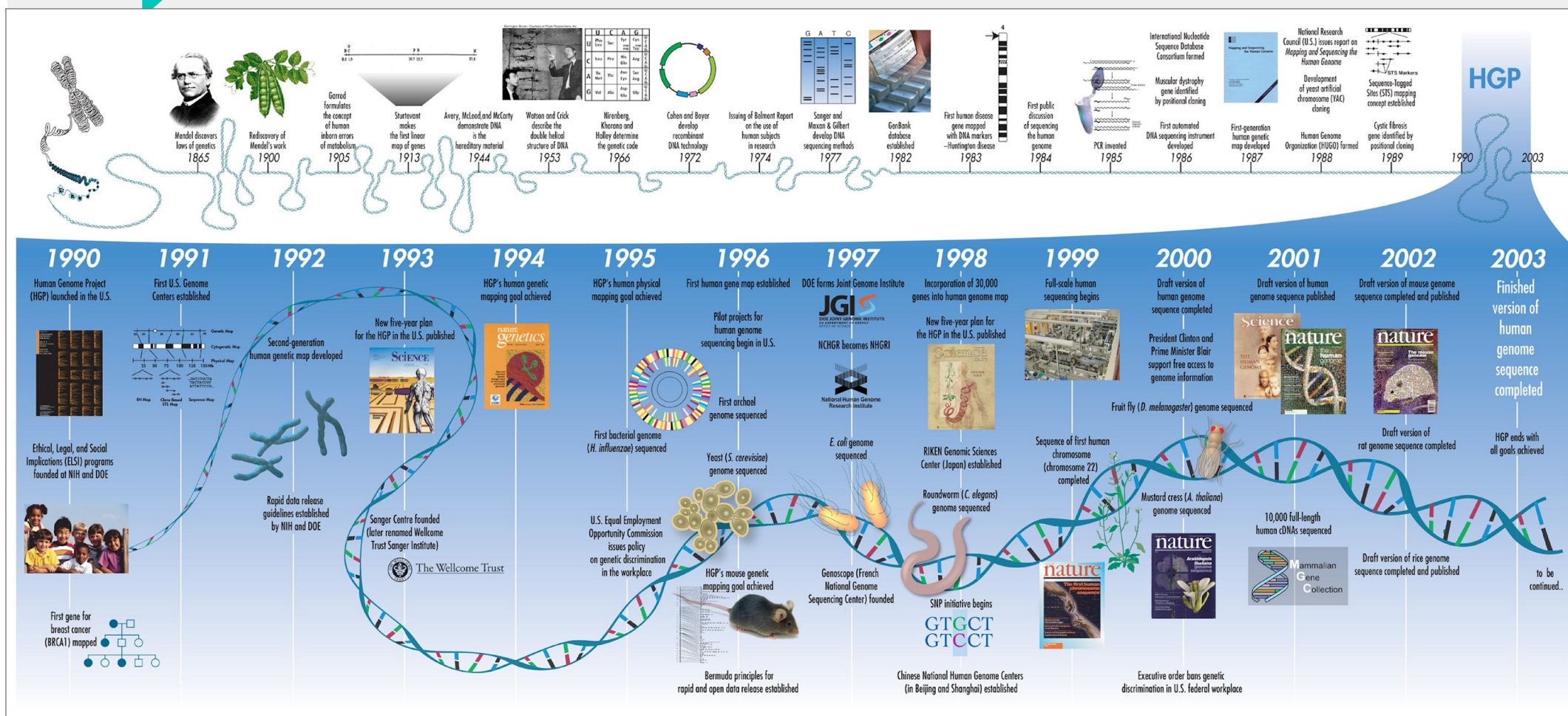


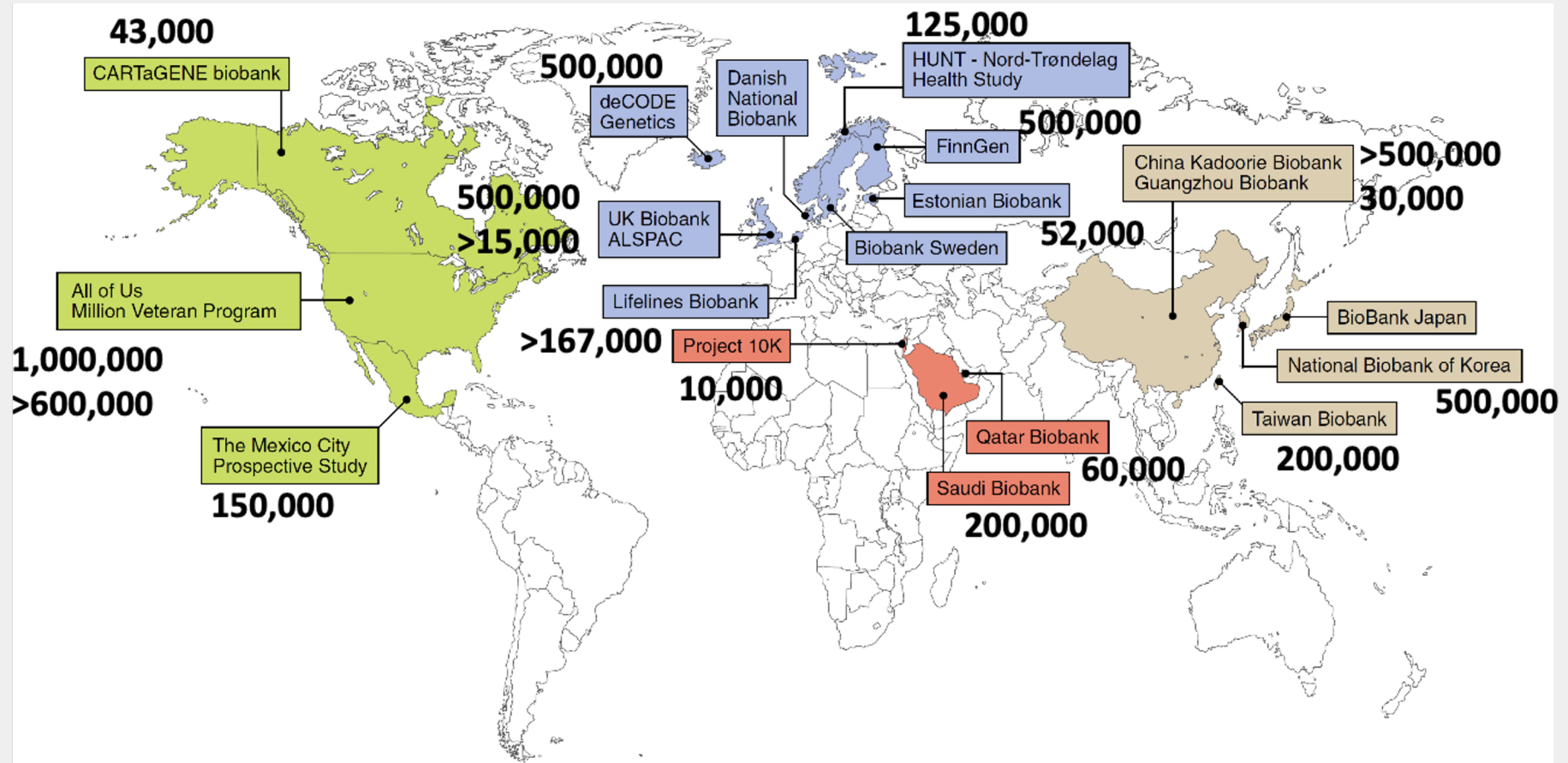
Taiwan Biobank

Su Ming-Wei wei@ibms.sinica.edu.tw

Human Genome Project



Global biobanks



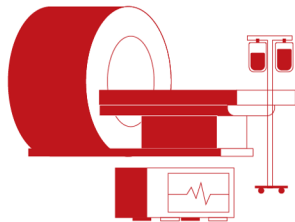
Why Taiwan ?

Holo Taiwanese
Hakka Taiwanese
Mainlanders
Taiwanese indigenous peoples
Taiwanese new immigrants

