



IMPACT OF HUMAN GENETICS ON DRUG R&D

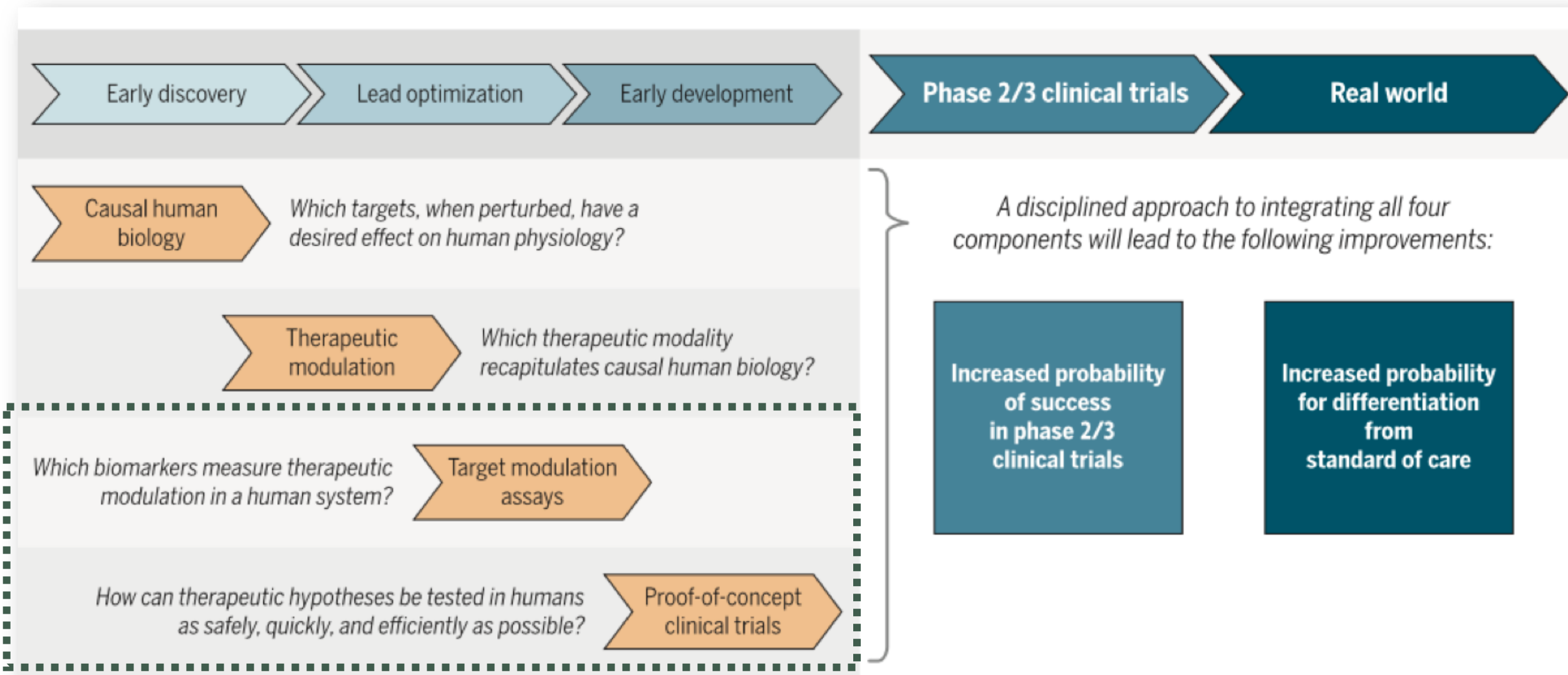


Robert Plenge
Harvard Medical School, Executive Education
June 5, 2018



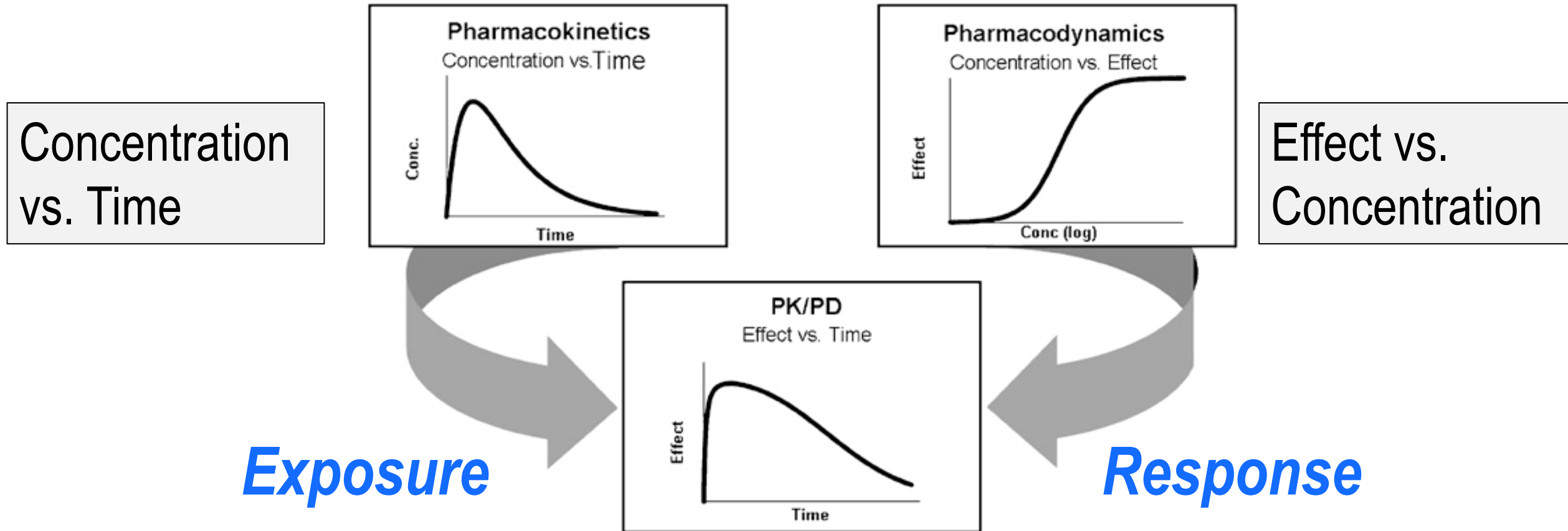
Agenda

- **Introduction**
 - Why human genetics?
- **Day 1:**
 - The model
 - Picking targets and pathways
 - Matching modality and mechanism
- **Day 2:**
 - Predictive biomarkers
 - Clinical development
 - Emerging resources



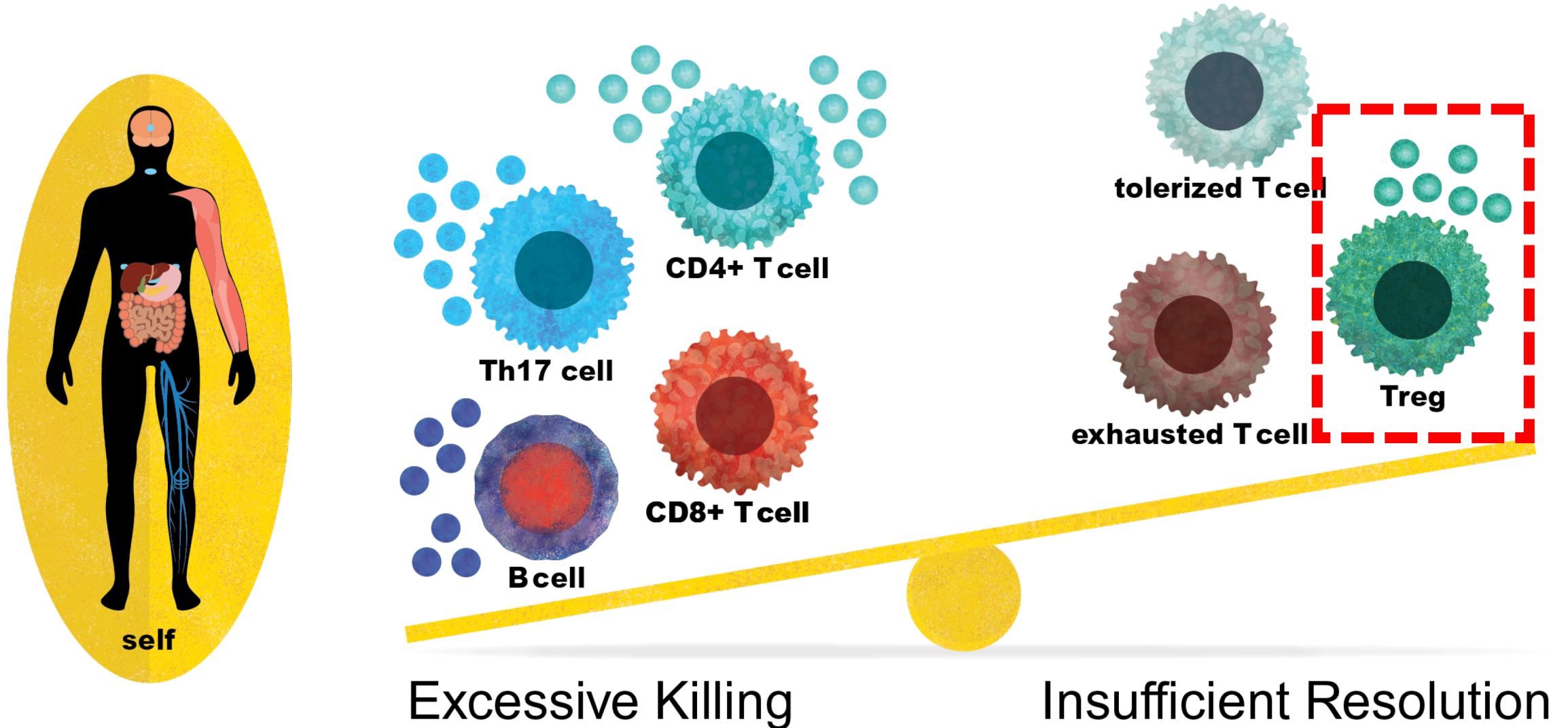
What is a biomarker?

- **Pharmacokinetic (PK)** – what the body does to the drug
- **Pharmacodynamic (PD)** – what the drug does to the body

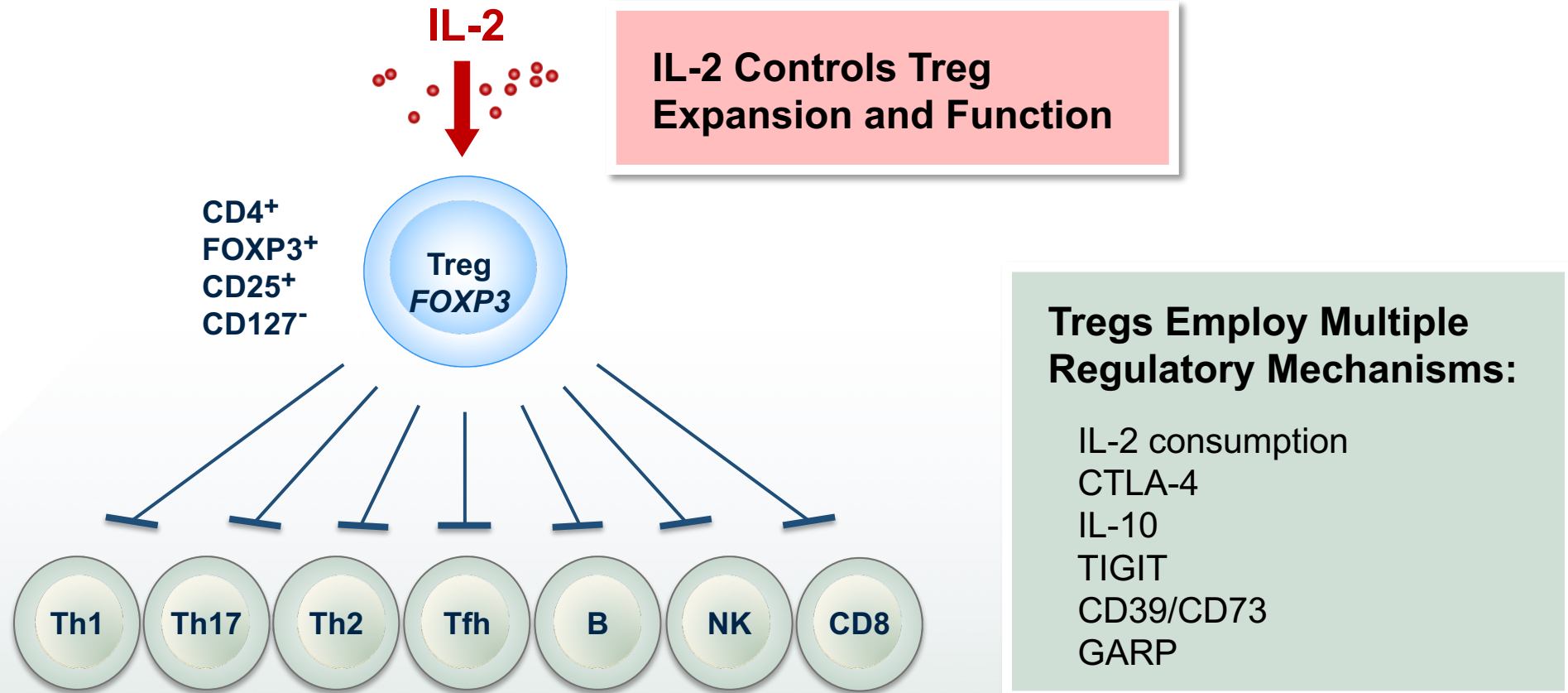


Human genetics can help select
PD biomarkers and model
exposure-response relationship

