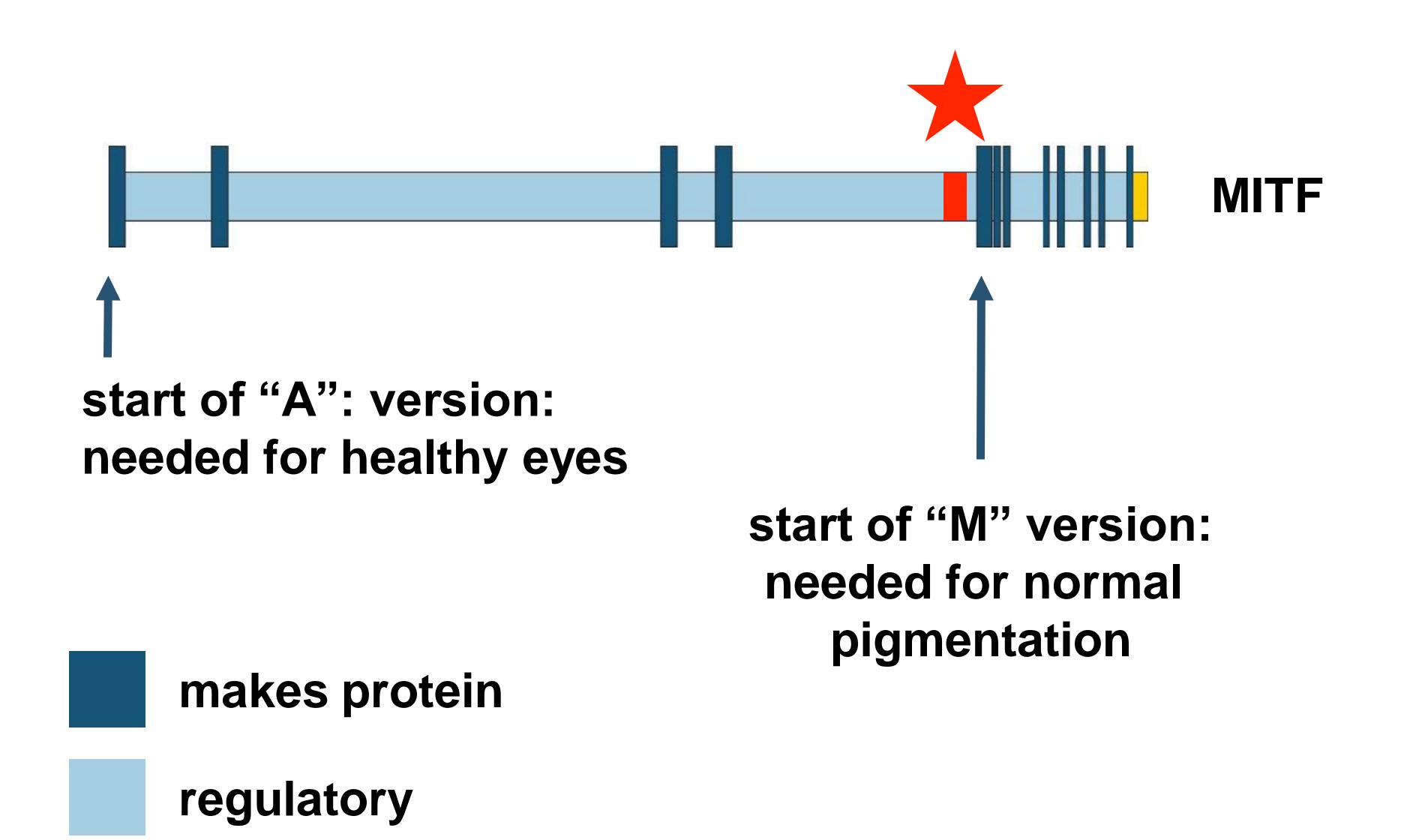
# Genome-wide association study (GWAS)

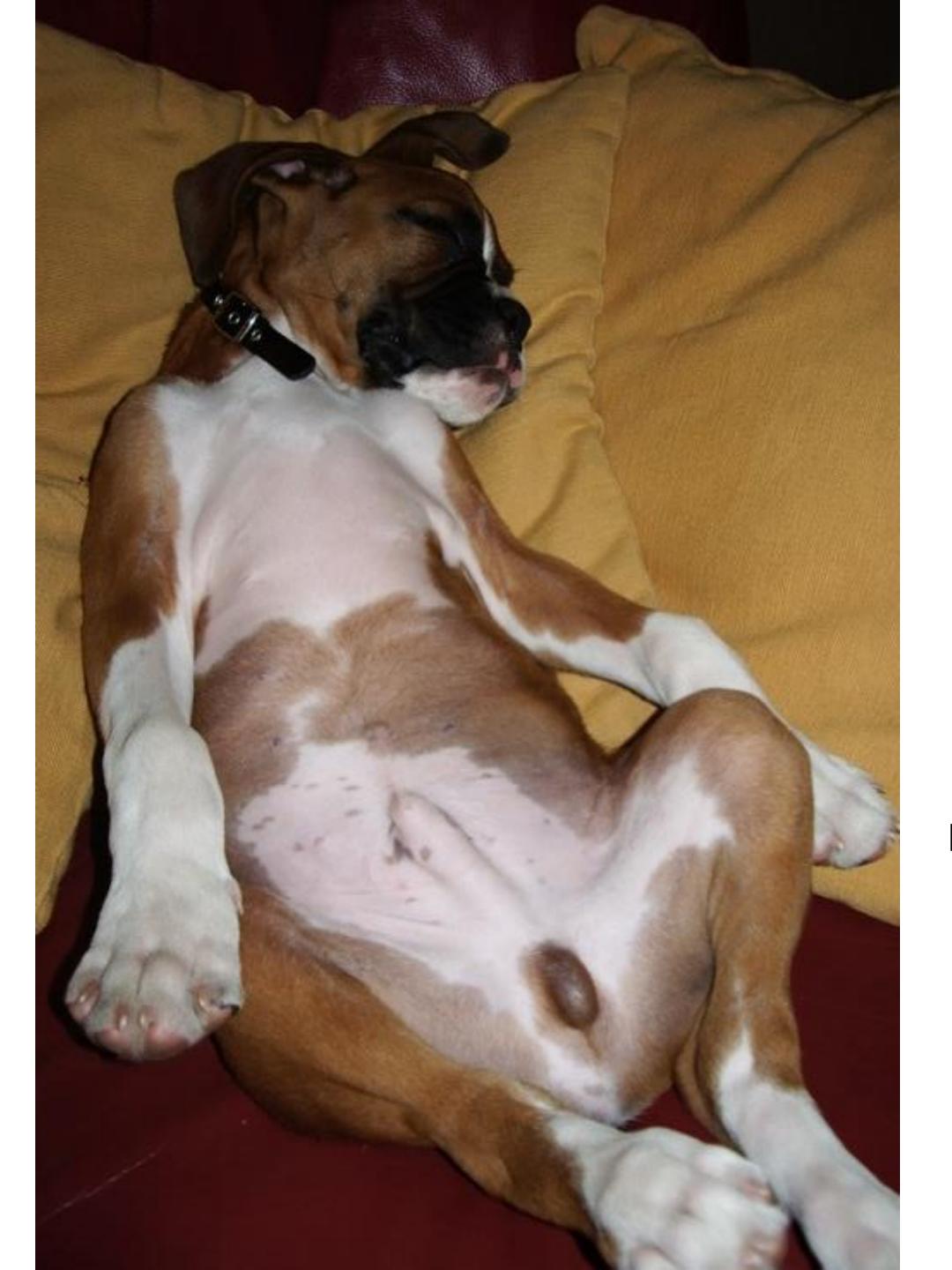
For each SNP, ask "Is this SNP correlated with my trait?"



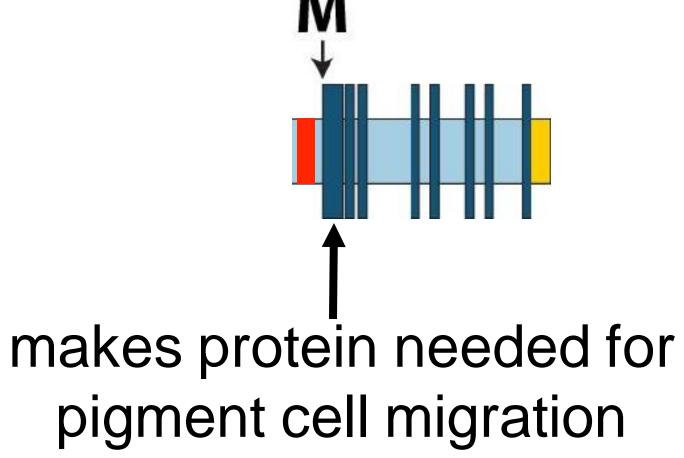
# Find region with most correlated SNPs







# hypothesis: regulation of M is disrupted



# Illustrates power of dog genetics



Mice with broken MITF protein:

White

Deaf

**Blind** 

**Dead** 



Dogs with MITF regulatory variants:

White
Rarely deaf
Normal eyes
Not dead

# Compulsive disorder in dogs

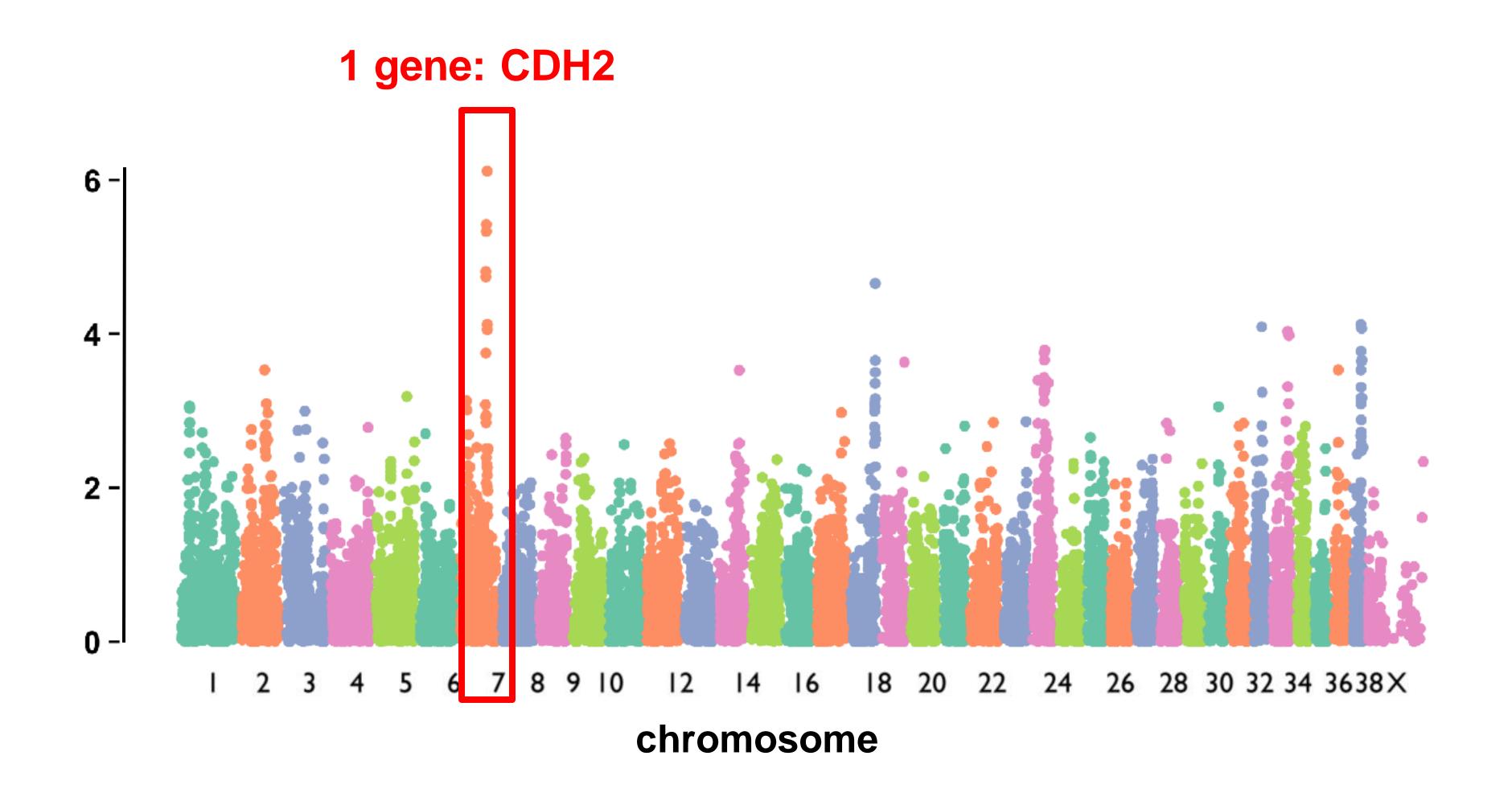




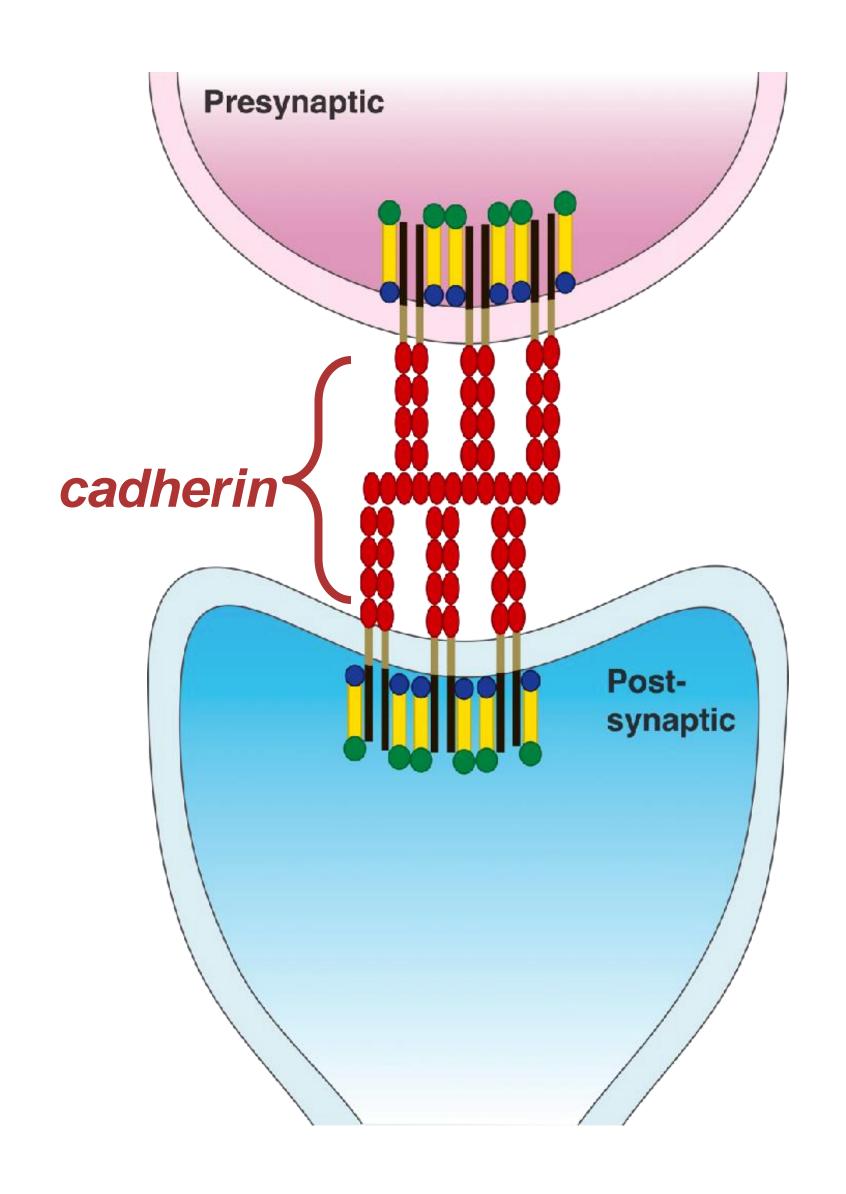


normal behavior done too much distressing, time-consuming and impairing onset in adolescence highly heritable poor response to treatment (including SSRIs)

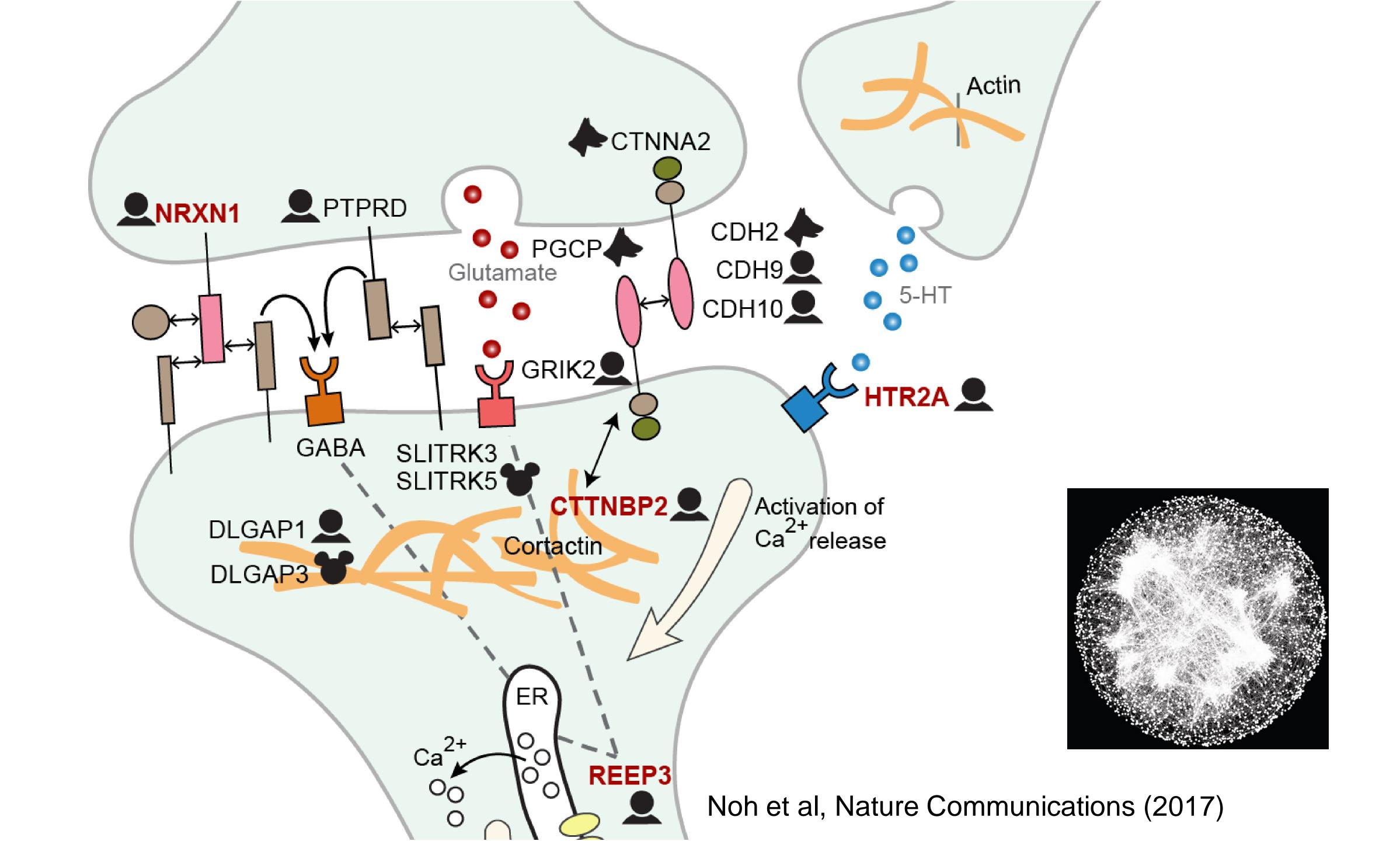
# Compare genomes of 92 affected and 67 healthy dobermans



### Function of CDH2



- Neural cadherin
- Found in glutamatergic synapses
- Synaptic plasticity (learning and memory)



# Can we predict which dobermans will get OCD?

# NO





# Pet genomics medicine runs wild

Genetic testing for dogs is big business. It is too easy for companies to sell false hope, warn Lisa Moses, Steve Niemi and Elinor Karlsson. They call for regulation.

Read more: karlssonlab.org/pets/

# Problem #1: we've only figured out part of the story

How much of the OCD risk in dobermans did we explain?



