

# Accelerating Translational Medicine using Heterogeneous Data: A Case for Better Metadata

Purvesh Khatri  
Institute for Immunity, Transplantation and Infection  
Center for Biomedical Informatics Research  
Department of Medicine  
Stanford University

Email: [pkhatri@stanford.edu](mailto:pkhatri@stanford.edu)  
[@purveshkhatri](#)

# “Reproducibility Crisis”

Essay

## Why Most Published Research Findings Are False

*PLoS Medicine 2005*

John P. A. Ioannidis

## Estimating the reproducibility of psychological science

*Science 2015*

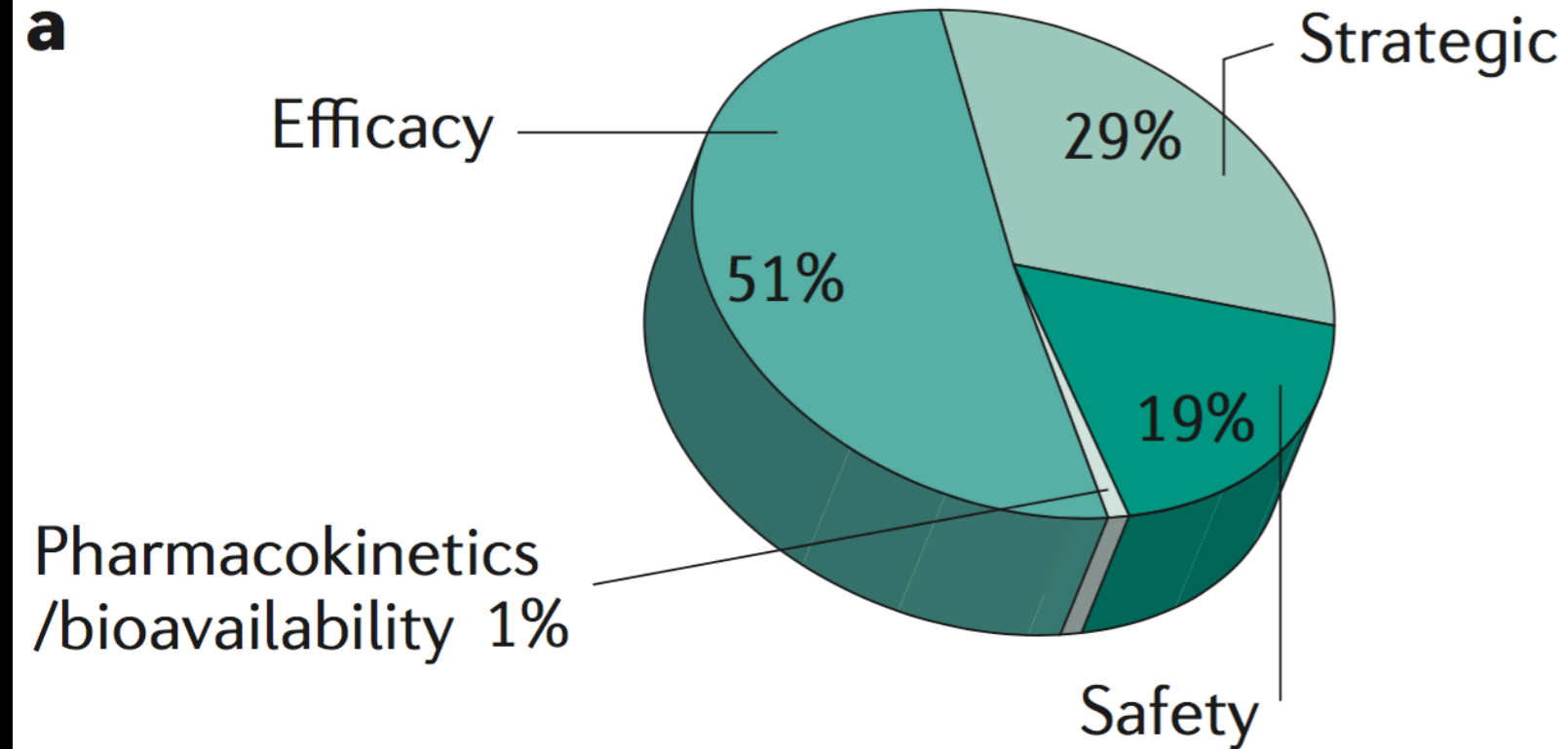
Open Science Collaboration\*

## Raise standards for preclinical cancer research

*Nature 2012*

# Lack of reproducibility affects translation

## Phase II failures: 2008–2010

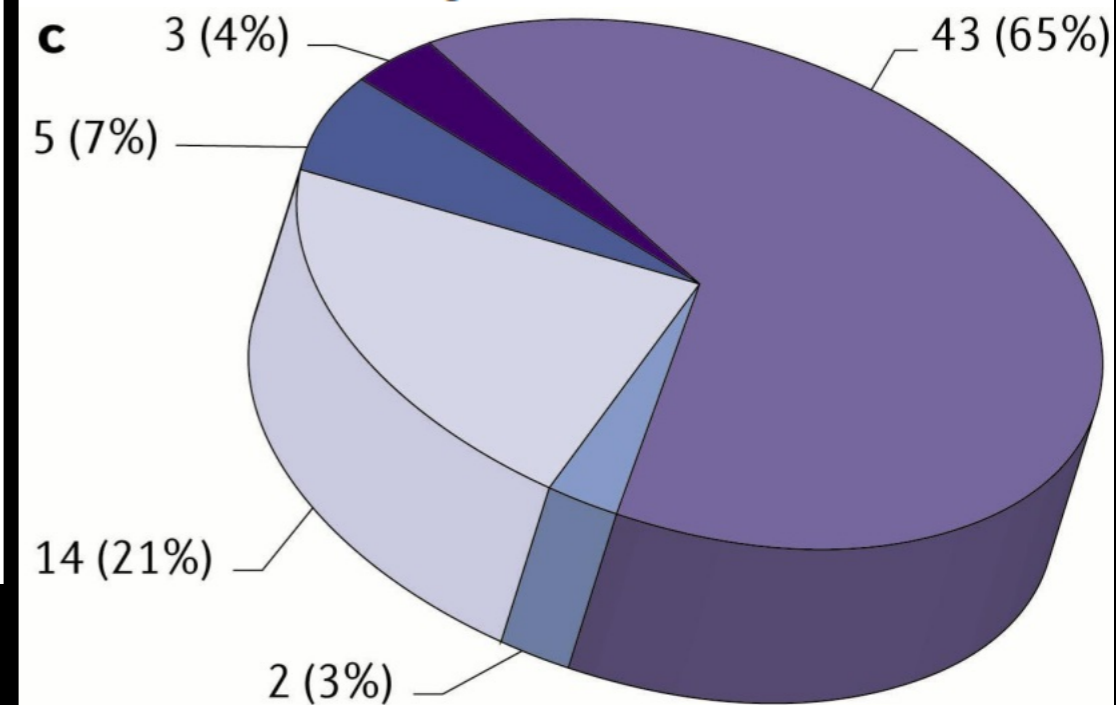


*Nat Rev Drug Discovery 2011*

- Phase II success rate reduced from 28% to 18%

## Believe it or not: how much can we rely on published data on potential drug targets?

Florian Prinz, Thomas Schlange and Khusru Asadullah



- Inconsistencies
- Not applicable
- Literature data are in line with in-house data
- Main data set was reproducible
- Some results were reproducible

*Nat Rev Drug Discovery 2011*

# Reasons for lack of reproducibility - Methods and Models

## STATISTICAL ERRORS

*Nature 2014*

*P* values, the ‘gold standard’ of statistical validity, are not as reliable as many scientists assume.

## **Of Mice and Not Men: Differences between Mouse and Human Immunology**

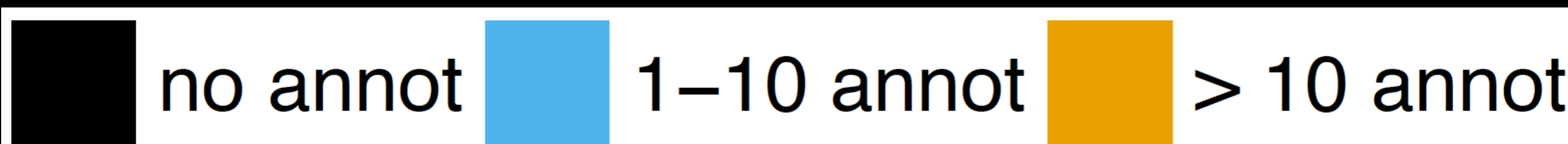
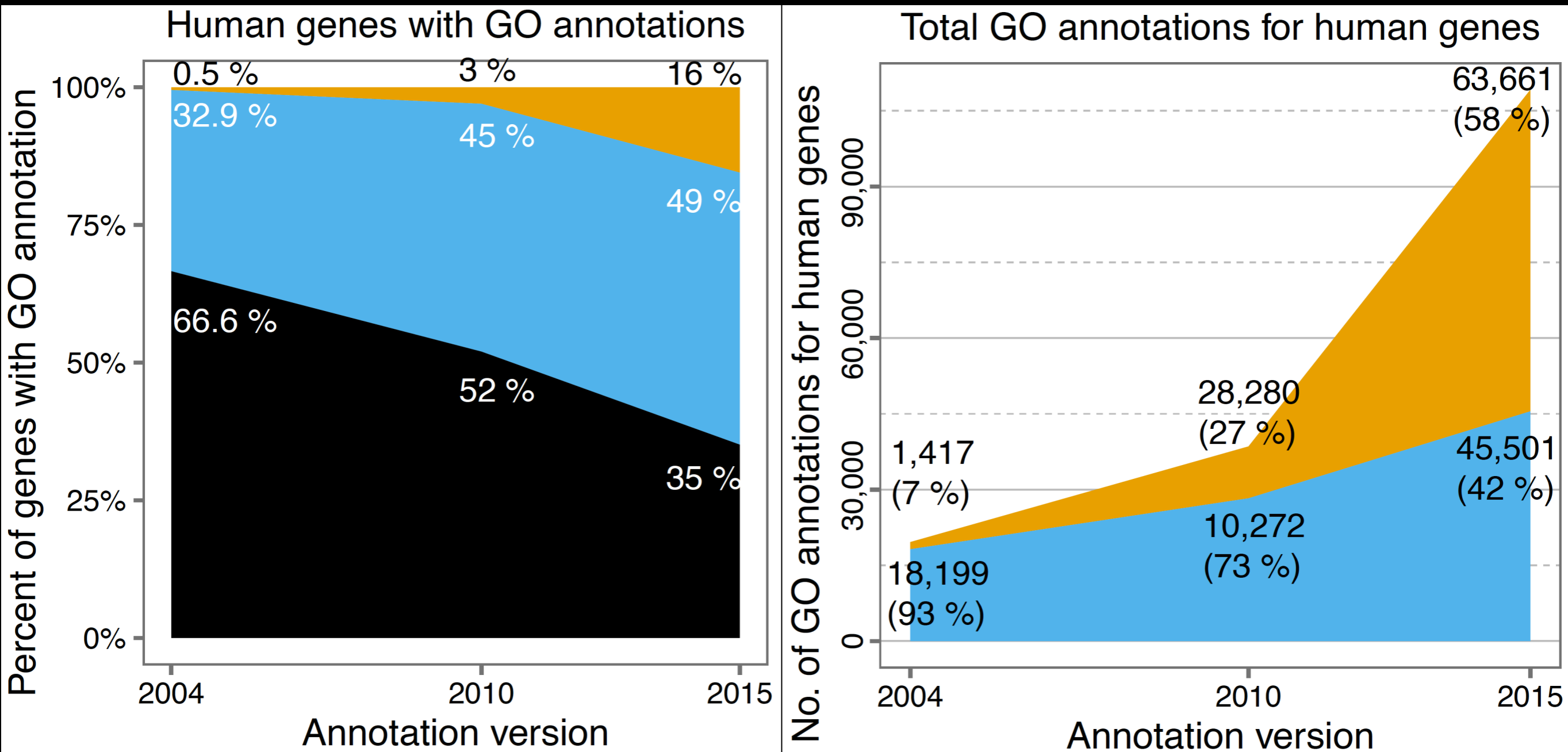
*Javier Mestas and Christopher C. W. Hughes<sup>1</sup>*

