

The National Precision Medicine Strategy in Singapore: Securing Public and Community Trust for data sharing

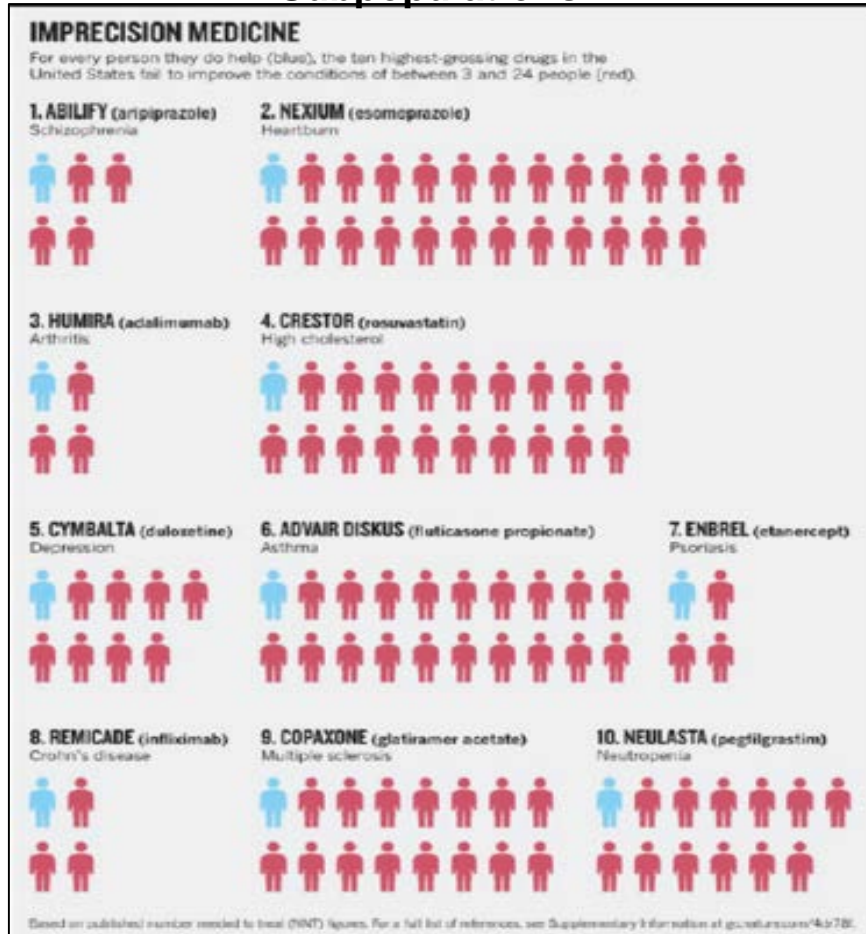
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National University of Singapore

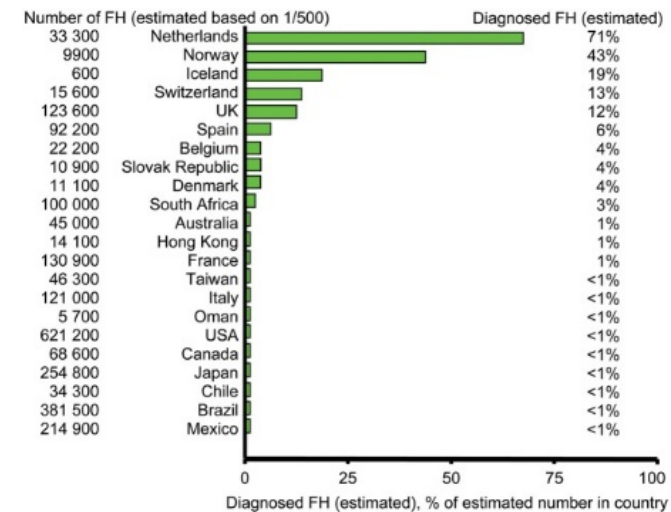
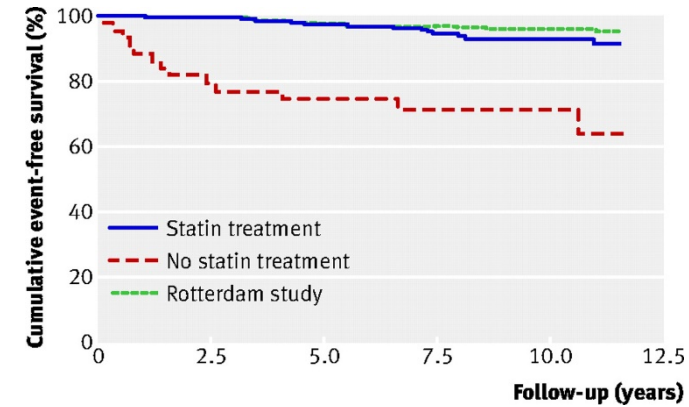
Why Precision Medicine?

A Need for New Clinical Paradigms

Most Treatments Benefit or Harm Subpopulations



Some patients who would benefit from treatment are not being treated

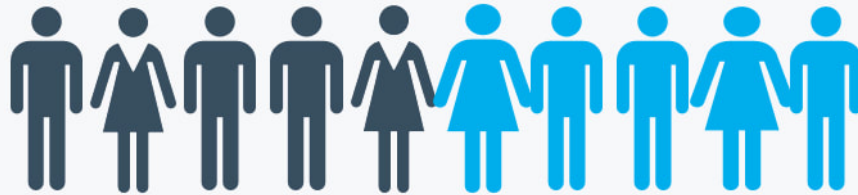


A Need for New Therapies

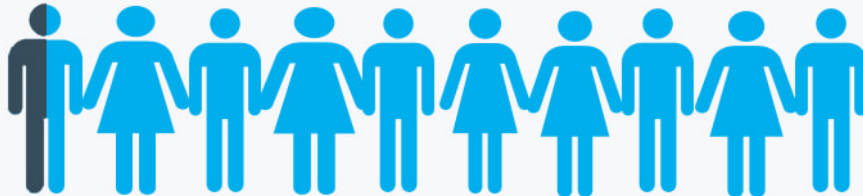
THE PROBLEM



10%
OF US POPULATION
AFFECTED BY A RARE
DISEASE
~30 Million in the US



50%
OF THOSE AFFECTED BY A
RARE DISEASE ARE
CHILDREN



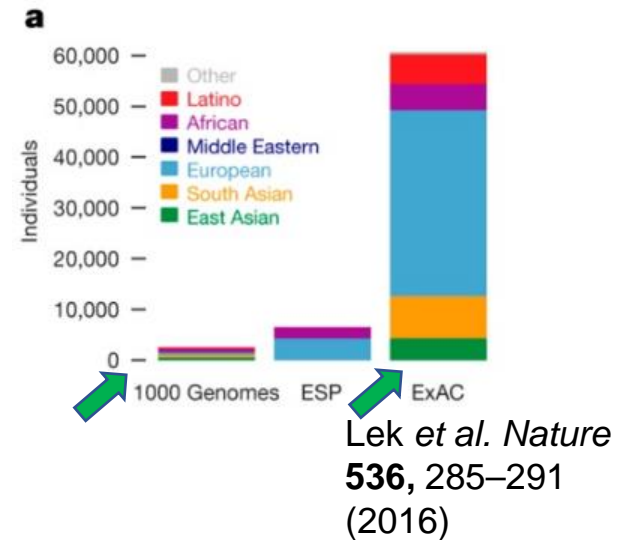
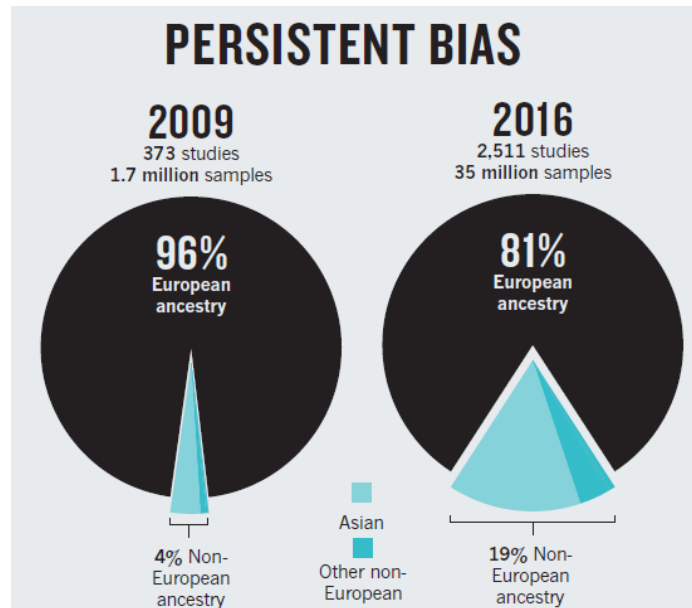
95%
AFFECTED BY A RARE
DISEASE HAVE NO FDA
APPROVED DRUG
TREATMENT

Why Asia?