The immune system is imbalanced in I&I diseases



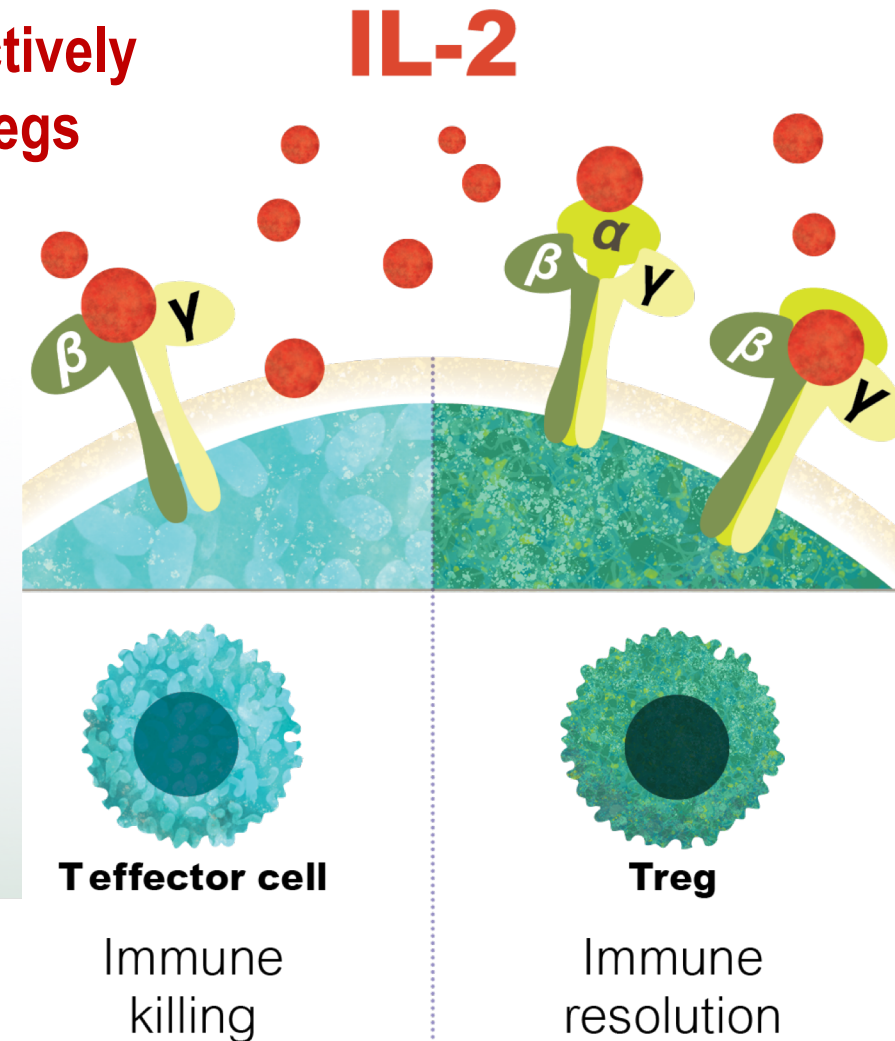
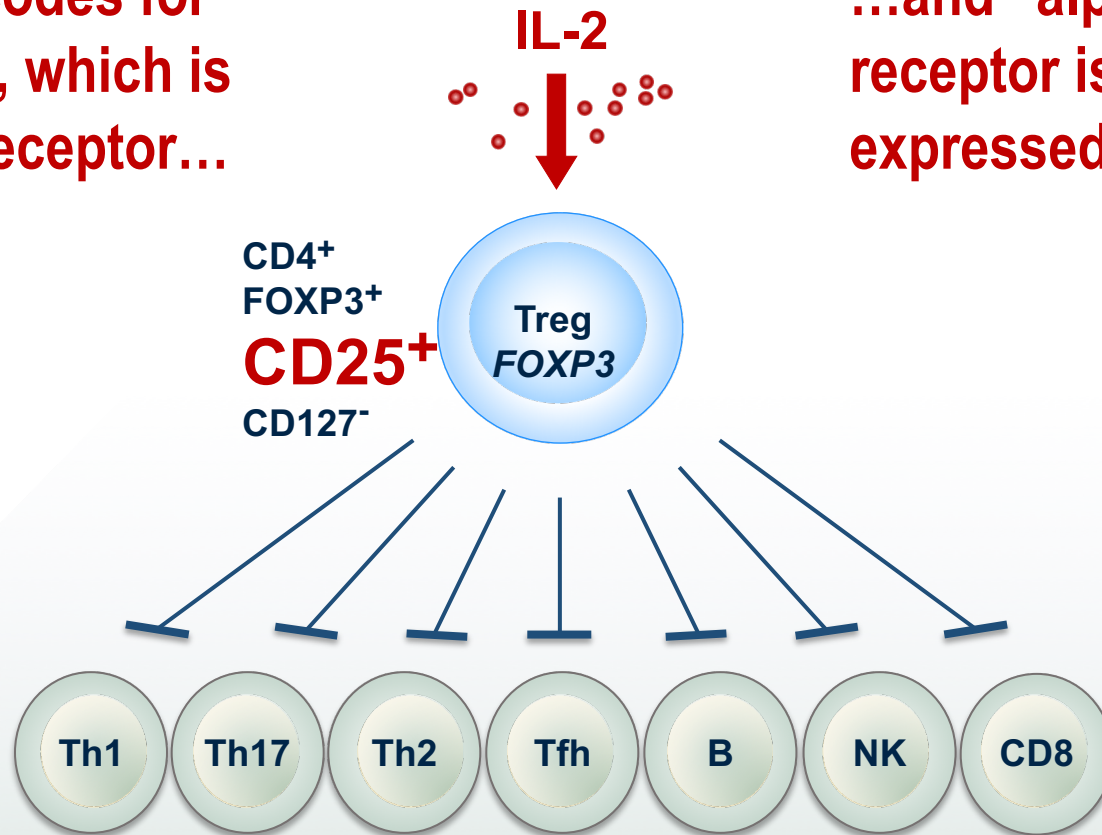
Regulatory T cells (Tregs) are key modulators of immune homeostasis



Regulatory T cells are key regulators of immune homeostasis

IL2RA gene codes for CD25 protein, which is the “alpha” receptor...

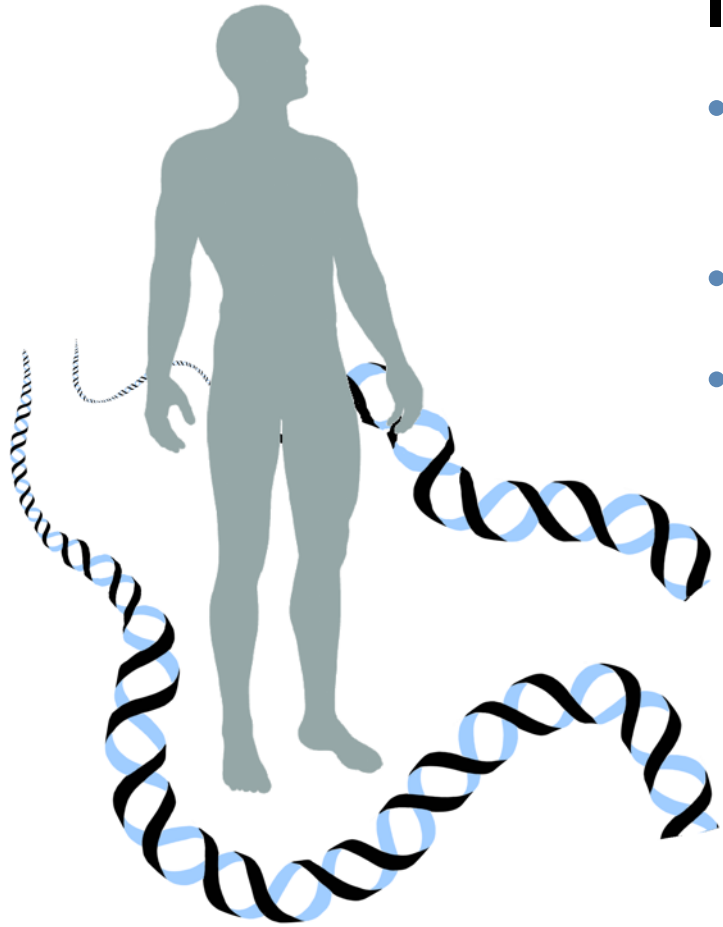
...and “alpha” receptor is selectively expressed on Tregs



Human knockouts of *IL2RA* have severe autoimmunity

IPEX Syndrome

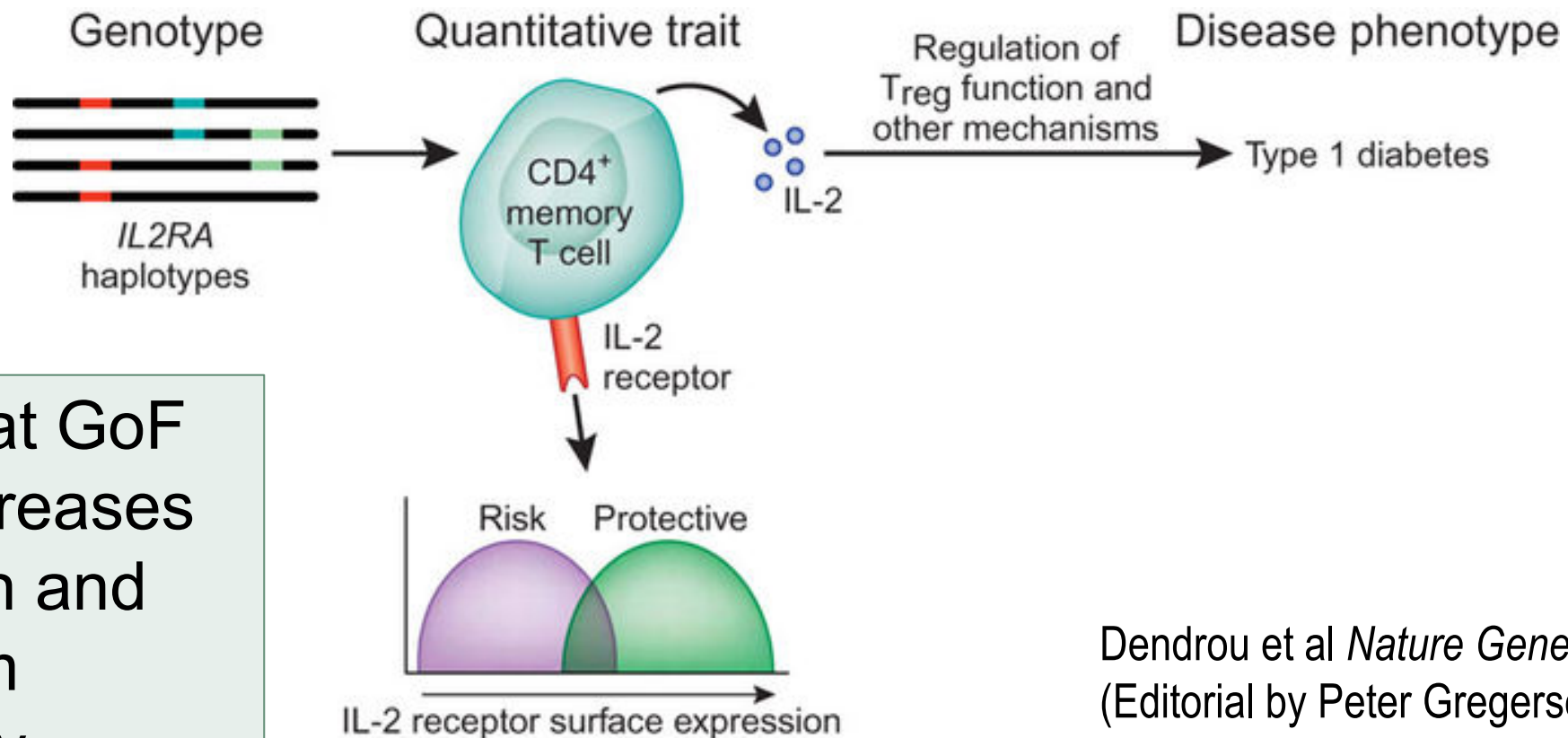
- Immune dysregulation, Polyendocrinopathy, Enteropathy, X-linked syndrome
- Rare, fatal immune disorder
- *Skin, intestinal, endocrine autoimmune disease*



- Reduced Treg cell levels and/or function
- Cured by hematopoietic stem cell transplantation
- Loss-of-function mutations in **FOXP3** gene
- Also caused by nonfunctional alleles of **IL2RA**

Common *IL2RA* variants predispose to multiple autoimmune diseases

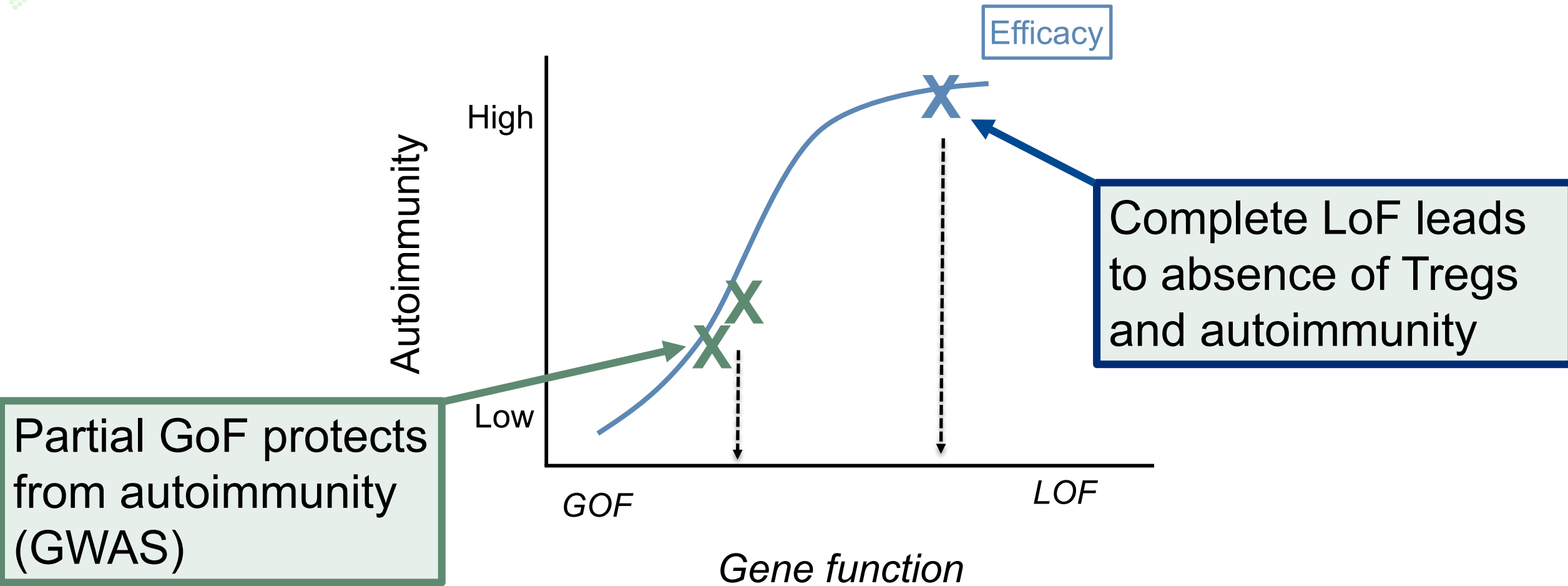
- Story is complicated, but...protective allele is associated with higher expression on CD4⁺ memory T cells



Suggests that GoF on Tregs increases Treg function and protects from autoimmunity

Dendrou et al *Nature Genetics* (2009)
(Editorial by Peter Gregersen)

Function-phenotype dose-response curve for *IL2RA*

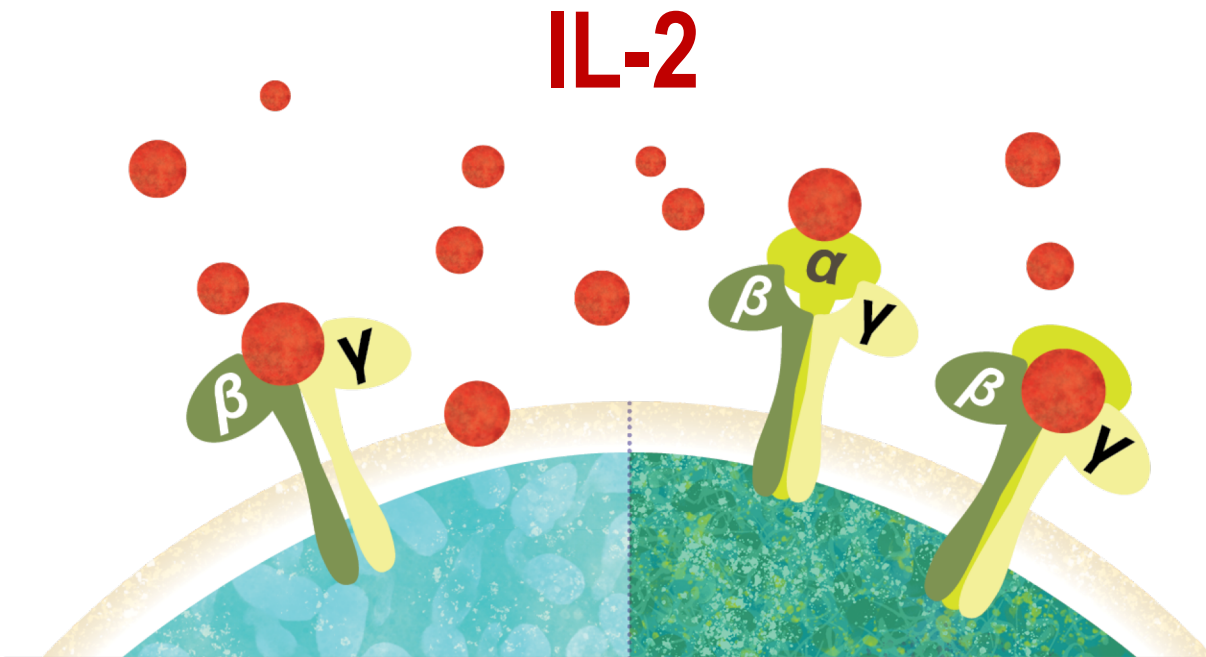


Therapeutic hypothesis

***Agonizing* CD25 (alpha subunit of IL2 receptor) will selectively expand Tregs and treat a wide-variety of autoimmune disorders**