*J of Immunology 2004*

**Genomic responses in mouse models poorly mimic human inflammatory diseases**

*PNAS 2013*

# Our biological knowledge is incomplete and biased



Lack of biological and technological  
heterogeneity is a significant problem

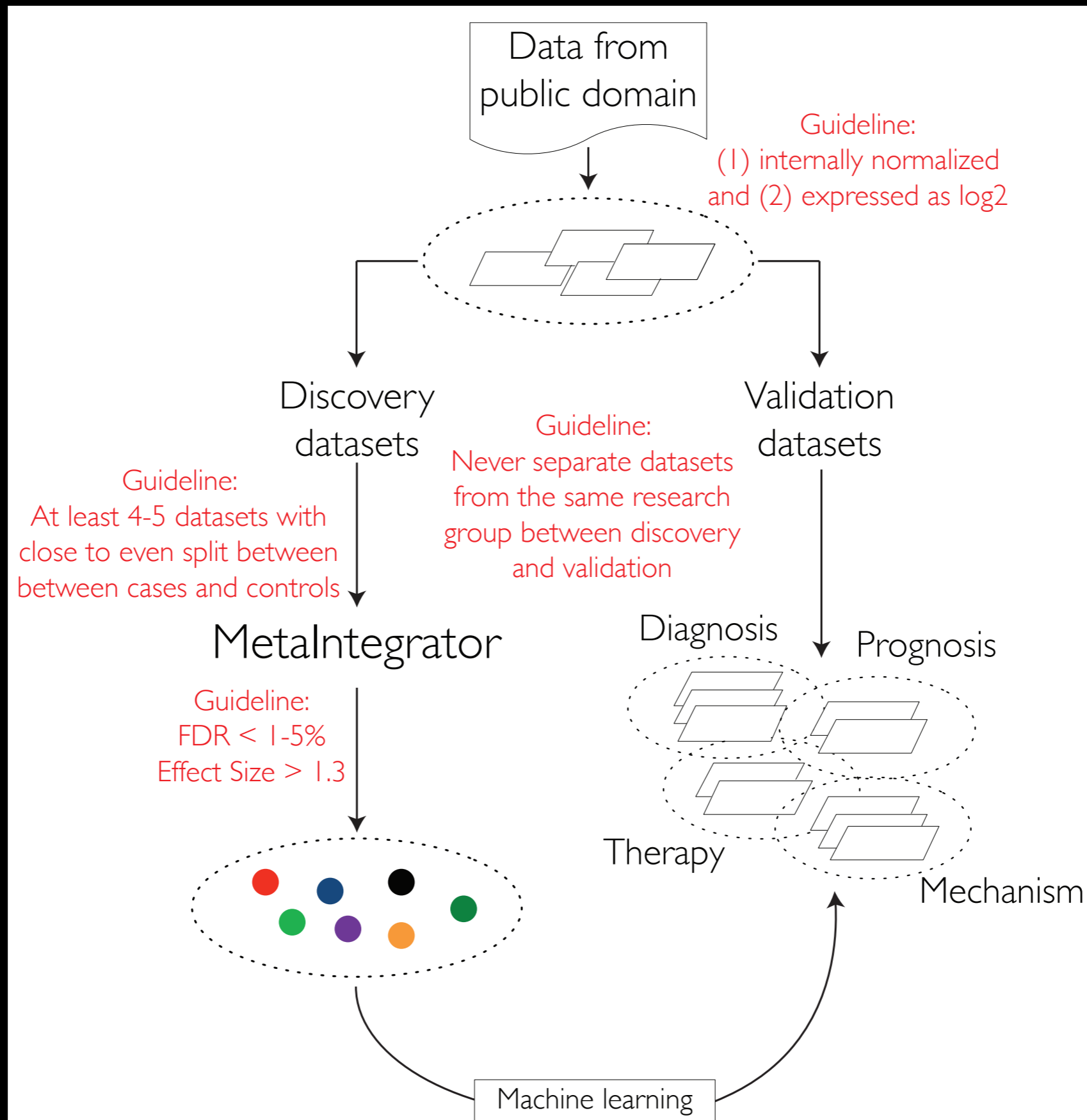
# Traditional approach - reduce heterogeneity

- Single cohort
  - Clinical homogeneity
  - Minimize technical variance
  - Internal validation
- Does not capture heterogeneity of a disease
- Results are difficult to generalize

# Embrace heterogeneity

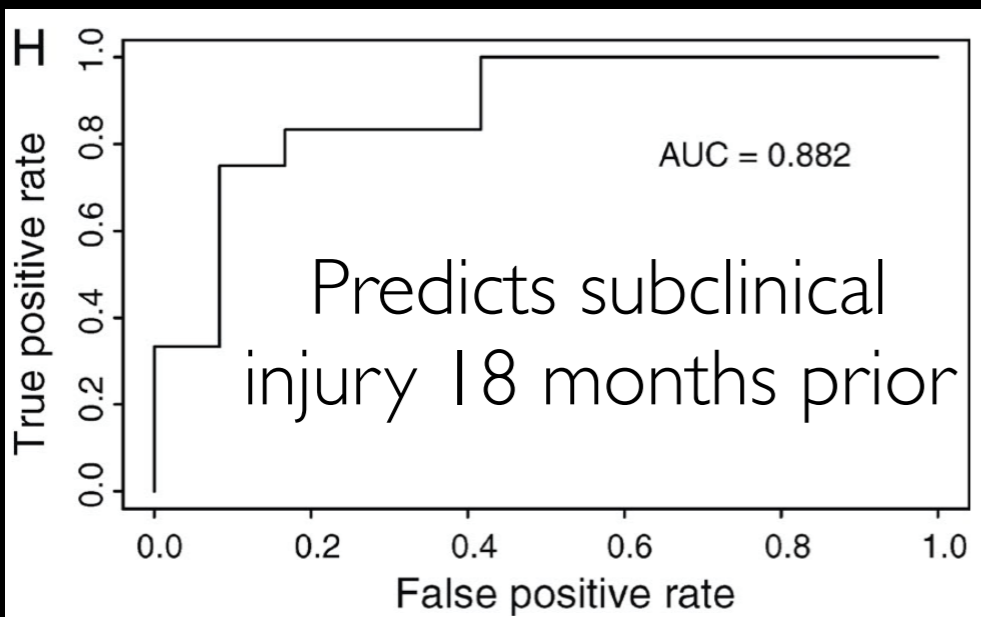
- Public data - multiple datasets asking the same question
  - Clinical heterogeneity
  - Different treatments
  - Different technologies
- Generalizable results
- Unexpected results are more “believable”
- “*Dirty data*” - integration is challenging

# Framework for leveraging heterogeneity



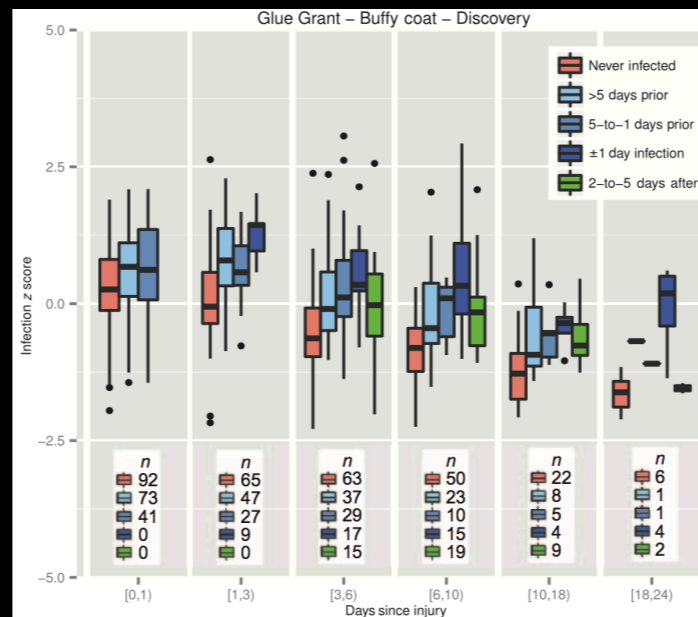
# Diagnostic and Prognostic Markers using Heterogeneous Data

