

# Pharmacogenomics for Cardiovascular Care

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January 17, 2019  
PGxP4 Symposium

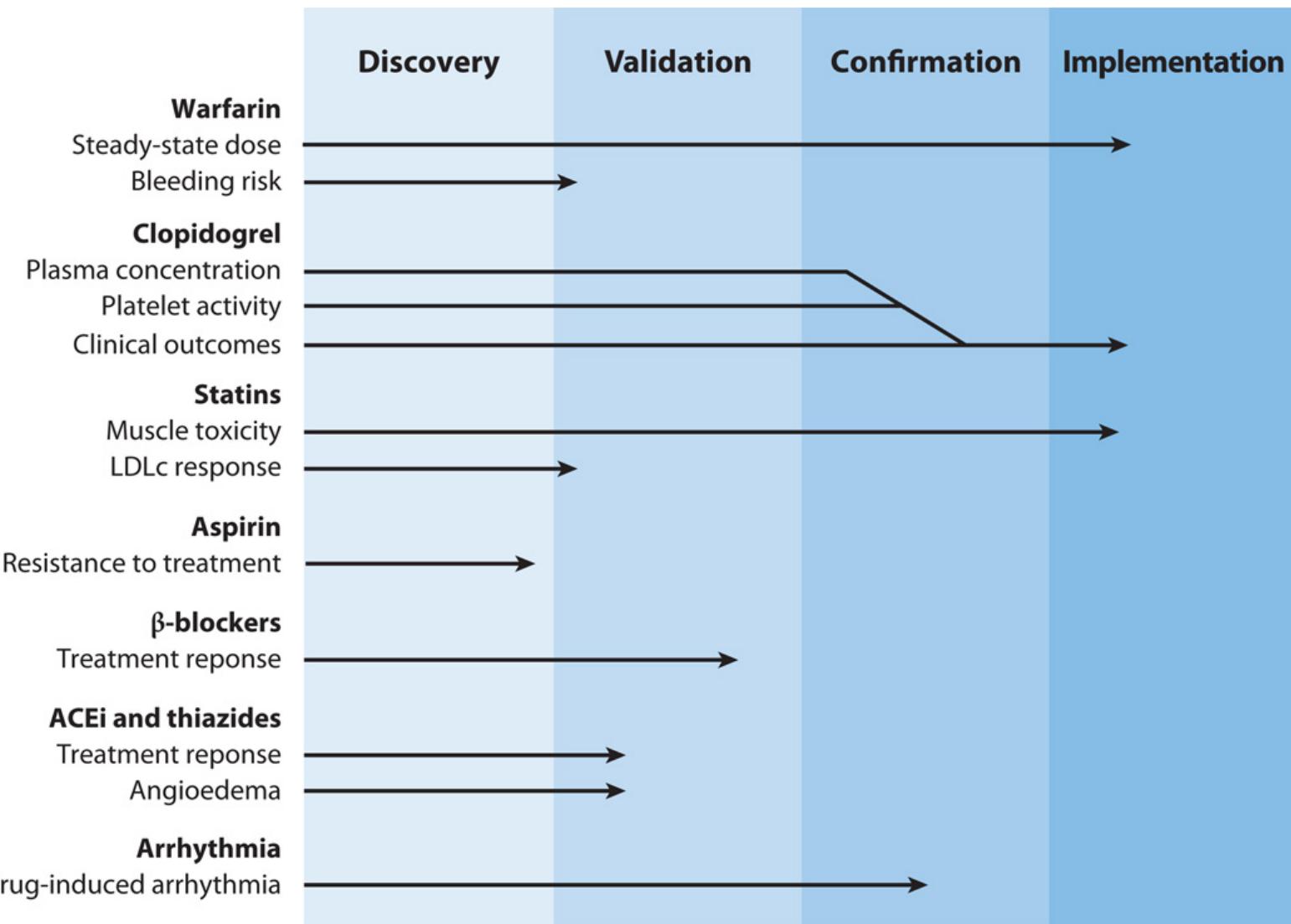
@jasonhkarnes



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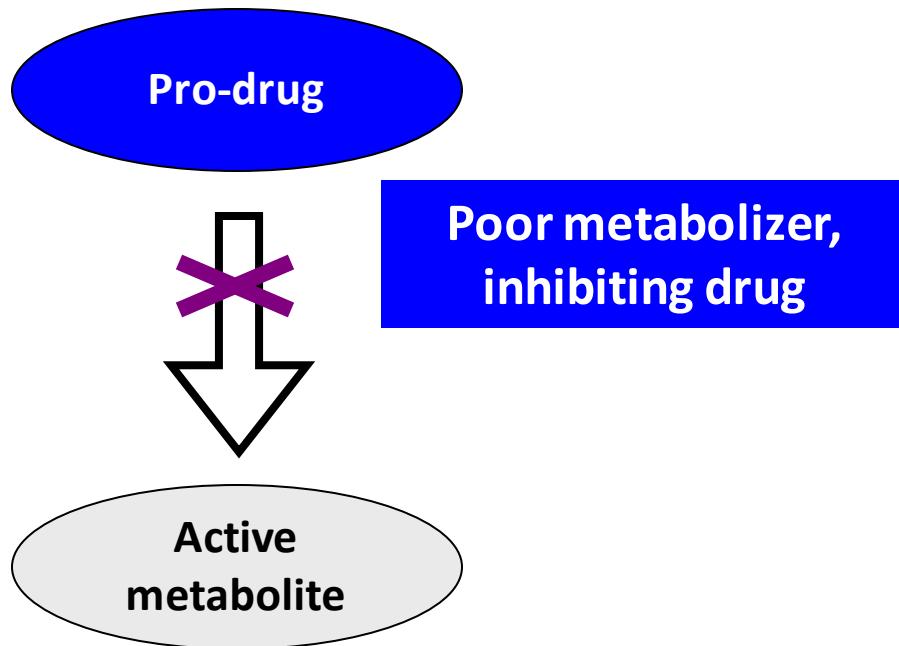


# State of the evidence in cardiovascular pharmcogenomics



# Where pharmacogenomics matters

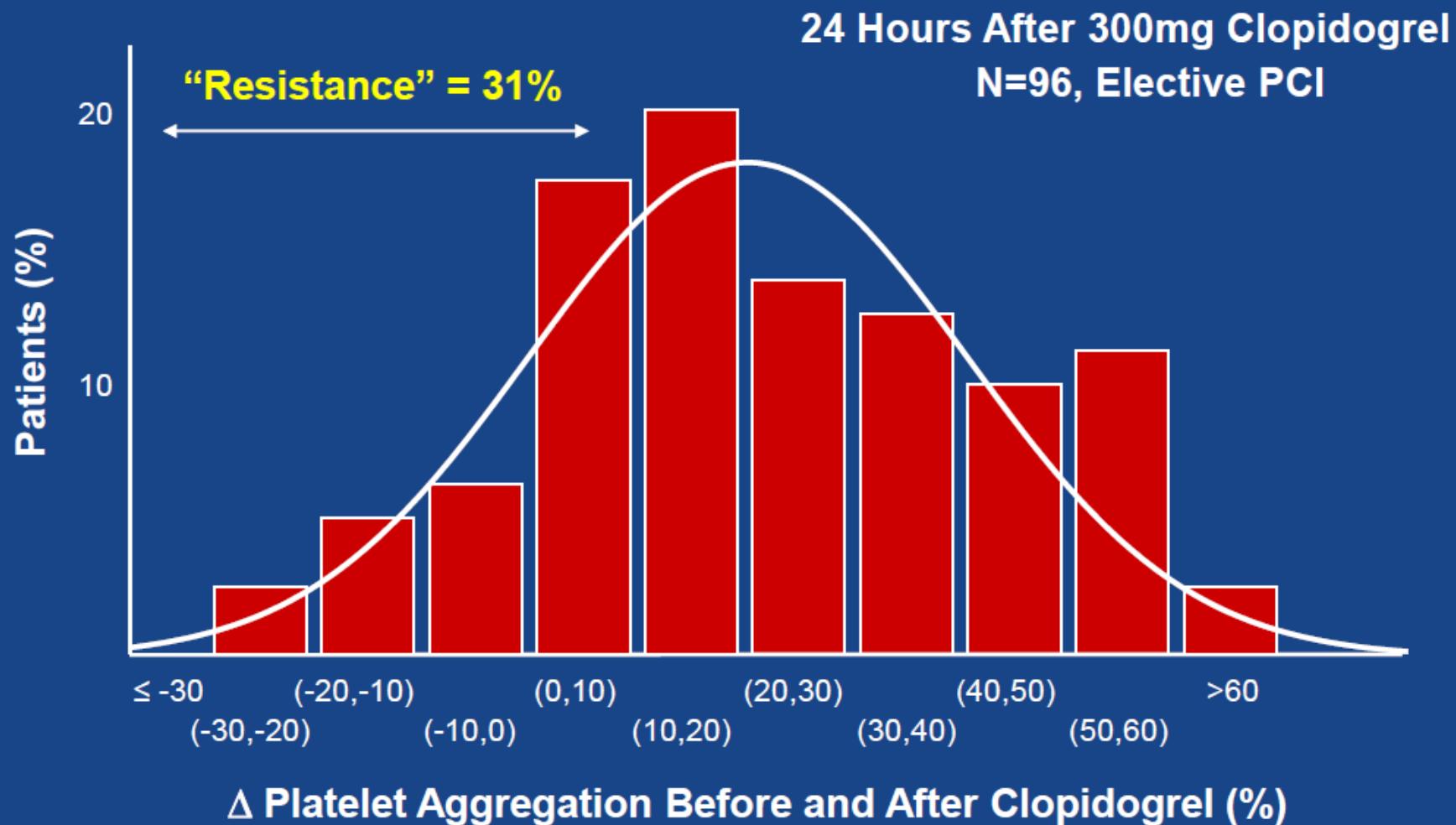
## Single pathway to bioactivation: High-risk pharmacokinetics



