Shameless advertisements

- My team offers several student internships.
- Check them out at careers.roche.com. Keyword: *predictive modeling and data analytics,* or *PMDA.*

What are good drug targets and how to find them?

Mathematical and Computational Biology in Drug Discovery (MCBDD), Module I

Dr. Jitao David Zhang, March 2022

Outline

- Always write down numbers and possibilities for inference.
- We review biological foundations of target identification.
- Genetics doubles the success rate of target identification.

Exercise of *inference* (I)

I have three pills and two hamsters. The two hamsters look identical, while one carries a genetic mutation that affects its response to the pills.

1. Pill A makes both hamsters sleep.
2. Pill B makes neither animal sleep.
3. Pill C makes one animal sleep but not the other.

Now I pick a pill, feed it to one hamster, and the hamster falls asleep. What's the probability that the pill makes the other animal sleep, too?

Solution: ⅔, not ½ or ⅓.

- We name the hamsters H1 and H2.
  - We cannot tell between H1 and H2 optically.
  - Upon treatment with pill A, H1 and H2 fall asleep.
  - Upon treatment with pill B, H1 and H2 stay awake.
  - Let's assume that upon treatment with pill C, H1 will sleep and H2 will stay awake. Once can switch the labeling of H1 and H2, without affecting the results.
- Having observed that one hamster, either H1 or H2, falls asleep, the option of pill B is excluded.
- The asleep hamster can be either H1 or H2. So three options are equally possible:
  - Pill A was given to H1, and H1 fell asleep;
  - Pill A was given to H2, and H2 fell asleep;
  - Pill C was given to H1, and H1 fell asleep.
- The possibility that the pill makes the other hamster asleep (i.e. the Pill A) is ⅔.

	H1	H2
Pill A	Sleep	Sleep
~~Pill B~~	~~Awake~~	~~Awake~~
Pill C	Sleep	Awake

Exercise of *inference* (II)

The company *Fränzi and Friends* developed a new quick test at home for SARS-Cov-2, which is pending regulatory agency's review. The test has been shown to have a sensitivity of 99% and a specificity of 99%.

Suppose that Fred uses the test by *Fränzi and Friends* and the test was positive. Assume that 5% of the population is in fact infected. Was is your guess about the probability that Fred is indeed infected?

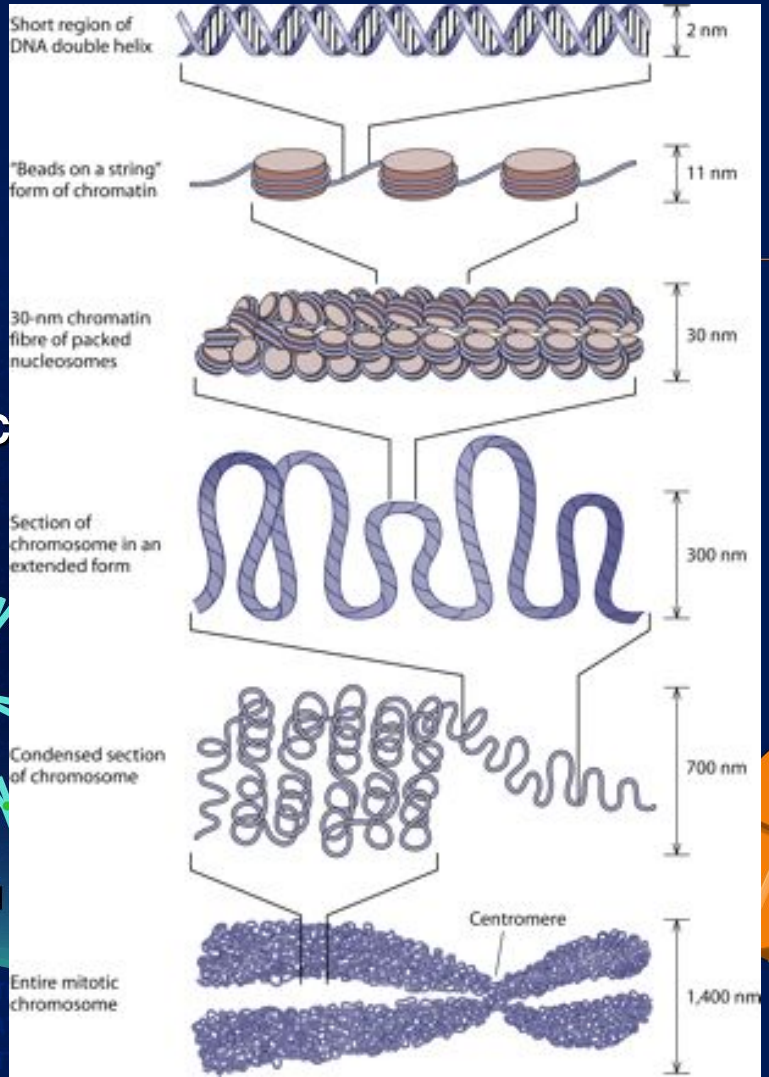
(Sensitivity is predicted true positive divided by all true positive; specificity is predicted true negative divided by all true negative).

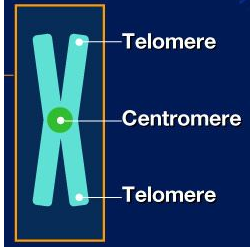
Exercise of *inference* (II) - variants

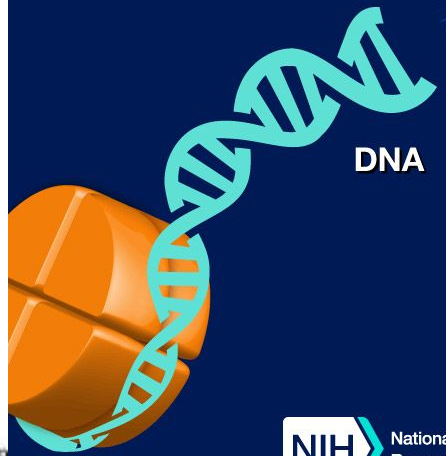
The company *Fränzi and Friends* developed a new quick test at home for SARS-Cov-2 which is pending regulatory agency's review. When test with 100 SARS-Cov-2 patients, 99 report positive and one reports negative. When test with 100 healthy volunteers, 99 report negative and one reports positive.

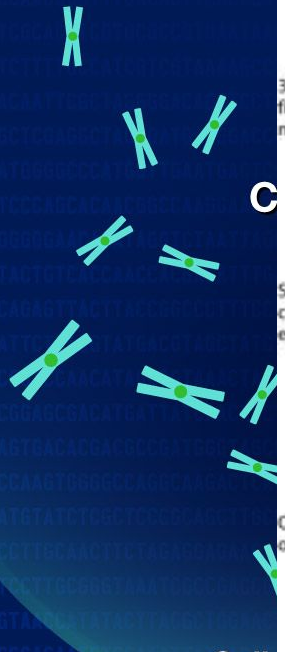
Suppose that Fred uses the test by *Fränzi and Friends* and the test was positive. There are 30,000 people in the city where Fred lives; among them 1,500 are infected with SARS-Cov-2. What is the likelihood that Fred is truly infected given his positive test?