IL2 “muteins” selectively bind to CD25 (*alpha* subunit of IL2R)

IL-2



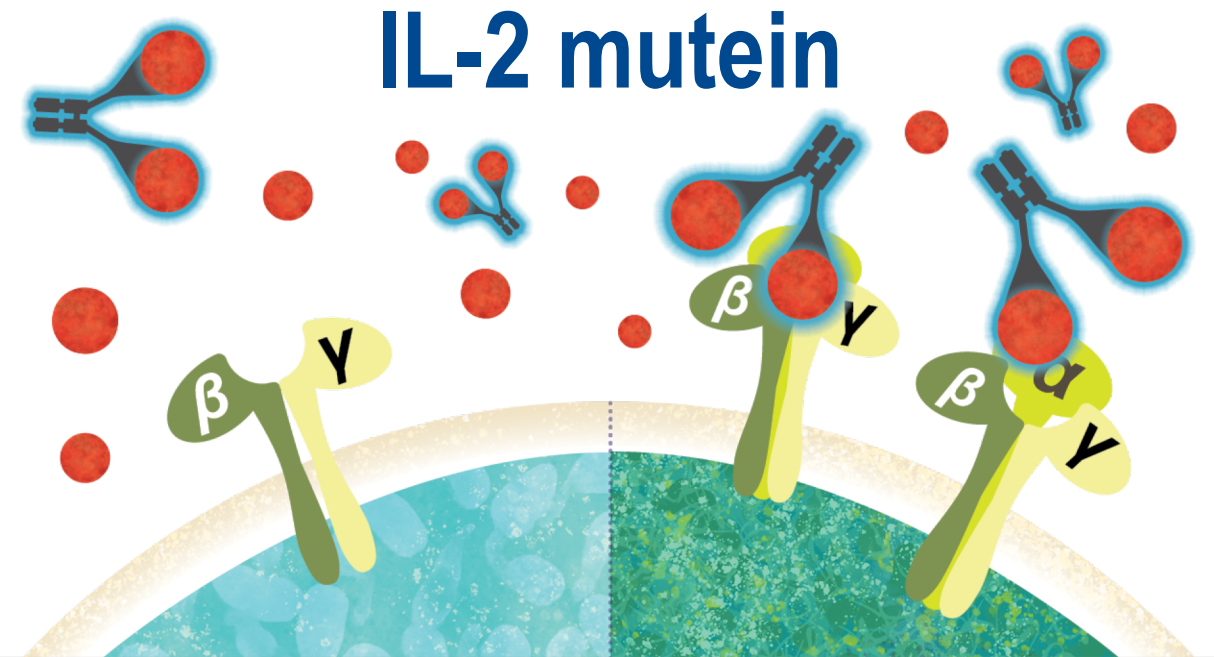
T effector cell

Immune
killing

Treg

Immune
resolution

IL-2 mutein



T effector cell

Immune
killing

Treg

Immune
resolution

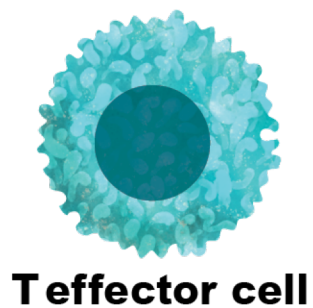
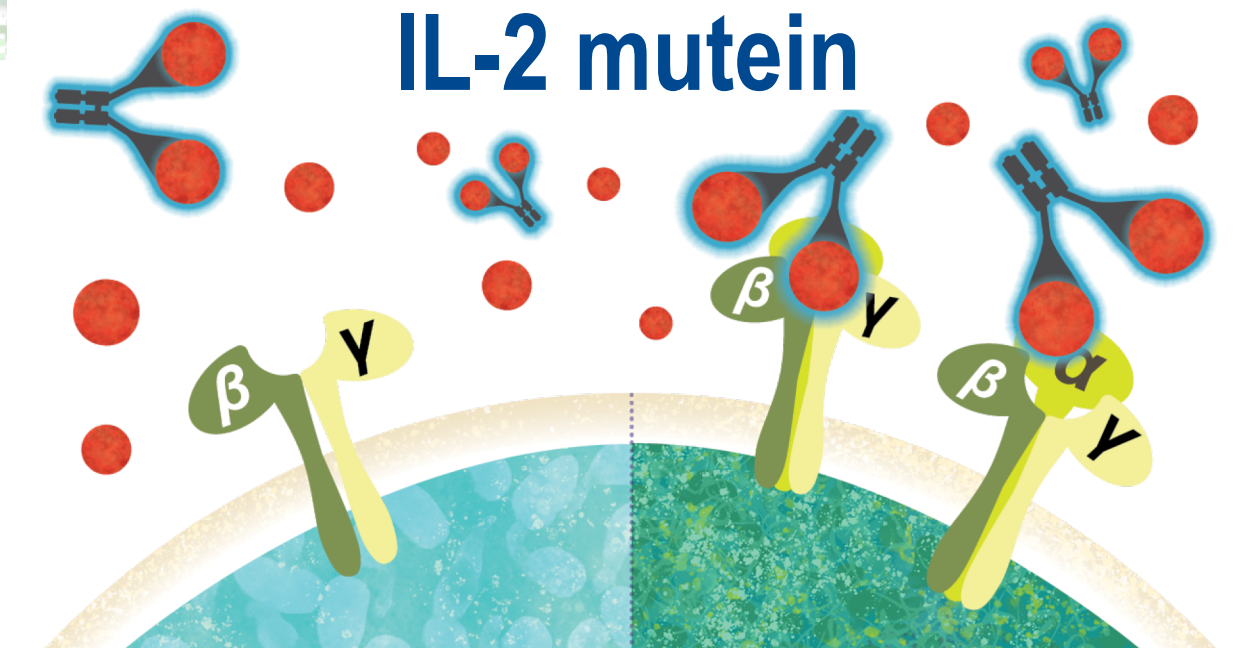
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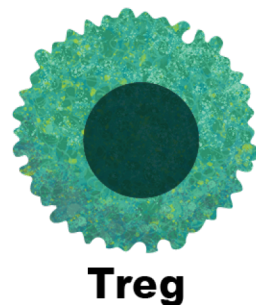
What PD biomarkers should be used to measure exposure-response in Phase 1?

Treg : T effector ratio is a good PD biomarker

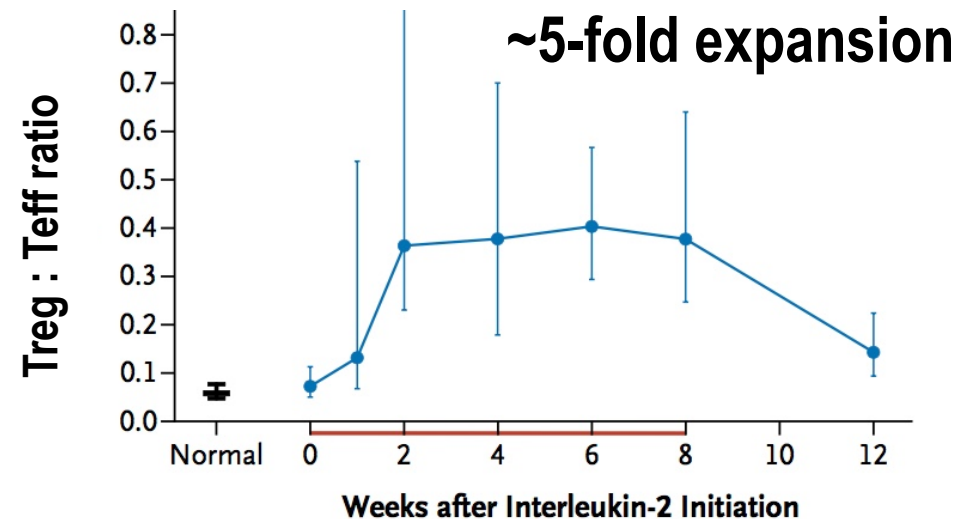
IL-2 mutein



Immune
killing



Immune
resolution



Koreth et al *NEJM* (2011)

Therapeutic hypothesis

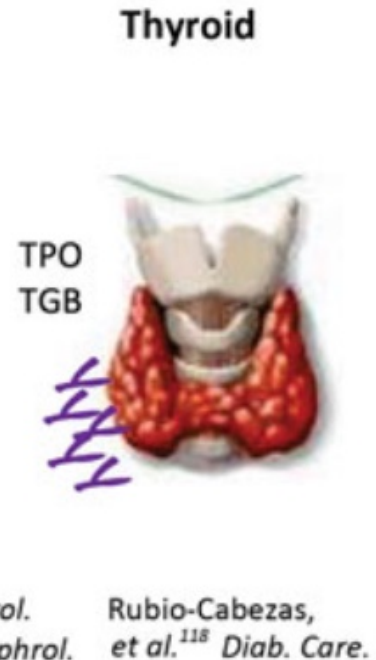
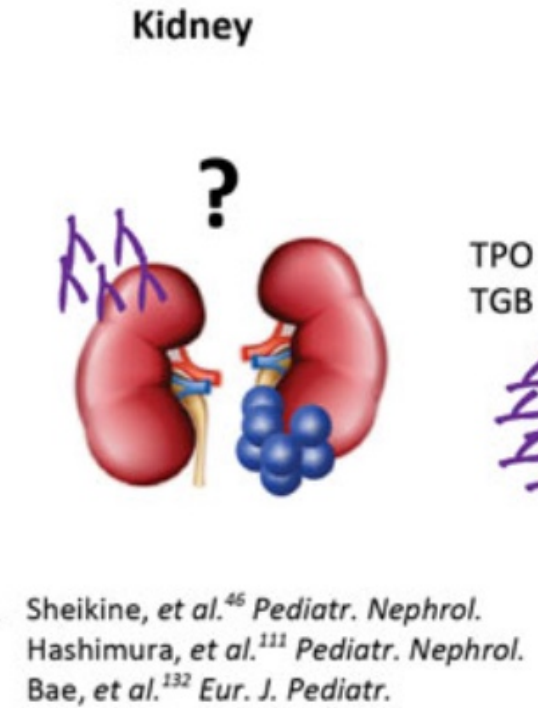
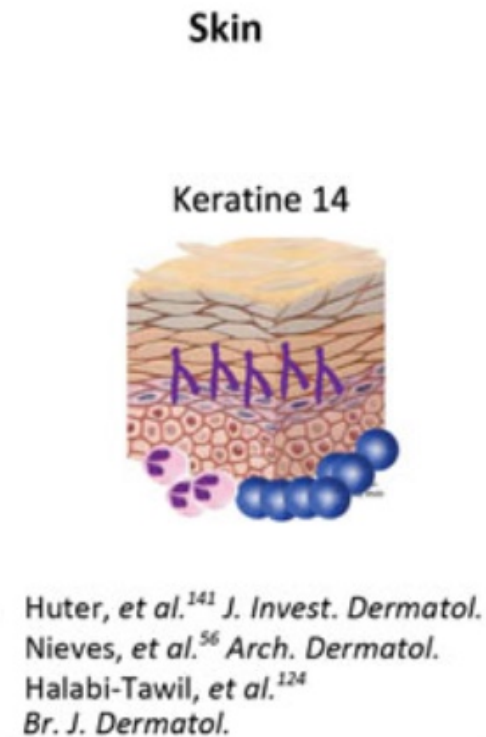
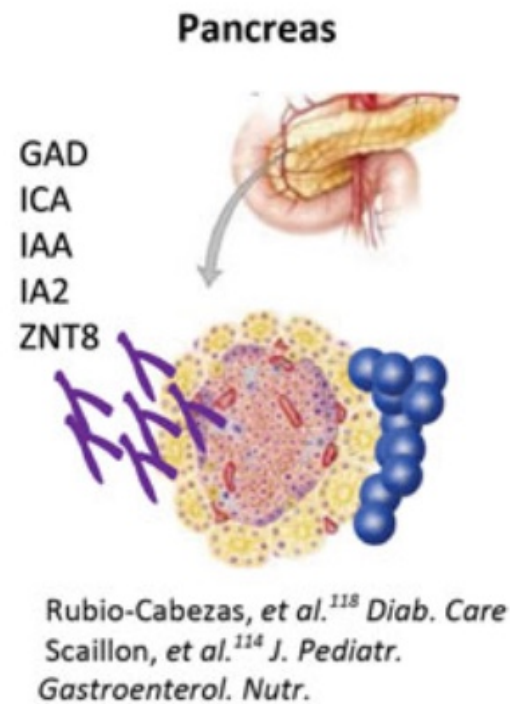
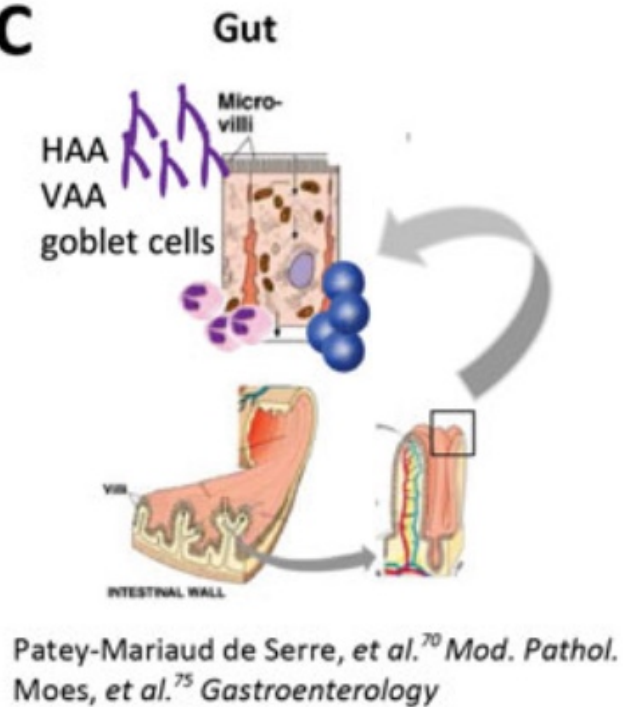
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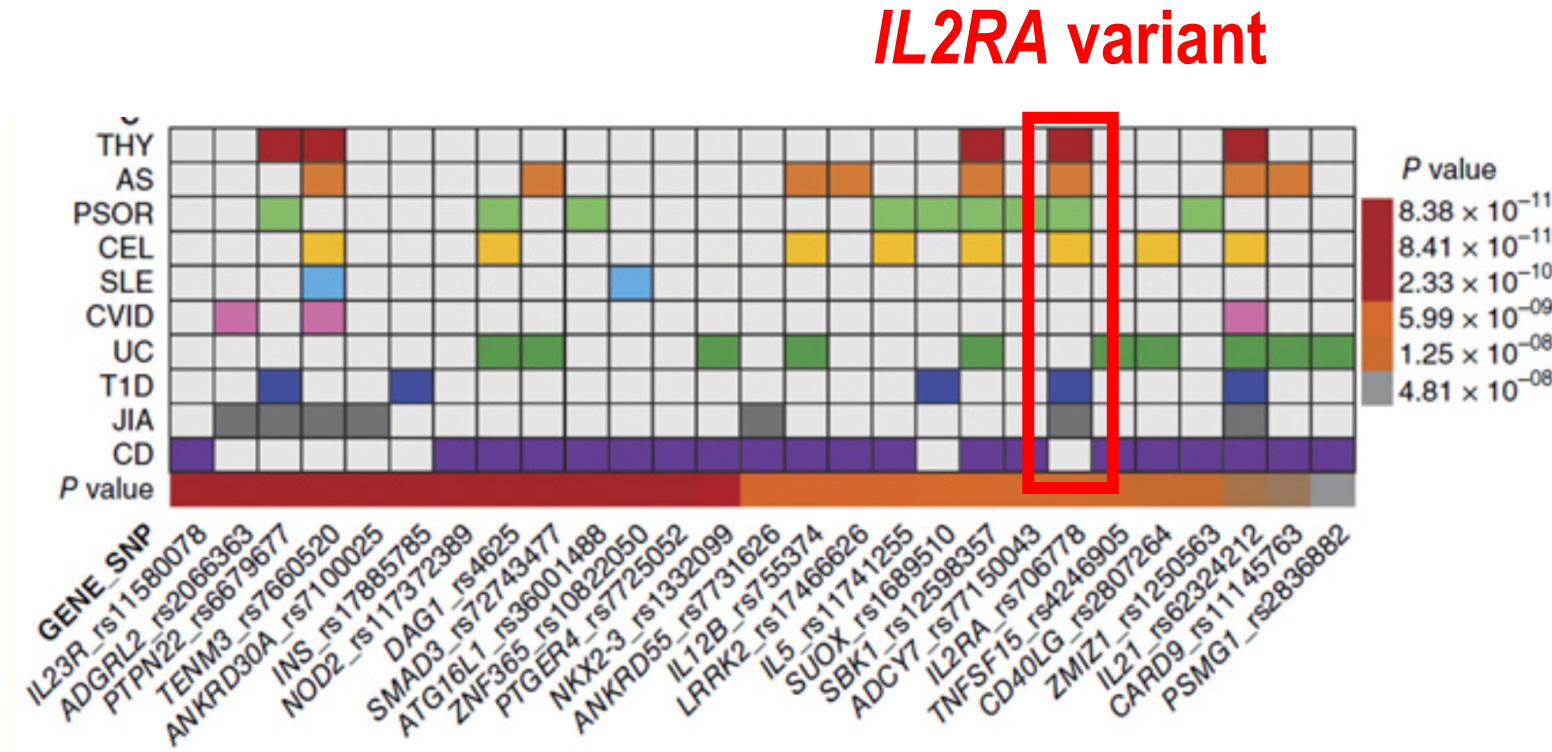
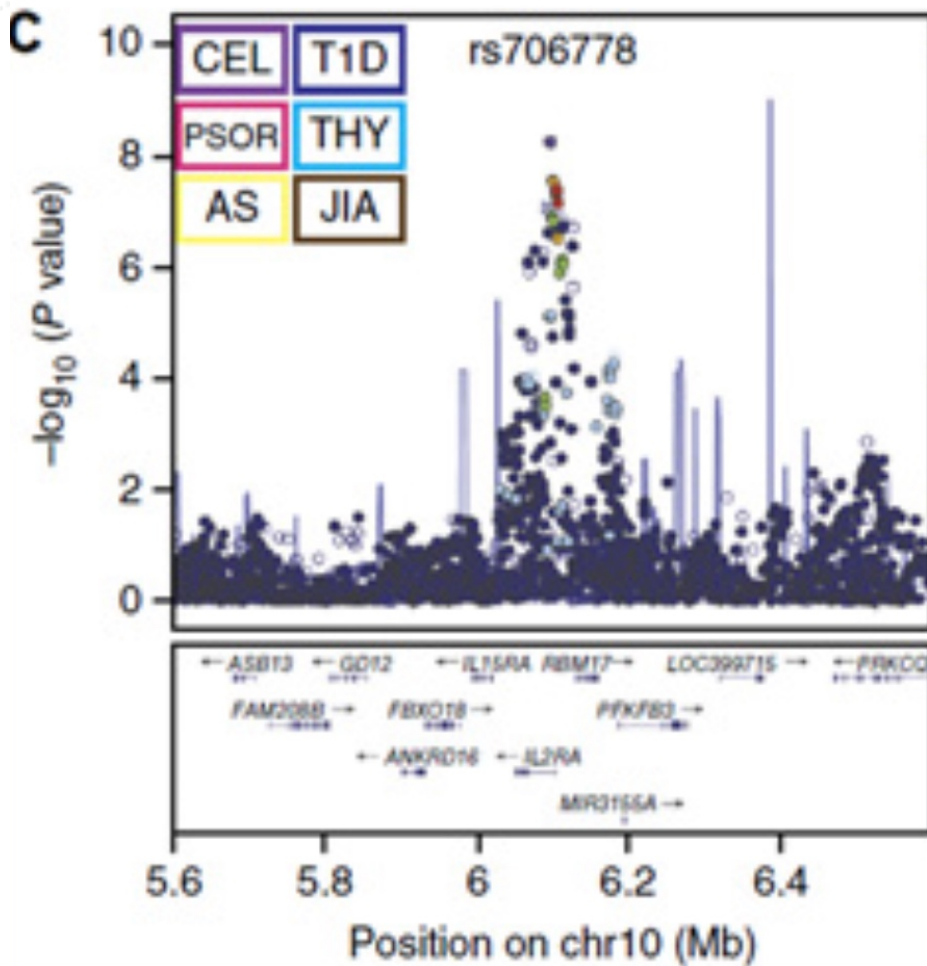
What indications should be pursued for PoC?