- encainide
- clopidogrel
- tamoxifen
- codeine



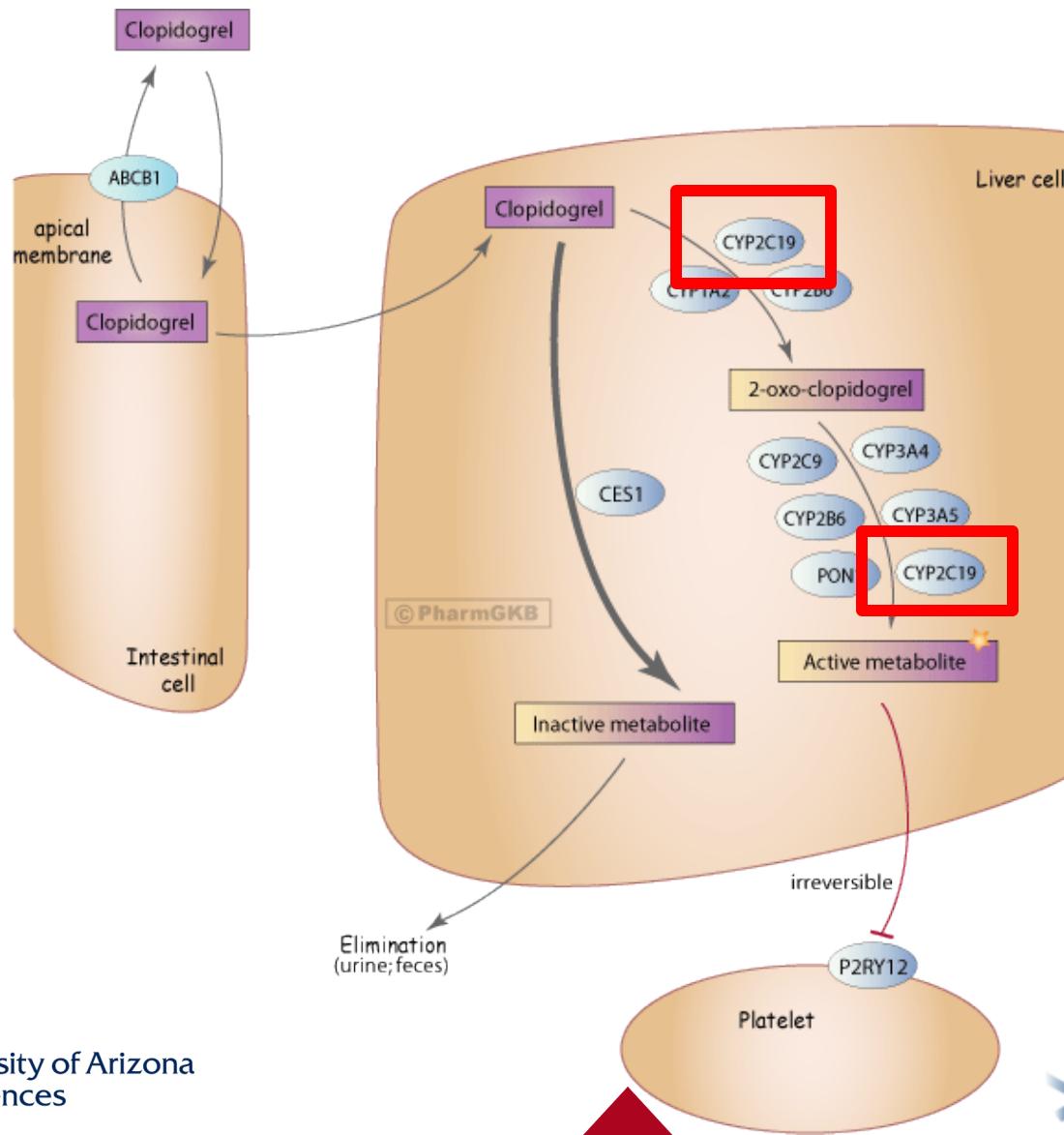
# Variable Response to Clopidogrel



“Resistance” =  $\leq 10\%$   $\Delta$  platelet aggregation

Gurbel PA et al., Circulation 2003;107:2908-2913

# Clopidogrel pharmacokinetic and pharmacodynamic pathways



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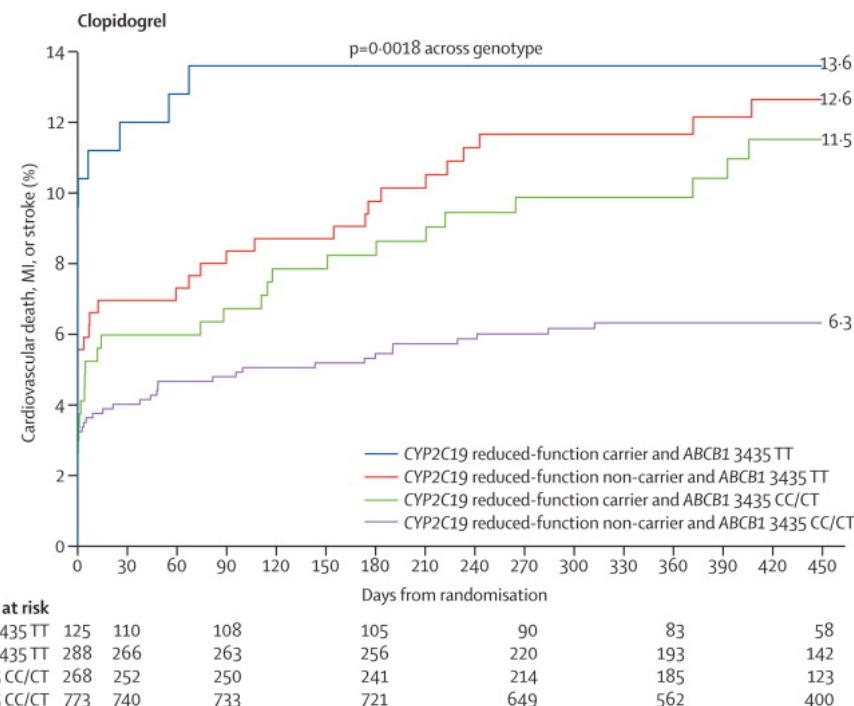
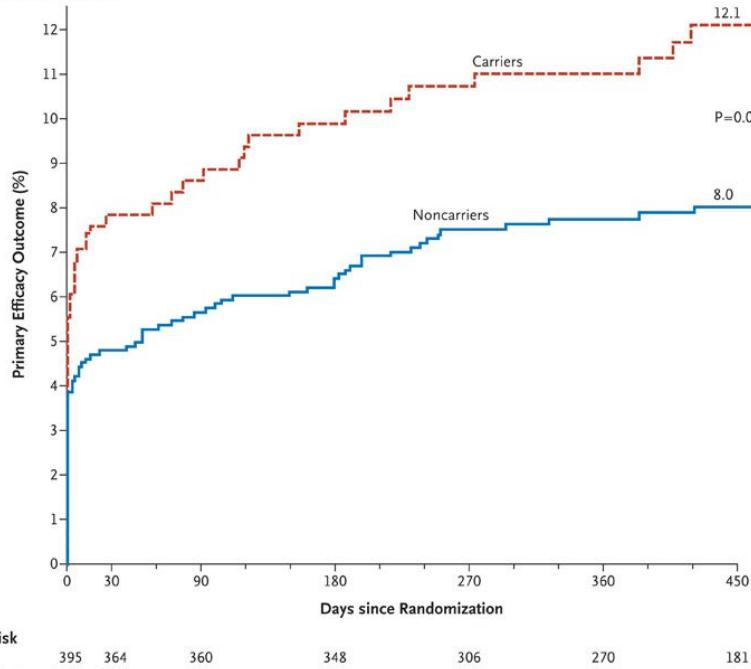
PG KB **PharmGKB**

# **CYP2C19 metabolizer phenotypes based on genotypes**

<b>Phenotype (% patients)</b>	<b>Genotypes</b>	<b>Diplotype examples</b>
Ultrarapid metabolizer (~5-30%)	One or more gain of function alleles	*17/*17, *1/*17
Extensive metabolizer (~35-50%)	two copies of functional alleles	*1/*1
Intermediate metabolizer (~18-45%)	one reduced and one nonfunctional allele	*1/*2, *1/*3
Poor metabolizer (~2-15%)	no functional alleles	*2/*2, *2/*3, *3/*3



## A Primary Efficacy Outcome

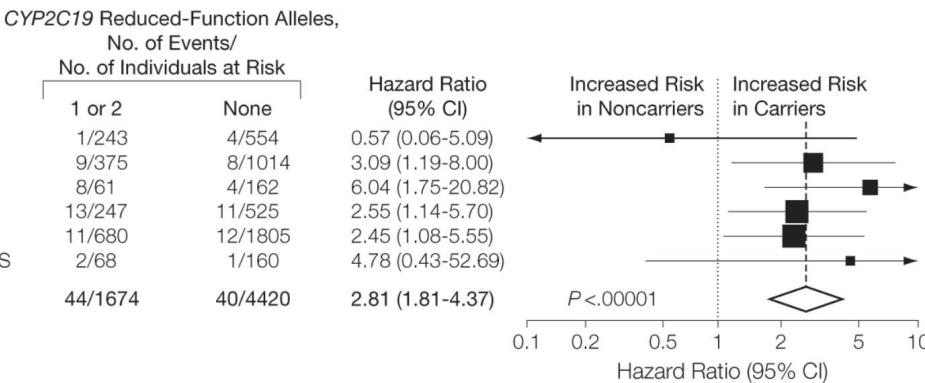


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	Number at risk	Cardiovascular death, MI, or stroke (%)
CYP2C19 reduced-function carrier and ABCB1 3435 TT	125	13.6
CYP2C19 reduced-function non-carrier and ABCB1 3435 TT	288	12.6
CYP2C19 reduced-function carrier and ABCB1 3435 CC/CT	268	11.5
CYP2C19 reduced-function non-carrier and ABCB1 3435 CC/CT	773	6.3

