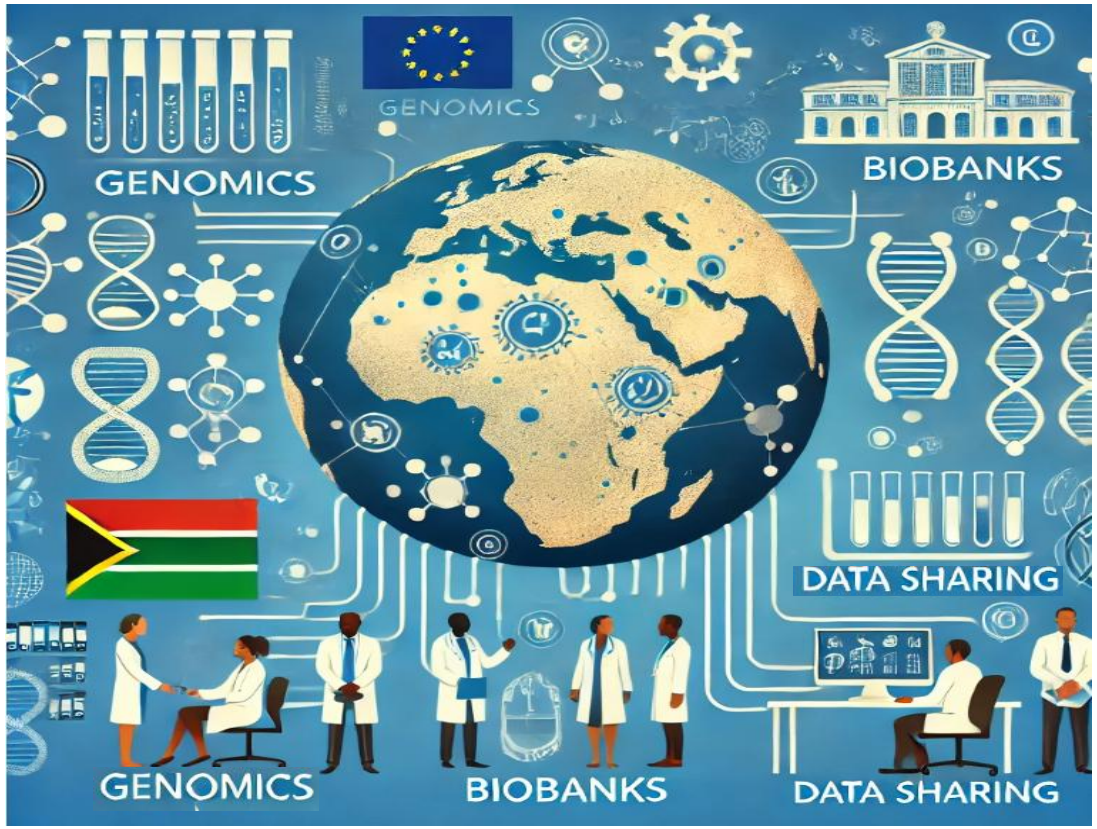
Personalized Medicine in Africa: Unlocking Potential Through Genetics and Global Partnerships



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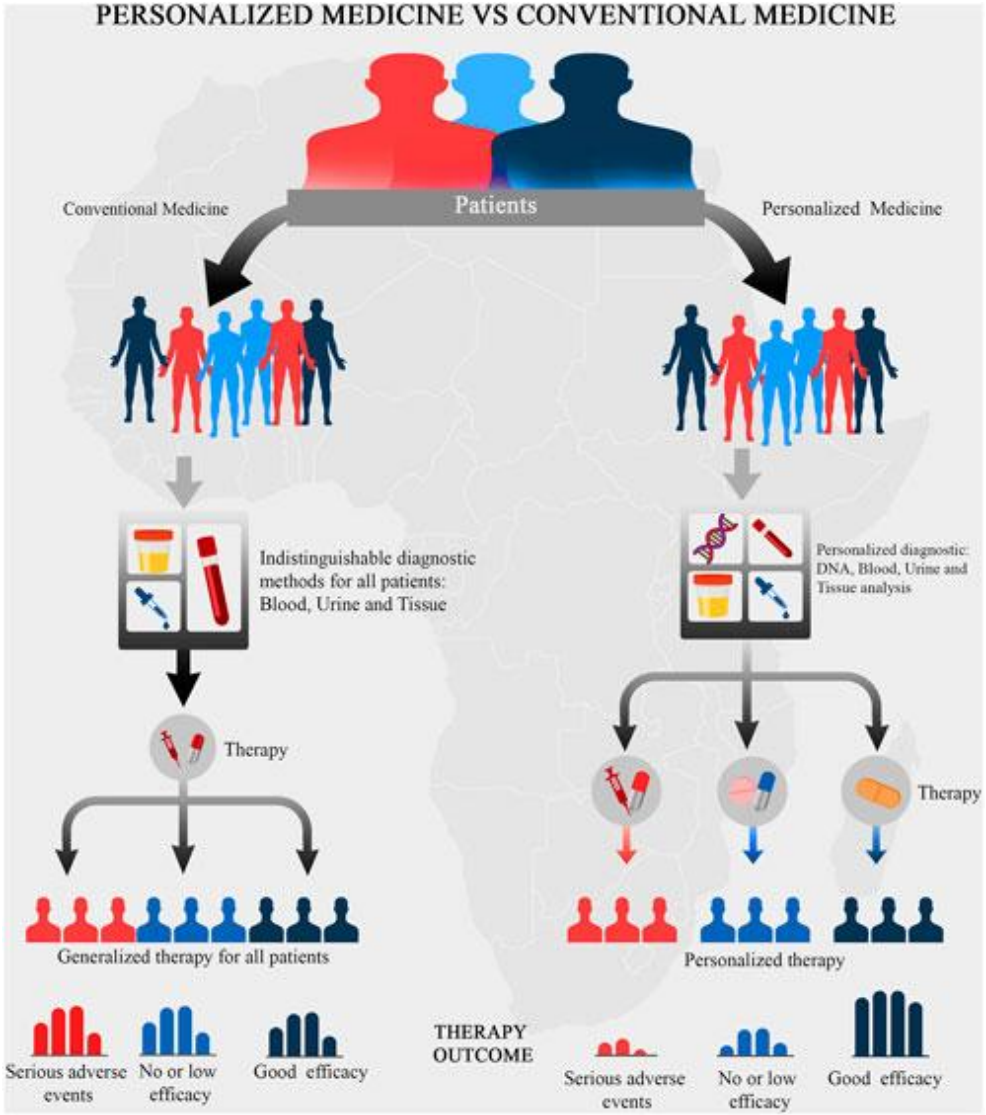
Muhimbili University of Health and Allied Sciences, Tanzania

IC PerMed Engagement Meeting, 10 June 2025

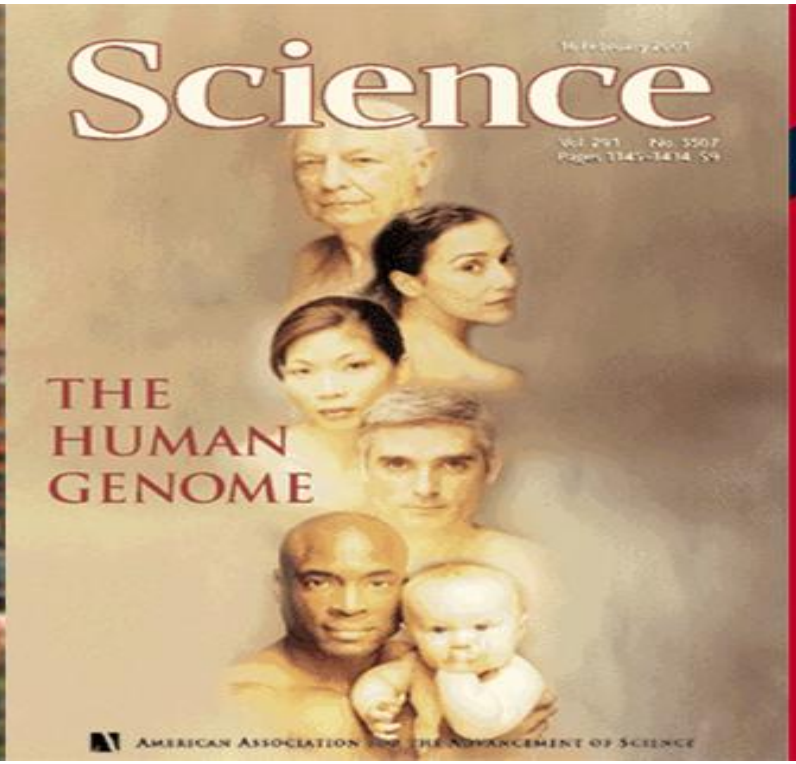
What is personalized medicine?

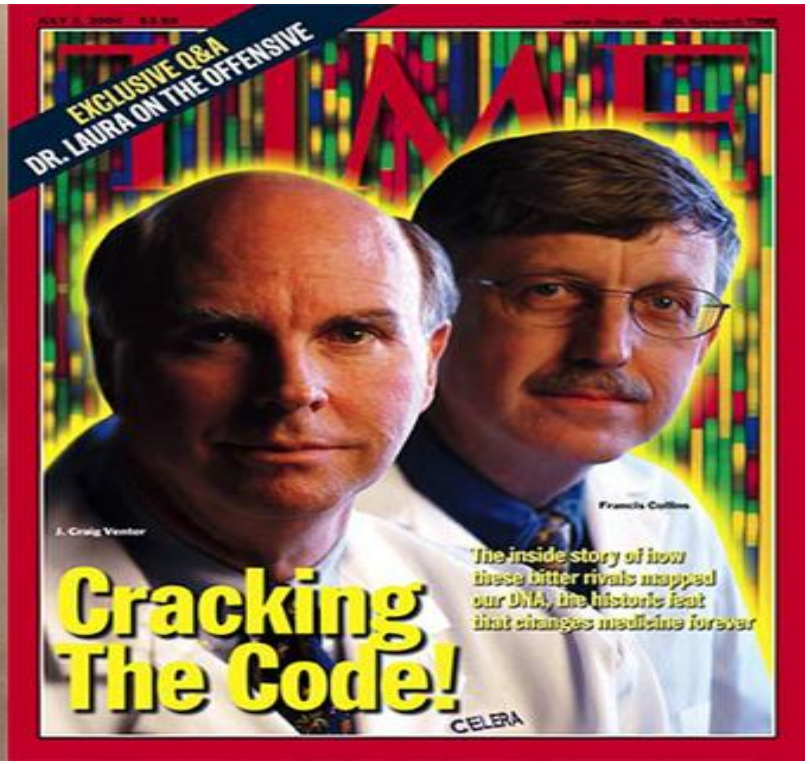
- Personalized medicine is an emerging practice of medicine that uses an individual's genetic profile, lifestyle and environment to guide decisions made about the prevention, diagnosis, and treatment of disease.
- Knowledge of a patient's genetic profile can help doctors select the proper medication or therapy and administer it using the proper dose or regimen.
- Personalized medicine is being advanced through data from the Human Genome Project.



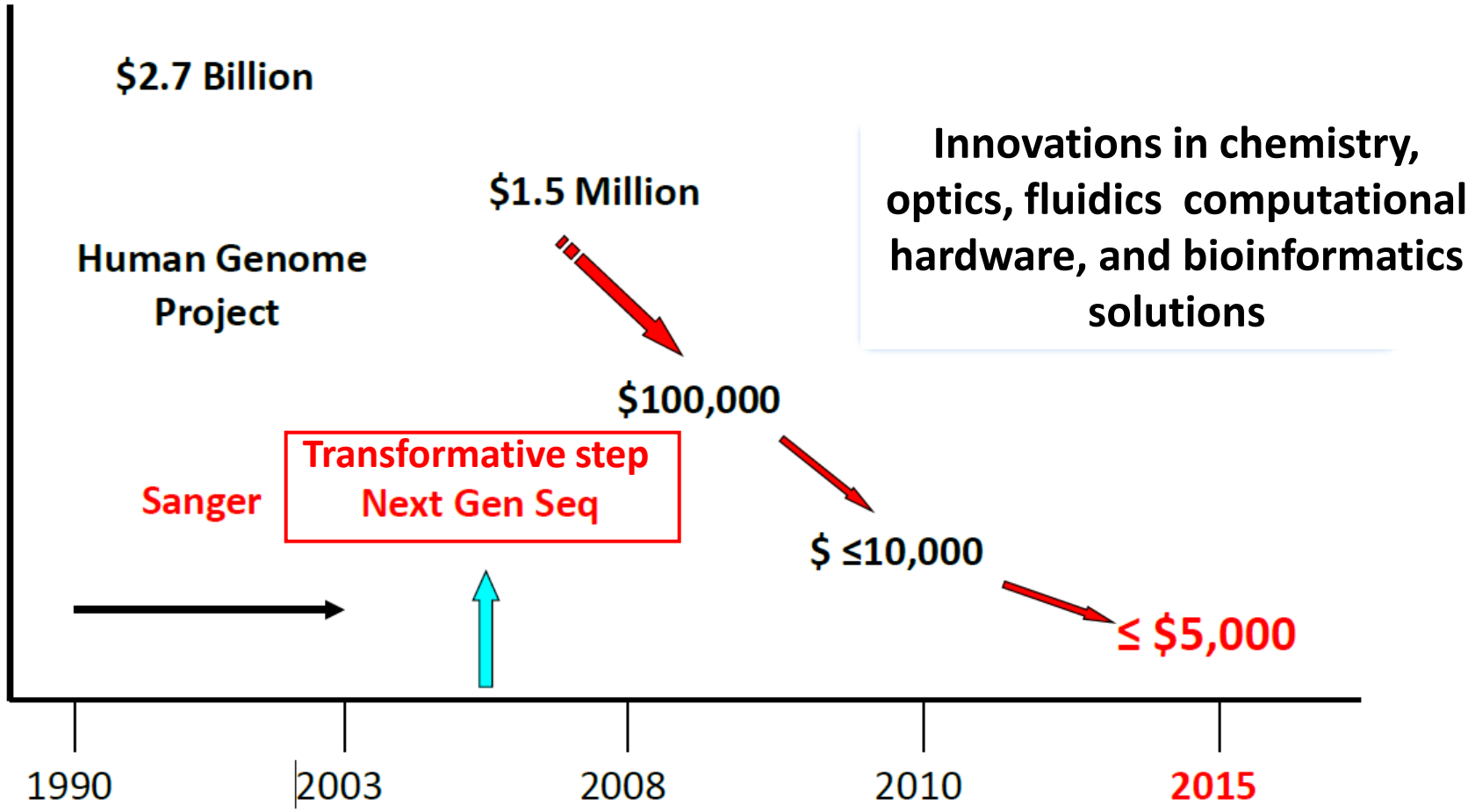
HUMAN GENOME PROJECT

"What more powerful form of study of mankind could there be than to read our own instruction book?"
-Francis S. Collins