**Why Taiwan's Health Care System
is the Best in the World**



Well-trained
medical personnels



New equipment



Diverse professions



www.president.gov.tw

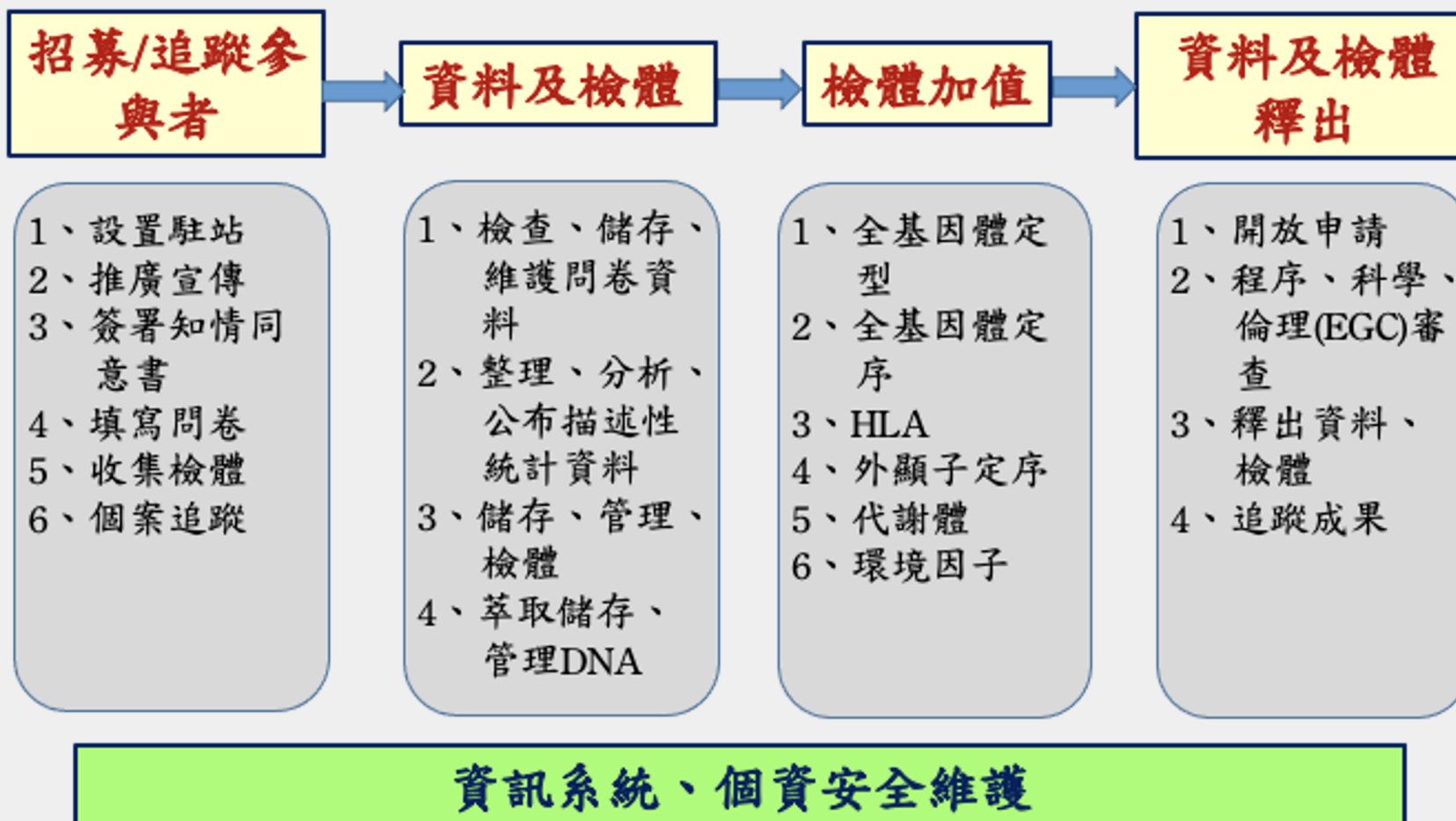
<https://ogme.edu.tw/lc/culturalGroups>

<https://tendashsix.com/taiwan-medical-service-ranked-first/>

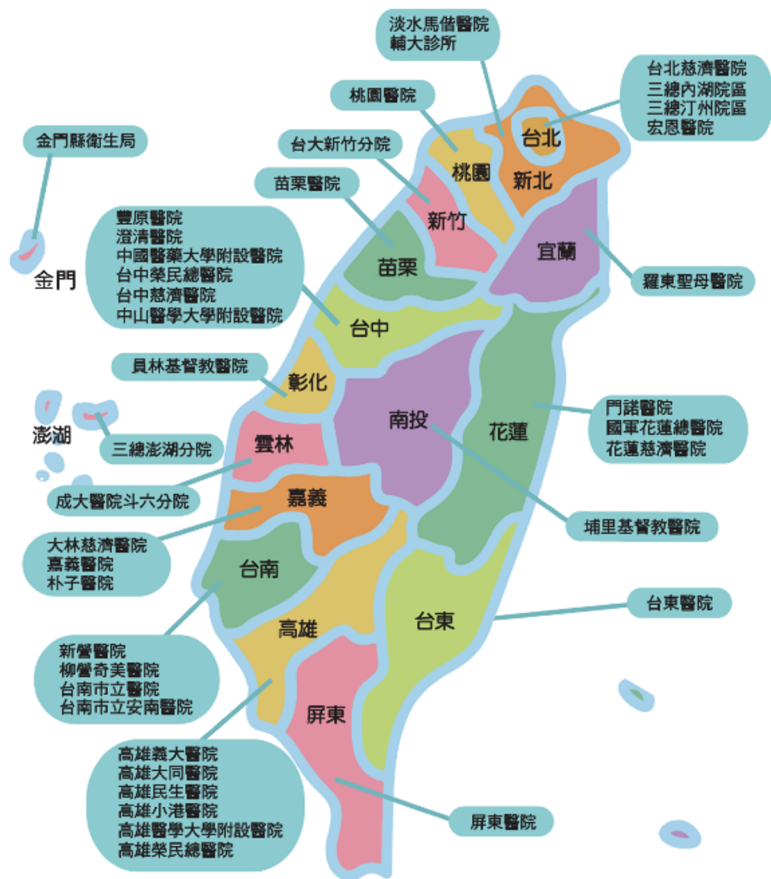
TWB

- 主管機關：衛生福利部
- 設置者：中央研究院
- 依2010.2.3 總統府頒布執行之《人體生物資料庫管理條例》設置
- 設有倫理委員會，針對資料庫之管理等有關事項進行審查及監督
- 2012.10.24 取得設置許可
- 第一個主管機關核准設置之人體生物資料庫
- 2012.11.8 開始正式收案 預計目標20萬社區民眾

TWB infrastructure



參與流程



取得您的同意



進行問卷訪談



2021.04 available data and samples

200,000
(> 20 years old)
General population

參與個案

144,990

完成第一輪追蹤個案

35,950

健康資訊

生活習慣問卷	~ 166,438筆
身體檢查數據	~ 166,409筆
血清生化數據	~ 166,339筆
進階追蹤影像	~ 20,408筆

遺傳資訊 (筆數)

• 全基因定型	116,066
• 全基因定序	2,010
• 人類白血球組織抗原分型	1,102
• DNA 甲基化定序	2,474


環境暴露資訊

• 血液代謝體核磁共振光譜	869
• 尿液塑化劑與三聚氰胺	1,353

生物檢體 (管數)

• DNA (管)	697,439
• 血漿 (0.4 c.c. 每管)	1,725,817
• 尿液 (1.5c.c. 每管)	1,028,789

<https://www.biobank.org.tw/index.php>



首頁 最新消息 收案統計 關於資料庫釋出 ▾ 檔案下載 使用者註冊/登入

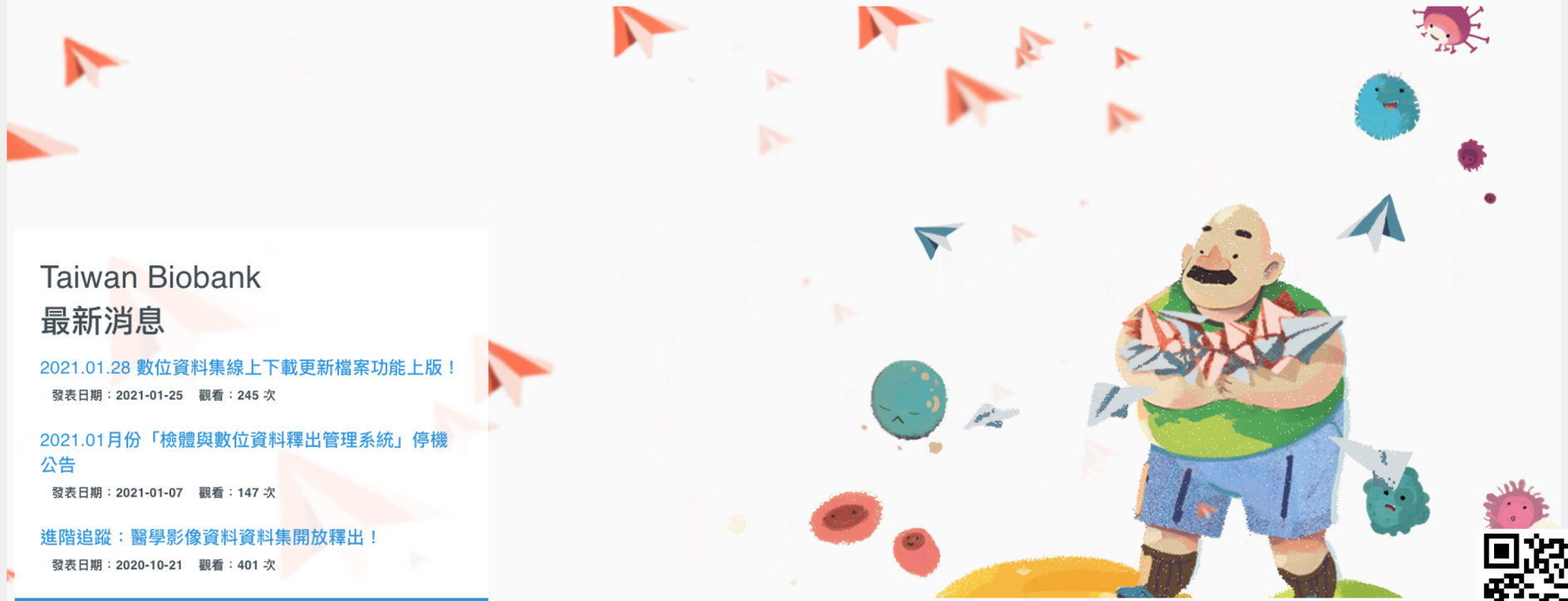
Taiwan Biobank 最新消息


2021.01.28 數位資料集線上下載更新檔案功能上版！
發表日期：2021-01-25 觀看：245 次

2021.01月份「檢體與數位資料釋出管理系統」停機公告
發表日期：2021-01-07 觀看：147 次

進階追蹤：醫學影像資料資料集開放釋出！
發表日期：2020-10-21 觀看：401 次

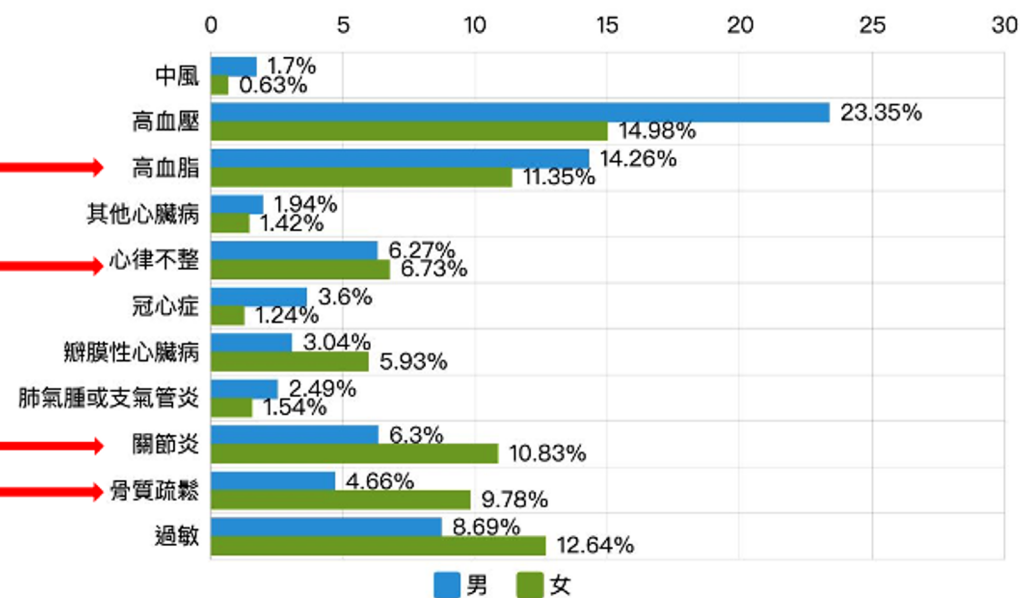
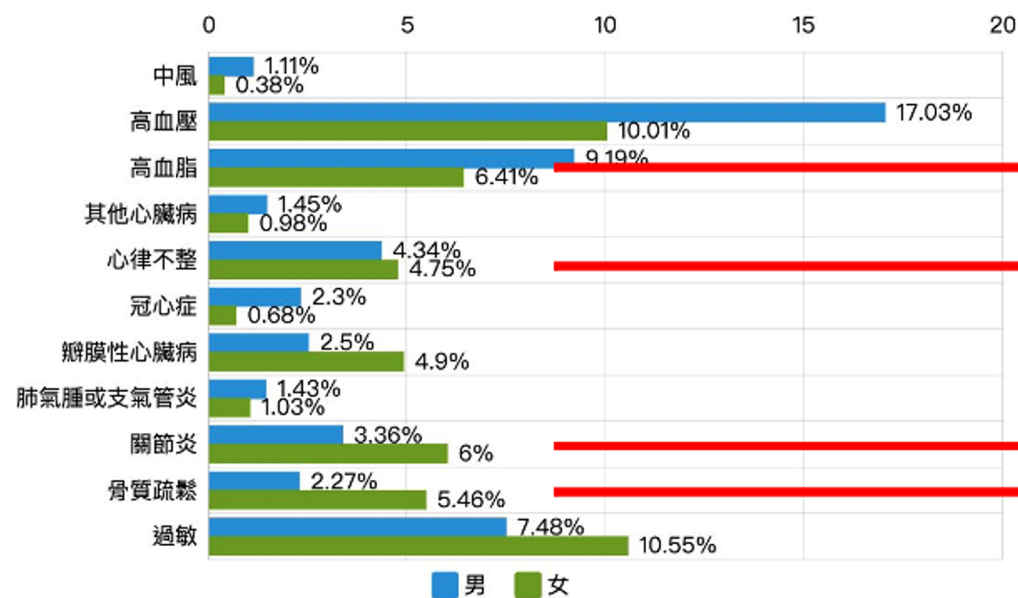
[了解 更多](#)





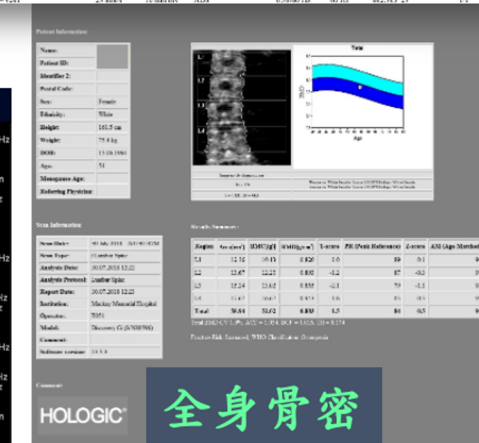
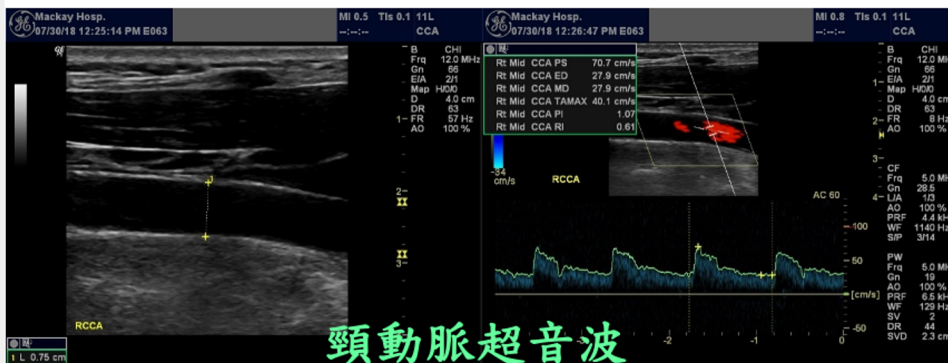
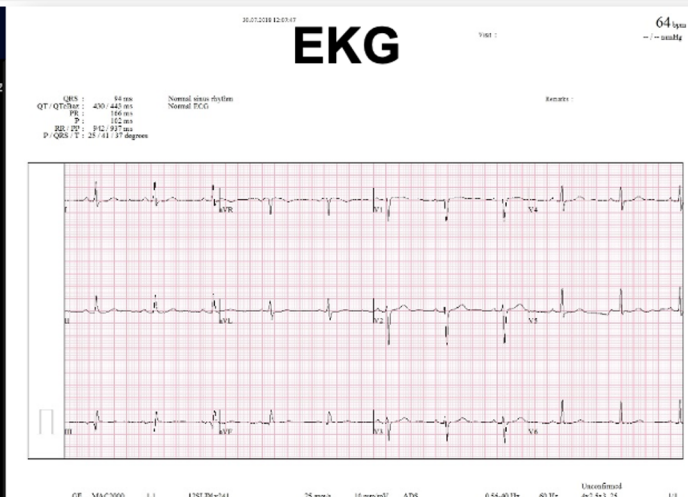
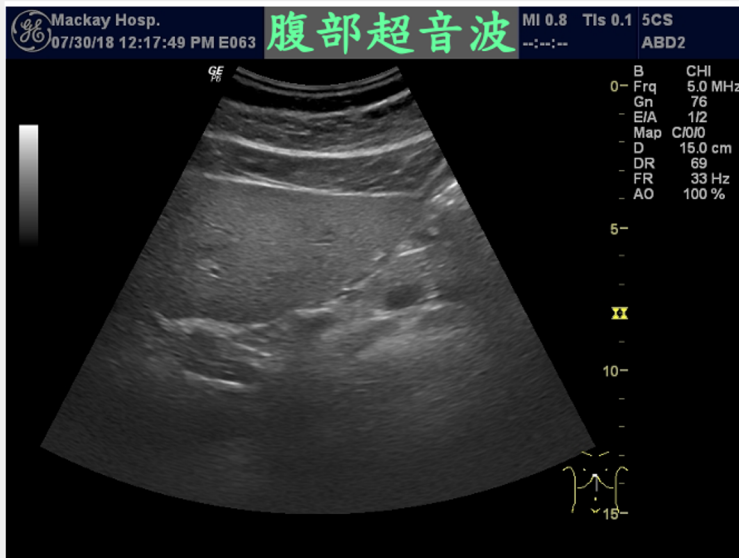
<https://reurl.cc/jqjqNZ>