Common rejection module  
across all solid organs



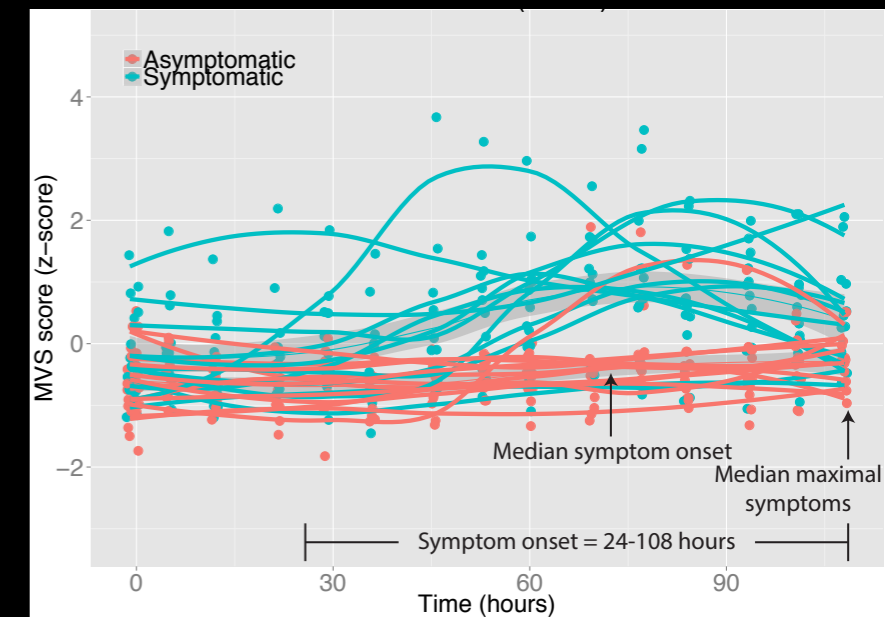
Khatri et al.  
*J Exp Med* 2013

Sepsis diagnosis  
1-to-5 days prior



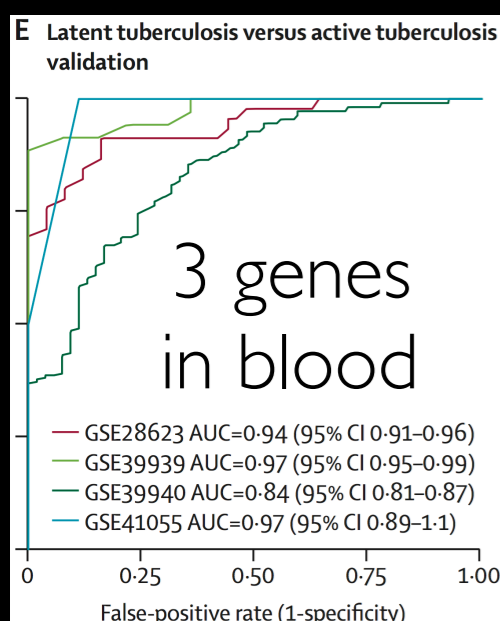
Sweeney et al.  
*Sci Trans Med* 2015

Common host response  
to viral infections



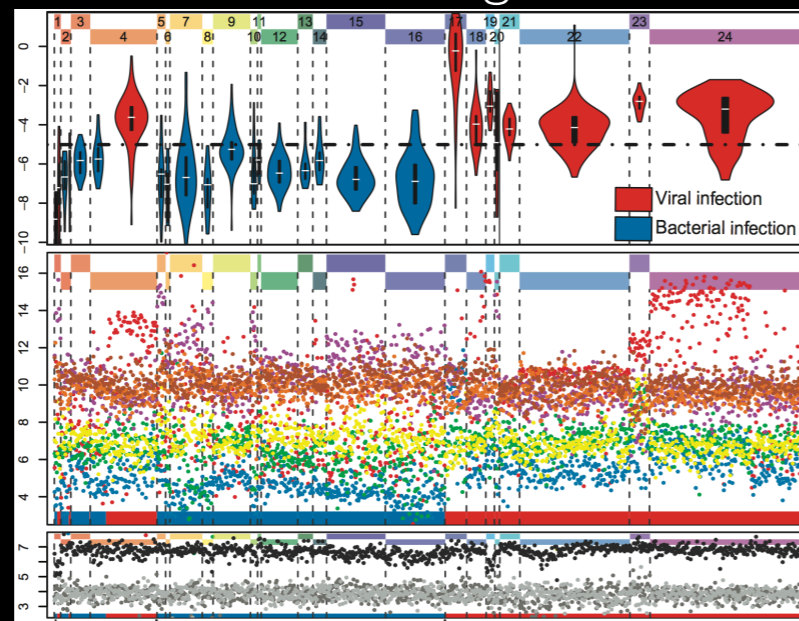
Andres-Terre et al.  
*Immunity* 2015

TB - satisfies  
WHO TPP



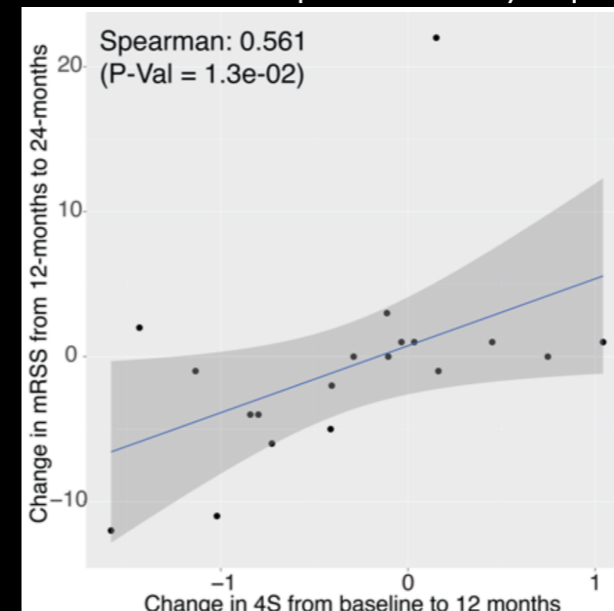
Sweeney et al.  
*Lancet Resp Med* 2016

Bacterial vs viral  
infection diagnosis



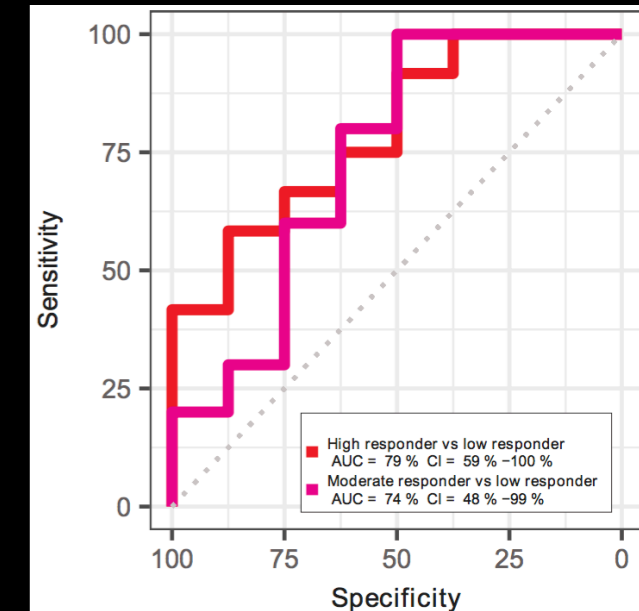
Sweeney et al.  
*Sci Trans Med* 2016

Scleroderma - predicts  
treatment response 1 yr prior



Lofgren et al.  
*JCI Insight* 2016

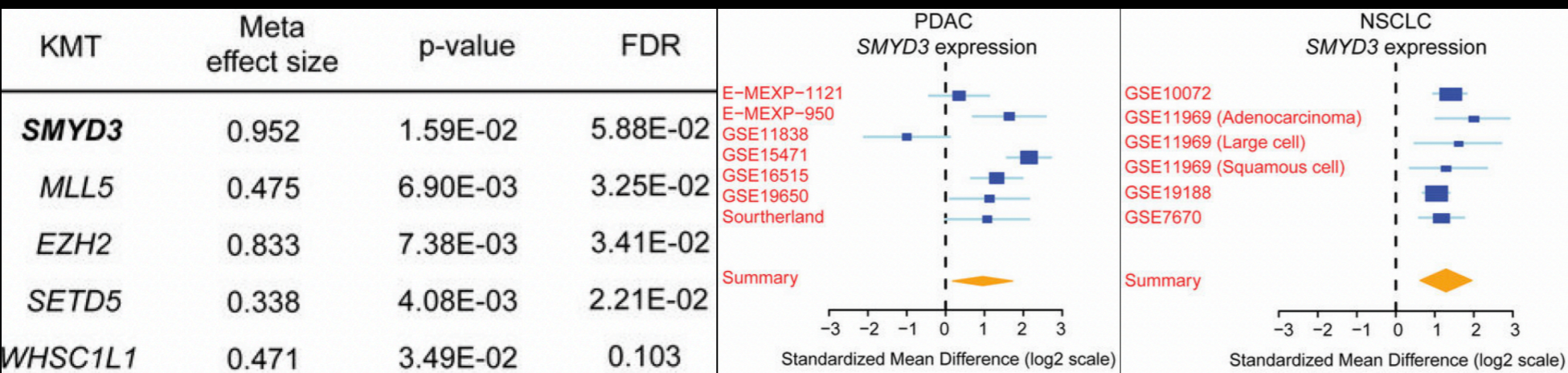
Predict response  
to vaccine at baseline