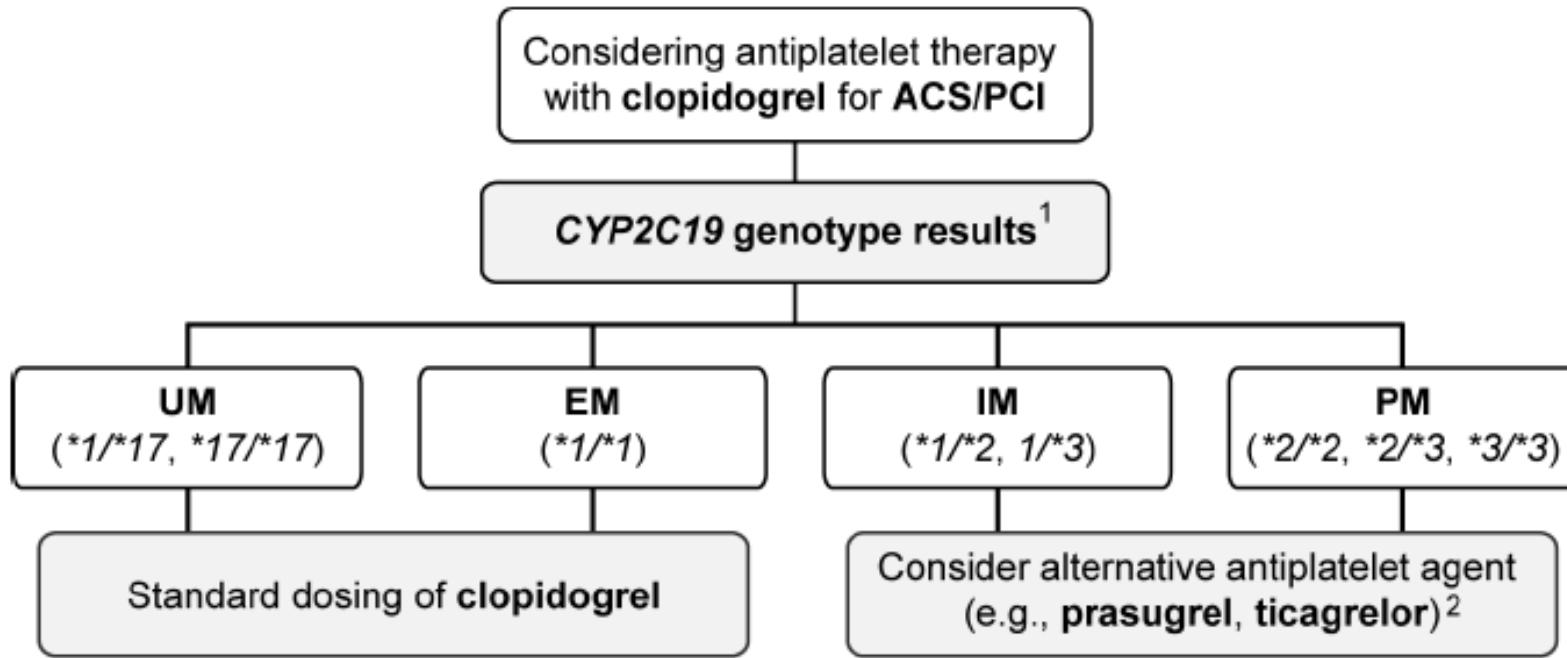
A

Carriers of 1 or 2 CYP2C19 Reduced-Function Alleles vs Noncarriers

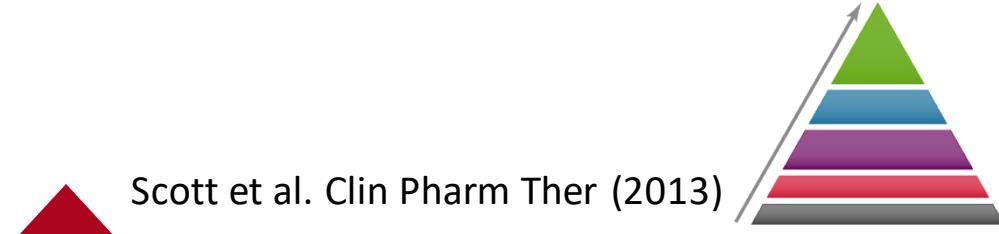


- Mega JL et al. Lancet 2010;1312–1319  
 Mega JL et al. JAMA. 2010;304(16):1821-1830  
 Mega JL et al. N Engl J Med 2009;360:354-362

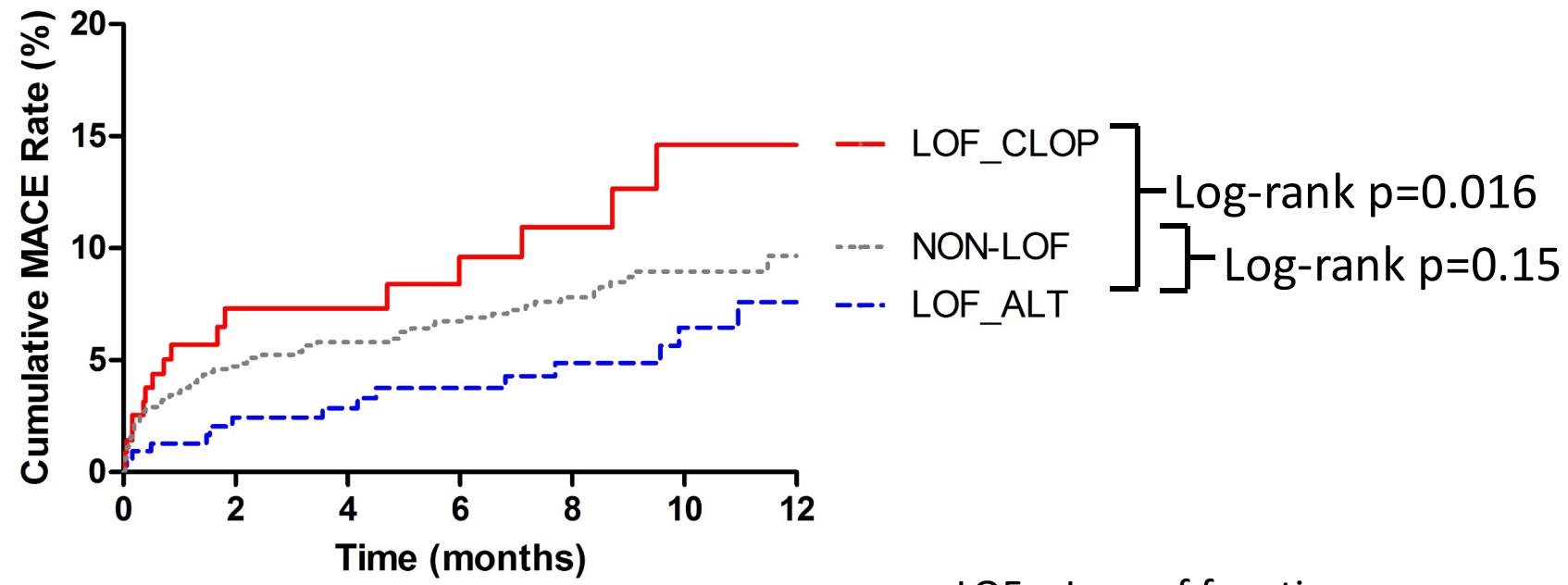
# CPIC: Clinical recommendations for *CYP2C19* and clopidogrel



- CPIC recommendations if genotype is already available
- ACC/AHA recommend case by case genotyping
- Not supported by RCTs



# Emerging Data: CYP2C19 and outcomes with clopidogrel



NO. at risk							
LOF_CLOP	226	112	89	76	63	39	3
NON-LOF	1243	759	636	577	451	293	28
LOF_ALT	346	245	221	195	161	112	9

LOF = Loss of function

Adjusted Hazard Ratio

LOF-CLOP vs LOF ALT: 2.21 (1.13-4.33) p=0.021

LOF-ALT vs non-LOF: 0.81 (0.48-1.35) p=0.41

# Clinical implementation

**HEO Popup**

## Clopidogrel Poor Metabolizer Rules

**Genetic testing has been performed and indicates this patient may be at risk for inadequate anti-platelet response to clopidogrel (Plavix) therapy**

This patient has been tested for CYP2C19 variants, and the presence of the **\*2/\*2** genotype has identified this patient as a **Poor metabolizer** of clopidogrel. Poor metabolizers treated with clopidogrel at normal doses exhibit higher rates of stent thrombosis/other cardiovascular events.