Chromosome



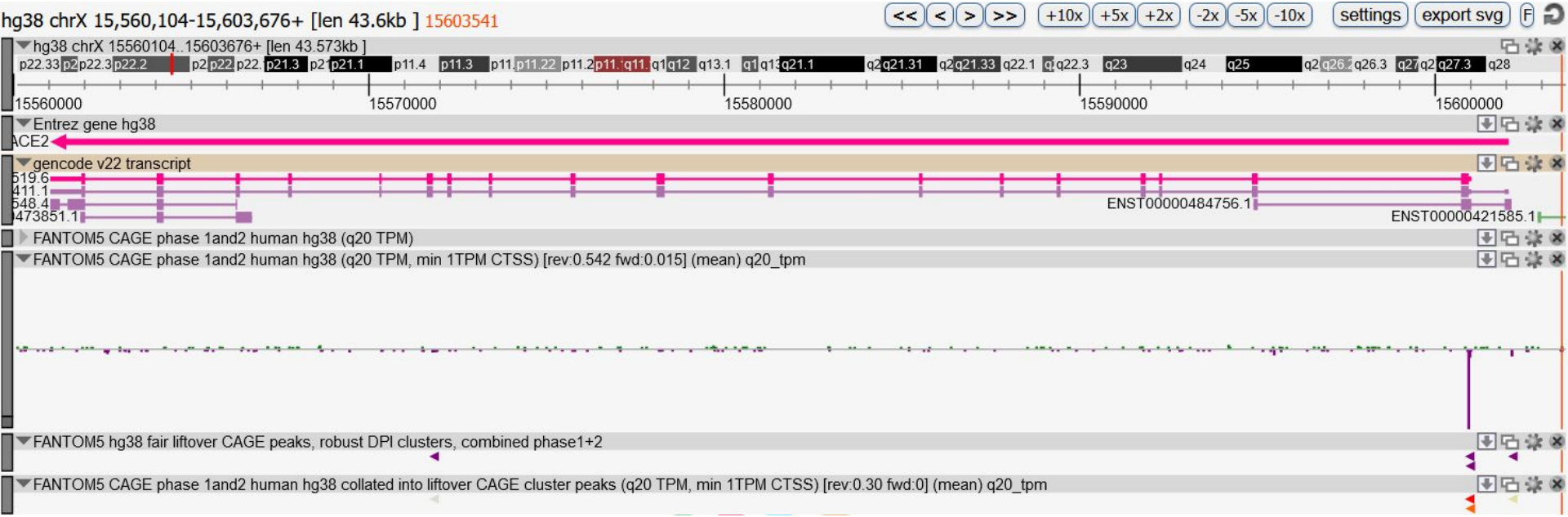






NIH National Human Genome Research Institute

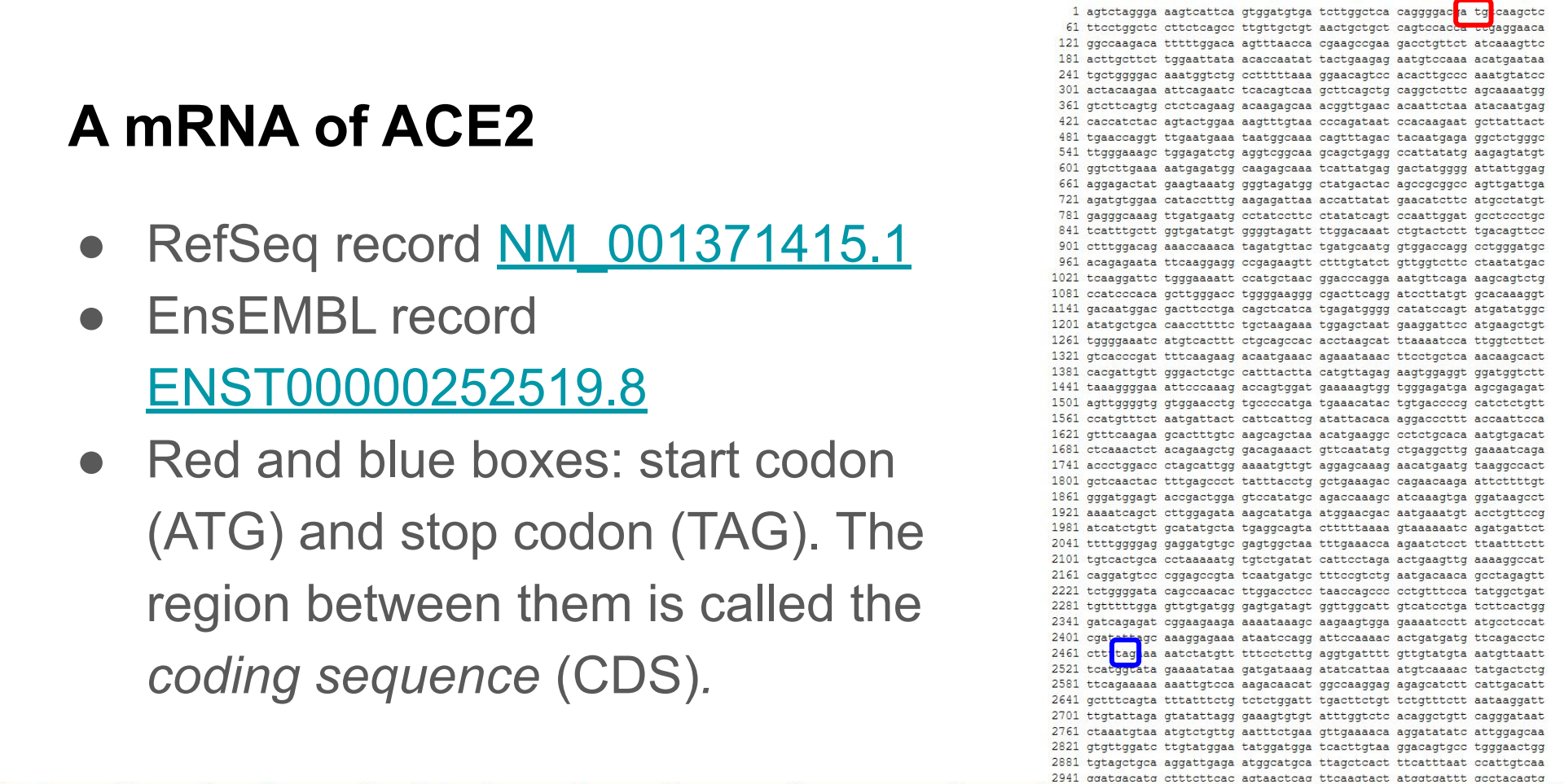
Gene structure and gene expression



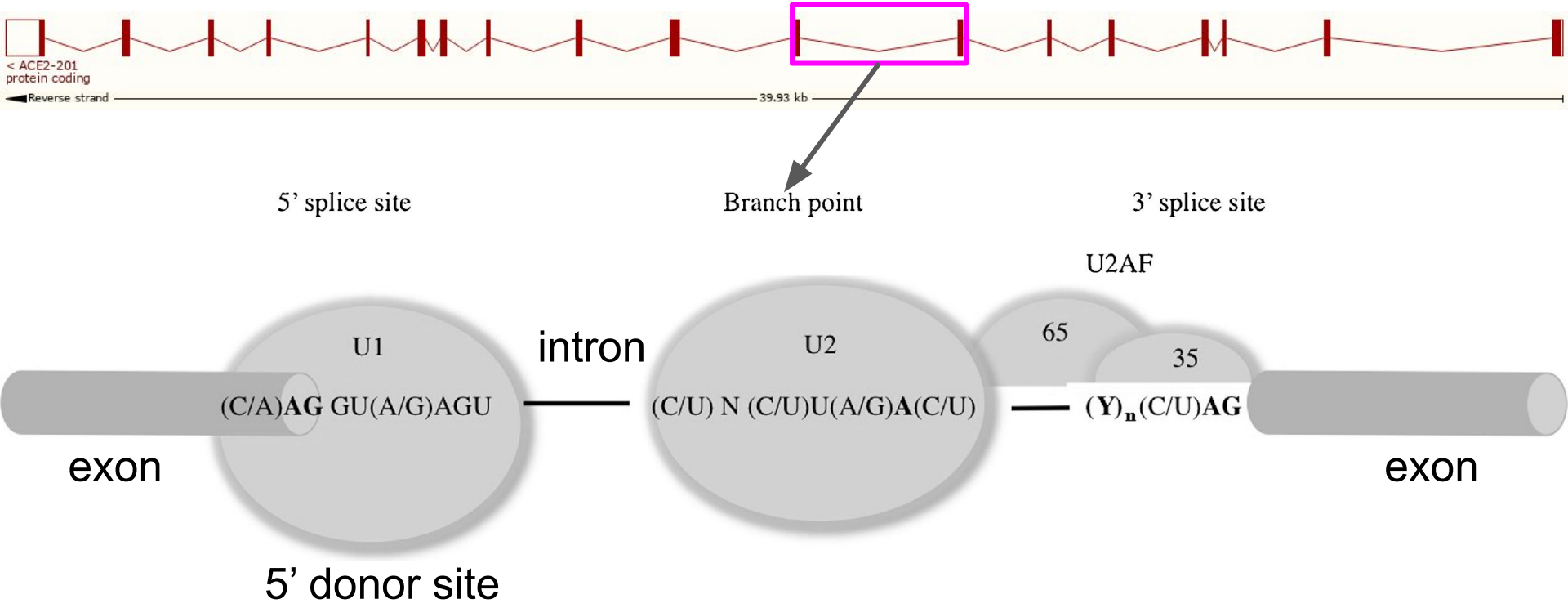
ACE2 viewed in [FANTOM5/ZENBU]

A mRNA of ACE2

- RefSeq record NM_001371415.1
- EnsEMBL record ENST00000252519.8
- Red and blue boxes: start codon (ATG) and stop codon (TAG). The region between them is called the *coding sequence* (CDS).



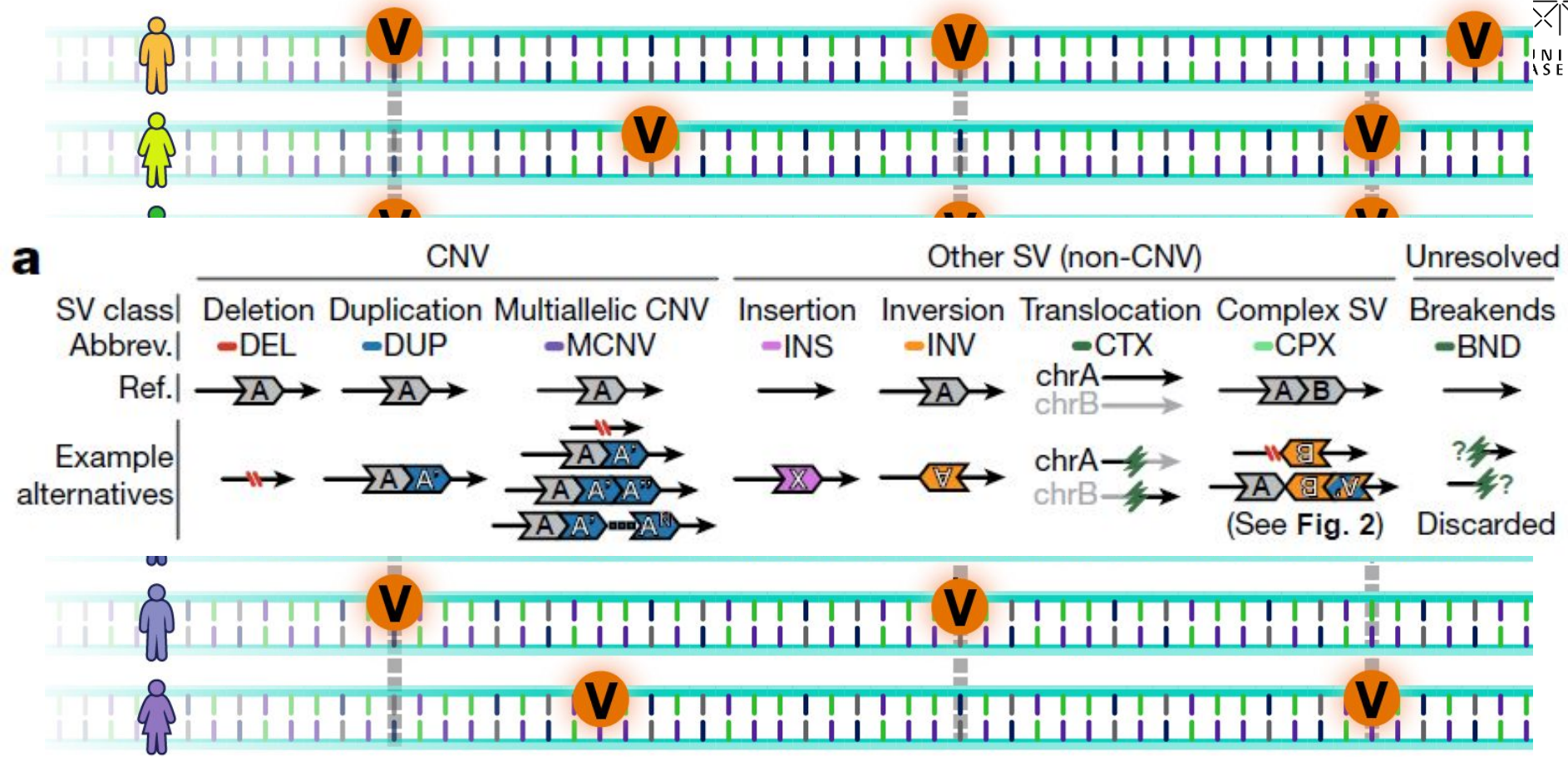
The splicing code



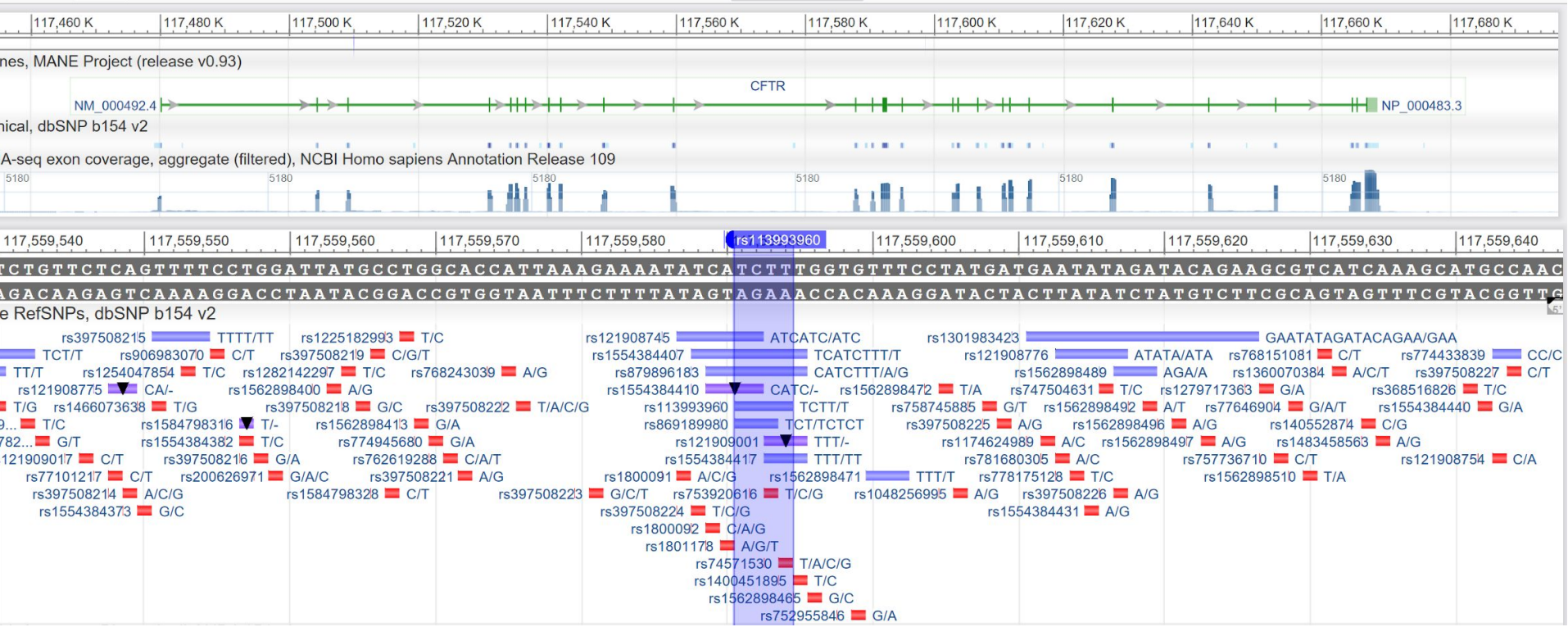
Person one

A G A C G C T

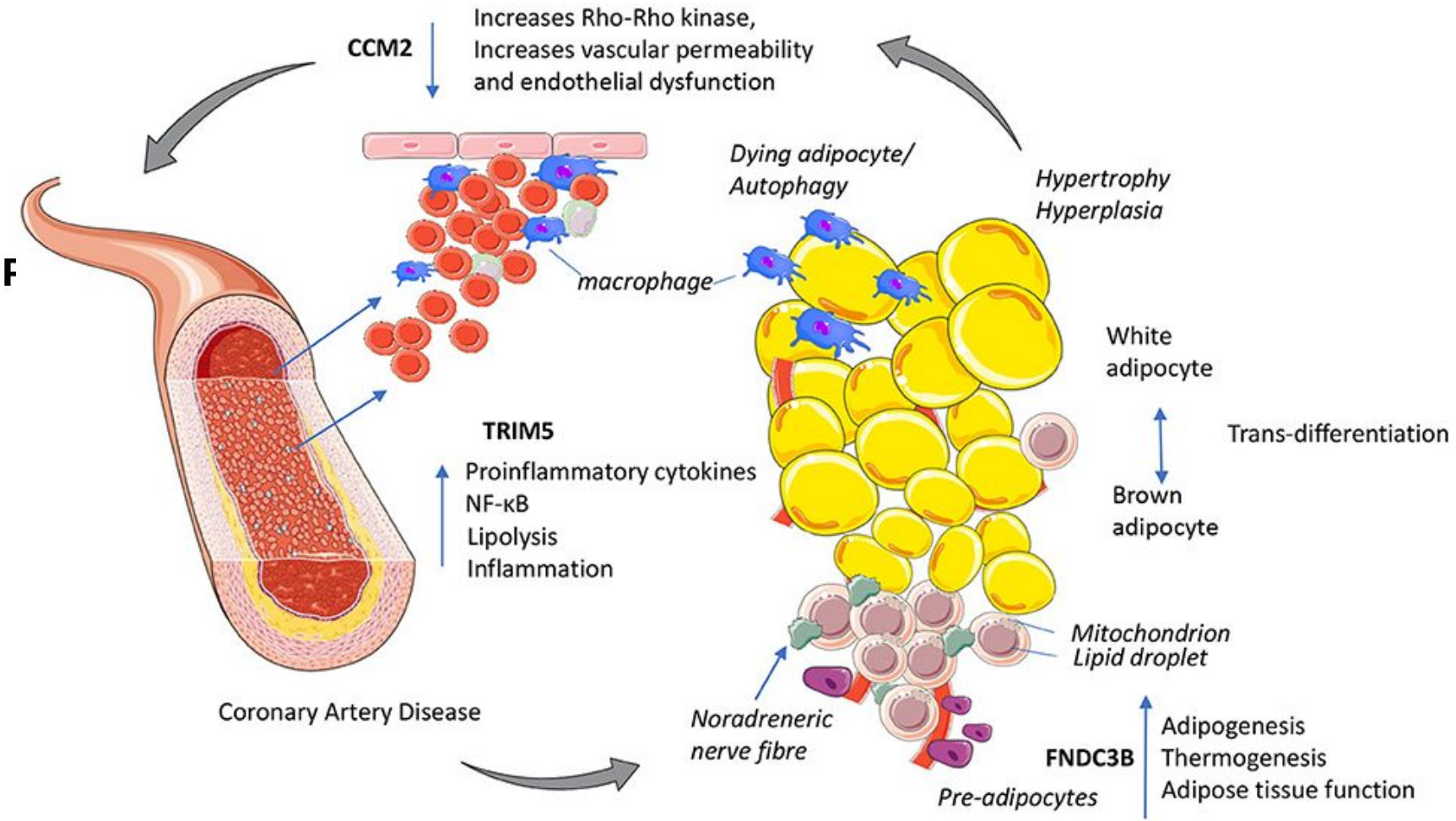
Variant ID	Source	HGVS Consequence	VEP Annotation	LoF Curation	Clinical Significance	Flags	Allele Count
17-7579817-C-T	E	c.74+22G>A	intron		Likely benign		1
17-7579831-C-T	E	c.74+8G>A	splice region		Likely benign		1
17-7579924-G-A	E G	c.-12C>T	5' UTR		Likely benign		7
17-7579932-G-C	E	c.-20C>G	5' UTR		Likely benign		2
17-7578142-C-A	E G	c.672+35G>T	intron		not provided		9
17-7577142-C-A	E	p.Gly266Ter	stop gained		Pathogenic		1
17-7578188-C-A	E	p.Glu221Ter	stop gained		Pathogenic		1
17-7578263-G-A	E	p.Arg196Ter	stop gained		Pathogenic		1
17-7576928-TAGGAA...	E	c.920-14_920-3delTGC...	splice region		Uncertain significance		2
17-7578171-C-A	E G	c.672+6G>T	splice region		Uncertain significance		2
17-7578171-C-T	E	c.672+6G>A	splice region		Uncertain significance		1
17-7579934-C-T	G	c.-22G>A	5' UTR		Uncertain significance		1
17-7565206-T-A	G	c.*51A>T †	3' UTR				1
17-7565222-C-T	G	c.*35G>A †	3' UTR				1