Rare LoF IPEX mutations guide indication selection

C



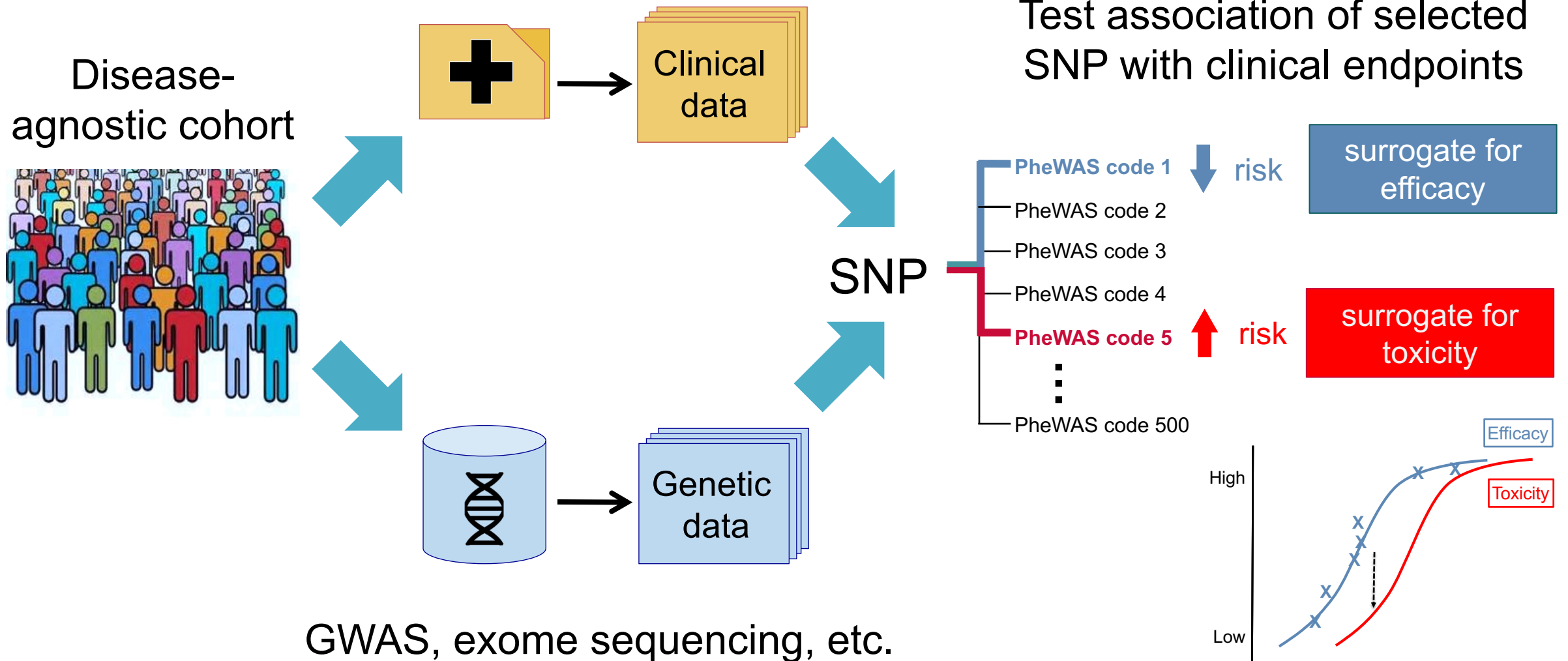
Common GoF GWAS variants guide indication selection

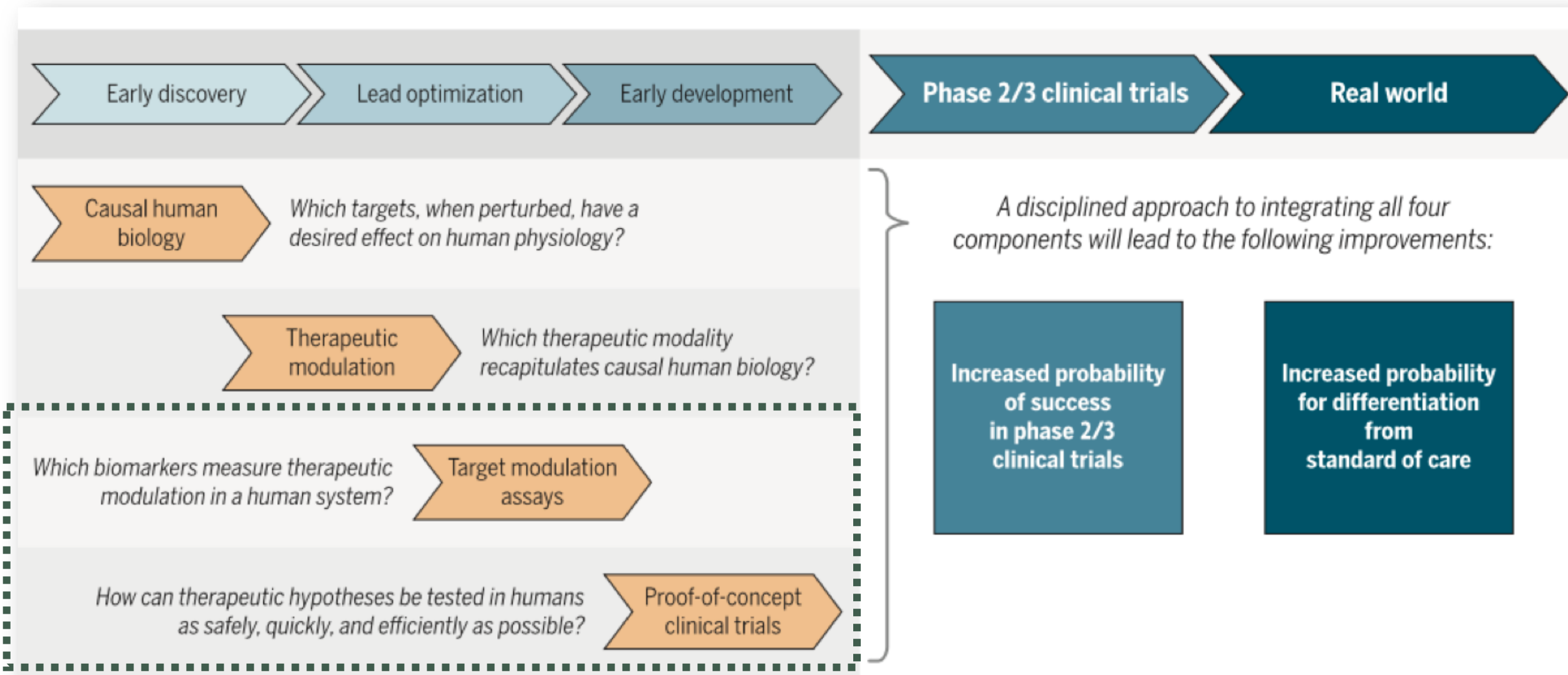


Psoriasis, inflammatory arthritis, type 1 diabetes, other

Phenome-wide association studies (PheWAS)

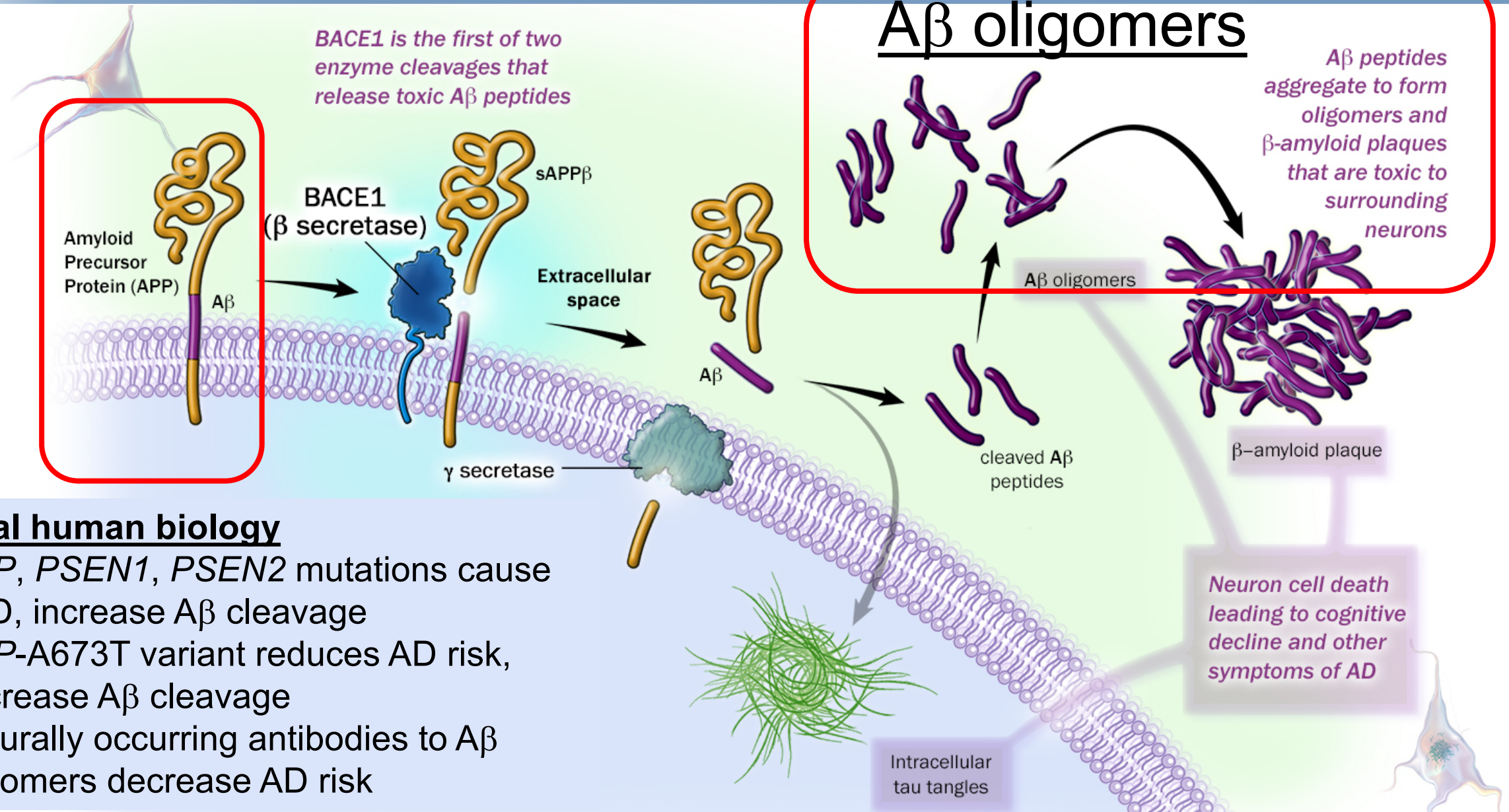
EHRs, Claims, Questionnaires, etc.





