



2023.10.10 (Tue)  
*UIDP Tokyo Forum*

# **“Genome School” For catching up with the rapidly evolving technologies**

**Yutaka Suzuki**

Life Science Data Analysis Center,  
Graduate School of Frontier Sciences,  
The University of Tokyo



## “Genome School” as a recurrent education program:

## To deal with the changing era of genome sciences

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GREETING



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東京大学 大学院新領域創成科学研究科 基礎システム専攻 教授  
徳永 朋祥  
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## ゲノム科学の発展と社会実装の 推進に寄与する人材を育てます。

本スクールは、現在発展の著しいゲノム関連解析技術とそこから産生されるデータを、近い将来に社会の広い範囲に活用できる人材を育成することを目標とするものです。

ゲノム関連の生体情報は、その個人を特徴づける最も基盤的なデータです。これをマルチモーダルな活動データ、いわゆるビッグデータと紐づけて活用していくには、様々なアイデアを創造し、それを大胆に試行し、企画していける力（思考力・企画力）が求められます。また、現在のコロナ感染症、あるいはがんゲノム等を活用する個別化医療について、特にバイオ関連産業においては、その取り込みという喫緊の課題に即戦力的に対応する力（先端知の実践的な活用力）が求められます。また、これらの能力は、長期的な経営戦略や行政判断においても必須のものと言えます。

そこで本スクールは、これらの能力を育成するために、次の2部からなるコースを開講することといたしました。



東京大学 統合ゲノム医科学情報連携研究機構 機構長  
東京大学 医科学研究所 教授  
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ゲノムスクール スクール長  
生命データサイエンスセンター センター長  
東京大学 大学院新領域創成科学研究科 メディカル情報生命専攻 教授  
鈴木 穰  
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ゲノムスクール

検索

## Delegate Companies for the first “Genome School” (1-Nov 2023)

Company	Category
Hitachi High Tech	Biotech
Agilent	Biotech
Vizgen	Biotech
Nikon	Camera
Iwai Chemistry	Chemistry
Shiseido	Cosmetics
Mitsui Chemical	Diagnosis
G&G	Diagnosis
SONY	Electric
Mitsui Knowledge Inc	IT
Bitz	IT
Amerief	IT
Dynacom	IT
TechMatrix	IT
Fuji Film	Pharma
Eli Lilly	Pharma
Astellas	Pharma
Novogene	Service Provider
Sumisho Pharma International	Trader

(19 companies of various categories)

## Module 1: Lectures by Distinguished Professors at U Tokyo

Date	Topic	Lecturer	
1-Nov	Opening	Yoshinori Murakami	
		Yutaka Suzuki	
13-Nov	BioBank	Yoichiro Kamatani	
		Koichi Matsuda	
20-Nov	BioInformatics	Yuichi Shiraishi	
		Tatsuhiko Tsunoda	
21-Nov	Common Diseases	Norio Ozaki	
		Seitaro Nomura	
27-Nov	Infectious Diseases	Yoshihiro Kawaoka	
		Hiroshi Yotsuyanagi	
28-Nov	Cancers	Hiroyuki Aburatani	
		Shunpei Ishikawa	
4-Dec	DataBase	Riu Yamashita	
		Seiya Imoto	
11-Dec	Policy Making	Cabinet Office	
		AMED	



## Sequencing core lab at LISDAC, Univ. of Tokyo

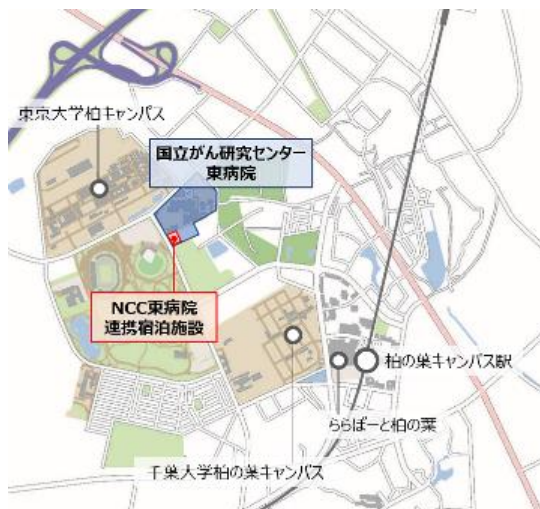
- Sequencer : NovaSeq6000 x 2台 WGS : 50,000/year
- Sequencer : NovaSeq6000 (DX) x 1台
- Sequencer : MGI T7 x 1; G400 x 1
- Sequencer : PromethION x 4 WGS : 10,000/year
- Robot : XT-AUTO/Hamilton/Analytik Jena
- Robot (MGI) : STP3000/NE960
- Nano dispenser : Mosquito (LV/HV/Dragonfly)
- QC : TapeStation/FemtoPulse
- シングルセル : 10X Chromium x 3
- Pathology : Microtome/Cryostat  
/Keyence+ CODEX x 2
- **※Xenium/StereoSeq in preparation**
- (Cluster server: 800 core; Luster 600Gb/Tape 1PB+ GPUx12)

-(Cluster server@KOG: 2500 core; Luster 2PB/Tape 6PB+ GPUx40)

Secure Computational System



Allow me to talk about cancers, not bones, joints or muscle...



## National Cancer Center East Hospital

Application of our omics platforms



## Domestic collaboration at LISDAC



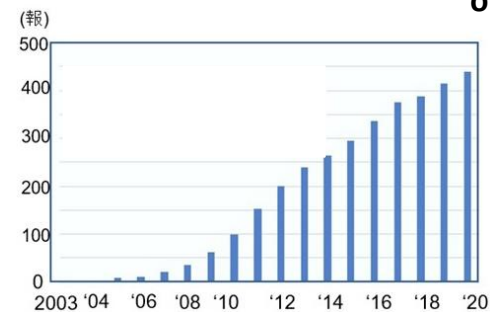
## Achievements of Bio Bank Japan Project

	2021	2022
<b>DNA sequencing</b>		
NovaSeq6000	119	130
MGI T7		3
<b>Single cell analysis</b>		
scRNA-seq	38	43
TCR reperpoir	7	3
scATAC-seq	3	
scMulti	7	13
<b>long read sequencing</b>		
PromethION	7	13
<b>Spatial analysis</b>		
Visium	15	26
CODEX		13
<b>Proteome analysis</b>		
Olink		1

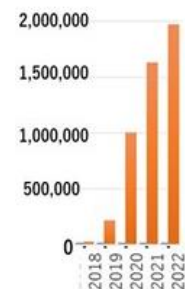
### International Collaborations



### Published papers



### Distribution of biomaterials



**Nature 17 papers**  
**Nature Genetics 72 papers**

# Background (1)

## Rapid Updates of the Analytical Instruments in 2022-2023

### • DNA Sequencer

#### Short read (update)



NovaSeq X  
\$2-3/Gb (\$200/100Gb=30X)

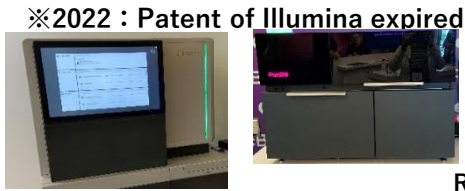


T7 (MGI)



Element Genomics

\$1/Gb (\$100/100Gb=30X)



Singular Genomics

※2022 : Patent of Illumina expired



Onso (PacBio)

#### Long read(Update)



Revio (PacBio)

\$10-20/Gb (\$1000-2000)



PromethION (ONT)

**“complete genome”  
(Telomere to Telomere)**

Fidelity Q30 (99.9%)

### • “Functional” Genomics

#### Spatial (mRNA)



Visium ver2  
(10X Genomics)



Xenium  
(10X Genomics)



Stomics  
(BGI)

#### Spatial(Protein)



Fusion (Akoya)

#### Serum protein



Olink



# Background (1)

## Investments on Genome “Sequencing” as a national policy

### Genome sequencing as a national policy



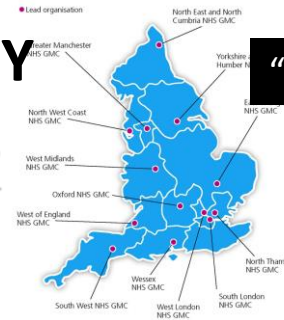
**US: Precision Medicine Initiative (PMI): 11 B JPY**

**“US ALL”**



**UK: Genomics England: 33 B JPY**

**“UK BioBank”**



**“Our Future Health”**



Let's prevent disease together



Our Future Health will be the UK's largest ever health research programme, bringing people together to develop new ways to prevent, detect and treat diseases.