a
CNV
Other SV (non-CNV)
Unresolved
SV class
Deletion
Duplication
Multiallelic CNV
Insertion
Inversion
Translocation
Complex SV
Breakends
Abbrev.
DEL
DUP
MCNV
INS
INV
CTX
CPX
BND
Ref.
chrA
chrB
Example alternatives
(See Fig. 2)
Discarded

Cystic fibrosis

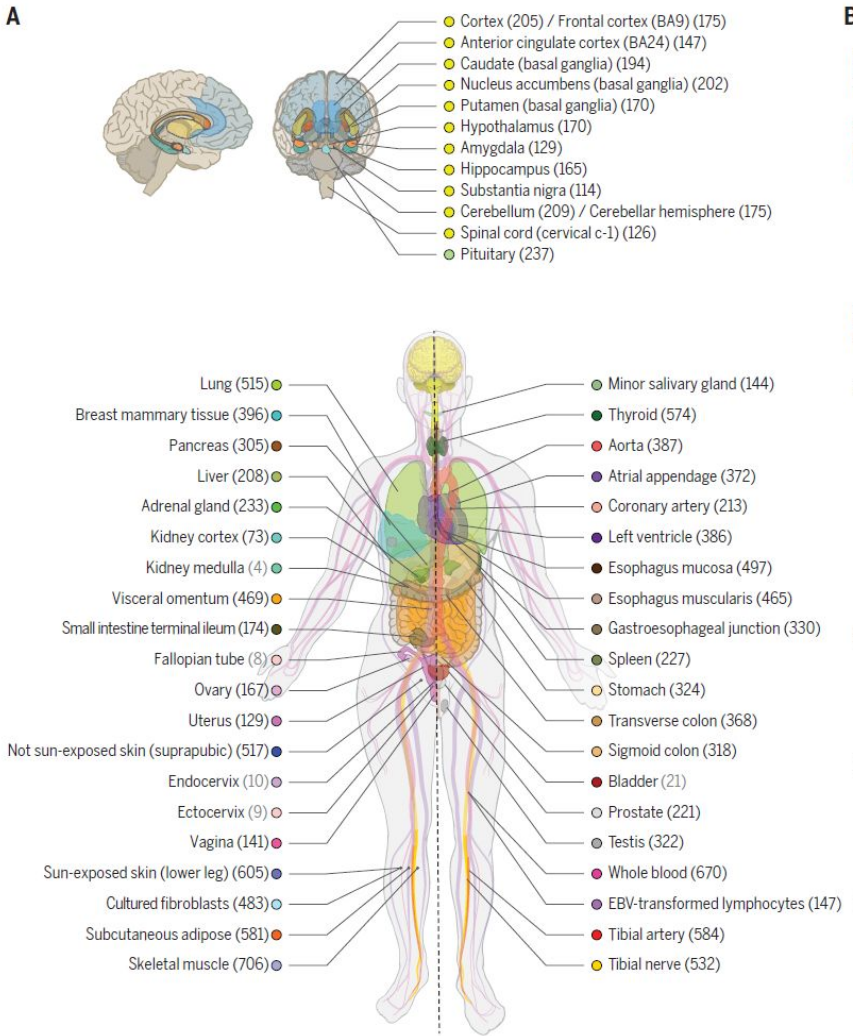


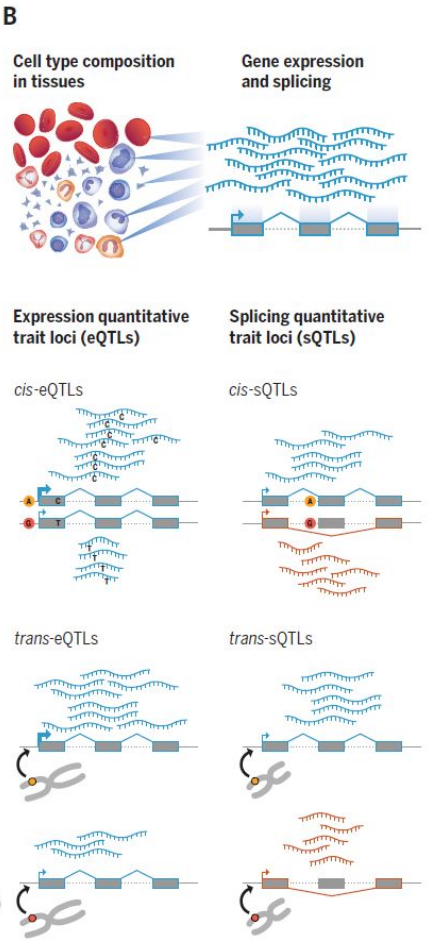
The *CFTR* gene (Chr 7), and rs113993960, the most common cause of CF


CCM2
Increases Rho-Rho kinase,
Increases vascular permeability
and endothelial dysfunction
Dying adipocyte/
Autophagy
Hypertrophy
Hyperplasia
macrophage
White
adipocyte
Trans-differentiation
Brown
adipocyte
TRIM5
Proinflammatory cytokines
NF-κB
Lipolysis
Inflammation
Mitochondrion
Lipid droplet
Coronary Artery Disease
Noradreneric
nerve fibre
FNDC3B
Adipogenesis
Thermogenesis
Adipose tissue function
Pre-adipocytes

Dna Se

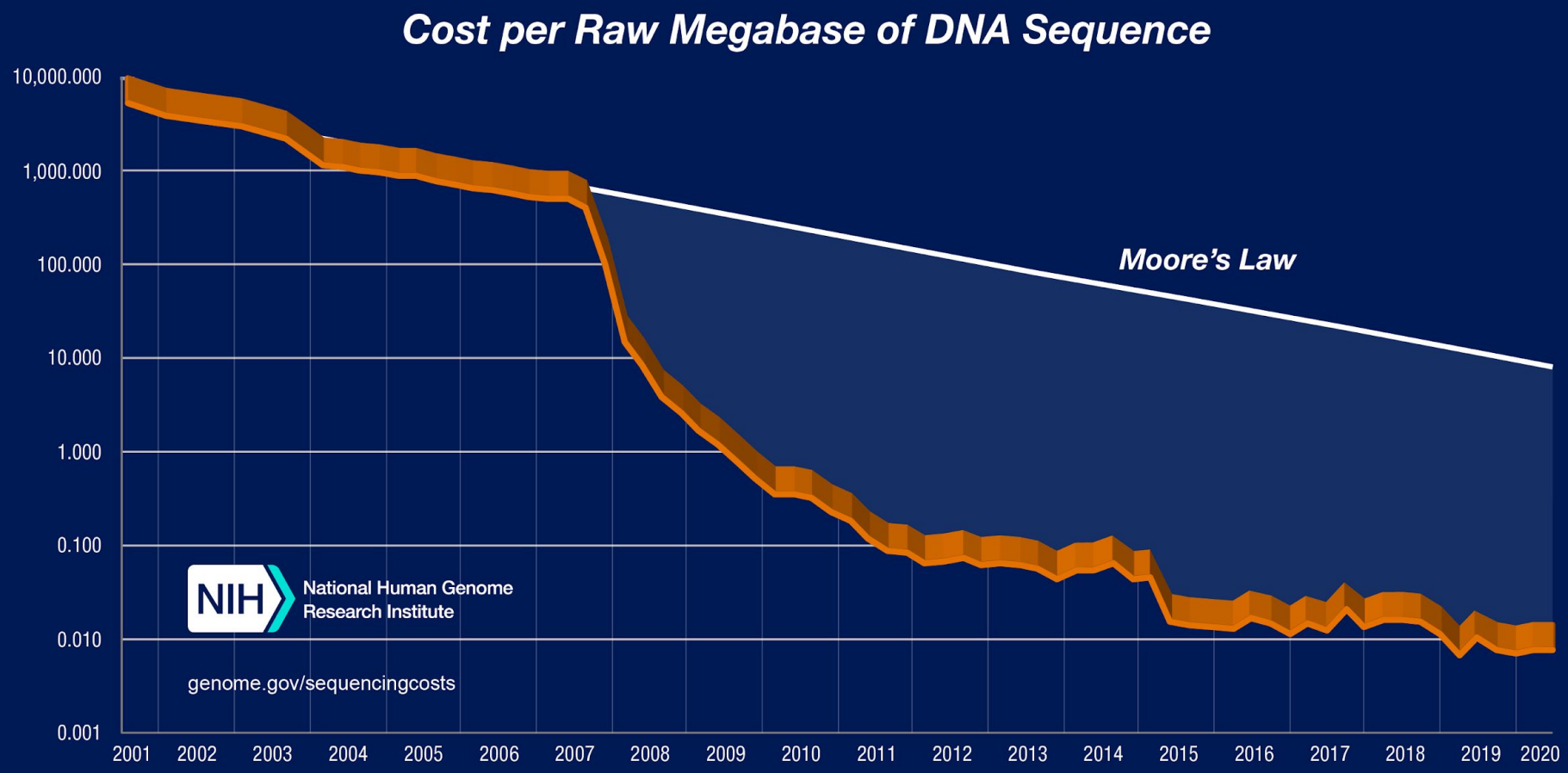
FACT SHEETS
genome.gov





GTEx (v8)