A Global Missing Gap : Asian Genomic Data

Having trouble finding Chinese genomic data?

Charlotte Whicher | 08 September 2016 | Product, Team Blog Post, Data Collection, Chinese Control Data, Repository, The China Kadoorie Biobank, The Singapore Genome Variation Project, GigaDB, GigaScience, Beijing Genomics Institute, Genome Asia 100K



Genetic Misdiagnoses and the Potential for Health Disparities

Arjun K. Manrai, Ph.D., Birgit H. Funke, Ph.D., Heidi L. Rehm, Ph.D., Morten S. Olesen, Ph.D., Bradley A. Maron, M.D., Peter Szolovits, Ph.D., David M. Margulies, M.D., Joseph Loscalzo, M.D., Ph.D., and Isaac S. Kohane, M.D., Ph.D.

NEJM, 2016

Diseases that manifest differently in Asians

Disease Risk Factors and Asian Diversity



Chinese

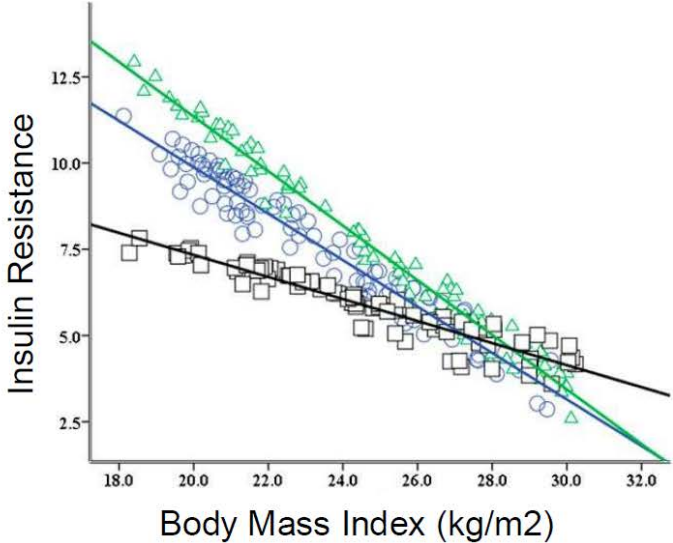


Malay



Indian

Impact of obesity on insulin resistance is stronger in Chinese and Malay populations



Chin Meng Khoo et al. (2014) Diabetes

Diseases that are only seen in Asians

© American College of Medical Genetics and Genomics

ARTICLE | Genetics
inMedicine

Corrected: Correction

Population genomics in South East Asia captures unexpectedly high carrier frequency for treatable inherited disorders

Table 2 Summary of pathogenic variants detected

Disease name	Gene	Transcript	Genomic coordinates (hg19)	Gene change	AA change	Number of carriers	SEC/ExAC_All	SEC/ExAC_EAS
Citrin deficiency	SLC25A13	NM_014251.2	Chr7:95818684delCATA	c.852_855delTATG	p.M285fs	12	24.07	1.95
			Chr7:95822344C>T	c.615+5G>A	splicing	4	24.24	1.15
			Chr7:95751240insCCCCGGG	c.1663_1664insGAGATTA	p.A555fs	3	19.92	1.39
			CAGCCACCTGTAATCTC	CAGGTGGCTGCCCGGG				
Wilson disease	ATP7B	NM_000053.3	Chr7:95822471G>A	c.493C>T	p.Q165X	1	NA*	NA*
			Chr13:52532469C>A	c.2333G>T	p.R778L	5	15.04	NA*
			Chr13:52520508G>A	c.2351C>T	p.T784M	2	0.93	12.03
			Chr13:52544627C>A	c.1543+1G>T	splicing	1	NA*	NA*
Phenylketonuria	PAH	NM_000277.1	Chr12:103246714G>A	c.721C>T	p.R241C	3	18.05	1.39
Glutaric aciduria, type I	GCDH	NM_000159.3	Chr19:13010280A>C	c.1244-2A>C	splicing	3	24.70	1.83
Molybdenum cofactor deficiency	MOCS2	NM_002203.3	Chr5:52405544G>A	c.16C>T	p.Q6X	2	NA**	NA**
Methylmalonic acidemia with homocystinuria	MMACHC	NM_015506.2	Chr1:45974001C>T	c.394C>T	p.R132X	1	6.05	NA**
			Chr1:45974520G>A	c.482G>A	p.R161Q	1	6.02	6.02
Methylmalonic aciduria	MUT	NM_000255.3	Chr6:49409685C>T	c.1677-1G>A	splicing	1	73.16	6.03
			Chr6:49425427->AA	c.729_730insTT	p.D244fs	1	36.03	3.03
Biotinidase deficiency	BTD	NM_000060.4	Chr3:15686120C>T	c.757C>T	p.P253S	1	NA*	NA*
Aceruloplasminemia	CP	NM_032383.4	Chr3:148927953C>	c.607+1delG	splicing	1	24.36	2.01
PTS deficiency	PTS	NM_000317.2	Chr11:112103928G>A	c.286G>A	p.D96N	1	NA*	NA*
Segawa syndrome	TH	NM_000207.2	Chr11:2189135C>T	c.605G>A	p.R202H	1	6.02	6.02
Alpha Mannosidosis	MAN2B1	NM_000528.3	Chr19:12759988C>G	c.2398G>C	p.G800R	1	NA*	NA*
Holocarboxylase synthetase deficiency	HLC5	NM_000411.6	Chr21:38308963C>	c.782delG	p.G261fs	1	25.11	2.08
TOTAL						46		