follow-up program



Characteristics	Male (%)	female (%)
BMI		
<18.5	1.29	4.42
18.5-24	35.83	56.96
24-27	35.25	22.58
>27 (Obesity)	27.62	16.05
Waist-Hip Ratio		
M \geq 0.92; F \geq 0.88	36.05	30.00
Body Fat Rate (male, female)		
\leq 17% , \leq 20%	12.42	2.02
17-23% , 20-27%	39.11	20.02
23-25%, 27-30%	16.02	17.81
>25% , >30%	32.45	60.11

advance follow-up program



distribution of urinary melamine and phthalate metabolites

Urinary metabolites ($\mu\text{g/g}$ crea.)	TWB (n=1,155)	NHANES (n=2,974) ^a
Melamine ($\mu\text{g}/\text{mmol}$ crea.)	0.46 (0.43-0.49)	---
MEHP	11.37 (10.69-12.09)	N.D. ^b
MEOHP	8.17 (7.81-8.54)	3.70 (3.49-3.92)
MEHHP	12.68 (12.06-13.33)	5.86 (5.62-6.12)
MECPP	19.17 (18.36-20.02)	9.14 (8.58-9.74)
MCMHP	3.88 (3.61-4.16)	--
MBzP	1.04 (0.98-1.1)	4.63 (4.06-5.28)
MnBP	20.51 (19.46-21.61)	10.2 (9.53-10.9)
MiBP	8.38 (7.92-8.87)	8.71 (8.06-9.42)
MEP	12.86 (11.82-13.99)	34.7 (31.0-39.0)
MMP	2.22 (2.09-2.36)	---
MiNP	N.D. ^b	N.D. ^b

^aData from the urine samples of 2015-2016 for the U.S. population from the National Health and Nutrition Examination Survey. (NHANES, 2019)

^bN.D., the chemical was analyzed but the proportion of results below limit of detection was too high to provide a valid result.

data and tubes



~1.5 PB



~3 million tubes

ISO certificate

ISO/IEC 27001 for management system



ISO/IEC 29100 for personal information protection



link NHIRD - TWB projects

通過倫審共 91 案	已串連	EGC 倫審中
	18 案	5 案
總計	23 案	

1. 臺灣人體生物資料庫為生物醫學研究的目的而建立，且經參與者「事前同意」及完善的「事後退出」流程，保障參與者權利
2. IRB EGC 雙重保障

TWB-NHIRD



身分證號+Release ID
實體加密後傳輸



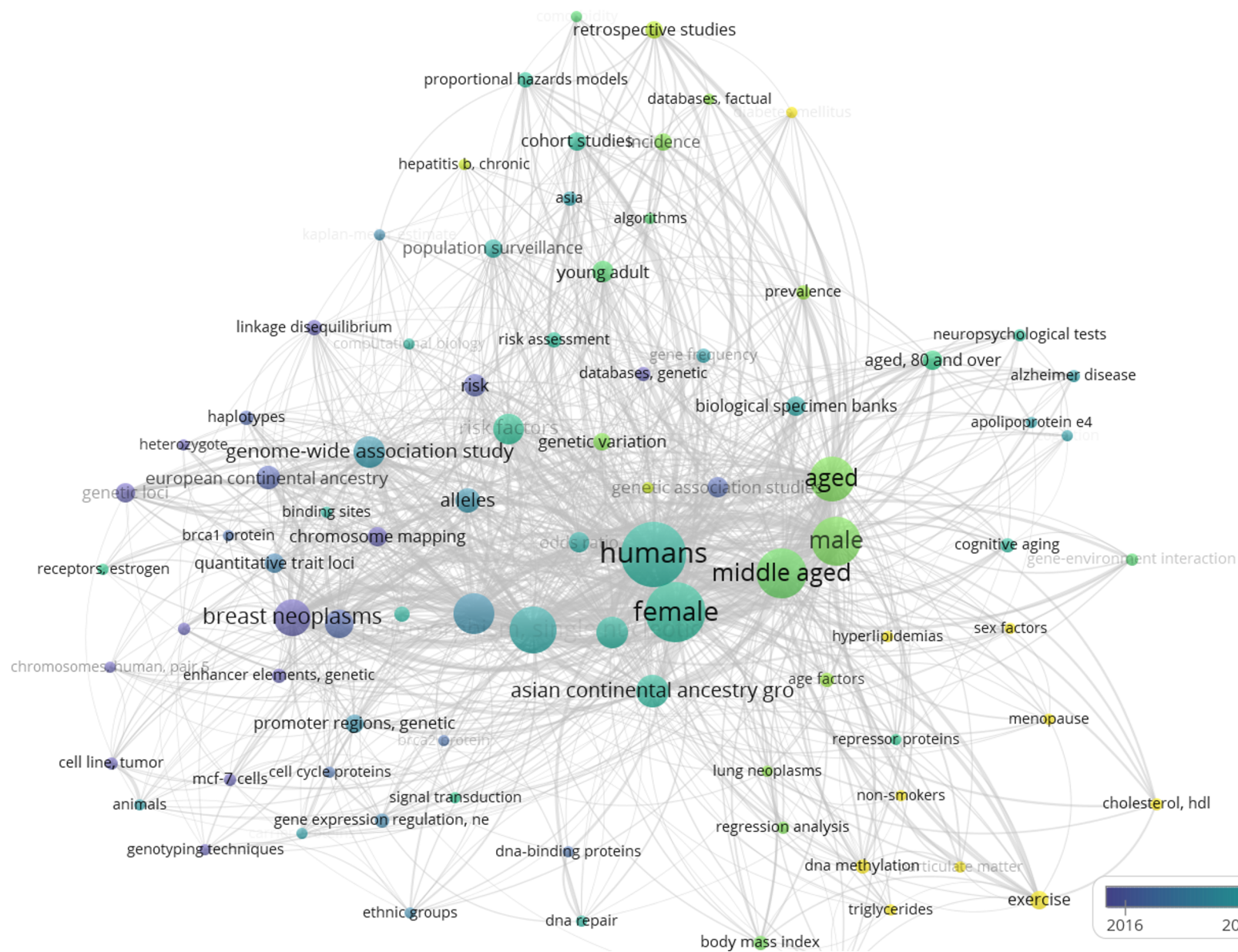
Release ID + TWB data

1. Release ID + TWB data 加密傳輸
2. email Key to 申請者



TWB - NHIRD

Diseases	Sex	TWB (%)	NHIRD (%)
Diabetes	Male	10.98	12.53
	Female	7.25	8.84
Hypertension	Male	29.12	26.7
	Female	16.86	17.08
Hyperlipidemia	Male	26.69	26.09
	Female	20.51	21.05



- 全國設置40個駐站
- 14萬一般民眾參與，追蹤3萬5千例
- 完整生活問卷、檢測資料、生物檢體
- 數位資訊 1.2 Petabyte (PB)
- 生物檢體 >300萬管，
- 資訊安全及隱私保護獲國際雙認證

- 設置Taiwan View公開網站
- 建立基因體學、表觀基因體學、代謝體學、及環境暴露等資訊
- 一般民眾之描述性統計分析
- 申請者成功串聯健保資料庫
- 成功國際傳輸

- 2,000 例全基因體序列
- 開發國人專屬全基因體定型晶片TWB2
- 10萬筆全基因體定型
- 建立以GRCh38版人類基因體參考序列
- 基因體定型晶片之基因體插補
- 完成逾2,000筆尿液塑化劑代謝物分析

- 支援41個機構之141件計畫
- 釋出數位資料超過九千萬人次、生物檢體近18萬管
- 申請者發表相關國際期刊逾200篇
- 開發釋出申請系統，優化申請流程，提升便捷與安全之異地服務系統