But it doesn't always work!

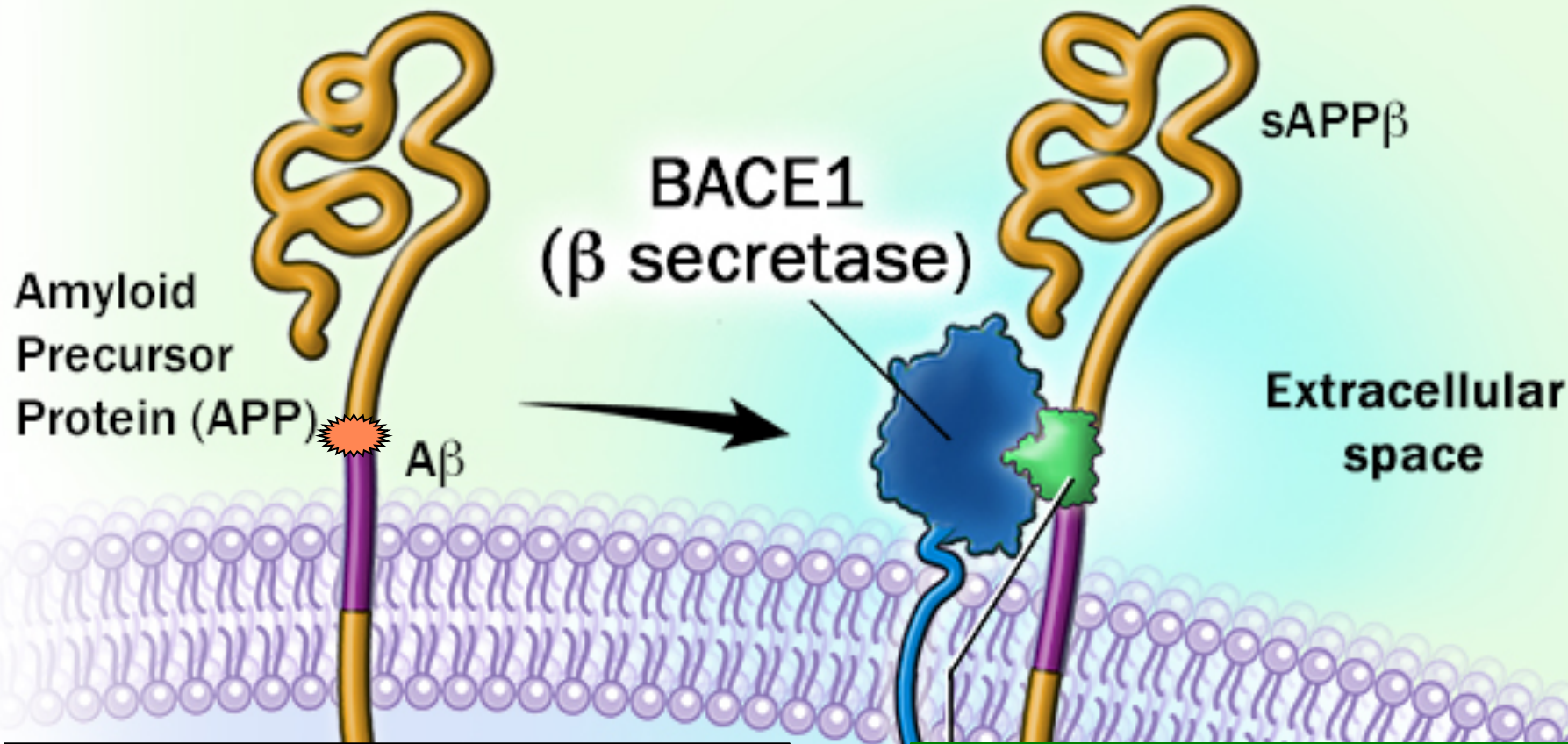
Amyloid hypothesis and Alzheimer's disease: *the role of the APP gene and BACE1 in disease initiation*



Causal human biology

- *APP*, *PSEN1*, *PSEN2* mutations cause FAD, increase Aβ cleavage
- *APP*-A673T variant reduces AD risk, decrease Aβ cleavage
- Naturally occurring antibodies to Aβ oligomers decrease AD risk

Therapeutic hypothesis: *BACE-inhibition blocks release of toxic A β and reduces AD progression*

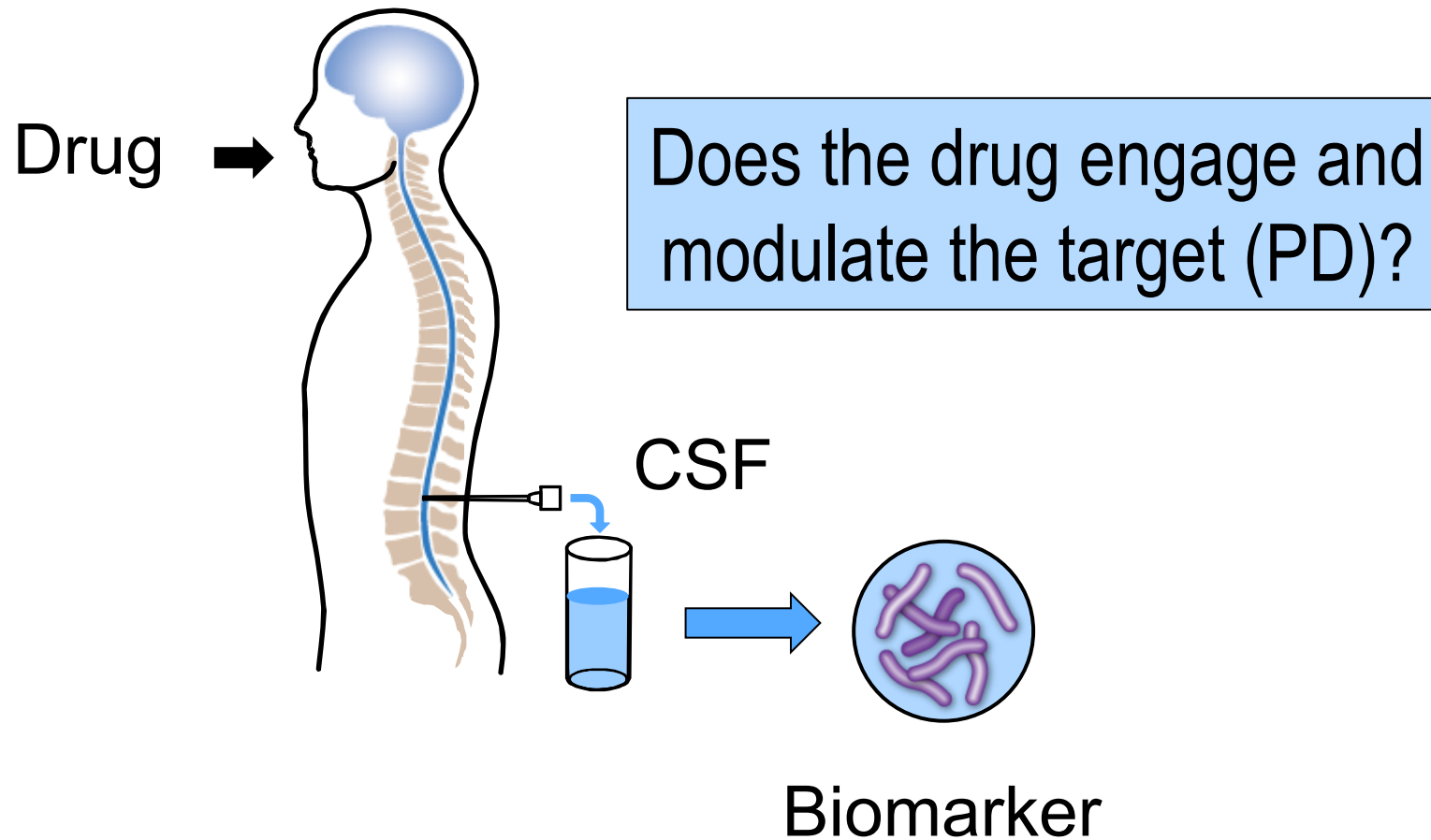


(3) Decrease in A β oligomers in brain protect from AD

(1) Protective APP mutation reduces BACE1 cleavage in vitro

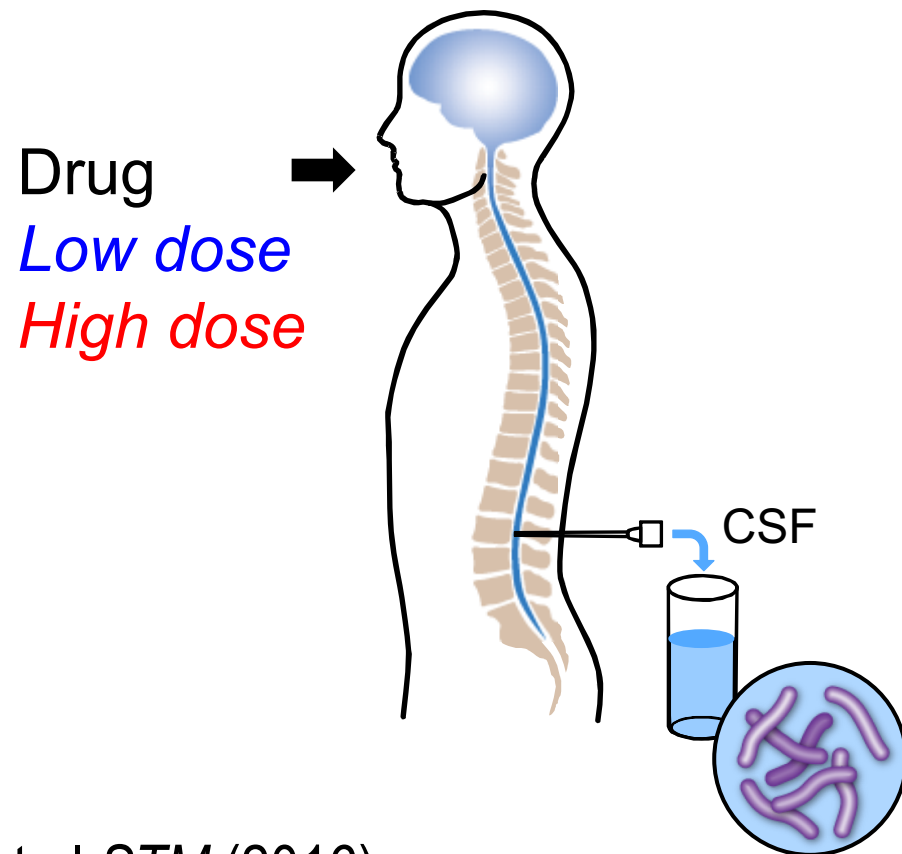
(2) BACE1 inhibitor mimics APP mutation and blocks first step in release of toxic Ab peptides

A β peptide levels measured in CSF serve as a quantitative biomarker for target modulation

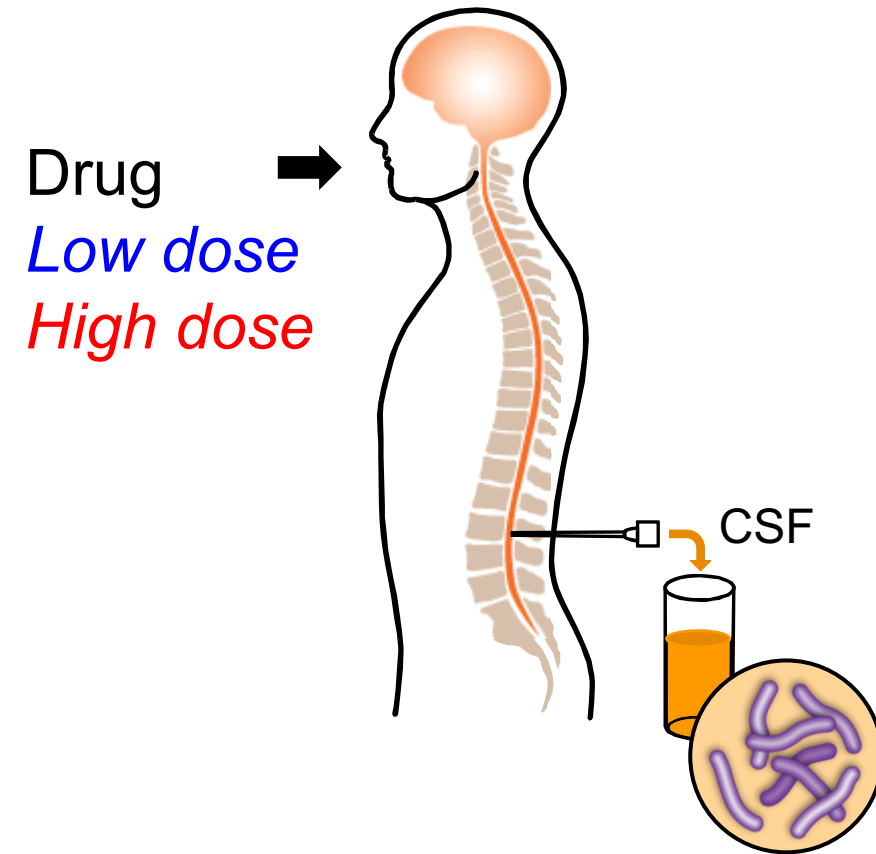


Is there a dose-dependent relationship in human subjects?

Healthy Volunteers

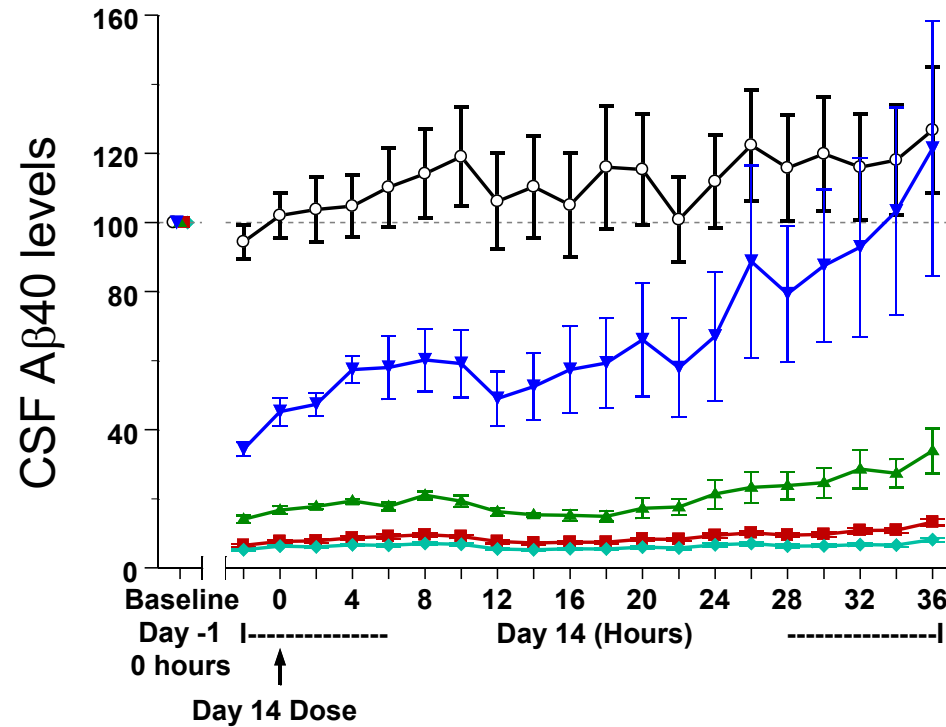


Alzheimer's Patients



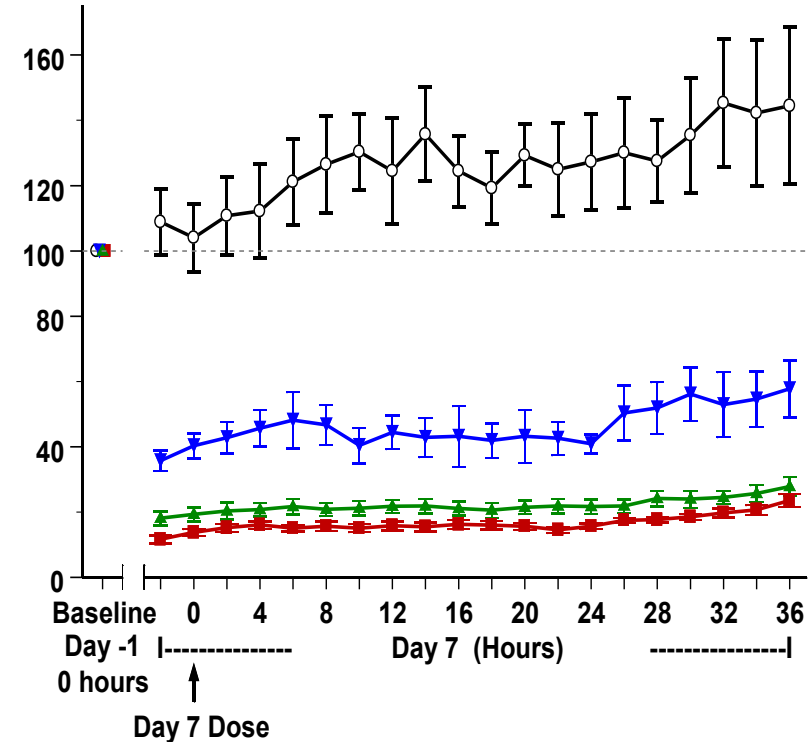
MK-8931 lowers A β levels in CSF from healthy volunteers and Alzheimer's disease patients