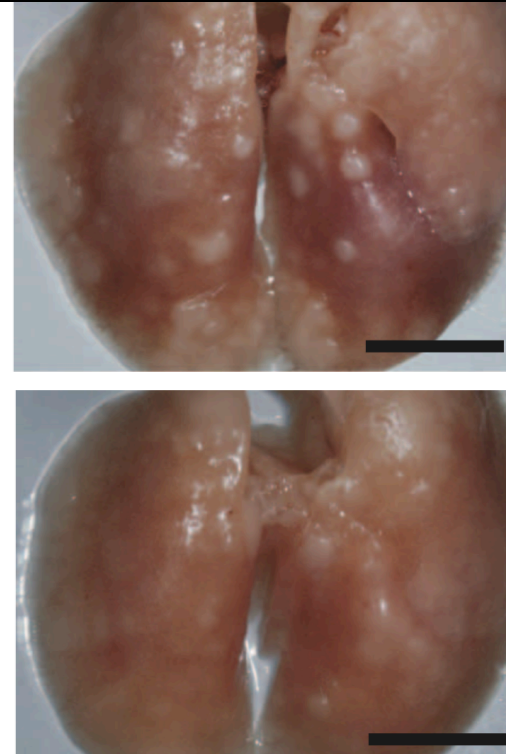
HIPC-CHI  
*Sci Immunology* 2017

# Target Discovery using Heterogeneous Data

Mazur et al. Nature 2014

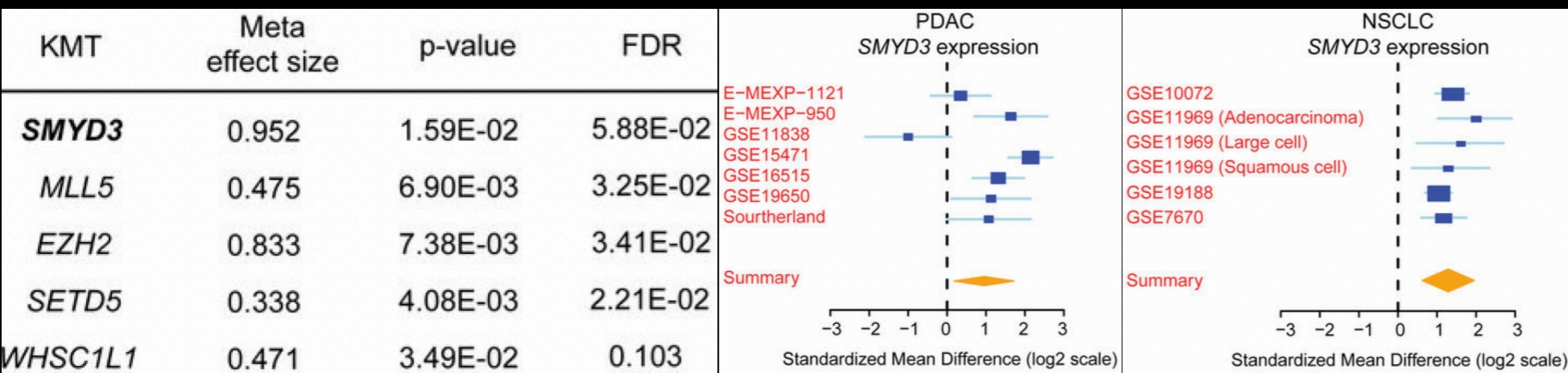


Kras  
Kras;Smyd3

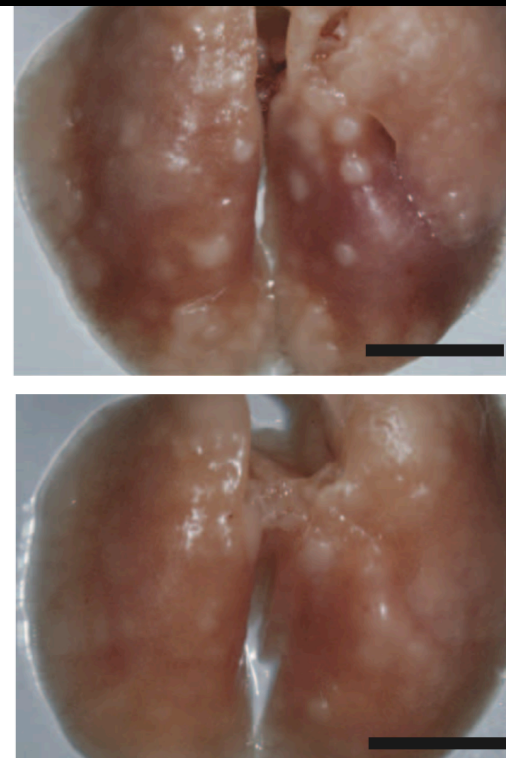


# Target Discovery using Heterogeneous Data

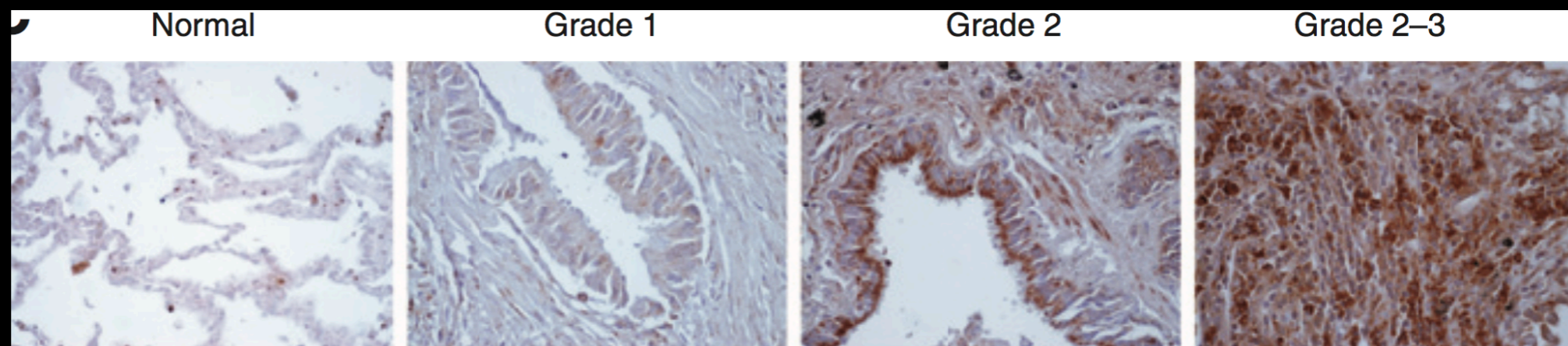
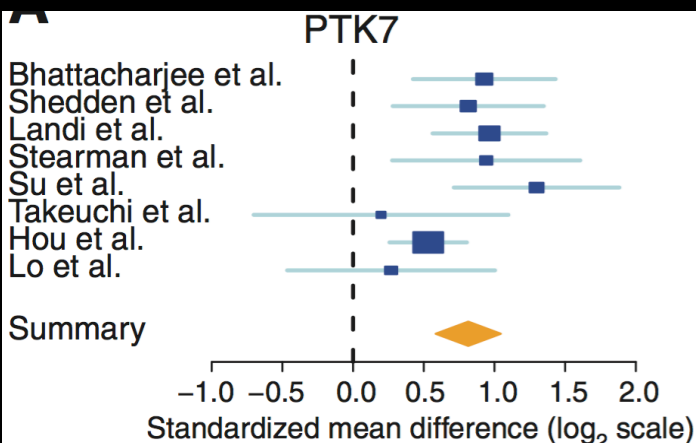
Mazur et al. Nature 2014



Kras  
Kras;Smyd3



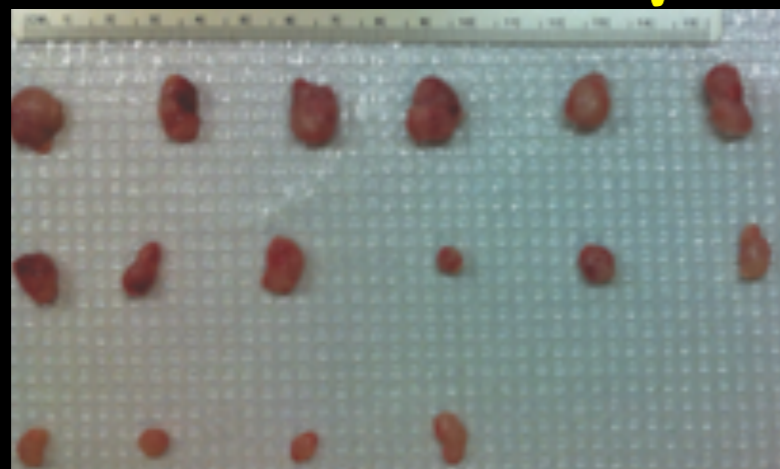
Chen\*, Khatri\* et al. Cancer Research 2014



shCtrl

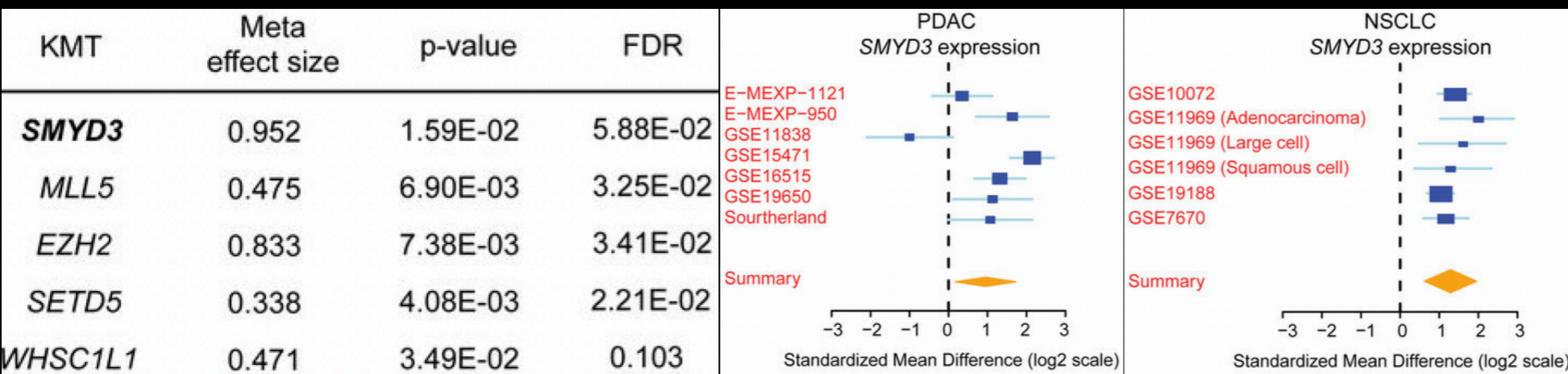
shPTK7

shPTK7

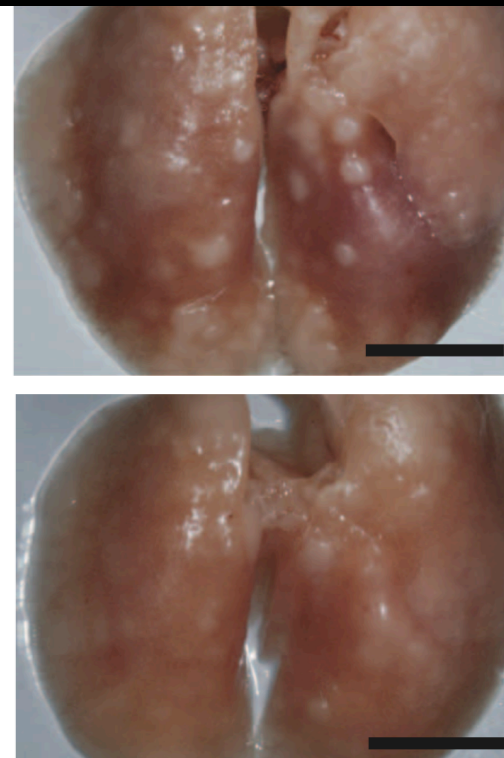


# Target Discovery using Heterogeneous Data

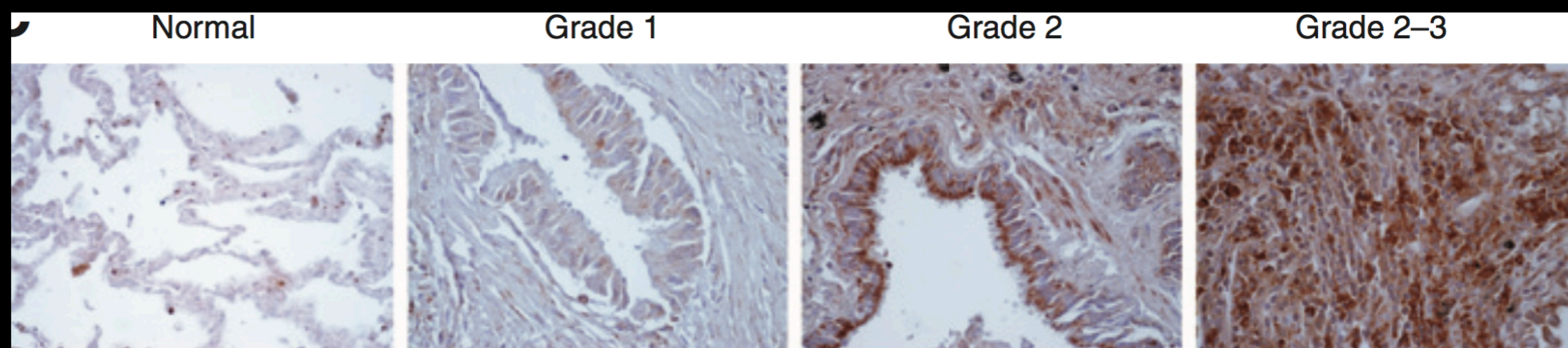
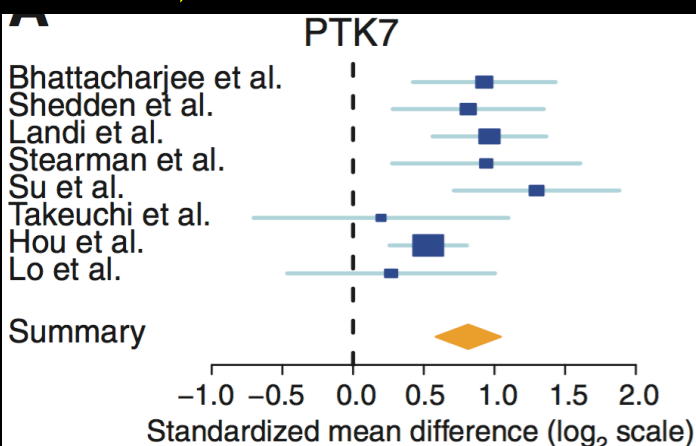
Mazur et al. Nature 2014



Kras; Smyd3



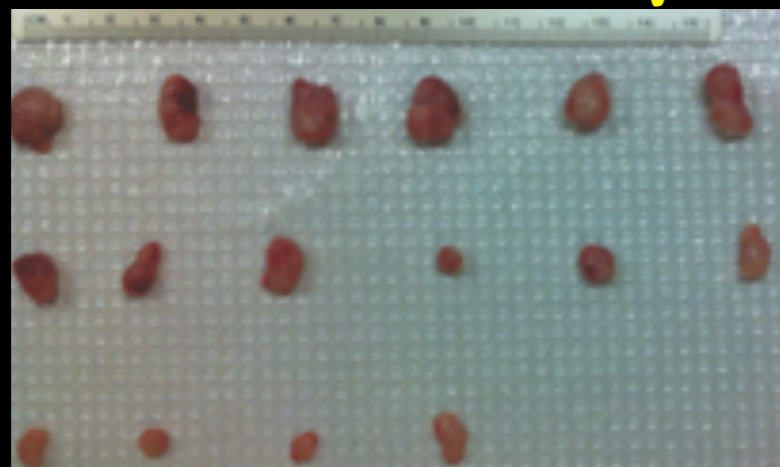
Chen\*, Khatri\* et al. Cancer Research 2014



shCtrl

shPTK7

shPTK7



SCIENCE TRANSLATIONAL MEDICINE | RESEARCH ARTICLE

CANCER

**A PTK7-targeted antibody-drug conjugate reduces tumor-initiating cells and induces sustained tumor regressions**

Marc Damelin,<sup>1\*†</sup> Alexander Bankovich,<sup>2\*</sup> Jeffrey Bernstein,<sup>2</sup> Justin Lucas,<sup>1</sup> Liang Chen,<sup>1</sup> Samuel Williams,<sup>2</sup> Albert Park,<sup>2</sup> Jorge Aguilar,<sup>2</sup> Elana Ernstoff,<sup>1</sup> Manoj Charati,<sup>1</sup> Russell Dushin,<sup>3</sup> Monette Aujay,<sup>2</sup> Christina Lee,<sup>2</sup> Hanna Ramoth,<sup>2</sup> Milly Milton,<sup>2</sup> Johannes Hampl,<sup>2</sup> Sasha Lazetic,<sup>2</sup> Virginia Pulito,<sup>1</sup> Edward Rosfjord,<sup>1</sup> Yongliang Sun,<sup>3</sup> Lindsay King,<sup>3</sup> Frank Barletta,<sup>1</sup> Alison Betts,<sup>3</sup> Magali Guffroy,<sup>1</sup> Hadi Falahatpisheh,<sup>1</sup> Christopher J. O'Donnell,<sup>3</sup> Robert Stull,<sup>2</sup> Marybeth Pysz,<sup>2</sup> Paul Escarpe,<sup>2</sup> David Liu,<sup>2</sup> Orit Foord,<sup>2</sup> Hans Peter Gerber,<sup>1</sup> Puja Sapra,<sup>1†</sup> Scott J. Dylla<sup>2†</sup>

# A comment from an NIH grant reviewer

## Weaknesses

- PI completely inexperienced in scleroderma – seems to like bright objects and flits from one shiny project to another without focus.