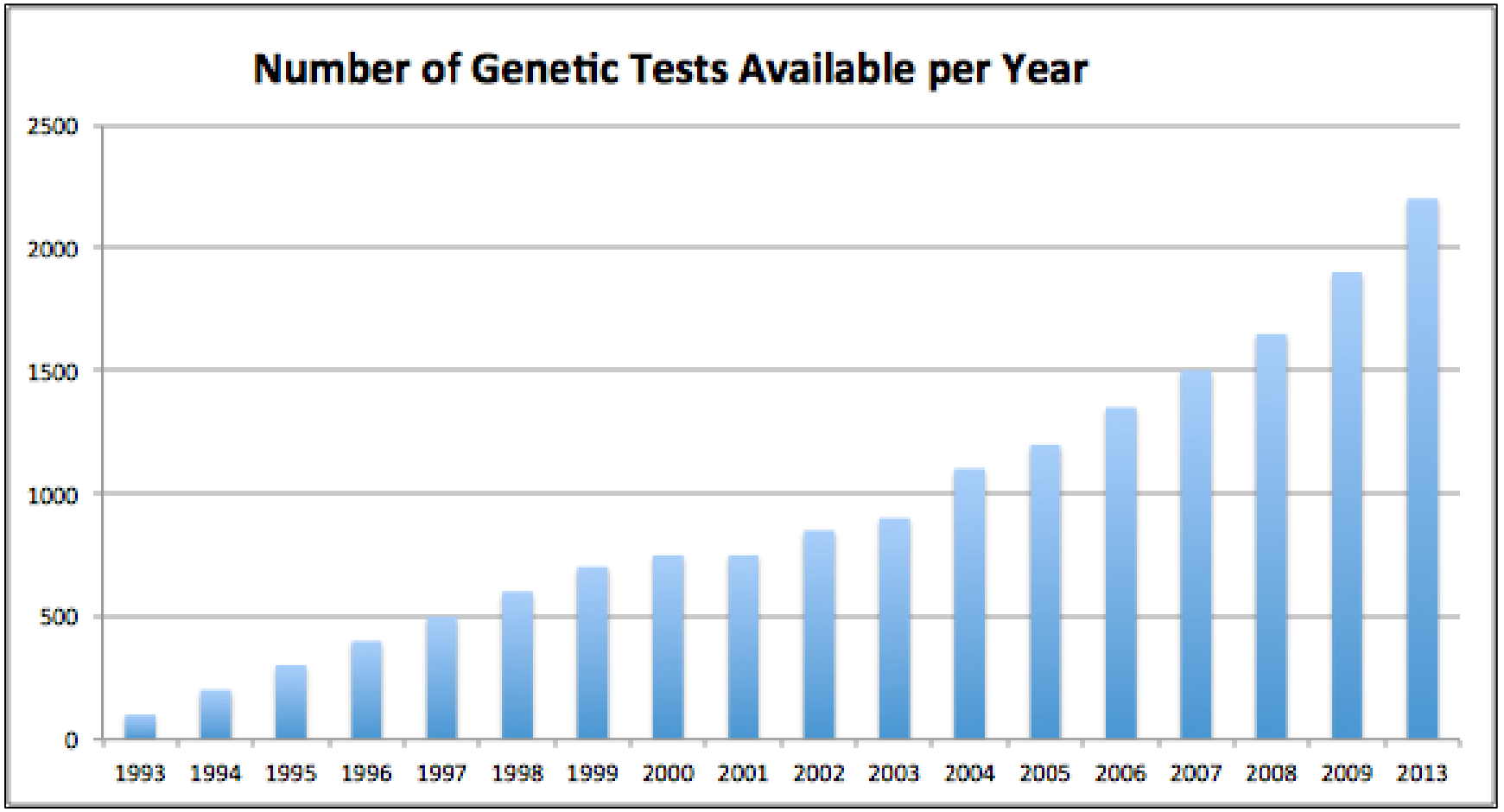




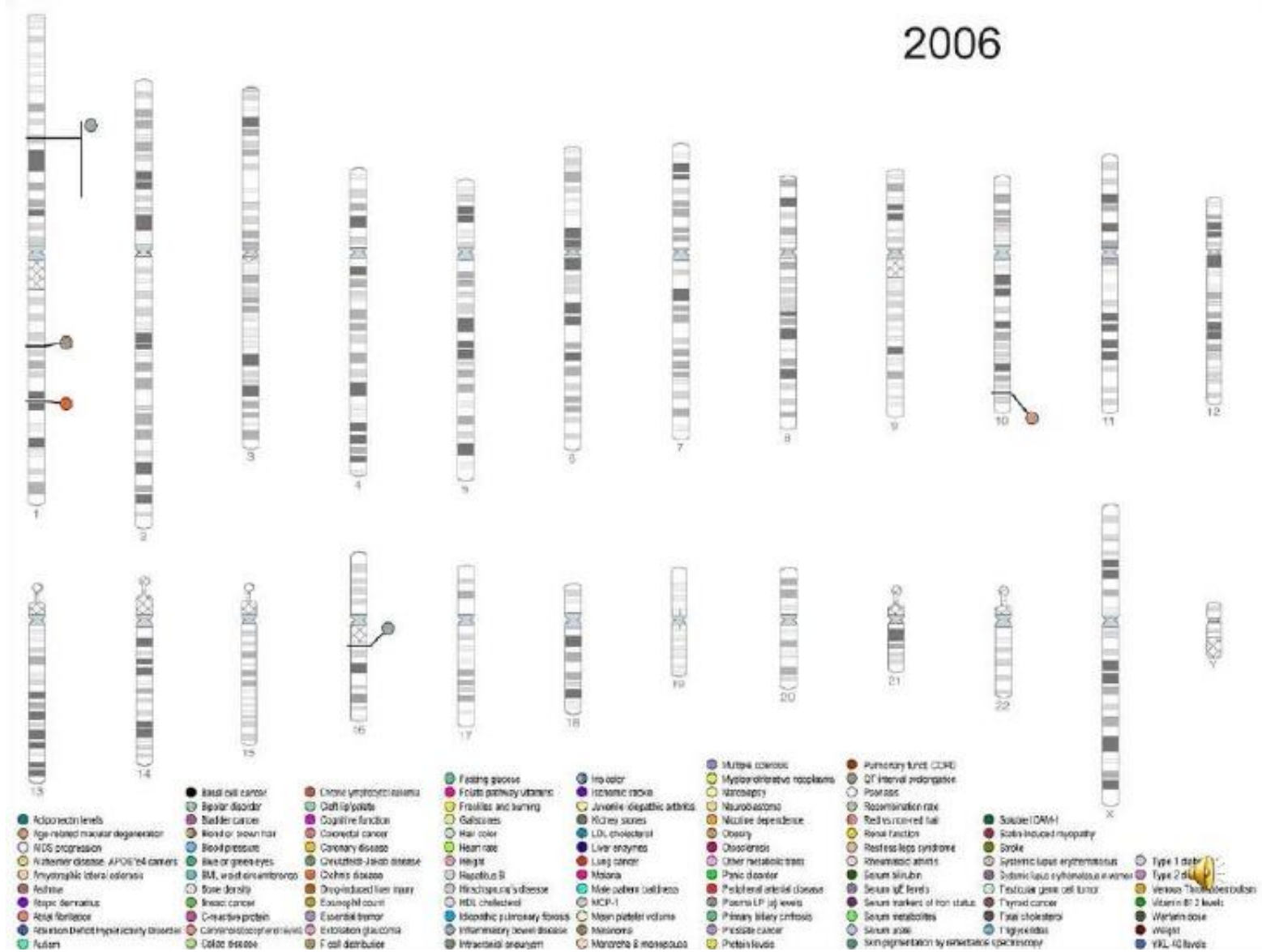
Cost of NGS

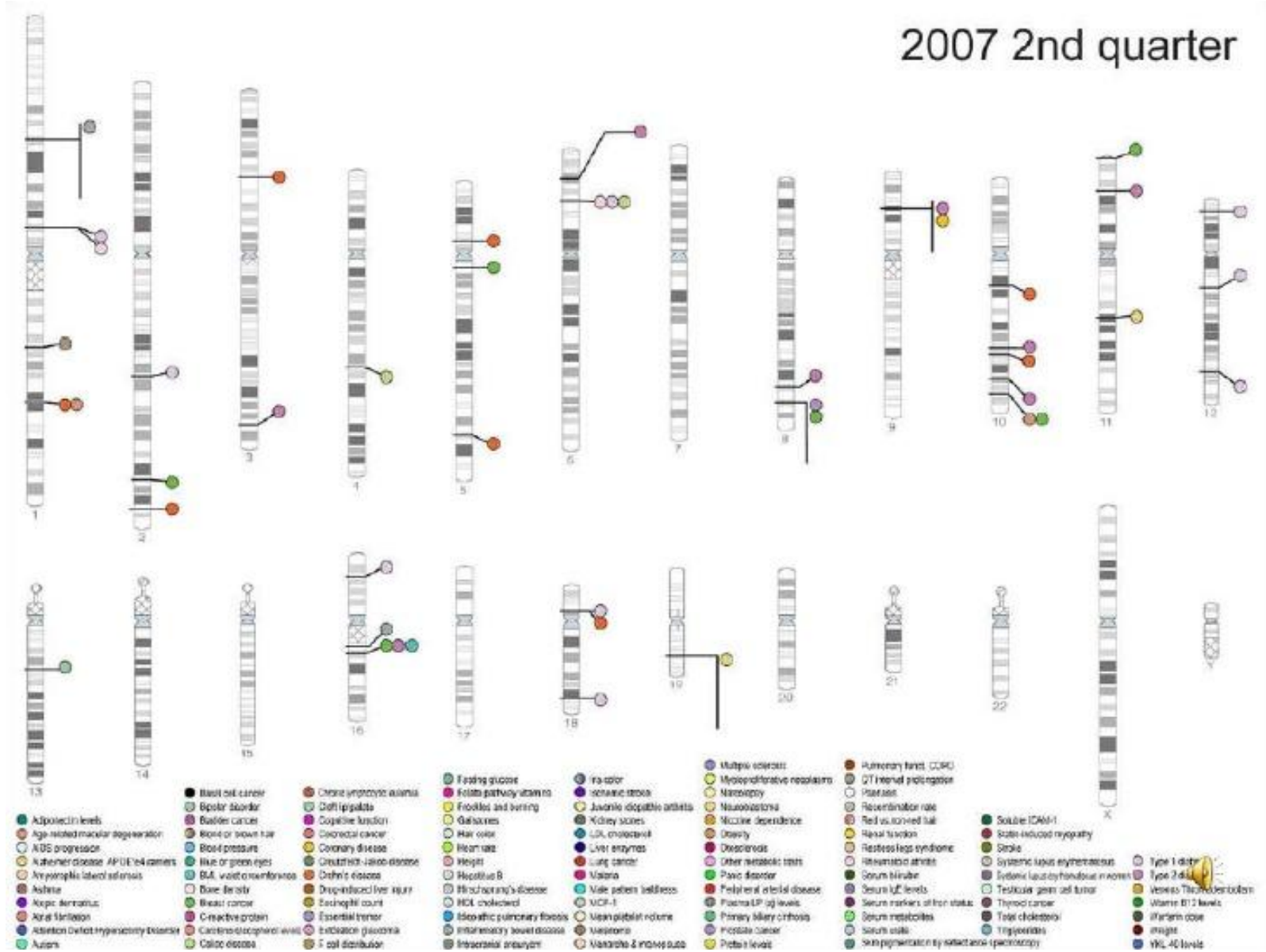

$2.7 Billion
$1.5 Million
Human Genome Project
Innovations in chemistry, optics, fluidics computational hardware, and bioinformatics solutions
$100,000
Transformative step
Next Gen Seq
Sanger
$ ≤10,000
≤ $5,000
1990
2003
2008
2010
2015