Multi-dose, healthy volunteers



—○— Placebo (N=10)
—▼— MK-8931 10 mg (N=6)
—▲— MK-8931 40 mg (N=6)
—■— MK-8931 150 mg (N=9)
—◆— MK-8931 250 mg (N=9)

Multi-dose, AD patients



>90% lowering

Quantitative PK-PD modeling estimates effective dose

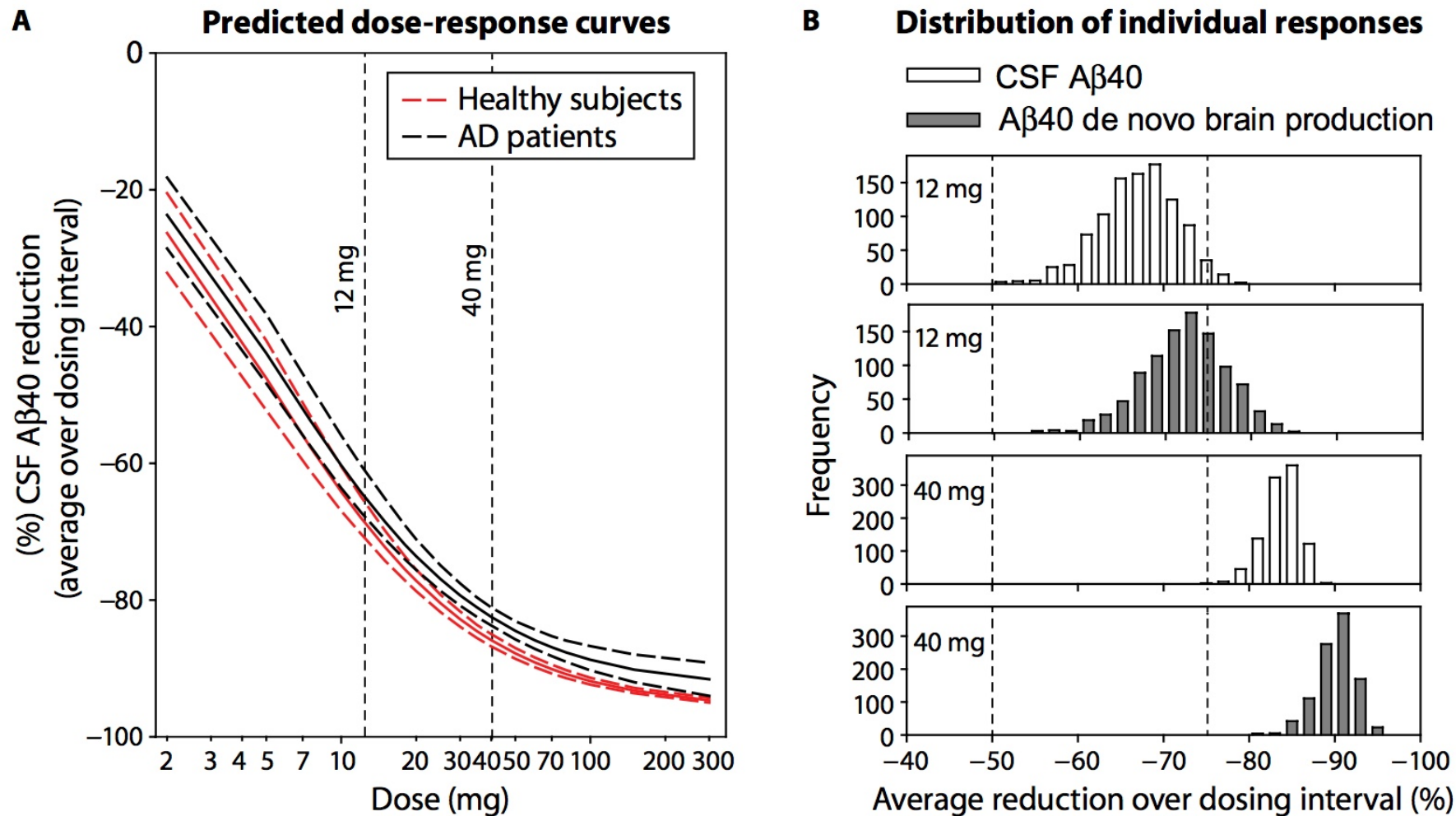
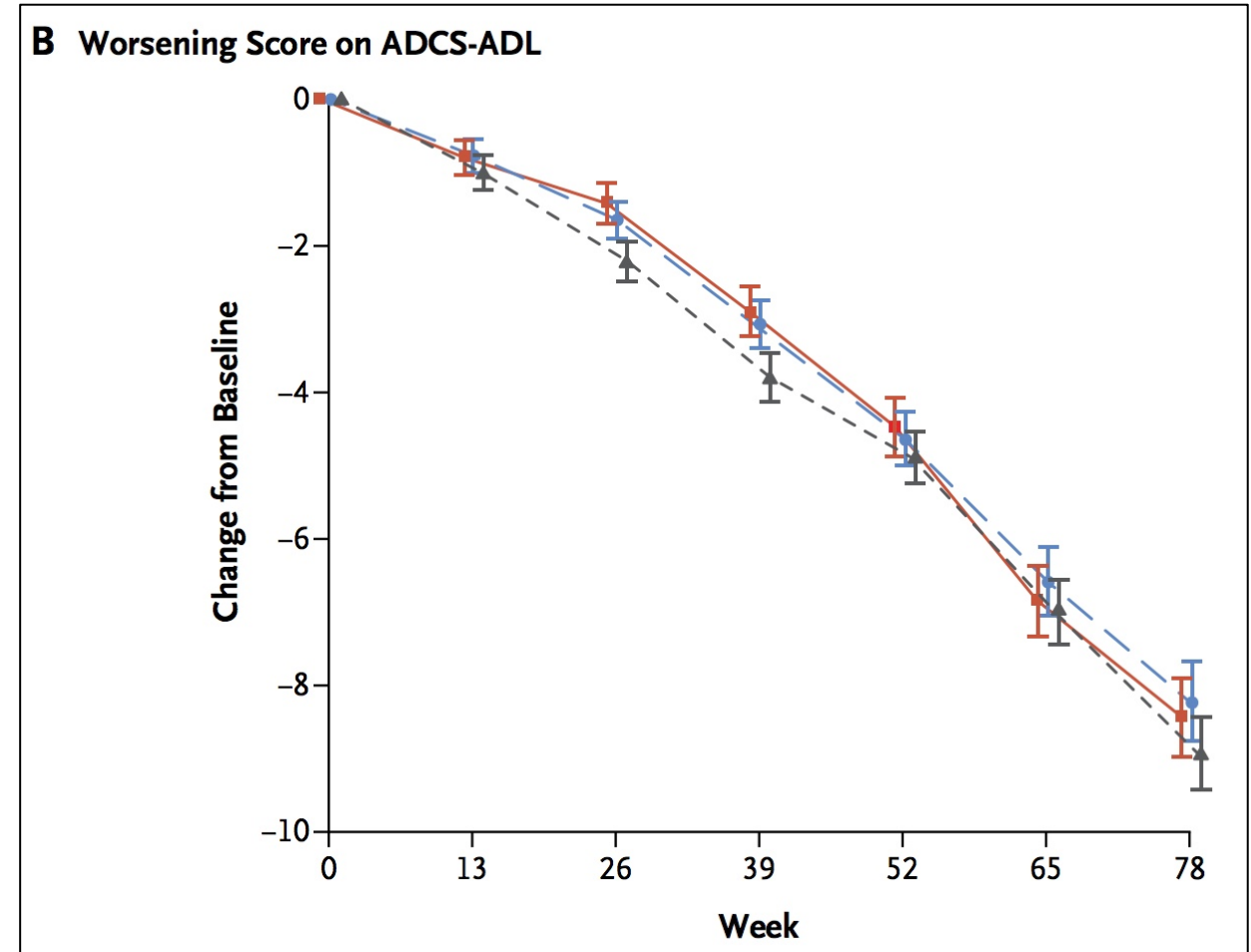
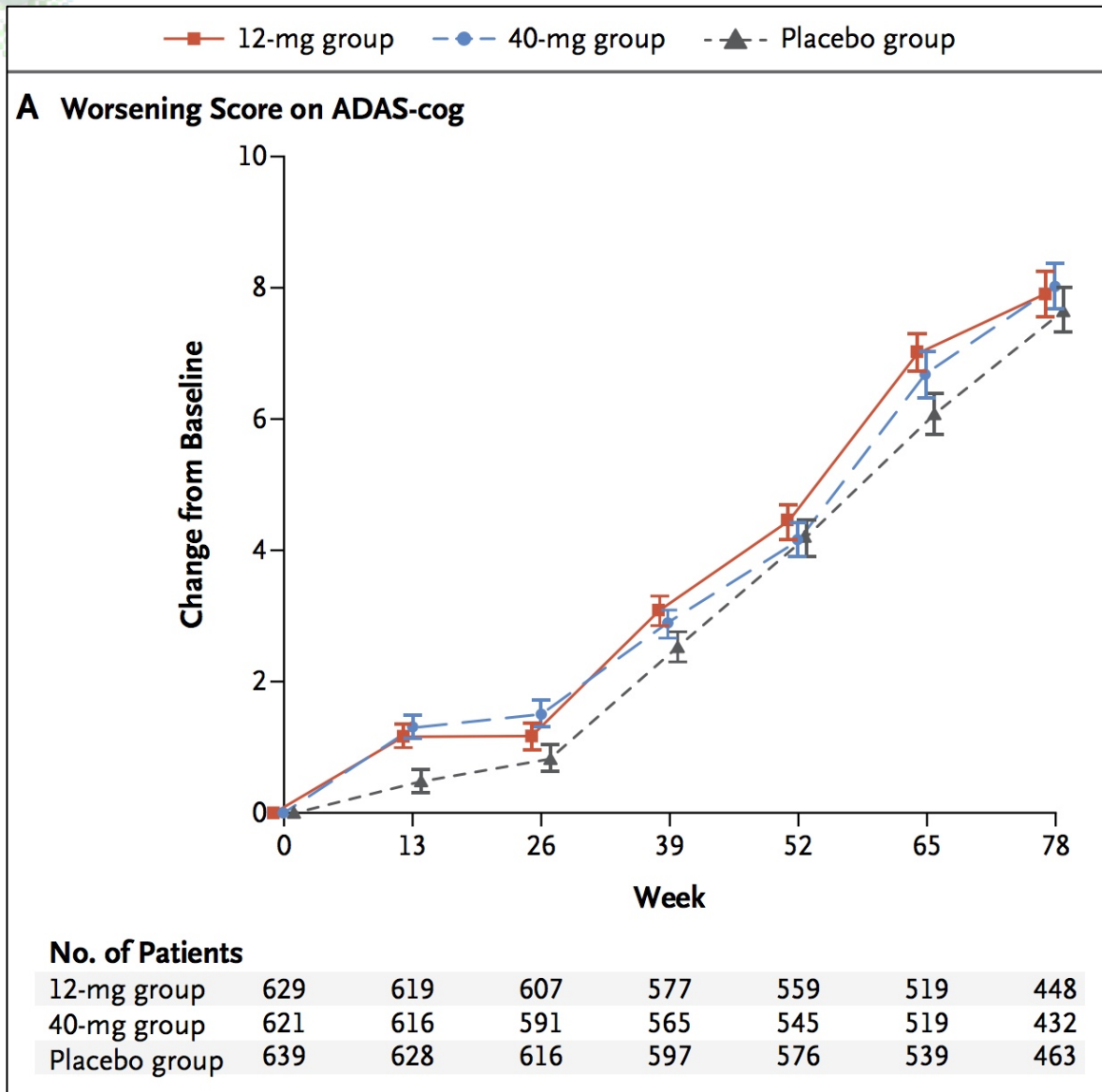


Fig. 7. Simulated steady-state verubecestat dose-response curves and predicted distribution of individual responses. A prospectively planned mechanistic PK/PD model was generated that used data across all time points, CSF PD end points, and studies to develop an integrated characterization of verubecestat effects in humans. (A) The solid and dashed lines represent the median and 90% confidence interval, respectively, of 1000 replicates of the response in a typical AD patient (black line) and a healthy nonelderly adult subject (red line). (B) Simulated distributions of individual CSF A β 40 and de novo brain A β 40 production in AD patients ($n = 1000$ subjects per dose level).

But not every therapy against a genetic target is successful...