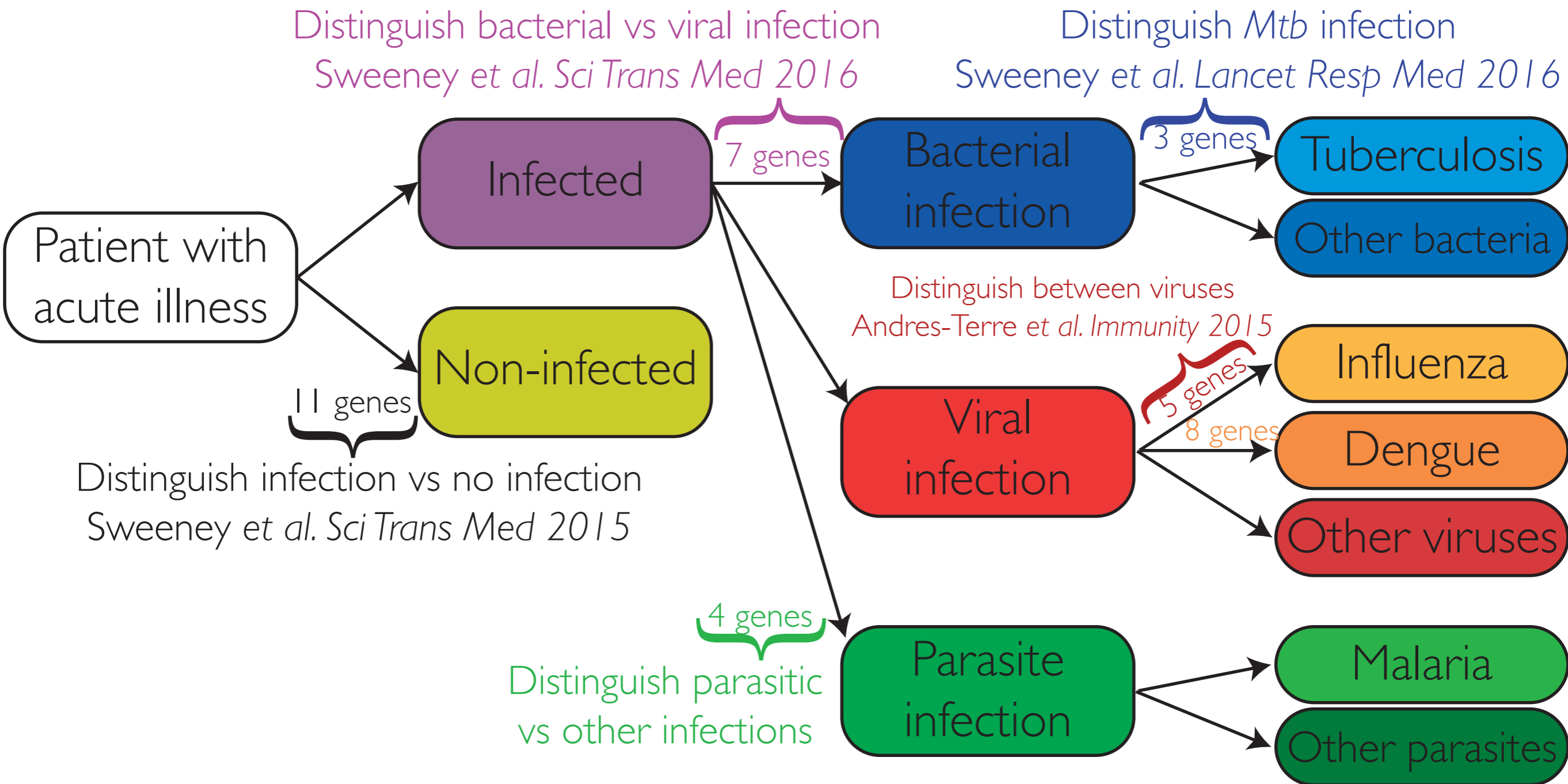
# A comment from an NIH grant reviewer

## Weaknesses

- PI completely inexperienced in scleroderma – seems to like bright objects and flits from one shiny project to another without focus.

But...there is a method to my ADD!