# Problem #1: we've only figured out part of the story

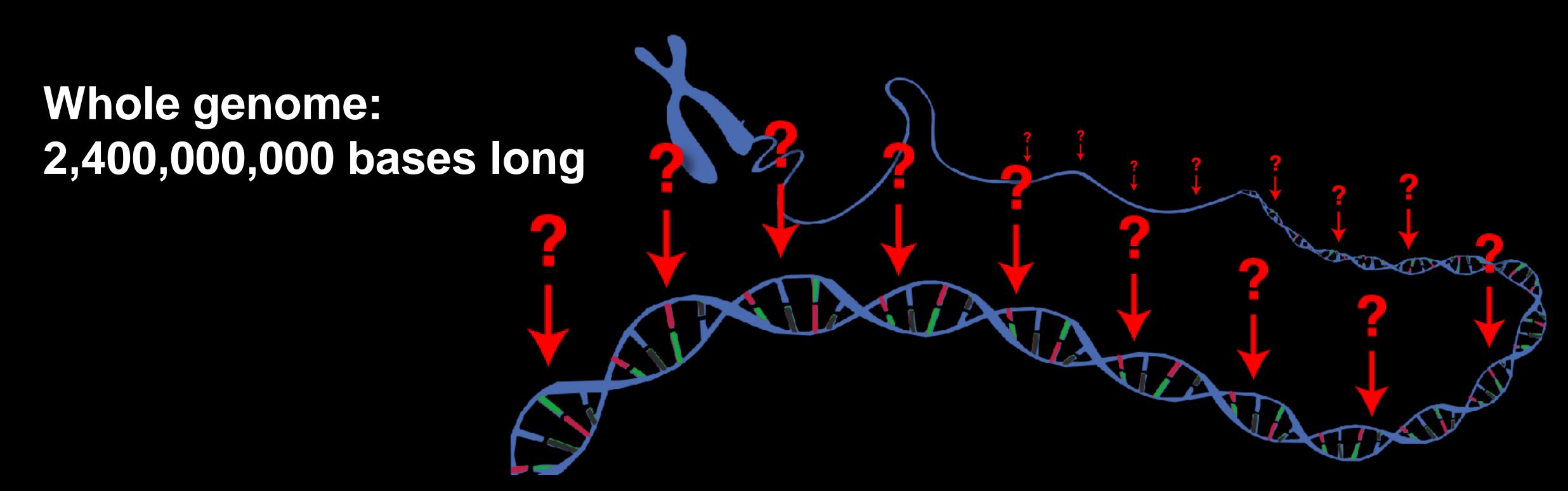


# Problem #2: We didn't find the "causal" mutation

2008: 20,000 SNPs

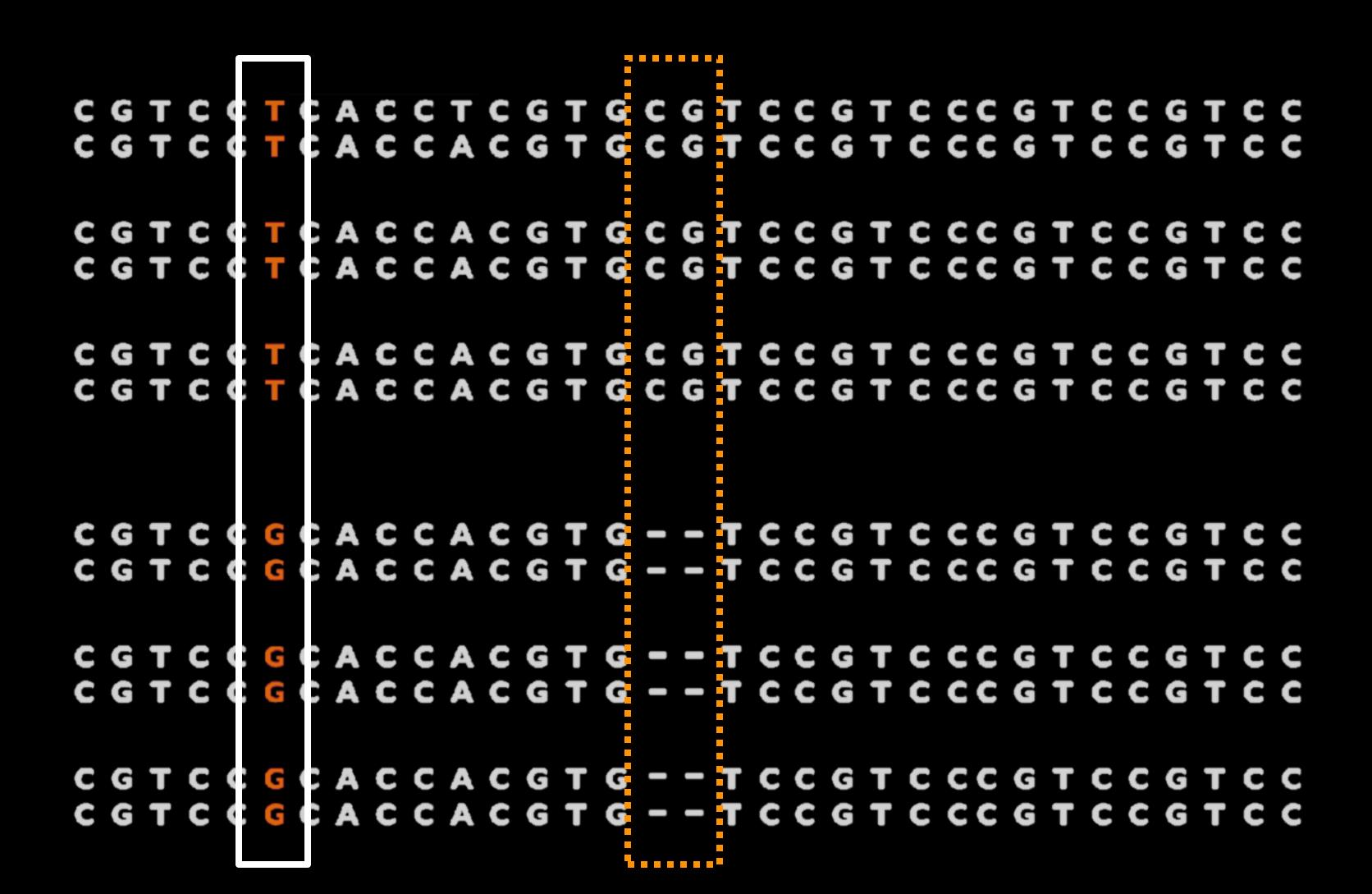
2014: 150,000 SNPs

2017: 600,000 SNPs



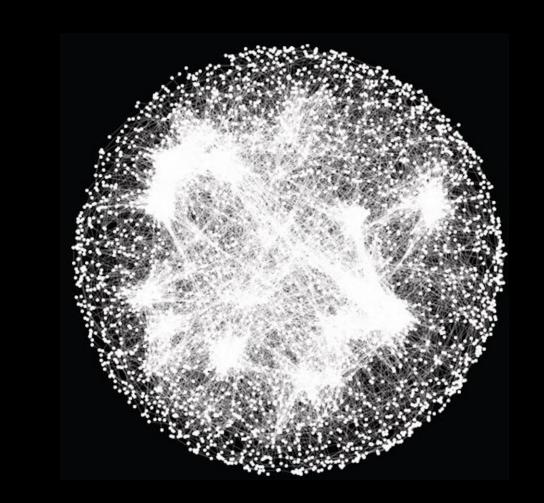
# Problem #2: We didn't find the "causal" mutation

A good marker in dobermans may not work in other breeds (or mutts)



# Problem #3: Genes interact with one another

The effect of the CDH2 variant may be different in different dogs (with different personalities?)











# Problem #4: We never tested predictive power

Scientists:

Can we find a change in DNA connected to this disease? Can it help us understand the biology of the disease?

Breeders: How do I breed healthier, more successful dogs?

Owners: Will my dog get sick?

# Solution:

We need BIG sample sizes

# ARTICLE

# Biological insights from 108 schizophrenia-associated genetic loci

Schizophrenia Working Group of the Psychiatric Genomics Consortium\*

Schizophrenia is a highly heritable disorder. Genetic risk is conferred by a large number of alleles, including common allele

36,989 cases and 113,075 controls

the findings. Many findings have the potential to provide entirely new insights into aetiology, but associations at DRD2 and several genes involved in glutamatergic neurotransmission highlight molecules of known and potential therapeutic relevance to schizophrenia, and are consistent with leading pathophysiological hypotheses. Independent of genes expressed in brain, associations were enriched among genes expressed in tissues that have important roles in immunity, providing support for the speculated link between the immune system and schizophrenia.

# The goal:

Predict whether a puppy is likely to be successful Put dogs into the right jobs

### **Step 1. Correlation**

Get DNA for a group of dogs

For each dog, find out if they have disease or trait

find genetic variants correlated with trait

### Step 2. Develop a predictive test

Get DNA for a NEW group of dogs

For each dog, find out if they have disease or trait

Develop test to predict which dogs will have trait from DNA

### Step 3. Validate predictive test

Get DNA for a NEW group of dogs

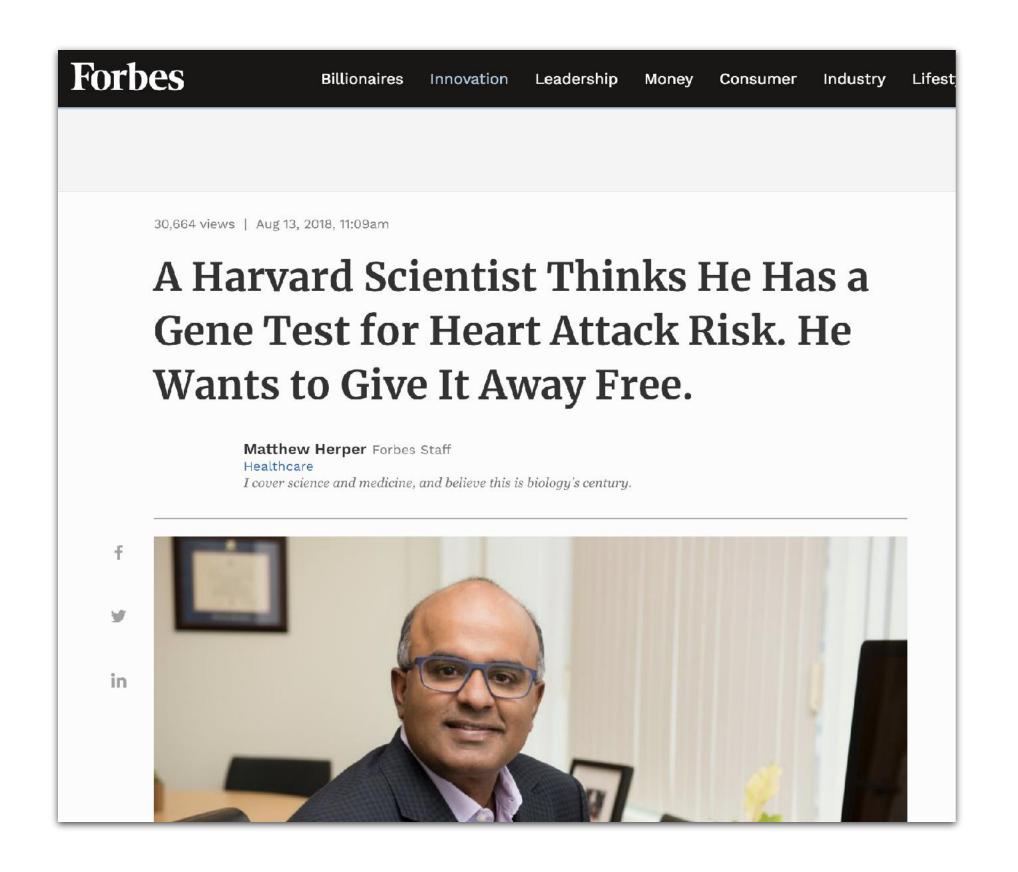
For each dog, find out if they have disease or trait

Validate genetic test

# Does genetic prediction work?

New genetic test for heart disease risk in humans

For each person: combines information from 6 million SNPs into 1 "polygenic risk score"



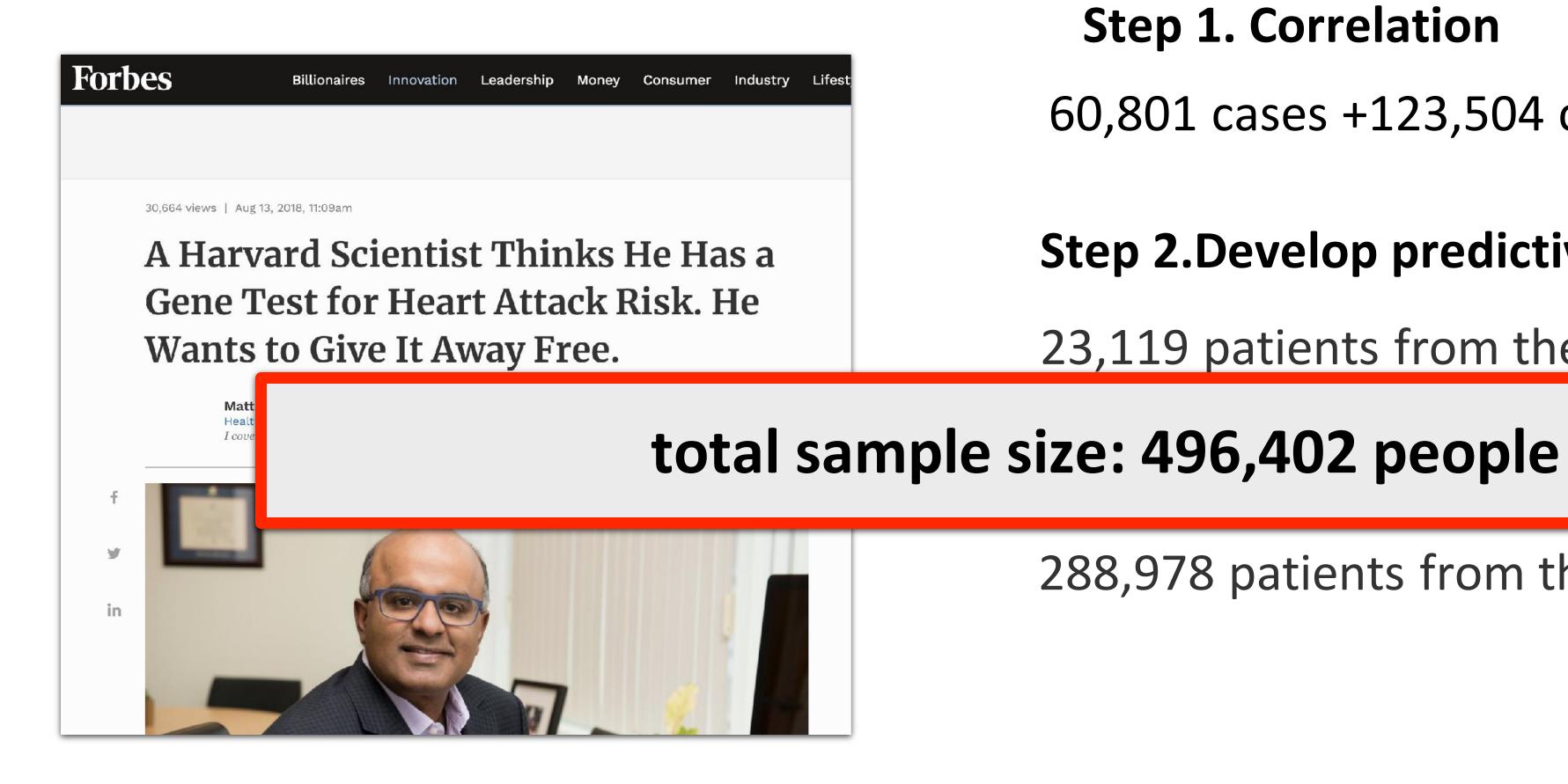
**High Risk Score + unhealthy lifestyle** 