**Treatment modification is recommended if not contraindicated:**

Prescribe prasugrel (EFFIENT) **10 mg** daily and stop clopidogrel (PLAVIX), startdate 10 AM

**Due to increased risk of bleeding compared to clopidogrel, prasugrel should not be given to patients:**

- that have a history of stroke or transient ischemic attack **\*\*\* Not known; please check StarPanel**  
**(Caution patient's age: 76 years)**
- that are greater than 75 years of age  
**(Caution patient's weight: 0 kgs)**
- whose body weight is less than 60 kg

Click here for [more information](#)

**If prasugrel (EFFIENT) not selected, please choose desired action:**

Increase maintenance dose of clopidogrel (PLAVIX) **150 mg** daily, startdate 10AM

Maintain requested daily dose of clopidogrel (PLAVIX) **75 mg** daily, startdate 10AM

**If not using prasugrel, please select a reason:**

Contraindicated for prasugrel  
 Potential side effects  
 Patient opts for clopidogrel  
 Other (Specify)

Click here for [more information](#)

**Note:** The Vanderbilt P&T Committee has recommended that prasugrel (if not contraindicated) should replace clopidogrel for Poor metabolizers; if this is not

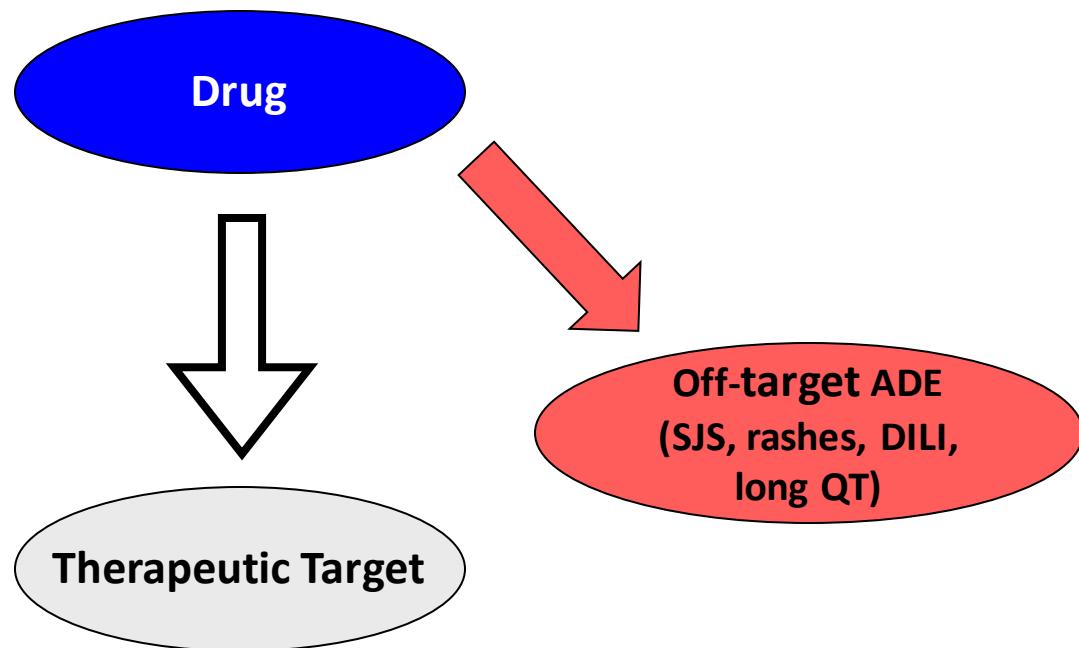
**Cancel** **Order**

**Back** **Home** **Close**



# Where pharmacogenomics matters

## Off-target serious adverse effects



- simvastatin
- carbamazepine
- clozapine
- haloperidol
- abacavir
- antibiotics



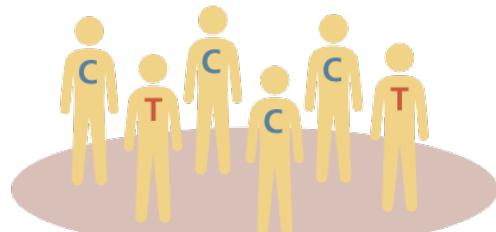
# Simvastatin and muscle toxicity

- Statins have wide therapeutic index and severe ADRs relatively uncommon
- Most common statin-related ADR is skeletal muscle toxicity
  - Myalgias (pain) – 1-5% patients
  - Myopathy (pain with evidence of muscle degradation) – 1 in 1,000 patients
  - Rhabdomyolysis (severe muscle damage with acute kidney injury), 1 in 100,000 patients
- Risk factors: age, statin dose, concomitant fibrates

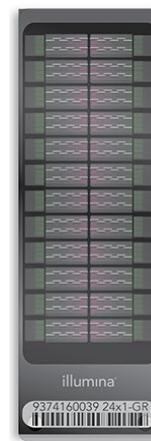


# Genome-wide association study (GWAS)

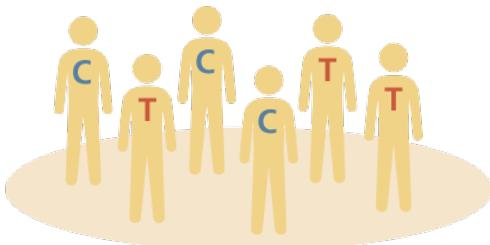
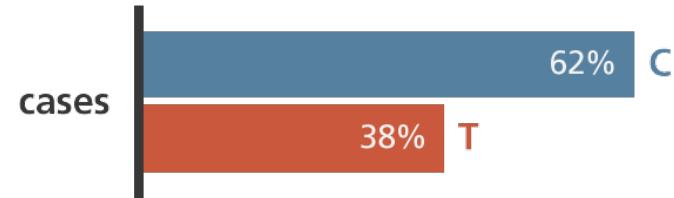
Identify cases and controls



Genotype a million SNPs across the genome



Statistical analysis for SNPs association with case



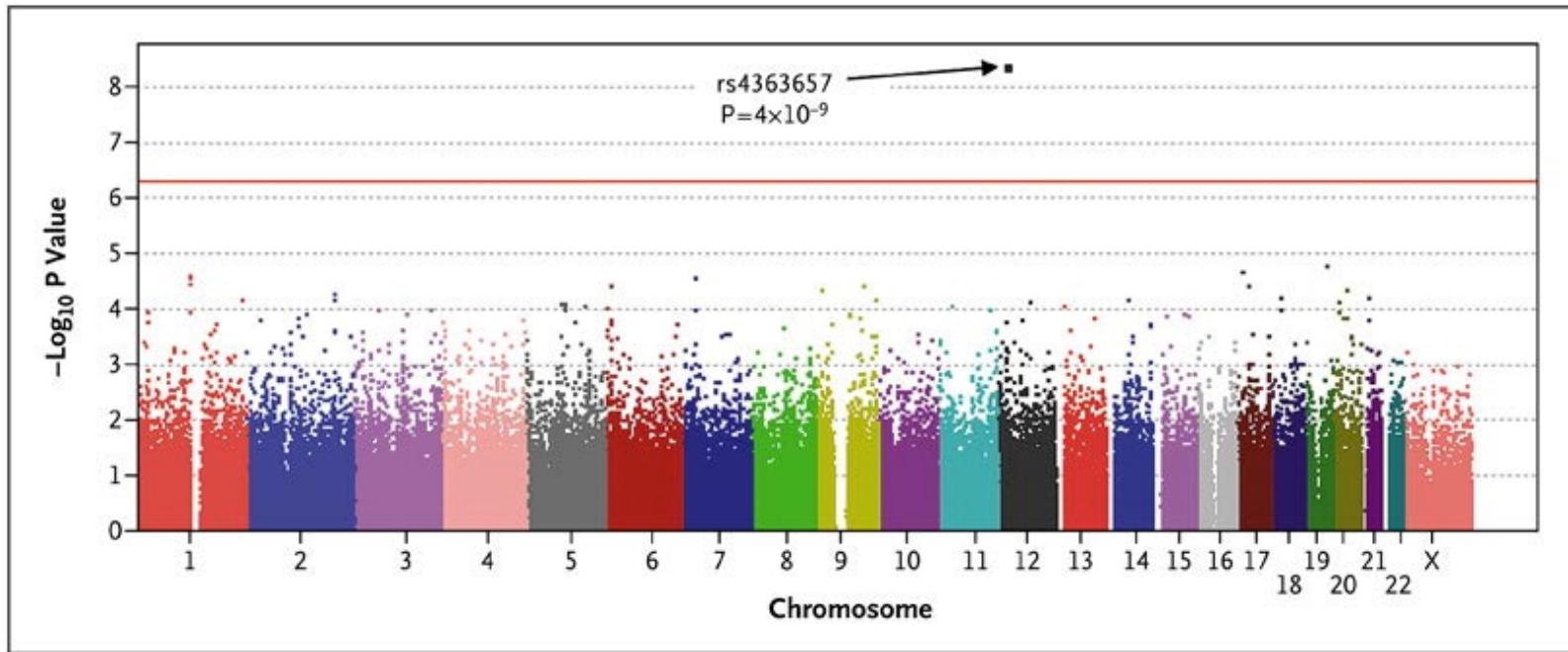
A case-control genome-wide association study investigating genetic variants associated with heart disease.



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Image credit: Genome Research Limited

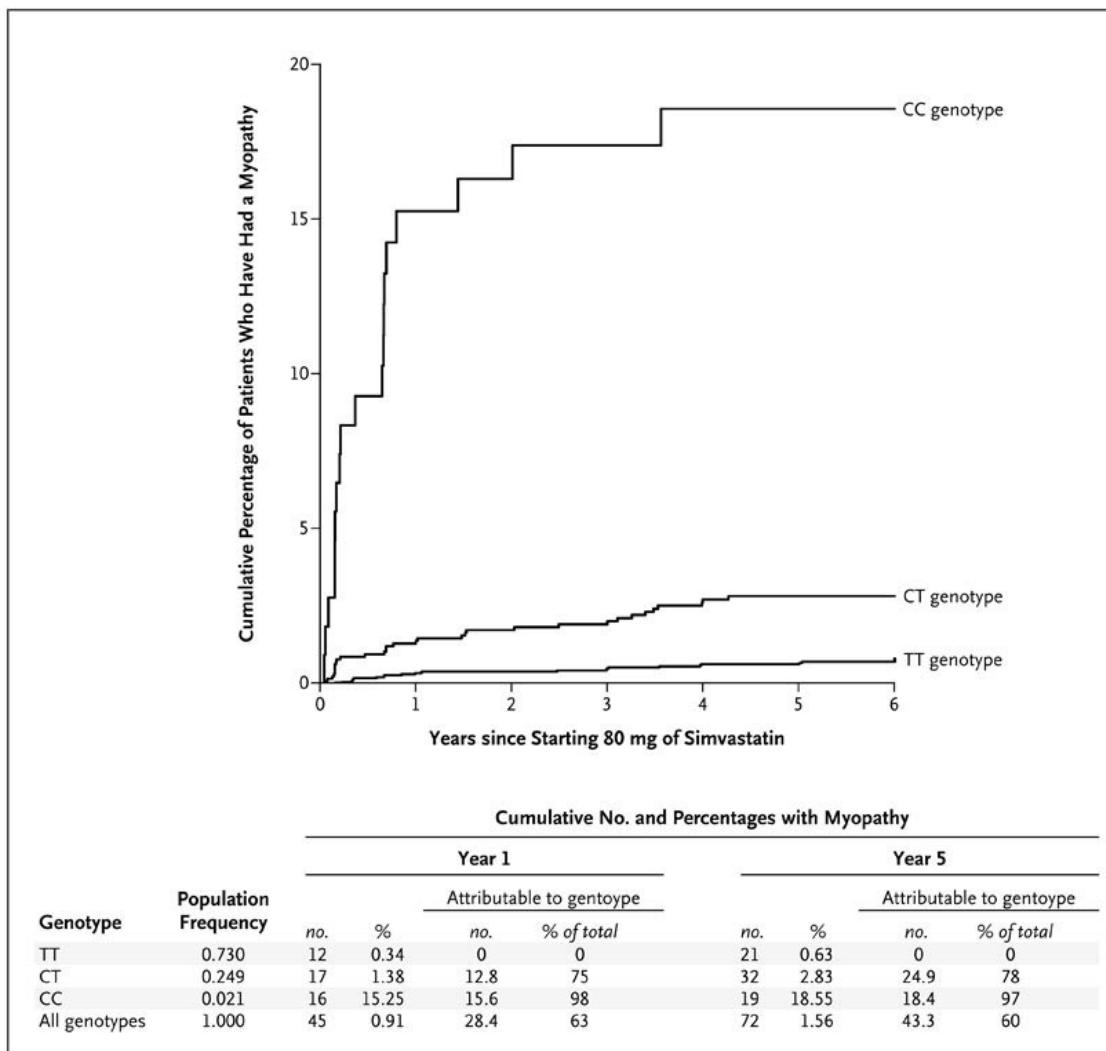
# *SLCO1B1* Variants and Statin-Induced Myopathy