# “Reading the immune response” to build phylogeny of host response to infectious diseases



# High-priority target product profiles for new tuberculosis diagnostics: report of a consensus meeting

28–29 April 2014

Geneva, Switzerland



World Health  
Organization

## Executive summary

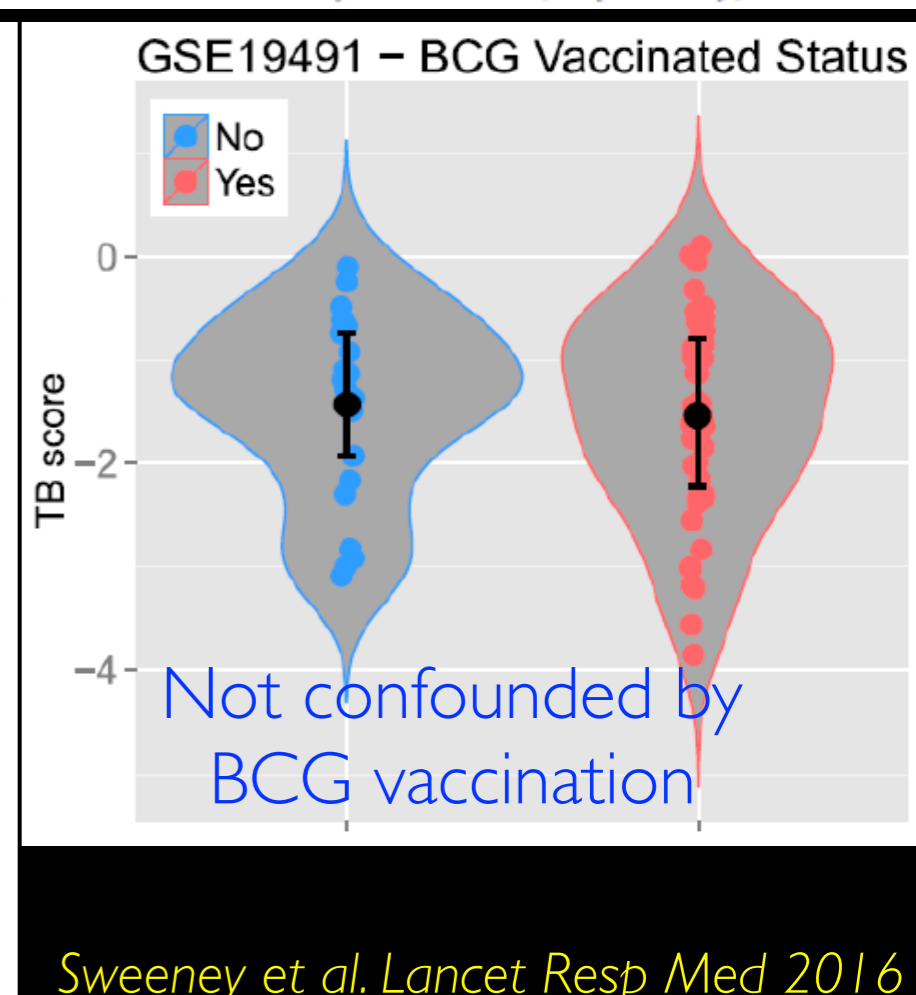
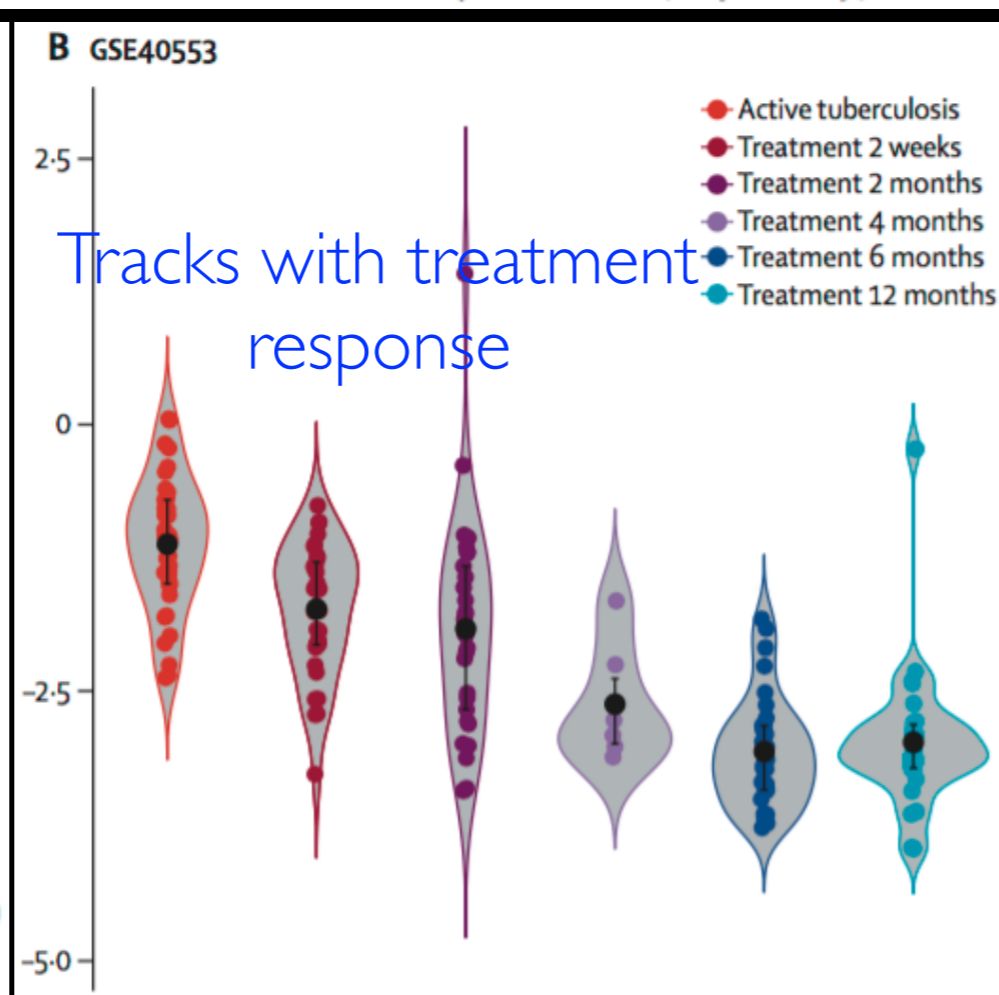
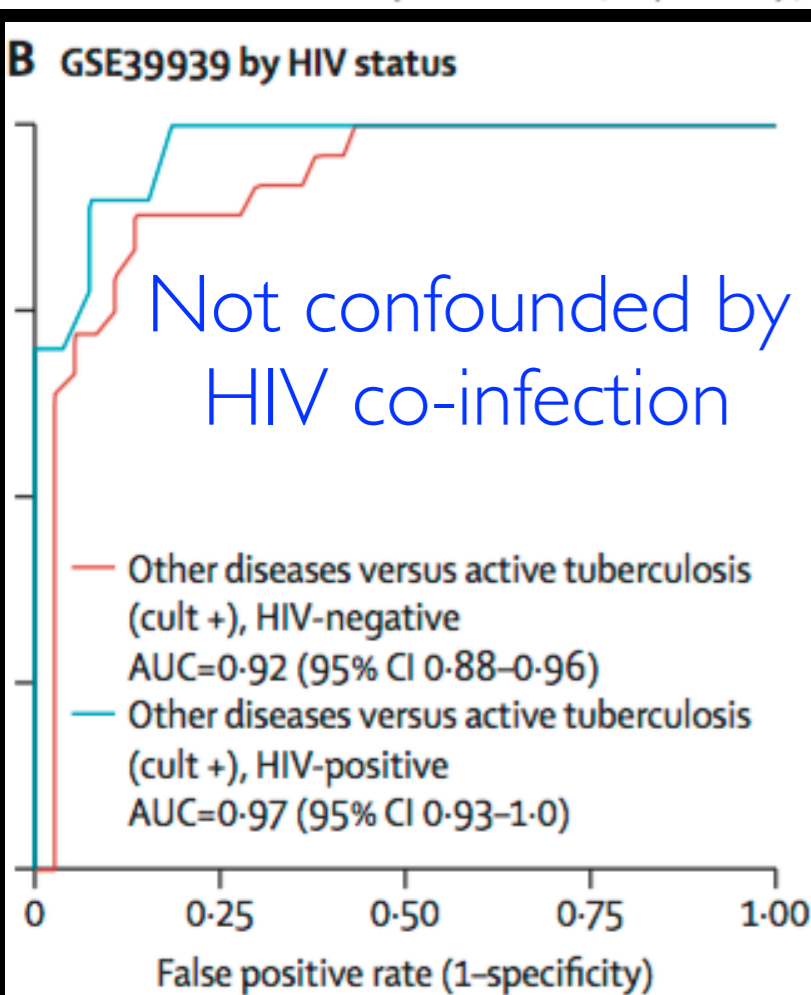
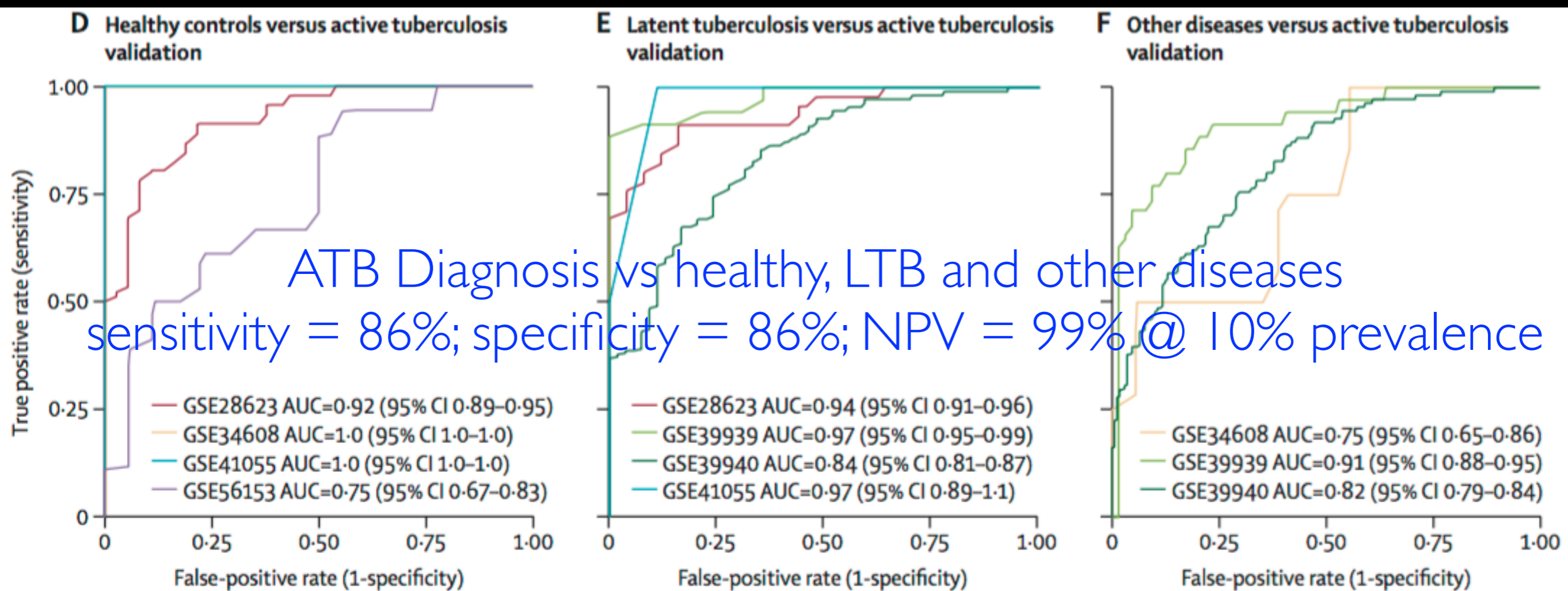
---

- a point-of-care non-sputum-based test capable of detecting all forms of TB by identifying characteristic biomarkers or biosignatures (known as the biomarker test);
- a point-of-care triage test, which should be a simple, low-cost test that can be used by first-contact health-care providers to identify those who need further testing (the triage test);
- a point-of-care sputum-based test to replace smear microscopy for detecting pulmonary TB (the smear-replacement test);
- a rapid drug-susceptibility test that can be used at the microscopy-centre level of the health-care system to select first-line regimen-based therapy (the rapid DST test).

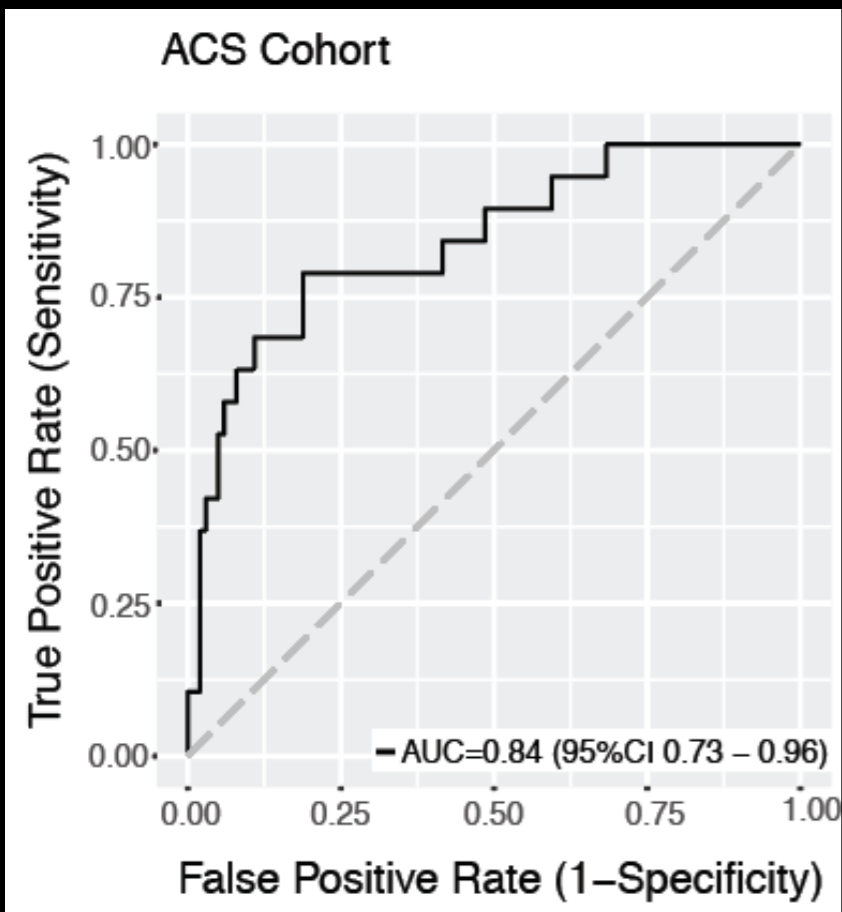
	Year	Reference	Platform	Use	Country	Age	HIV status	Active tuberculosis culture or smear	Healthy controls	Latent tuberculosis	Other disease	Active tuberculosis	Treatment	Total	Miscellaneous
GSE19491	2010	Berry <sup>8</sup>	GPL6947	Discovery	South Africa, UK, USA	Adults	Negative	Positive	86	69	193	31	..	409	Other disease breakdown: 28 ASLE, 82 PSLE, 31 Still's, 52 <i>Streptococcus</i> and/or <i>Staphylococcus</i> infection; post-treatment samples not used.
GSE25534	2010	Maertzdorf <sup>30</sup>	GPL1708	Validation	South Africa	Adults	Negative	Positive	6	19	..	19	..	44	Two-colour array (on-chip comparisons between healthy controls, latent tuberculosis, and active tuberculosis)
GSE28623	2011	Maertzdorf <sup>22</sup>	GPL4133/ GPL6480	Validation	The Gambia	Adults	Negative	Positive	3	21	..	46	..	108	..
Cliff Combined Dataset	2013	Cliff <sup>3</sup>	GPL570	Validation	South Africa	Adults	Negative	Positive	..	..	..	36	117	153	Treatment measured at 1, 2, 4, and 26 weeks
GSE34608	2012	Maertzdorf <sup>24</sup>	GPL4133/ GPL6480	Validation	Germany	Adult	Negative	Positive	18	..	18	8	..	44	Other diseases all sarcoid
GSE37250	2014	Kaforou <sup>7</sup>	GPL10558	Discovery	Malawi, South Africa	Adults	Positive and negative	Positive	..	167	175	195	..	537	See reference for other disease distributions; 194 patients with other diseases reported but only 175 available with microarrays.
GSE39939	2014	Anderson <sup>6</sup>	GPL10558	Validation	Kenya	Children	Positive and negative	Positive and negative	..	14	64	44 negative, 35 positive	..	157	Other diseases breakdown: 33 pneumonia, 5 sepsis, 7 malnutrition, 19 other
GSE39940		Anderson <sup>6</sup>		Validation	Malawi, South Africa	Children	Positive and negative	Positive	..	54	169	111	..	334	Other diseases breakdown: 86 pneumonia, 8 CLD, 11 URI, 34 other infections, 12 malignancy, 18 other
GSE40553	2012	Bloom <sup>9</sup>	GPL10558	Validation	South Africa, UK	Adults	Negative	Positive	..	..	..	36	130	166	Treatment measured at 0.5, 2, 4, 6, and 12 months. Two cohorts followed. Latent tuberculosis not used; overlaps with GSE19491
GSE41055	2013	Verhagen <sup>10</sup>	GPL5175	Validation	Venezuela	Children	Negative	Positive and negative	9	9	..	7 negative; 2 positive	..	27	..
GSE42834	2014	Bloom <sup>9</sup>	GPL10558	Discovery	UK, France	Adults	Negative	Positive	118	..	123	40	..	281	Other diseases breakdown: 83 sarcoidosis, 24 pneumonia, 16 cancer
GSE56153	2012	Ottenhoff <sup>23</sup>	GPL6883	Validation	Indonesia	Adults	Negative	Positive	18	..	..	18	35	71	Treatment measured at 8 and 28 weeks
GSE62147	2015	Tientcheu <sup>29</sup>	GPL6480	Validation	The Gambia	Adults	Negative	Positive	..	..	..	26	26	52	<i>M africanum</i> and <i>M tuberculosis</i>
GSE74092	2015	Maertzdorf <sup>12</sup>	RT-PCR array GPL21040	Validation	India	Adults	Negative	Positive	76	..	..	113	..	189	<i>KLF2</i> not present in these data

ASLE=adult systemic lupus erythematosus. PSLE=paediatric systemic lupus erythematosus. CLD=chronic lung disease. URI=upper respiratory infection.