high risk of heart disease

**High Risk Score + healthy lifestyle** 

average risk of heart disease

# Does genetic prediction work?



### **Step 1. Correlation**

60,801 cases +123,504 controls

### Step 2. Develop predictive test

23,119 patients from the UK

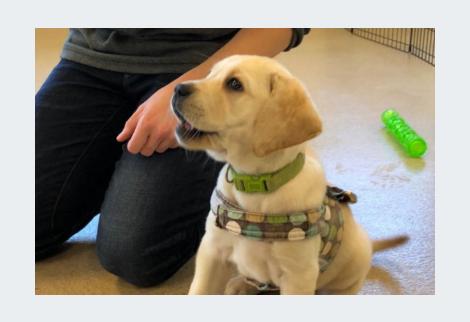
288,978 patients from the UK



# We're combining information from complementary studies









Pet dogs

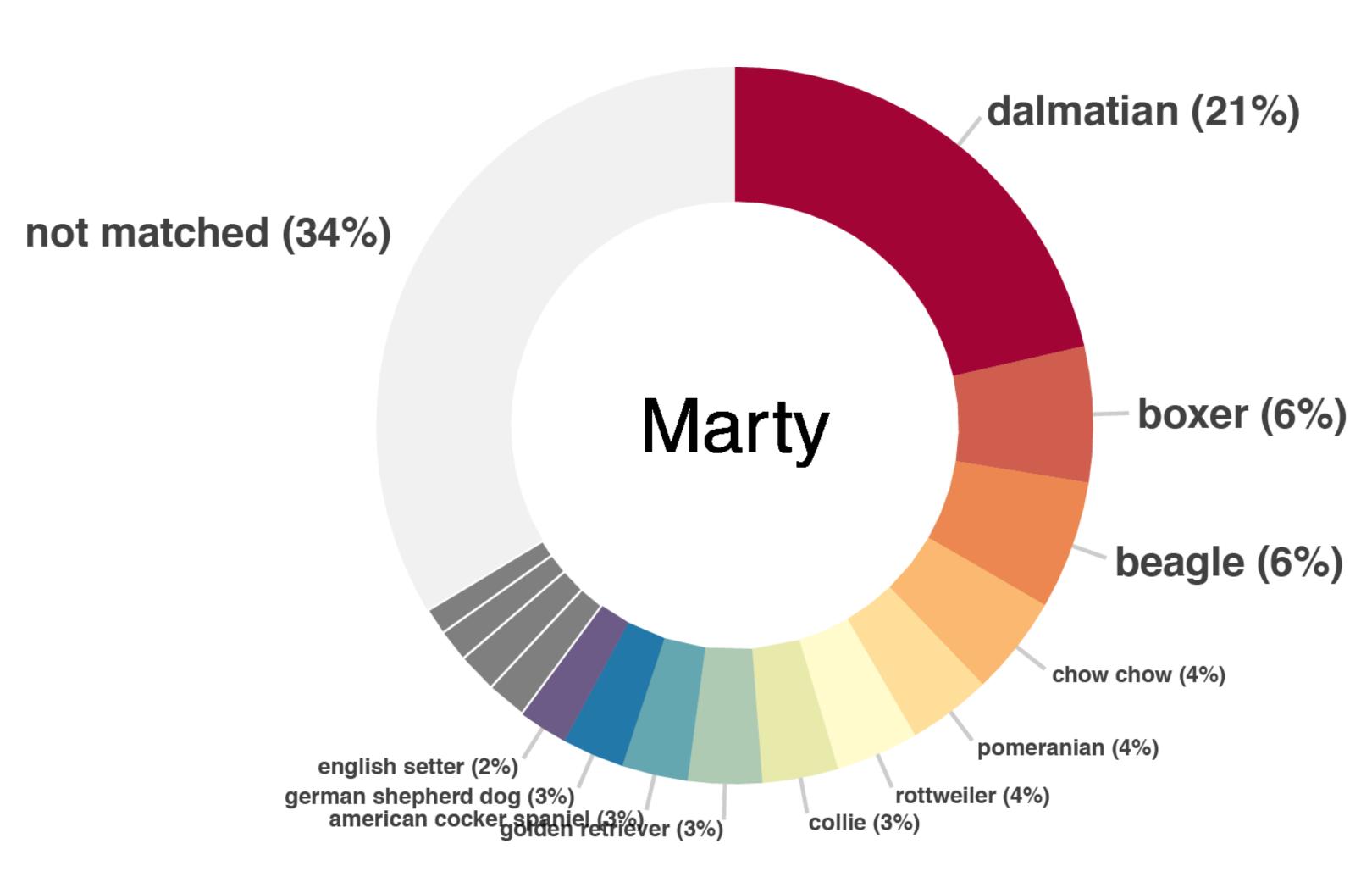
Purpose-bred working dogs

Wolf-dog hybrids

very large sample size	moderate sample size	small sample size
very diverse ancestry	breeds & intentional mixes	spectrum of wolf/dog mixes
owner reported phenotypes	phenotyped by professionals	phenotyped by researchers
no / weak selection on behavior (some historical selection)	strong selection on behavior	mixes of behaviorally distinct populations

# We're studying all dogs





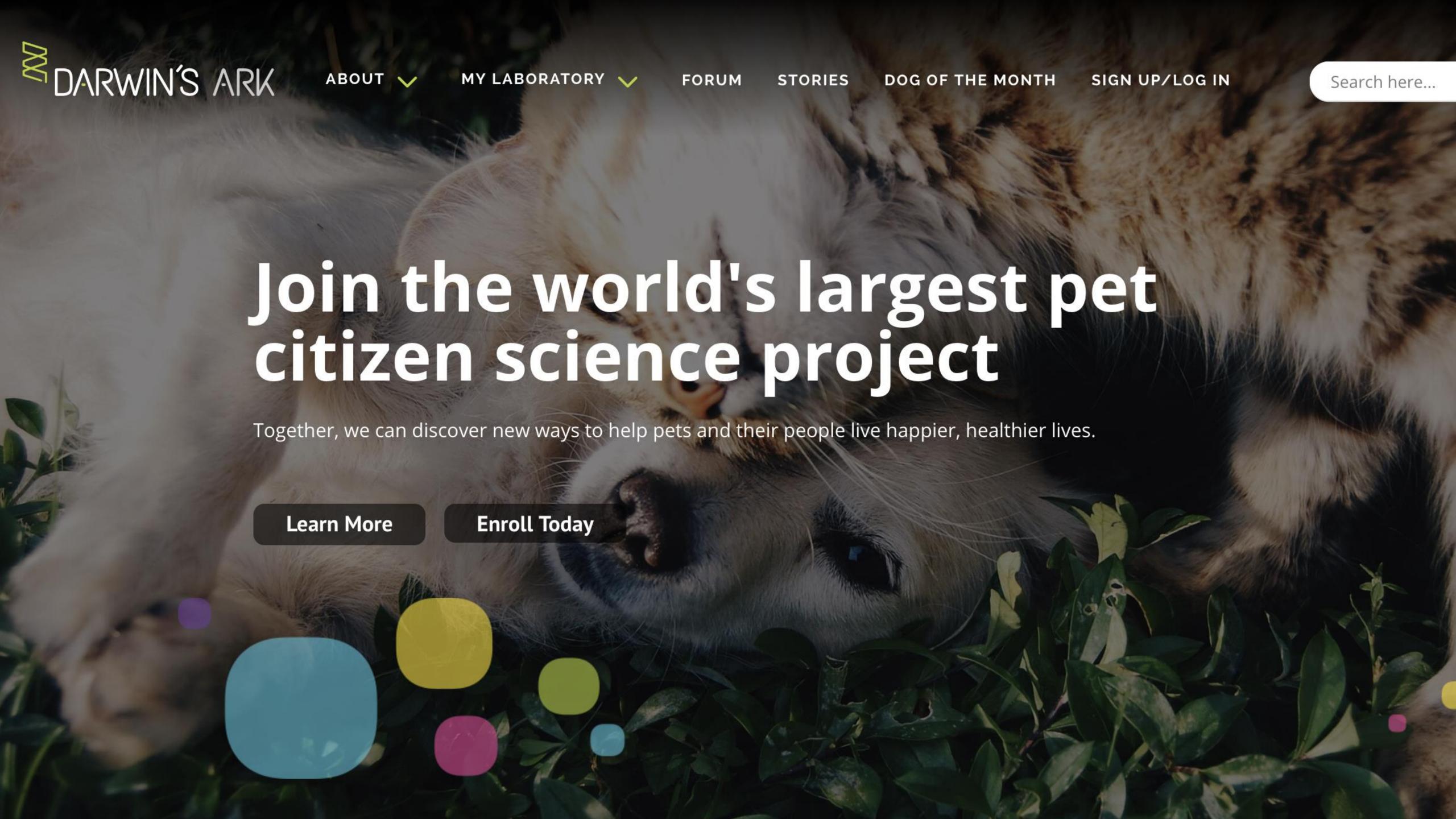
# We're using low-pass (1x) sequencing rather than arrays

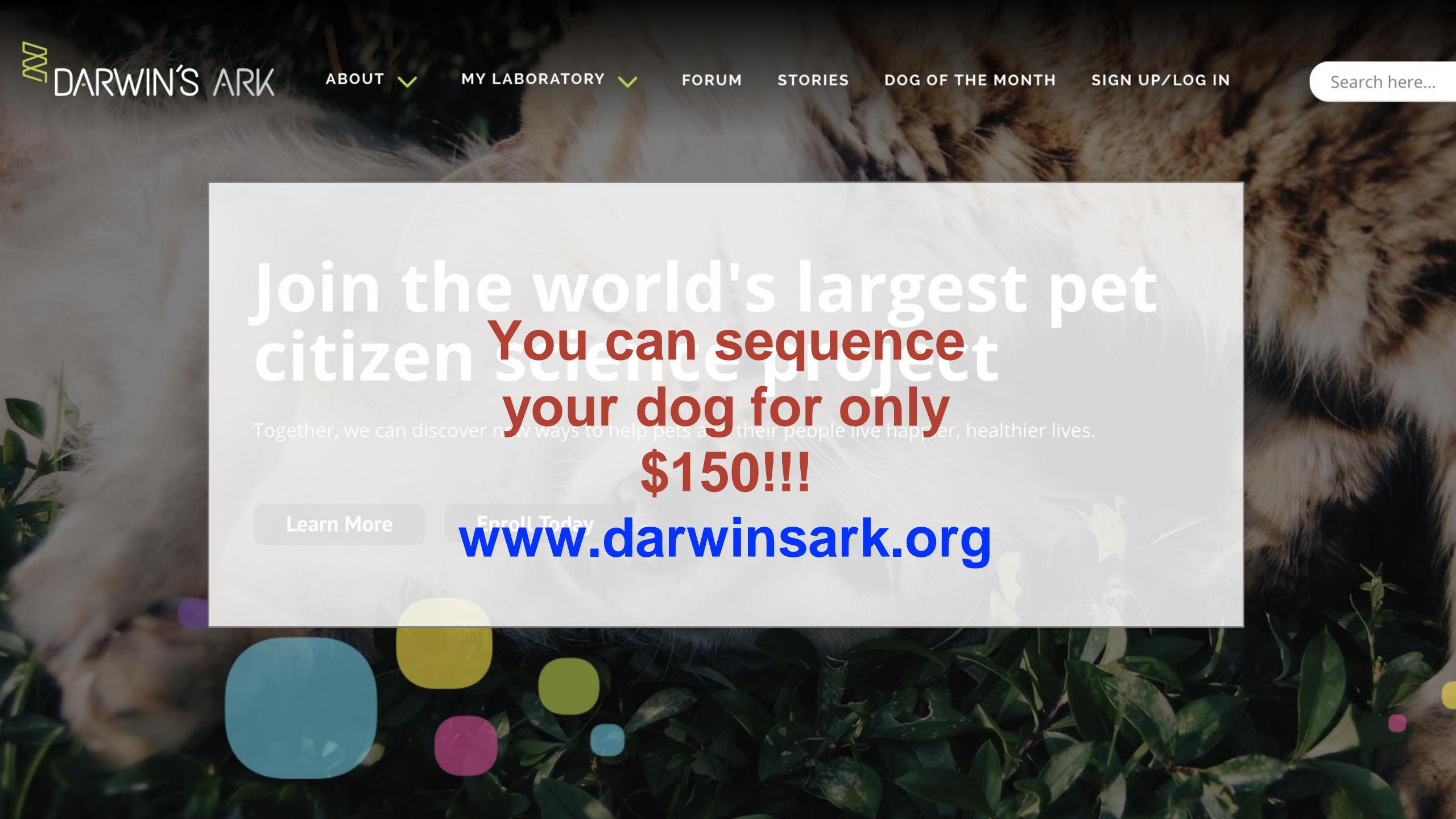
Validated in 10 very mixed breed dogs with 30x WGS data



	30x Whole Genome Sequencing	Genotyping	Low-pass sequencing*
Cost	~\$1,400	\$100-\$200	<\$100
# SNPS typed	>30 million	<800,000	7-9 million
Amount of DNA required	>500 nanograms	>500 nanograms	2-5 nanograms
Average accuracy vs 30x	N/A	98.75%	99.14%*

<sup>\*</sup> Higher accuracy possible with more stringent parameters (fewer SNPs called)

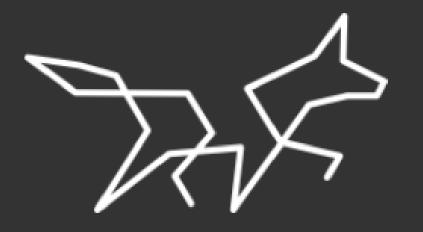




### The "Science" of Citizen Science

Darwin's Ark lets ordinary citizens become scientific partners. Our projects, such as Darwin's Dogs, combine genetics and behavior to advance the understanding of complex diseases.

We're a non-profit that subscribes to the open science model. This means **we do not own and will never sell your pet's data**. You contribute to an open source database and we share all the new discoveries we find freely with you and researchers around the world. Together we can advance health care for pets and their humans. For details on our process, see our Frequently Asked Questions.