National Human Genome Research Institute


Cost per Raw Megabase of DNA Sequence
10,000.000
1,000.000
100.000
10.000
1.000
0.100
0.010
0.001
Moore's Law
NIH
National Human Genome Research Institute
genome.gov/sequencingcosts
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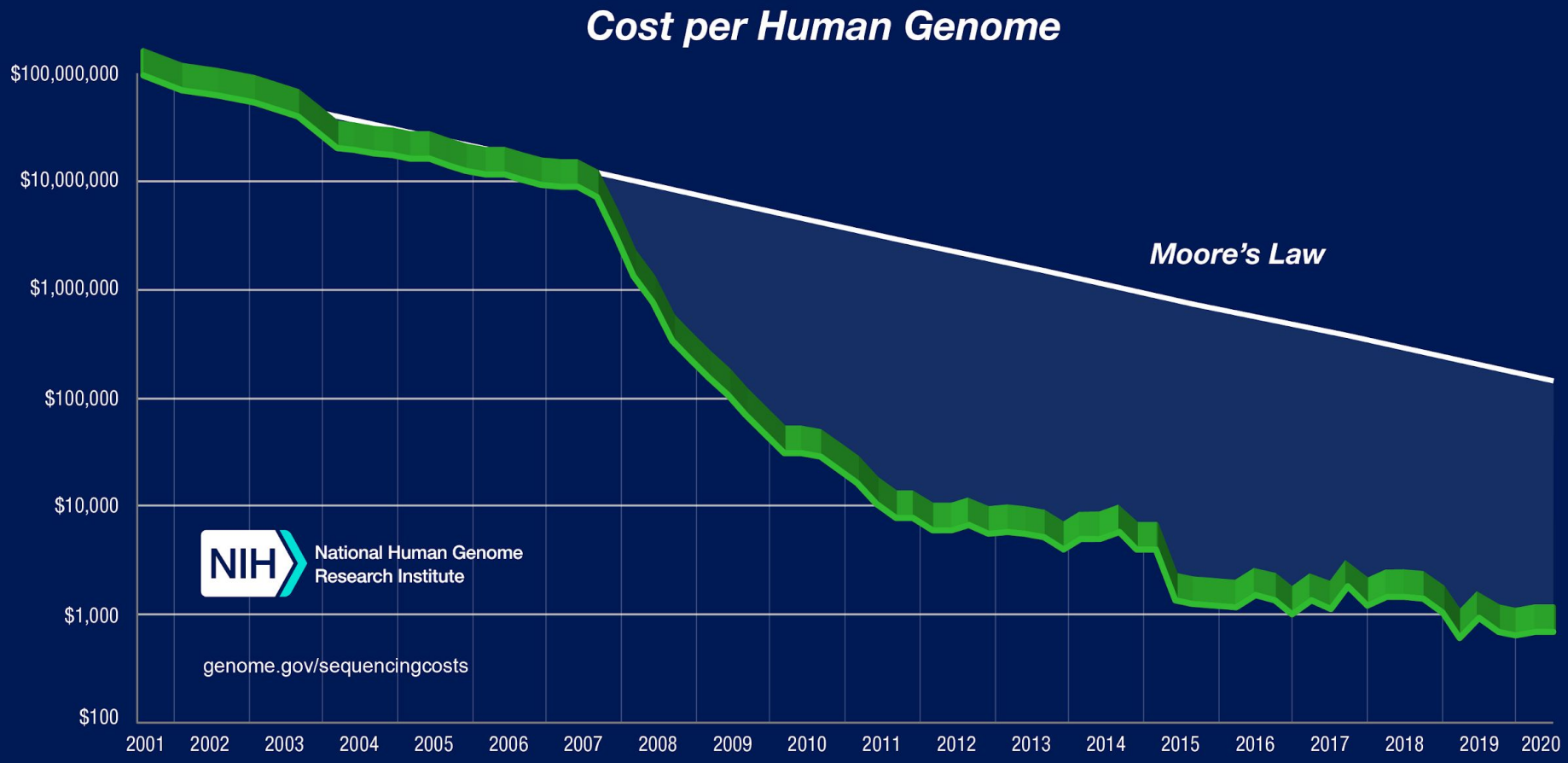
Cost per Human Genome
$100,000,000
$10,000,000
$1,000,000
$100,000
$10,000
$1,000
$100
Moore's Law
NIH
National Human Genome Research Institute
genome.gov/sequencingcosts
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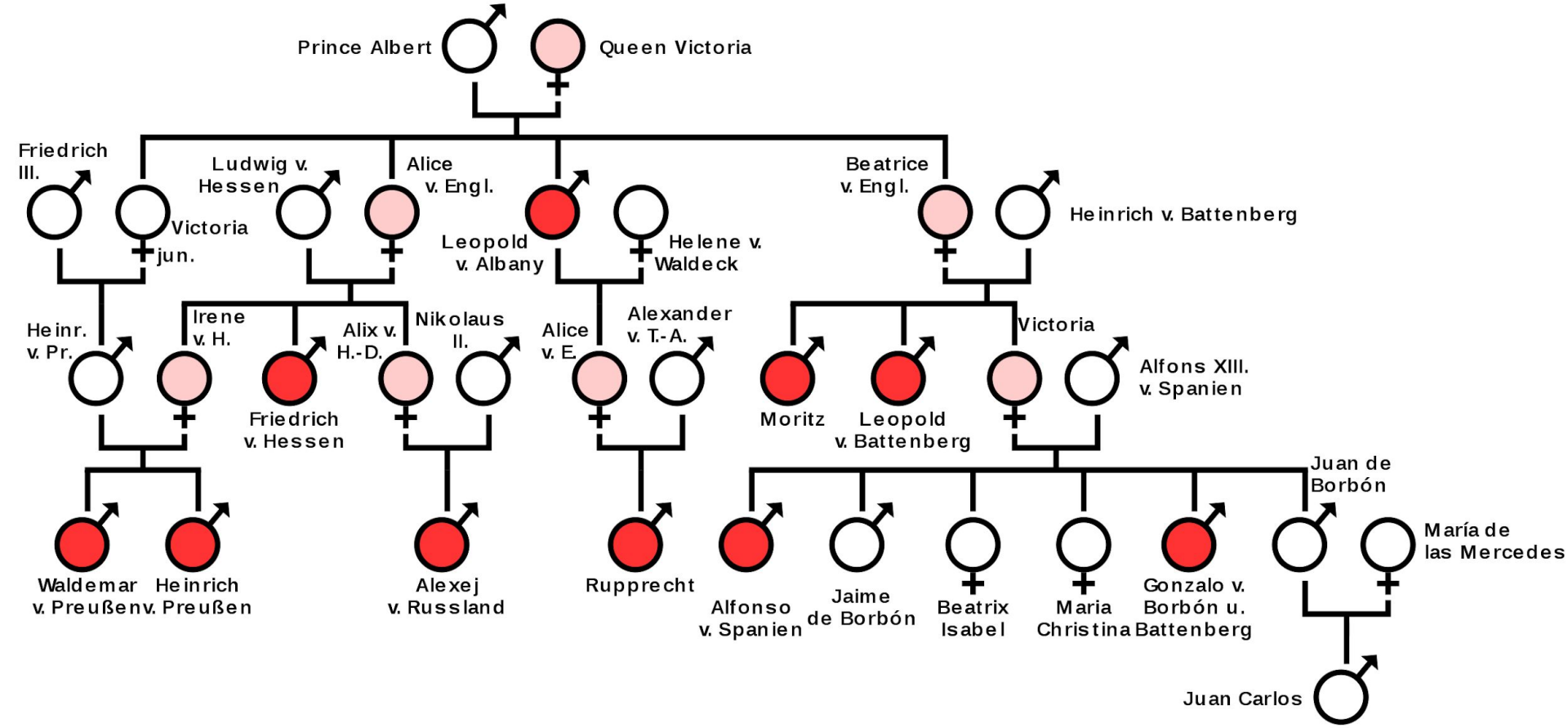
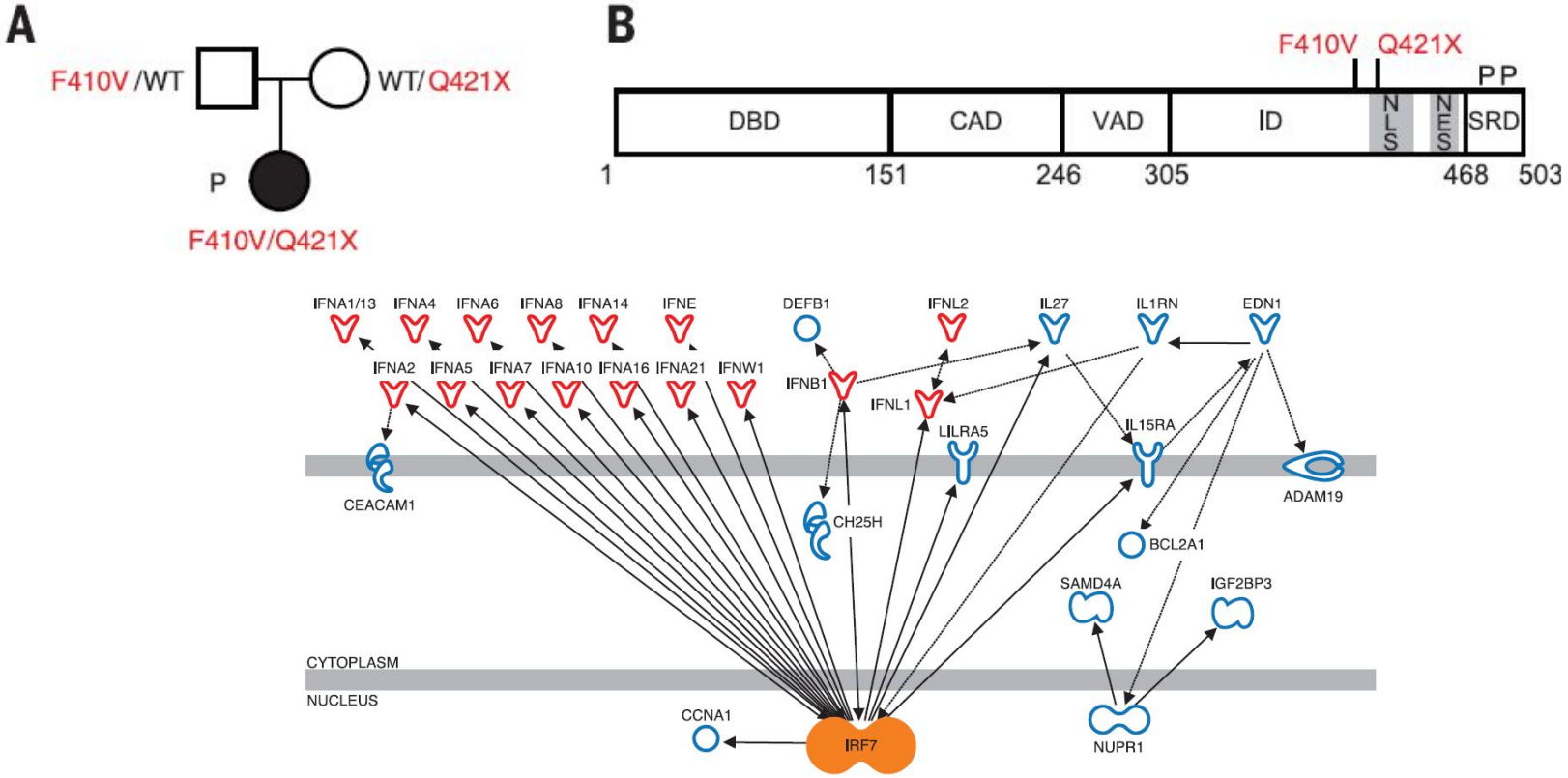


Prussia (1889-1945) | Prussia (1900-1904) | of Russia (1904-1918) | Teck (1907-1928) | Asturias (1907-1938) | Spain (1914-1934)

Life-threatening influenza infection in human IRF7 deficiency detected by trio sequencing



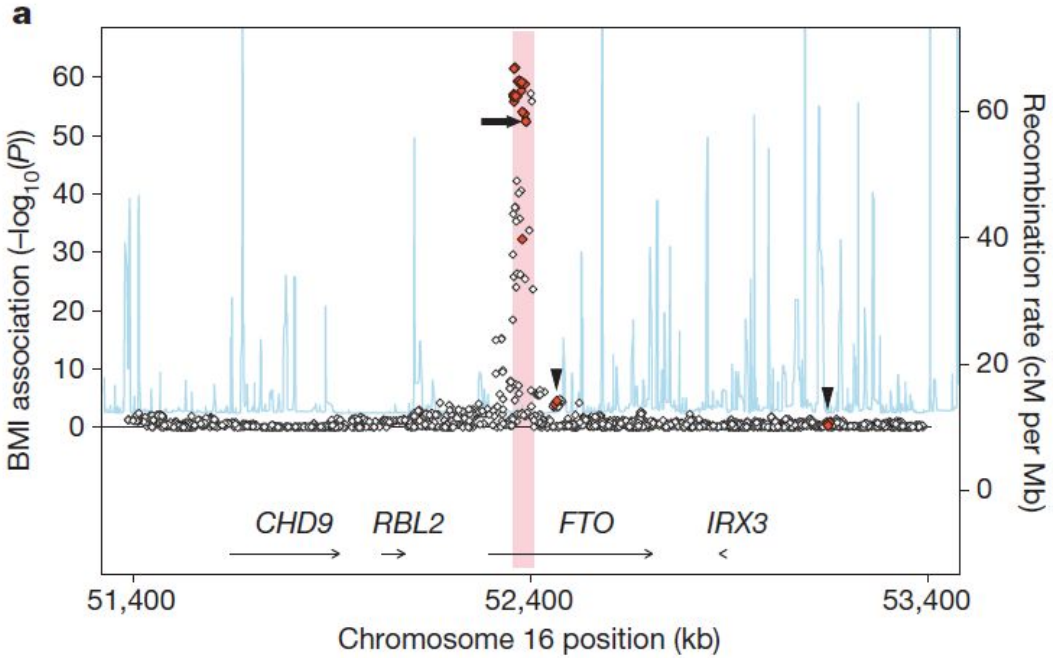
Exercise of *inference* (III)

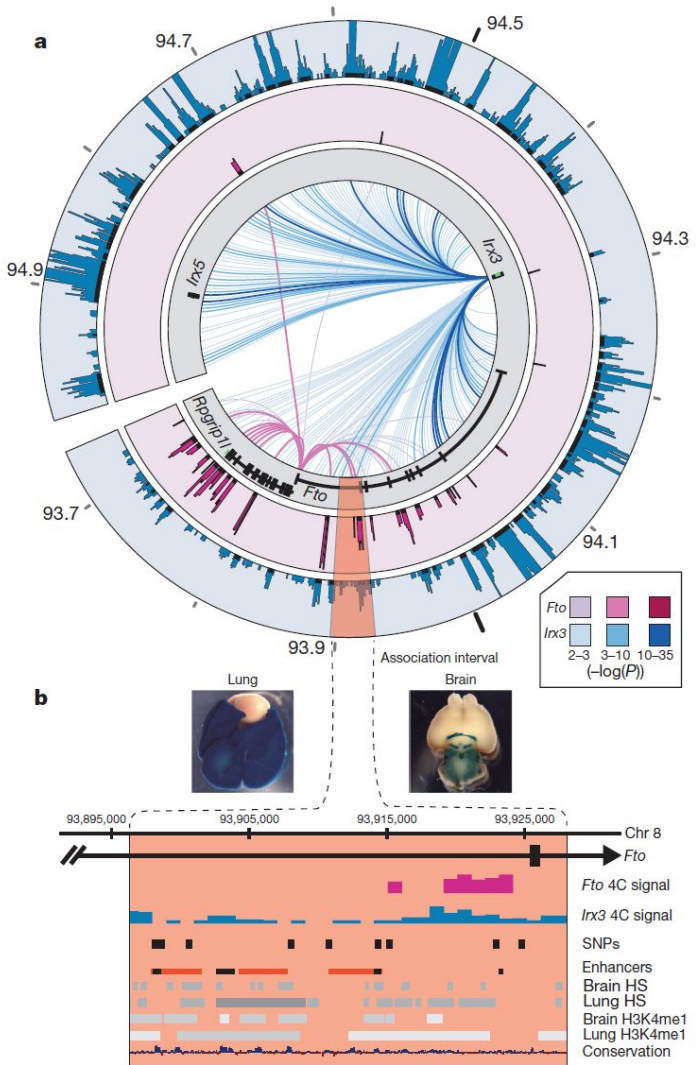
- Cao and Moult (BMC Genomics, 2014) reported studied overlap between drug targets and GWAS hits.
- Use the data in the Table 1 of the paper (cloned here) to answer following the following two questions:
  a. Assuming we know *nothing* about a gene (let's call it gene *WKN1*), what is the probability that the gene is a target for a disease listed here?
  b. Assuming that we know nothing about another gene *WKN2* but that it is a GWAS hit for a disease, what is the probability that *WKN2* is a target for that disease?