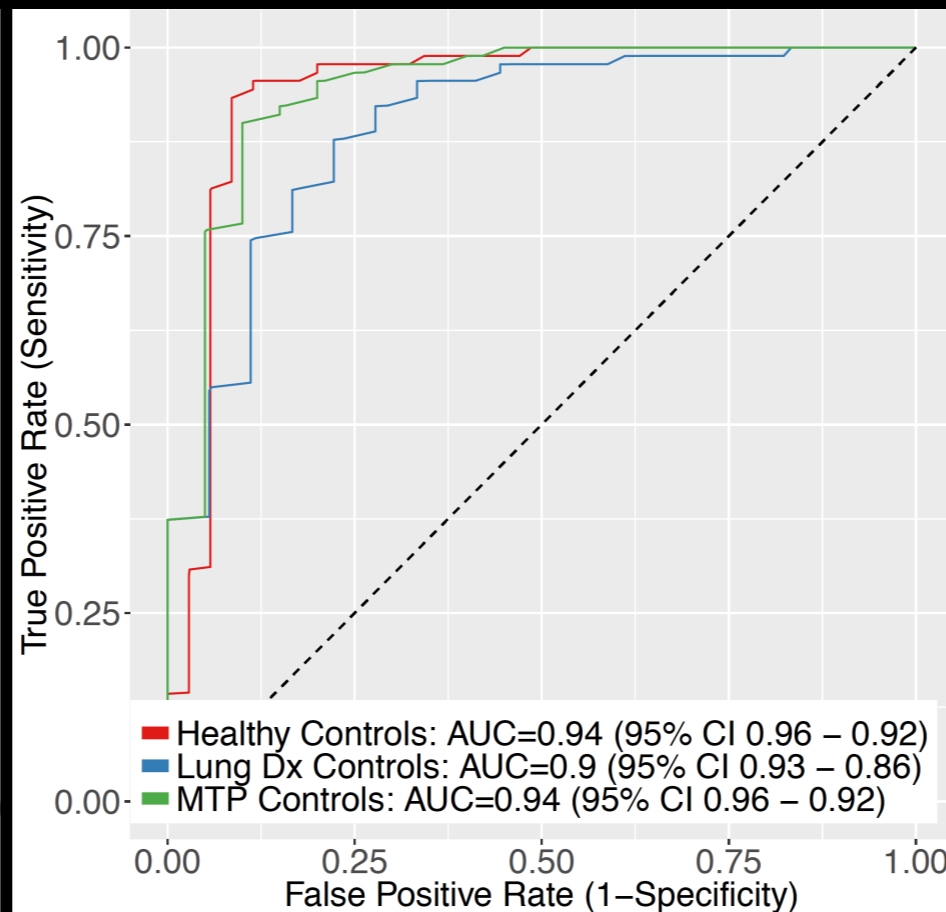
**Table:** Summary table of all datasets that matched inclusion criteria (whole blood, clinically active pulmonary tuberculosis)



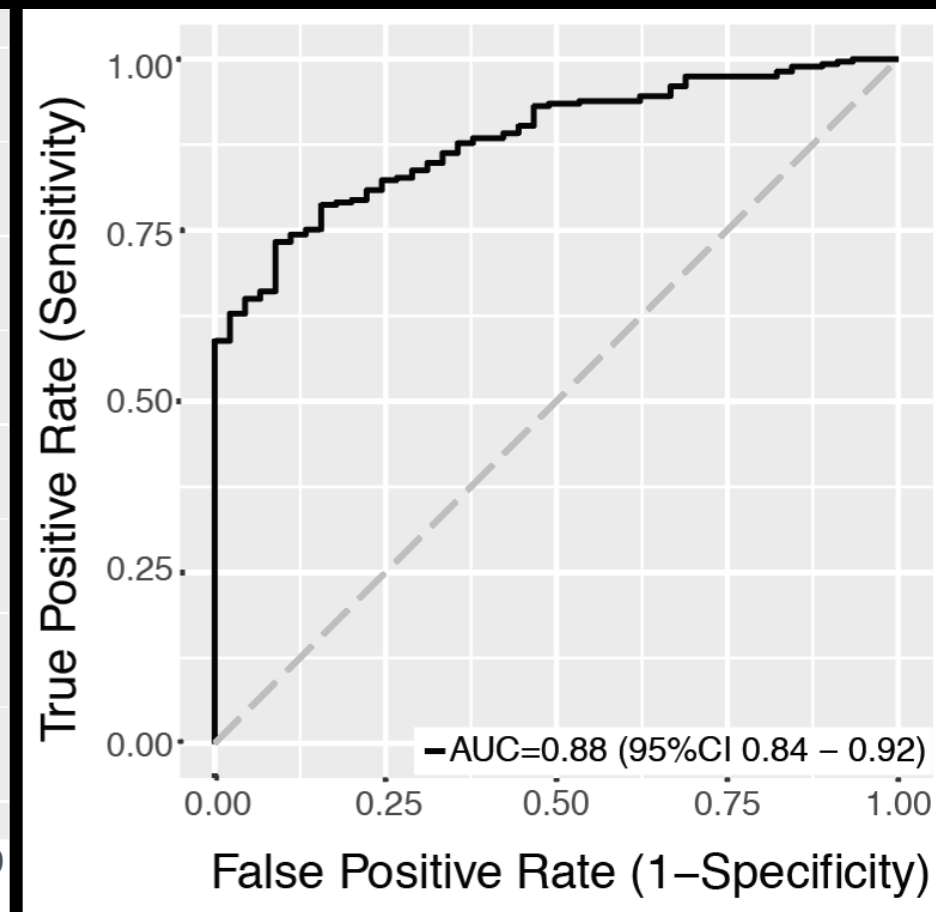
# 3-gene signature distinguishes ATB in prospective cohorts