收
案

加
值

資
訊

釋
出

Taiwan Biobank - 垂直整合



垂直整合



健康資訊

生活型態問卷、生理檢測、血液生化檢測、生物檢體

基因資訊

全基因體定型、全基因體定序、全外顯子定序、DNA 甲基化、人類白細胞抗原

環境暴露數據

核磁共振代謝體、尿液三聚氰胺
尿液塑化劑代謝物

族群世代長期追蹤

中醫問卷、心電圖、全身骨密度、頸部超音波
腹部超音波、甲狀腺超音波、腸道菌相*、穿戴式裝置*、新興檢體*

*規劃中

串聯整合

環保署空氣品質監測資料庫

體育署體適能調查資料庫

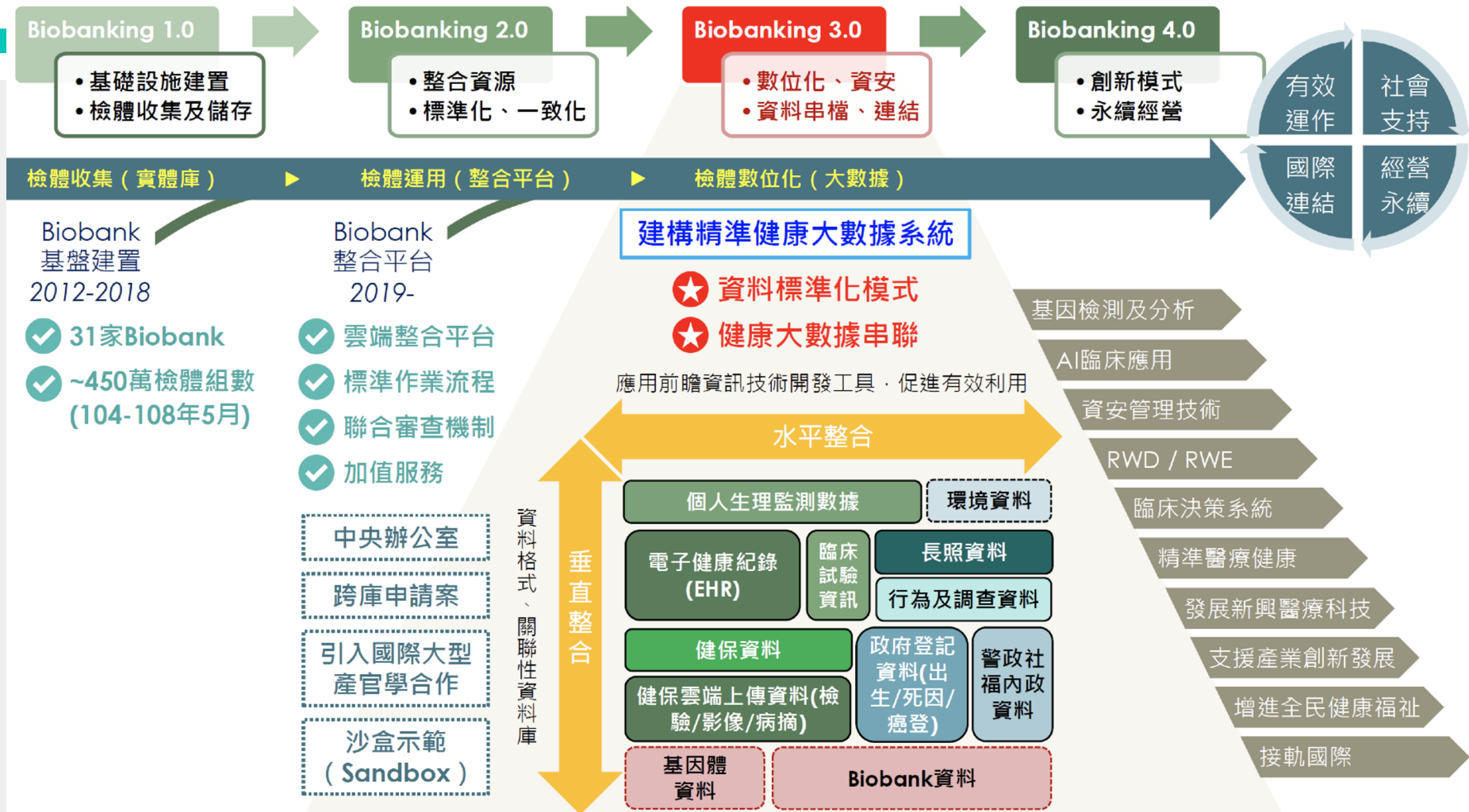
健保資料庫

國民健康署國民營養調查

長照資料

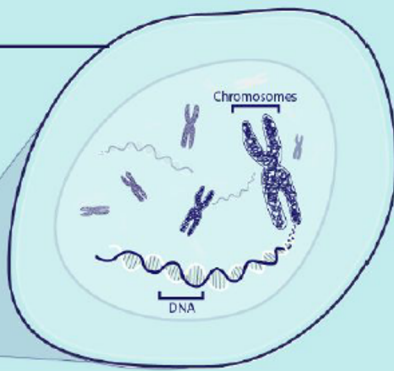
健康大數據 ➤ ➤ ➤ 精準健康照護系統

建構以大數據為基礎之國家精準健康架構



Human cell

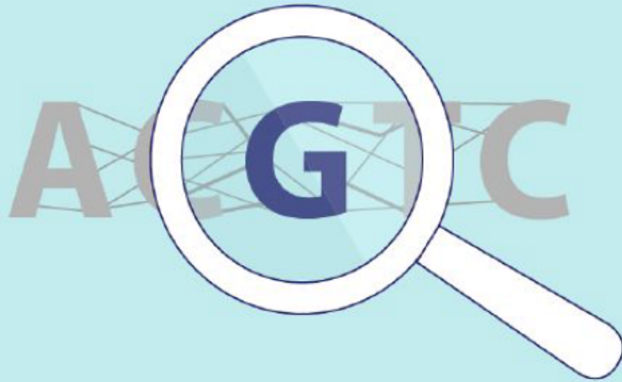
Most cells in the human body have a **complete** set of genes



Your **genome** is one whole set of all your genes plus all the DNA between your genes.

There are around **20,000** genes in your **genome**

Now



We know that the non-gene (non-coding) parts of your genome may have a role to play so we look at the whole thing, every single letter, and how the different parts work together.

5% [**were analysed**
Only the active genes were looked at



Your genome

with

3 Billion

pairs of letters in the human genome

AAGTAATATGC
TTCTAGGCGTC
TCAAGATGCAT
CTAGCACAGC
GCCCTTTATTA
TCTCTATACTCA
ACTACTAGGGC
TATTTTCATATCT
AAATAC**G**CTCG
AGGCTACTGAC
TTATGCTATCG
ATCTCGAGCGC
TDCCGTAATTT
TCGCGAATCAG
AAGTAATATGC
TTCTAGGCGTC
TCAAG**A**TGCAT
CTAGCACAGC
GCCCTTTATTA