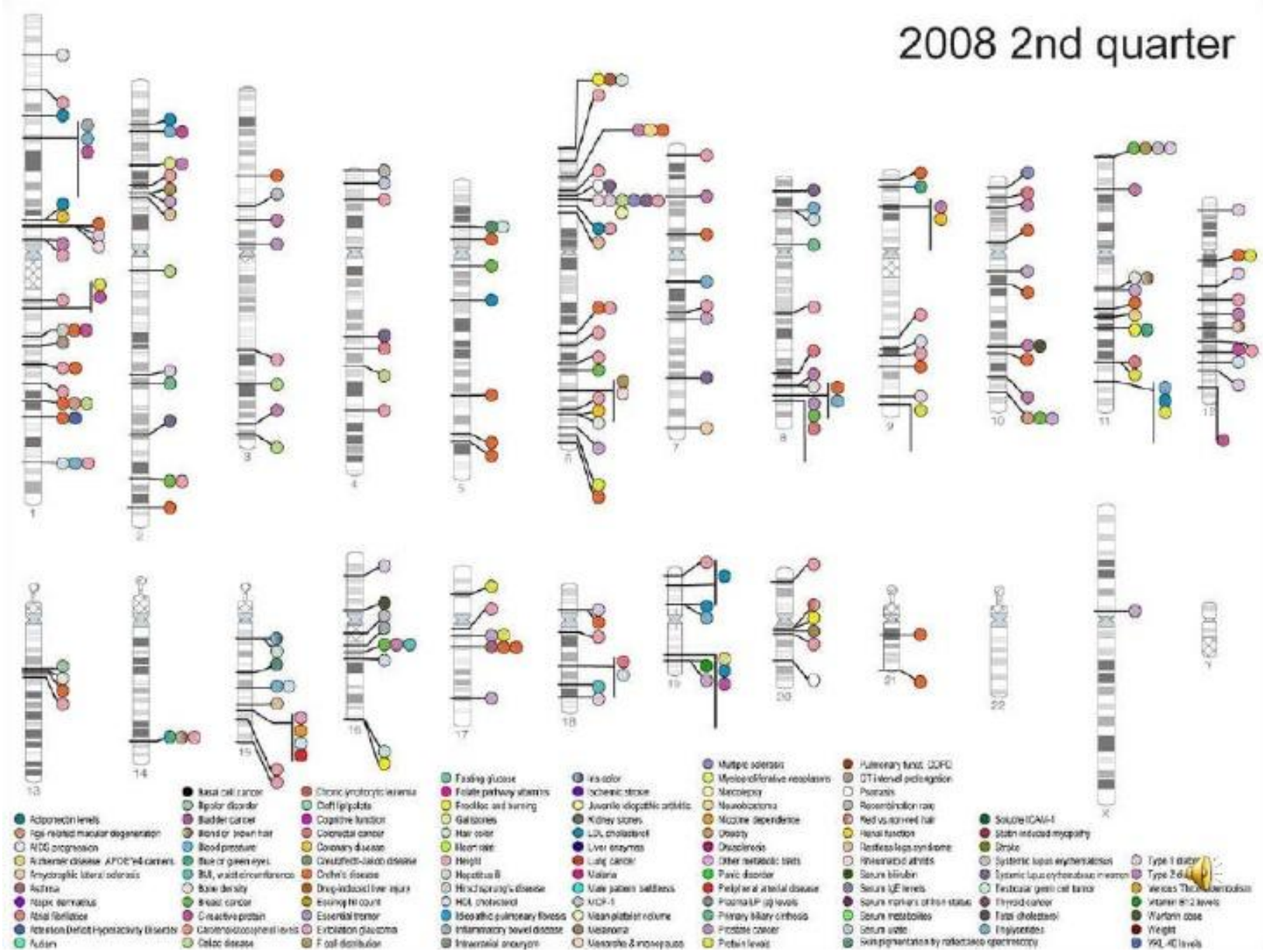
Clinical Genetic Test Consultation Service

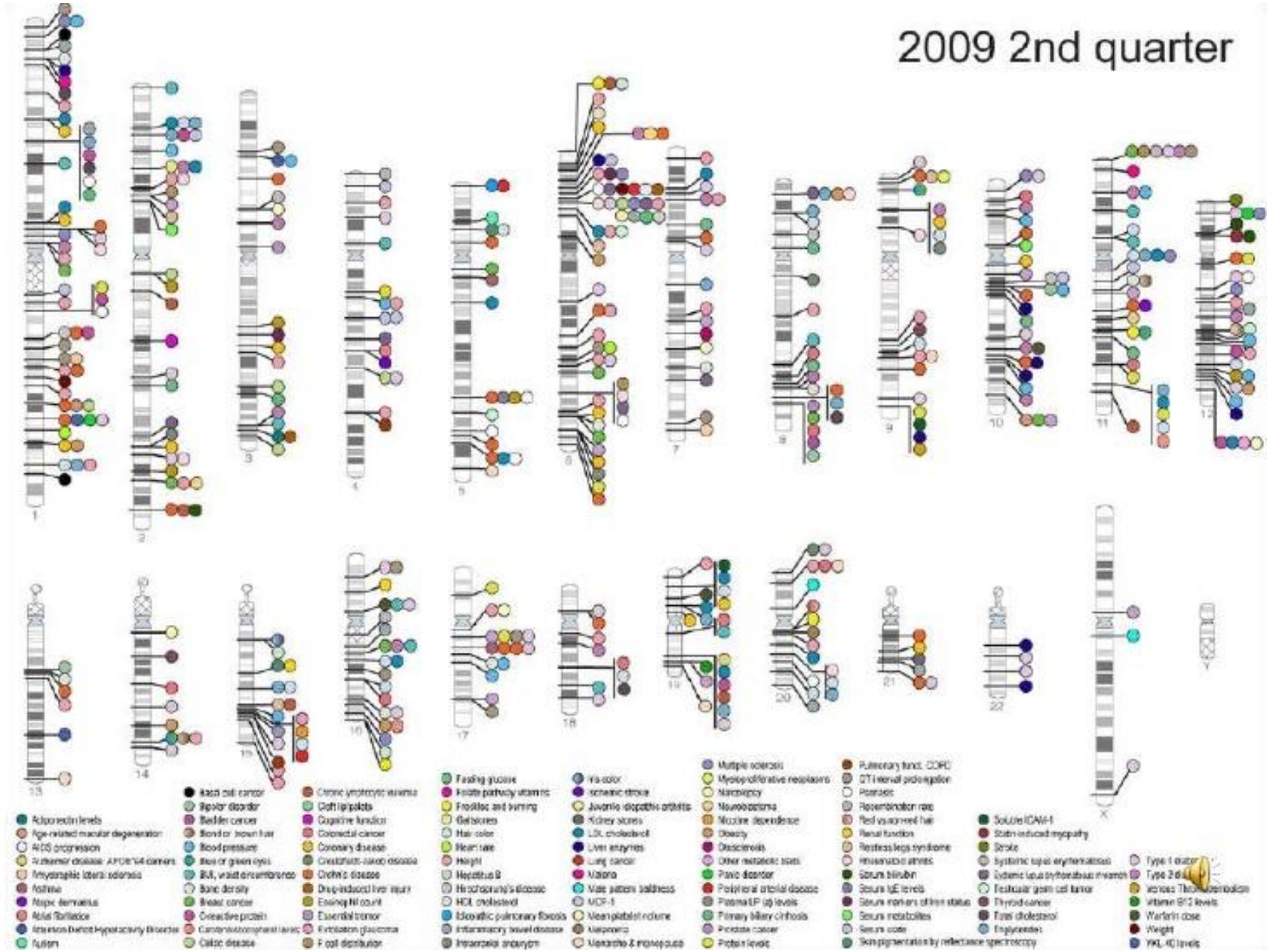


The CDC estimates that genetic tests for use in the clinical setting have been developed for approximately 2,000 diseases


2006
Adiponectin levels
Age-related macular degeneration
AIDS progression
Alzheimer disease, APOE ε4 carriers
Amyotrophic lateral sclerosis
Asthma
Atopic dermatitis
Atrial fibrillation
Attention Deficit Hyperactivity Disorder
Autism
Basal cell carcer
Bipolar disorder
Bladder cancer
Blond or brown hair
Blood pressure
Blue or green eyes
BMI, waist-to-hip ratio
Bone density
Breast cancer
C-reactive protein
Carcinoembryonic antigen levels
Celiac disease
Chronic lymphocytic leukemia
Cleft lip/palate
Cognitive function
Colorectal cancer
Coronary disease
Creutzfeldt-Jakob disease
Crohns disease
Drug-induced liver injury
Eosinophil count
Essential tremor
Exfoliation glaucoma
F cell distribution
Fasting glucose
Folate pathway vitamins
Freckles and tanning
Gallstones
Hair color
Heart rate
Height
Hepatitis B
Hirschsprung's disease
HDL cholesterol
Idiopathic pulmonary fibrosis
Inflammatory bowel disease
Intracranial aneurysm
Iris color
Ischemic stroke
Juvenile idiopathic arthritis
Kidney stones
LDL cholesterol
Liver enzymes
Lung cancer
Malaria
Male pattern baldness
MCP-1
Mean platelet volume
Melanoma
Menarche & menopause
Multiple sclerosis
Myeloproliferative neoplasms
Nanogiary
Neuroblastoma
Nicotine dependence
Obesity
Osteoporosis
Other metabolic traits
Panic disorder
Peripheral arterial disease
Plasma LP (a) levels
Primary biliary cirrhosis
Prostate cancer
Protein levels
Pulmonary funct. (COPD)
QT interval prolongation
Psoriasis
Recombination rate
Red blood cell traits
Renal function
Restless legs syndrome
Rheumatoid arthritis
Serum bilirubin
Serum IgE levels
Serum markers of iron status
Serum metabolites
Serum urate
Skin pigmentation by reflectance spectroscopy
Soluble ICAM-1
Statin-induced myopathy
Stroke
Systemic lupus erythematosus
Systemic lupus erythematosus in women
Testicular germ cell tumor
Thyroid cancer
Total cholesterol
Triglycerides
Type 1 diabetes
Type 2 diabetes
Venous Thromboembolism
Vitamin B12 levels
Warfarin dose
Weight
VKL-40 levels