Zak et al. *Lancet* 2016  
Adolescents  
LTB vs ATB  
RNAseq

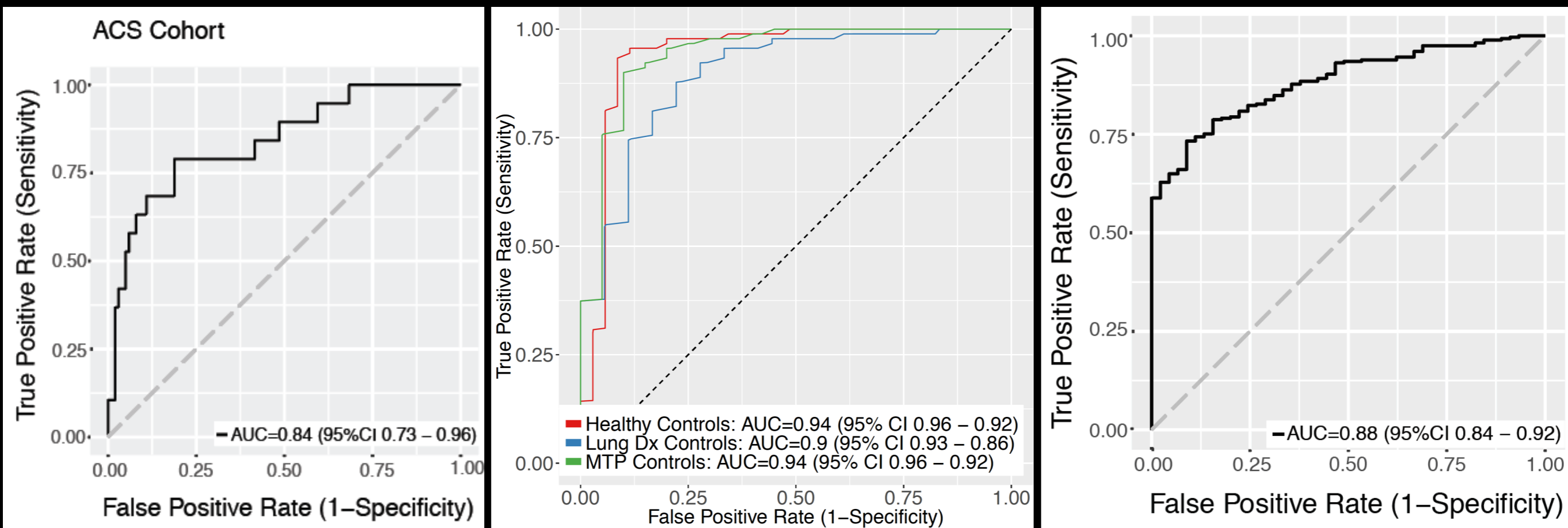


Zak et al. *Tuberculosis* 2017  
Adults  
ATB vs controls  
RNAseq



Warsinske et al.  
Active screen in adults  
ATB vs controls  
PCR

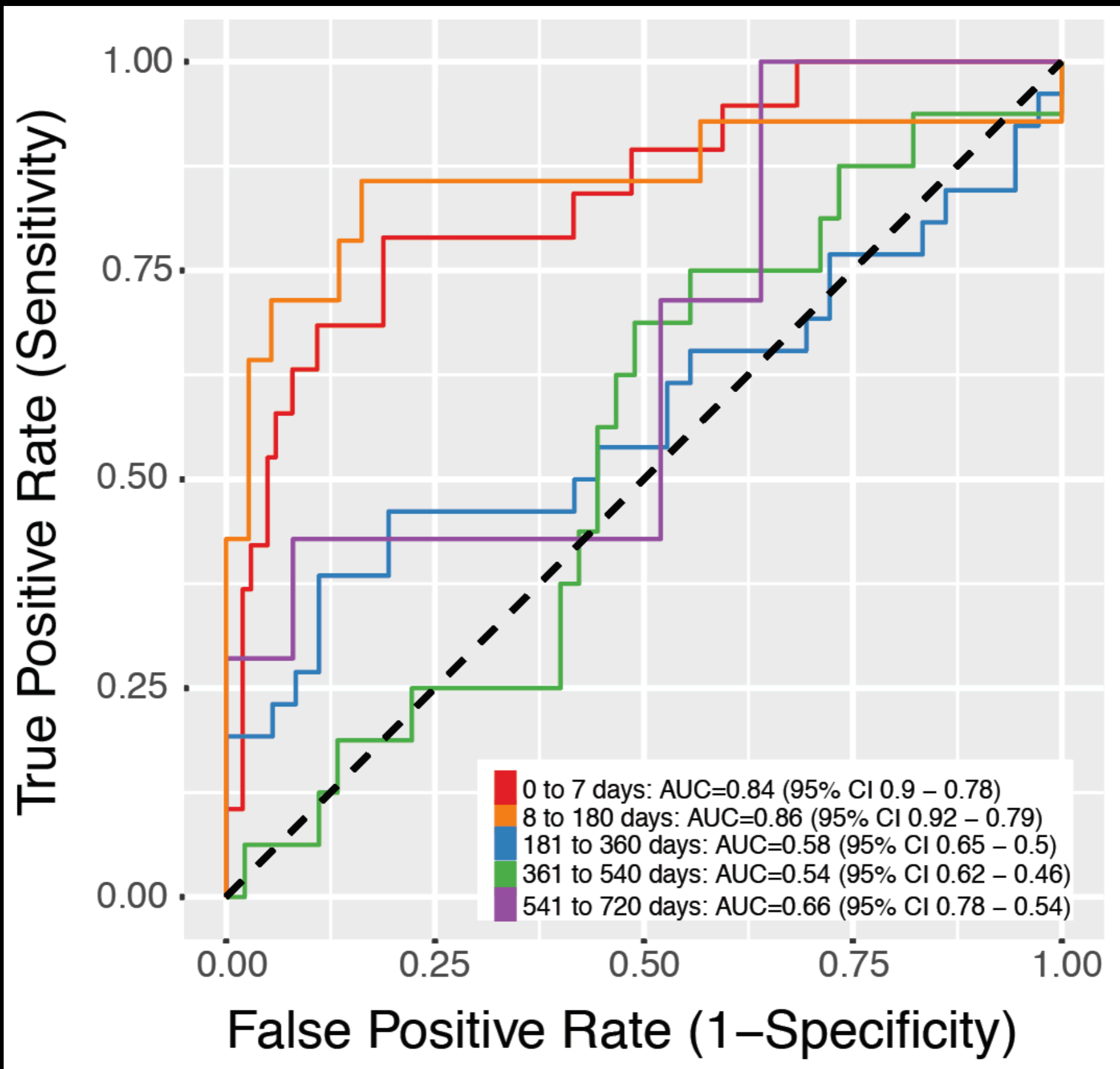
# 3-gene signature distinguishes ATB in prospective cohorts



**Table 3** Maximized sensitivity values obtained from the ROC analysis of *GBP5*, *DUSP3* and *KLF2* combinations in WB cohort test. *Francisco et al. J of Infection 2017*

	<i>GBP5</i>	<i>DUSP3</i>	<i>KLF2</i>	<i>GBP5,DUSP3</i>	<i>GBP5,KLF2</i>	<i>DUSP3,KLF2</i>	<i>GBP5,DUSP3,KLF2</i>
<b>ATB vs HC</b>							
AUC	0.85	0.73	0.62	0.84	0.86	0.77	0.85
95%CI	0.81-0.90	0.67-0.78	0.56-0.68	0.80-0.89	0.82-0.91	0.72-0.82	0.81-0.89
Sensitivity	80.6%	61.8%	31.3%	77.8%	77.8%	66.0%	85.5%
Specificity	90.9%	78.0%	96.7%	89.5%	87.1%	82.3%	70.8%

# 3-gene signature predicts progression from LTB to ATB



# Where we are today



Image courtesy:  
Chloe McDougall

# Where we are today



# Where we want to go



Image courtesy:  
Chloe McDougall

# Where we are today



Better  
metadata

# Where we want to go



Image courtesy:  
Chloe McDougall

# Where we are today



Better  
metadata

# Where we want to go

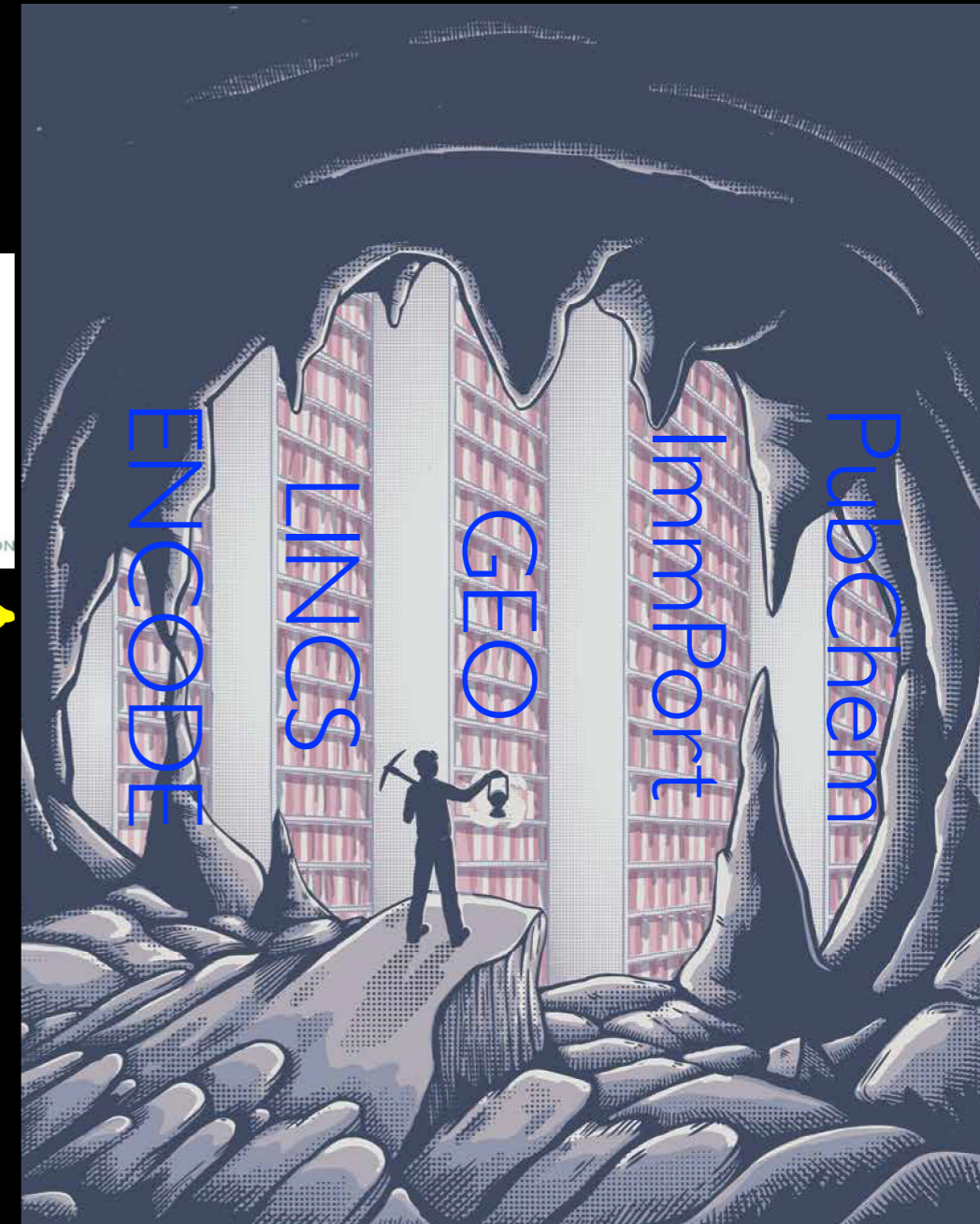
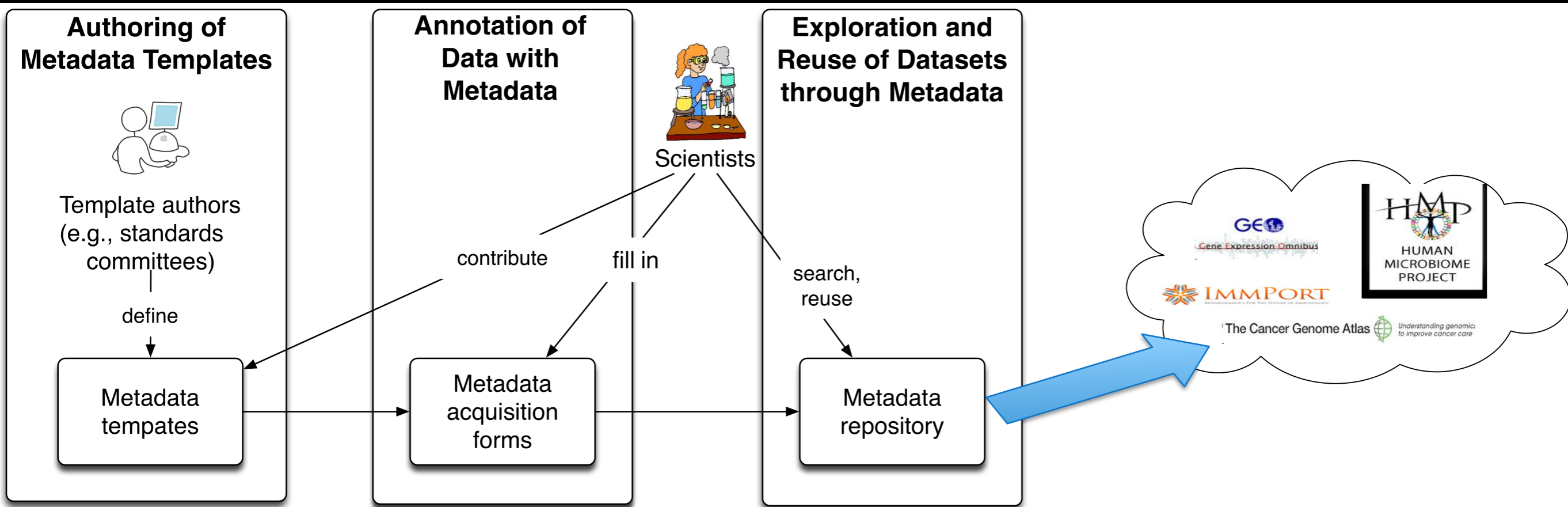


Image courtesy:  
Chloe McDougall

# The CEDAR approach to better metadata



- Template editor
- Metadata editor
- Metadata repository

Courtesy: Mark Musen

# Summary

- Heterogeneity: a blessing in disguise
- Leverage biological and technical heterogeneity
  - Increase reproducibility
  - Accelerate translational medicine
- “Data reproducibility” versus “reporting reproducibility”
- Need for better metadata
  - CEDAR



# Acknowledgements

Khatri Lab  
 Tim Sweeney  
 Shane Lofgren  
 Marta Andres-Terre  
 Winn Haynes  
 Michele Donato  
 Steven Schaffert  
 Francesco Vallania  
 Erika Bongen  
 Aurelie Tomczak  
 Ravi Shankar  
 Tej Deepak Azad  
 Brandon Turner  
 Matthew Daniel Li  
 Madeleine Scott  
 Andrew Liu  
 Lindsay Braviak  
 Caroline Braviak

SIMR students  
 Andrew Tam  
 Charles Liu  
 Sophia Luo  
 Jeffrey Cheng  
  
 PJ Utz  
 Alex Kuo  
 Peggie Cheung  
  
 Shirit Einav  
 Yuan Jin Tan  
 Elena Bekerman  
  
 Mark Davis  
 Cristina Tato  
 Helen McGuire  
  
 Nigam Shah  
 Katie Quinn

## Clinical collaborators

Jason Andrews	Lyle Moldawer
Julio Croda	Hector Wang
Benjamin Tang	Patrick Carroll
Angela Rogers	Gabriel Escobar
Ashham Mansur	Jeffrey Freeman