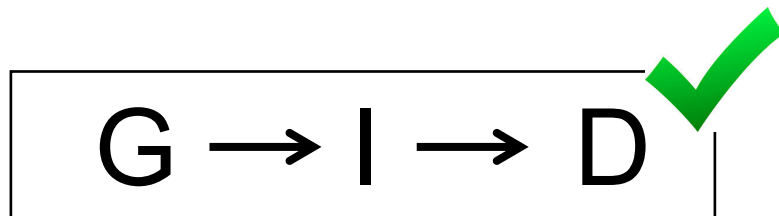
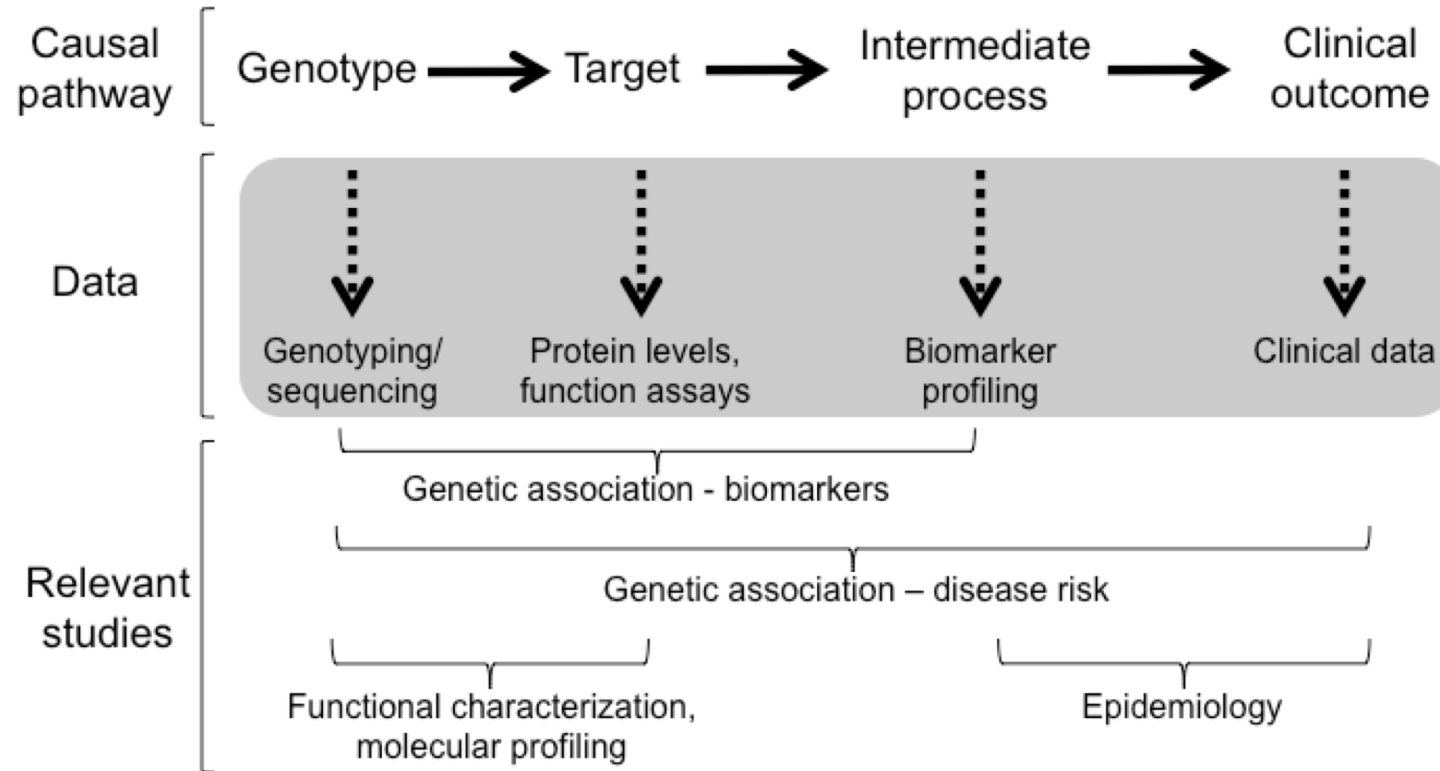
Egan et al *NEJM* (2018)

Key points about biomarkers and why genetic targets fail

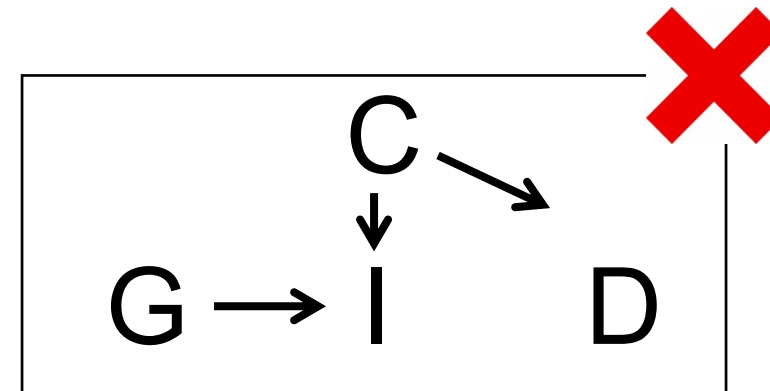
- Essential to have robust PD biomarkers and PK/PD model to predict safety / efficacy
- Ideally, quantitative PK/PD model should be firmly rooted in human genetics
- Even so, not all therapies based on genetic targets will lead to approved drugs
 - Genetics is lifelong, drugs are not
 - Not all genetic phenotypes are good surrogates for drug discovery
 - Modality and molecular mechanism may not be precisely matched
 - Intervention may not sufficiently test therapeutic hypothesis

There are emerging resources to help maximize human genetics for drug discovery and development

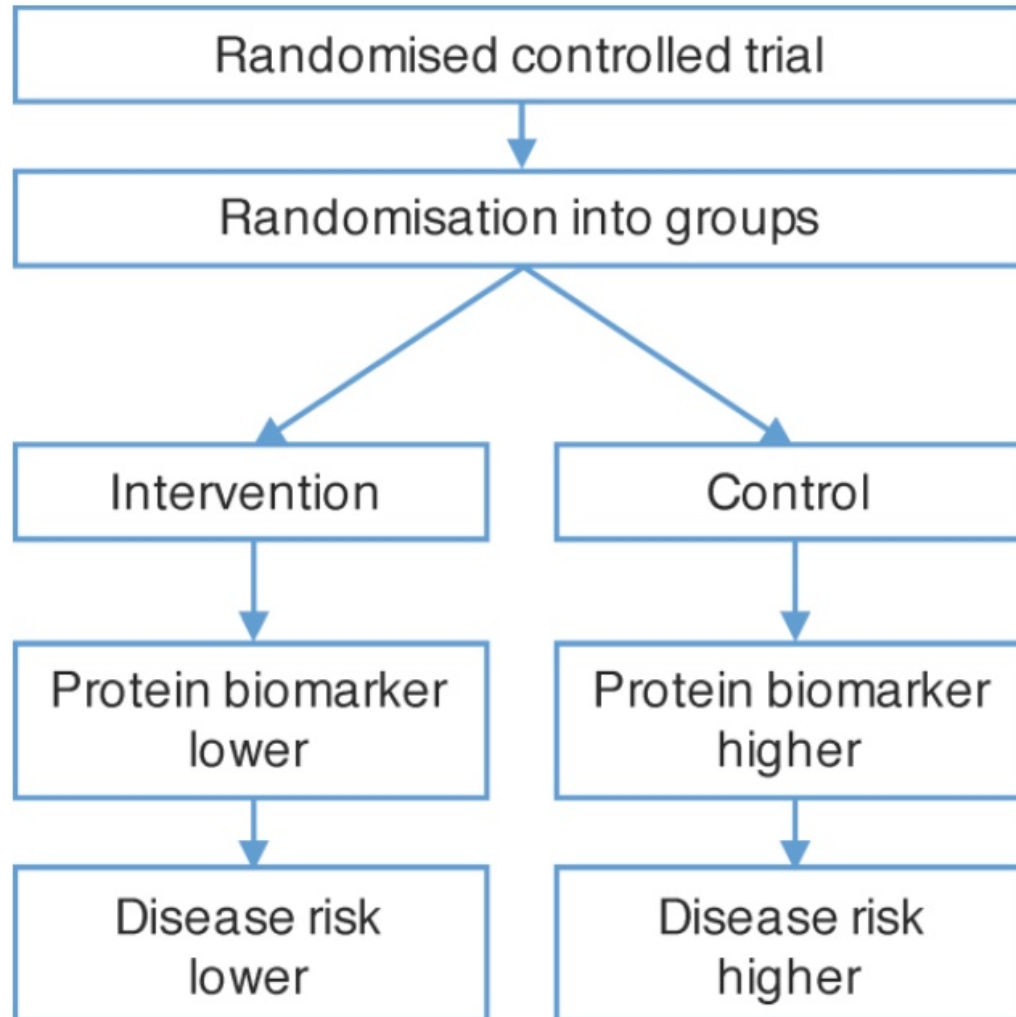
Genetics can bridge biomarker with clinical data, establishing a causal link for drug discovery



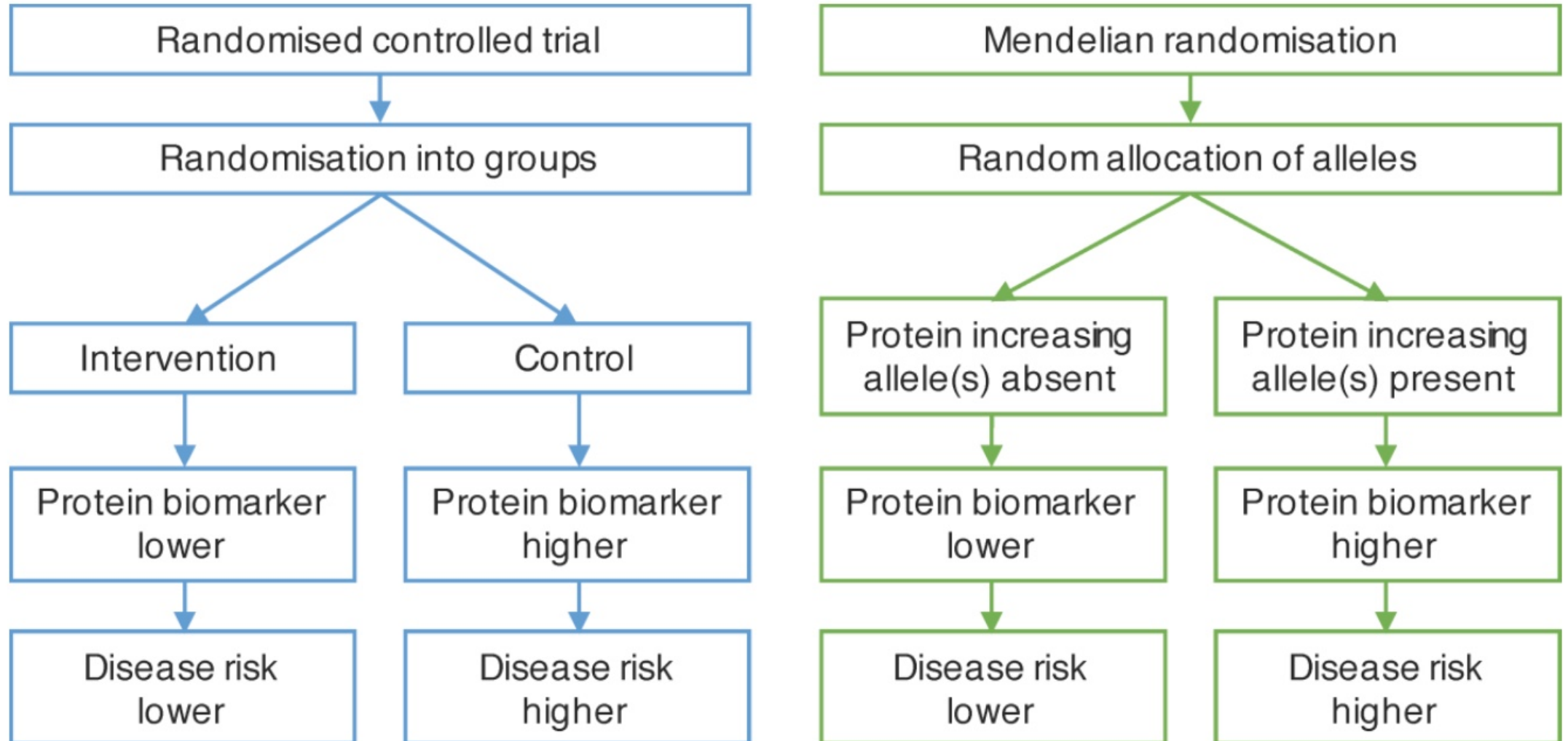
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Mendelian randomization: *nature's clinical trial*



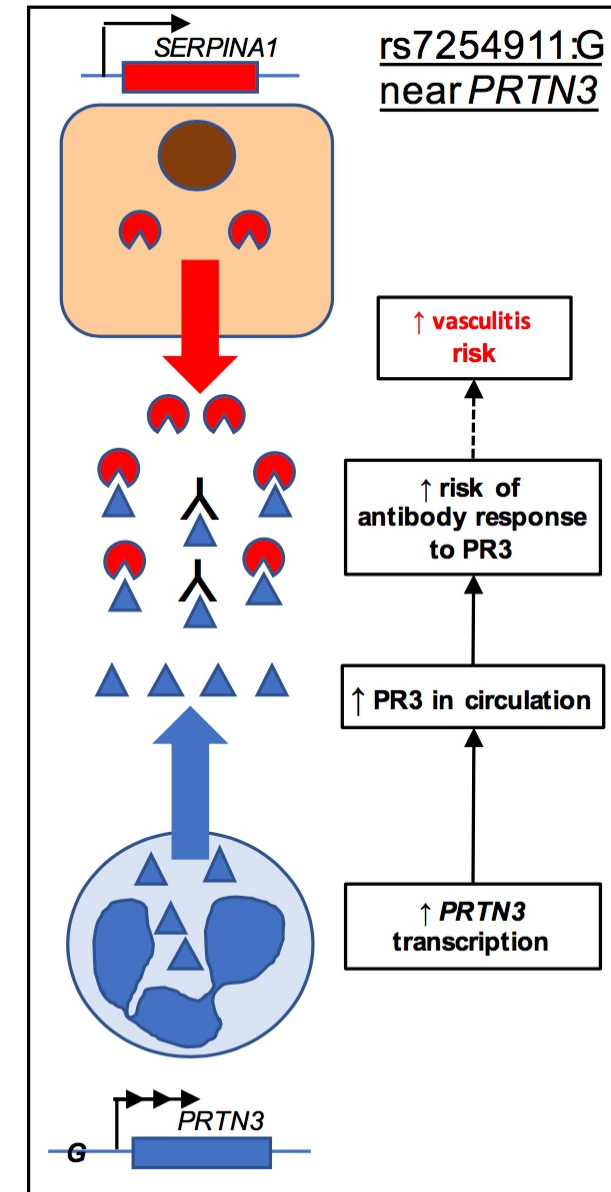
Mendelian randomization: *nature's clinical trial*



MR example: *PRTN3* and ANCA+ vasculitis

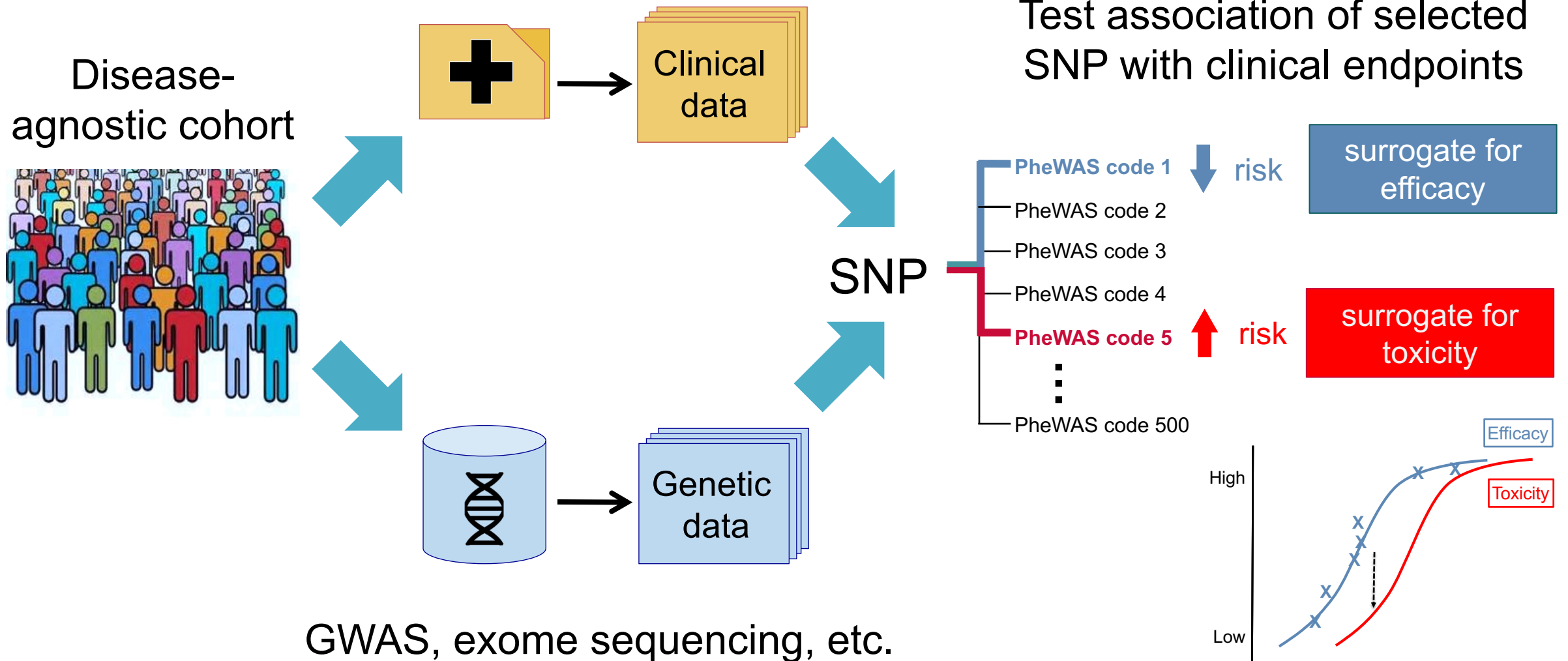
- Tested 3,622 plasma proteins in 3,301 healthy individuals from INTERVAL population cohort
- Identified 1,927 genetic associations with 1,478 proteins
- Example: *PRTN3* GoF allele increases PR3 protein and increases risk of PR3-associated vasculitis
- Therapeutic hypothesis: eliminating PR3 protein or deleting autoantibody secreting B cells may treat vasculitis