- Results of Tests for a Trend in the Association between Myopathy and Each SNP Measured in the Genomewide Association Study.
- x axis is  $-\log(p \text{ value})$  so a dot (representing a SNP) at 8 on the x axis has a p value of  $p=1\times 10^{-8}$  or  $p=0.00000001$



# Risk of myopathy associated with 80 mg daily simvastatin by *SLCO1B1* rs4149056 genotype



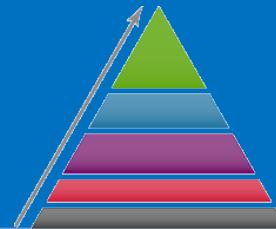
The University of Arizona  
Health Sciences

The SEARCH Collaborative Group. N Engl J Med  
2008;359:789-799



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# CPIC: Clinical recommendations



- Simvastatin metabolized primarily by CYP3A4 and transported into liver primarily by SLCO1B1 (OATP1B1)
- Avoid 80 mg simvastatin in all patients (FDA)
  - Exception in patients taking this dose for over a year without signs/symptoms of muscle toxicity
- *SLCO1B1* genotyping may apply to other statins, but not currently sufficient evidence
- Simvastatin-induced muscle toxicity can still occur in absence of rs4149056

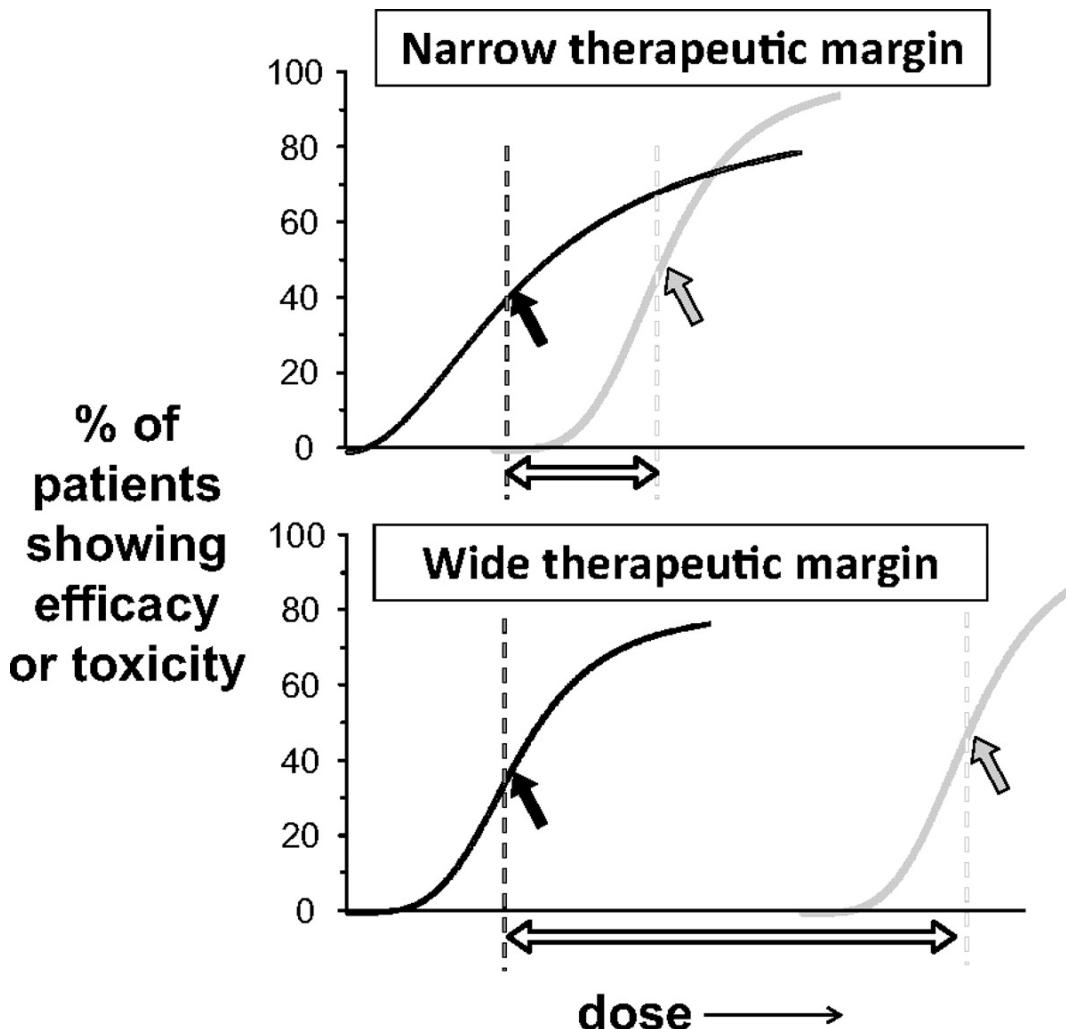
**Table 2 Dosing recommendations for simvastatin based on *SLCO1B1* phenotype**

Phenotype	Implications for simvastatin	Dosing recommendations for simvastatin <sup>a,b</sup>	Classification of recommendations <sup>c</sup>
Normal function	Normal myopathy risk	Prescribe desired starting dose <sup>b</sup> and adjust doses of simvastatin based on disease-specific guidelines	Strong
Intermediate function	Intermediate myopathy risk	Prescribe a lower dose or consider an alternative statin (e.g., pravastatin or rosuvastatin); consider routine CK surveillance	Strong
Low function	High myopathy risk	Prescribe a lower dose or consider an alternative statin (e.g., pravastatin or rosuvastatin); consider routine CK surveillance	Strong

CK, creatine kinase.

<sup>a</sup>In all cases, the potential for drug-drug interaction should be evaluated before initiating a prescription. <sup>b</sup>The US Food and Drug Administration recommends against 80 mg (unless already tolerated for 12 months). <sup>c</sup>See the **Supplementary Material** online (text section titled "Levels of Evidence") for additional details regarding the three-tiered system used to grade the quality of evidence.