**Japan ( BioBank and Database infrastructure )**

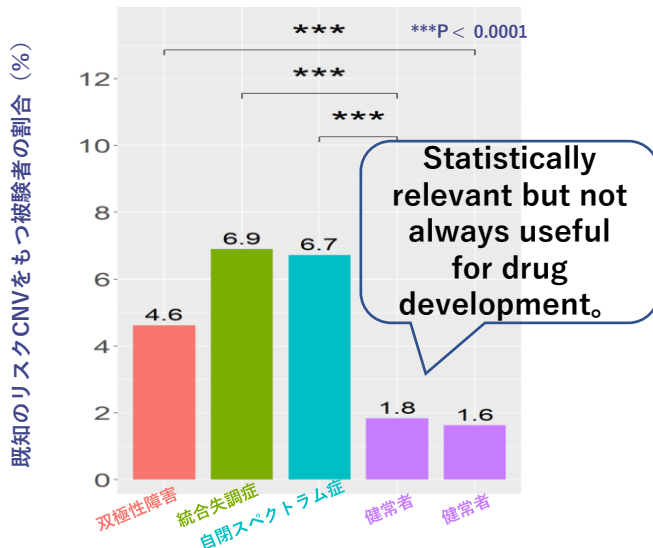
- Launch of C-CAT at National Cancer Center.
- BioBank Projects: BBJ, ToMMo, NBNC

# “Functional” analysis of Genomes; Beyond the sequencing

## PCDH15 as an “associated gene” of Bipolar Disease

8,708 cases of Genome sequencing

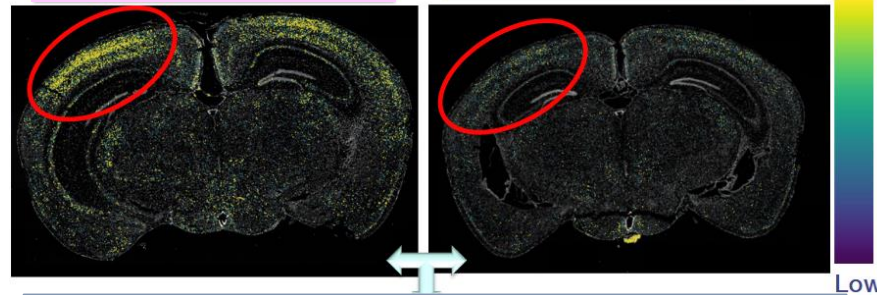
- BPD: 1,818 cases
- SCZ: 3,014 cases
- ASD: 1,205 cases
- Healthy: 2,671 individuals



## Spatial Gene Expression Analysis of the Disease model/ Patients

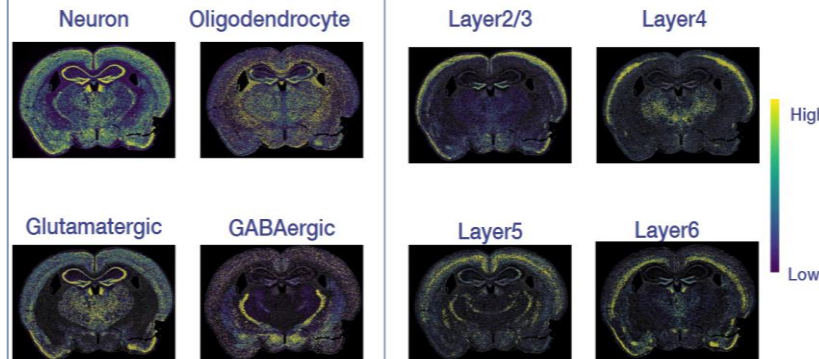
PCHD KO mice

WT mice



Gene Expression aberration in Frontal Cortex

## Xenium: in situ profiling



Validation using post mortal human brains

# Perspectives on clinical applications

Towards "Next Generation" Precision Medicine

Patients separation  
Driver mutation (genome)

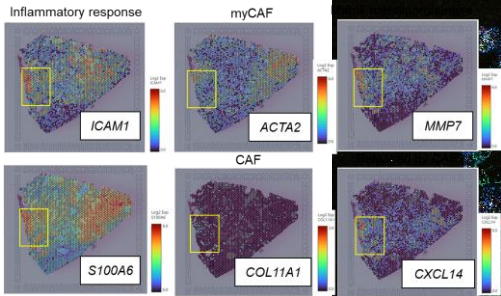
- Global
- Static
- >"Molecular targeting drugs"

Also considering pathological info.