Sun, Maranville et al *Nature* (2018)

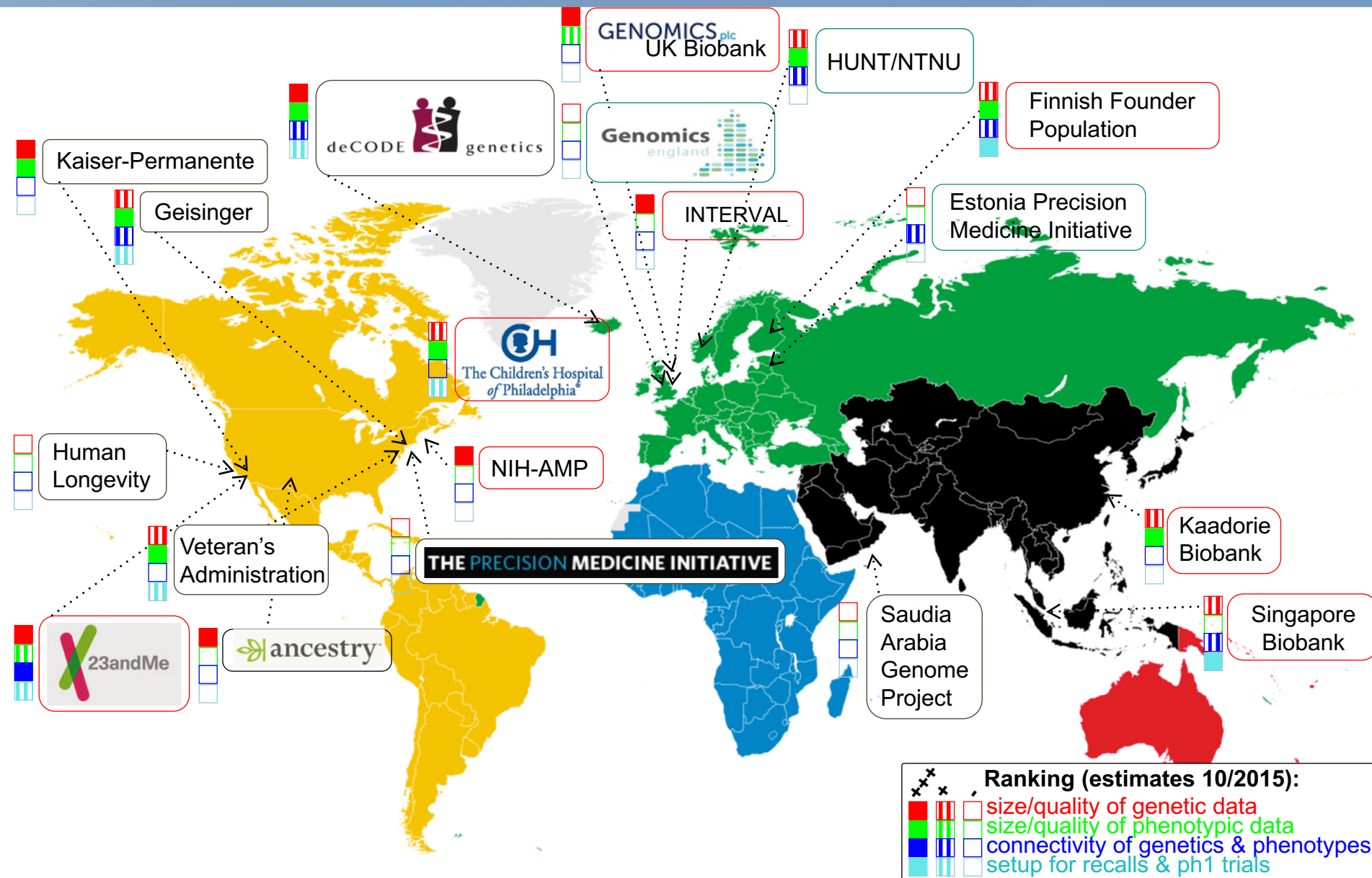


Phenome-wide association studies (PheWAS)

EHRs, Claims, Questionnaires, etc.

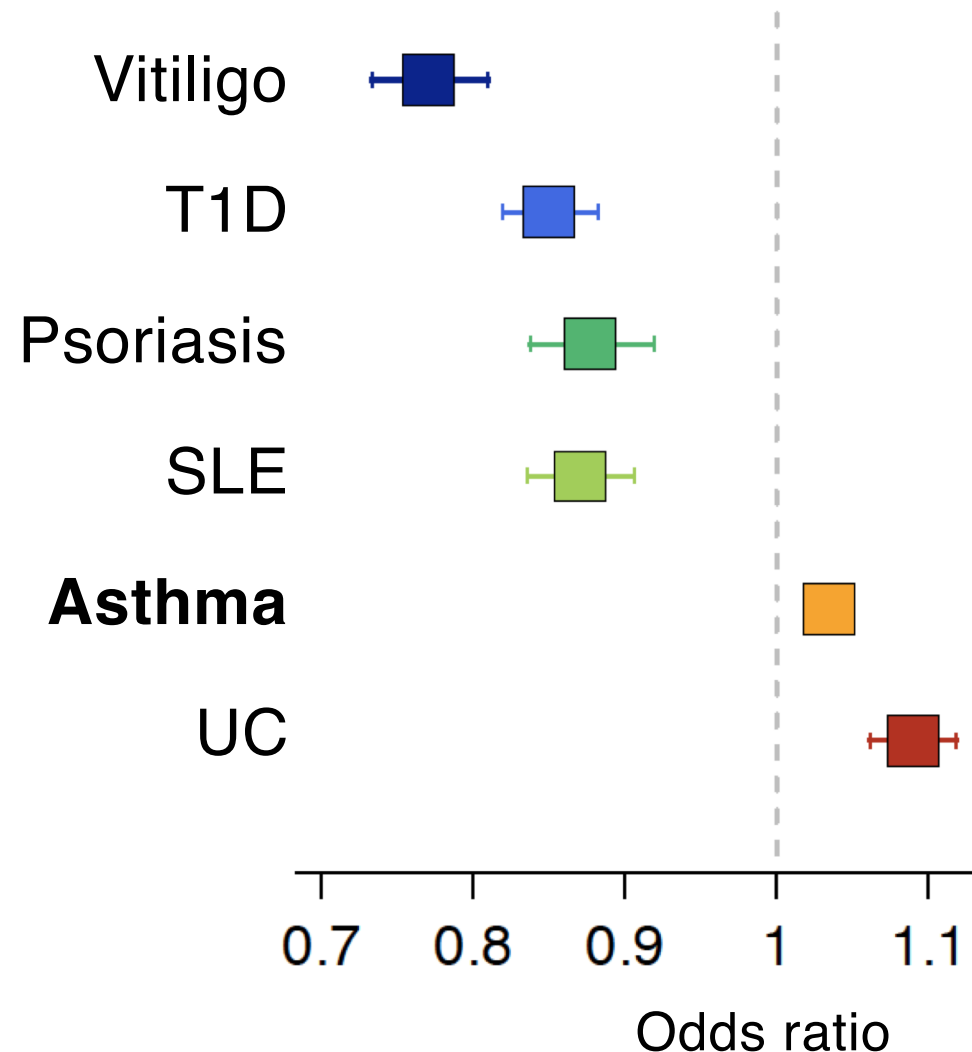


Population cohorts as unique genetic resource



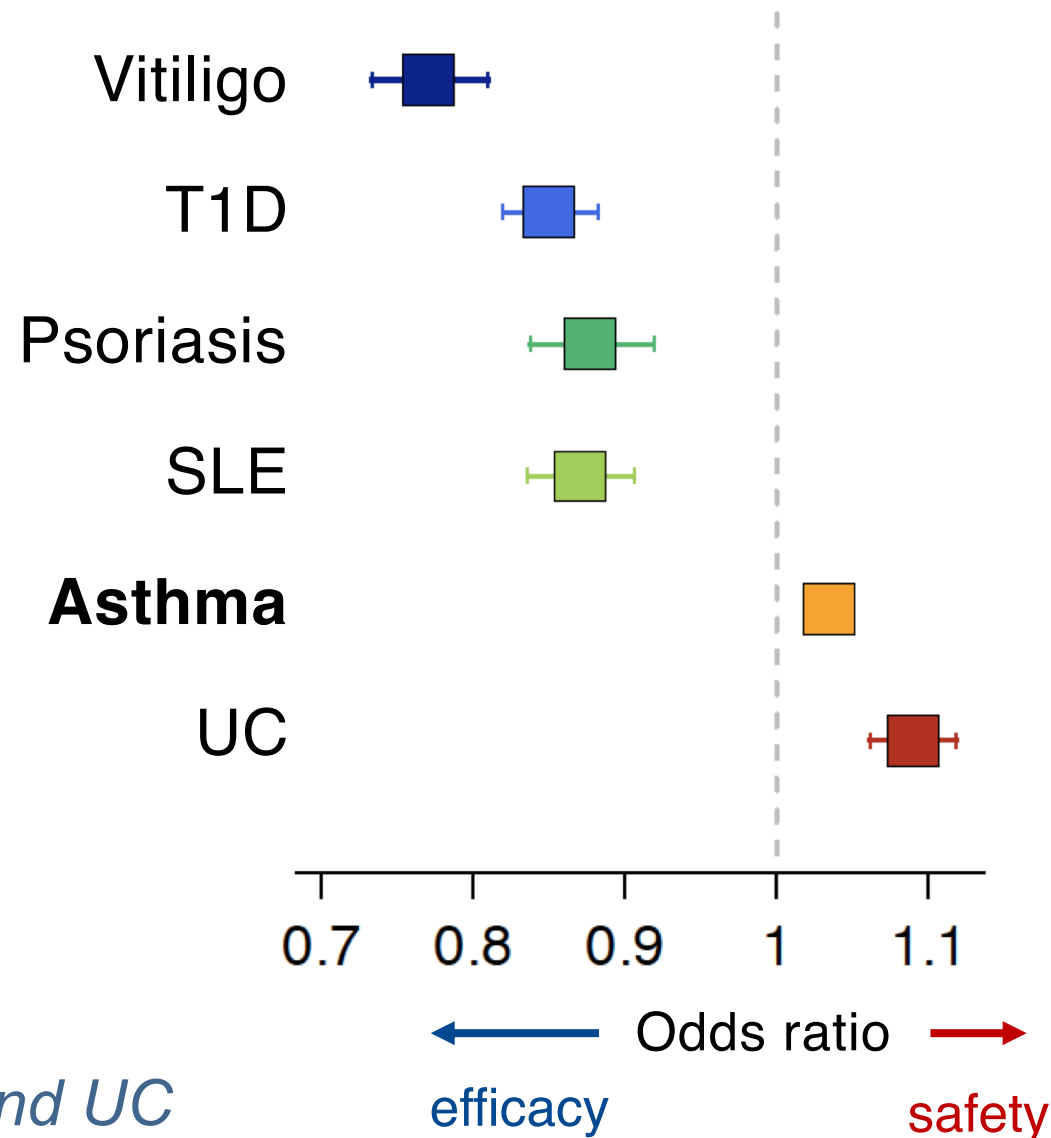
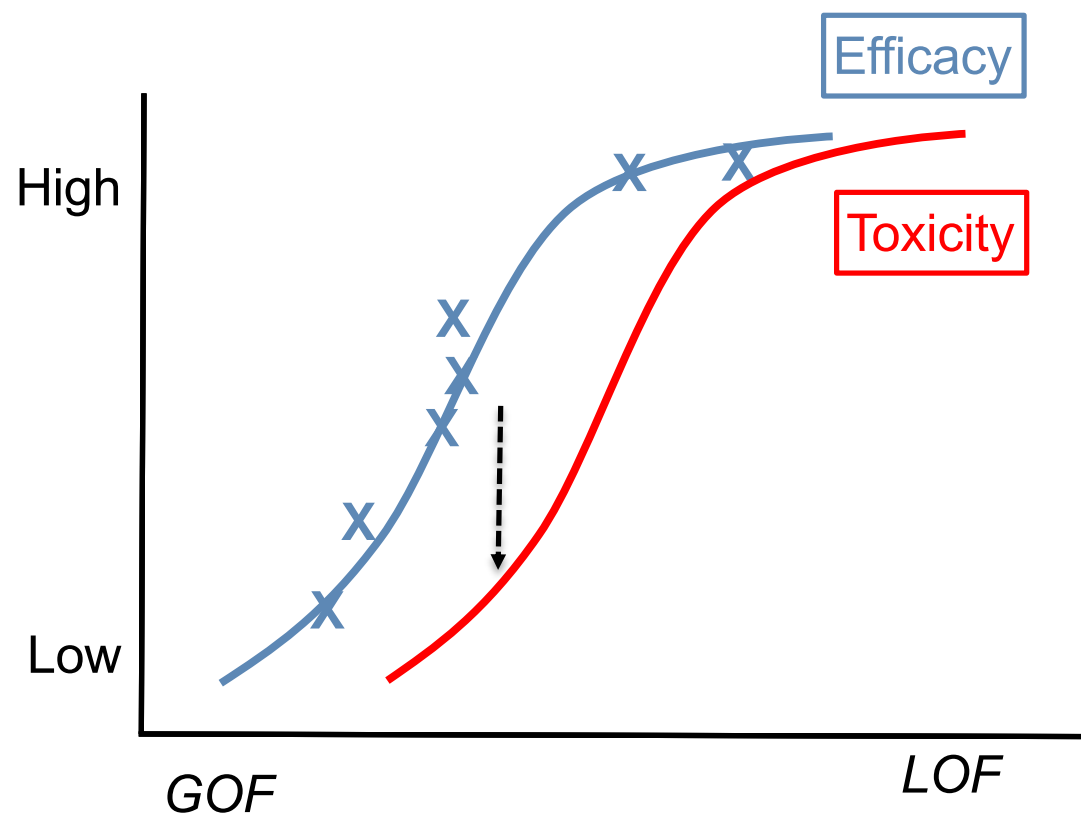
PheWAS example: *IFIH1*, autoimmunity, asthma

- PheWAS in ~800,000 individuals from four population cohorts
- Tested 25 SNPs for association with 1,683 clinical endpoints
- 10 novel associations discovered
- Example: *IFIH1* LOF allele protects from autoimmunity (known) but increases risk of asthma (novel finding)
- Therapeutic hypothesis: inhibiting *IFIH1* may be effective in some autoimmune diseases but may make asthma worse



Diogo et al *under revision*

Predicted impact of therapeutic inhibition of IFIH1



Beneficial effect for some autoimmune diseases, but increase risk of asthma and UC