Offline activities of Module I

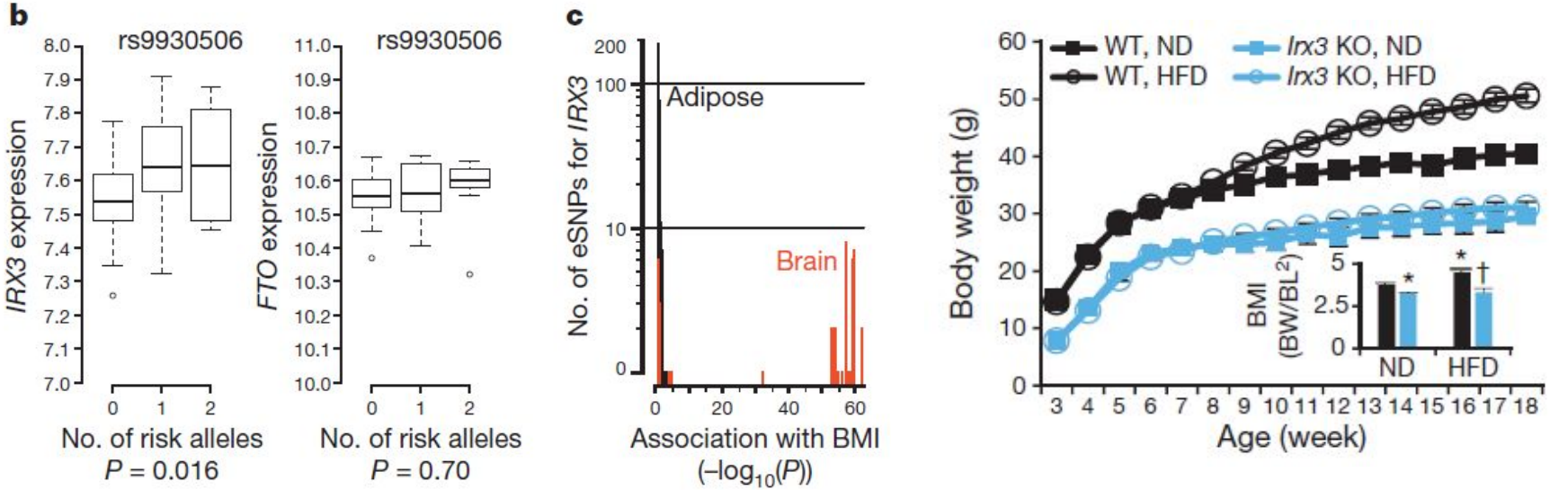
Due on March 31st, https://forms.gle/KQm4GQxxBq1odVgE9

Is FTO a good target for obesity?

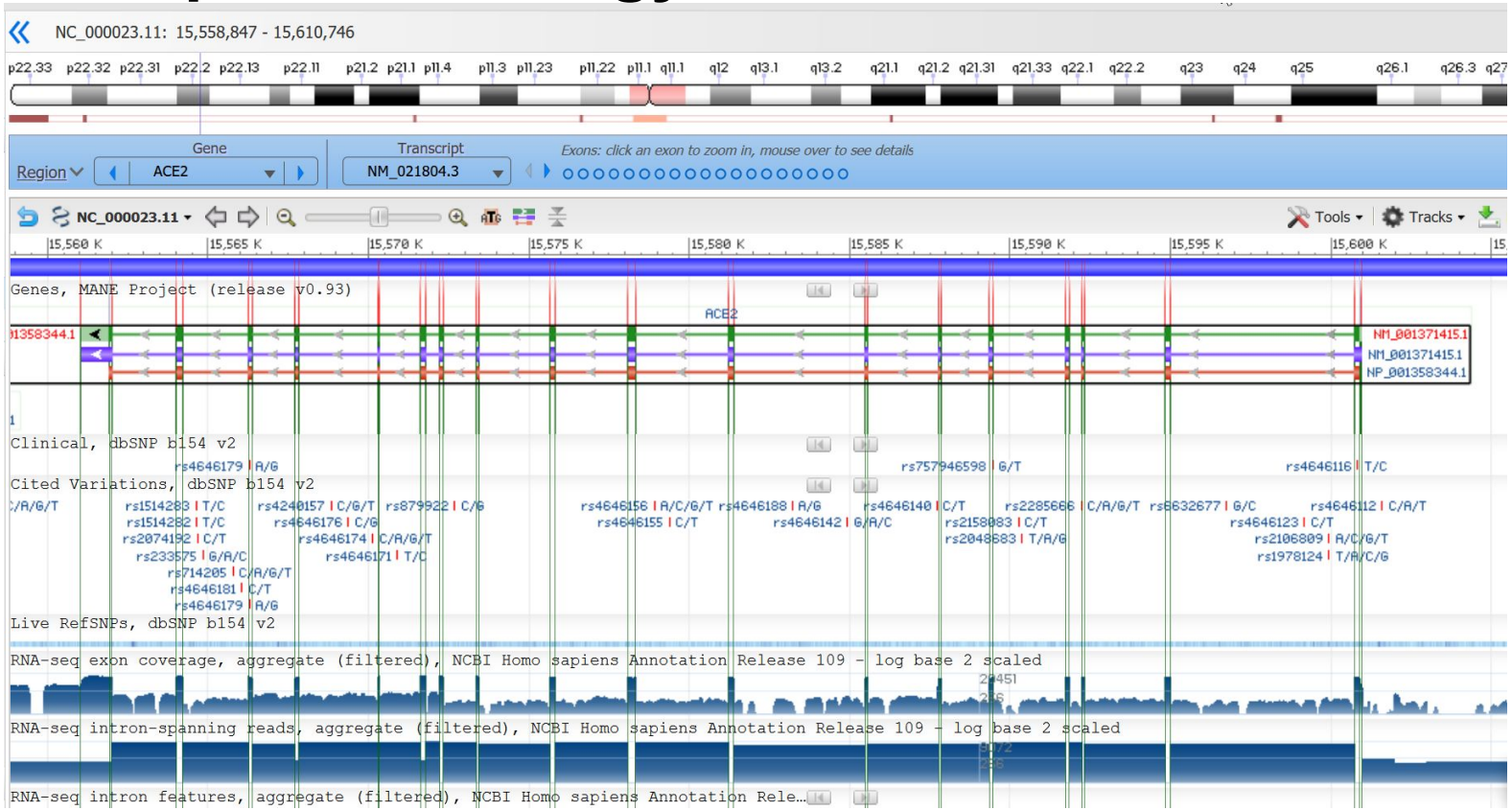




If at all, IRX3 is a more probable target



Recap of the biology we talked about last time



ACE2 viewed in [NCBI Genome Browser]

The Human Genome and Variations

Gene Structure and gene expression

DNA and RNA sequencing

Recap of the math we talked about last time

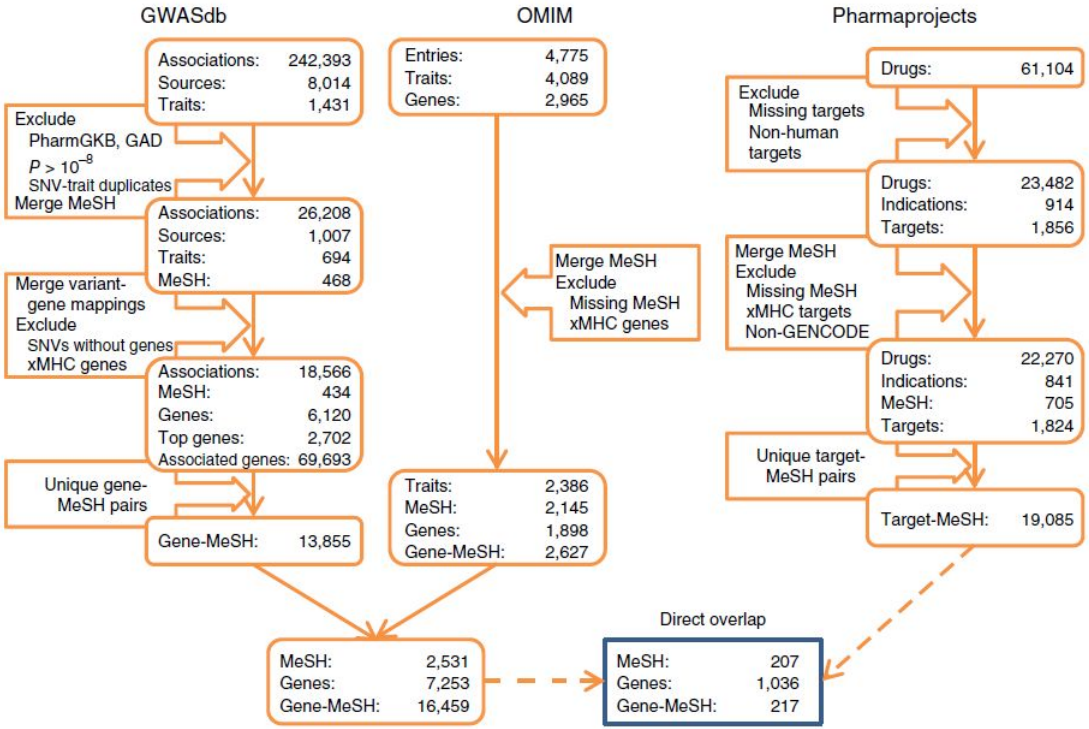
- ***Always* write down your probabilities.**
- The probability theory and the Bayes theorem for inference.

	Sensitivity	Specificity
NPS	86% (90% CI 77–93)	99.93% (90% CI 99.77–99.99)
Saliva	92% (90% CI 83–97)	99.96% (90%CI 99.85–100)

NPS = nasopharyngeal swabs. Yokota *et al.*, 2020

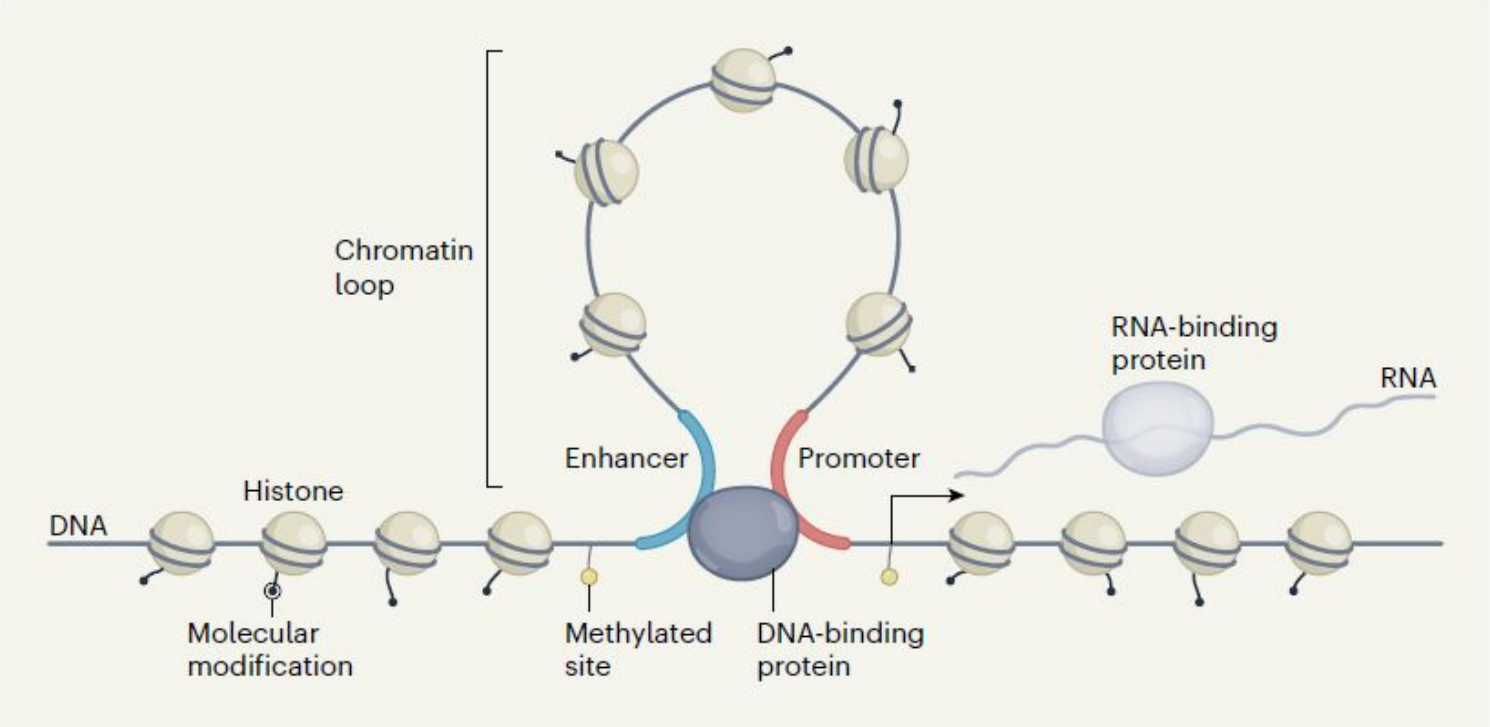
- A list of approved serological tests and their accuracy can be found here;
- *Does He Have It?* by Bill Casselman (AMS)