2007 2nd quarter


2008 2nd quarter


2009 2nd quarter

Published Genome-Wide Associations as of July 2019

p≤5X10-8 for 17 trait categories

Normal variation

Eye colour

Differences in response to diet/medication

Obesity
Effect of antidepressants

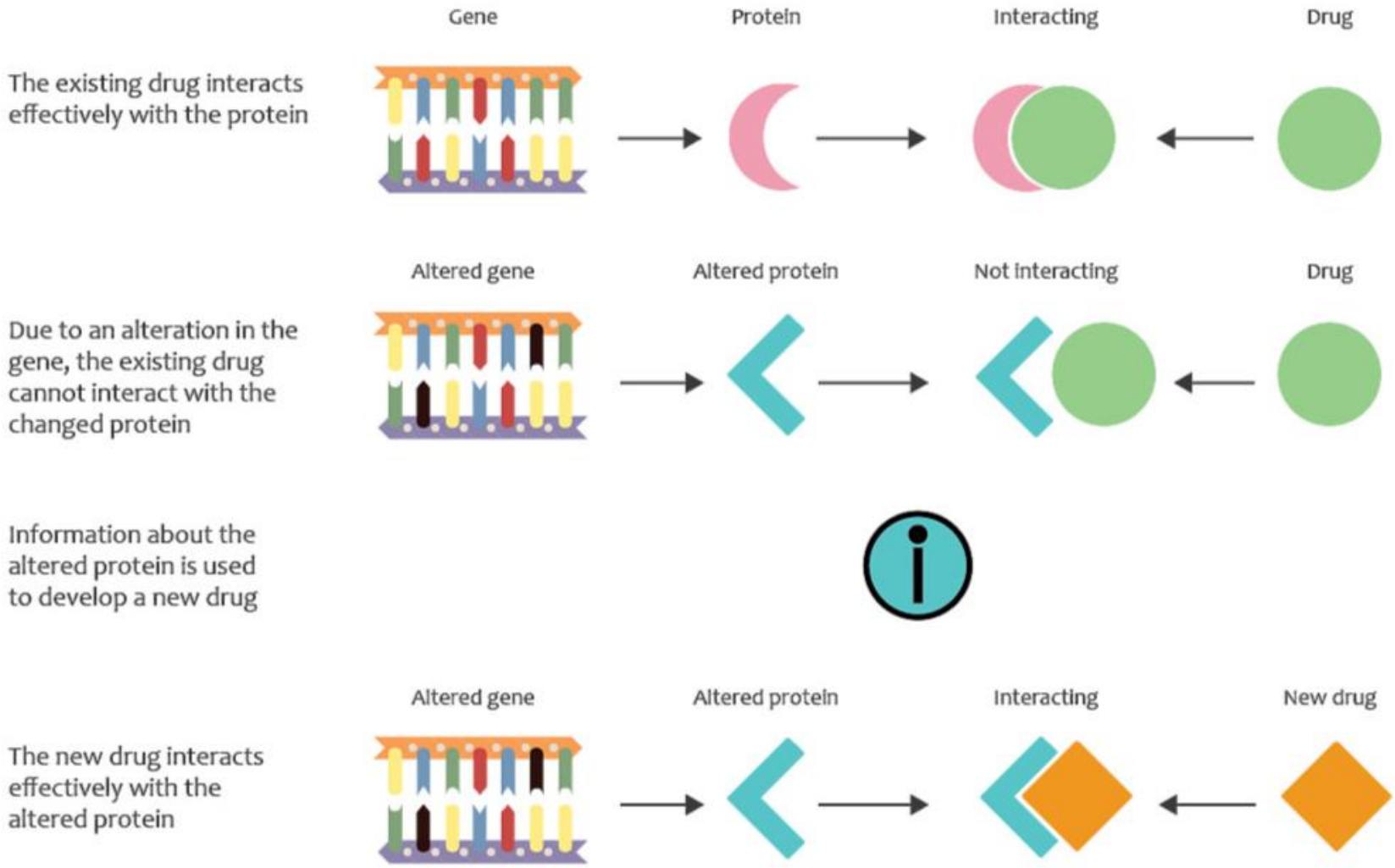
Influence likelihood of disease

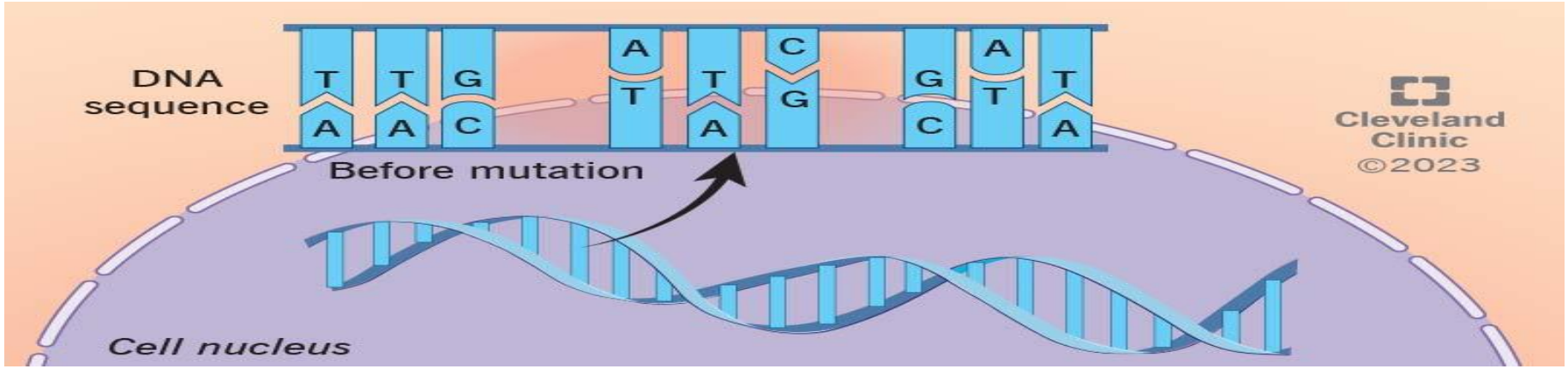
Diabetes
Coeliac disease

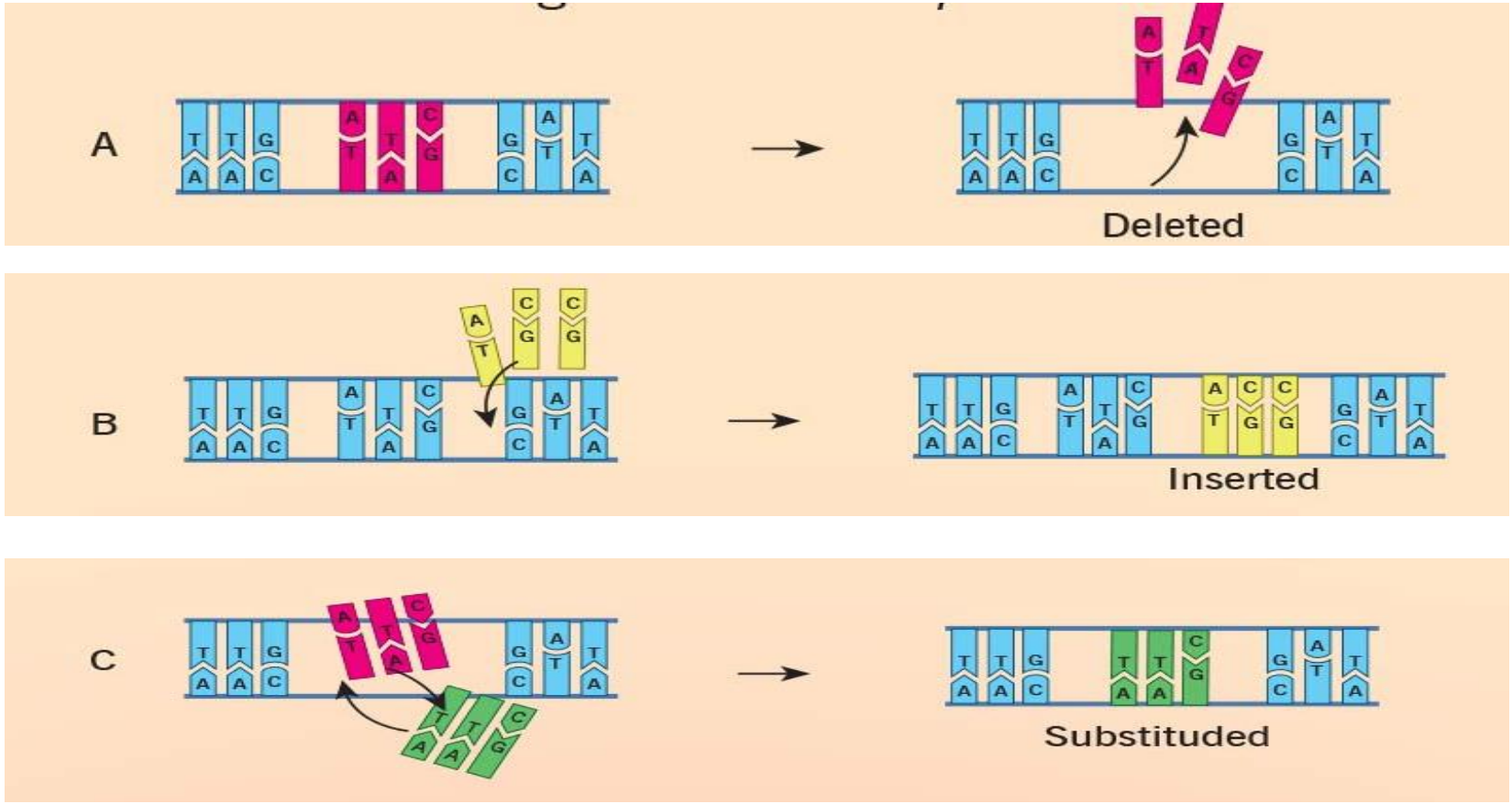
Directly result in a genetic condition

PKU
Familial hypercholesterolaemia

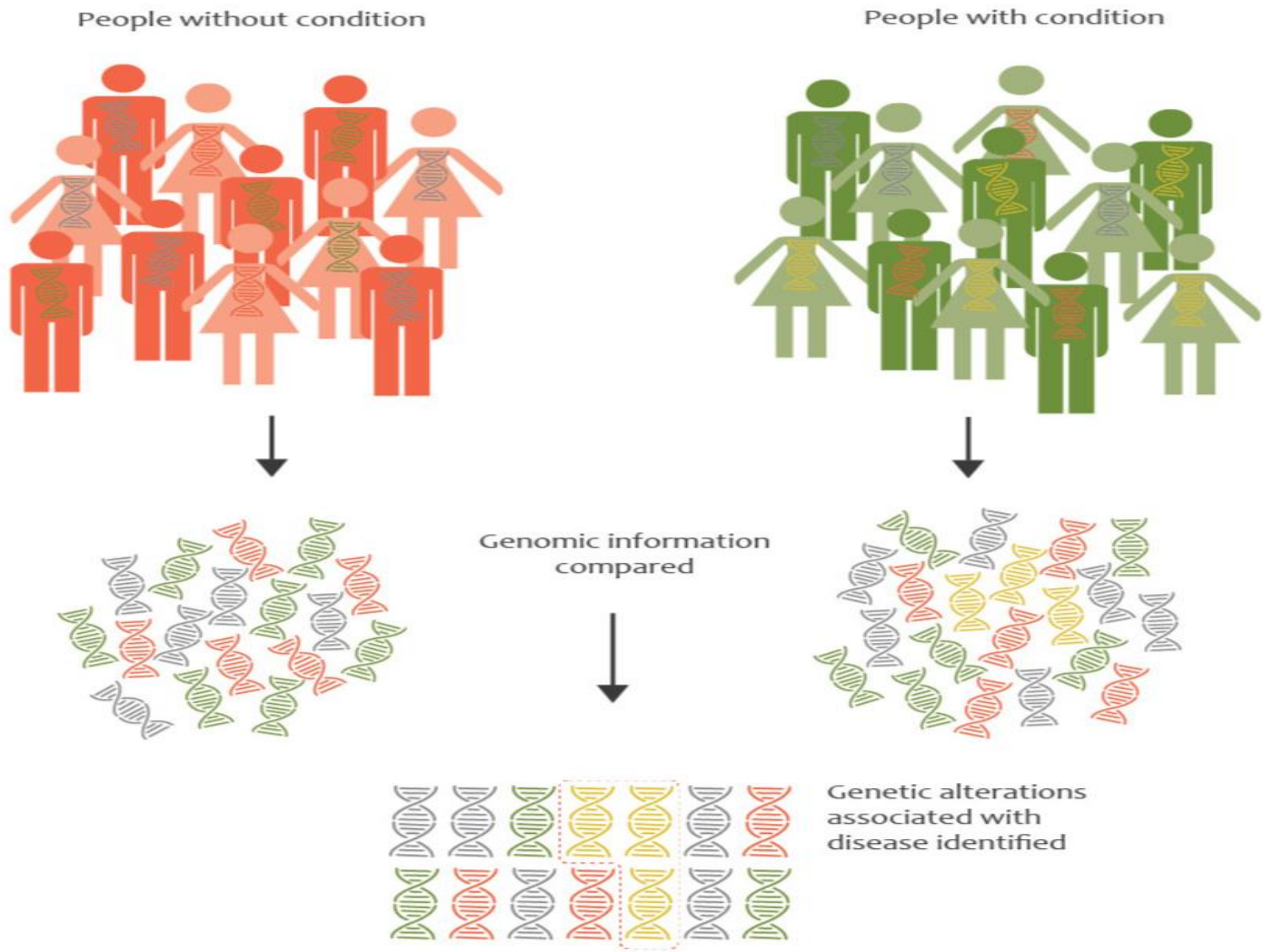
Using genomic information to develop new treatments - an example of drug-protein interaction




