

# Personalized/Precision Medicine

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Disclosure:

Alan Shuldiner is an employee of the Regeneron Genetics Center, a subsidiary of Regeneron Pharmaceuticals Inc. and is also the John Whitehurst Professor of Medicine (part-time) at the University of Maryland School of Medicine

# Lecture Outline

- Precision/Personalized Medicine
  - Definition
  - Genetic architecture of human traits and disease 101
  - Opportunities for prevention, diagnosis and treatment of rare (monogenic) and common (polygenic) disease
  - Pharmacogenetics
    - Variable drug response (pharmacodynamics)
    - Variable drug metabolism (pharmacokinetics)
    - Adverse events/Safety
    - Challenges of implementing evidence-based pharmacogenetics into patient care
  - Application of human genetics in therapeutic development
    - Identification of new therapeutic targets (efficacy)
    - Derisking therapeutic targets (safety)
    - New indications for therapeutic targets





# **Precision Medicine Initiative**



https://www.whitehouse.gov/precision-medicine

January 30, 2015

# What is Precision Medicine?

FDA

Precision medicine is the use of information from a patient's genome or other biomarkers to:

- predict individual disease susceptibility,
- better define disease prognosis,
- tailor medication, medical device use, diet and lifestyle...

...to more effectively prevent or treat disease and minimize adverse treatment effects.

In short, Precision Medicine enables health care providers to prescribe the right intervention for the right patient at the right time to prevent or treat disease.

"4 P's" of Precision Medicine – predictive, personalized, preemptive, participatory



# How is Genetic Information Used in Medicine Today?



- Diagnostic testing (e.g., factor V Leiden, hemochromotosis)
- Newborn screening (e.g., PKU, MSUD, sickle cell)
- Carrier testing (CF, Tay-Sachs)
- Prenatal testing (e.g., above diseases, chromosomal abnormalities)



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- Rare(ish)
  - Hemochromotosis 1/200
  - a-1-antitrypsin deficiency 1/1700
  - Cystic fibrosis 1/3000
  - Neurofibromatosis 1/3000
- Monogenic
- High penetrance
- High sensitivity and specificity

Whole Exome Sequencing is the Standard of Care for Diagnosis of Rare Genetic Conditions

Total number of monogenic diseases for which the molecular basis is known (11/6/2019) = **6,528** 

## https://www.omim.org/

ORIGINAL ARTICLE

FDA

Whole-Genome Sequencing in a Patient with Charcot–Marie–Tooth Neuropathy

Clinical assessment incorporating a personal genome



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### Euan A Ashley, Atu DIAGNOSTICS

Alexander A Morga Katrin Sangkuhl, Jo Abraham M Rosenl

Summary Background Th remains unclea

Rapid Whole-Genome Sequencing for Genetic Disease Diagnosis in Neonatal Intensive Care Units

Carol Jean Saunders,<sup>1,2,3,4,5</sup> Neil Andrew Miller,<sup>1,2,4</sup> Sarah Elizabeth Soden,<sup>1,2,4</sup> Darrell Lee Dinwiddie,<sup>1,2,3,4,5</sup> Aaron Noll,<sup>1</sup> Noor Abu Alnadi,<sup>4</sup> Nevene Andraws,<sup>3</sup> Melanie LeAnn Patterson,<sup>1,3</sup> Lisa Ann Krivohlavek,<sup>1,3</sup> Joel Fellis,<sup>6</sup> Sean Humphray,<sup>6</sup> Peter Saffrey,<sup>6</sup> Zoya Kingsbury,<sup>6</sup> Jacqueline Claire Weir,<sup>6</sup> Jason Betley,<sup>6</sup> Russell James Grocock,<sup>6</sup> Elliott Harrison Margulies,<sup>6</sup> Emily Gwendolyn Farrow,<sup>1</sup> Michael Artman,<sup>2,4</sup> Nicole Pauline Safina,<sup>1,4</sup> Joshua Erin Petrikin,<sup>2,3</sup> Kevin Peter Hall,<sup>6</sup> Stephen Francis Kingsmore<sup>1,2,3,4,5†</sup>