22,567

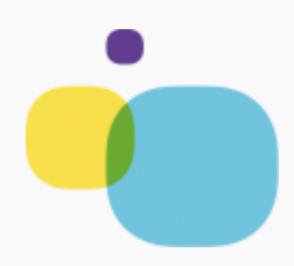
DOGS REGISTERED



2,487,298

ANSWERS COLLECTED

~5000 DNA samples collected ~1500 sequenced



# **Elinor's Laboratory**



>EDIT DESCRIPTION

### CITIZEN SCIENTISTS

MY DOGS + Add a Dog

#### **Primary Owner**



**Elinor Karlsson** Member Since 2016-10-23 elinork@gmail.com

>EDIT

Other Members

♣ Invite People



0 Likes

### Darwin 🚳

- > EDIT
- > CONTACT FOR MORE HELP

Born 2003-11-24

**Order DNA Kit** 

Free Kit Waitlist

8

**Survey Status** 

2 / 21 Surveys

**Next Surveys** 

>Communication >The Great Outdoors

View All >

### Question 1/10



Play

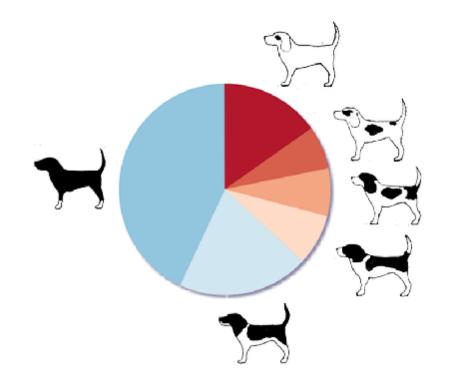
## Darwin enjoys life



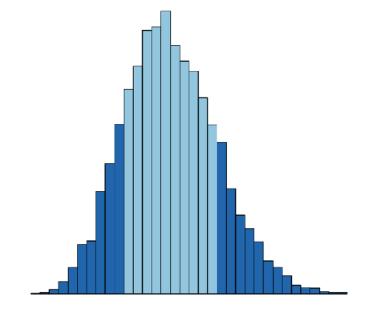
Next

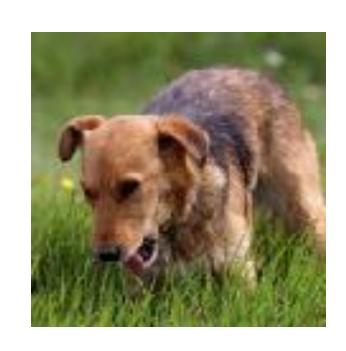
#### 200+ questions per dog

- 1. Morphology
- 2. Selected behaviors
- 3. Complex behavioral traits & disorders
- 4. Traits suggested by dog behavior experts (IAABC)
- 5. Food & food allergy related traits







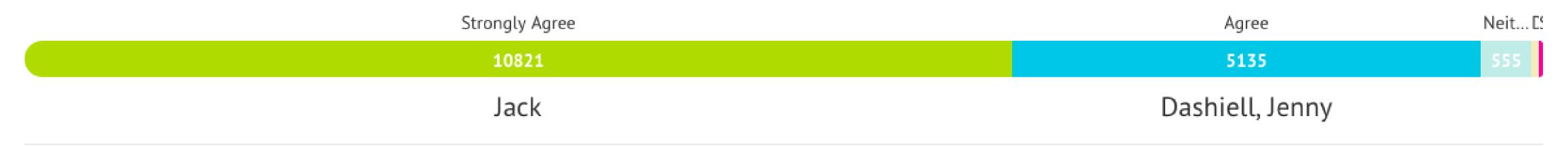




#### Returning results: how does your dog compare?

#### **Today: Simple trait comparisons**





#### Your dog wants to play



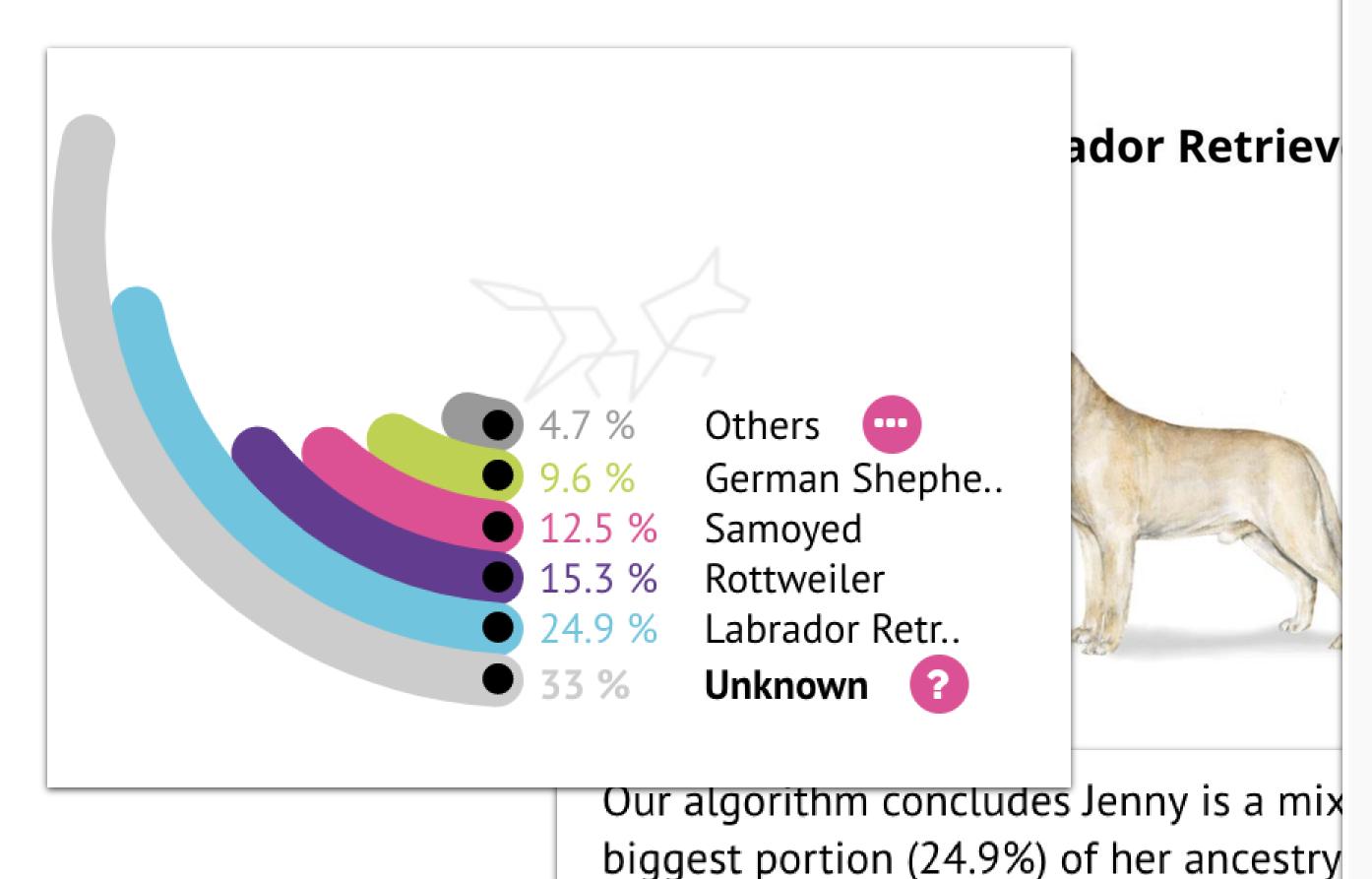
#### Your dog becomes aggressive when excited



#### Returning results: what is your dog's breed ancestry?

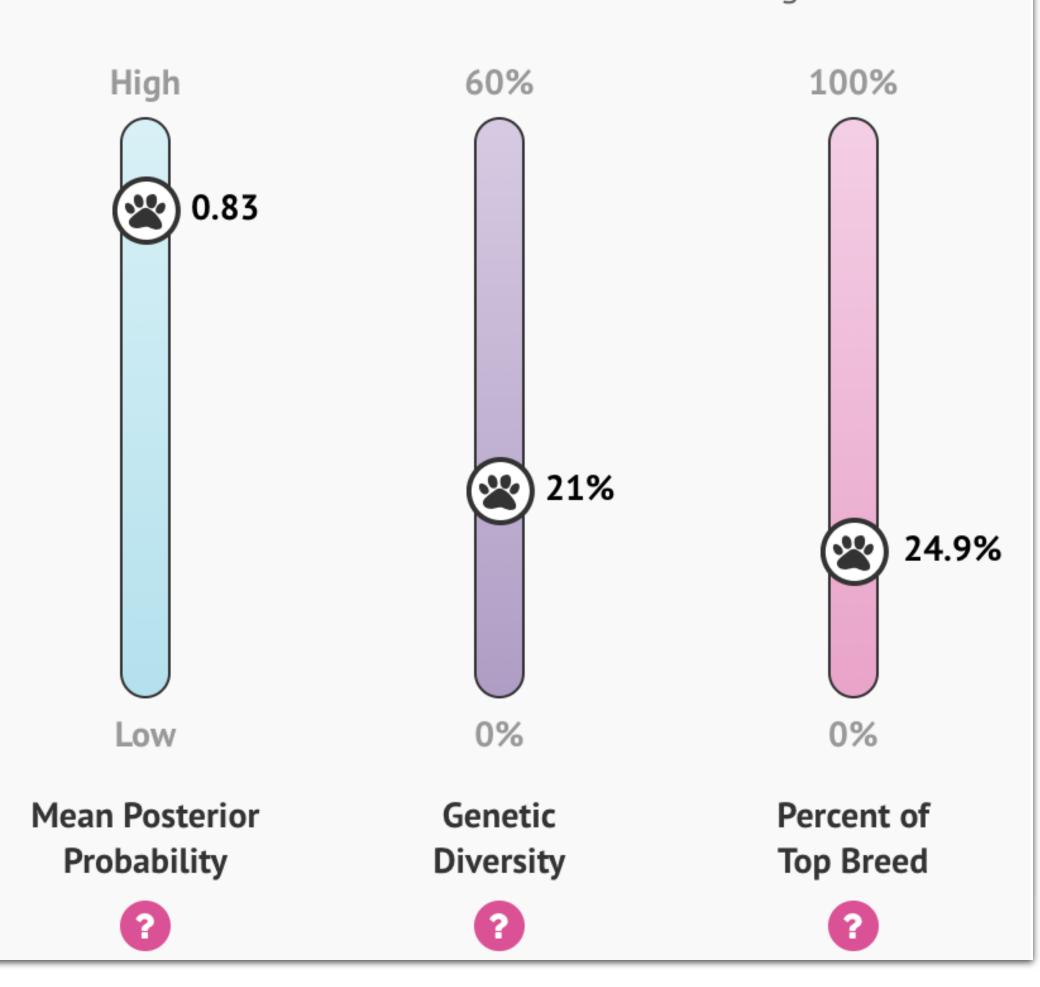
Retriever, but we find other breeds as w

#### **Today: Breed results**



How did we get these results?

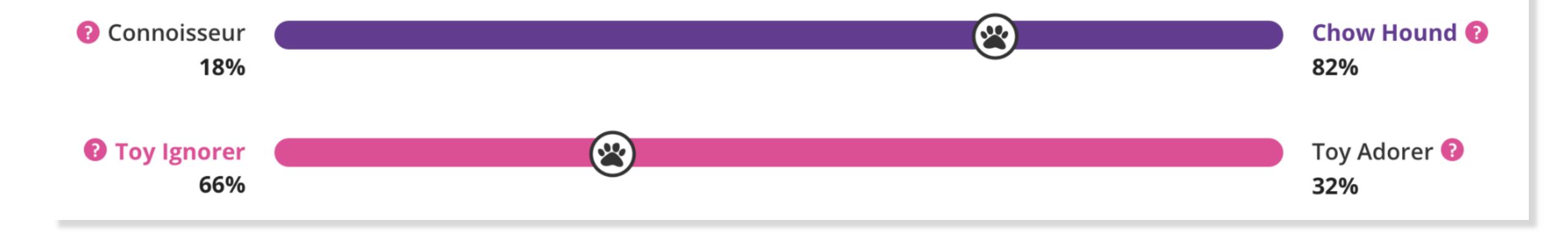
We used a combination of three statistics and Jenny's DNA results to decide that she was a mixed breed dog.