AA amino acid; SEC Singapore Exome Consortium; ExAC Exome Aggregation Consortium

* Allele count not available in ExAC

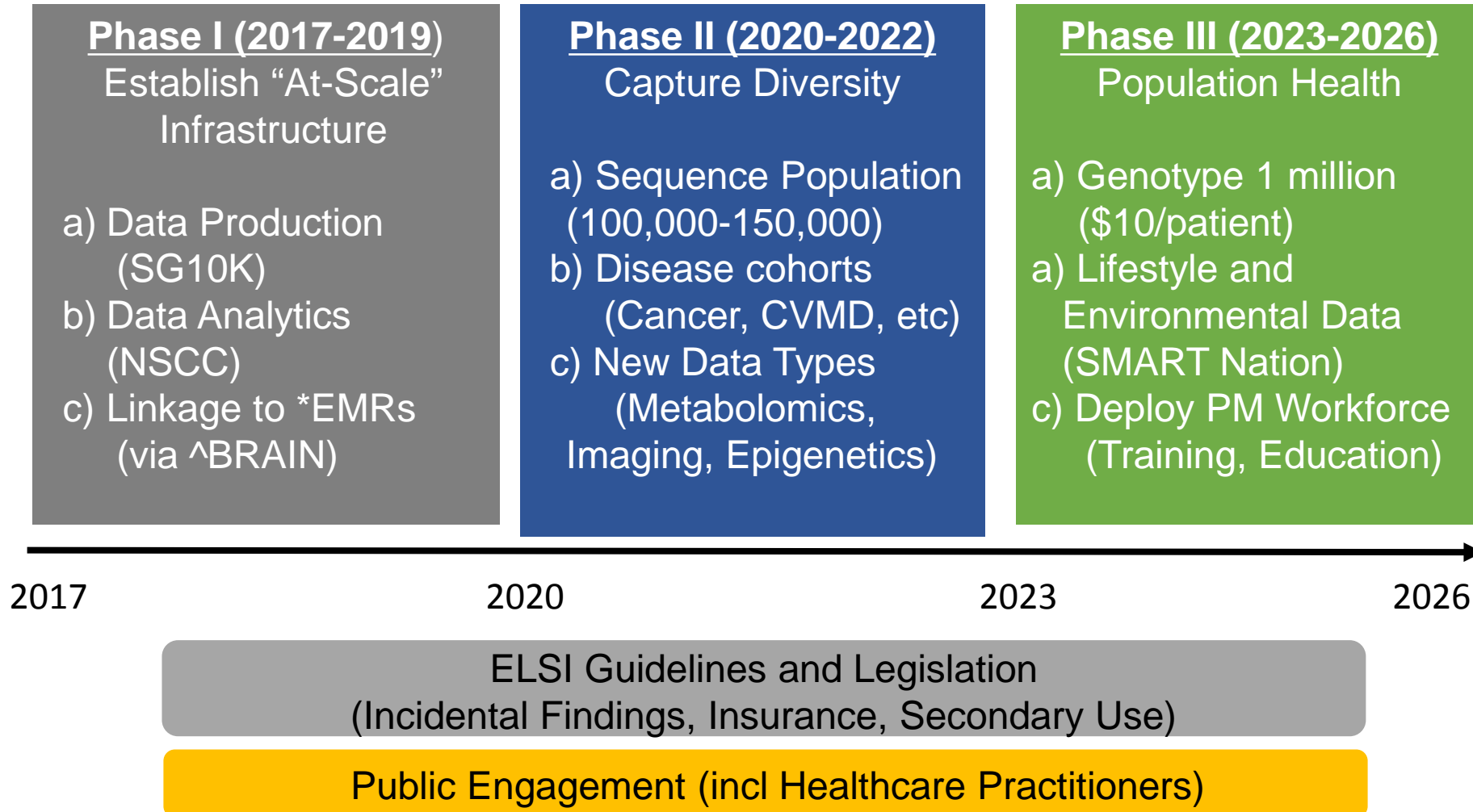
** Allele count = 0 in ExAC

10-year Singapore Precision Medicine Roadmap

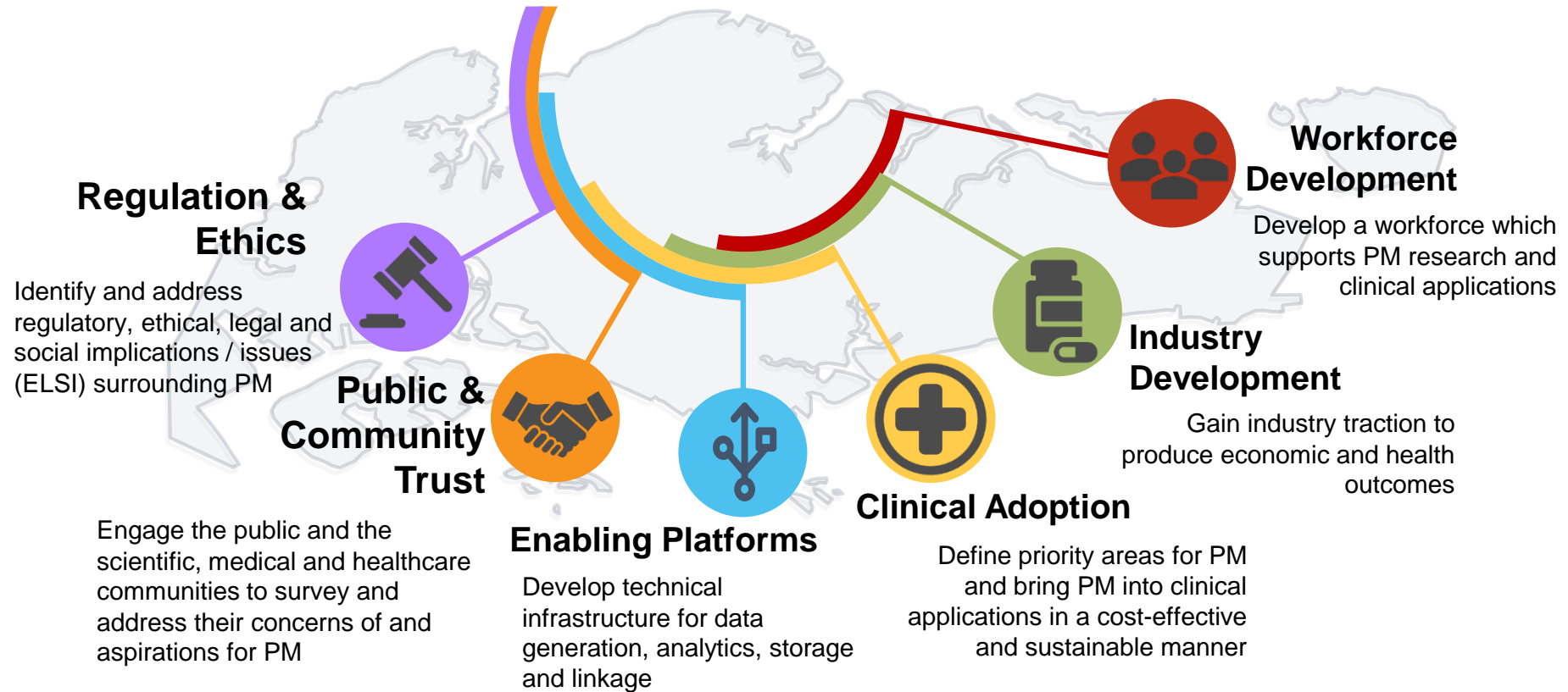
Real-time Genomic-Clinical Data Vault of 1,000,000 Singaporeans

Three Phases : Term-Limited, with Clear Go/No-Go Milestones

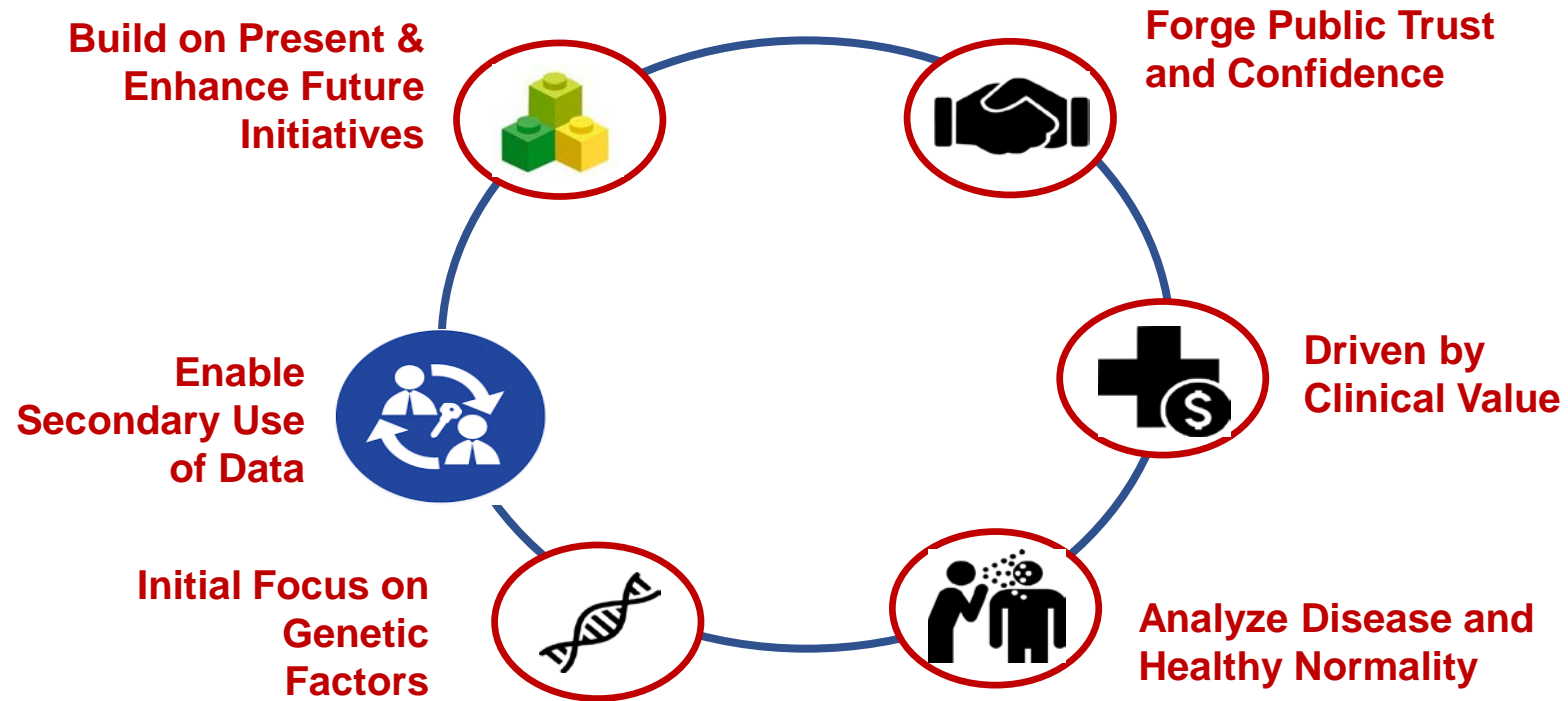
Endorsed by HBMS IAC, RIEC (Non-Ministerial), NRF SAB