ORIGINAL ARTICLE

# Clinical application of exome sequencing in undiagnosed genetic conditions

Anna C Need,<sup>1</sup> Vandana Shashi,<sup>2</sup> Yuki Hitomi,<sup>1</sup> Kelly Schoch,<sup>2</sup> Kevin V Shianna,<sup>1</sup> Marie T McDonald,<sup>2</sup> Miriam H Meisler,<sup>3</sup> David B Goldstein<sup>1,4</sup>

#### BRIEF REPORT

### October 24, 2019

### Patient-Customized Oligonucleotide Therapy for a Rare Genetic Disease

J. Kim, C. Hu, C. Moufawad El Achkar, L.E. Black, J. Douville, A. Larson, M.K. Pendergast, S.F. Goldkind, E.A. Lee, A. Kuniholm, A. Soucy, J. Vaze, N.R. Belur, K. Fredriksen, I. Stojkovska, A. Tsytsykova, M. Armant, R.L. DiDonato, J. Choi, L. Cornelissen, L.M. Pereira, E.F. Augustine, C.A. Genetti, K. Dies, B. Barton, L. Williams, B.D. Goodlett, B.L. Riley, A. Pasternak, E.R. Berry, K.A. Pflock, S. Chu, C. Reed, K. Tyndall, P.B. Agrawal, A.H. Beggs, P.E. Grant, D.K. Urion, R.O. Snyder, S.E. Waisbren, A. Poduri, P.J. Park, A. Patterson, A. Biffi, J.R. Mazzulli, O. Bodamer, C.B. Berde, and T.W. Yu

- 6-year old girl with insidious onset of blindness, ataxia, seizures and developmental regression
- Work-up revealed Batten's disease due to mutations in *MFSD8*, a rare neurodegenerative disease with very poor prognosis.
- An allele-specific oligonucleotide (ASO) was designed to correct missplicing caused by the mutation Successful in correcting splicing in the patient's cells
- Toxicity tested in rats
- N of 1 human clinical trial initiated (escalating doses)



N ENGL J MED 381;17 NEJM.ORG OCTOBER 24, 2019

## Genetics of "Typical" Common Diseases:

## Interaction between genetic susceptibility, the environment, and time



# Some Common Diseases with a Known Genetic Component



- Diabetes
- Cancer
- CVD (coronary disease, stroke, heart failure)
- Osteoporosis
- Pulmonary disease (asthma, COPD)
- Eye diseases (glaucoma, macular degeneration)
- Neurodegenerative disorders (Alzheimer, Parkinsons)
- Psychiatric diseases (bipolar, schizophrenia)
- Immune diseases (asthma, rheumatoid arthritis, SLE, MS)



### https://www.ebi.ac.uk/gwas/

### 14

FDA

## Polygenic Risk Score (PRS): Combining hundreds/thousands of genetic variants, eac

Combining hundreds/thousands of genetic variants, each with small effect on risk for a given disease



- To predict disease risk in individual patients
  - More aggressive preventive care
  - Inform actuary tables for health/life insurance
- To select high-risk patients for clinical trials
- Generalizable across populations?

Source: Nature Genetics

# Genetic Architecture of Human Diseases and Traits



# FDA

# Pharmacogenomics

The study of how genetic makeup affects responsiveness to drugs (efficacy) and adverse side effects

*"The right medication for* 

the right patient at the

right time."



**Treat with medication** 

Prevent lack of efficacy and adverse reactions/death

# Goals for Pharmacogenomic Studies for Clinical Trials

- Provide a molecular understanding of drug response in patients
  - » Inform patient stratification strategies for enrichment of clinical studies or diagnostic development
  - » Identify targets/pathways associated with non-responders
  - » Inform follow-up programs or identify potential drug combinations to explore
- Provide a molecular understanding of drug safety for patients
  - » Identify patients at risk for developing AE's
- Provide a molecular understanding of PK variability for patients
- Understand disease pathogenesis:
  - » Understand baseline patient subgroups with differential progression and disease pathology, may use this information to stratify future clinical studies
  - » Inform target discovery
- Development of a program database of genotyped/sequenced patients as a resource for novel disease gene discovery

# Maximizing the Use of Genetic Data from Clinical Trials



· Identify new indications for therapeutic target

Variability of Clopidogrel Response: The Amish Pharmacogenomics of Antiplatelet Intervention (PAPI) Study

- 668 healthy subjects treated with clopidogrel for 1 week
- Platelet aggregation measured before and after therapy

The population "responds" to clopidogrel but there is great inter-individual variation in response

Heritability of clopidogrel response =  $0.7 \rightarrow$  GENETICS !