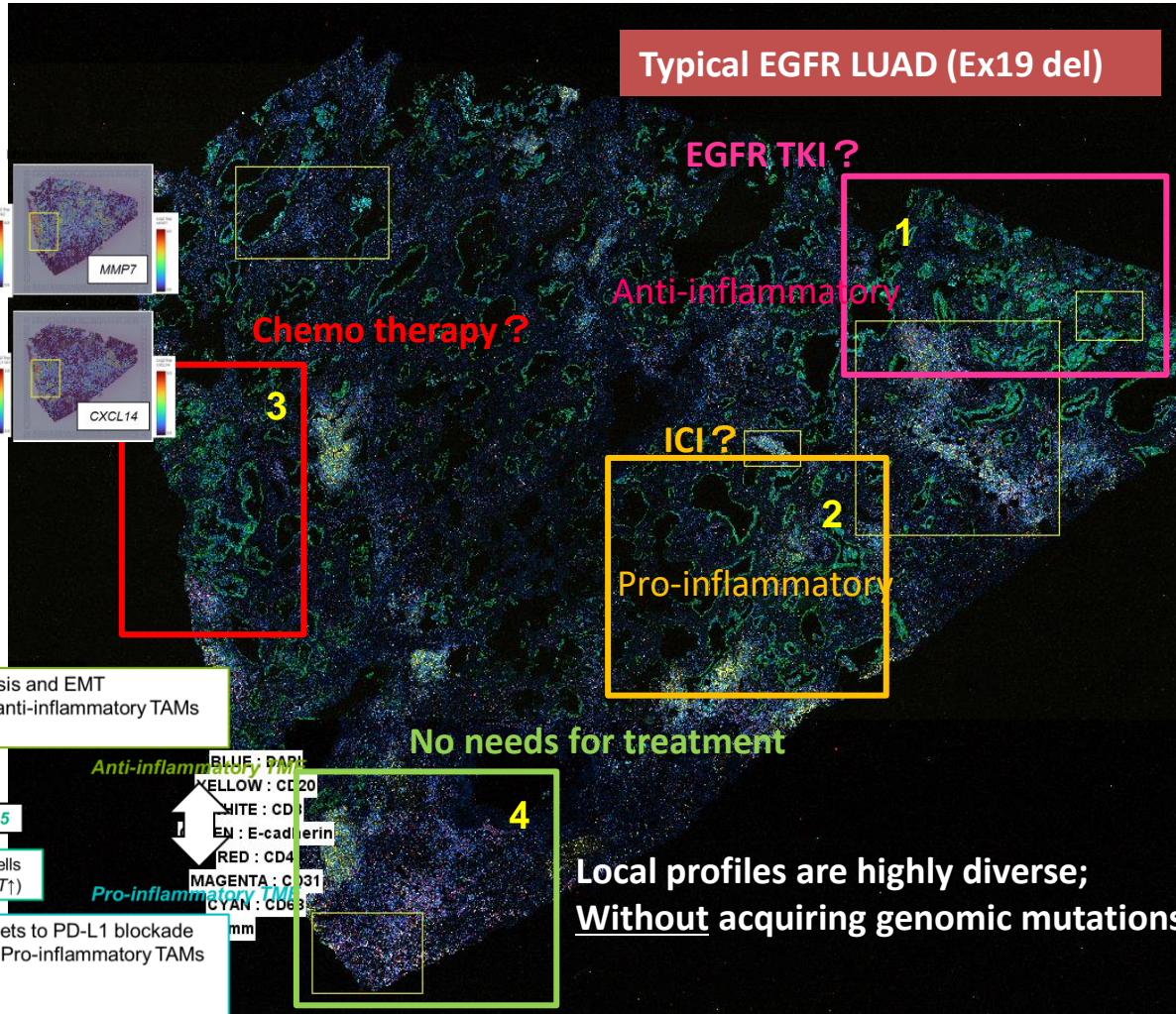
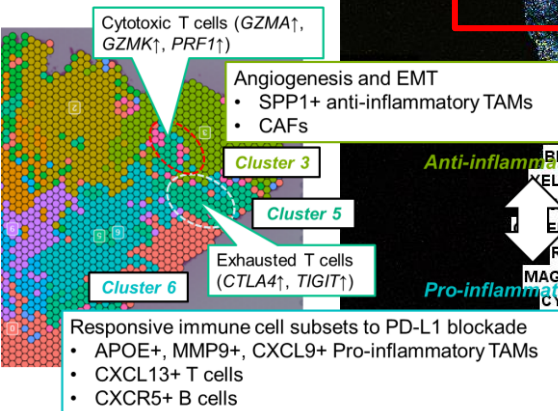
- More precise medicine
- Local/Dynamic
- >Novel concept
- DDS/Combination therapy

For complete elimination

## Local behavior



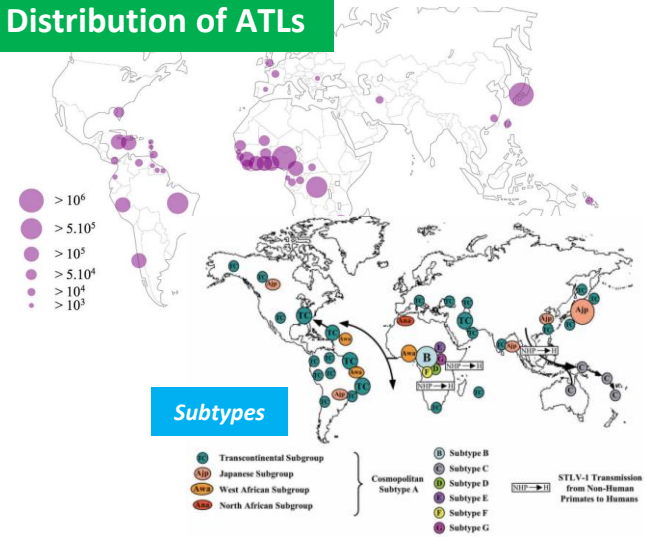
## Modeling



Local profiles are highly diverse;  
Without acquiring genomic mutations

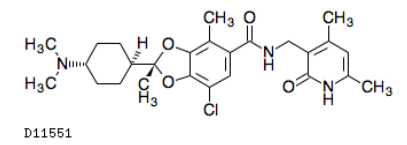
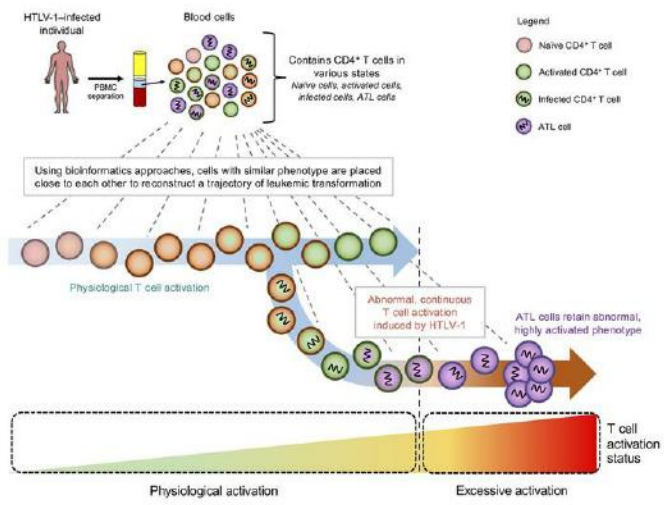
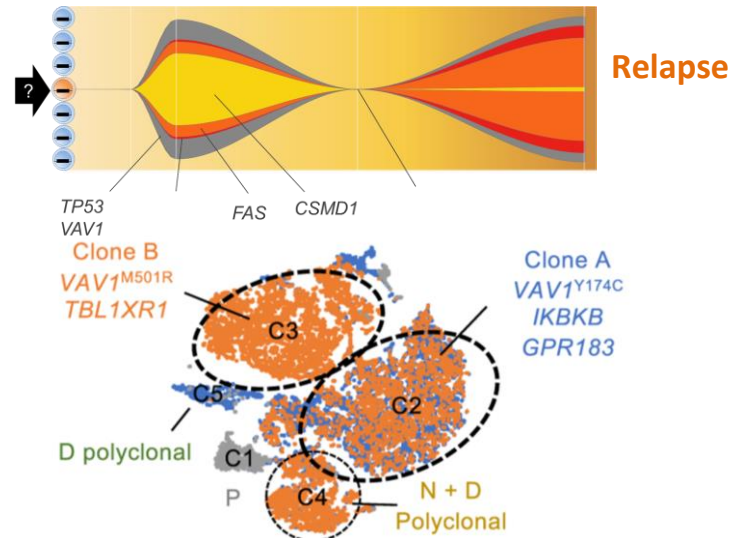
# Regional Cancers: ATL (Adult T cell Leukemia)