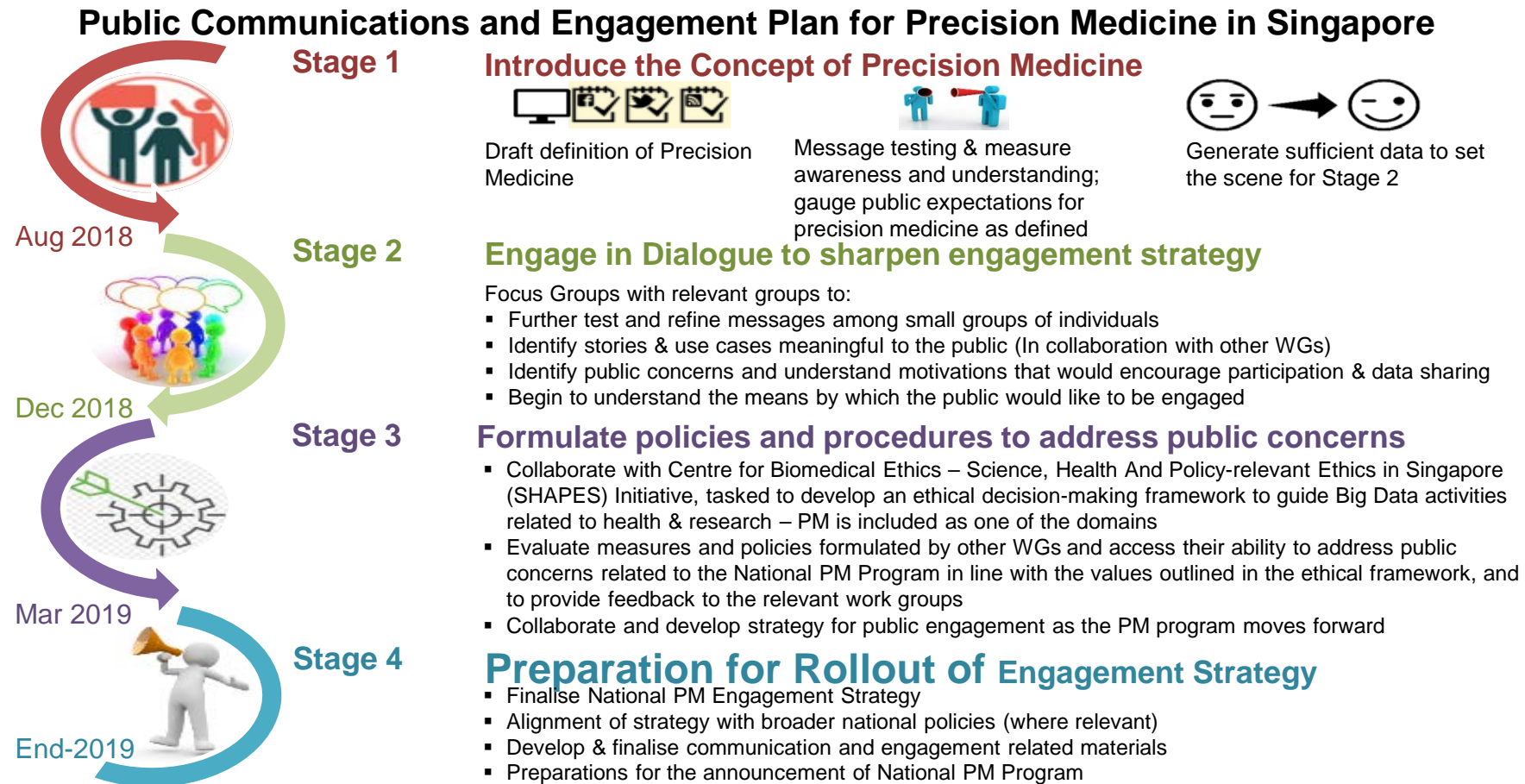
NATIONAL PRECISION MEDICINE STEERING COMMITTEE- WORKGROUPS



National Precision Medicine-Guiding Principles



Public and Community Trust Workgroup Roadmap



Public Concerns towards Precision Medicine



Survey Participants interviewed @Singapore Science Centre

- Educators
- Student and Senior volunteers

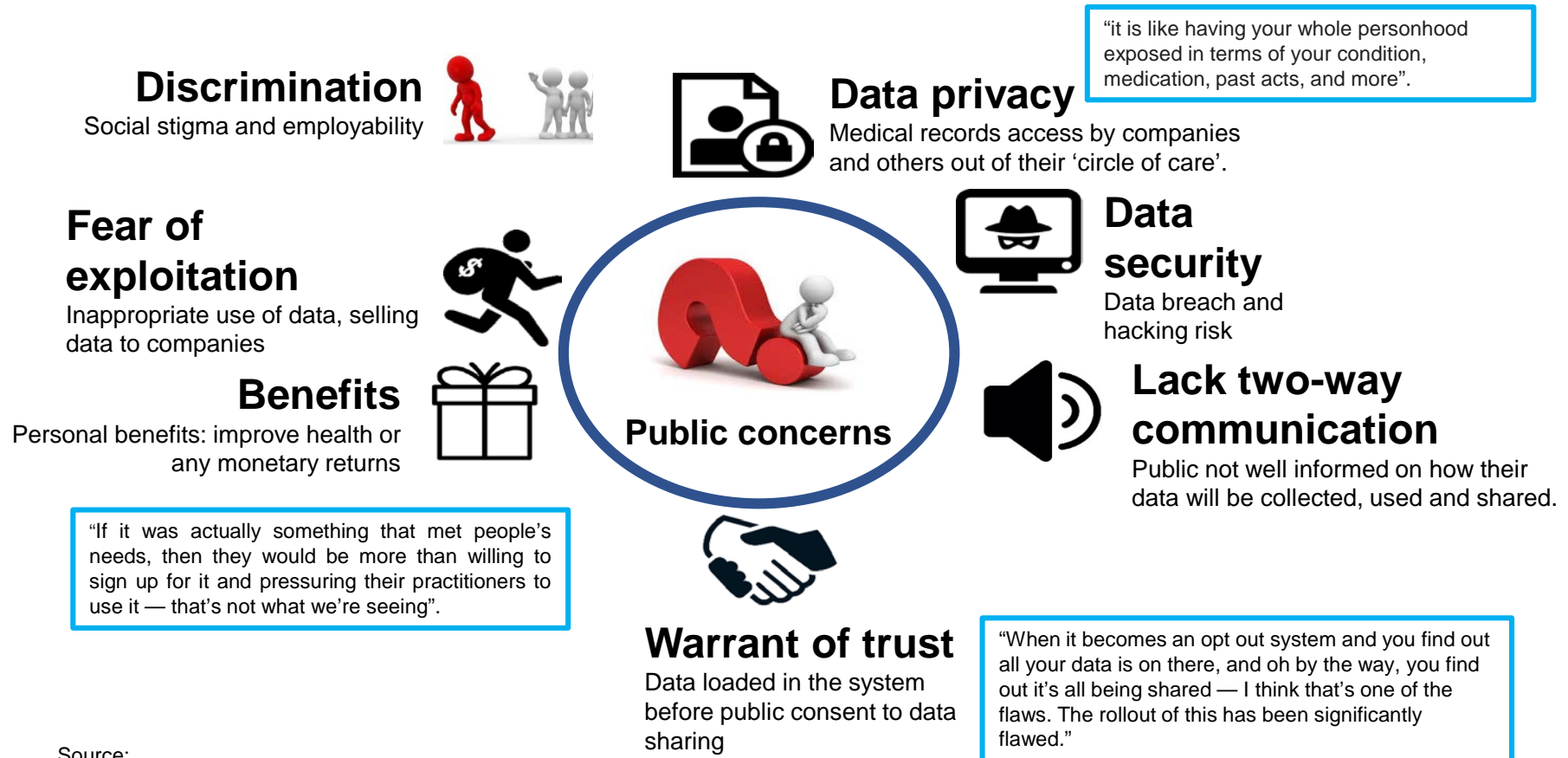


Public survey @Maker Faire (Tampines Hub)

Top Concerns (examples):

- **Affordability:** *“Precision medicine sounds expensive, like Chatterbox chicken rice versus Kopitiam chicken rice.”*
 - Is sequencing to prevent disease more cost-effective than funding resources to encourage healthy lifestyles?
- **Personal benefit:** *“What’s in it for me?”*
 - Would they get money, discounted/free treatment, or preferred access to precision medicine when it’s available?
- Insurance companies and employers using information for discrimination
- Privacy and security of data: How would information be processed/kept?