# Do you think we got Scruffy's breed mix right? Not Sure Next

#### Returning results: personality profiles

Soon: Personality profiles from surveys



#### Returning results: morphology predictions

#### **Future: Morphology predictions**



X-Small
under 15 lbs
Chihuahua, Pomeranian,
Shih Tzu, Papillon



Small
15-30 lbs
West Highland White Terrier,
Boston Terrier, Dachshund,
Jack Russell Terrier



Medium
30-50 lbs
Corgi, English Springer Spaniel,
English Bulldog



Large 50-75 lbs Golden Retriever, Labrador Retriever, Standard Poodle, German Shorthair Pointer



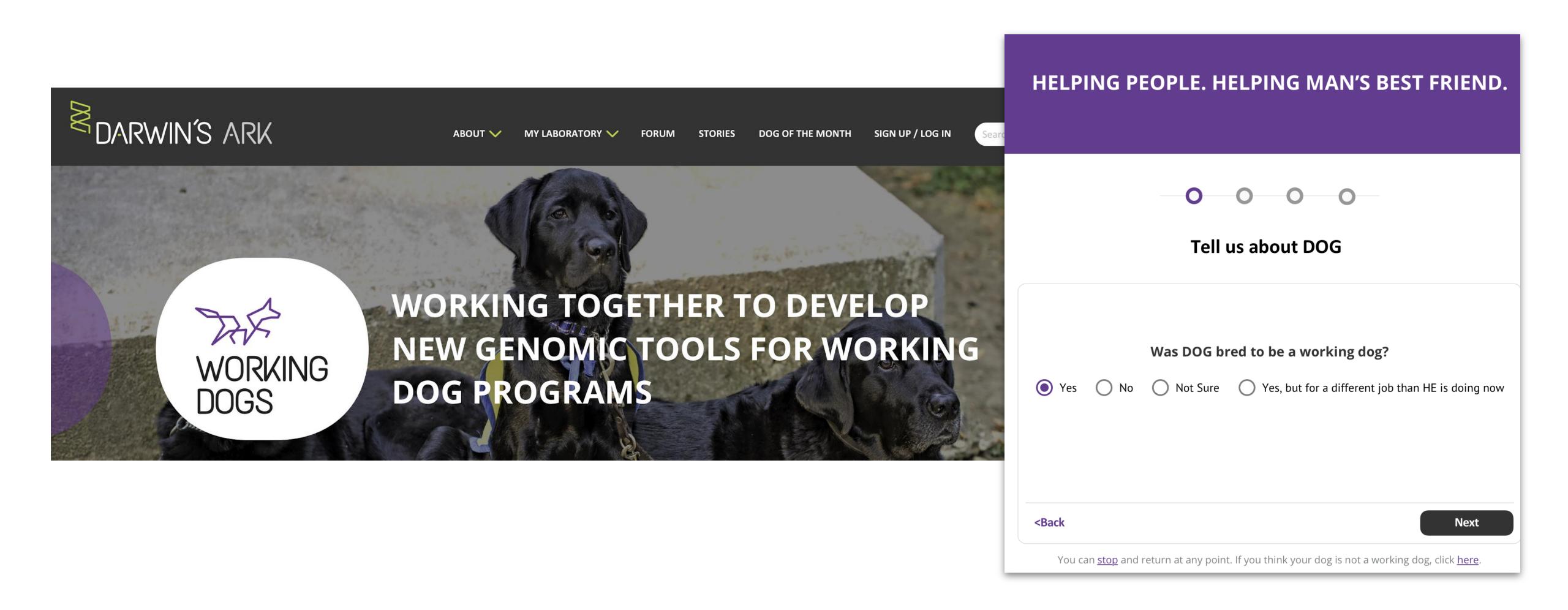
X-Large
75 lbs and Greater
Leonberger, Irish Wolfhound,
Great Dane, Newfoundland



We predicted **Pirl** with size 2.7 (±0.5), Larger than 68% of dogs.

#### Coming soon: "Working Dog" portal on Darwin's Ark site

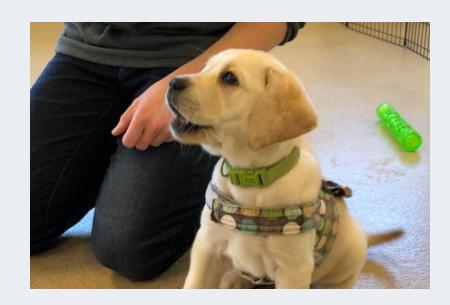
Any dog owner can enroll their working dog.



#### Our approach: ask same question in different ways









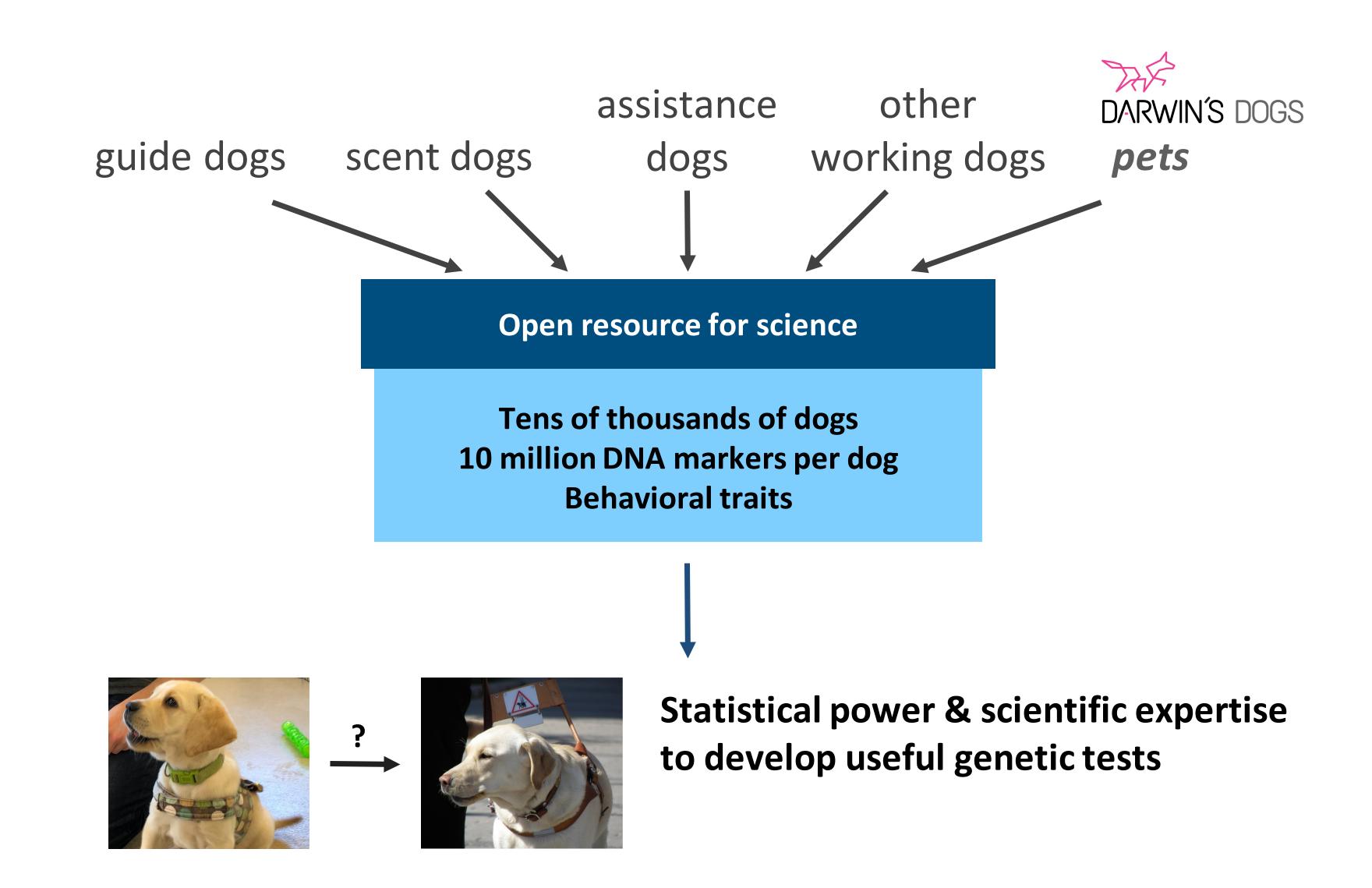
#### Pet dogs

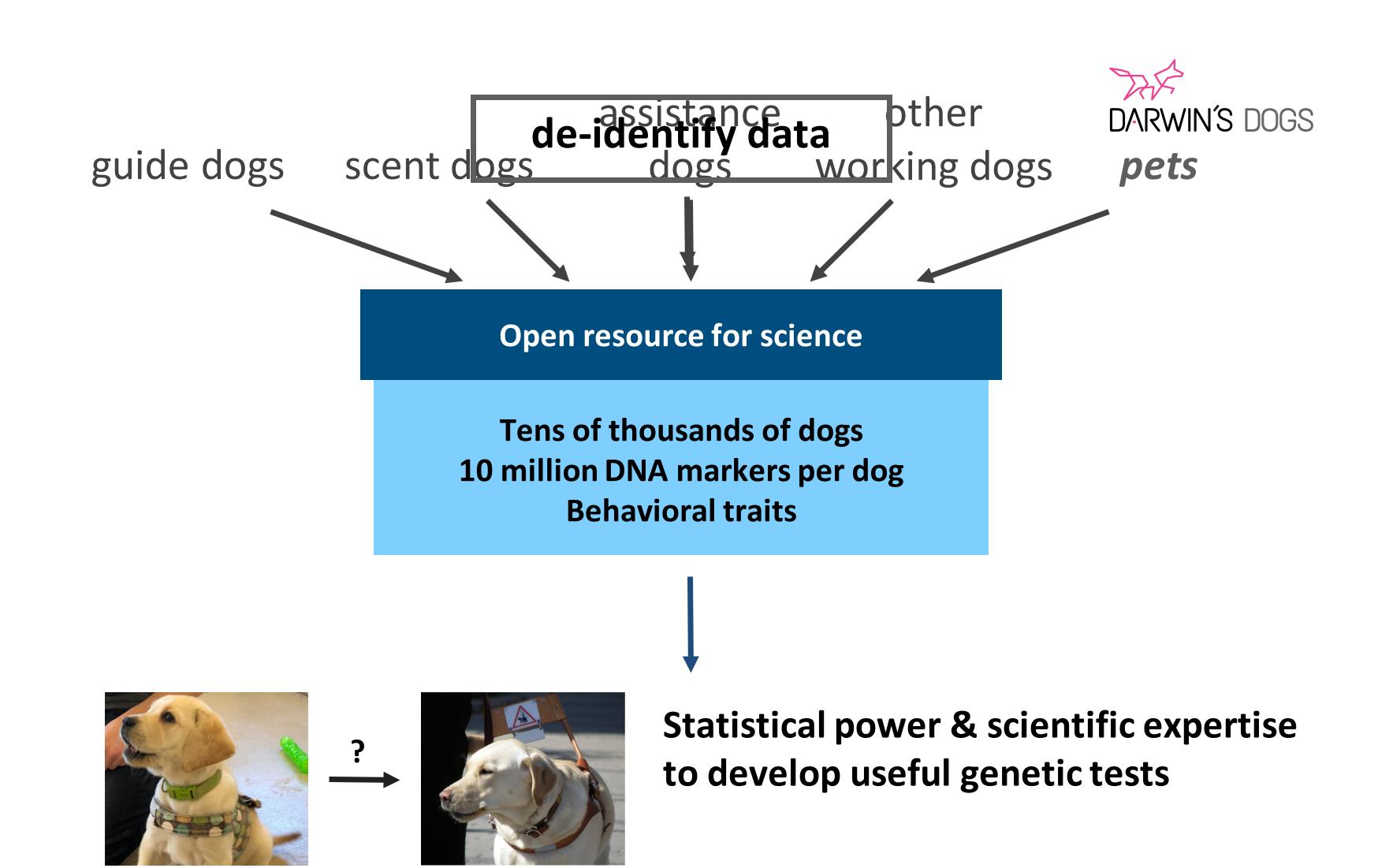
#### Purpose-bred working dogs

Wolf-dog hybrids

very large sample size	moderate sample size	small sample size	
very diverse ancestry	breeds & intentional mixes	spectrum of wolf/dog mixes	
owner reported phenotypes	phenotyped by professionals	phenotyped by researchers	
weak selection on behavior & health (some historical selection)	strong, ongoing selection on behavior & health	mixes of behaviorally distinct populations	