## Distribution of ATLs



Yamagishi et al Nat Commu 2021

## Changes of clonal structure



Clones expanded in the relapse are being analyzed

**Valemetostat (just approved in Japan; Under review in FDA)**

Yamagishi et al under review

# As one of the first test sites worldwide; Xenium set up



**CDP ID: 9GT3BT**

## Base panel (202)

PCOLCE2	F3	F2RL3	FOXJ1	LGALS2	CYTIP	TCL1A	CTSK
PH16	GATA2	CCND1	HEPACAM2	CD1C	LILRA1	VAMP8	MMP9
FRZB	KIT	ACE2	SOX4	CD1E	LILRA5	PF4	PLA2G7
LMOD1	SLC18A2	FOXJ1	MEDAG	CLEC10A	LILRB2	TUBB1	TREM2
PLN	BIRC3	TSTD1	MLLT11	FCGR2B	AQP9	KRT14	AGT
RERGL	RGS13	C16orf89	WT1	HLA-DQB2	CD163	KRT5	COL21A1
TNNT2	ADGRL4	HSD17B11	FSCN1	ITGBL1	CD300E	ASPM	FOXS1
JUND	PLVAP	PTP4A1	LRRC70	LTBP2	CLEC4E	MKI67	NTN4
SDC4	APOLD1	EREG	LYVE1	POSTN	OLR1	UBE2C	THY1
TMPRSS2	TM4SF18	FGF18	MMRN1	SPP1	CSPG4	DAPL1	CCL23
WSB1	CD3E	GREM2	NTS	ASCL2	KCNK3	KLF5	PLA1A
RND1	CD40LG	LGR6	PDPN	CCKAR	LAMC3	KLK11	RGS5
ELN	CXCR6	PAMR1	PROX1	ISG20	LGALS3BP	TP63	SELP
FGFR4	GPR171	SCARA3	CXCL5	LIMD2	LG4	CCDC78	
GDF10	IL2RG	SYNPO2	MSR1	MYOM2	CRELD2	TP73	
PDGFRA	LAT	CCNO	RETN	KRT81	DNAJB9	FDCSP	
WNT2	TRAT1	CYP2F1	TREM1	KRT86	PIM2	LPO	
BMX	PIK3IP1	MUC5AC	ALDH1A3	LCK	PLA2G2D	NDRG2	
GIMAP7	CD8A	SPDEF	CALB2	ASCL1	POU2AF1	ODAM	
GJA5	CLEC2D	UPK1B	PRG4	CALCA	PRDX4	PRB1	
IGFBP3	NTRK2	VMO1	RGS4	CHGA	TNFRSF13B	S100A1	
SOX17	SMAD6	CCL13	RPS4Y1	CHGB	TNFRSF17	SLC12A2	
BANK1	ACE	GPR34	MMP7	FURIN	CLEC4C	AK1	
CD19	CYP3A5	MS4A4A	MUC5B	TRH	LILRB4	ETV5	
FCMR	FRY	ATP6V1G3	PI3	CD48	MPEG1	LAMP3	
SELL	PRX	CFTR	TMEM45A	CFP	PTCRA	MALL	
VPREB3	SLC14A1	CLDN25	CCL22	CLEC12A	SPIB	SELENBP1	

## Custom panel (100)

CDH1	PDCD1	FAP	MET	NECTIN2
COL1A1	ICOS	COL11A1	ERBB2	MZB1
PECAM1	CD274	IL6	AKR1C1	SCGB3A2
PTPRC	IDO1	ACTA2	GSR	GZMA
CD74	HLA-A	MMP11	ATF4	
CD4	HLA-DPB1	CXCL13	ATF6	
GATA3	MARCO	CXCR5	HYOU1	
TBX21	FABP4	CXCL9	XBP1	
RORC	NKX2-1	CXCL14	OAS2	
CCR7	FOXA1	APOE	HMGA1	
CCL21	HOPX	C1QC	KDR	
NCAM1	CAV1	CD44	SLC2A1	
GZMB	NAPSA	LGR5	DUOX1	
PRF1	SFTPC	TGFB1	AXL	
ITGAE	SFTPB	CTNNB1	KRT8	
CD68	SFTPD	ZEB1	SMAD4	
ITGAM	SCGB3A1	VIM	NFKB1	
ITGA3	SCGB1A1	VEGFA	RHOA	
CD33	FOXA2	ICAM1	HNF4A	
FOXP3	YAP1	FOS	IL1B	
IL2RA	REST	TNC	TNF	
CTLA4	SOX2	WEE1	CD80	
TIGIT	SOX9	TP53	CD86	
LAG3	SPARC	EGFR	PVR	

## US/SW/SG/JP Staffs

✳️ With 10X CEO/CTO



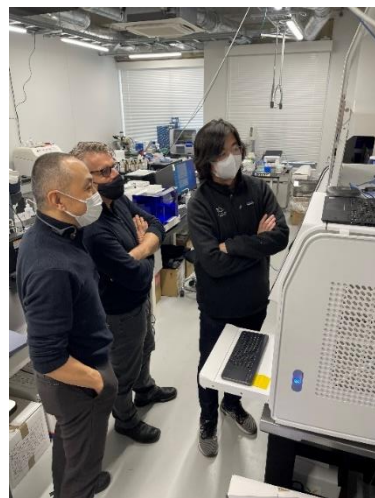
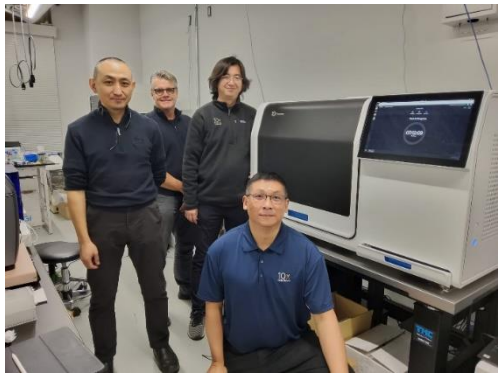
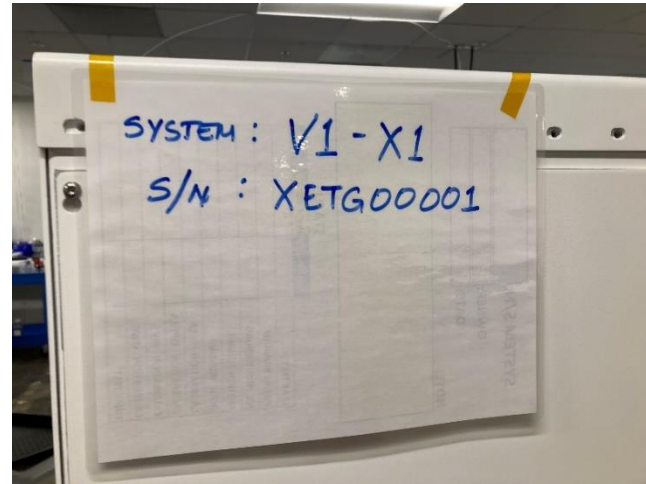
# 10x Team Set UP



California, US



Kashiwa U Tokyo

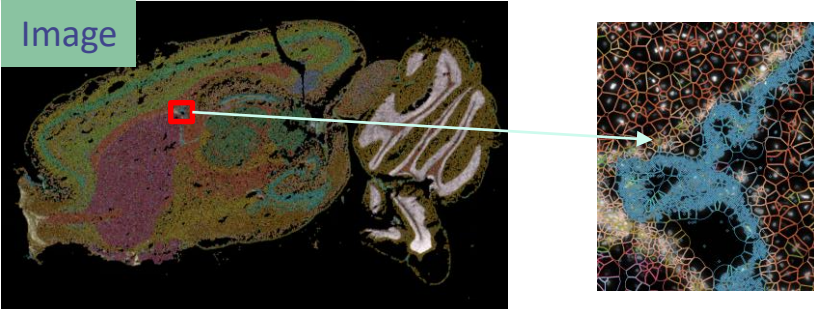


# Output Data Format

## Spatial Analysis

Mouse brain (Xenium explore)

### Image



### mRNA coordinates

```
overlaps_nucleus", "feature_name", "x", "y", "z", "count", "control_probe_counts", "control_code"
281483566645249, -1, 0, "Lyz2", 639.2887, 609.10046, 12.225598, 40.0
281483566645250, -1, 0, "Lyz2", 641.2621, 400.46677, 12.176018, 40.0
281483566645251, -1, 0, "Nrxp3", 644.0111, 776.96045, 12.318884, 40.0
281483566645252, -1, 0, "Lyz2", 645.5328, 55.875877, 12.4246435, 40.0
281483566645253, -1, 0, "Bhlhe40", 648.7455, 544.4293, 12.210579, 40.0
281483566645254, -1, 0, "Lyz2", 651.8875, 453.28986, 12.198851, 40.0
281483566645255, -1, 0, "Lyz2", 652.56384, 697.9203, 12.311746, 40.0
281483566645256, -1, 0, "Lyz2", 653.0201, 240.30208, 12.224723, 40.0
```