Impact by a factor of ~2 estimated by Nelson *et al.*

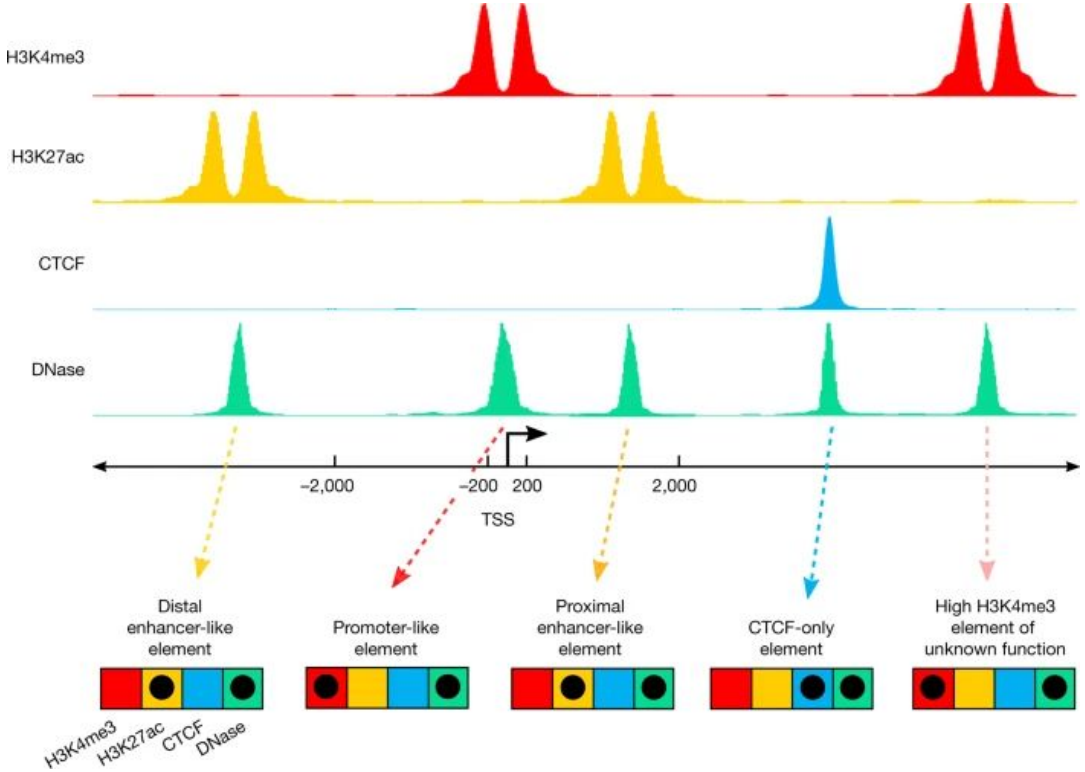


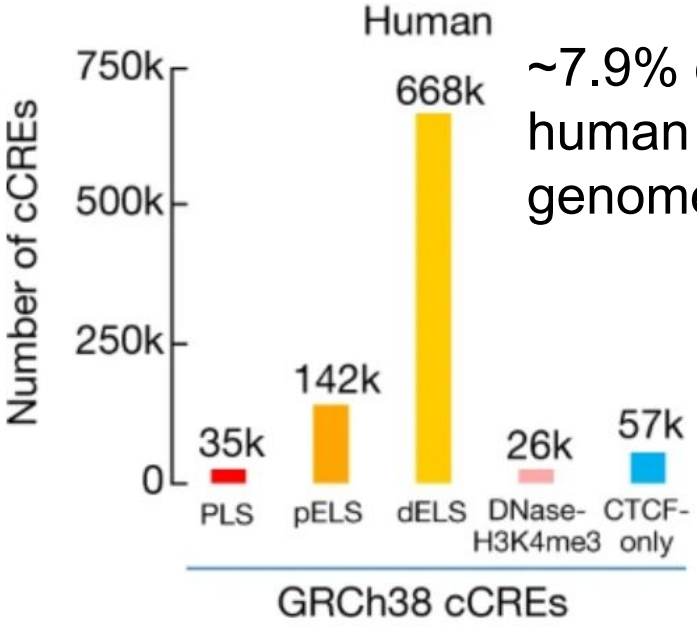
Disease ⟷ Gene ⟷ Drug

Much of the non-coding genome is junk, some is regulatory



Candidate cis-regulatory elements (cCRE)



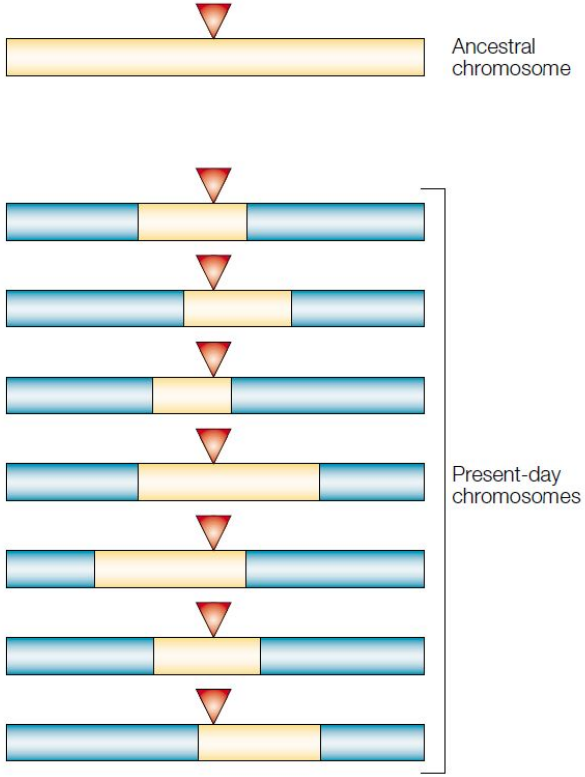


~7.9% of human genome

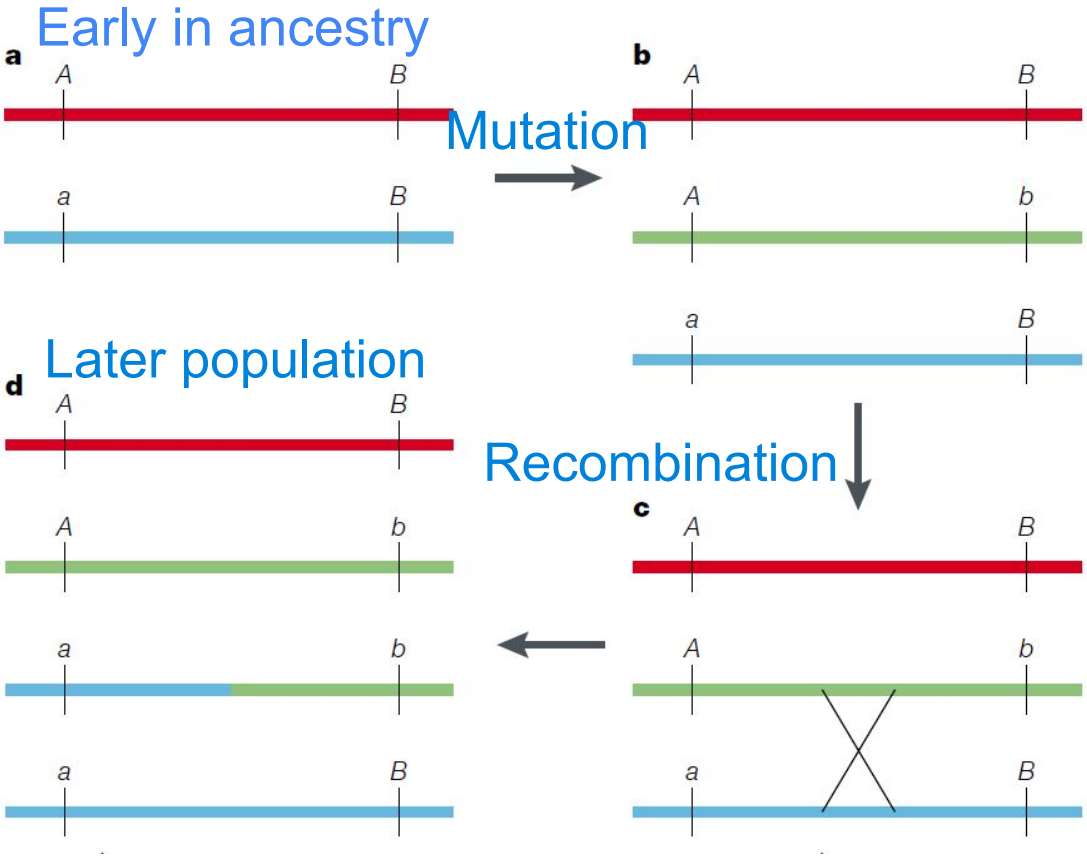
https://screen.encodeproject.org/

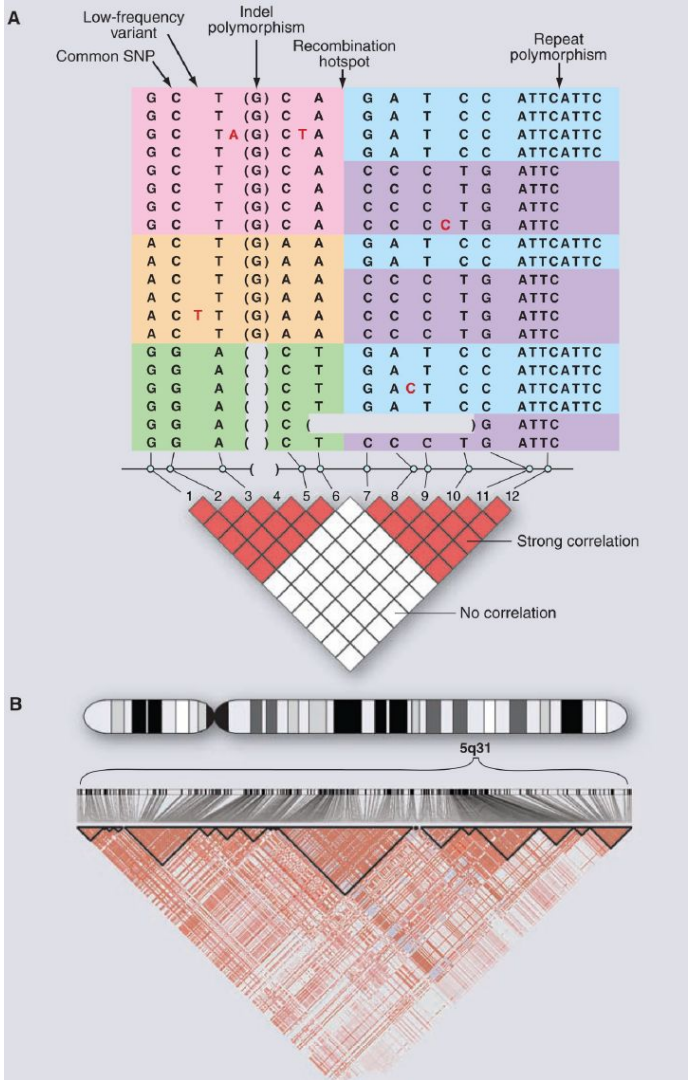
Linkage Disequilibrium in human genome

Particular alleles (single gene copies) at neighbouring loci tend to be co-inherited. For tightly linked loci, this might lead to associations between alleles in the population. This property is known as linkage disequilibrium (LD).