# Where Pharmacogenomics Matters

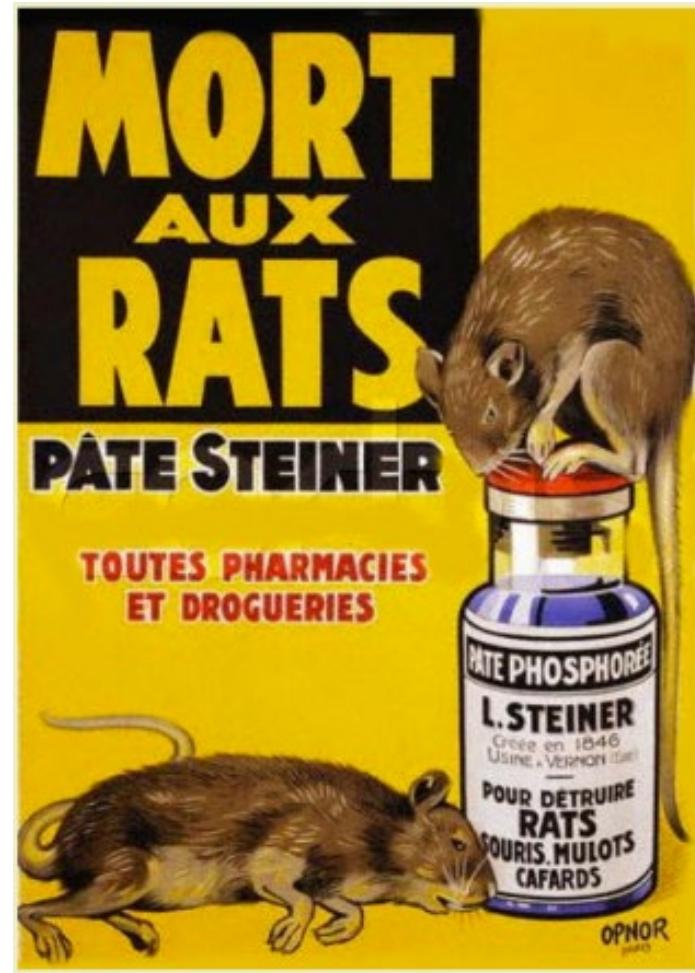
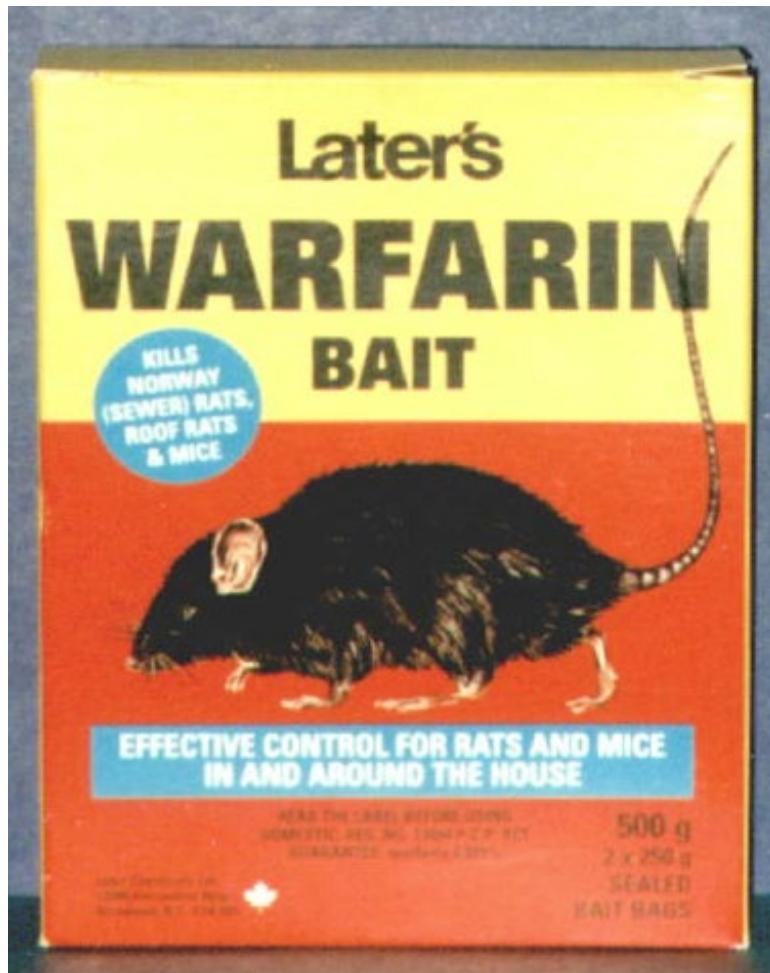


Drugs with narrow therapeutic windows

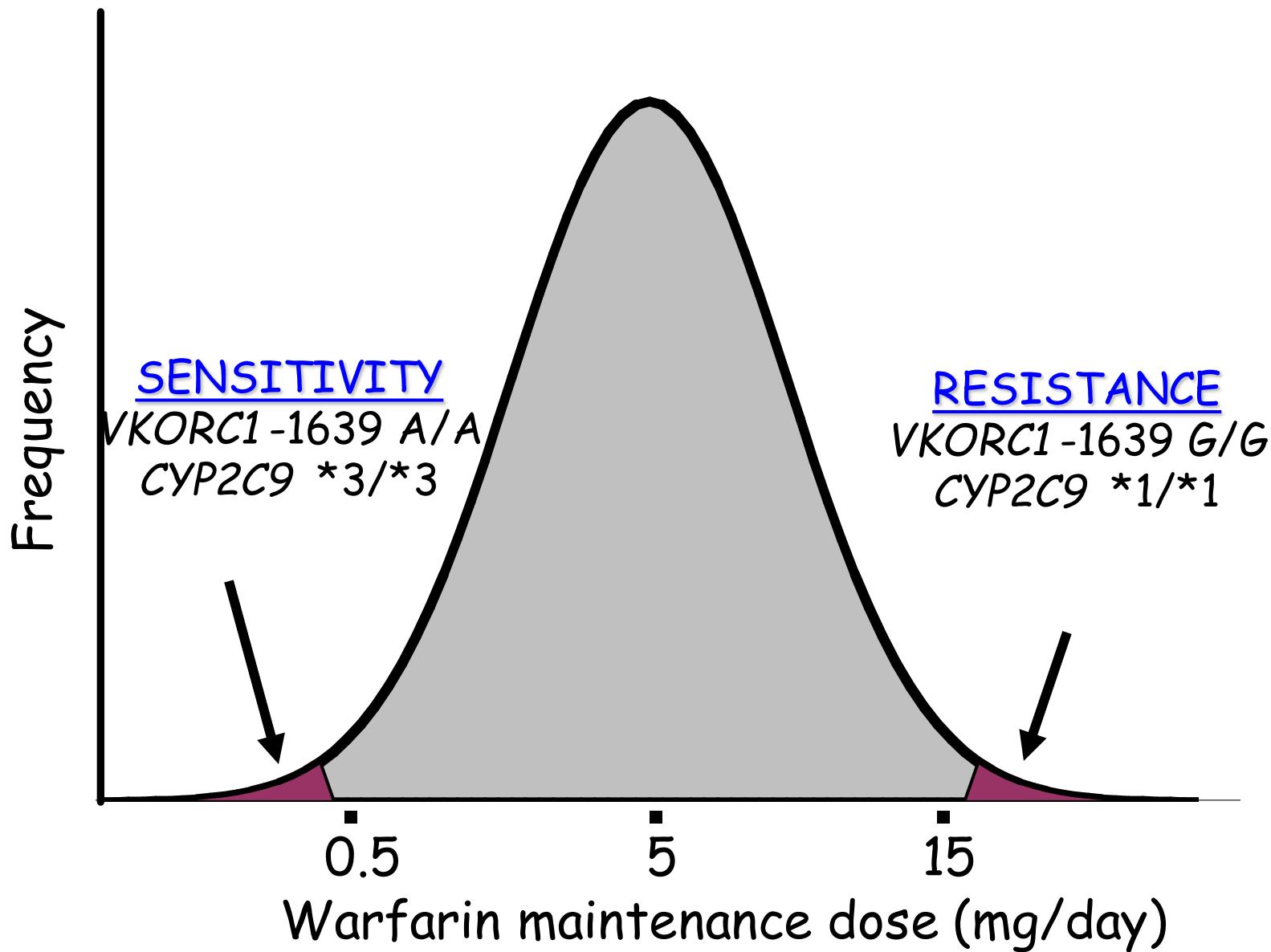
- warfarin
- lithium
- digoxin
- some antibiotics (vancomycin)



# Warfarin



# Inter-individual variability in warfarin dose



# Warfarin package insert

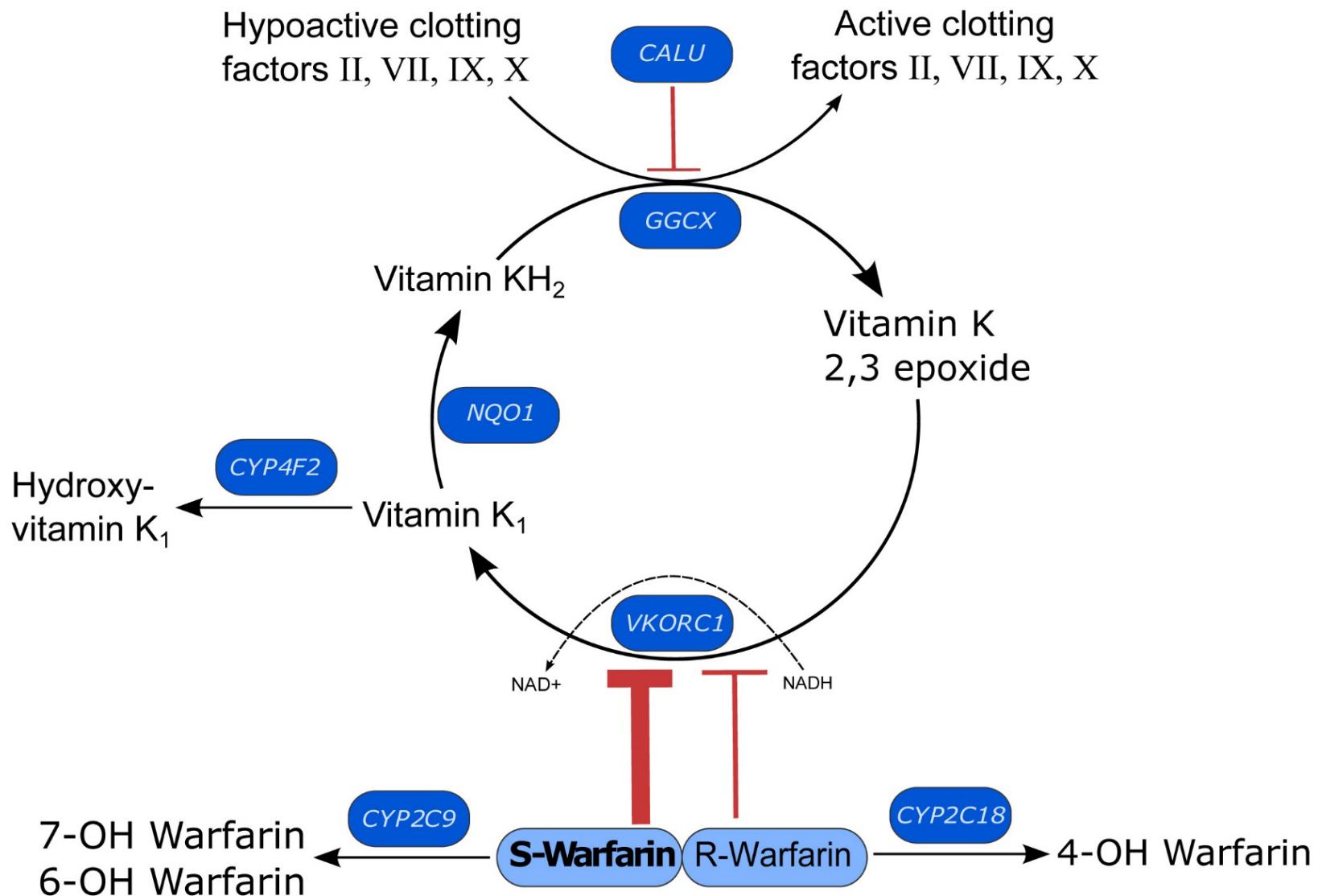
**Table 1: Three Ranges of Expected Maintenance COUMADIN Daily Doses Based on CYP2C9 and VKORC1 Genotypes<sup>†</sup>**

VKORC1	CYP2C9					
	*1/*1	*1/*2	*1/*3	*2/*2	*2/*3	*3/*3
GG	5-7 mg	5-7 mg	3-4 mg	3-4 mg	3-4 mg	0.5-2 mg
AG	5-7 mg	3-4 mg	3-4 mg	3-4 mg	0.5-2 mg	0.5-2 mg
AA	3-4 mg	3-4 mg	0.5-2 mg	0.5-2 mg	0.5-2 mg	0.5-2 mg

<sup>†</sup>Ranges are derived from multiple published clinical studies. VKORC1 -1639G>A (rs9923231) variant is used in this table. Other co-inherited VKORC1 variants may also be important determinants of warfarin dose.