### Cell/Nucleus coordinates

```
script_counts", "control_probe_counts", "control_code"
273.476.35328125, 36.80234375
2.7629, 0.213662346027, 7.7173, 2.14237612466, 16.76, 0, 18, 9, 4828125, 4.0640625
3, 836.3118560791015, 7371.93876953125, 370, 0, 0, 370, 205, 37062500000002, 64.93468750000001
4, 820.2961730957031, 7369.998046875, 242, 0, 0, 242, 157.95656250000002, 49.581562500000004
5, 842.2104949951172, 7338.1296875, 372, 0, 0, 372, 404.058125, 12.23734375
6, 831.3291046142577, 7396.638574218749, 123, 0, 0, 123, 62.812343750000004, 12.869531250000001
```

### mRNA count per cell

```
541 245060 15666824
1 1 4
2 1 5
9 1 1
11 1 3
12 1 3
```

## Single cell (Fixed)

```
%%MatrixMarket matrix coordinate integer general
%%metadata_json: [{"software_version": "cellranger-7.1.0", "format_version": 2}]
18082 10301 27984338
2 1 1
7 1 1
19 1 2
21 1 1
27 1 3
32 1 1
35 1 1
```

1st line : gene name  
2nd line : cell ID  
3rd line : Expression

## Olink (Proteome)

```
SampleID;Index;OlinkID;UniProt;Assay;MissingFreq;Panel;Panel_Lot_Nr;PlateID;QC_Warning;LOD;NPX;Normaliz
sample_001;1;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0.3
sample_009;2;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0.3
sample_017;3;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;-0
sample_025;4;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0
sample_035;5;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0
sample_043;6;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0
sample_051;7;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;-0
sample_054_1;8;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0
sample_269_1;9;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0
sample_125;10;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;-0
sample_056;11;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;-0
sample_269_1;12;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;0
sample_002;13;O1D20419;P60568;IL2;0.9659;Inflammation;B04411;Olink_Plate_Layout_0831_mod;PASS;0.5811;-0
```

NPX-normalized expression data

All the data is "numbers", therefore, does not contain any personal information



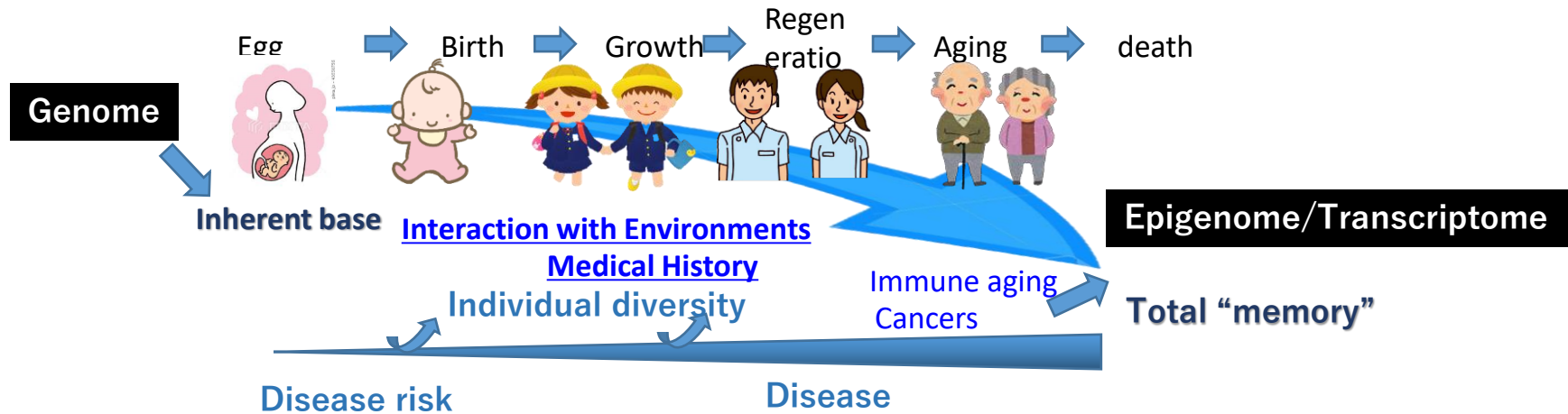
Easier data sharing??

# Possible pre-symptomatic disease stage

## (Hypothesis)

Kashima et al Exp Mol Med. 2022

- Risks of various diseases may be inferred from the “omics” status at the given time
- Omics status should be described as the modification to the original genome sequence



## (Action)

- Single cell analysis of health/elderly individuals...



**Some individuals are originally less reactive regarding their immune responses ?**



# Actions at Japanese Government

健康・医療戦略推進本部 [▶ 本文△](#)

**Cabinet Office: Strategic meeting**

[トップ](#)
[健康・医療戦略推進本部](#)
[関係会議](#)
[健康・医療戦略／医療分野研究開発推進計画](#)
[資料](#)

## ゲノム医療協議会

### 設置根拠及び構成員

[▶ ゲノム医療協議会の開催について\(PDF/263KB\)](#)

### 開催状況

31-Mar New Technologies  
30-Jun Data Sharing

回数	年月日	配布資料等
第12回	令和5年6月30日	<a href="#">議事次第 (配布資料)</a> <a href="#">議事概要(PDF/497KB)</a>
第11回	令和5年3月31日	<a href="#">議事次第 (配布資料)</a> <a href="#">議事概要(PDF/519KB)</a>
第10回	令和4年12月23日	<a href="#">議事次第 (配布資料)</a> <a href="#">議事概要(PDF/641KB)</a>



国立研究開発法人 日本医療研究開発機構  
 Japan Agency for Medical Research and Development

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## AMED: R&D Grant of 2.5B JPY for three years

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[イベント](#)
[事務手続き](#)

[トップ](#) > [公募情報](#) > 令和5年度「ゲノム医療実現バイオバンク利活用プログラム (ゲノム医療実現推進プラットフォーム・先端ゲノム研究開発) /ゲノム創薬基盤推進研究事業 [ゲノム研究を創薬等出口に繋げる研究開発プログラム]」に係る公募について

[公募情報](#)
若手あり
 令和5年度「ゲノム医療実現バイオバンク利活用プログラム (ゲノム医療実現推進プラットフォーム・先端ゲノム研究開発) /ゲノム創薬基盤推進研究事業 [ゲノム研究を創薬等出口に繋げる研究開発プログラム]」に係る公募について

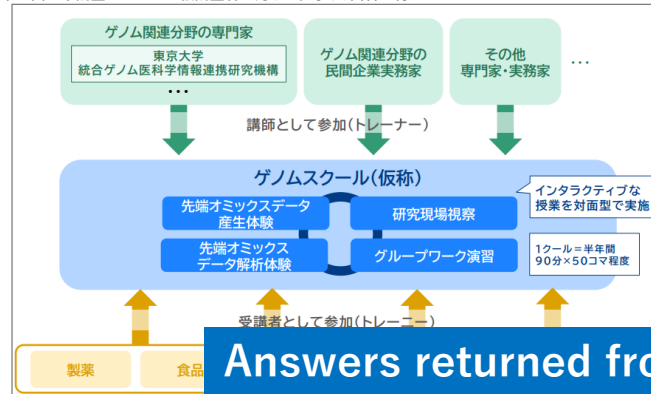
# Questionnaire to Private Companies: ~Needs for the "Genome School"??