### Shuldiner et al (2009) JAMA

## PAPI-1: Clopidogrel Response GWAS to Functional Variant to Clinical Outcome



Shuldiner et al (2009) JAMA

# FDA Boxed warning: Plavix (3/20/2010; updated 5/2019):

### WARNING: DIMINISHED ANTIPLATELET EFFECT IN PATIENTS WITH TWO LOSS-OF-FUNCTION ALLELES OF THE CYP2C19 GENE

The effectiveness of Plavix results from its antiplatelet activity, which is dependent on its conversion to an active metabolite by the cytochrome P450 (CYP) system, principally CYP2C19 [see Warnings and Precautions (5.1), Clinical Pharmacology (12.3)]. Plavix at recommended doses forms less of the active metabolite and so has a reduced effect on platelet activity in patients who are homozygous for nonfunctional alleles of the CYP2C19 gene, (termed "CYP2C19 poor metabolizers"). Tests are available to identify patients who are CYP2C19 poor metabolizers [see Clinical Pharmacology (12.5)]. Consider use of another platelet P2Y12 inhibitor in patients identified as CYP2C19 poor metabolizers.

## Clopidogrel Pharmacogenomics The perfect storm for individualized anti-platelet therapy?

- Plavix (clopidogrel) off patent (inexpensive)
- Progeny of clopidogrel prasagrel, ticagrelor -FDA approved (expensive; higher bleeding risk)
- Cyp2C19 \*1\*1 → clopidogrel
  - Cyp2C19 \*2/\*2 → prasugrel, ticagrelor (or other alternatives)
  - \*1/\*2 (intermediate metabolizers)?







# Why aren't most cardiologists performing genetic testing?

- Lack of prospective randomized clinical trials
  - Does pgx improve outcomes?
  - What is the optimal clinical algorithm for its application?
  - Is it cost effective?
  - Who will pay for a RCT?
- Health care provider education (and expectations)
- Logistics of genetic testing
  - Point-of-care, CLIA, etc.
- Reimbursement
- Ethical and legal considerations
- Despite above: Patients 'get it' and want it!

#### ORIGINAL ARTICLE

#### A Genotype-Guided Strategy for Oral P2Y<sub>12</sub> Inhibitors in Primary PCI

 Daniel M.F. Claassens, M.D., Gerrit J.A. Vos, M.D., Thomas O. Bergmeijer, M.D., Renicus S. Hermanides, M.D., Ph.D., Arnoud W.J. van 't Hof, M.D., Ph.D., Pim van der Harst, M.D., Ph.D., Emanuele Barbato, M.D., Ph.D., Carmine Morisco, M.D., Ph.D., Richard M. Tjon Joe Gin, M.D., Folkert W. Asselbergs, M.D., Ph.D., Nethol, Mosterd, M.D., Ph.D., Jean-Paul R. Herrman, M.D., Ph.D., Willem J.M. Dewilde, M.D., Ph.D., Paul W.A. Janssen, M.D., Ph.D., Cornelis Boersma, Pharm.D., Ph.D., Arnthonius de Boer, M.D., Ph.D., Cornelis Boersma, Pharm.D., Ph.D., Vera H.M. Deneer, Pharm.D., Ph.D., and Jurriën M. ten Berg, M.D., Ph.D.

October 24, 2019

ABSTRACT

#### BACKGROUND

It is unknown whether patients undergoing primary percutaneous coronary intervention (PCI) benefit from genotype-guided selection of oral P2Y<sub>12</sub> inhibitors.