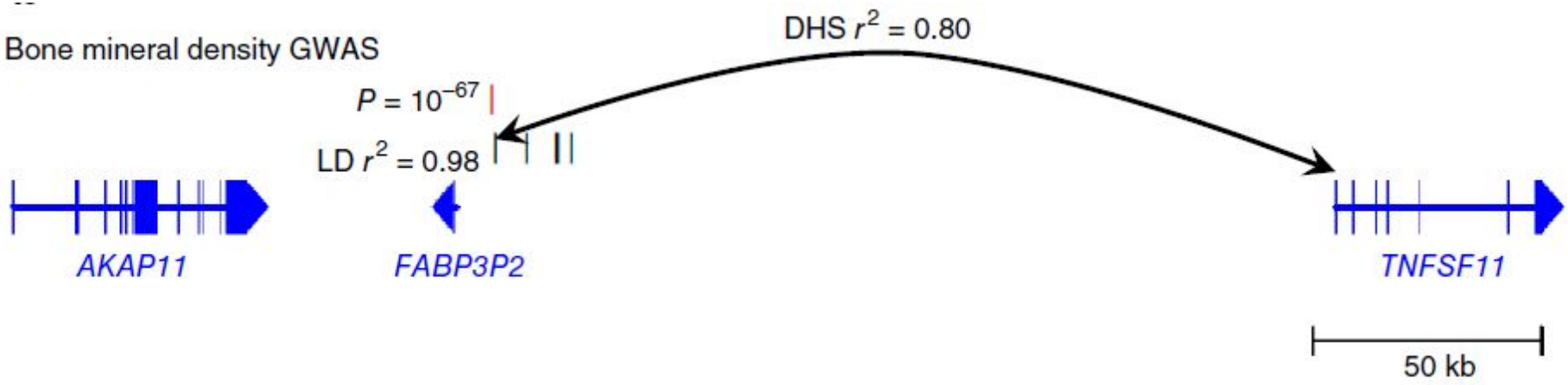


Population genetics helps with disease mapping





Correlation between DNase I hypersensitive (DHS) sites helps linking genetic variants with genes



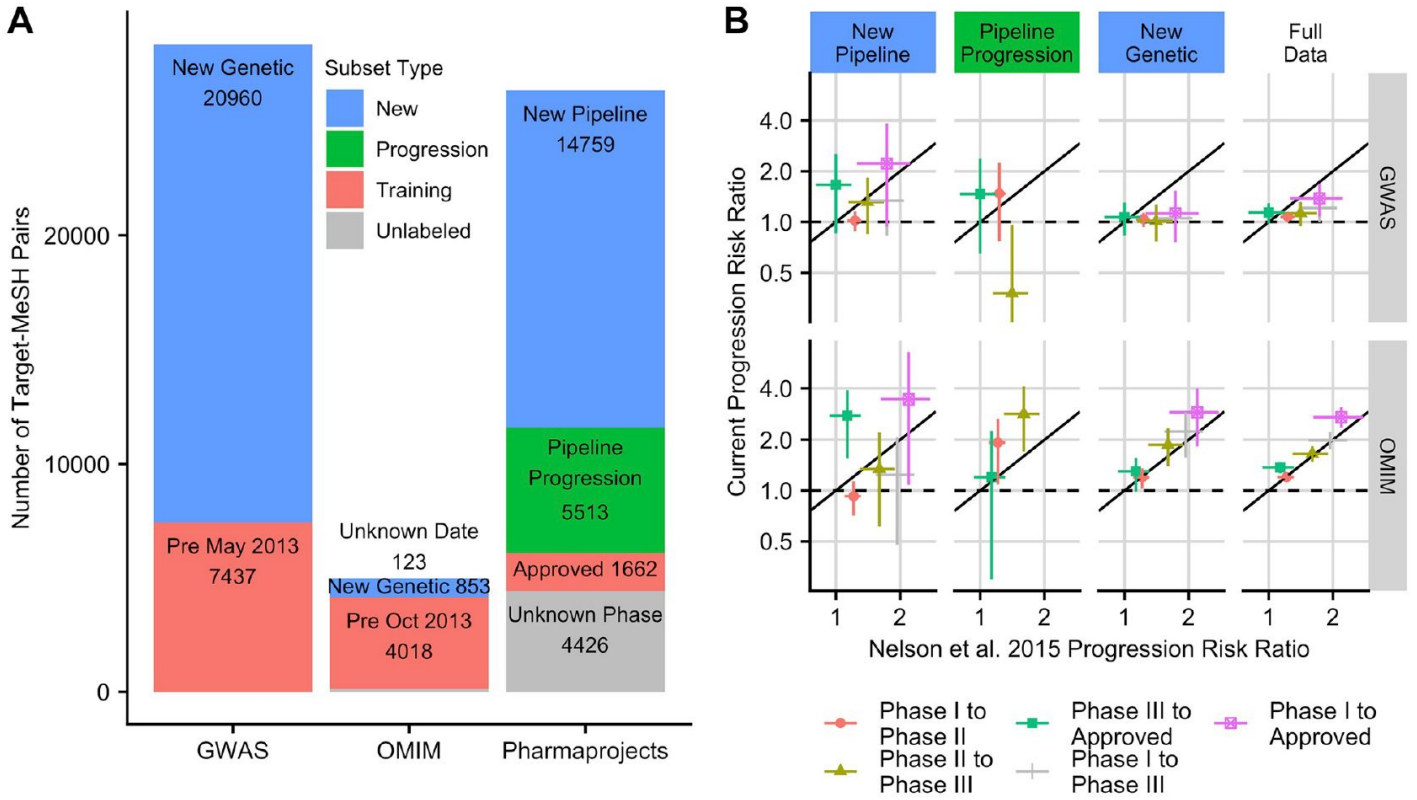
Nelson *et al.* inferred that genetic support offers an likelihood ratio ~2

Table 1 The relative value of genetic support for the probability that a target-indication pair progresses along the drug development pipeline, based on historical drug trial information

	p(progress|genetic support)/(progress|no genetic support)		
Progression	GWASdb and OMIM	GWASdb	OMIM
Phase I to phase II	1.2 (1.1–1.3)	1.2 (1.1–1.3)	1.2 (1.1–1.3)
Phase II to phase III	1.5 (1.3–1.7)	1.4 (1.2–1.7)	1.6 (1.3–1.9)
Phase III to approval	1.1 (1.0–1.2)	1.0 (0.8–1.2)	1.1 (0.9–1.3)
Phase I to phase III	1.8 (1.5–2.1)	1.8 (1.4–2.1)	1.9 (1.5–2.3)
Phase I to approval	2.0 (1.6–2.4)	1.8 (1.3–2.3)	2.2 (1.6–2.8)

Values give the ratio of the probability of a target-indication pair progressing given genetic support to the probability of progressing without genetic support; 95% confidence intervals are given in parentheses.

Follow-up study by King *et al.*, 2019



Genes with *biologically understandable* genetic association are more likely to be good targets

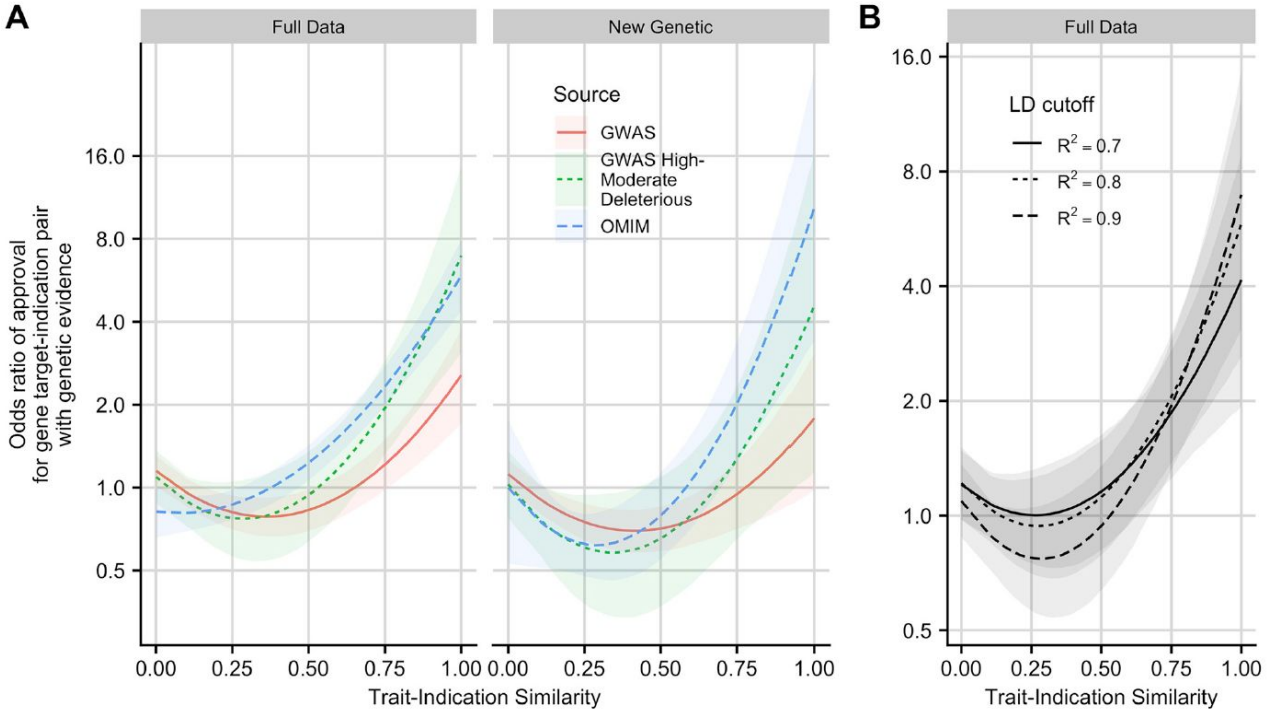
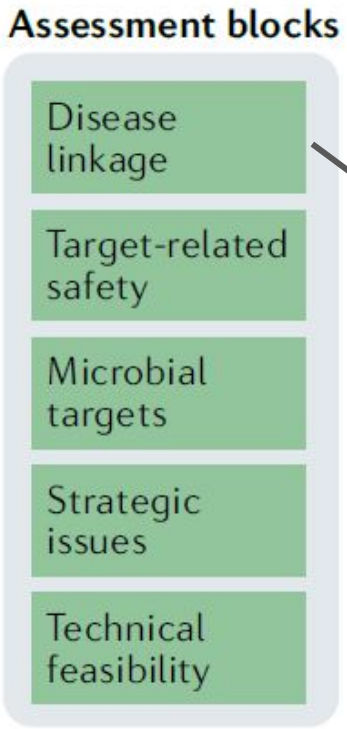


Fig 2. Estimated odds ratio of gene target-indication pair attaining approval, as a function of similarity between drug indication and the most similar trait associated with the target. A: Left: All genetic associations. Right: Only genetic associations reported after 2013 download. B: Effect of LD expansion threshold R^2 on the estimated approval odds ratio of a drug gene target-indication pair supported by a GWAS high-moderate deleterious variant. Posterior median and pointwise 95% credible interval from Bayesian logistic regression.

Discussion

What other evidences can we use to increase the likelihood that a gene is a good drug target?

GOT-IT recommendations for target-disease linkage



AB1: target–disease linkage (human targets)

1. Is the target perturbation a cause or consequence of the human disease process?
2. Is the therapeutic relevance (such as human connection) of models used sufficiently high for decision-making?
3. Is the target expression pattern known (that is, within the anticipated patient population)?
4. Is the target manipulation process clinically relevant?
5. Is the read-out used to detect target-dependent processes disease-relevant?
6. Is the stimulus used to activate or influence target-dependent processes disease-relevant?
7. Are the biological consequences of an observed effect size known?

Public resources for target assessment

AB1: target–disease linkage (human targets)

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5. Is the read-out used to detect target-dependent processes disease-relevant?
6. Is the stimulus used to activate or influence target-dependent processes disease-relevant?
7. Are the biological consequences of an observed effect size known?

- OpenTargets
- Online Mendelian Inheritance in Man (OMIM)

- Scattered in diverse information sources such as Wikipedia and literature

- Health: GTEx, The Human Protein Atlas
- Disease: Gene Expression Atlas, scattered

Public resources for target safety assessment

AB2: target-related safety (human targets)

8. Is the target selective and not genetically linked to other diseases (or phenotypes or organ systems)?
9. Is there prior knowledge on safety of the target or reported evidence for the role of the target in a known pathway and/or physiological process that may be harmful if disrupted?
10. Are in vitro or pharmacologically relevant animal models available for safety testing?
11. Do models used for safety testing translate well to humans?
12. Are safety biomarkers available and can adverse effects be monitored and/or predicted by safety biomarkers?
13. Is there sufficient confidence that a necessary safety window has been or can be established?
14. Is the disease life-threatening (at what stage of the disease is the target of relevance)?
15. Is the tissue distribution of the target known (in humans or in animals)?