Public Concerns on Contributing Data to National Platforms



Source:
P&CT WG, Care.data, My Health Record, and Your DNA, Your Say

Ethics of data use

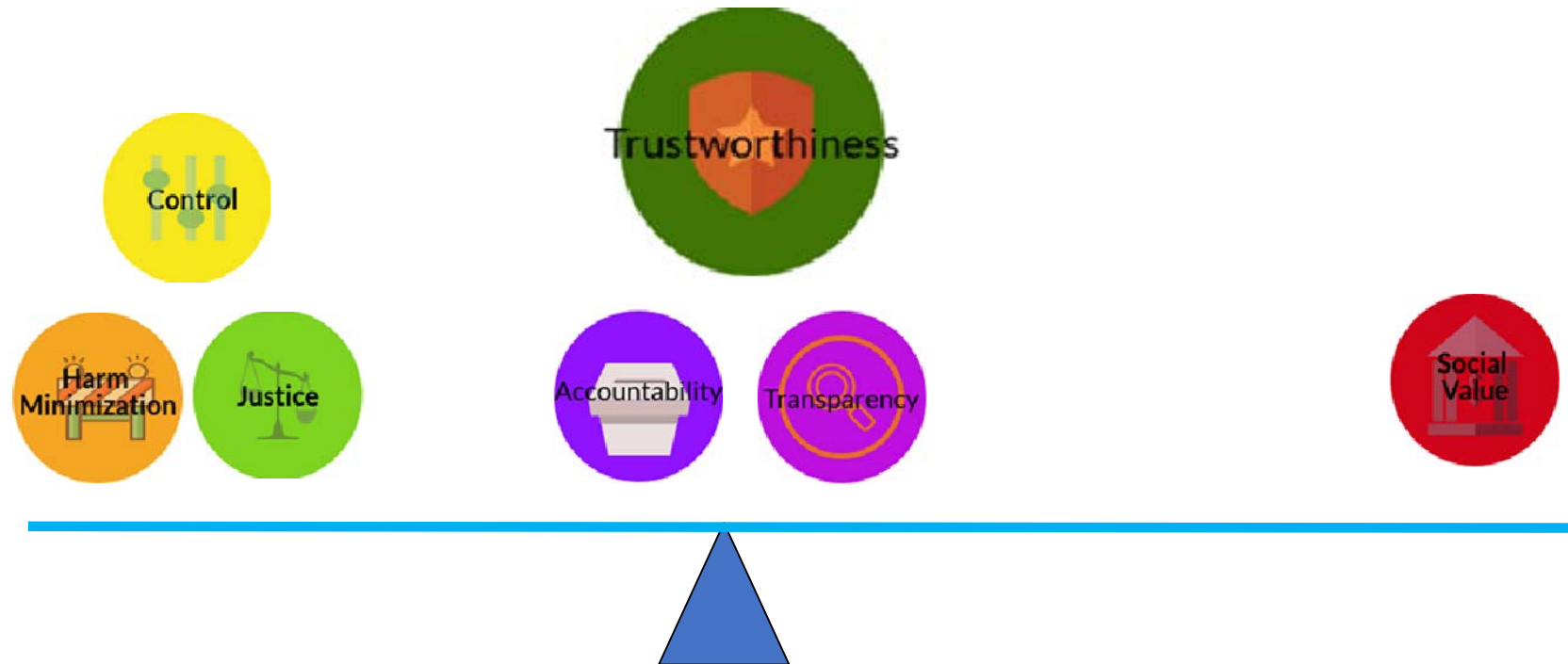


From: Where is the human in the data? A guide to ethical data use

Gigascience. 2018;7(7). doi:10.1093/gigascience/giy076

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Balancing our values



Our Survey Pool

300 attendees of Science Festival satellite events and One-North Festival



Makers Faire

- Science/tech inventions and crafts at **Tampines Hub**
- Public – students, parents, visitors to mall
- 10,000 attendees over 3 days
- 62 surveys (makers & public who paid \$10 for Makers Faire entry)



Science Buskers

- Science/tech demonstrations at **Plaza Singapura**; competition
- Public – students, parents, visitors to mall
- 20,000 attendees over 2 days (free admission)
- 106 surveys (almost all students, parents, attendees of Buskers)

Case Studies

Please read the description of genes below.

Genes carry the codes that determine how our bodies function, the way we look and how we behave. Changes in the codes (gene variants) can cause disease, or determine how we respond to drugs or other things in our environment (food, exercise, toxins). Gene variants can be passed down from parents to children. Understanding how gene variants cause disease allows us to diagnose diseases, develop new drugs or choose the right drug or the right patient to maximize benefits and minimize side effects. The following are some examples of how this might occur.

Please read the case study, which is based on actual patient cases, then answer questions 1 and 2.

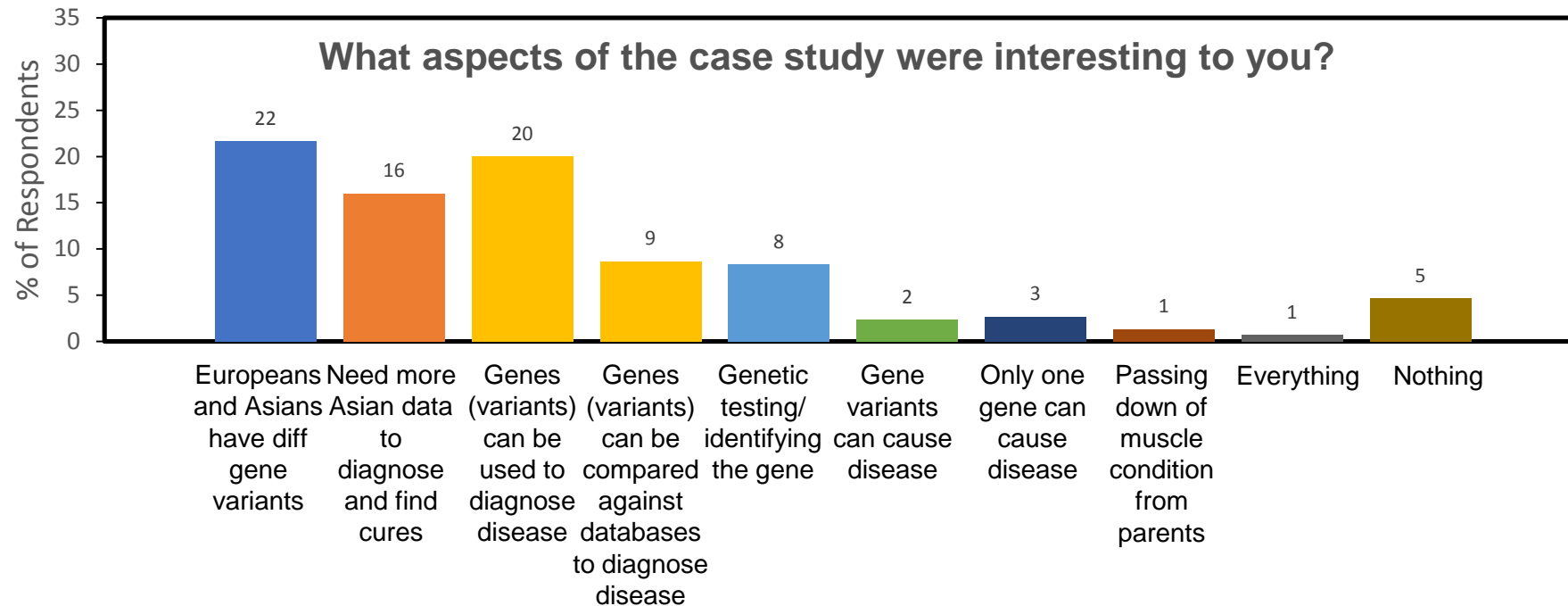
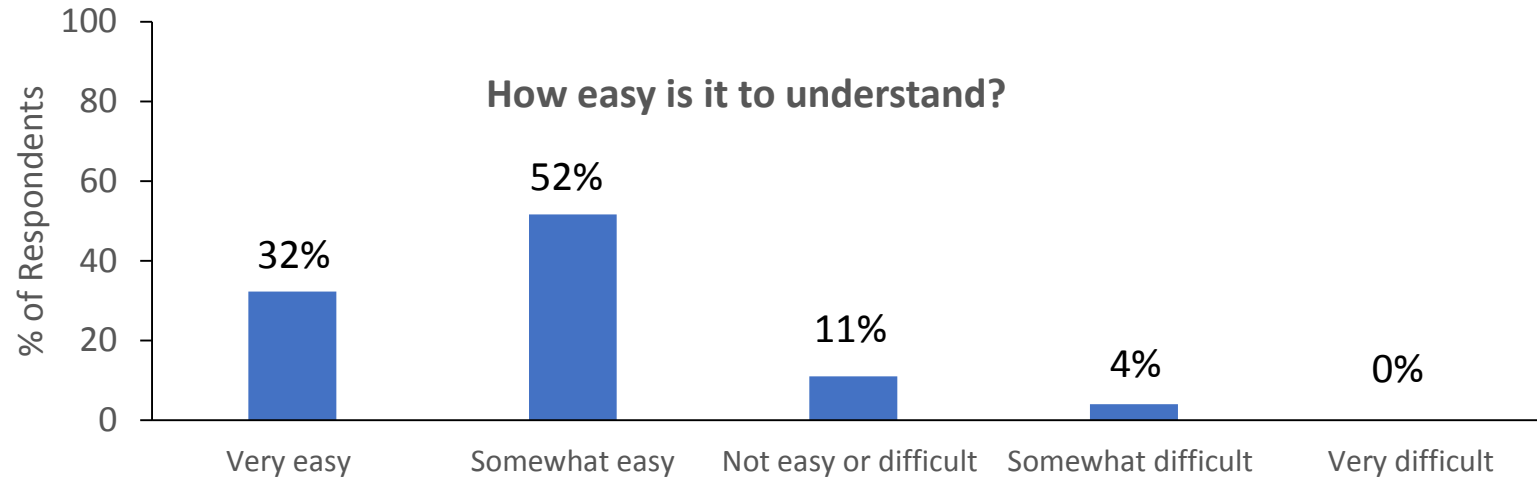
Case Study 1: Using Genetic Testing to Find an Elusive Diagnosis