#### METHODS

We conducted a randomized, open-label, assessor-blinded trial in which patients dergoing primary PCI with stent implantation were assigned in a 1:1 ratio to a either a P2Y, inhibitor on the basis of early CYP2C19 genetic testing (genotyp group) or standard treatment with either ticagrelor or prasugrel (standar group) for 12 months. In the genotype-guided group, carriers of CYP2C19\*3 loss-of-function alleles received ticagrelor or prasugrel. received clopidogrel. The two primary outcomes were net advers defined as death from any cause, myocardial infarction, defi rombosis, stroke, or major bleeding defined according to Platelet Inhibit tient Outcomes (PLATO) criteria - at 12 months (primary combined out ted for noninferiority, with a noninferiority margin of 2 percentage point he absolute difference) mary bleeding outcome and PLATO major or minor bleeding at 12 month

#### RESULTS

For the primary analysis, 2488 patients were of udded: 1242 in the sector and group and 1246 in the standard-treatment group. The primare sector outcome occurred in 63 patients (5.7%) in the group/pe-guided group on 73 patients (5.9%) in the standard-treatment group (absolute different of 0.7 percentage points; 95% confidence interval [CI], -2.0 to 0.7; Pe-Outper noninferiority]. The primary bleeding outcome occurred in 122 patients (9.8%) in the genotype-guided group and in 156 patients (12.5%) in the standard-treatment group (hazard ratio, 0.78; 95% CI, 0.61 to 0.98; Pe-0.04).

#### CONCLUSIONS

In patients undergoing primary PCI, a CVP2C19 genotype-guided strategy for selection of oral P2Y<sub>12</sub> inhibitor therapy was noninferior to standard treatment with ticagrelor or prasugrel at 12 months with respect to thrombotic events and resulted in a lower incidence of bleeding. (Funded by the Netherlands  $Vog_{20}$ and Development; POPular Genetics ClinicalTrials.gov number, Net-Netherlands Trial Register number, NL2872.) The primary combined outcome occurred in 63 patients (5.1%) in the genotype-guided group and in 73 patients (5.9%) in the standard-treatment group (absolute differences -0.7%; 95% confidence interval [CI], -2.0 to 0.7; P<0.001 for noninferiority.

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his article was published on Septembe

is article.

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In patients undergoing primary PCI, a CYP2C19 genotypeguided strategy for selection of oral P2Y12 inhibitor therapy was noninferior to standard treatment with ticagrelor or prasugrel at 12 months with result to thrombotic events and resulted in a lower incidence of bleeding.

# Examples of Ready for Prime Time PGX:

http://www.pharmgkb.org/page/cpic

- TPMT/Thiopurines
- CYP2C19/Clopidogrel
- CYP2C9-VKORC1/Warfarin
- HLA-B\*5701/Abacavir
- CYP2D6/Codeine, SSRIs, ADHD drugs, Tamoxofen
- SLCO1B1/Simvastatin
- HLA-B/\*1502/Carbamazepine
- IL28B/interferon
- CYP2D6/SSRIs
- UGT1A1/irinotecan



# Cancer: Leading the Way in Personalized Medicine

(http://www.fda.gov/drugs/scienceresearch/researchareas/pharmacogenetics/ucm083378.htm)



- Her-Neu2/Trastuzumab (Herceptin), everolimus
- ER/tamoxifen
- Brc-Abl-C-Kit/ Imatinib (Gleevac)
- EGFR/gefitinib, cetuximab, erlotinib, panitumumab
- KRAS/cetuximab, panitumumab
- ALK/crizotinib
- BRAF/vemurafenib
- PD1/PDL1 checkpoint inhibitors and tumor neoantigens



# The Reality of Therapeutic Development in 2019

- Despite increased investment in R+D in the pharmaceutical industry, the number of new molecular entities is not increasing
- >90% of molecules that enter Phase I clinical trials fail to demonstrate sufficient safety and efficacy to gain regulatory approval
- Most failures occur in Phase II clinical trials
  - 50% due to lack of efficacy
  - 25% due to toxicity
- Pre-clinical models may be poor predictors of clinical benefit
- Compounds supported by human genetics evidence are substantially more likely to succeed

# The Potential for Human Genetics to Accelerate Target Identification, Validation and Drug Development



## Congenital Insensitivity to Pain (CIP) and SCN9A: Human Genetics Provides Insights Into New Pain Drug Targets





- CIP  $\rightarrow$  pain free burns, fractures, childbirth, etc
- Extremely rare: <1/1,000,000 prevalence
- Mutations in SCN9A cause insensitivity to pain
- Efforts to mimic the effects of pain insensitivity through therapeutics blocking the corresponding protein are being pursued