DNA sequence
Before mutation
Cell nucleus
Cleveland Clinic ©2023


A
Deleted
B
Inserted
C
Substituded

How researchers compare genomic information to identify genetic alterations



Genetic variation in the African population

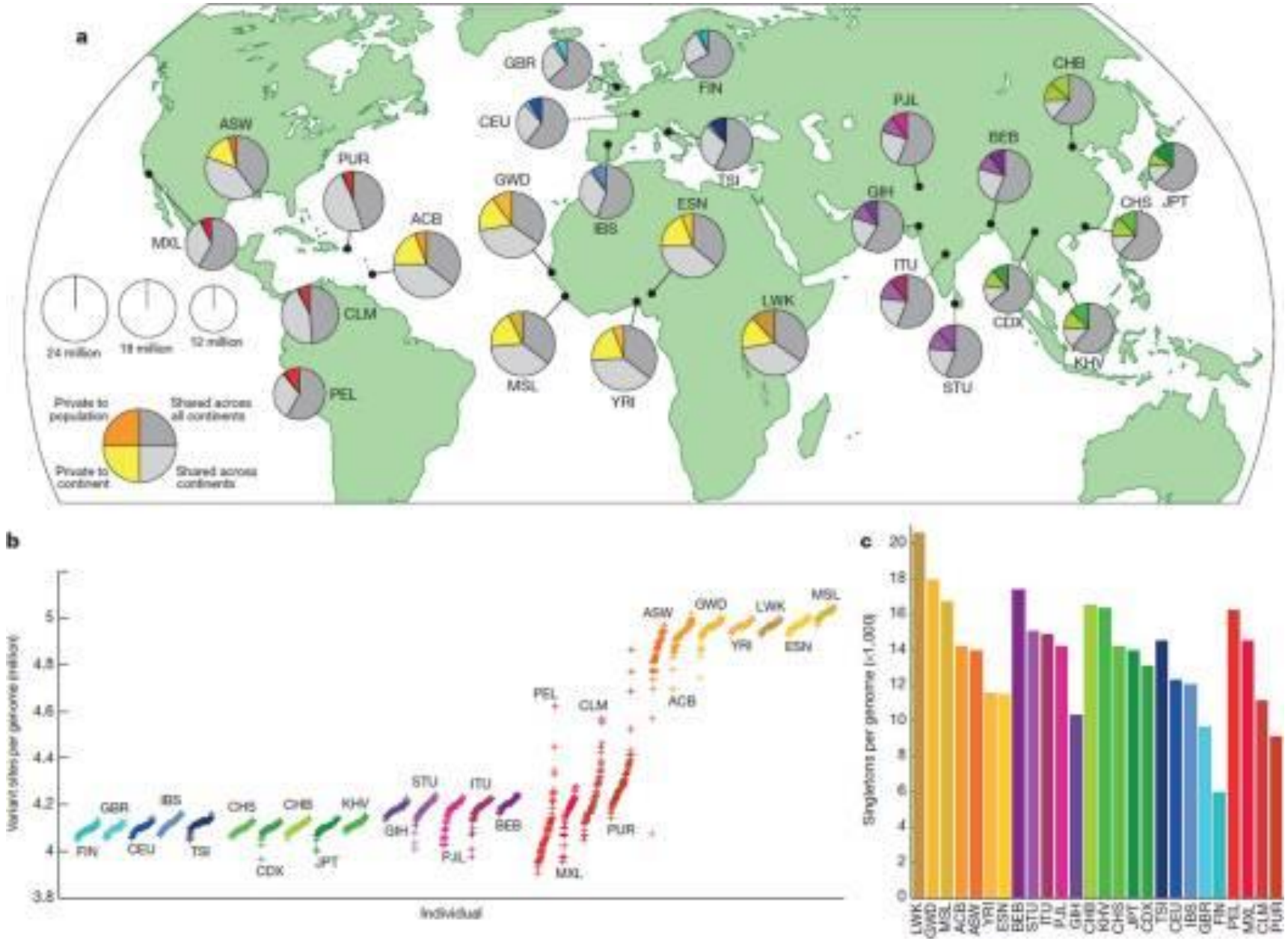
1.4 billion people

Africa is the worlds second largest and second most populous continent

54 countries, >3000 ethnic groups, >2100 languages

~50% of the African population are children <18 years old

By 2050, 40% of the world's children will live in Africa


a
GBR
FIN
CEU
TSI
CHB
PJL
ASW
PUR
BEB
GWD
IBS
ESN
GIH
CHS
JPT
ACB
MXL
ITU
CLM
LWK
CDX
KHV
MSL
YRI
STU
PEL
24 million
18 million
12 million
Private to population
Shared across all continents
Private to continent
Shared across continents
b
Variant sites per genome (million)
5
4.8
4.6
4.4
4.2
4
3.8
FIN
GBR
CEU
IBS
TSI
CDX
CHS
JPT
CHB
KHV
GIH
STU
PJL
ITU
BEB
MXL
PEL
CLM
PUR
ACB
ASW
GWD
YRI
LWK
ESN
MSL
Individual
c
Singletons per genome (×1,000)
20
18
16
14
12
10
8
6
4
2
0
LWK
GWD
MSL
ACB
ASW
YRI
ESN
BEB
STU
ITU
PJL
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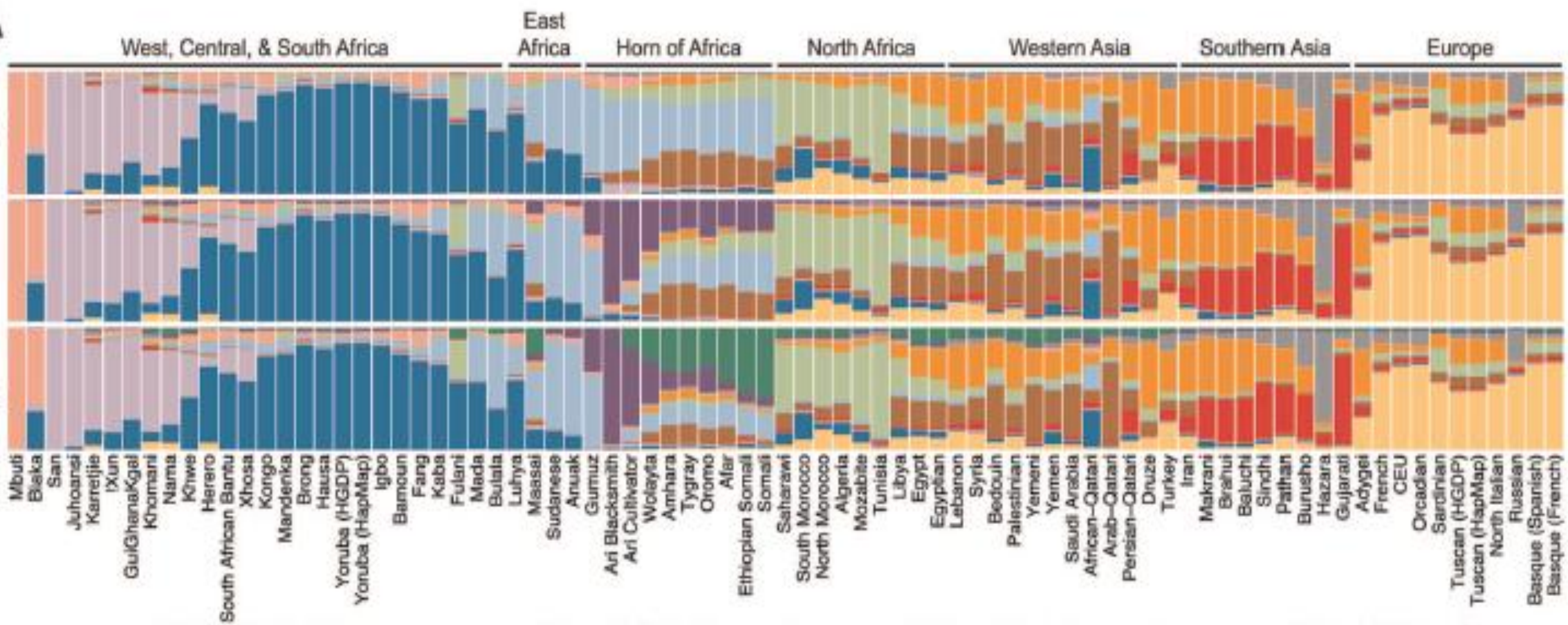
CHB
KHV
CHS
JPT
CDX
TSI
CEU
IBS
GBR
FIN
PEL
MXL
CLM
PUR


A
West, Central, & South Africa
East Africa
Horn of Africa
North Africa
Western Asia
Southern Asia
Europe
10
11
12
Mbuti
Biaka
San
Juhoansi
Karretjie
!Xun
GuiGhanaKgal
Khomani
Nama
Khwe
Herero
South African Bantu
Xhosa
Kongo
Mandenka
Brong
Hausa
Yoruba (HGDP)
Yoruba (HapMap)
Igbo
Bamoun
Fang
Kaba
Fulani
Mada
Bulala
Luhya
Maasai
Sudanese
Anuak
Gumuz
Ari Blacksmith
Ari Cultivator
Wolayta
Amhara
Tygray
Oromo
Afar
Ethiopian Somali
Somali
Saharawi
South Morocco
North Morocco
Algeria
Mozabite
Tunisia
Libya
Egypt
Egyptian
Lebanon
Syria
Bedouin
Palestinian
Yemeni
Yemen
Saudi Arabia
African–Qatari
Arab–Qatari
Persian–Qatari
Druze
Turkey
Iran
Makrani
Brahui
Baluchi
Sindhi
Pathan
Burusho
Hazara
Gujarati
Adygei
French
CEU
Orcadian
Sardinian
Tuscan (HGDP)
Tuscan (HapMap)
North Italian
Russian
Basque (Spanish)
Basque (French)

LETTERS
https://doi.org/10.1038/s41588-018-0273-y
nature genetics
OPEN

Corrected: Author Correction

Assembly of a pan-genome from deep sequencing of 910 humans of African descent

Rachel M. Sherman[1,2*], Juliet Forman[1,3], Valentin Antonescu[1], Daniela Puiu[1], Michelle Daya[4], Nicholas Rafaels[4], Meher Preethi Boorgula[4], Sameer Chavan[4], Candelaria Vergara[5], Victor E. Ortega[6], Albert M. Levin[7], Celeste Eng[8], Maria Yazdanbakhsh[9], James G. Wilson[10], Javier Marrugo[11], Leslie A. Lange[4], L. Keoki Williams[12], Harold Watson[13], Lorraine B. Ware[14], Christopher O. Olopade[15], Olufunmilayo Olopade[16], Ricardo R. Oliveira[17], Carole Ober[18], Dan L. Nicolae[16], Deborah A. Meyers[19], Alvaro Mayorga[20], Jennifer Knight-Madden[21], Tina Hartert[14], Nadia N. Hansel[5], Marilyn G. Foreman[22], Jean G. Ford[23], Mezbah U. Faruque[24], Georgia M. Dunston[25], Luis Caraballo[11], Esteban G. Burchard[26], Eugene R. Bleecker[19], Maria I. Araujo[27], Edwin F. Herrera-Paz[28], Monica Campbell[4], Cassandra Foster[5], Margaret A. Taub[29], Terri H. Beaty[30], Ingo Ruczinski[31], Rasika A. Mathias[5,30], Kathleen C. Barnes[4] and Steven L. Salzberg[1,2,29,31*]

We used a deeply sequenced dataset of 910 individuals, all of African descent, to construct a set of DNA sequences that is present in these individuals but missing from the reference human genome. We aligned 1.19 trillion reads from the 910 individuals to the reference genome (GRCh38), collected all reads that failed to align, and assembled these reads into contiguous sequences (contigs). We then compared all contigs to one another to identify a set of unique sequences representing regions of the African pan-genome missing from the reference genome. Our analysis revealed 296,485,284 bp in 125,715 distinct contigs present in the populations of African descent, demonstrating that the African pan-genome contains ~10% more DNA than the current human reference genome. Although the functional significance of nearly all of this sequence is unknown, 387 of the novel contigs fall within 315 distinct protein-coding genes, and the rest appear to be intergenic.

Since its initial publication[1,2], the human genome sequence has undergone continual improvements aimed at filling gaps and correcting errors. The latest release, GRCh38, spans 3.1 gigabases (Gb), with just 875 remaining gaps[3]. The ongoing effort to improve the human reference genome, led by the Genome Reference Consortium, has in recent years added alternate loci for genomic regions where variation cannot be captured by SNPs or small insertions and deletions (indels). These alternate loci, which comprise 261 scaffolds in GRCh38, capture a small amount of population variation and improve read mapping for some data sets.

Despite these efforts, the current human reference genome derives primarily from a single individual[4], thus limiting its usefulness for genetic studies, especially among admixed populations, such as those representing the African diaspora. In recent years, a growing number of researchers have emphasized the importance of capturing and representing sequencing data from diverse populations and incorporating these data into the reference genome

Article

High-depth African genomes inform human migration and health

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Open access
Check for updates

Ananyo Choudhury[1], Shaun Aron[1], Laura R. Botigué[2], Dhriti Sengupta[1], Gerrit Botha[3], Taoufik Bensellak[4], Gordon Wells[5,6], Judit Kumuthini[5,6], Daniel Shriner[7], Yasmina J. Fakim[8,9], Anisah W. Ghoorah[9], Eileen Dareng[10,11], Trust Odia[12], Oluwadamilare Falola[12], Ezekiel Adebiyi[12,13], Scott Hazelhurst[1,14], Gaston Mazandu[3], Oscar A. Nyangiri[15], Mamana Mbiyavanga[3], Alia Benkahla[16], Samar K. Kassim[17], Nicola Mulder[3], Sally N. Adebamowo[18,19], Emile R. Chimusa[20], Donna Muzny[21], Ginger Metcalf[21], Richard A. Gibbs[21,22], TrypanoGEN Research Group*, Charles Rotimi[7], Michèle Ramsay[1,23], H3Africa Consortium*, Adebowale A. Adeyemo[7]✉, Zané Lombard[23]✉ & Neil A. Hanchard[22]✉

The African continent is regarded as the cradle of modern humans and African genomes contain more genetic variation than those from any other continent, yet only a fraction of the genetic diversity among African individuals has been surveyed[1]. Here we performed whole-genome sequencing analyses of 426 individuals—comprising 50 ethnolinguistic groups, including previously unsampled populations—to explore the breadth of genomic diversity across Africa. We uncovered more than 3 million previously undescribed variants, most of which were found among individuals from newly sampled ethnolinguistic groups, as well as 62 previously unreported loci that are under strong selection, which were predominantly found in genes that are involved in viral immunity, DNA repair and metabolism. We observed complex patterns of ancestral admixture and putative-damaging and novel variation, both within and between populations, alongside evidence that Zambia was a likely intermediate site along the routes of expansion of Bantu-speaking populations. Pathogenic variants in genes that are currently characterized as medically relevant were uncommon—but in other genes, variants denoted as 'likely pathogenic' in the ClinVar database were commonly observed. Collectively, these findings refine our current understanding of continental migration, identify gene flow and the response to human disease as strong drivers of genome-level population variation, and underscore the scientific imperative for a broader characterization of the genomic diversity of African individuals to understand human ancestry and improve health.