#### Focus on getting HUGE datasets





**SHORT TERM:** Type variants linked to diseases

MEDIUM TERM: Accelerate breeding program progress

LONG TERM: Develop new tools for genetic prediction





**SHORT TERM:** Type variants linked to diseases

**SHORT TERM:** Type variants linked to diseases

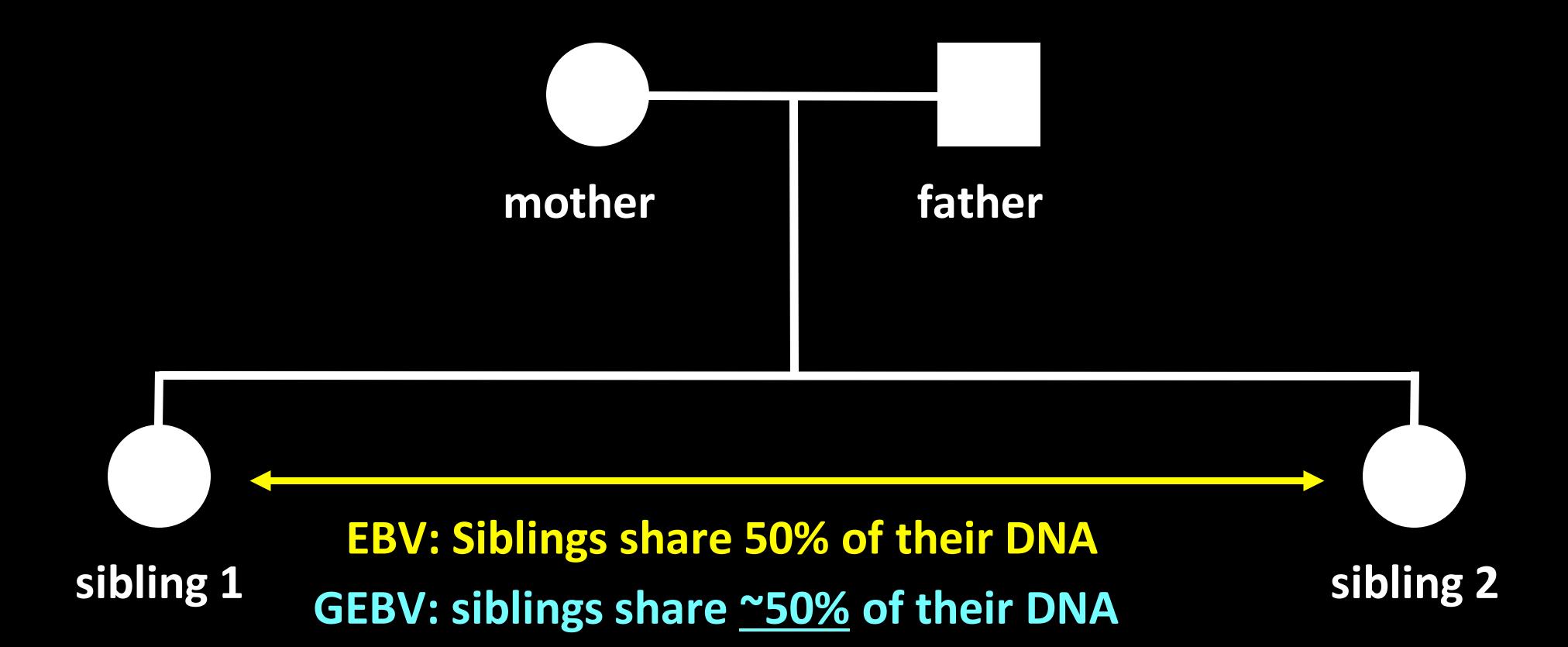
Work with organizations to figure out what tests are useful in their dogs now Caveat: need to assess low-pass sequencing accuracy & speed

MEDIUM TERM: Accelerate breeding program progress

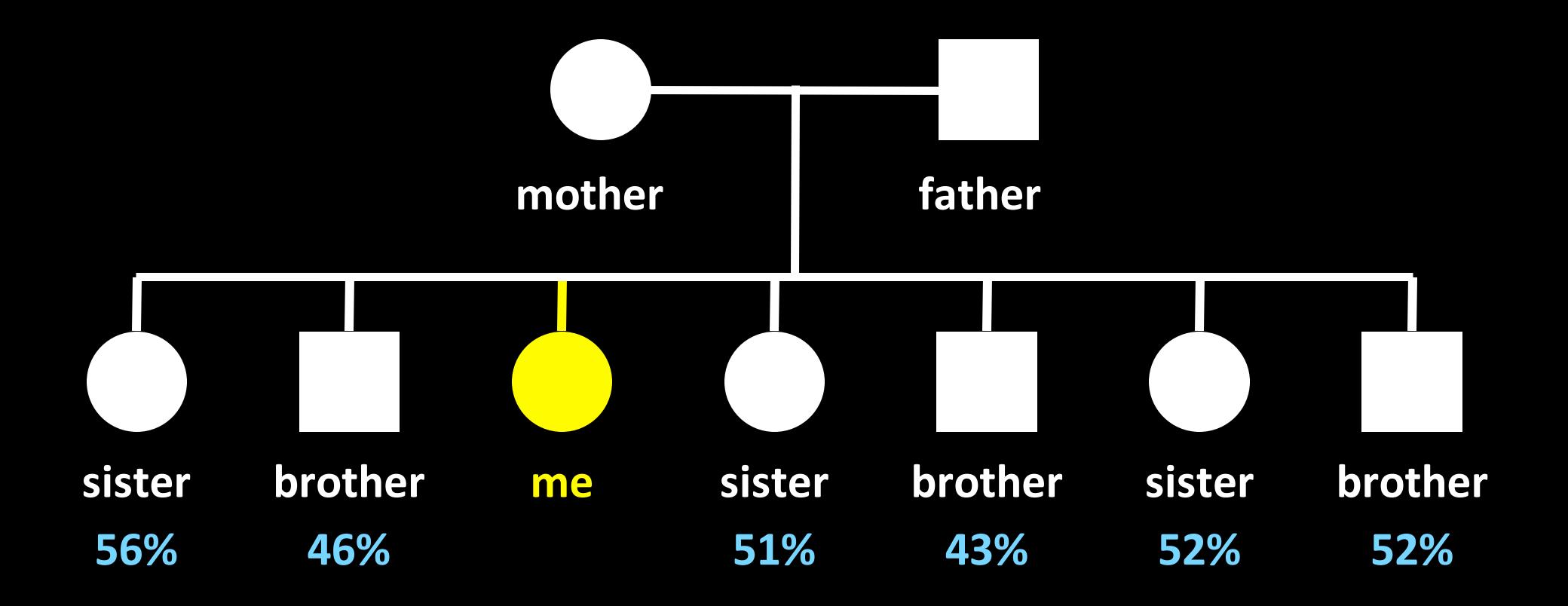
#### Breeding for better dogs through genomic selection

Select dogs for breeding based on their performance and the performance of their relatives

No genetic testing: Estimated Breeding Value With genetic testing: Genomic Estimated Breeding Value (GEBV)







MEDIUM TERM: Accelerate breeding program progress with more accurate GEBVs (even for programs with smaller pedigrees)

LONG TERM: Develop new tools for genetic prediction

LONG TERM: Understand & treat diseases better -

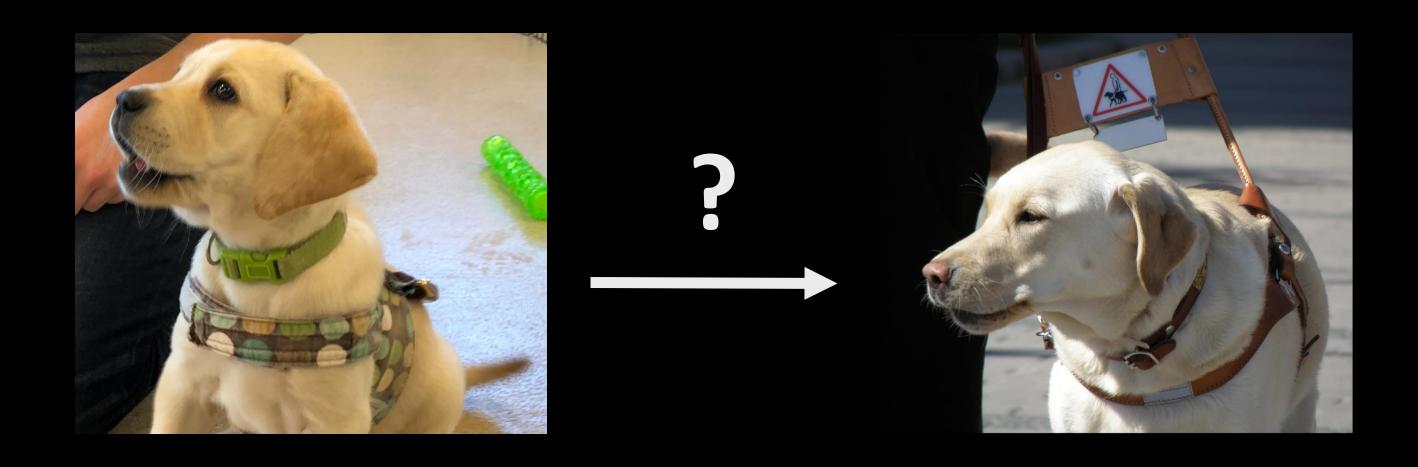
in dogs and their humans

#### Dog genomics is in its infancy

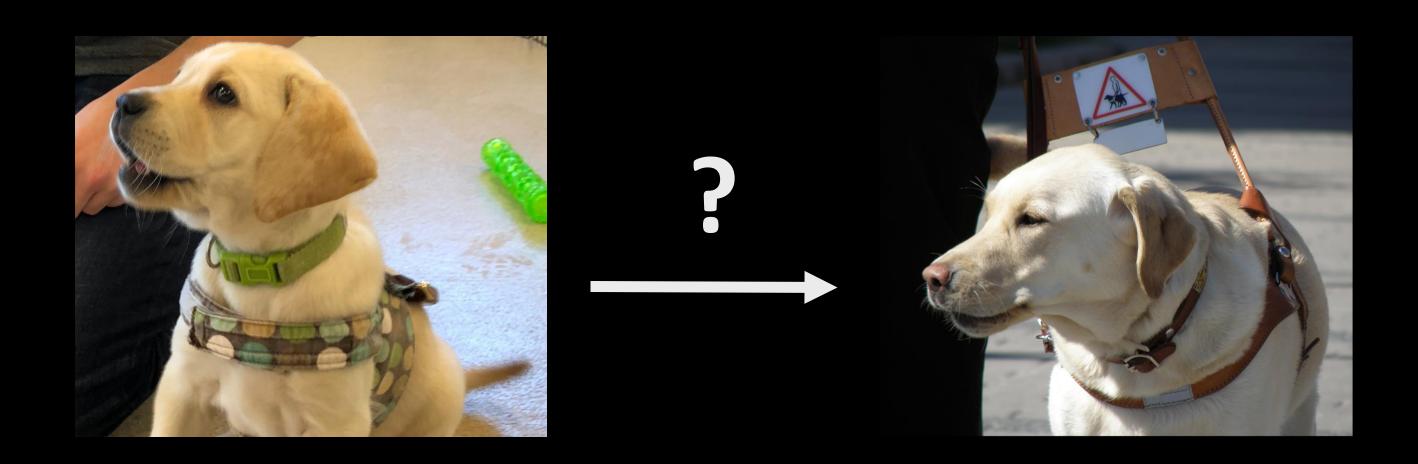
We can't yet predict diseases or traits (except for a few easy ones)

We'll never be perfect (environment matters a lot!)

Genomics can be powerful tool - if we think big



## We need new approaches



Is this puppy worth the cost of training?

## We need new approaches



How do we breed more dogs that succeed?

## We need new approaches



Which job is this dog suited to?

## Will it work?

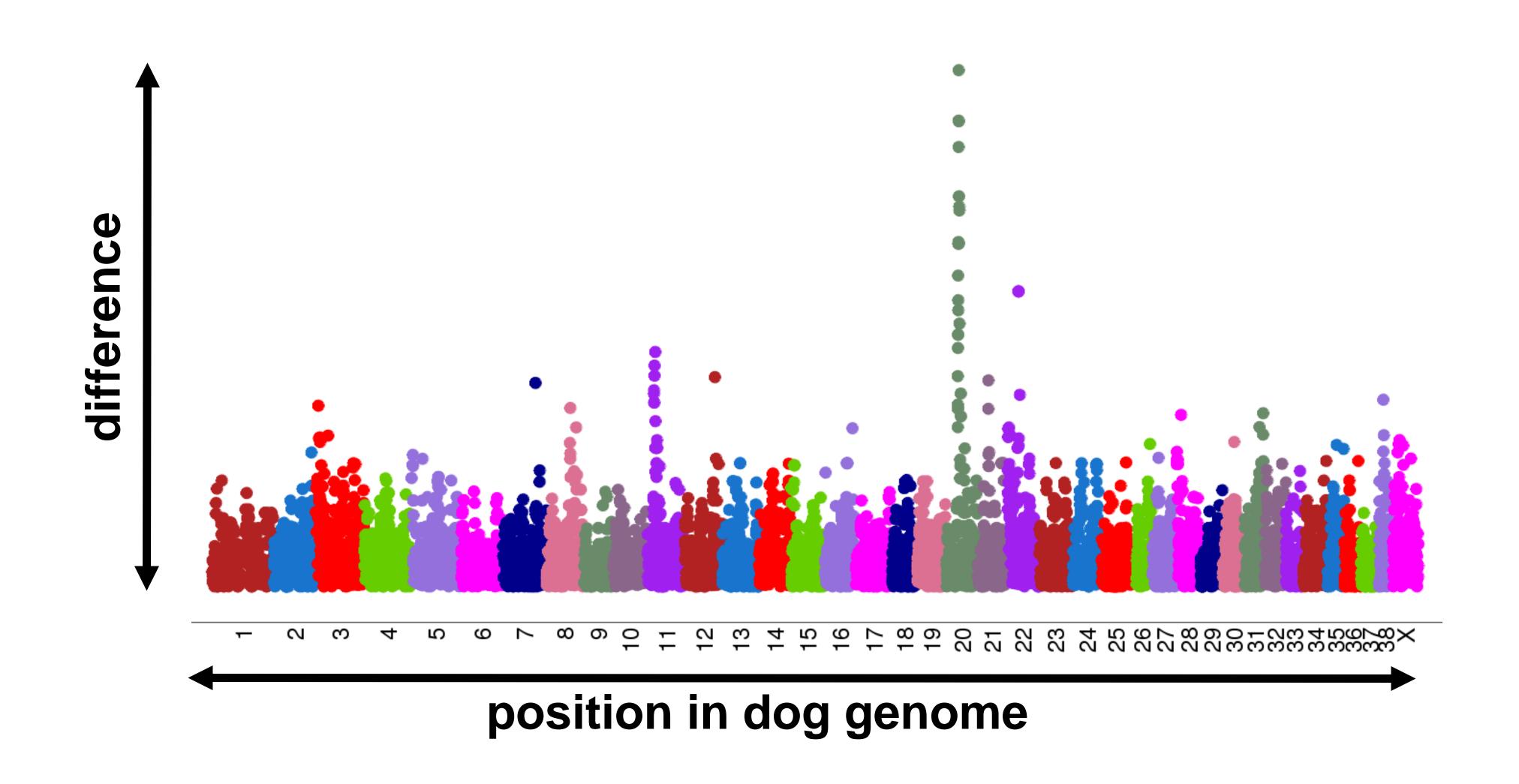
YES!