# Application of Human Genetics to Accelerate Novel Target Identification and Clinical Development





## Human Genetics Validation and Derisking of New Lipid Lowering Targets

### ...and T2D as a potential new indication for ANGPTL4 inhibition

The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

#### Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease

Frederick E. Dewey, M.D., Viktoria Gusarova, Ph.D., Colm O'Dushlaine, Ph.D., Omri Gottesman, M.D., Jesus Trejos, M.S., Charleen Hunt, Ph.D.,
Cristopher V. Van Hout, Ph.D., Lukas Habegger, Ph.D., David Buckler, Ph.D., Ka-Man V. Lai, Ph.D., Joseph B. Leader, Ph.D., Michael F. Murray, M.D.,
Marylyn D. Ritchie, Ph.D., H. Lester Kirchner, Ph.D., David H. Ledbetter, Ph.D., John Penn, M.S., Alexander Lopez, M.S., Ingrid B. Borecki, Ph.D.,
John Penn, M.S., Alexander Lopez, M.S., Ingrid B. Borecki, Ph.D.,
John D. Overton, Ph.D., Jeffrey G. Reid, Ph.D., David J. Carey, Ph.D.,
Andrew J. Murphy, Ph.D., George D. Yancopoulos, M.D., Ph.D., Aris Baras, M.D.,
Jesper Gromada, Ph.D., D. M.S.c., and Alan R. Shuldiner, M.D.



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#### Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease

F.E. Dewey, V. Gusarova, R.L. Dunbar, C. O'Dushlaine, C. Schurmann, O. Gottesman, S. McCarthy, C.V. Van Hout, S. Bruse, H.M. Dansky, J.B. Leader, M.F. Murray, M.D. Ritchie, H.L. Kirchner, L. Habegger, A. Lopez, J. Penn, A. Zhao, W. Shao, N. Stahl, A.J. Murphy, S. Hamon, A. Bouzelmat, R. Zhang, B. Shumel, R. Pordy, D. Gipe, G.A. Herman, W.H.H. Sheu, I-T. Lee, K.-W. Liang, X. Guo, J. Rotter, Y.-D.I. Chen, "W.E. Kraus, S.H. Shah, S. Darruauer, A. Small, D.J. Rader, A.B. Wulff, B.G. Nordestgaard, A. Tybjærg: Hansen, A.M. van den Hoek, H.M.G. Princen, D.H. Ledbetter, D.J. Carey, \* J.D. Overton, J.G. Reid, W.J. Sasiela, P. Banerjee, A.R. Shuldiner, I.B. Borecki, T.M. Teslovich, G.D. Yancopoulos, S.J. Mellis, J. Gromada, and A. Baras