What Did We (Africans) Learn Post HGV Project?

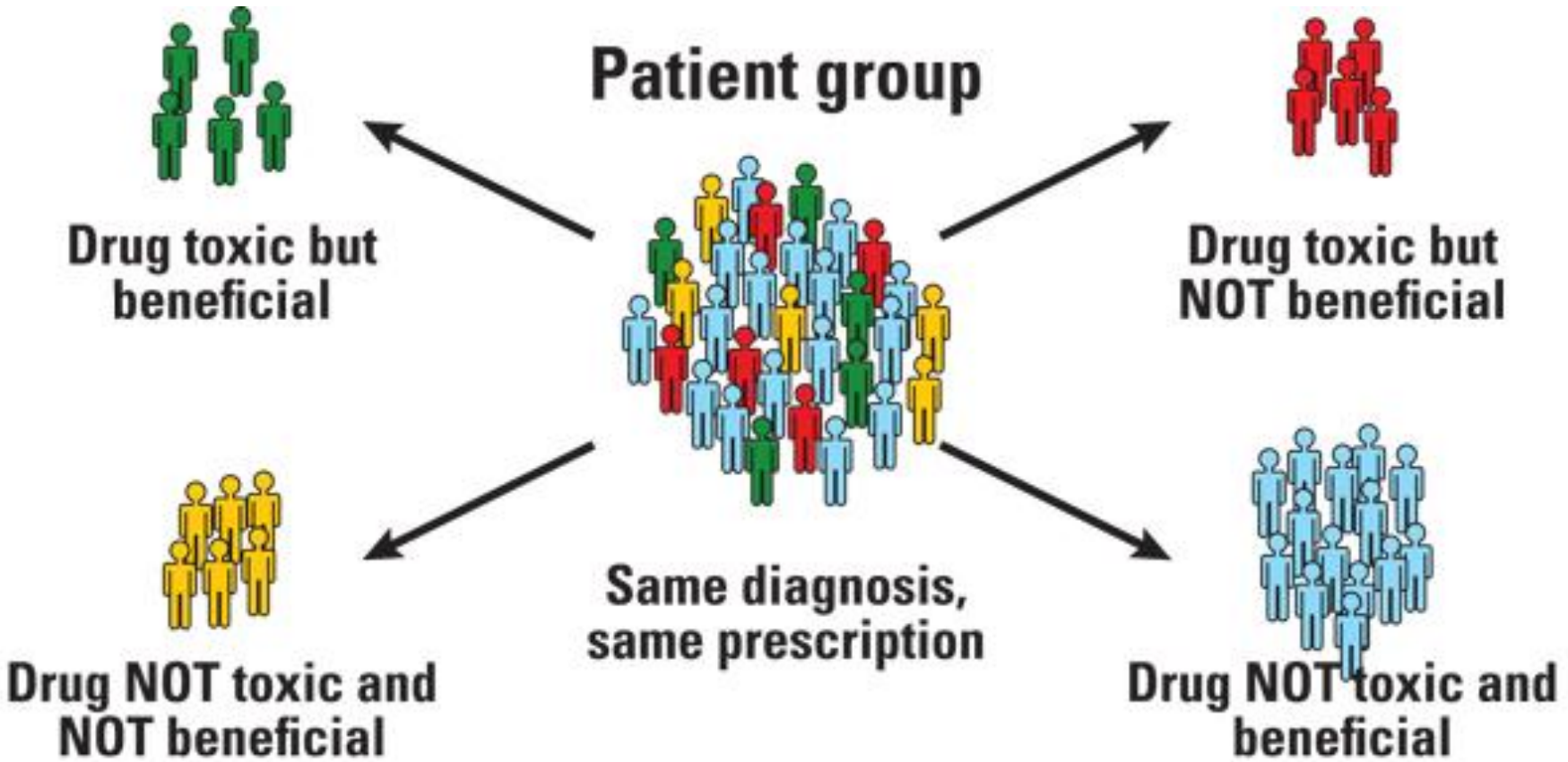
- Importance of genotyping
- Importance of phenotyping
- Road towards precision medicine

Diagnostics

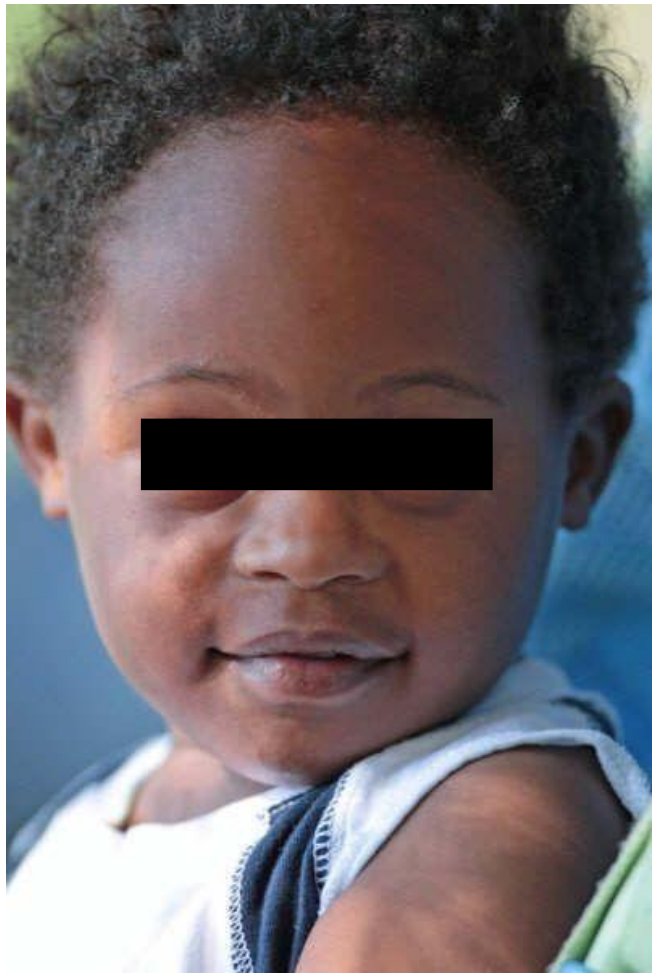
Benign Variants Misclassified as Pathogenic in Genetic Reports

Seven patients, all of African or unspecified ancestry, received reports between 2005 and 2007 that they had one of two variants, *TNNI3* P82S or *MYBPC3* G278E, that were classified as "pathogenic" or "presumed pathogenic" (Table 1); these variants were later reclassified as benign. In five of the seven reports, P82S or G278E was the most pathogenic variant reported to the patient. Six additional patients with inconclusive or positive genetic-testing results that were reported later were listed as having one of these two variants, which were characterized as being of "unknown significance" or "pathogenicity debated." Among the 13 patients, 9 had a clinical diagnosis of hypertrophic cardiomyopathy, 2 had clinical features of hypertrophic cardiomyopathy, and 1 had clinical symptoms of hypertrophic cardiomyopathy. Five of the 13 patients had a documented family history of hypertrophic cardiomyopathy. From the records available, it was not possible to determine whether the families affected by the reclassification of these variants were recontacted.