# Multiple genes affecting warfarin dose



> [Warfarin Dosing](#)

> [Clinical Trial](#)

> [Outcomes](#)

> [Hemorrhage Risk](#)

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User:

Patient:

[Version 2.40](#)

Build : April 05, 2013

## Required Patient Information

Age:

Sex:

Ethnicity:

Race:

Weight:  lbs or  kgs

Height: ( feet and  inches) or ( cms)

Smokes:

Liver Disease:

Indication:

Baseline INR:

Target INR:

Randomize & Blind

Amiodarone/Cordarone® Dose:  mg/day

Statin/HMG CoA Reductase

Inhibitor:

Any azole (eg. Fluconazole):

Sulfamethoxazole/Septra/Bactrim/Cotrim/Sulfatrim:

## Genetic Information

[VKORC1-1639/3673](#):

[CYP4F2 V433M](#):

[GGCX rs11676382](#):

[CYP2C9\\*2](#):

[CYP2C9\\*3](#):

[CYP2C9\\*5](#):

[CYP2C9\\*6](#):

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**> ESTIMATE WARFARIN DOSE**



The  
Heart

# Randomized controlled trials for warfarin pharmacogenomic testing

Study	Sample size (n)	Control group dosing algorithm	Clinical Factors included in algorithm(s)	Comparator Group (% TTR)	Genotype-Guided Group (% TTR)**	p value
Pirmohamed et al. 2013 (EU-PACT)	454	Fixed dose*	Age, Height, Weight, Amiodarone	60.3%	67.4%	<0.001
Kimmel et al. 2013 (COAG)	955 700 (non-AA) 255 (AA)	Clinically-derived dose	Age, Race, Smoking status, BSA, Amiodarone, Target INR,	45.4%  46.1% (non-AA) 43.5% (AA)	45.2%  48.8% (non-AA) 35.2% (AA)	0.91  0.15 (non-AA) 0.0003 (AA)
Verhoeft et al. 2013 (EU-PACT)***	548	Clinically-derived dose	Age, Sex, Height, Weight, Amiodarone	60.2%	61.6%	0.52

\*Fixed dose algorithm used no clinical factors and started with 10mg (day 1) and 5mg (days 2 and 3).

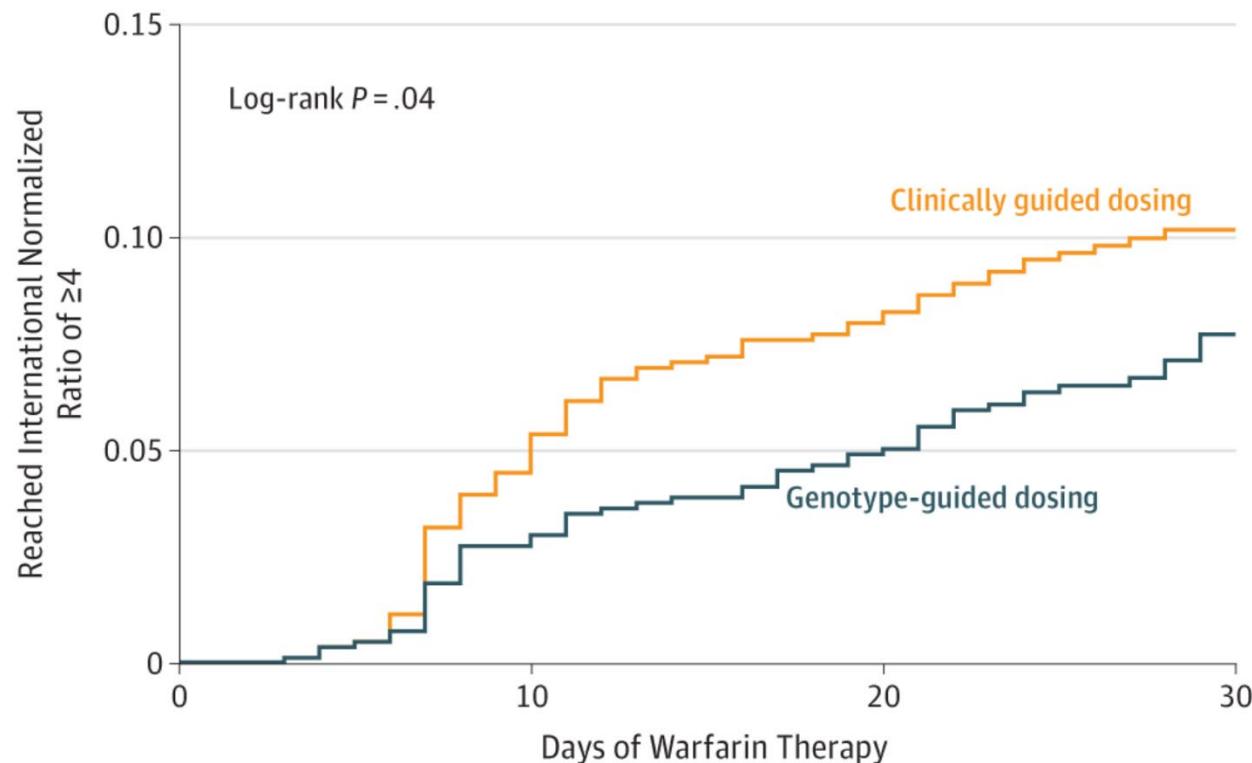
\*\* All genotype-guided algorithms included clinical factors and genetic factors CYP2C9 \*2, \*3, and VKORC1 -1639A (or VKORC1 1173T).

\*\*\*Study administered warfarin derivatives acenocoumarol and phenprocoumon.



From: **Effect of Genotype-Guided Warfarin Dosing on Clinical Events and Anticoagulation Control Among Patients Undergoing Hip or Knee ArthroplastyThe GIFT Randomized Clinical Trial**

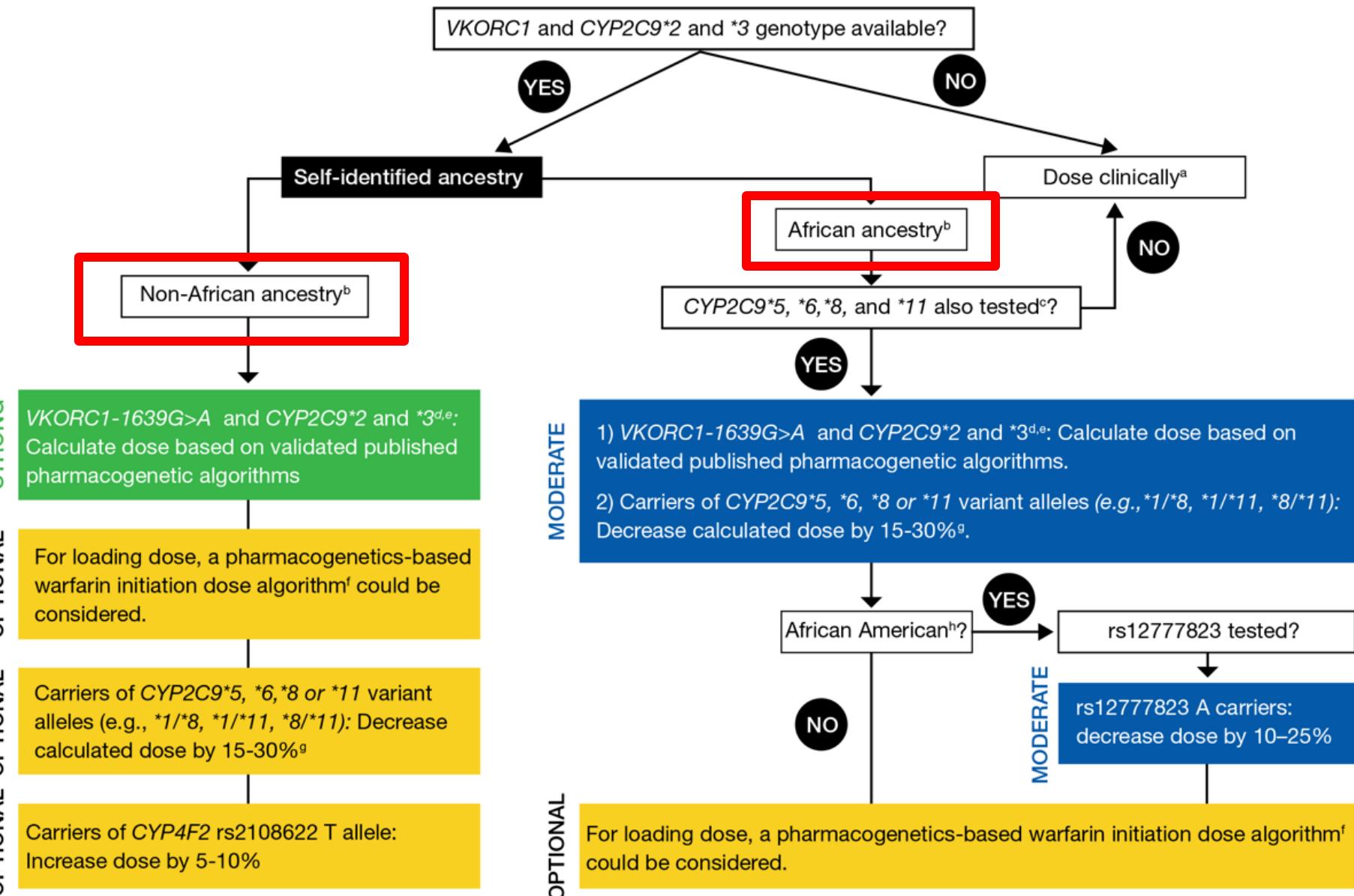
JAMA. 2017;318(12):1115-1124. doi:10.1001/jama.2017.11469