95%

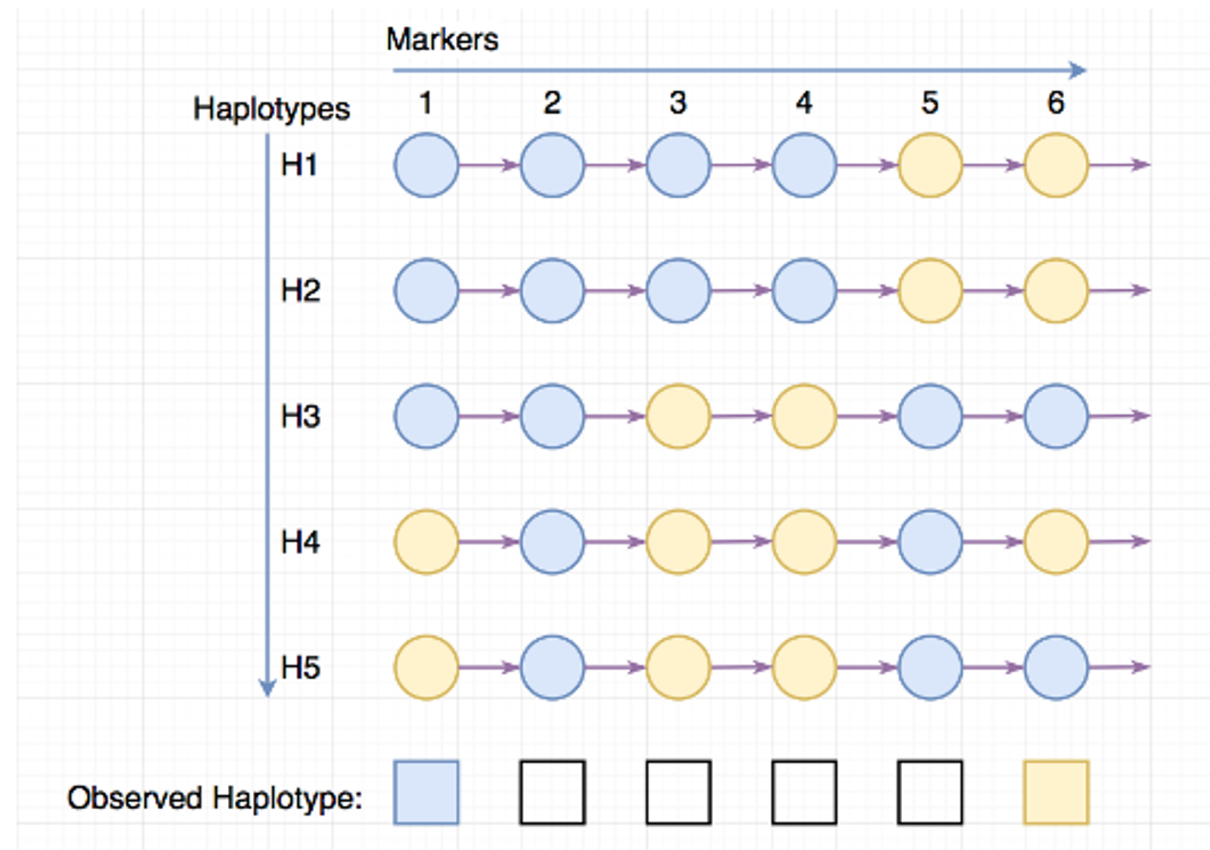
were unused

All the non-gene sections that we didn't understand were disregarded as useless

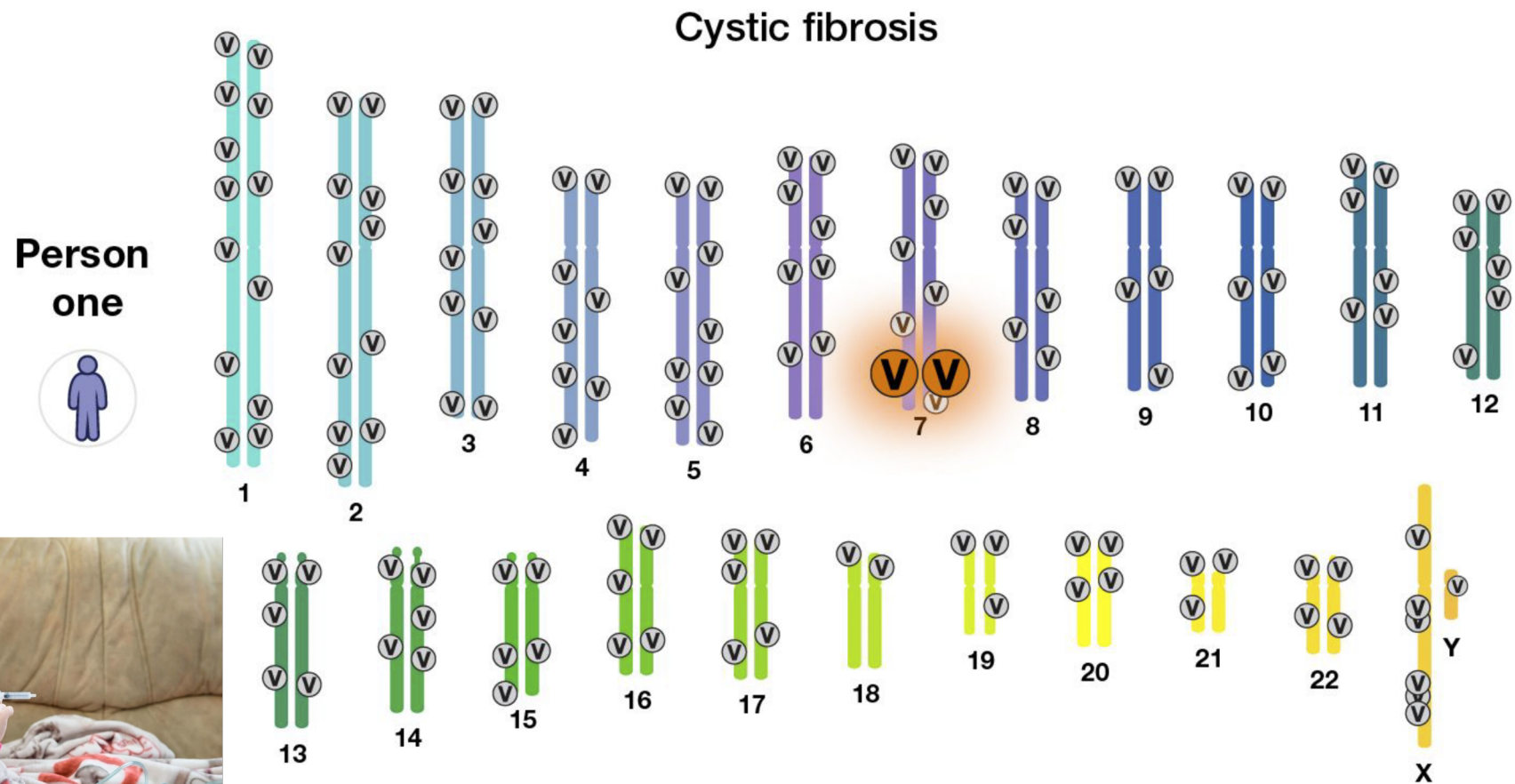


臺灣 BIOBANK • 健康世代
Taiwan Biobank 中央研究院 • 臺灣人體生物資料庫

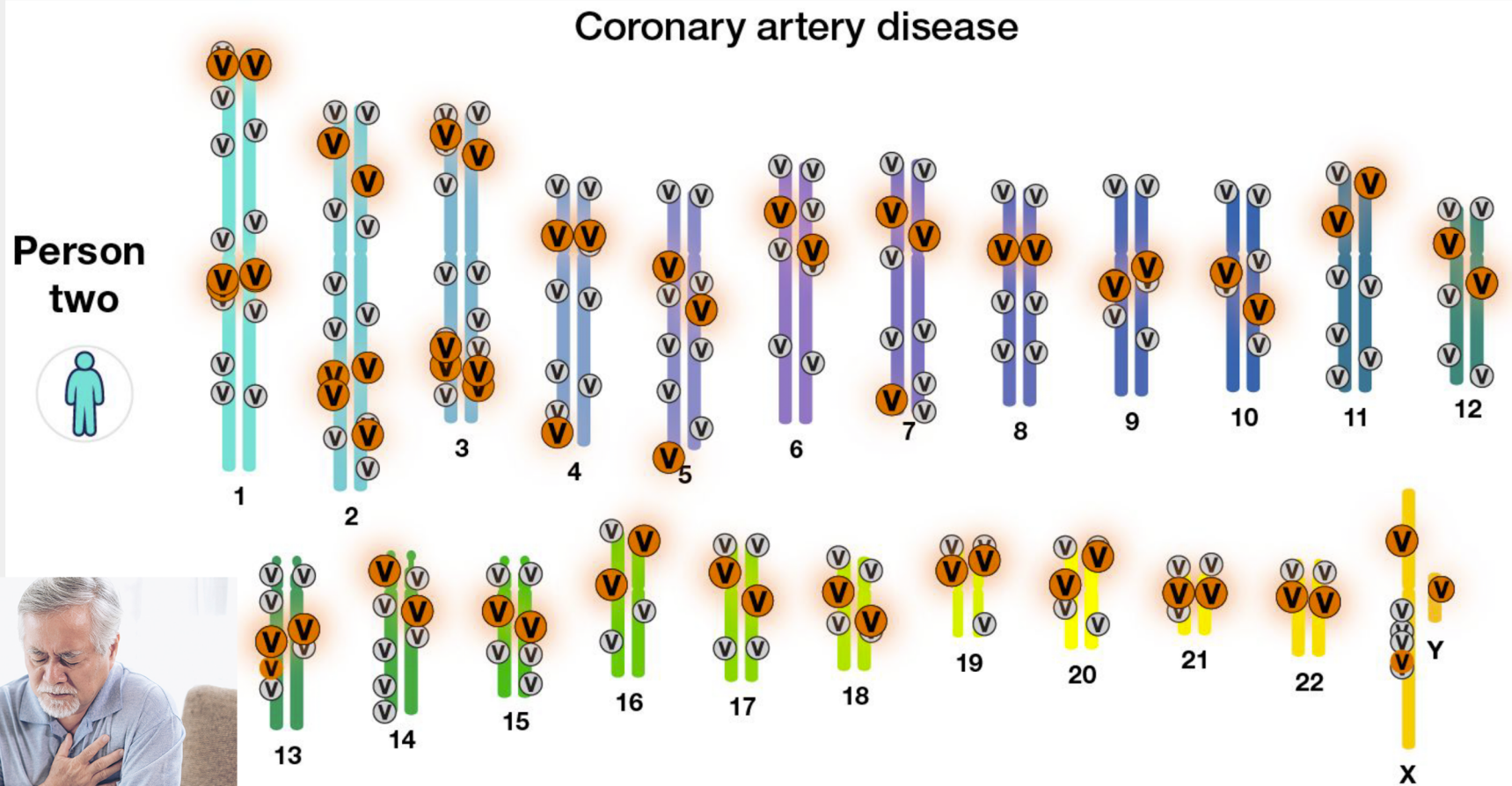
chip design



cystic fibrosis (囊狀纖維化) → transmembrane conductance regulator (CFTR) gene on chromosome 7.

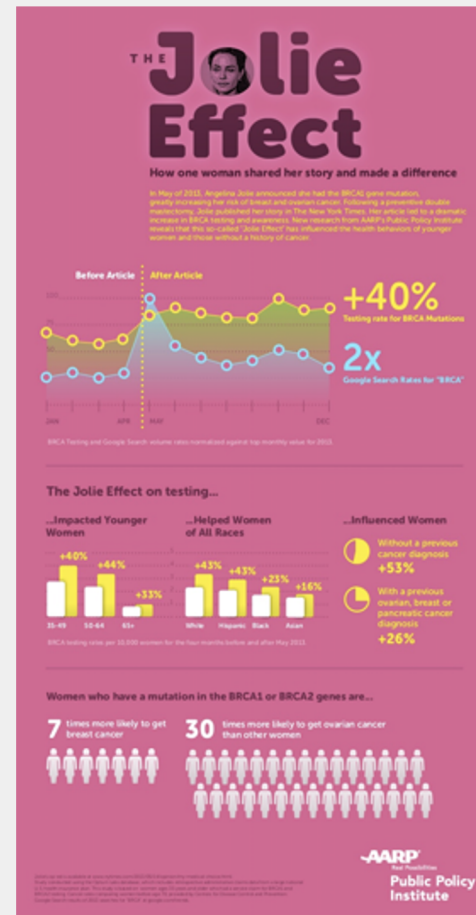


complex diseases (polygenic disease)

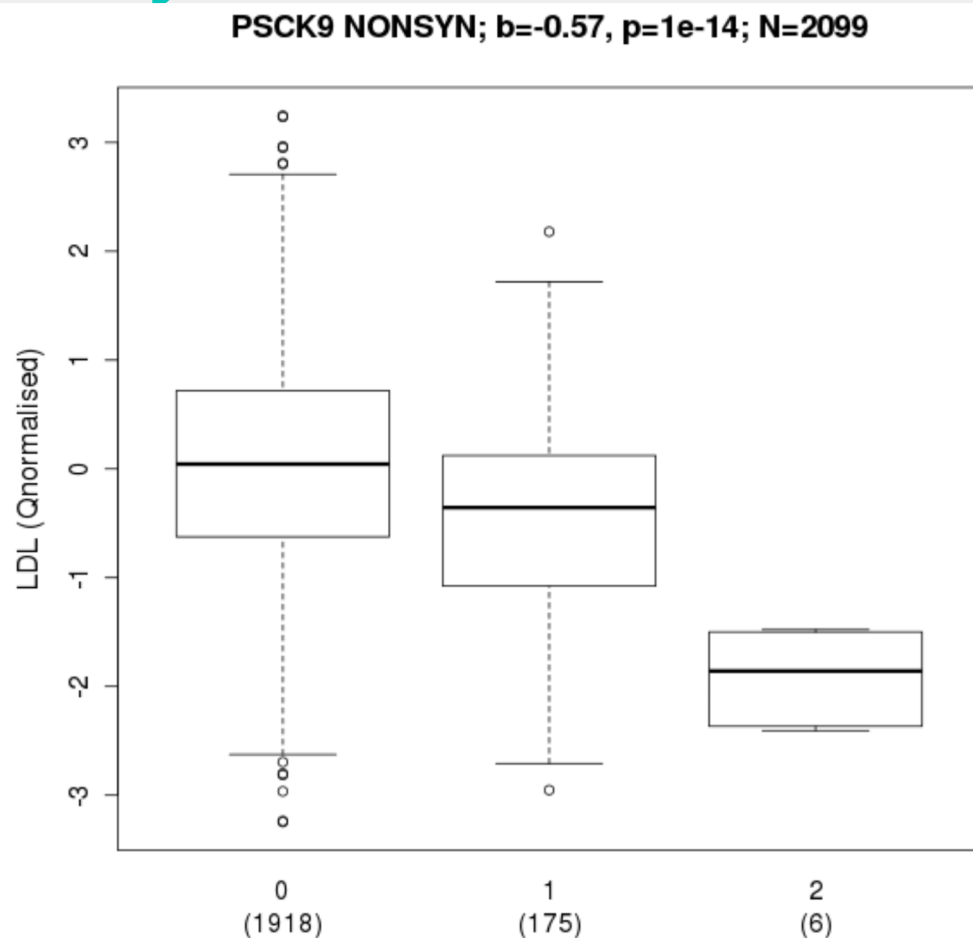


sigle gene

Jolie Effect

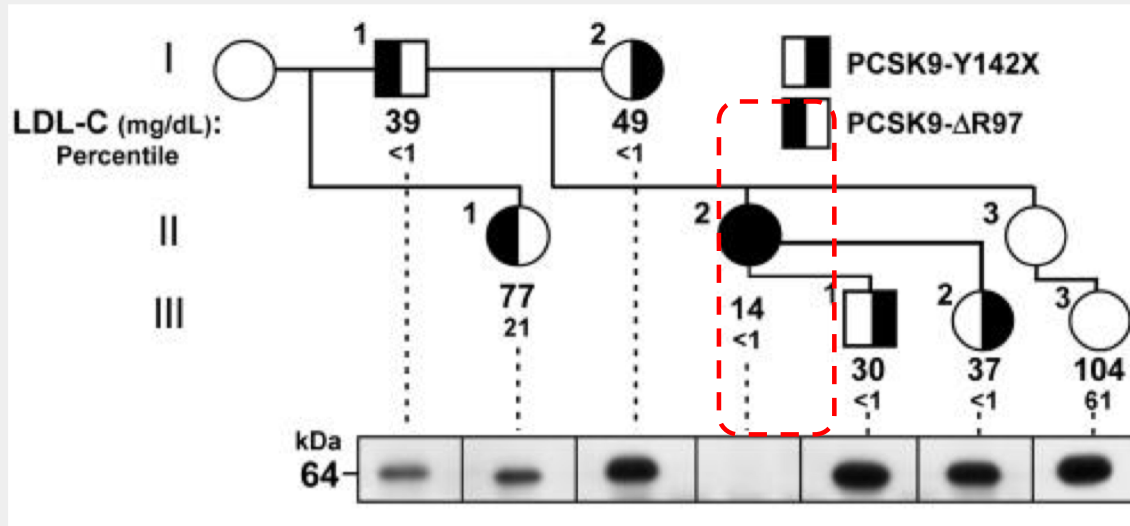


GENETIC VARIANT “RS11591147” IN PCSK9



- Carriers of T variant have lower levels of LDL cholesterol than carriers of G variant
- LDL is a strong risk factor for heart disease

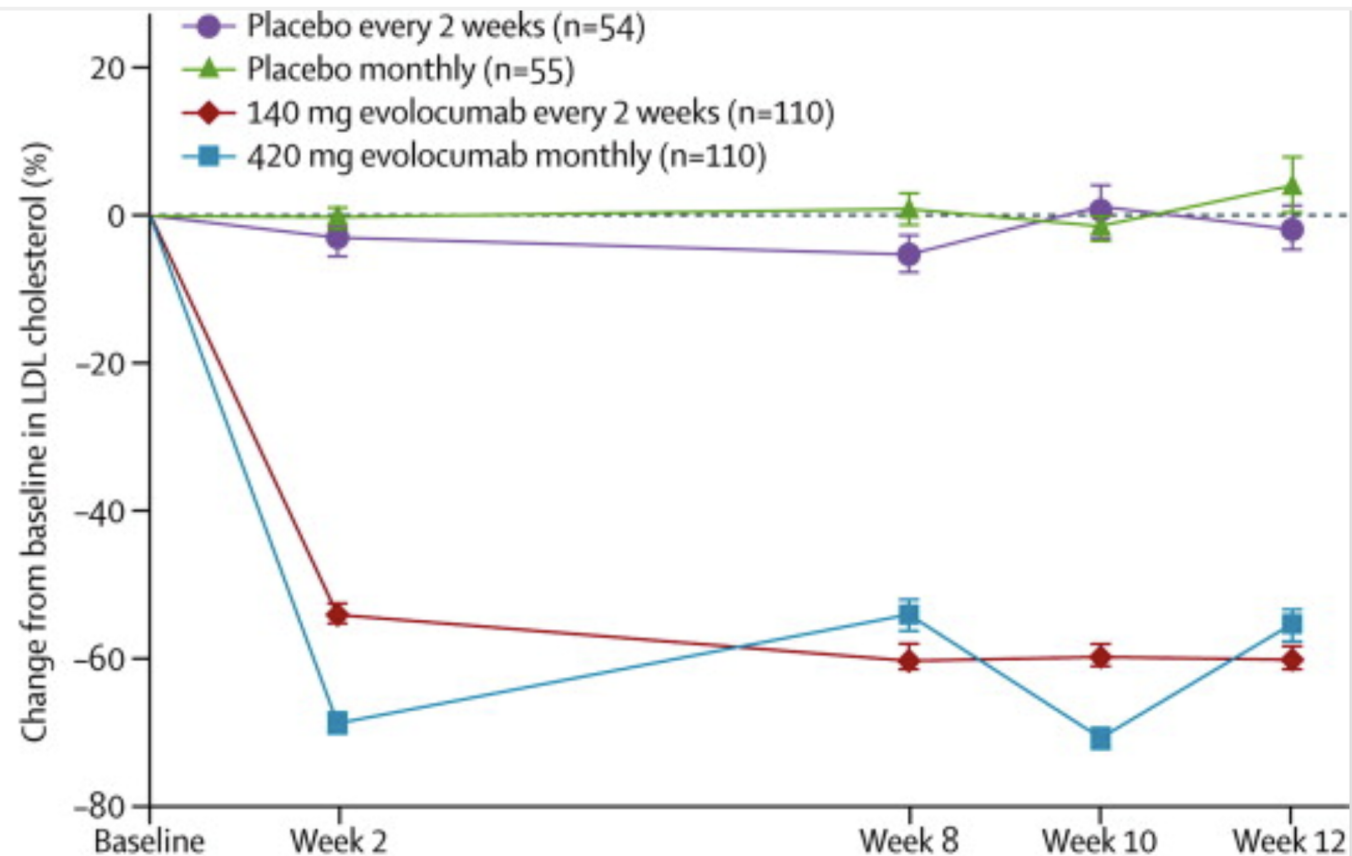
A HUMAN KNOCK-OUT OF PCSK9 (2006)



Individual **II.2** has zero working copies of PCSK9 gene

- no circulating PCSK9 and an LDL-C of only 14 mg/dL
- apparently healthy, fertile, normotensive, college-educated woman with normal liver and renal function tests who works as an aerobics instructor
- Why is this very interesting observation? Inhibiting PCSK9 might be a safe way to reduce LDL

PCSK9 inhibition with evolocumab (AMG 145) in heterozygous familial hypercholesterolaemia (RUTHERFORD-2): a randomised, double-blind, placebo-controlled trial



Evolocumab every 2 weeks	..	↑	↑	↑	↑	↑	↑
Evolocumab monthly	..	↑	..	↑	..	↑	..