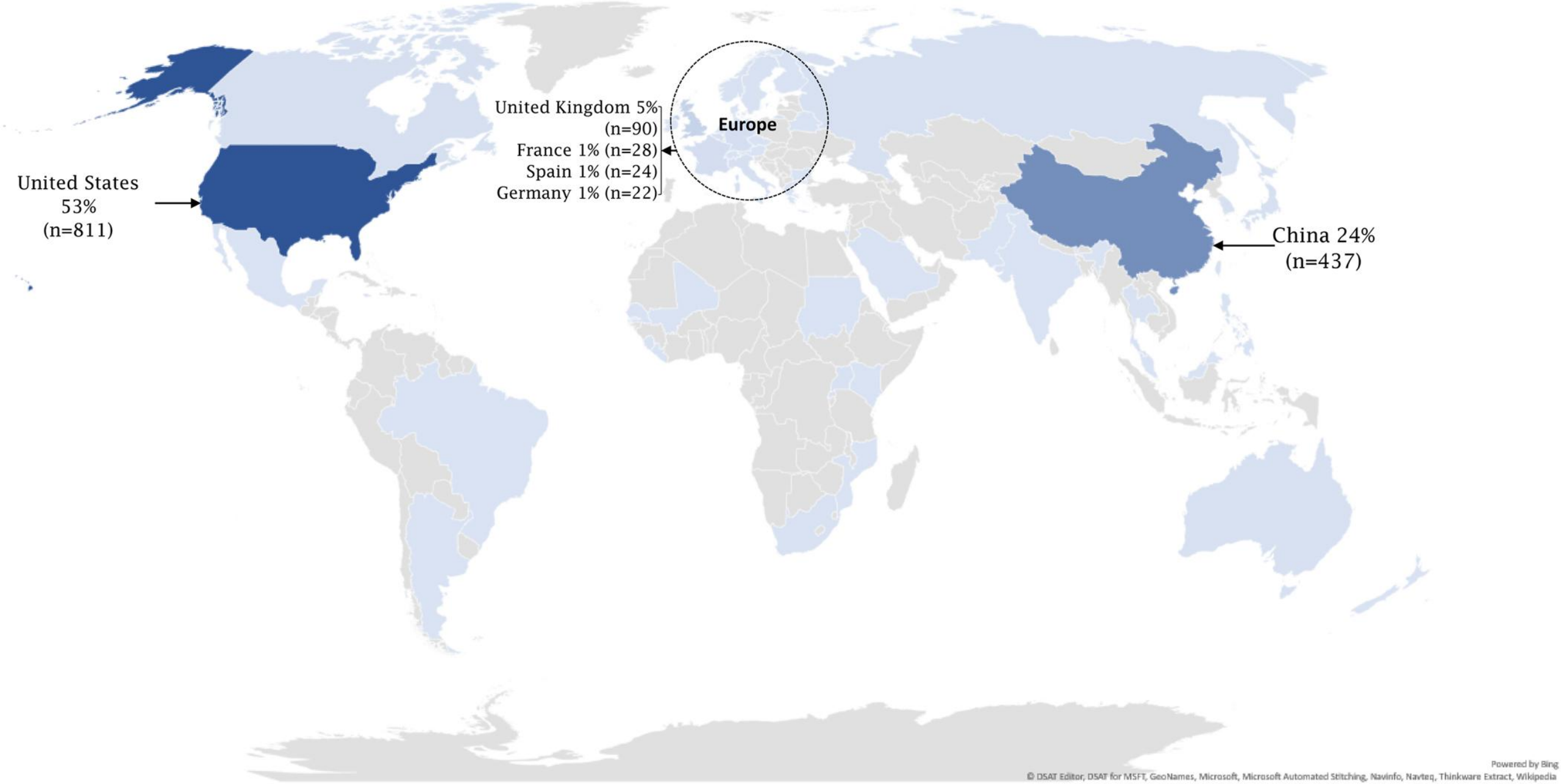
Pharmacogenomics

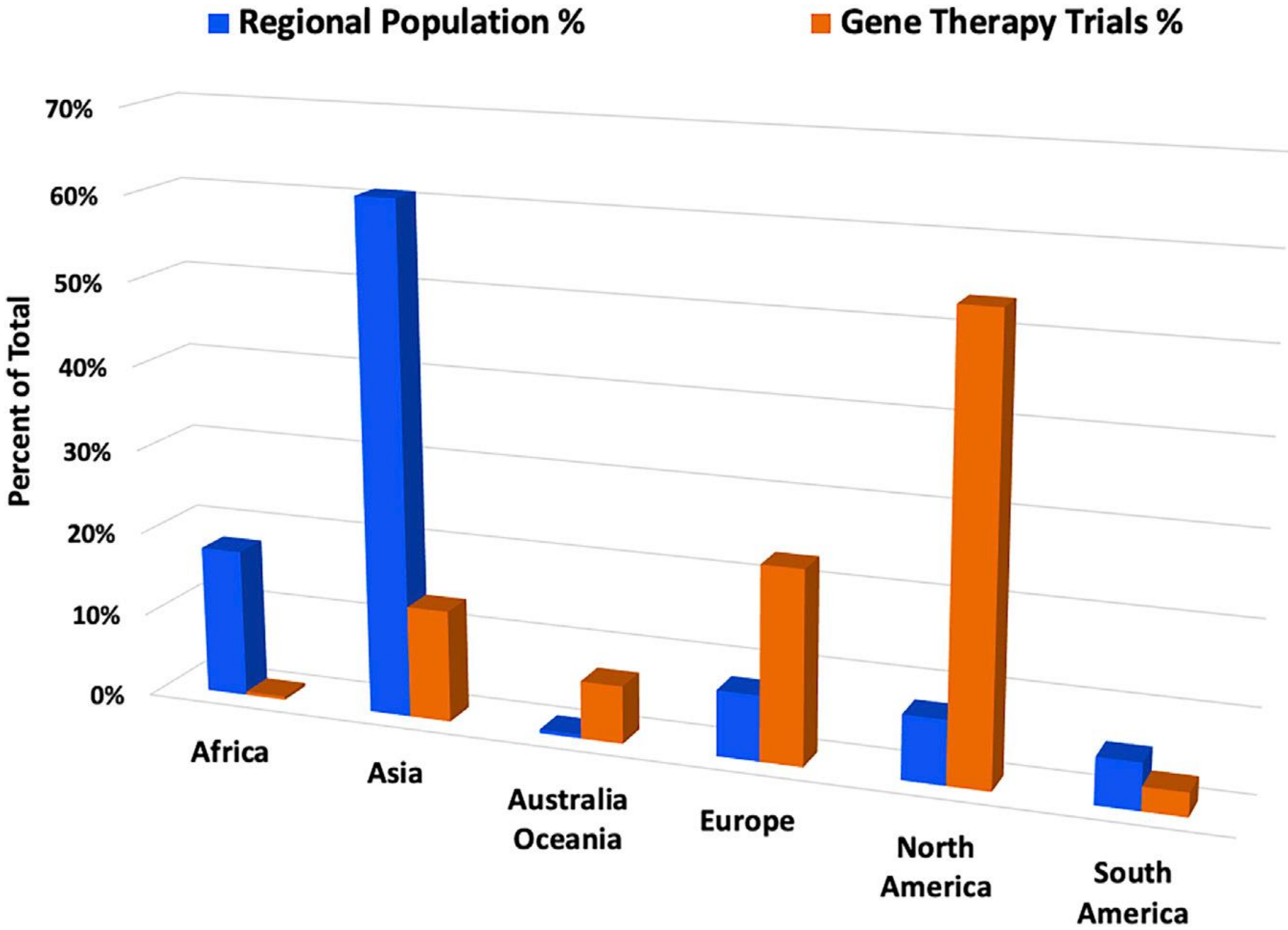


Phenotyping



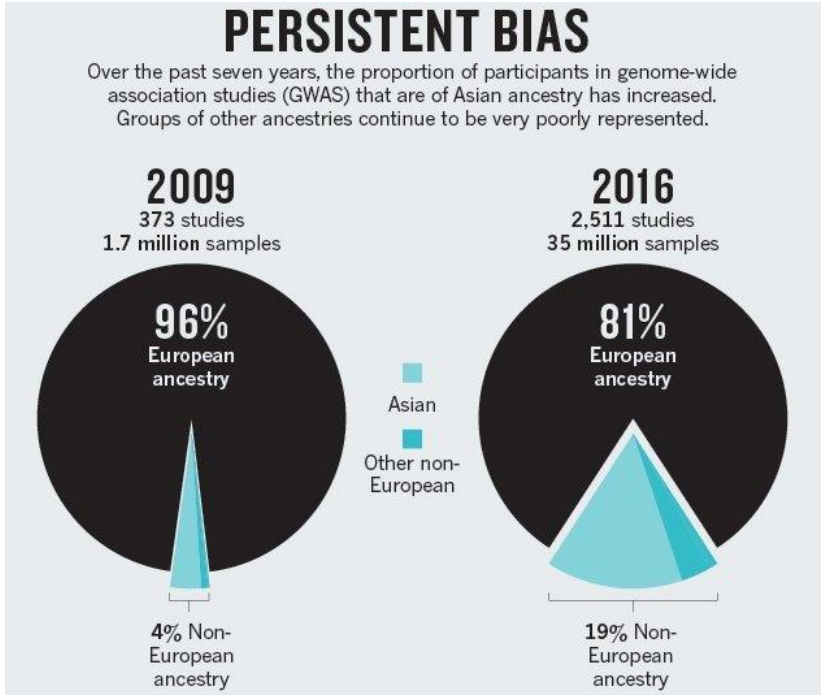
Gene therapy clinical trials



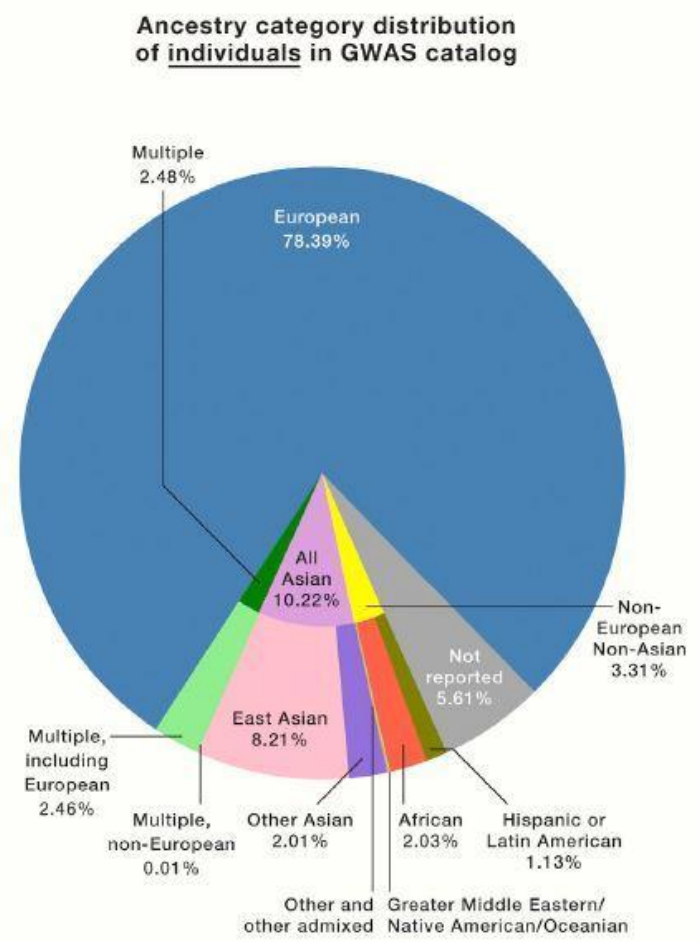

Regional Population %
Gene Therapy Trials %
70%
60%
50%
40%
30%
20%
10%
0%
Percent of Total
Africa
Asia
Australia
Oceania
Europe
North
America
South
America

Despite repeated calls, the Genomics Eurocentric bias is on the rise!!!