## Recurrent program at U Tokyo, DSTEP



## ゲノムスクール(仮称)

以下の図は本調査においても被調査者に対して表示し、回答を得た



Answers returned from >100 companies

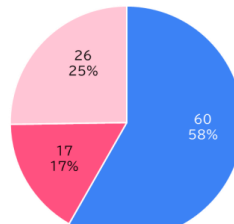
コミュニティの形成・他分野への拡がり

## プログラム利用意向

回答者全体のうち、ゲノム人材育成プログラムの参加意向として最も多かったのは「はい」(60人)、次いで「わからない」(26人)、「いいえ」(17人)の順であった

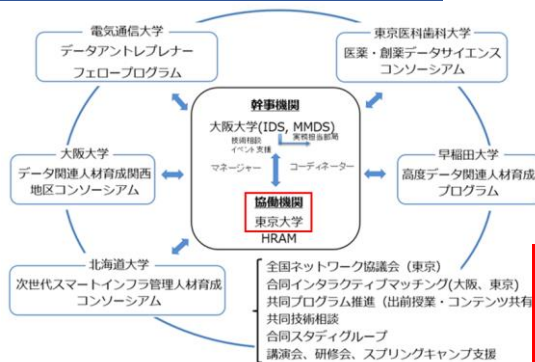
Q26: 東京大学統合ゲノム医科学情報連携研究機構では、リカレント教育(学びなおし)の場として以下のようなゲノムスクール(仮称)の設置を検討しております。このようなゲノム人材育成プログラムがあった場合、あなたの所属する企業・団体は参加してみたいと思いませんか。

ゲノム人材育成プログラム参加意向(n=103)単一回答



Immediate Needs for "GenomeSchool" YES= 58%

## Education Network "D-DRVE"



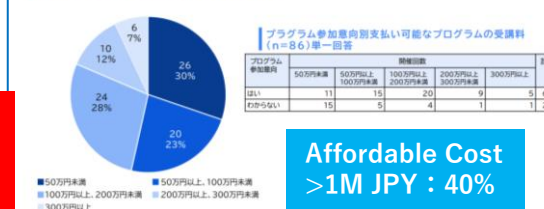
## プログラム受講料

ゲノム人材育成プログラムの参加意向について「はい」及び「わからない」の回答者(n=30)のうち、支払い可能なプログラムの受講料で、最も多かったのは「50万円未満」(26人)、次いで「100万円以上、200万円未満」(24人)の順であった

Q31: Q.26のゲノム人材育成プログラムについて、受講料はどの程度までお支払い可能でしょうか。 ※複数回答可でお考え下さい。

※イメージ図のように1クール=半年間 90分×50コマ程度としてお考え下さい。

支払い可能なプログラムの受講料(n=86)単一回答 Q26で「はい/わからない」と回答した場合



Affordable Cost >1M JPY : 40%

# GTB Bio-innovation Promotion Areas

## 5. Kawasaki Area

The Open Innovation City with Direct Access to Haneda Airport



## 3. HOTS HILL

(Hongo/Ochonomizu/Tokyo Station Area)  
The Largest Concentration of Academia in GTB



From Press Release

## 4. Nihonbashi Area

Global life science business hub in the heart of Tokyo



From LINK-J HP

## 1. Tsukuba Area

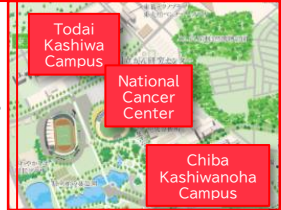
The Biggest Science City with Various Institutions

From brochure



## 2. Kashiwanoha Area

The Smart City with Top-Tier Universities and the National Cancer Center



From Kashiwanoha Smart City HP

## 6. Yokohama Area

Innovative City Focusing on Health and Medical Care



## 7. Shonan Area

An Innovation Hub with the Largest Wet Lab, in Collaboration with Neighbouring Hospitals



Shonan Health Innovation Park

## 8. Chiba/Kazusa Area

The Research Base of Plant, Immunological Medicare and Biomanufacturing



Note 1) In addition to areas above, Shinjuku, Shinano, Waseda, Tsukiji, Daiba, Tokorozawa, and Wako are emerging areas.  
Note 2) As new areas are developed, area definition maybe restructured.

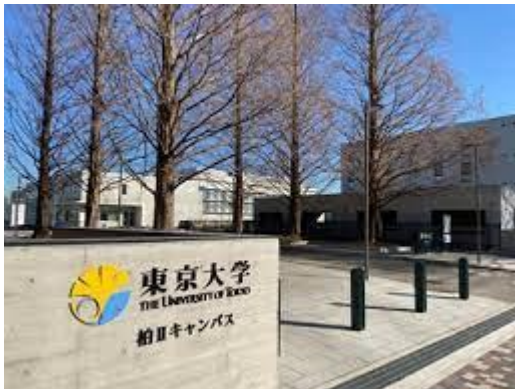
## Japan's Bioeconomy Strategy and Greater Tokyo Biocommunity





# Module 1: +Practice at Genome Core Lab at U Tokyo, Kashiwa II Campus

Learning the latest Spatial/single cell analysis



3

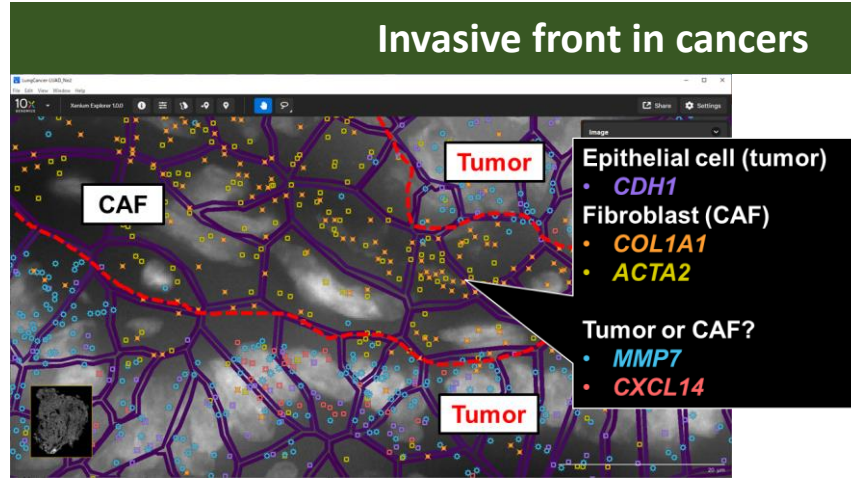
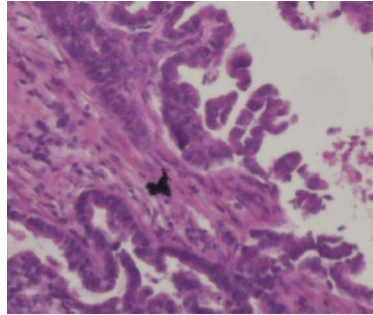
月	火	水	木	金	土	日
				1	2	3
4	5	6	7	8	9	10
11	12	13	14	15	16	17
18	19	20	21	22	23	24
25	26	27	28	29	30	31

演習・サイトビジット      講義

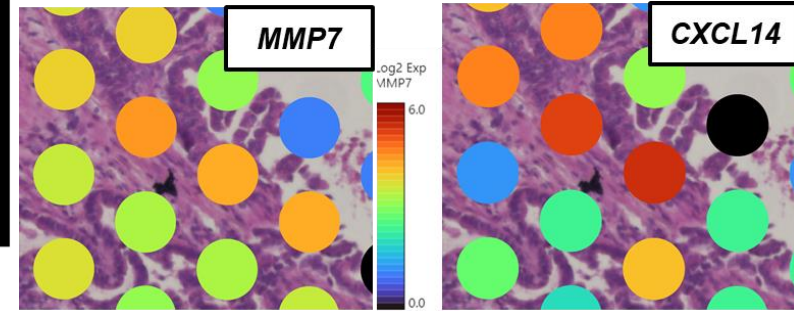
・講義スケジュールの日程等含む詳細につきましては、決定次第こちらに掲載いたします