Access to data from Asian individuals can help diagnose rare genetic conditions in children. It helped the parents of Clara, 3, finally discover the cause of their daughter's severe breathing problems.

After many negative tests, Clara's doctor decided to try genetic sequencing. The test was performed on a blood sample from Clara. It revealed many gene variants, but only one was causing her disease. By comparing Clara's variants against databases containing thousands of genes from many people, Clara's doctor eliminated the variants that were also in healthy people. But he was stuck after that because the databases were mainly of European people.

Fortunately, he knew researchers who were studying Asian patients. With their help, he found a variant in Clara that was also in another person with similar symptoms. He diagnosed Clara with a rare genetic muscle condition, and started her on a medication to strengthen her muscles.

What We Found: How easy was the case to understand?



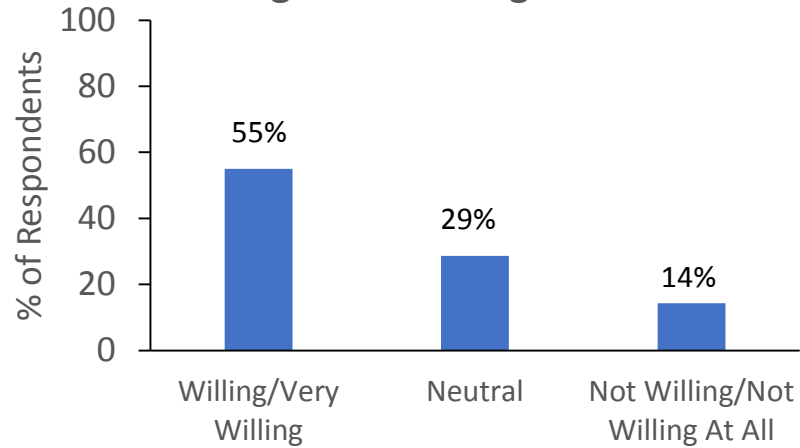
Explanation of a Potential Precision Medicine Program

What a Precision Medicine Program Could Involve

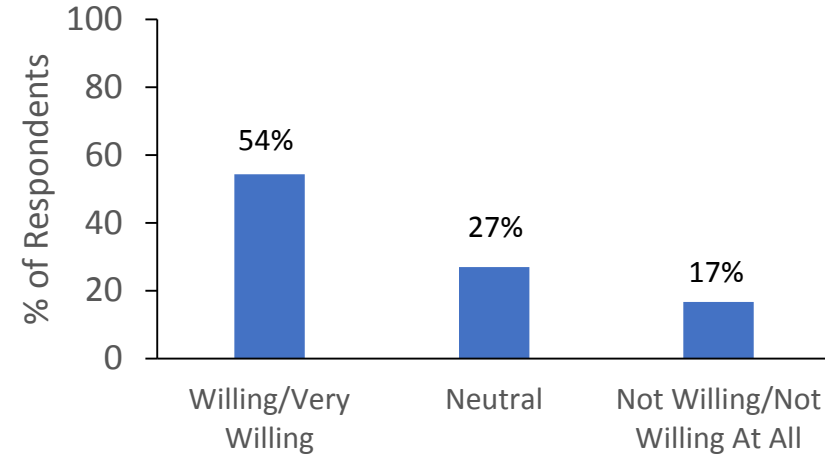
Since each individual is unique, doctors and scientists need access to genetic, medical and lifestyle data from a large number of individuals to understand how different individuals develop disease and respond to different treatments. This information will be stored in a database and will be as secure as your banking data. Doctors and scientists can access this anonymous information and use it to better prevent and treat diseases.

Willingness to Participate

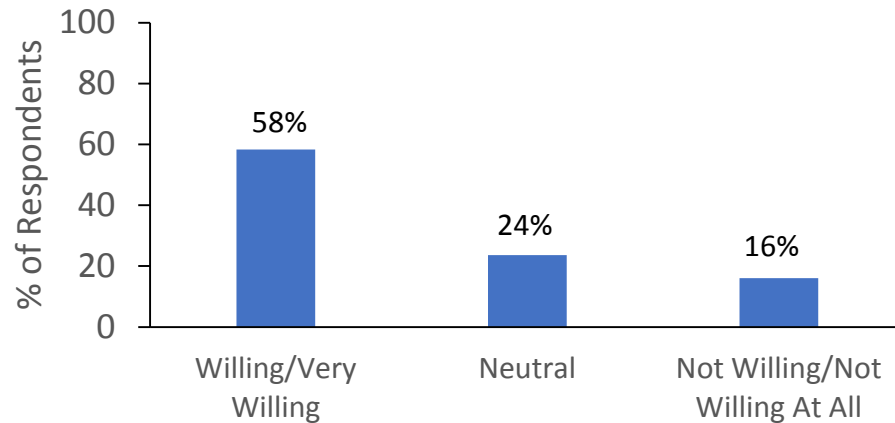
Provide a blood sample for genetic testing



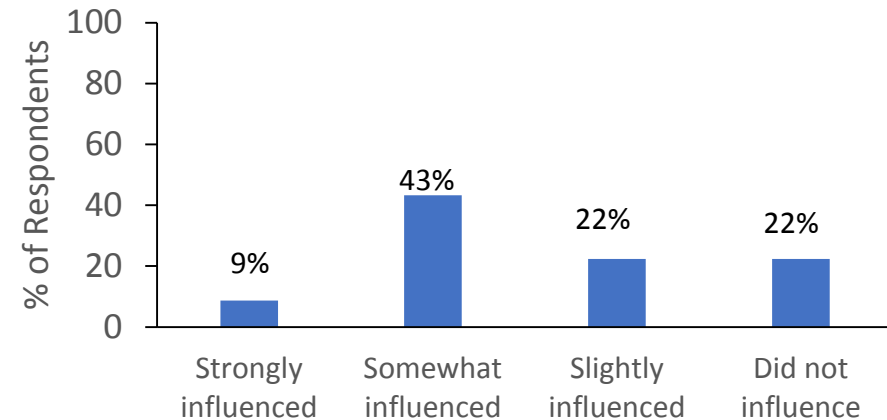
Access to anonymous medical records



Submit lifestyle data (diet, lifestyle, etc.) through questionnaires or mobile devices