- Comparative Toxicogenomics Database (CTD)

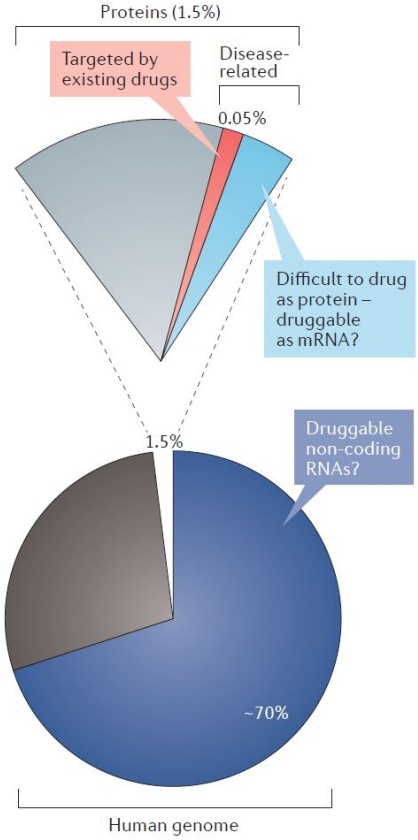
- DrugBank, DrugCentral
- FDA Adverse Event Reporting System (FAERS)

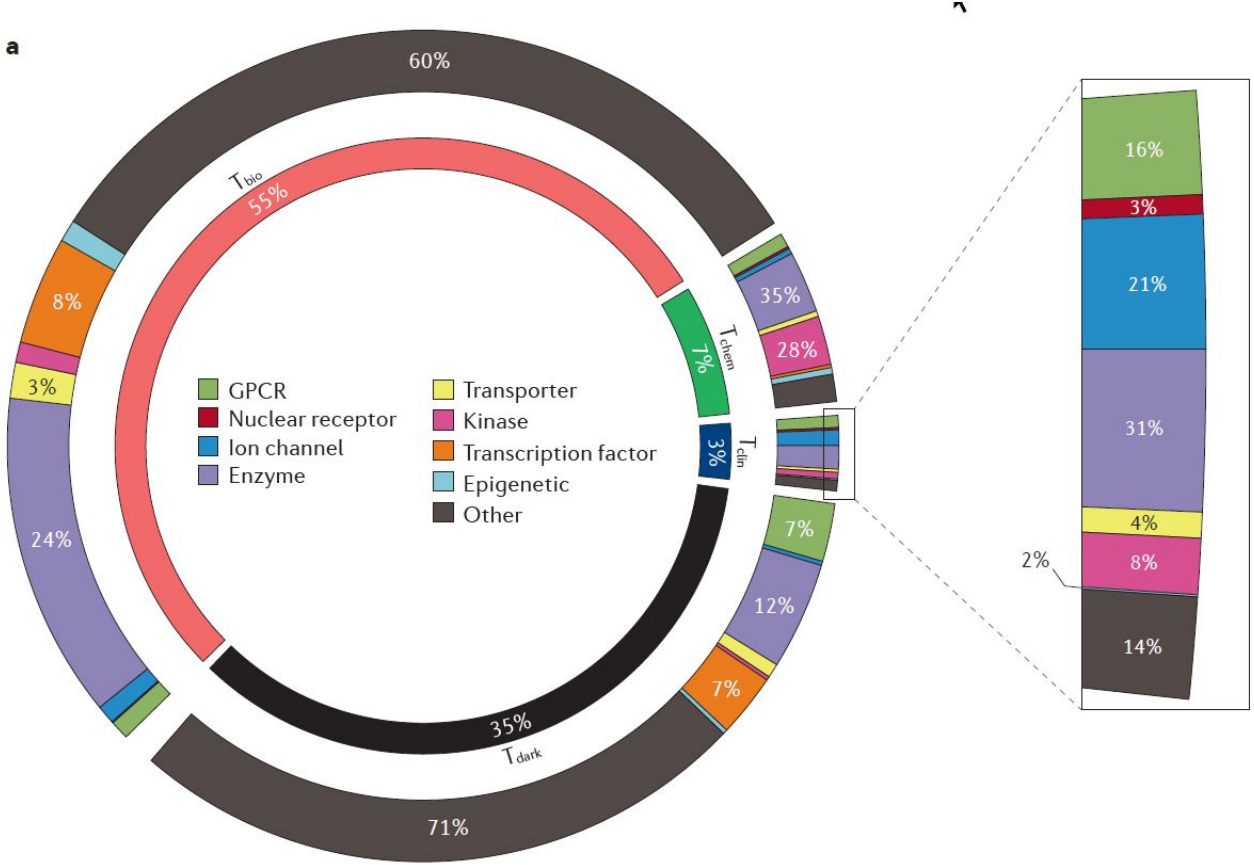
- NCBI HomoloGene
- ENSEMBL ComparaGenom
- Mouse Genome Informatics (MGI)

Other important information resources

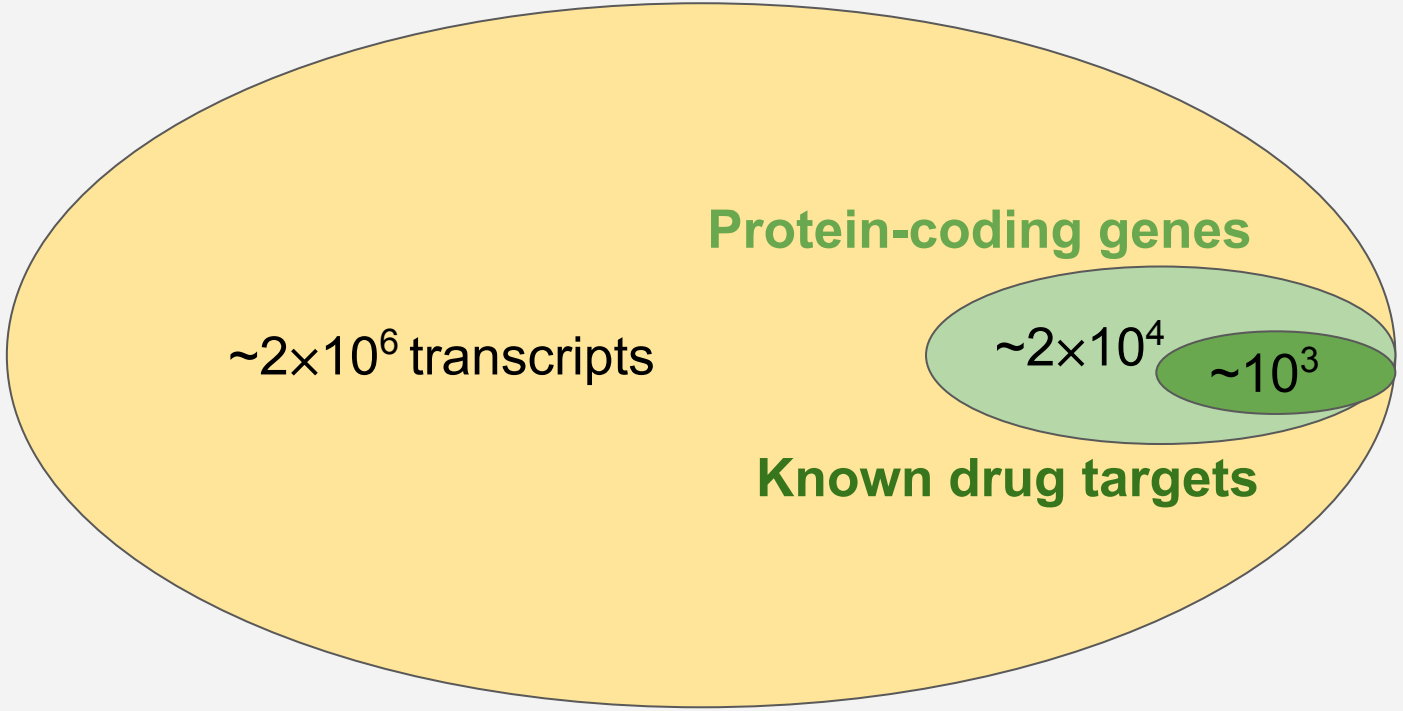
- **Genomic variations**: gnomAD, dbSNP, and TCGA for oncology;
- **Protein domain and static structure**: InterPro, Pfam, and PDB;
- **Interaction network and pathway**: BioGRID, IntAct, Reactome, and KEGG;
- **Gene expression profiles associated with the target**: NCBI GEO (Gene Expression Omnibus), ARCHS4

Challenge #1: little experience for much of the genome



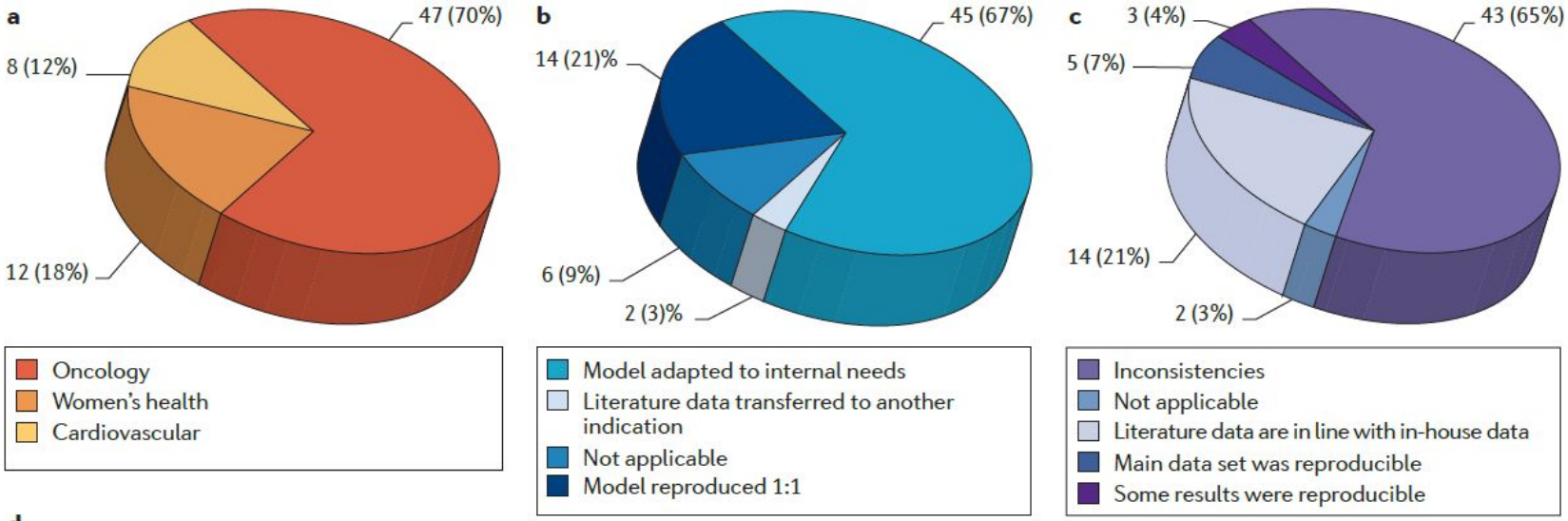


Protein, RNA, or DNA as target?



~3×10^9 DNA bases from maternal and paternal each

Challenge #2: Lack of reproducibility



d

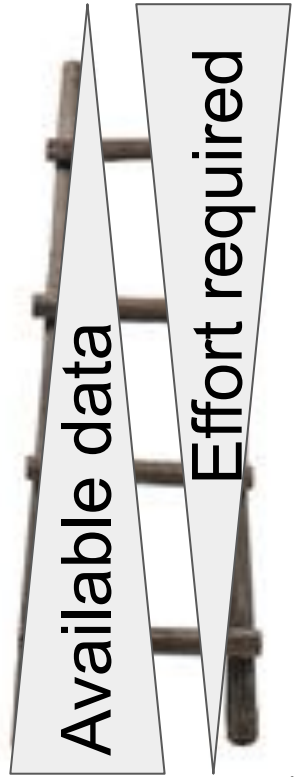
	Model reproduced 1:1	Model adapted to internal needs (cell line, assays)	Literature data transferred to another indication	Not applicable
In-house data in line with published results	1 (7%)	12 (86%)	0	1 (7%)
Inconsistencies that led to project termination	11 (26%)	26 (60%)	2 (5%)	4 (9%)

Challenge #3: The Target Ladder

3. [**Real-world test**] What would happen if we inhibit the activity of the kinase domain in the *WKN3* gene in patients with Alzheimer's Disease?

2. [**Intervention**] What would happen to human cells or to a rat model if we inhibit the activity of the kinase domain in the *WKN3* gene?

1. [**Association**] What are the evolutionary conservation, sequence, expression profile, expression regulation patterns, … of the *WKN3* gene?



Conclusions

- Genomics and genetics offer unprecedented opportunities and challenges for target identification and assessment;
- Target identification and assessment involves knowledge integration and experimental validation;
- A central task of mathematical and computational biology in drug discovery is to perform inference, i.e. using information to reduce uncertainty.

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Backup

An example of complementary views

We want to work on hepatocarcinoma (liver cancer) and have the following information about a potential target X:

- X is a receptor expressing on the surface of most cell types;
- Upon binding ligands, X activates innate immune response;
- Gene sequence of X is conserved in primates but *not* in rodents;
- Protein X interacts with protein Y, which is essential, namely Y knockout causes lethal embryos;
- Asian population has a unique genetic variant in the non-coding region of *X*;

Discussion: what are the consequences of having these information?

Questions from courses

- Why I recommended the GOT-IT paper? How can academia and industry work together towards good targets?
- Did sequencing cost always follow the Moore's law?
- What happens if there are ATGs (AUGs in RNA) in 5'-untranslated region?
  - In some cases, there are alternative start codons;
  - However, in most cases, the ATGs in 5'-untranslated region seem to be always ignored by the translational machinery. A study (Rogozin, Bioinformatics, 2001) suggested that those AUGs may ensure low basal expression and generate regulatory elements.
- Which target level (gene or protein) is more useful for the target identification? In the lecture, gene-level approach seems not so promising.
- Is blue eyeness a marker of Neanderthalian origin? *The story of OAC2*

Why autoimmune diseases are more prevalent in females, though one X chromosome is randomly inactivated?

- Sex hormone signaling plays an important role in immune functions, especially estrogens. The hormone signalling apparently explains a lot, but not all, sex differences in autoimmune diseases.
- Mutations of genes on the X-chromosome, as expected, cause many primary immunodeficiencies only in males, because they have only one copy of the X chromosome.
- One of the two X chromosomes in females indeed get inactivated during the embryo stage. However, about 15-20% genes regularly escape the inactivation, among others important genes involved in innate and adaptive immune response, including TLR7 and CD40L.
- There are a few other hypotheses besides X-inactivation escaping, including loss of mosaicism, reactivation, and haploinsufficiency.