Evolocumab and Clinical Outcomes in Patients with Cardiovascular Disease

Marc S. Sabatine, M.D., M.P.H., Robert P. Giugliano, M.D., Anthony C. Keech, M.D., Narimon Honarpour, M.D., Ph.D., Stephen D. Wiviott, M.D., Sabina A. Murphy, M.P.H., Julia F. Kuder, M.A., Huei Wang, Ph.D., Thomas Liu, Ph.D., Scott M. Wasserman, M.D., Peter S. Sever, Ph.D., F.R.C.P., and Terje R. Pedersen, M.D. for the FOURIER Steering Committee and Investigators*

FDA Approves Amgen's Repatha (evolocumab) to Prevent Heart Attack and Stroke



Dec 1 2017

In the Repatha cardiovascular outcomes study (FOURIER), [Repatha reduced the risk of heart attack by 27%](#), the [risk of stroke by 21%](#) and the risk of [coronary revascularization by 22%](#)..

precision medicine in Taiwan

Use of HLA-B*58:01 genotyping to prevent allopurinol-induced severe cutaneous adverse reactions in Taiwan: national prospective study

BMJ 2015;351:h4848 Sep 23, 2015

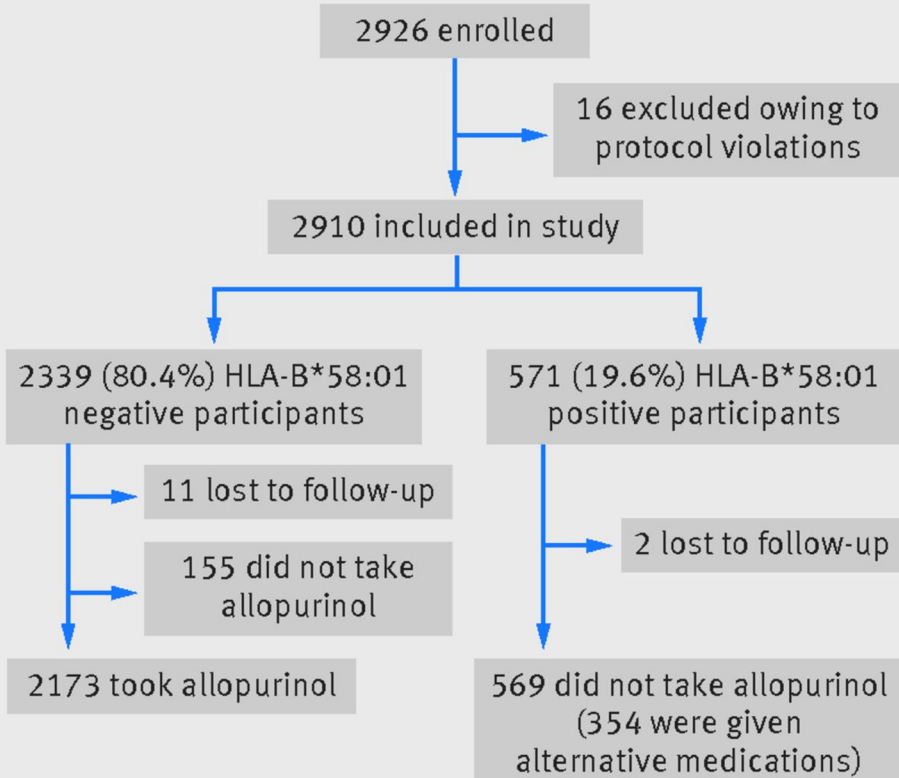
BMJ



Gout
Allopurinol
HLA-B*58:01



NHIRD-TWB → **reduce** health expenditures



Adverse event	HLA-B*58:01 positive participants receiving alternative drug treatment (n=354)	HLA-B*58:01 negative participants receiving allopurinol (n=2173)	Total (n=2910)
Mild cutaneous events			
Rash and itching	3*	94	97
Blisters	0	0	0
Oral ulcers	0	2	2
Rash, itching, oral ulcers, and fever	0	1	1
Rash, itching, and other adverse events	0	22	22

Records from the **National Health Insurance research database**
Incidence of SCARs ~0.3%

frequency distribution of pharmacogenetic phenotypes predicted by genotypes of TWB cohort

Gene	Drug	Rx ^a /year	EM	IM	PM	ADR ^b carrier rate
CYP2B6	Efavirenz	1,662,525	66.0%	30.5%	3.6%	
CYP2C19	Clopidogrel	63,664,076	39.8%	56.4%	3.8%	
CYP2C9	Celecoxib	65,058,810	93.6%	6.3%	0.1%	
CYP3A5	Tacrolimus	10,272,406	8.1%	40.6%	51.2%	
IL28	Peginterferon	40,941	88.6%	11.1%	0.3%	
NAT2	Isoniazid	7,885,251	28.8%	59.2%	12.0%	
SLCO1B1	Simvastatin	50,695,934	78.9%	19.9%	1.3%	
TPMT	Azathioprine	7,435,217	97.0%	2.9%	0.02%	
UGT1A1	Atazanavir	719,793	53.2%	39.8%	7.0%	
VKORC1	Warfarin	16,121,944	1.1%	19.2%	79.7%	
HLA-A*3101	Carbamazepine	17,078,849				2.0%
HLA-B*1502	Carbamazepine	17,078,849				4.1%
HLA-B*5701	Abacavir	3,049,217				0.2%
HLA-B*5801	Allopurinol	23,888,472				10.5%
MT-RNR1	Amikacin	321,561				4.7%

^aRx = prescriptions.

^bADR = adverse drug reactions.

NOTCH3 cysteine-altering variant is an important risk factor for stroke in the Taiwanese population

We queried the Taiwan Biobank database for cysteine-altering mutations in exons 2–24 of NOTCH3 within these genomes. The reference coding sequence of NOTCH3, NM_000435.3, was used for annotating the variants. (p.R544C (c.1630G>A), p.C853Y (c.2558G>A), and p.C884Y (c.2651G>A))

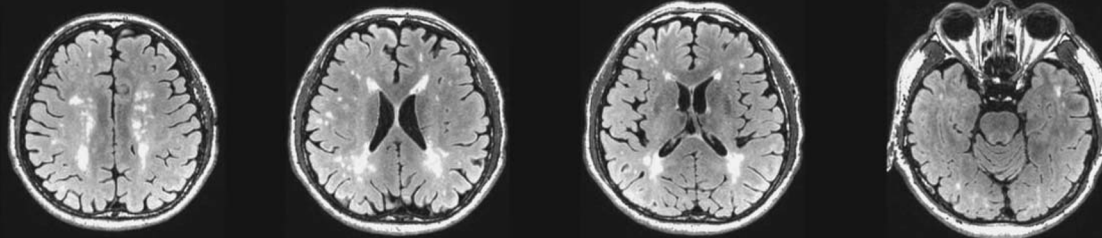
The cysteine-altering NOTCH3 variants identified from the Taiwan Biobank database were genotyped in the control participants and patients with stroke using the TaqMan genotyping assay

Only the NOTCH3 p.R544C variant was found in 4 individuals (TP-VGH (n =550))

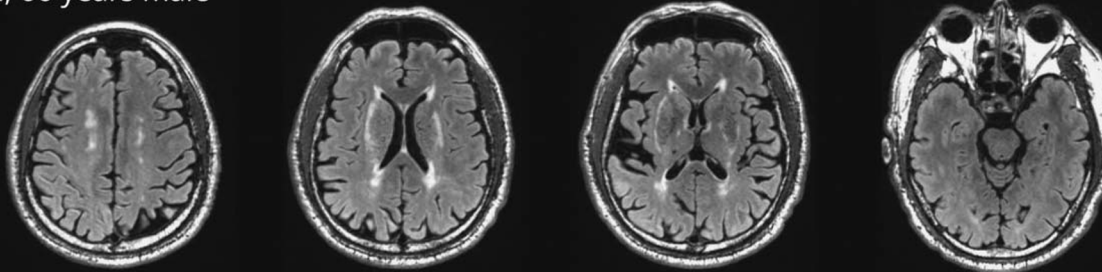
	Controls			Patients with stroke		
	Taiwan biobank (n = 6,488)	TP-VGH (n = 550)	Biobank + TP-VGH (n = 7,038)	TP-VGH (n = 350)	TC-VGH (n = 450)	TP-VGH + TC-VGH (n = 800)
Male	2,293 (35.3)	230 (41.8)	2,523 (35.8)	248 (70.9)	327 (72.7)	575 (71.9)
Age, y	48.4 ± 10.9	56.7 ± 15.0	49.1 ± 11.5	64.4 ± 13.6	67.5 ± 13.2	66.2 ± 13.5
Hypertension	682 (10.6)	186 (33.8)	868 (12.4)	248 (70.9)	329 (73.1)	577 (72.1)
Diabetes	300 (4.6)	72 (13.1)	372 (5.3)	130 (37.1)	168 (37.3)	298 (37.3)
Hyperlipidemia	388 (6.0)	138 (25.1)	526 (7.5)	129 (36.9)	181 (40.2)	310 (38.8)
Smoking habit	1,228 (18.9)	98 (17.8)	1,326 (18.8)	122 (34.9)	136 (30.4)	258 (32.4)
Alcohol consumption	387 (6.0)	108 (19.6)	495 (7.0)	56 (16.0)	87 (23.2)	143 (19.7)
Family history of stroke	1,146 (17.8)	—	—	40 (14.1)	14 (4.0)	54 (8.5)
NOTCH3 p.R544C mutation (+)	56 (0.9)	4 (0.7)	60 (0.9)	8 (2.3)	9 (2.0)	17 (2.1)

Physical examination revealed that they were free of neurologic deficits. Three of them received brain MRI scans, and all had a variable degree of leukoencephalopathy

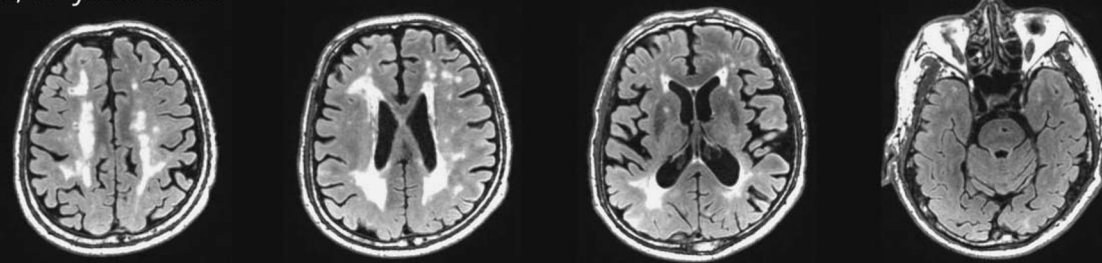
C-I, 59 years male



C-II, 66 years male



C-III, 67 years male



multi-gene

GWAS study

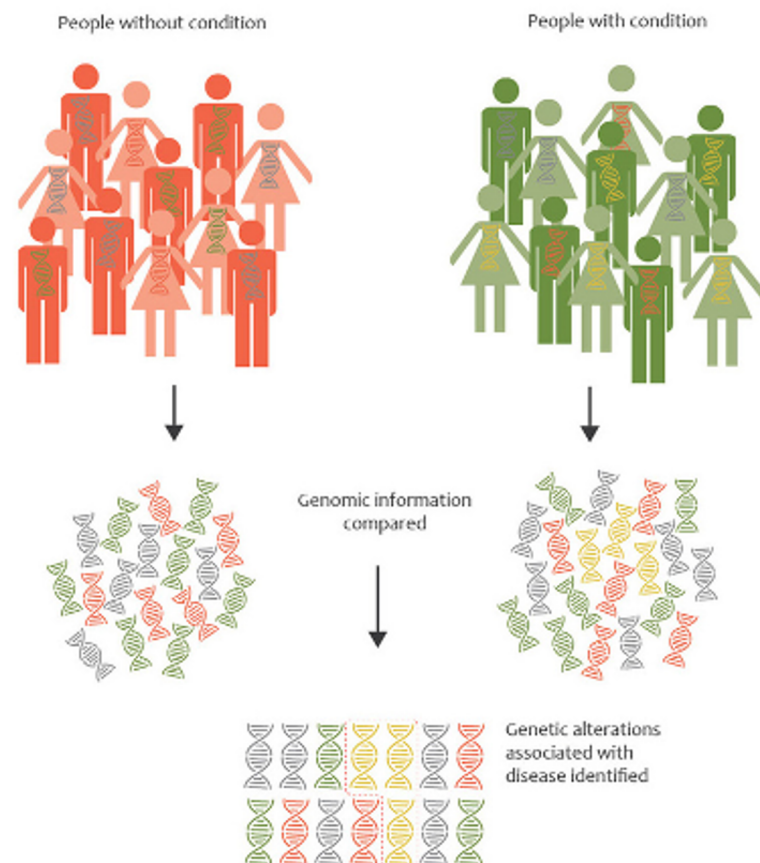
- 偏頭痛及阿茲海默氏症之全基因體關聯性研究-台北榮總
- 利用全基因關聯性研究於影響人類身高差異性之基因鑑定與功能性探討-中國醫藥大學
- 利用台灣生物資料庫探討成人肺功能變化之全基因體關聯研究-中央研究院
- Calculate polygenic risk score (PRS) for individual j using m SNPs