•

|                      | N Cases | N Controls |      |            |          |      | P Value               | Odds Ratio [95% CI]  |
|----------------------|---------|------------|------|------------|----------|------|-----------------------|----------------------|
| Discovery Study      |         |            |      |            |          |      |                       |                      |
| DiscovEHR            | 12,945  | 36,165     |      | <b>—</b>   |          |      | 4.2x10-02             | 0.90 [ 0.81 , 1.00 ] |
| Replication Studies  |         |            |      |            |          |      |                       |                      |
| T2DG/GT2D/DG         | 34,809  | 57,985     |      | ⊢∎         |          |      | 4.1x10-03             | 0.86 [ 0.79 , 0.93 ] |
| CGPS                 | 7.838   | 107.246    |      |            |          |      | 2.6x10-01             | 0.94 0.85 1.05       |
| DECODE               | 6,808   | 72,309     |      | L          | <b>.</b> |      | 5.0x10 <sup>-01</sup> | 0.96 0.85 1.08       |
| HUNT                 | 4,761   | 56,837     |      |            |          |      | 2.9x10 <sup>-02</sup> | 0.86 0.75 0.98       |
| MDC                  | 4.854   | 23,060     |      |            |          |      | 3.8x10 <sup>-02</sup> | 0.86 0.75 0.99       |
| UKBB                 | 5,741   | 106,597    |      | <b>-</b>   |          |      | 2.4x10-01             | 0.92 0.80 1.06       |
| EINT-C               | 5,143   | 7.300      | H    |            |          |      | 1.0x10 <sup>-03</sup> | 0.7510.63.0.891      |
| DiscovEHR-30K        | 3,456   | 22.372     | 1    |            |          |      | 6.4x10 <sup>-02</sup> | 0.84 0.70 1.01       |
| EINT-Q               | 4,257   | 4,293      |      |            |          | -    | 5.0x10 <sup>-01</sup> | 1.07 0.88 1.32       |
| MGI                  | 1,389   | 12,289 ⊢   |      |            |          |      | 4.2x10 <sup>-02</sup> | 0.72 0.51 1.00       |
| DUKE                 | 1,630   | 4,903      |      |            |          |      | 3.9x10 <sup>-02</sup> | 0.7010.49.0.981      |
| ENOR                 | 1,347   | 19,504 ⊢   |      |            |          |      | 2.7x10-01             | 0.77 0.48 1.23       |
| UPENN                | 733     | 4.066      |      |            |          |      | 9.7x10 <sup>-01</sup> | 1.02 0.36 2.88       |
| Combined-replication | 82,766  | 498,761    |      | •          |          |      | 5.0x10-09             | 0.88 0.85, 0.92      |
| Combined-all         | 95,711  | 534,926    |      | •          |          |      | 6.3x10 <sup>-10</sup> | 0.89 [ 0.85 , 0.92 ] |
|                      |         |            | 1    | 1          |          |      |                       |                      |
|                      |         | 0.45       | 0.61 | 0.82       | 1.11     | 1.50 |                       |                      |
|                      |         |            |      | Odds ratio |          |      |                       |                      |

In 95,711 T2D cases and 534,926 controls, carriers of p.E40K carriers have a ~11% reduced odds of diabetes per allele (OR 0.89, 95%CI 0.85- 0.92, p= $6.3x10^{-10}$ )

- In 32,015 T2D cases and 84,006 controls, carriers of rare pLOFs of ANGPLT4 have a 29% reduced OR of T2D (OR 0.81, 95%CI 0.49-0.99, p = 0.04)
- pE40K non-diabetic carriers have lower glucose and increased insulin sensitivity

# DiscovEHRy of a New Drug Target for Chronic Liver Disease

DA

The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

## A Protein-Truncating HSD17B13 Variant and Protection from Chronic Liver Disease

N.S. Abul-Husn, X. Cheng, A.H. Li, Y. Xin, C. Schurmann, P. Stevis, Y. Liu,
J. Kozlitina, S. Stender, G.C. Wood, A.N. Stepanchick, M.D. Still, S. McCarthy,
C. O'Dushlaine, J.S. Packer, S. Balasubramanian, N. Gosalia, D. Esopi, S.Y. Kim,
S. Mukherjee, A.E. Lopez, E.D. Fuller, J. Penn, X. Chu, J.Z. Luo, U.L. Mirshahi,
D.J. Carey, C.D. Still, M.D. Feldman, A. Small, S.M. Damrauer, D.J. Rader,
B. Zambrowicz, W. Olson, A.J. Murphy, I.B. Borecki, A.R. Shuldiner, J.G. Reid,
J.D. Overton, G.D. Yancopoulos, H.H. Hobbs, J.C. Cohen, O. Gottesman,
T.M. Teslovich, A. Baras, T. Mirshahi, J. Gromada, and F.E. Dewey

N ENGL J MED 378;12 NEJM.ORG MARCH 22, 2018

# Summary and Conclusions



From New Yorker

"Here's my sequence..."

- "4 P's" of Precision Medicine predictive, personalized, preemptive, participatory
- The genomic architecture of human traits and disease is a continuum from rare large effect genetic variants that cause highly penetrant monogenic diseases to many common small effect genetic variants that in aggregate influence susceptibility to common (polygenic) diseases
- A deeper understanding of the genomic architecture of human traits and disease offer opportunities for precision medicine
  - Diagnosis and novel treatments for highly penetrant monogenic diseases
  - Polygenic risk scores (PRS) to stratify patients at risk for common diseases
  - Pharmacogenetics
- Human genetics can identify novel therapeutic targets more likely to be effective and safe in man

FD/A