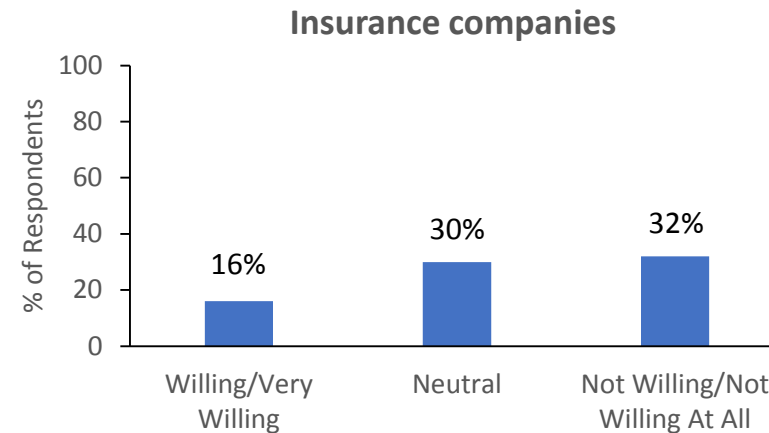
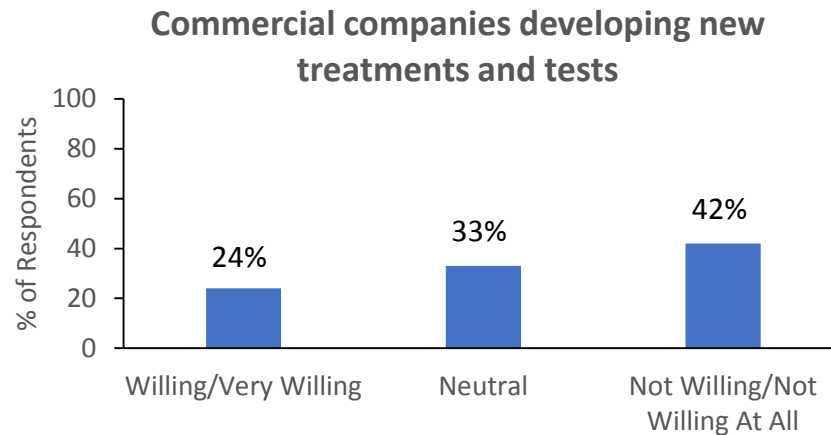
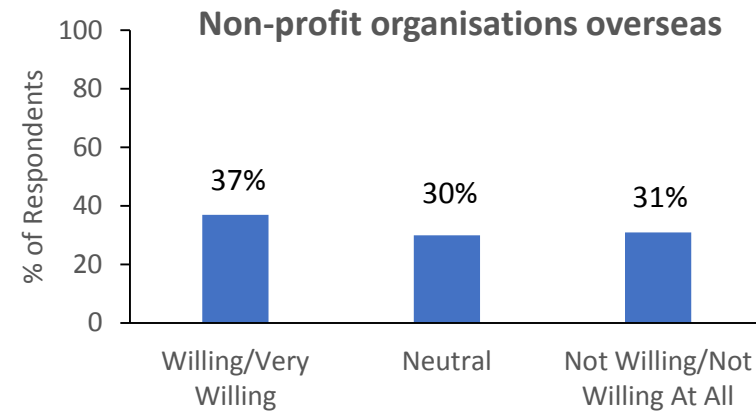
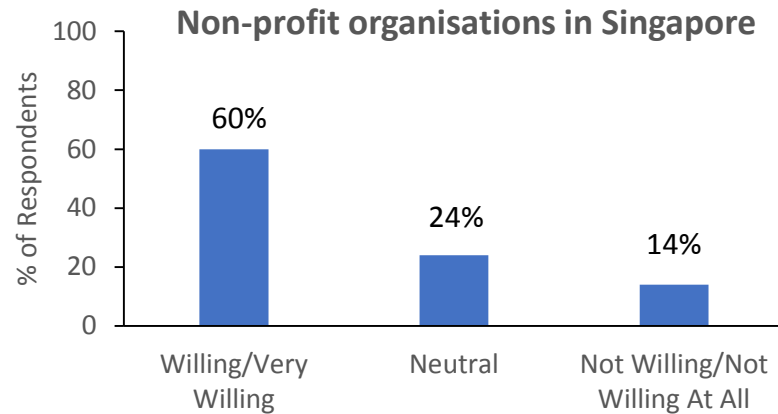


Did reading the case studies influence your willingness to participate?