$$PRS_j = \frac{\sum_{i=1}^m \ln(OR_i) \times SNP_{ij}}{m}$$

where

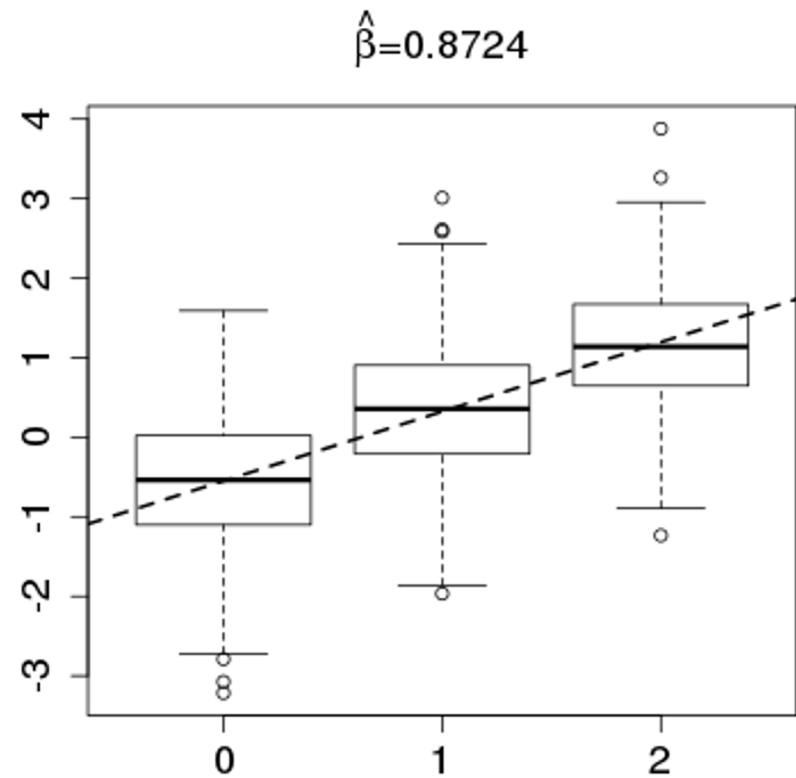
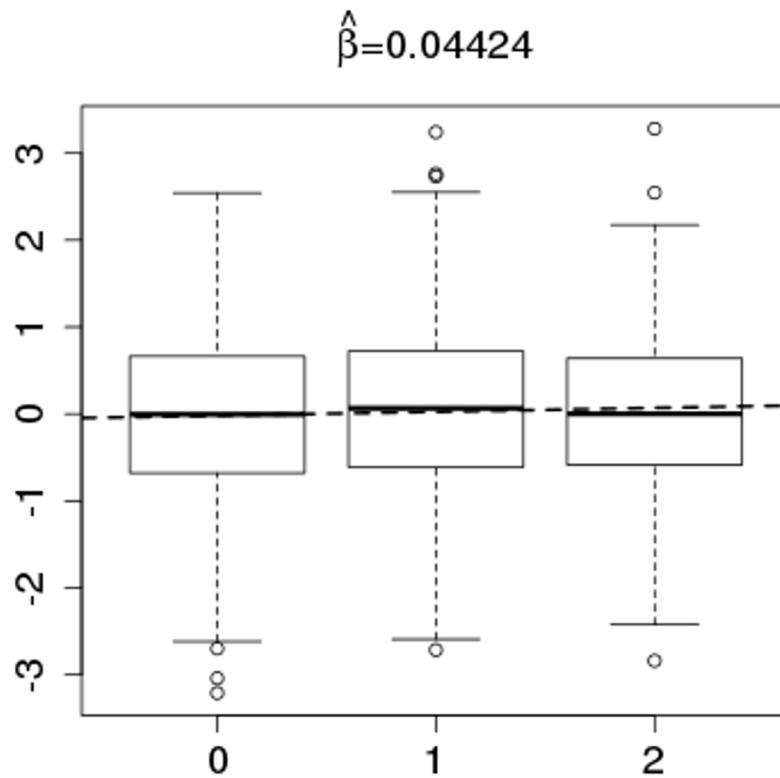
- $\ln(OR_i)$ = effect size for SNP i from discovery sample
- SNP_{ij} = number of risk alleles (0,1,2) for SNP i, individual j in target sample
- m = number of SNPs considered in test set

Purcell / ISC et al. Common polygenic variation contributes to risk of schizophrenia and bipolar disorder Nature 2009

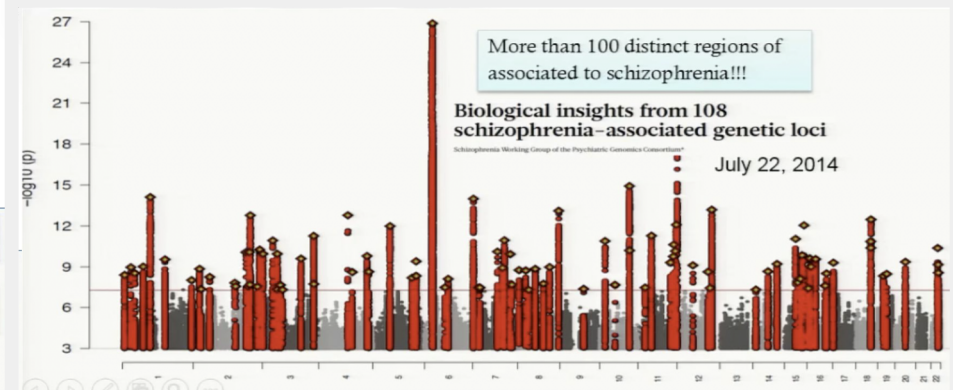


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Yamou Biobank
中央研究院 • 臺灣人體生物資料庫

association study



the power of sample size - schizophrenia | psychiatric genomics consortium



polygenic risk score

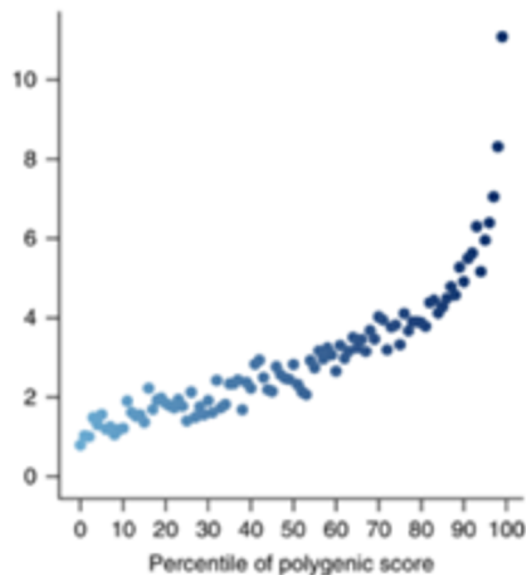
Discovery GWAS

	Weight*	Risk Allele	
SNP1	0.2	A	
SNP2	-0.3	C	
SNP3	0.1	G	
Individual	Alleles SNP1	Alleles SNP2	Alleles SNP3
1	AT	AA	CG
2	AA	CA	GG
3	TT	AC	CG
4	TT	AA	GG
5	TA	CA	GC
6	AT	CA	CG
7	AA	AA	GG
8	AA	CC	CG
9	TA	CC	GC
10	AT	AA	CG

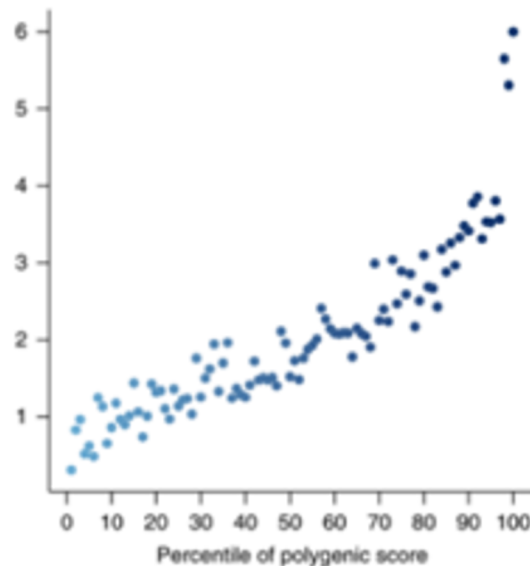
PRS:

Individual	SNP 1	SNP 2	SNP 3	PRS
1	0.2+0.0	0.0+0.0	0.0+0.1	0.3
2	0.2+0.2	-0.3+0.0	0.1+0.1	0.3
3	0.0+0.0	0.0-0.3	0.0+0.1	-0.2
4	0.0+0.0	0.0+0.0	0.1+0.1	0.2
5	0.0+0.2	-0.3+0.0	0.1+0.0	0.0
6	0.2+0.0	-0.3+0.0	0.0+0.1	0.0
7	0.2+0.2	0.0+0.0	+0.1+0.1	0.6
8	0.2+0.2	-0.3-0.3	0.0+0.1	-0.1
9	0.0+0.2	-0.3-0.3	0.1+0.0	-0.3
10	0.2+0.0	0.0+0.0	0.0+0.1	0.3

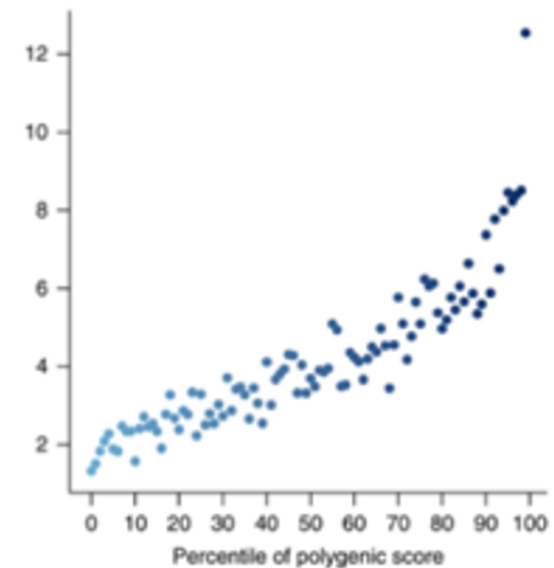
disease risk prediction



Prevalence of Coronary Artery Disease



Prevalence of Type 2 Diabetes



Prevalence of Breast Cancer

"...it is time to contemplate the inclusion of polygenic risk prediction in clinical care, and discuss relevant issues."