# Single cell resolution measurement of the “disease” cells

## Invasive front in cancers



## Previous platform



### Alzheimer's Disease

アルツハイマー病で死亡した患者の脳の断面図

拡大図の前面  
海馬

### ゾンビを退治する

米ウェイク・フォレスト大学医学大学院のミランダ・オー率いるチームは、海馬など、記憶に不可欠な領域に潜む老化細胞(ゾンビ細胞)を発見した。この細胞は自然に死滅せず、有毒物質を放出する。オーのチームは薬でゾンビ細胞を殺して、記憶力を回復できるかどうか調べている。下の拡大画像にはアルツハイマー病の影響が見てとれる。黄色はタウタンパク質。その濃度は進行性の脳疾患の指標となる。青はストレスを示唆する分子、赤紫は修復不能な損傷の兆候、緑はゾンビ細胞による炎症を示す。特に、大きな細胞に青、赤紫、緑がすべてあれば、それはゾンビ細胞とみていい。

細胞

ゾンビ細胞

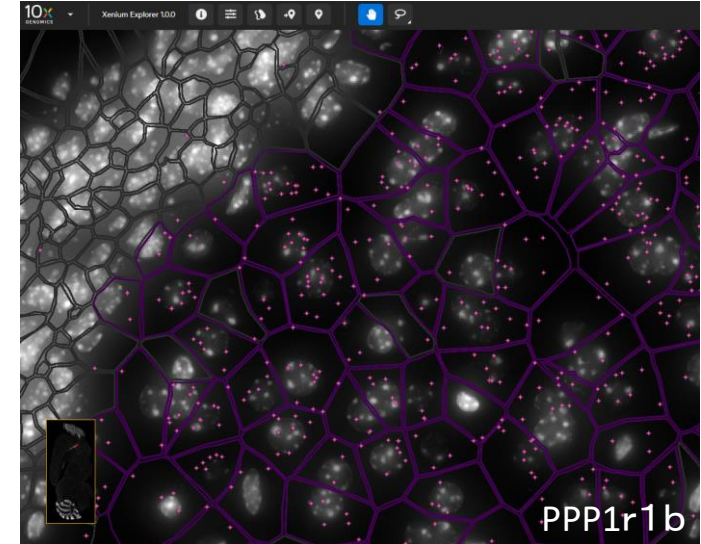
© 2023 LESAN WU, NANSHIYU, COSMO, SIRI MIRANDA ODE AND TIMOTHY ODE, WAKE FOREST UNIVERSITY SCHOOL OF MEDICINE, CHEN XUEBIN AND CANTINI AT WFLU, UNIVERSITY OF WASHINGTON ALZHEIMER'S DISEASE RESEARCH CENTER

### NATIONAL GEOGRAPHIC

より長く  
より健康に  
生きる

科学で老化を  
止められるか?

Jan. 2023



画像(資料)提供: 日経ナショナル ジオグラフィック

# Time to re-start/further accelerate the international collaborations!!

- English
- ▶ HOME
  - ▶ ご挨拶
  - ▶ スピーカー



**14AGW** 第14回国際ゲノム会議

Complete human genome and beyond

会期: 10月4日(水)~6日(金)  
会場: 一橋講堂

 **Eric Green**  
@NHGRI\_Director

Day 3 of the 14th International Workshop on Advanced Genomics ended with an incredible meeting banquet. Nothing better than celebrating genomics with colleagues over Japanese food!

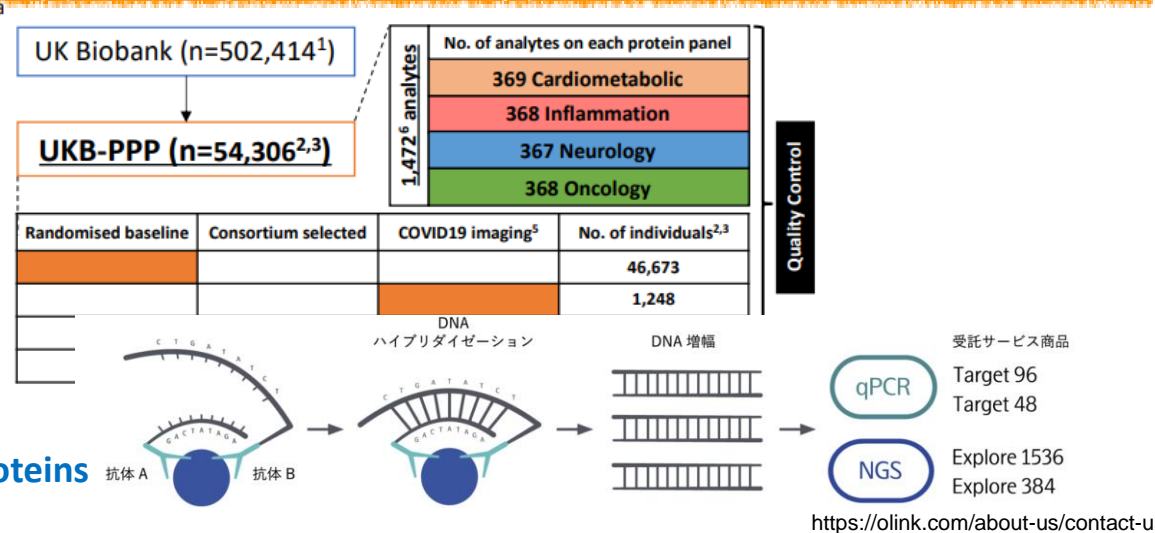
**Eric Green**  
Director, NHGRI, US



# Possibly diverse immune landscapes: Needs for the international collaboration;

## Genetic regulation of the human plasma proteome in 54,306 UK Biobank participants

Benjamin B. Sun<sup>1</sup>, Joshua Chiou<sup>2\*</sup>, Matthew Traylor<sup>3\*</sup>, Christian Benner<sup>4\*</sup>, Yi-Hsiang Hsu<sup>5\*</sup>, Tom G. Richardson<sup>3\*</sup>, Praveen Surendran<sup>6\*</sup>, Anubha Mahajan<sup>4\*</sup>, Chloe Robins<sup>7\*</sup>, Steven G. Vaszquez-Grinnell<sup>8\*</sup>, Liping Hou<sup>9\*</sup>, Erika M. Kvikstad<sup>8\*</sup>, Oliver S. Burren<sup>10</sup>, Madeleine Cule<sup>11</sup>, Jonathan Davitte<sup>7</sup>, Kyle L. Ferber<sup>12</sup>, Christopher E. Gillies<sup>13</sup>, Åsa K. Hedman<sup>14</sup>, Sile Hu<sup>3</sup>, Tinchu Lin<sup>15</sup>, Rajesh Mikkilineni<sup>16</sup>, Rion K. Pendergrass<sup>4</sup>, Corran Pickering<sup>17</sup>, Bram Prins<sup>10</sup>, Anil Raj<sup>11</sup>, Jamie Robinson<sup>1</sup>, Anurag Sethi<sup>11</sup>, Lucas D. Ward<sup>18</sup>, Samantha Welsh<sup>17</sup>, Carissa M. Willis<sup>18</sup>, Alnylam Human Genetics, AstraZeneca Genomics Initiative, Biogen Biobank Team, Bristol Myers Squibb, Genentech Human Genetics, GlaxoSmithKline Genomic Sciences, Pfizer Integrative Biology, Population Analytics of Janssen Data Sciences, Regeneron Genetics Center, Lucy Burkitt-Gray<sup>17</sup>, Mary Helen Black<sup>9</sup>, Eric B. Fauman<sup>2</sup>, Joanna M. M. Howson<sup>3</sup>, Hyun Min Kang<sup>13</sup>, Mark I. McCarthy<sup>4</sup>, Eugene Melamud<sup>11</sup>, Paul Nioi<sup>18</sup>, Slavé Petrovski<sup>10,19</sup>, Robert A. Scott<sup>6</sup>, Erin N. Smith<sup>20</sup>, Sándor Szalma<sup>20</sup>, Dawn M. Waterworth<sup>21</sup>, Lyndon J. Mitnau<sup>13</sup>, Joseph D. Szustakowski<sup>8\*</sup>, Bradford W. Gibson<sup>22\*</sup>, Melissa R. Miller<sup>2\*</sup>, Christopher D. Whelan<sup>1\*</sup>