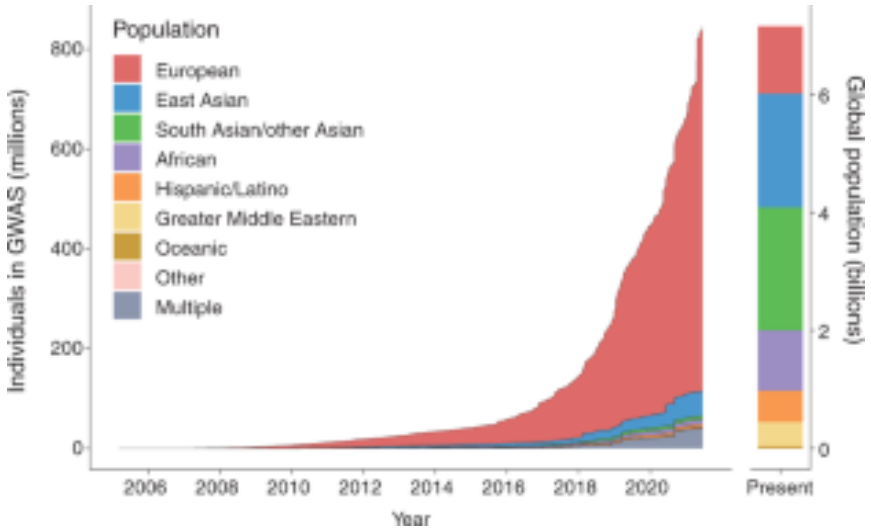
2016:
Europeans 81%
Africans 3%



2019:
Europeans 78.39%
Africans 2.03%

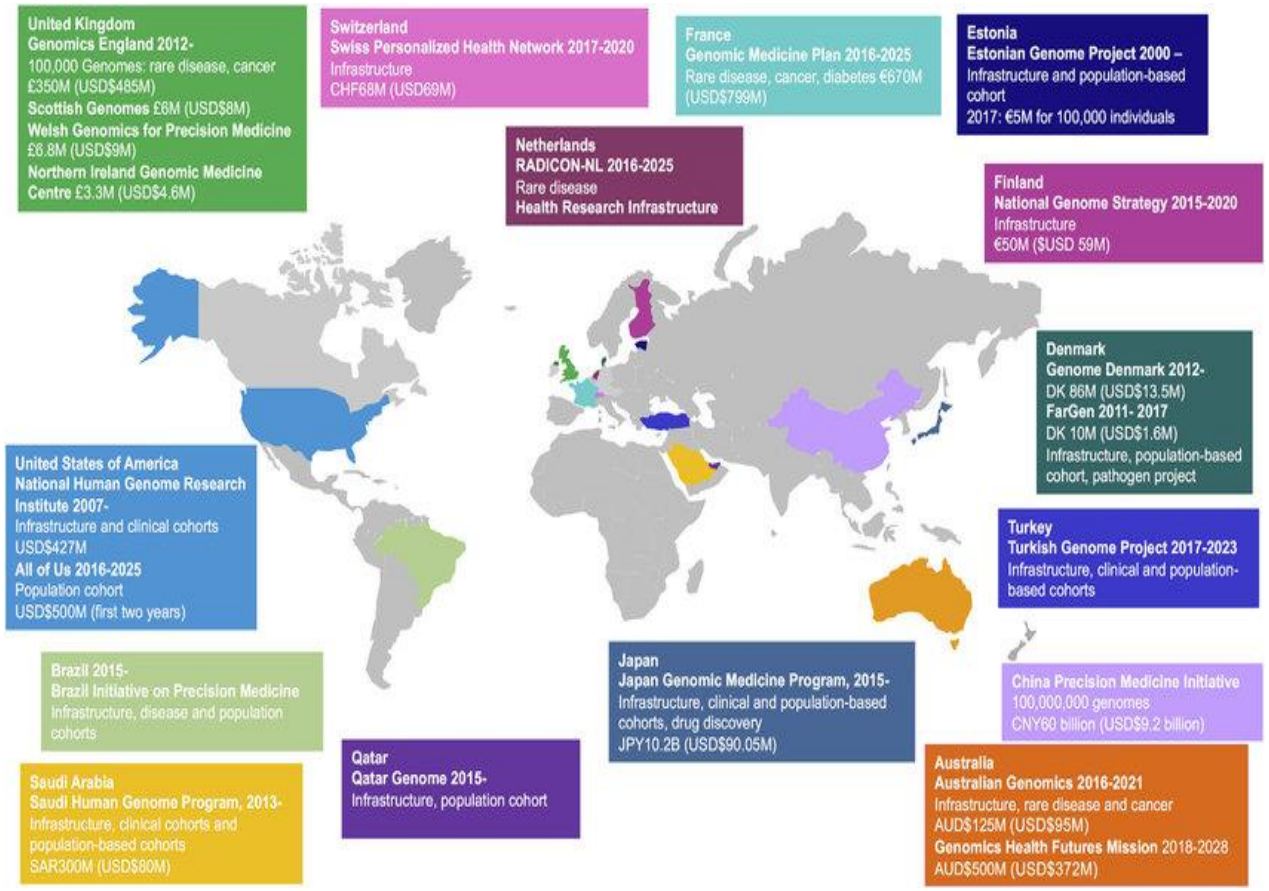


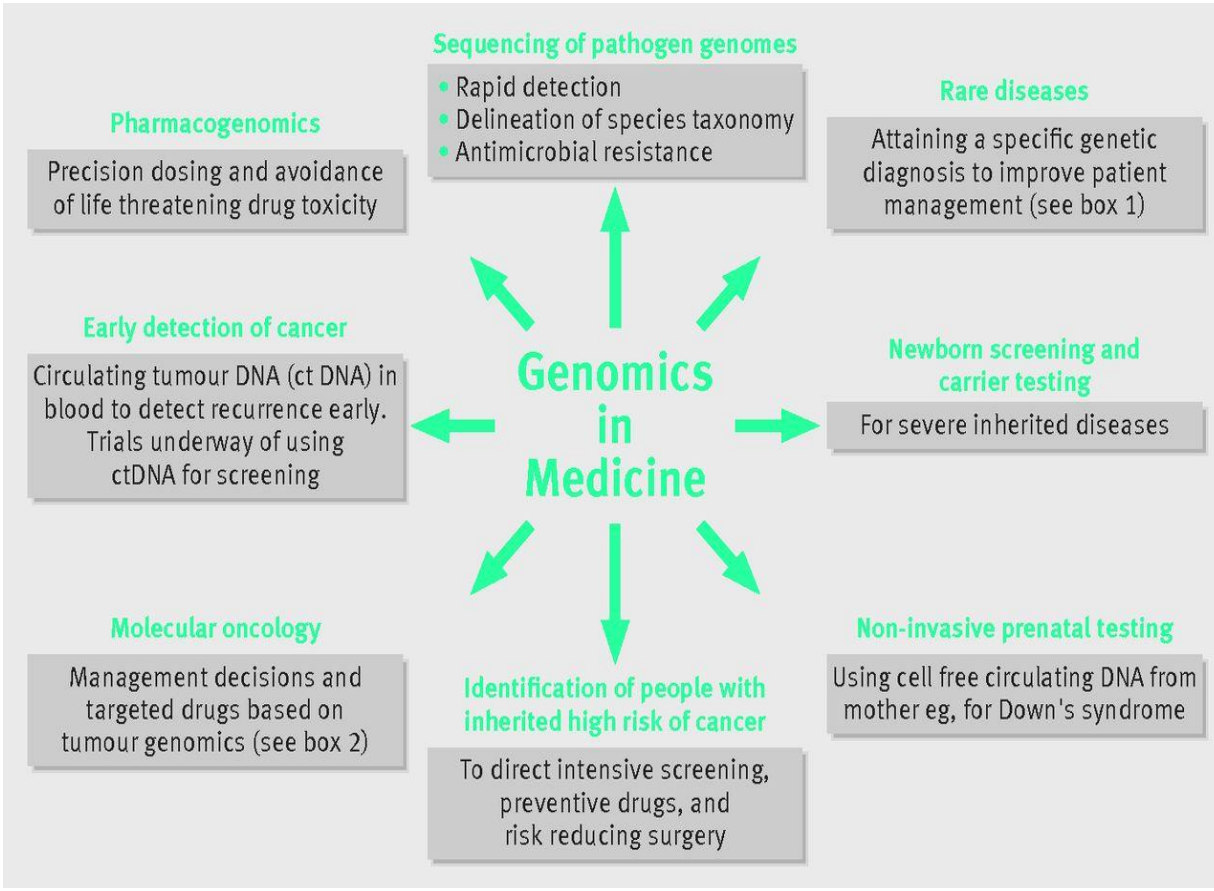
2022:
Europeans 86%
Africans 1.1%

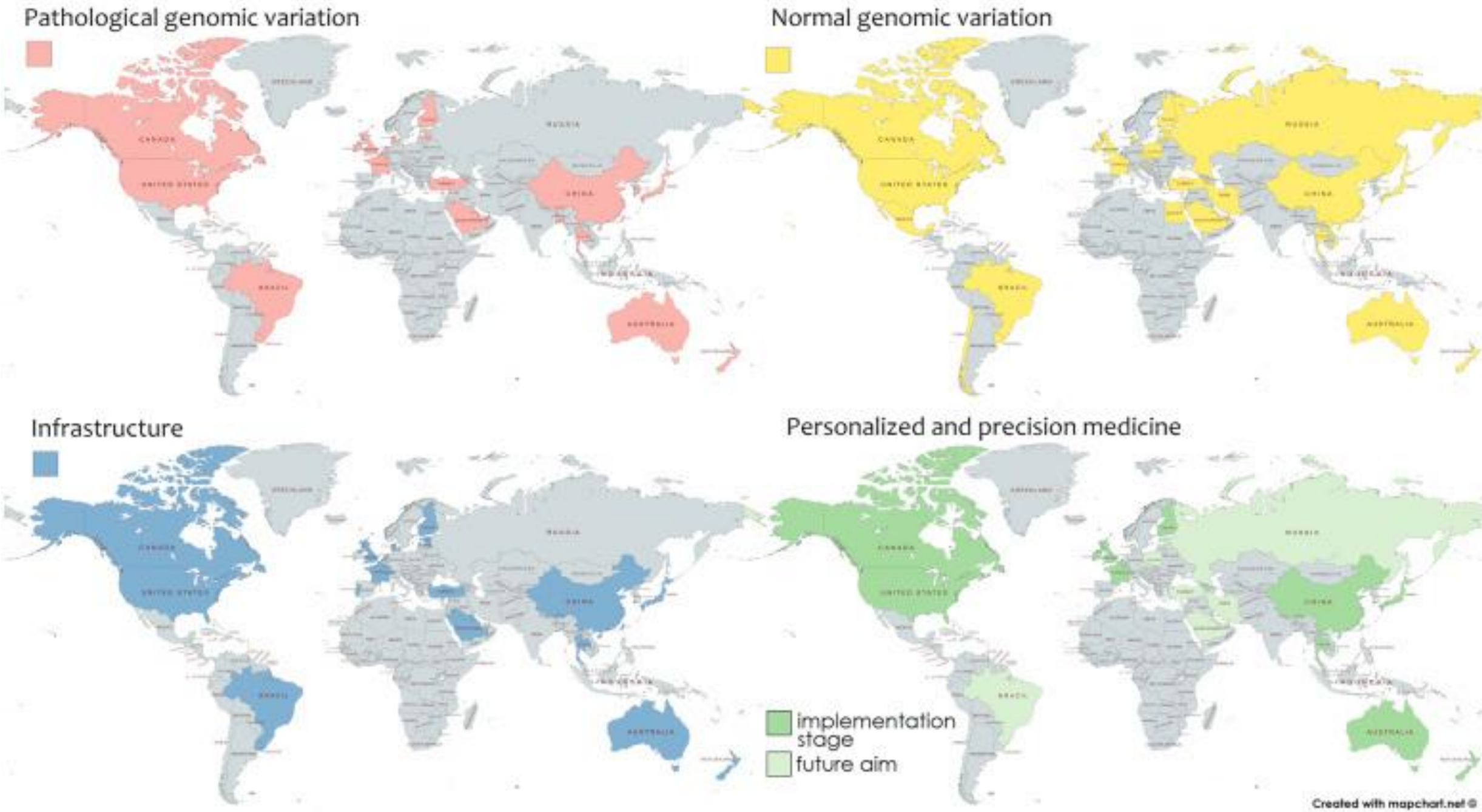


Courtesy: Prof Segun Fatumo

Global Status and Applications



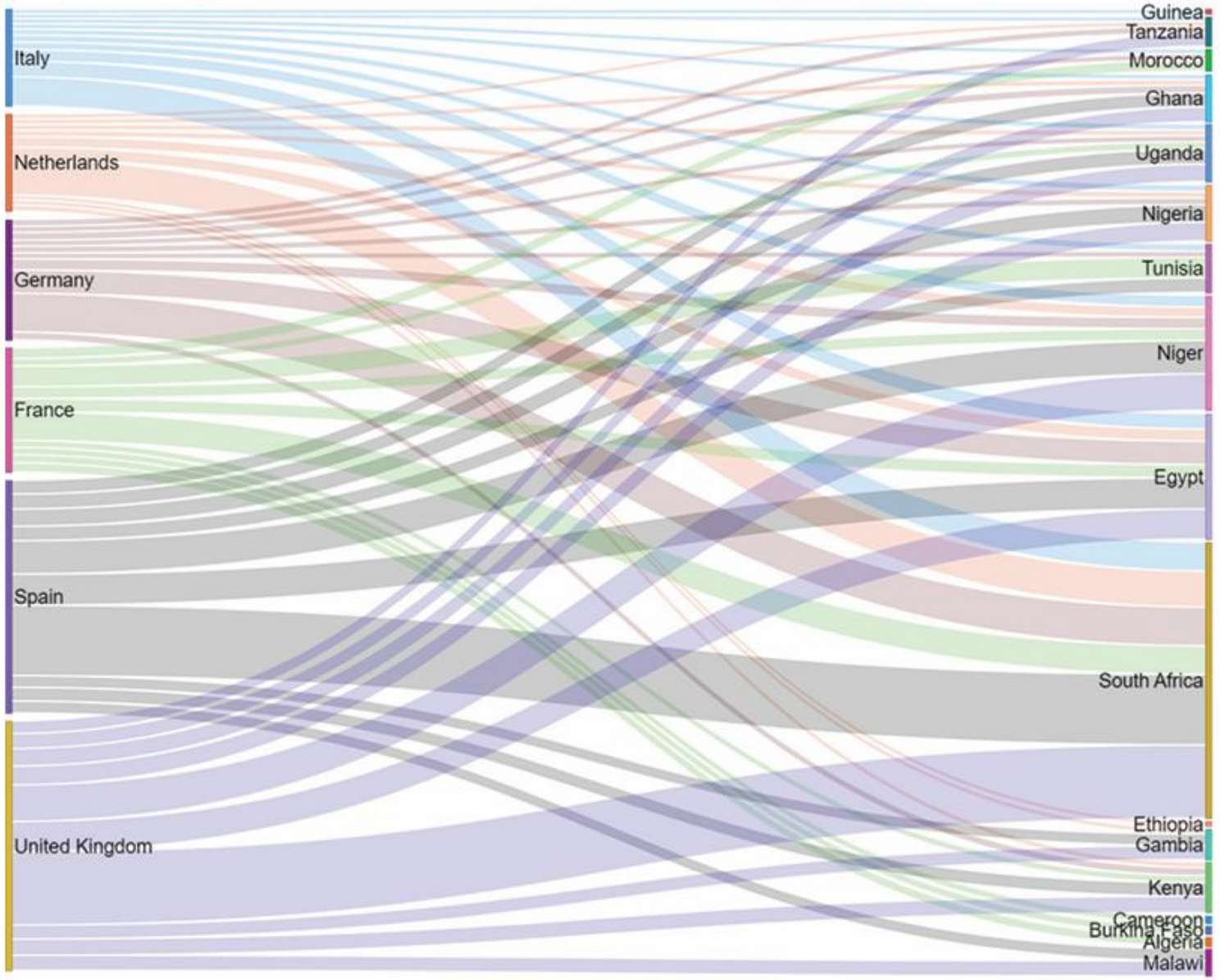



Pathological genomic variation
Normal genomic variation
Infrastructure
Personalized and precision medicine
implementation stage
future aim
Created with mapchart.net ©

Pressing issues in Africa

1. Building research capacity for infectious genomic research
2. Improving medical genetics and services
3. Setting up genetic testing for congenital diseases
4. Cytogenetic techniques as diagnostic tools – routine
5. Ethical considerations in genomics in Africa
6. Bio banking for genomic studies in Africa – socio-cultural issues
7. Standardized bio repositories : Resource for High quality samples in resource limited setting
8. Bioinformatics training challenges
9. Pharmacogenomics in Africa – challenges
10. Genetic syndromes in diverse populations - limitations

Co-authorship network between the highly active European countries (United Kingdom, France, Germany, Italy, Spain and the Netherlands) with their top African collaborating countries



EU-Africa PerMed

Action Plan to facilitate, foster and promote Personalised Medicine research collaboration between Europe and Africa

EU Africa PerMed has received funding from the European Union's Horizon 2020 Research and Innovation programme under grant agreement No 964333

Context of the Action plan

Key Objectives:	Facilitate collaboration in PM research.	Strengthen Africa-Europe bilateral STI relations.	**Core Features:**
Infrastructure development: Biobanks, genomic hubs.	Capacity building: Training, knowledge transfer.	Ethical and regulatory frameworks: FAIR principles and inclusivity.	**Why It Matters for Africa:**
	Provides tools to address local healthcare challenges.	Aims to build Africa's PM capacity and integrate it into healthcare systems.	

Strengths of the action plan

Infrastructure Development:
Biobanks and genomic hubs to address Africa’s research infrastructure gaps.
Enhanced bioinformatics networks for data analysis.
Capacity Building:
Focus on training and knowledge exchange to create skilled professionals.
Ethics and Governance:
Emphasis on FAIR principles, ethical data sharing, and regulatory frameworks.
Inclusivity:
Acknowledges the need for African representation in global research.

Challenges from an African perspective

- **Infrastructure Gaps:**
- Limited access to advanced research facilities.
- Reliance on external resources.
- **Sustainability Concerns:**
- Long-term funding and government buy-in.
- **Equity in Collaboration:**
- Risks of "helicopter science" and unequal partnerships.
- **Policy Gaps:**
- Lack of integration of PM into national health systems.

Opportunities for mutual benefit

- **Africa's Genetic Diversity:**
- Unparalleled opportunities for global genomic discoveries.
- **Knowledge Transfer:**
- European expertise in PM can strengthen Africa's research capacity.
- **Health Equity:**
- Collaborative projects can reduce health disparities and improve outcomes.

Actionable steps to implement the plan's recommendations

1

Promote African-Led Initiatives:

- Encourage African leadership in research and decision-making.

2

Tailor PM Strategies:

- Adapt solutions to Africa's socio-economic and cultural contexts.

3

Secure Long-Term Funding:

- Combine local and international funding sources.

4

Expand Training Programs:

- Include scientists, healthcare workers, and policymakers.

5

Leverage Existing Networks:

- Build on initiatives like H3Africa.

Health Economics of Personalised Medicine: Summary Table

- Every $1 invested in the Human Genome Project generated an estimated $141 in economic output.

Category	Key Statistic / Insight	Reference
Reduction in treatment cost	67% of psychiatric patients experienced overall cost reduction after pharmacogenomic intervention	Rinser, 2023 – LinkedIn article
Drug development savings	PM could lower drug development costs by ~17%, saving up to **$26 billion annually**	Sanogenetics blog
Oncology cost impact	Global implementation of PM in cancer could save **>$100 billion/year** by avoiding ineffective treatment	Socio-economics of PM in Asia (Routledge)
Cost-effectiveness baseline	Most PM interventions evaluated were cost-effective compared to standard care	Kewal K. Jain., 2009 – Springer Chapter

Africa's people must be able to write their own genomics agenda

Genomics on the continent is finally getting the attention it deserves – but funding needs to come from more diverse sources.