Khera et al. Nature Genetics 50, 1219–1224 (2018)

Precision medicine

Box 7. The GINA asthma treatment strategy

Adults & adolescents 12+ years

Personalized asthma management:

Assess, Adjust, Review response

Symptoms
Exacerbations
Side-effects
Lung function
Patient satisfaction



Confirmation of diagnosis if necessary
Symptom control & modifiable risk factors (including lung function)
Comorbidities
Inhaler technique & adherence
Patient goals

Treatment of modifiable risk factors & comorbidities
Non-pharmacological strategies
Education & skills training
Asthma medications

Asthma medication options:

Adjust treatment up and down for individual patient needs

PREFERRED CONTROLLER

to prevent exacerbations and control symptoms

STEP 1

As-needed low dose ICS-formoterol*

STEP 2

Daily low dose inhaled corticosteroid (ICS), or as-needed low dose ICS-formoterol*

STEP 3

Low dose ICS-LABA

STEP 4

Medium dose ICS-LABA

STEP 5

High dose ICS-LABA
Refer for phenotypic assessment ± add-on therapy, e.g. tiotropium, anti-IgE, anti-IL5/5R, anti-IL4R

Other controller options
Low dose ICS taken whenever SABA is taken†

Leukotriene receptor antagonist (LTRA), or low dose ICS taken whenever SABA is taken†

Medium dose ICS, or low dose ICS+LTRA#

High dose ICS, add-on tiotropium, or add-on LTRA#

PREFERRED RELIEVER

Other reliever option

As-needed low dose ICS-formoterol*

As-needed low dose ICS-formoterol*

As-needed low dose ICS-formoterol‡

As-needed low dose ICS-formoterol‡

* Off-label, data only with budesonide-formoterol (bud-form)
† Off-label, separate or combination ICS and SABA inhalers

‡ Low-dose ICS-form is the reliever for patients prescribed bud-form or BDP-form maintenance and reliever therapy
Consider adding HDM SLIT for sensitized patients with allergic rhinitis and FEV1 >70% predicted

For children 6–11 years, the preferred Step 3 treatment is low dose ICS-LABA or medium dose ICS.

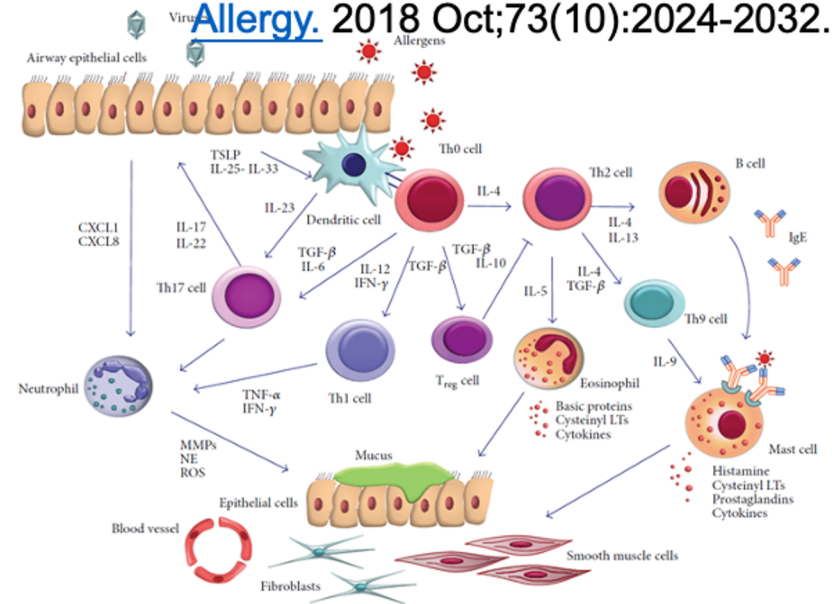
6. ADVAIR DISKUS (fluticasone propionate) Asthma



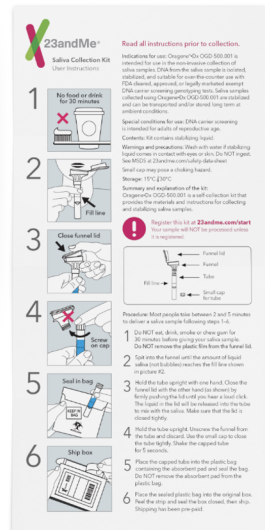
Nature 520, 609–611



Allergy. 2018 Oct;73(10):2024-2032.



Direct to consumer genetic testing (DTG)



For most health conditions (like diabetes or cancers), each person has some risk of developing the condition during their life. This diagram represents this as a bucket – a person experiences the condition when their bucket gets full up.

Most health conditions arise due to a combination of genetic and other risk factors.

● Genetic factors ■ Other factors



Everyone starts life with some genetic risk factors for the condition. Some people have very few, some people have a lot. You are born with this risk and you can't change it. Direct-to-consumer genetic tests aim to measure this risk (though their measurement is often far from perfect).



Over the course of life, people are exposed to other factors that increase the chance of them experiencing the condition.



If you had more genetic risk factors in your bucket to begin with, it takes fewer other risk factors to fill the bucket and result in the health condition.



Some of the other factors, you can't change, like your age. Some factors, you might be able to work on, like smoking, or alcohol intake.



Even if you have a 'high genetic risk' of a particular condition, for most health conditions, having a high genetic risk does not mean you'll get it.

By working on the factors you can change, you might be able to reduce the chance of developing a health condition, even if you have a high genetic risk.

Need for a Precision Health Eco-system



Economically Unsustainable

Current healthcare and human services industries



Treatment Decisions

Gap in accuracy



Evidence-Based Medicine

<50% is actually evidence-based



Chronic and Aging Populations

Require more care



Health Spending

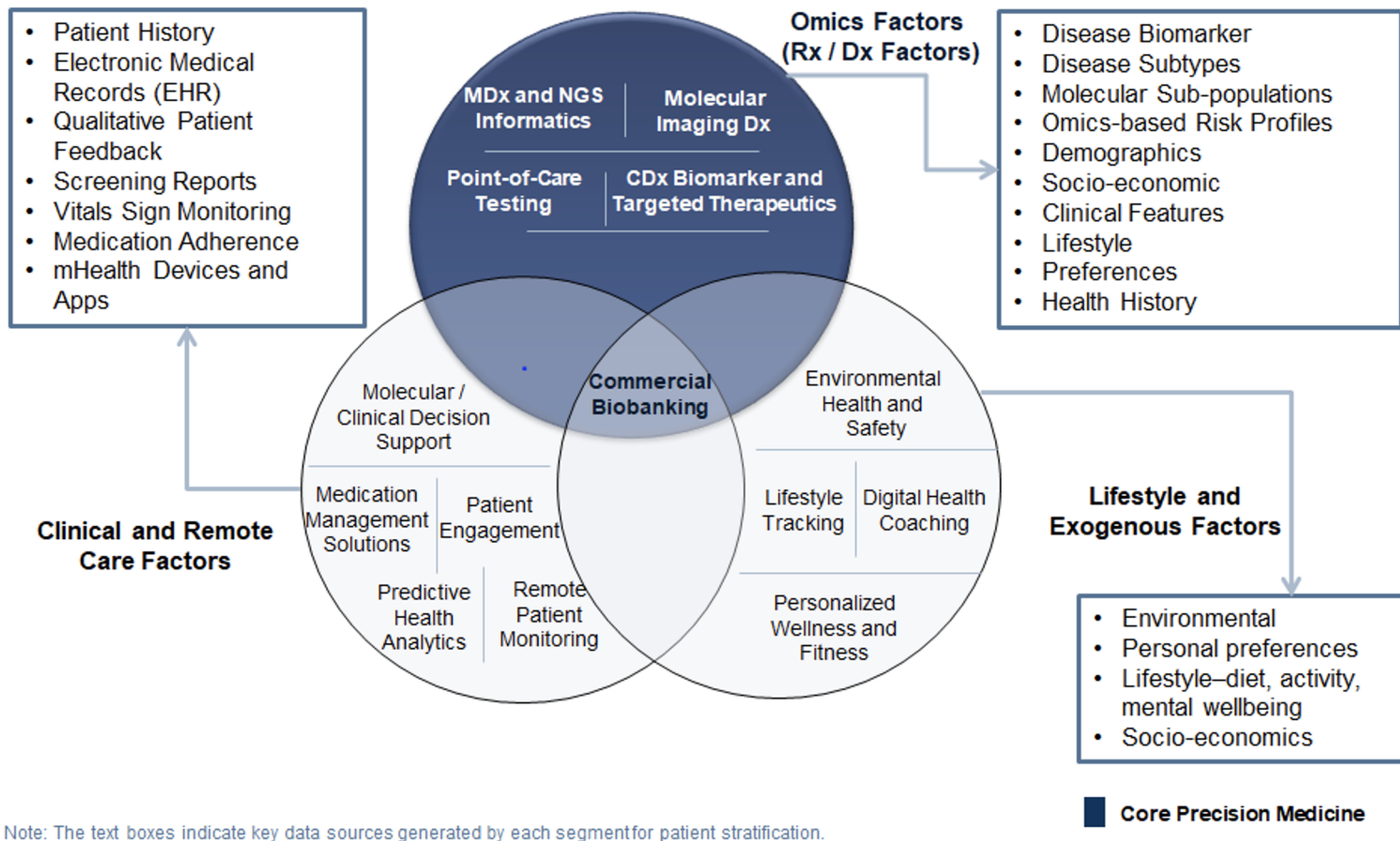
Disconnect with outcomes

The problem is one of precision and productivity, not of diseases, gadgets or healthcare

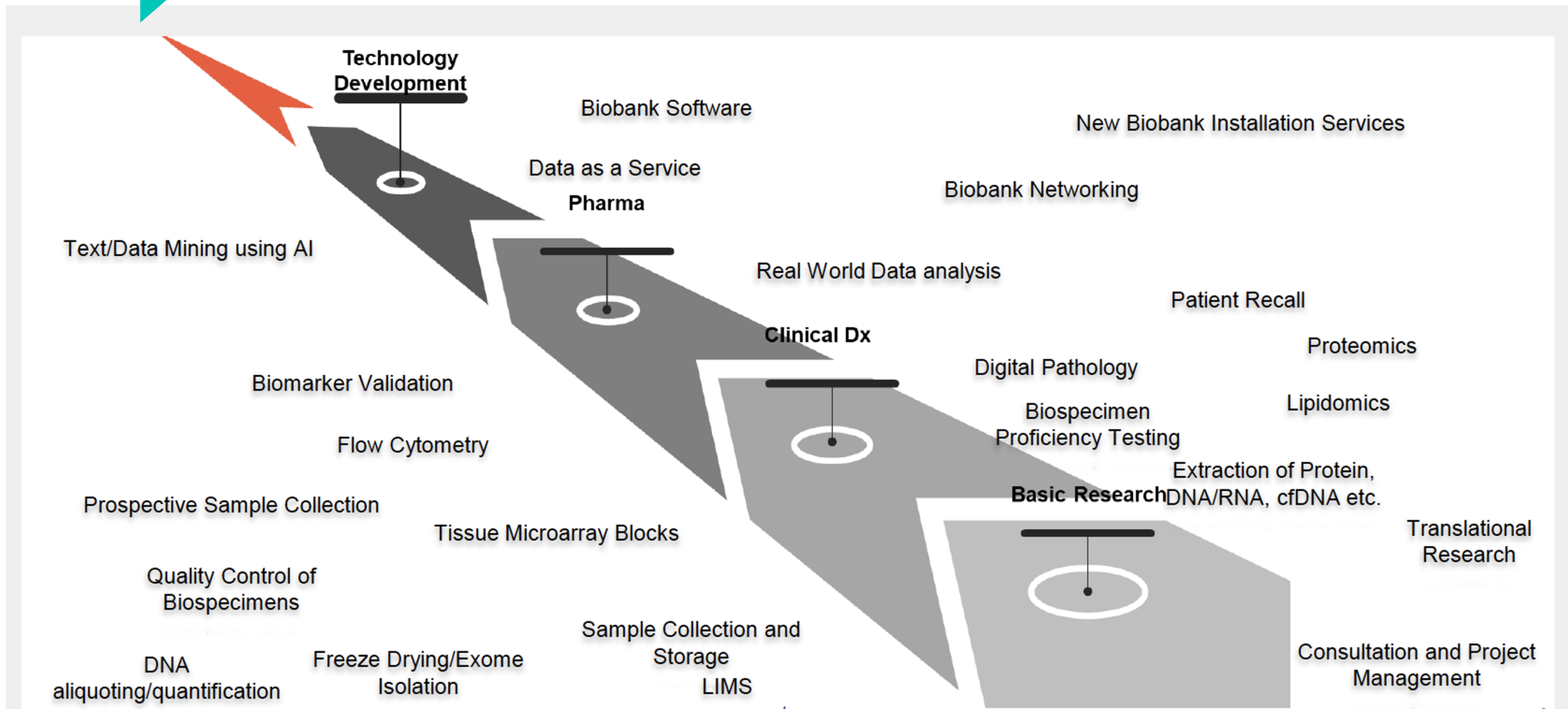


Now the new vision of healthcare is about Precision-based Predictive, Preventive and Participatory care models promoting social and financial inclusion.

Biobank - provide clinical research support that translates into bedside diagnostics and treatments, and advances research technologies into clinical applications



Biobank service



Lion man 35,000~40,000 years old