Olink : Plasma proteome → 3000 proteins

et al., <https://www.biorxiv.org/content/10.1101/2022.06.17.496443v1.full.pdf>

## Single cell cohort analysis (UKB: 0.5 M people)

## Status of "Frail" may be also reflected there

**RESEARCH ARTICLE SUMMARY**

**IMMUNOGENOMICS**

**Single-cell eQTL mapping identifies cell type-specific genetic control of autoimmune disease**

Seyhan Yazar<sup>1</sup>, Jose Alquicira-Hernandez<sup>1</sup>, Kristof Wing<sup>1</sup>, Anne Senabouth, M. Grace Gordon, Stacey Andersen, Qinyi Lu, Antonia Rowson, Thomas R. P. Taylor, Linda Clarke, Katia Maccora, Christine Chen, Anthony L. Cook, Chun Jimmie Ye, Kirsten A. Fairfax, Alex W. Hewitt<sup>1\*</sup>, Joseph E. Powell<sup>1\*</sup>

**INTRODUCTION:** The human immune system has evolved to maintain tissue homeostasis and target exogenous pathogens by regulating specialized cell populations. The genetic control of immune cell populations is complex, and substantial variation between individuals, identifying how people vary in susceptibility to disease and respond to pathogens.

**RATIONALE:** Our knowledge of how genetic differences contribute to immune variation at the cellular level has been limited by two main challenges in the generation of data at single-cell resolution. One of these challenges is to sequence from many individuals and the other is to sequence a large number of cells from each individual. Addressing these challenges is essential for understanding the genetic control of immune cell populations.

(63.6%) of which were cell type-specific. We show how eQTLs have dynamic allelic effects in B cells that are transitioning from naive to memory states. Overall, we identified a set of 1988 eSNP-eGene (a gene with an eQTL) pairs expressed across the B cell maturation landscape, of which 333 have a statistically significant change in their allelic effect as B cells differentiate. Of these, 66% were only identified from the dynamic eQTL analysis and were not observed when testing for effects independently in cell types, highlighting the importance of investigating cell state-specific effects that underlie immune cell function. We investigated how eQTLs affect the expression variation of essential immune genes in specific cell types and provided experimental support for established hypotheses of cellular mechanisms in complex autoimmune diseases.

**SINGAPORE SCIENTISTS TO HELP DEVELOP ASIAN IMMUNE DIVERSITY ATLAS**

14 Mar 2022

Scientists from A\*STAR's Genome Institute of Singapore (GIS) will work with scientists from RIKEN and Samsung Medical Center to develop a genetic reference for Asian populations, and deepen the understanding of the diversity of immune genes.

Four photos of the AIDA team in GIS from left: Dr Shwetha Sankaran, Dr Nimada Anil Raman, Dr Deepa Rajagopal, Dr Shyam Prabhakar, Mr Haroonabed Mohammed Amin. (Copyright: A\*STAR's Genome Institute of Singapore)

**RESOURCE**

<https://doi.org/10.1038/s43587-022-00198-9>

**nature aging**

Check for updates

## Multidimensional single-cell analysis of human peripheral blood reveals characteristic features of the immune system landscape in aging and frailty

Oscar Junhong Luo<sup>1,2,19</sup>, Wen Lei<sup>2,3,19</sup>, Guodong Zhu<sup>2,4,19</sup>, Zhiyao Ren<sup>1,5,6,19</sup>, Yudai Xu<sup>2,3</sup>, Chanchan Xiao<sup>2,3</sup>, Hongyi Zhang<sup>2,3</sup>, Junxiang Cai<sup>7</sup>, Zhiping Luo<sup>7</sup>, Lijuan Gao<sup>2,3</sup>, Jun Su<sup>8</sup>, Lei Tang<sup>9</sup>, Wei Guo<sup>9</sup>, Huanxing Su<sup>3,10</sup>, Zhang-Jin Zhang<sup>3,11</sup>, Evandro Fei Fang<sup>3,12</sup>, Yijun Ruan<sup>13</sup>, Sean Xiao Leng<sup>14</sup>, Zhenyu Ju<sup>15</sup>, Huiling Lou<sup>7</sup>, Junling Gao<sup>16</sup>, Nan Peng<sup>17</sup>, Jie Chen<sup>18</sup>, Zhijun Bao<sup>18</sup>, Feng Liu<sup>2,7</sup> and Guobing Chen<sup>2,3</sup>

S Yazar et al., Science 2022

OJ Luo et al., Nature Aging 2022





## 教育用の拠点のUpdate (東大柏拠点を例に)

- シーケンサー： NovaSeq6000 x 2台 **WGS：50,000/year**
- シーケンサー： NovaSeq6000 (DX) x 1台
- シーケンサー： MGI T7 x 1; G400 x 1
- シーケンサー： PromethION x 4 **WGS：10,000/year**

- Robot： XT-AUTO/Hamilton/Analytik Jena
- Robot (MGI)： STP3000/NE960
- Nano dispenser： Mosquito (LV/HV/Dragonfly)
- QC： TapeStation/FemtoPulse
- シングルセル： 10X Chromium x 3

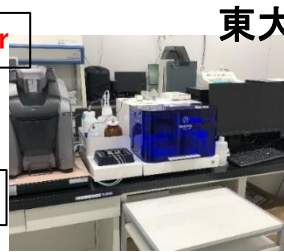
※Xenium/StereoSeq

- (Cluster server: 800 core; Luster 600Gb/Tape 1PB+ GPUx40)

国内有数のデータ産生・解析拠点

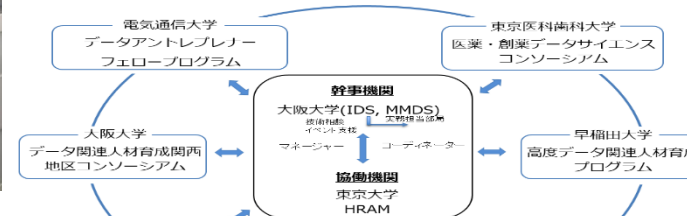
(Cluster server@KOG: 2500 core; Luster 2PB/Tape 6PB)

民間でも利用可能なデータ解析環境  
(NBDCの定める“機関外サーバー”基準を満たす)



## 東大柏の葉での既存の教育の枠組み

### 社会人リカレントプログラム”DTEP”



### 文科省データ人材育成ネットワーク “D-DRIVE”



# scRNA analysis for healthy (elderly) individuals: >100 samples analyzed so far

## “Kashiwanoha” Cohort study



Blood sampling

<50s, 50s, 60s, 70s, >80s  
>10 individuals for each



### 全体の流れ



Smart Watch

Apri for: Foods, Sleep, Exercise, Medical Check-ups