No. of patients

Clinically guided dosing	789	737	698	209
Genotype-guided dosing	808	771	739	216

# CPIC: Clinical Recommendations (2017)

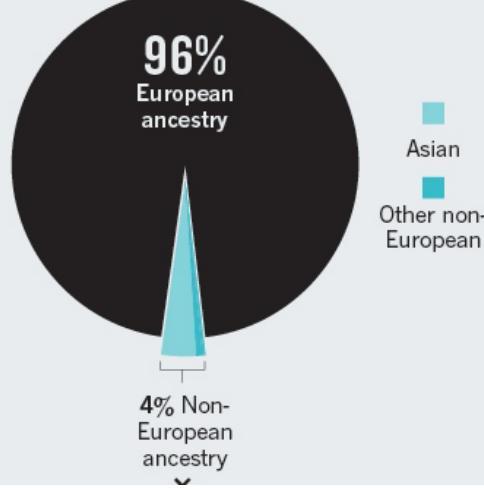


# Genomics is failing on diversity

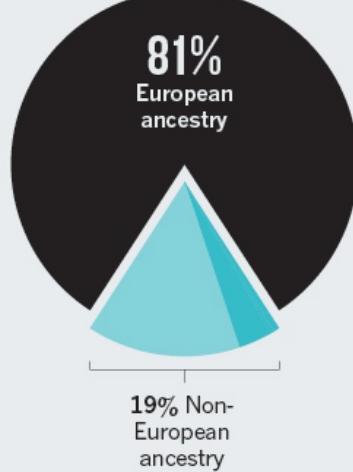
## PERSISTENT BIAS

Over the past seven years, the proportion of participants in genome-wide association studies (GWAS) that are of Asian ancestry has increased. Groups of other ancestries continue to be very poorly represented.

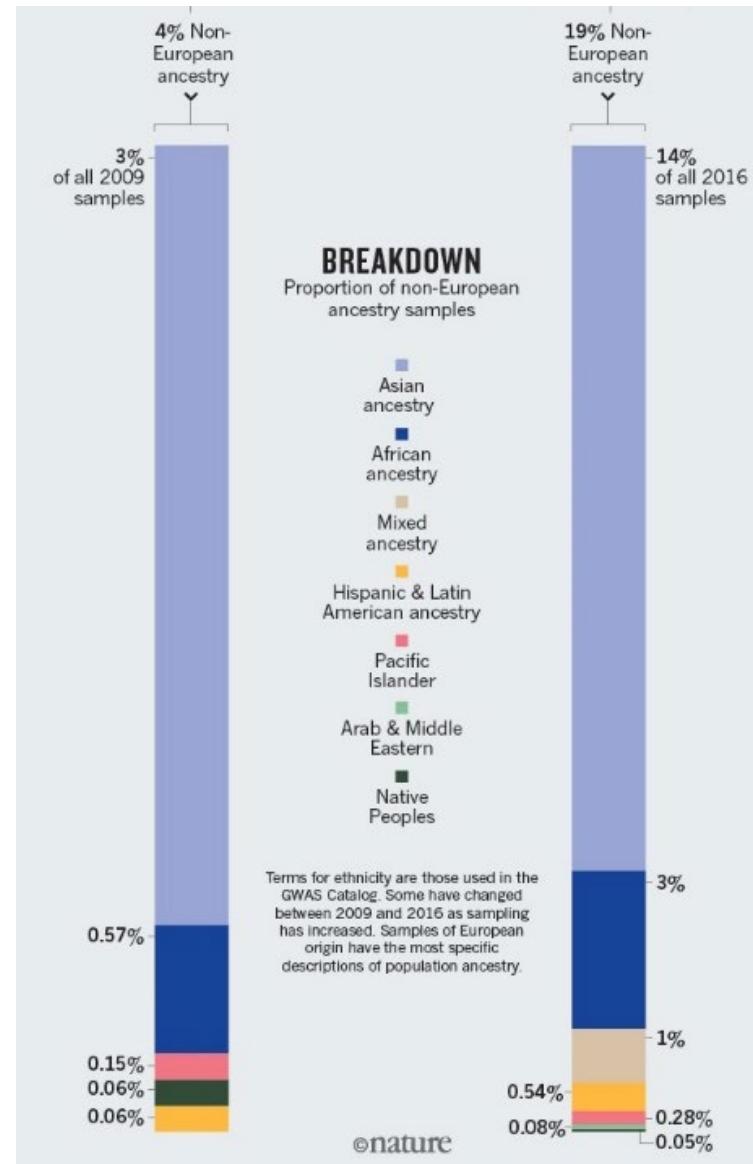
**2009**  
373 studies  
1.7 million samples



**2016**  
2,511 studies  
35 million samples



- Studies in whites may not be valid in other race/ethnic groups
- Without research, clinical testing may not be useful for non-whites



## Mission and Objectives



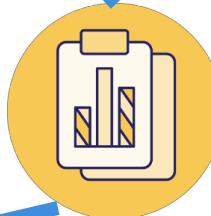
### Nurture relationships

with one million or more participant partners, from all walks of life, **for decades**



### Our mission

To accelerate health research and medical breakthroughs, **enabling individualized** prevention, treatment, and **care for all of us**

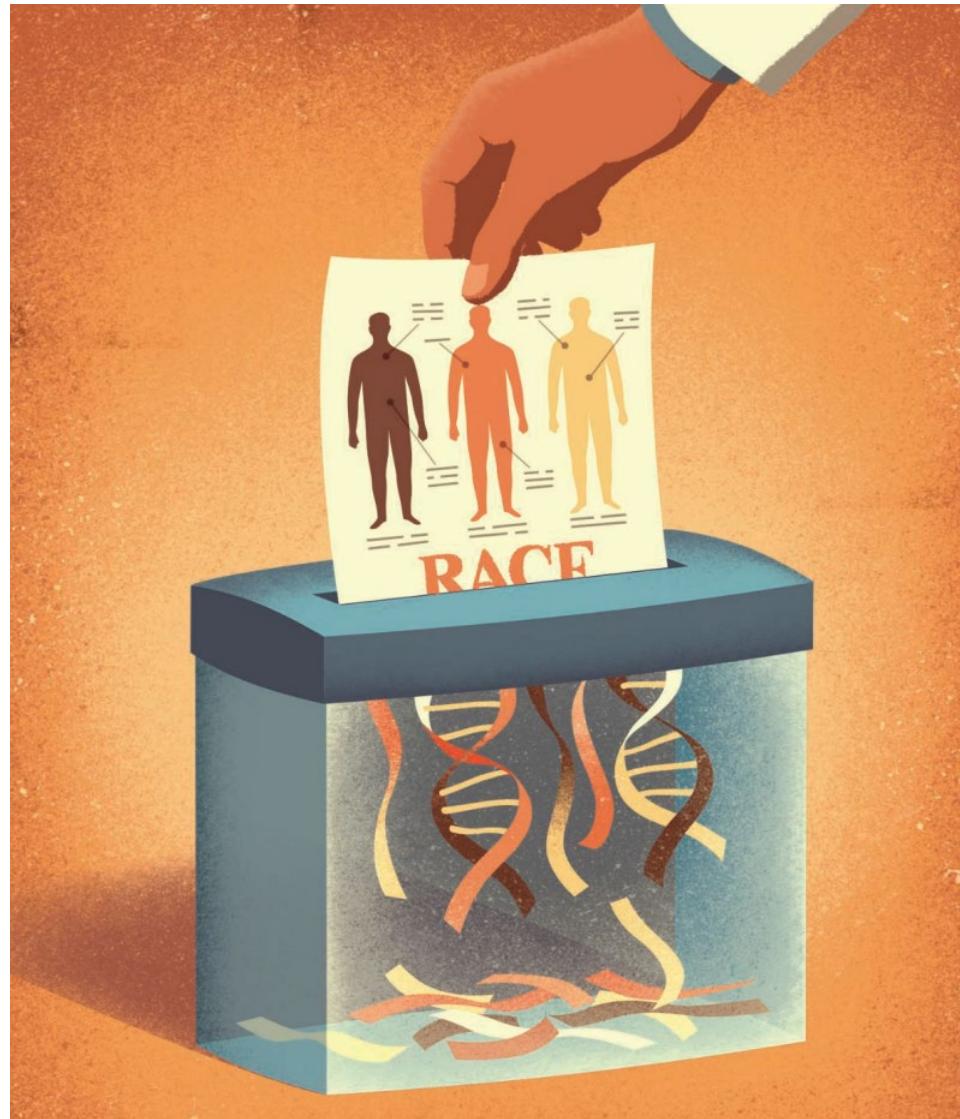


**Catalyze the robust ecosystem**  
of researchers and funders hungry to use and support it

**Deliver one of the largest, richest biomedical datasets ever**  
that is easy, safe, and **free to access**

**Goal of 50% of participants under-represented in biomedical research**

# Questions?



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Yudell et al. Science (2016)