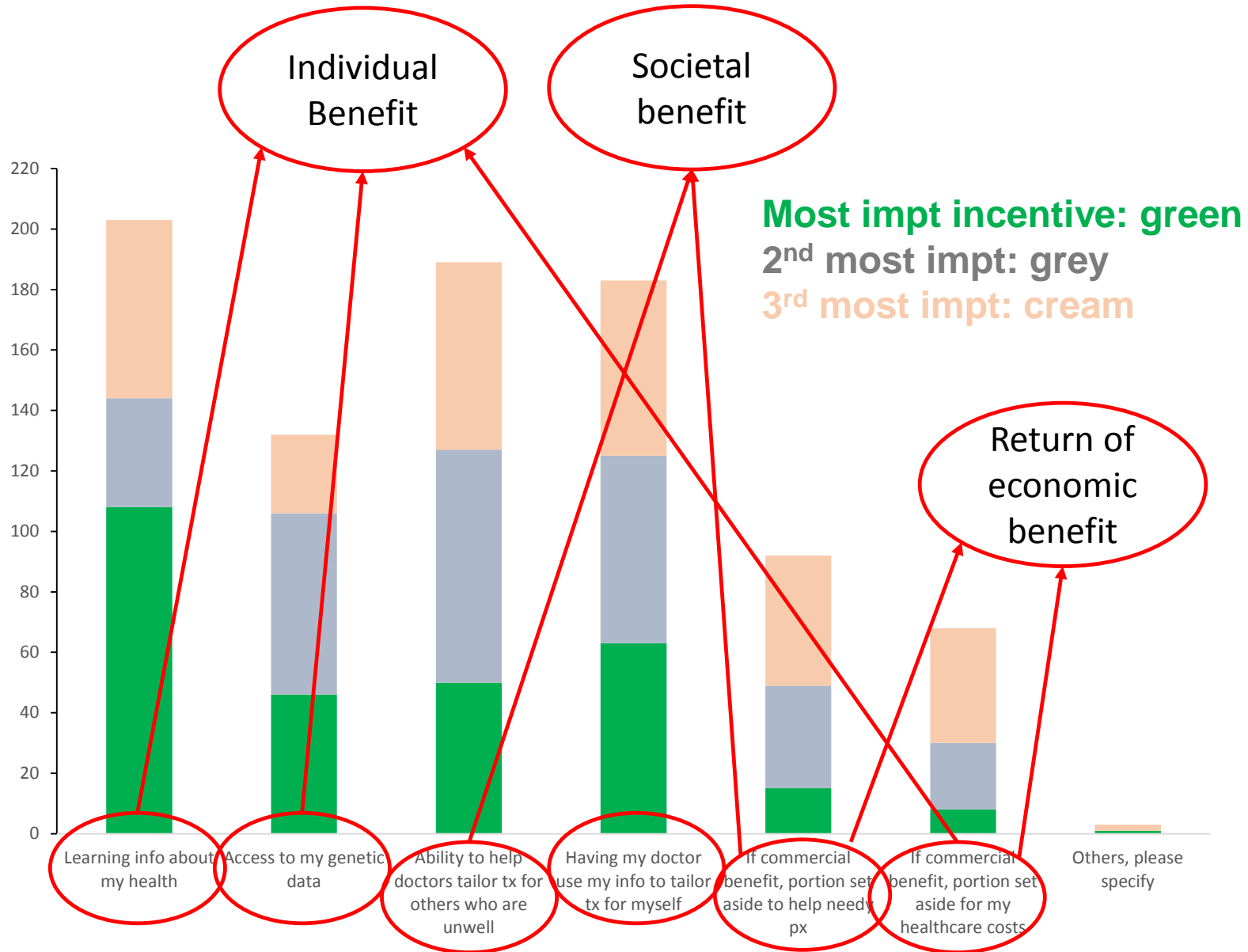


Willingness to Participate

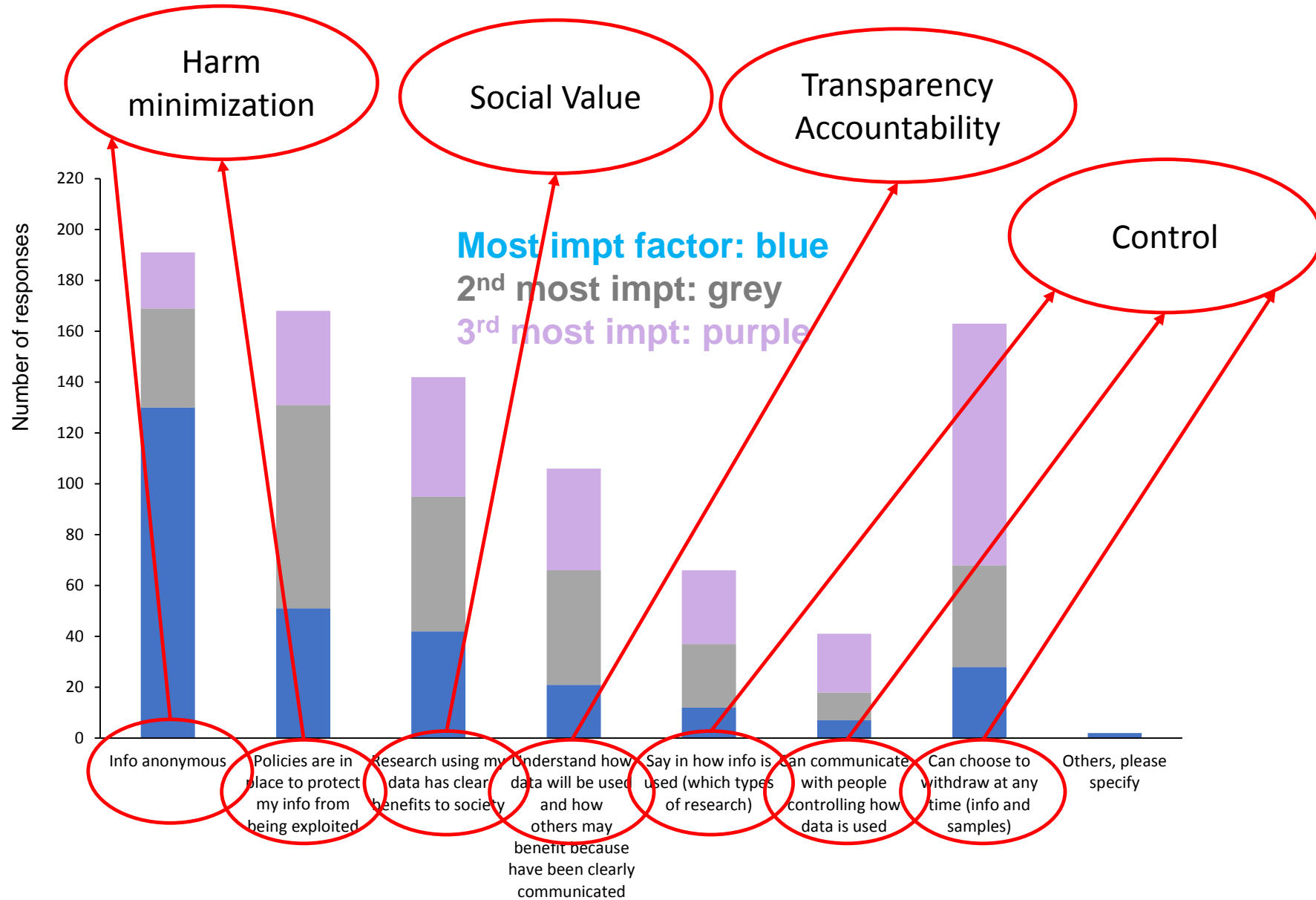
How willing would you be for **researchers from the following organisations** to access your anonymous information, including genetic and medical records?



Incentives For Participation



Factors Determining Participation



Genetic data may be inherently identifiable in today's environment

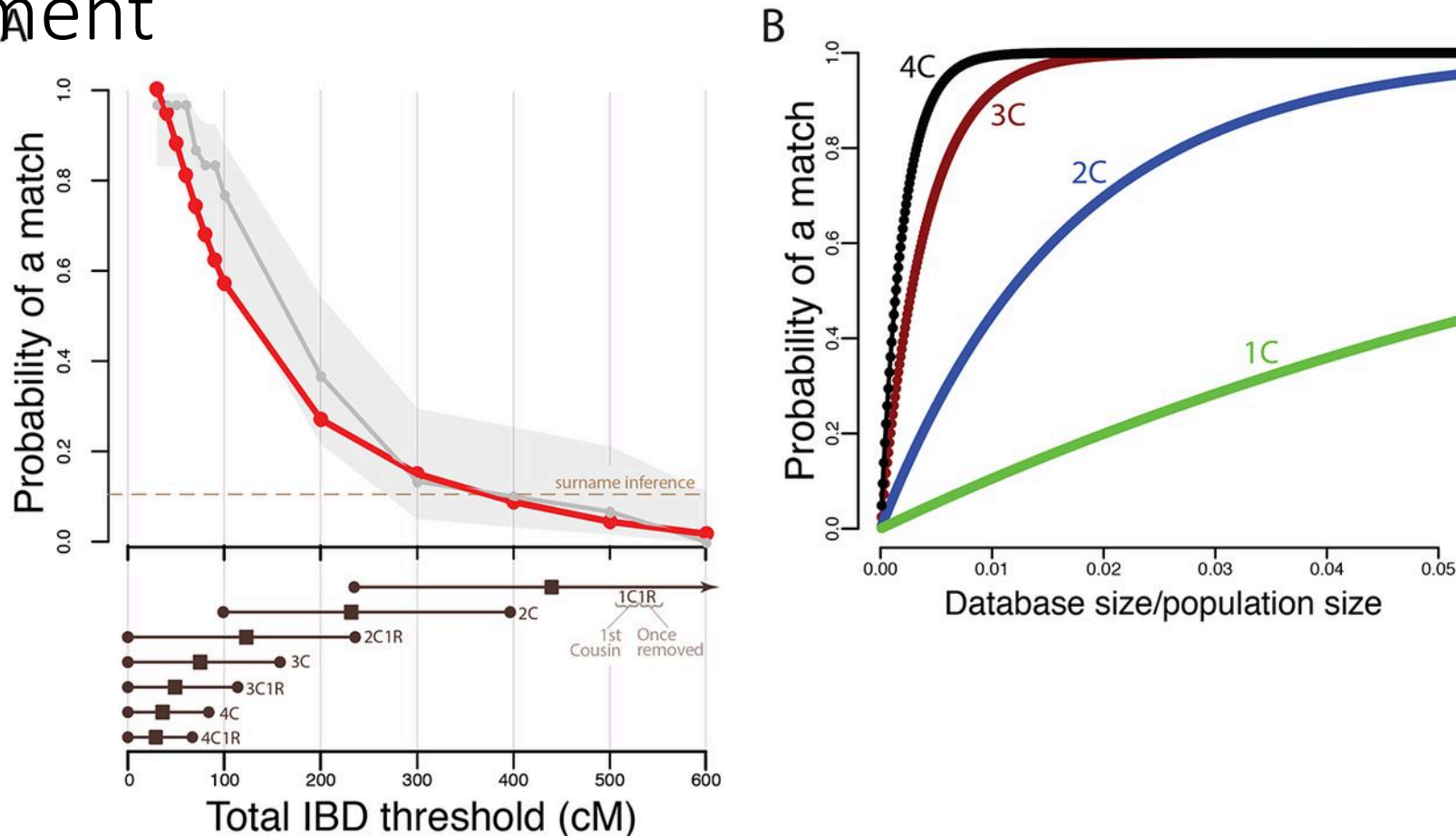


Fig. 1 The performance of long range familial searches for various database sizes.

Yaniv Erlich et al. *Science* 2018;science.aau4832



Key aspects of Public Trust and Engagement that are required for a successful program

Establishing a Social License

- Requires consistent messaging and engagement with the public and
 - Articulation of the benefits (societal/individual) of participation and manage the return of benefits
 - Stories Matter
 - Return of individual level data for healthcare
 - Articulation of the risks of participation and the steps taken to mitigate those risks
 - Risk of re-identification
 - Protection against discrimination

Governance and Data Access

- Policies and regulations need to be uniformly applied across data derived from multiple institutions
 - Ensure transparency and accountability
 - Who is using the data?
 - How is the data used?
 - Enable appropriate attribution of contributions and return of economic benefit
 - Allow for Co-governance (particularly by vulnerable populations) as a way to complement Consent

Security and Access Control

- Data security Framework
- encryption

Current & Proposed Capabilities