with <u>lots</u> of dogs

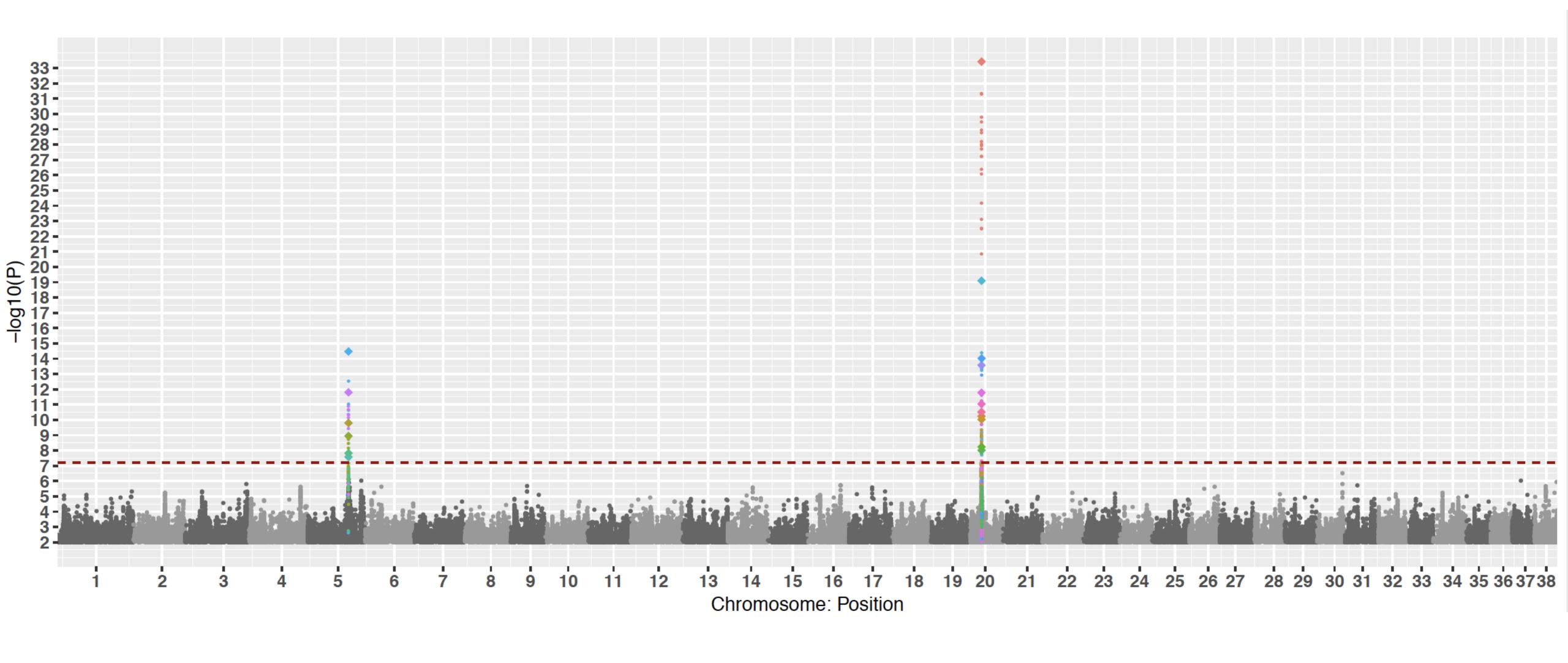
AND

lots of genetic data from each dog

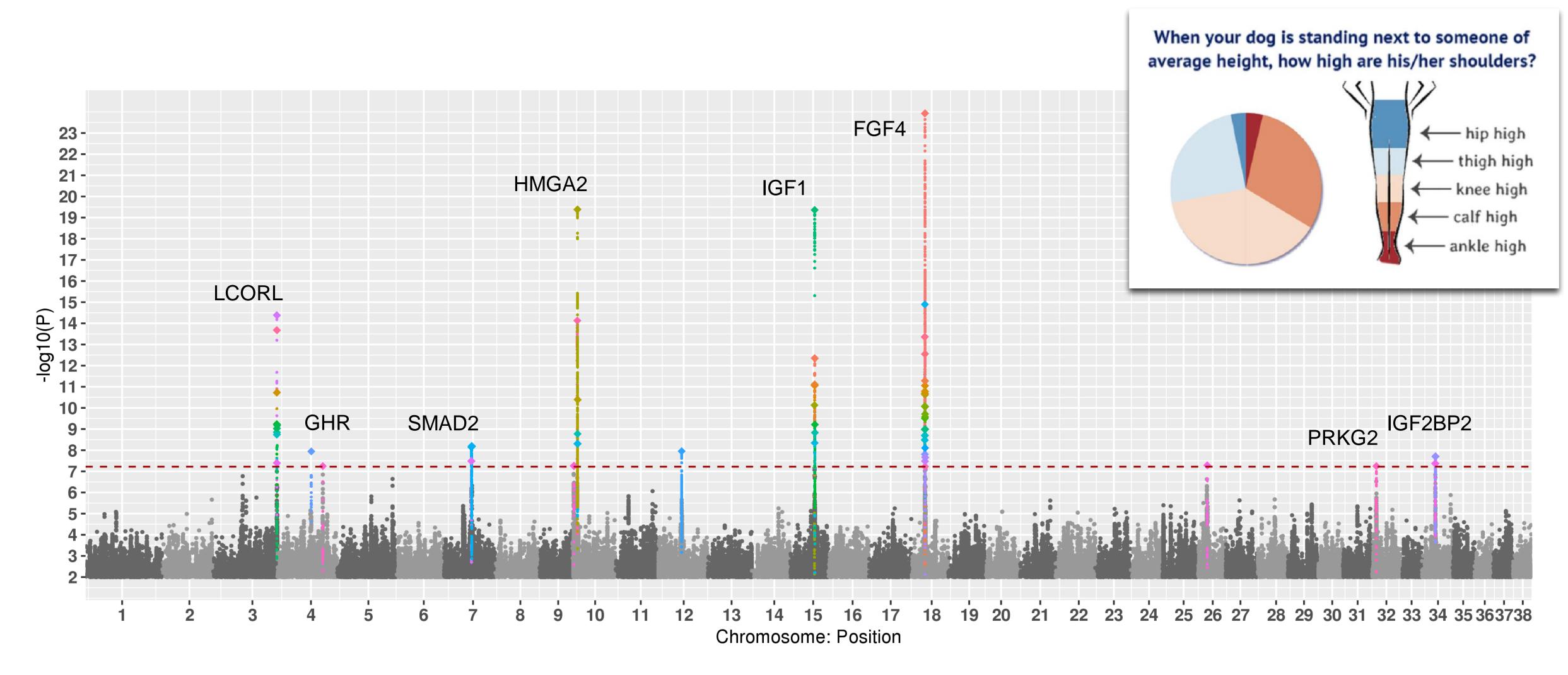
#### White coat color with 19 dogs & 20,000 markers



#### White coat color with 1000 dogs and 5-10 million markers



#### Size GWAS with 1000 dogs



Sutter et al 2007 | Koltes et al 2009 | Rimbault et al 2013 | Metzger et al 2013 | Aniek et al 2018 | Plassais et al 2019

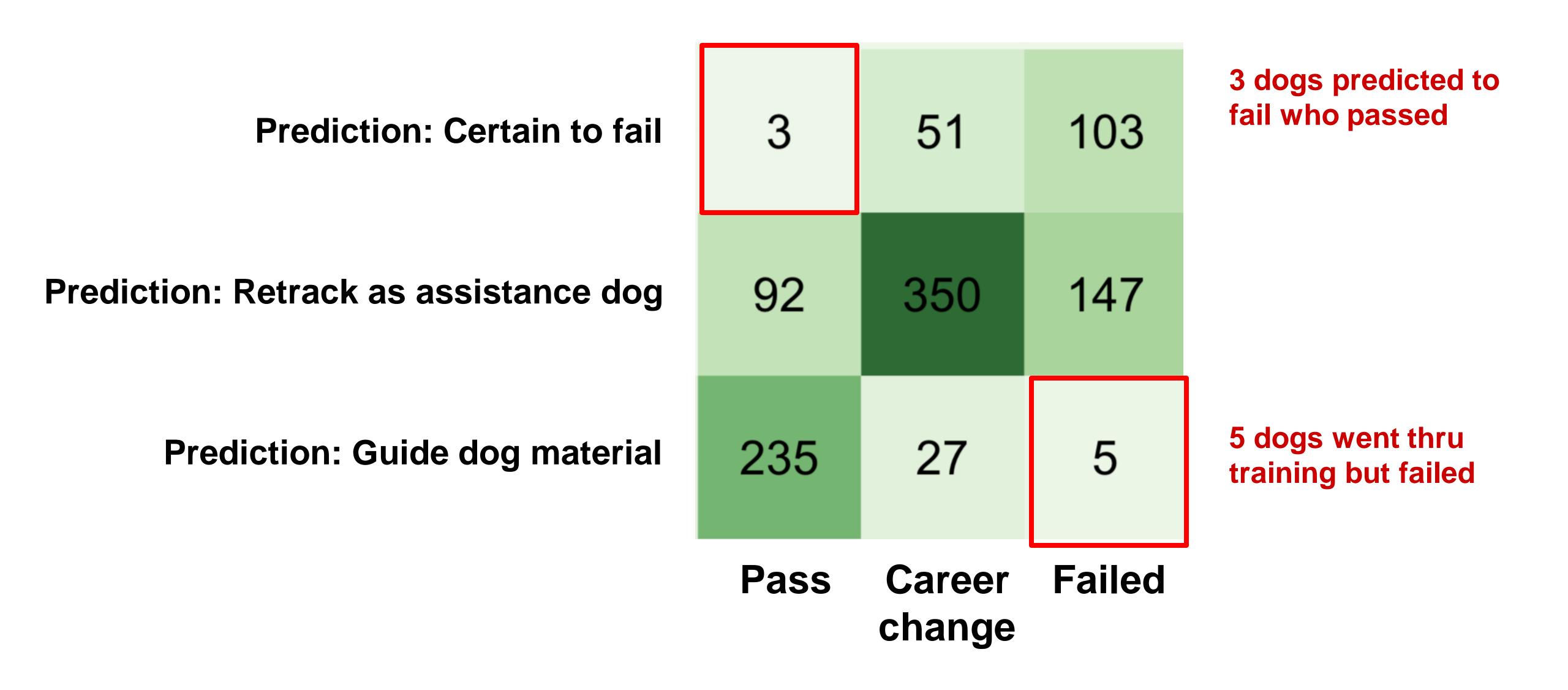
## Can we predict how big a dog will be?

Prediction: Thigh high	3	51	103
Prediction: Knee high	92	350	147
Prediction: Calf high	235	27	5
	Calf high	Knee high	Thigh high

## Hypothetical: What if we could predict behavior?

Prediction: Certain to fail	3	51	103
Prediction: Retrack as assistance dog	92	350	147
Prediction: Guide dog material	235	27	5
	Pass	Career change	Failed

#### Hypothetical: What if we could predict behavior?



#### Pilot project ongoing

- Inhibited with stress
- Activated with stress
- Harness sensitivity
- Thunderstorm phobia
- Hip dysplasia
- Cancer
- Other diseases





We'll start with most heritable traits (collab. with GEB and IWDBA)

## We're looking for new collaborations as Working Dog Project grows Have your own dog? Sign up today! darwinsark.org





The Manton Foundation





