KSBi-BIML 2026

Bioinformatics & Machine Learning(BIML) Workshop for Life Scientists

생명정보학 & 머신러닝 워크샵 (온라인)

Introduction to single cell multiomics technologies

황병진 _ 연세대학교

KSBI KOREAN SOCIETY FOR BIOINFORMATICS | 한국생명정보학회

본 강의 자료는 한국생명정보학회가 주관하는 BIML 2026 워크샵을 목적으로
제작된 것으로 해당 목적 이외의 다른 용도로 사용할 수 없음을 분명하게 알립니다.

이를 다른 사람과 공유하거나 복제, 배포, 전송할 수 없으며 만약 이러한 사항을 위반할 경우
발생하는 **모든 법적 책임은 행위자 본인에게 있음**을 알립니다.

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Bioinformatics & Machine Learning (BIML) Workshop for Life Scientists

한국생명정보학회가 주최하는 BIML-2026 동계 Bioinformatics &Machine Learning 교육 워크숍에 여러분을 초대합니다.

BIML 워크숍은 생명정보학 연구자들이 최신 AI바이오 분야의 인공지능 기반 분석 기술과 바이오 데이터 분석 기법을 이론과 실습을 통해 체계적으로 배울 수 있는 전문 교육 프로그램입니다. 2015년에 시작된 BIML 워크숍은 올해로 12년 차를 맞이하며, 국내 생명정보학 분야의 최초이자 최고 수준의 교육 프로그램으로 자리 잡았습니다. 이번 워크숍은 크게 인공지능바이오(AI바이오) 분야와 디지털바이오 분야, 두 분야로 구성됩니다.

AI바이오 분야에서는 생명정보 분석에 폭넓게 응용되고 있는 다양한 인공지능 기반 자료 모델링 기법을 다룰 예정입니다. 특히, 인공지능 심층학습을 활용한 단백질 구조 예측, 유전체 분석, 신약 개발에 대한 이론 및 실습 강의가 진행됩니다.

또한 디지털바이오 분야에서는 단일세포오믹스, 공간오믹스, 멀티오믹스, 메타오믹스에 대한 강의도 마련되어 있어, 연구자들의 분석 역량 강화에 실질적인 도움을 줄 것으로 기대됩니다.

또한 2024년부터 추가된 의료정보 자료 분석을 다루는 강의를 올해도 지속해서 운영하고자 합니다. 이는 최근 의료정보 자료 분석에 관한 연구 수요 증가를 반영한 것으로, 관련 연구를 수행하는 의과학자 및 의료정보 연구자들에게 유용한 지침을 제공할 것입니다.

또한, 올해도 생명정보학 기술의 다양화에 발맞춰 온라인 강좌를 대폭 확대했습니다. 올해는 무료 강좌 10개를 포함한 총 40개 이상의 강좌가 개설되며, 연구 주제에 맞는 강좌 추천과 강연료 할인 혜택도 제공합니다.

BIML-2026는 국내 주요 연구 중심 대학의 전임 교수 및 각 분야 최고 전문가들의 강의로 구성되어 있으며, 기초 이론부터 최신 연구 동향까지 아우르는 심도 있는 교육의 장이 될 것으로 확신합니다.

여러분의 많은 관심과 참여를 기대합니다!

2026년 2월

한국생명정보학회장 류 성 호

강의개요

Introduction to single cell multiomics technologies

단일 세포 기술의 발달로 유전체, 전사체, 단백체, 그리고 후성 유전제를 분석할 수 있는 기술들이 빠른 속도로 개발되고 있다. 하지만 실제 biological한 의미를 가진 세포를 정확하게 정의하기 위해서는 여러 표현형을 동시에 측정하는 멀티오믹스 기술이 요구된다. 예를 들어, 단일 세포 수준에서 RNA와 표면 단백질의 발현량을 동시에 측정하는 CITE-seq, 그리고 염색질 접근성(ATAC)과 전사체를 동시 분석하는 10x Multiome 및 sci-CAR와 같은 기술들이 대표적인 멀티오믹스(multiomics) 방법론에 해당한다. 본 강의에서는 최신 단일세포 멀티오믹스 데이터 종류들에 대해서 배우고, 이들이 어떻게 만들어지는지 기술적인 원리와 개념을 배우는 것을 목표로 한다. 또한 이런 기술들을 적용하여 실제 논문에서 분석된 예제들을 살펴본다.

강의는 다음의 내용을 포함한다:

- 단일세포 기술의 역사
- 단일세포 멀티오믹스 기술 I
- 단일세포 멀티오믹스 기술 II
- 단일세포 멀티오믹스 분석 방법론의 적용 예

* 교육생준비물:
  노트북 (이론강의로 파워포인트나 PDF가 문제없이 열리면 됨)

* 강의 난이도: 초급

* 강의: 황병진교수 (연세대학교 의과대학 의생명과학부)

Curriculum Vitae

Speaker Name: Byungjin Hwang, Ph.D.

▶ **Personal Info**

Name	Byungjin Hwang
Title	Assistant Professor
Affiliation	Yonsei University, Department of Biomedical Sciences

▶ **Contact Information**

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Research Interest

Single cell multi-omics, CRISPR engineering and Cancer-immunology

Educational Experience

2012	B.S. in Chemistry, Yonsei University, Korea
2018	Ph.D. in Genome engineering and Bioinformatics, Yonsei University, Korea

Professional Experience

2018-2022	Post-doc research fellow, Institute for Human Genetics, UCSF, USA
2022-2022	Visiting Scholar, University of Michigan, USA
2022-	Assistant Professor, Yonsei University, Severance Biomedical Science Institute, Korea

Selected Publications (5 maximum)

1. Connor A. Tsuchida, Nadav Brandes, Raymund Bueno, Marena Trinidad, Thomas Mazumder, Bingfei Yu, **Byungjin Hwang**, Christopher Chang, Jamin Liu, Yang Sun, Caitlin R. Hopkins, Kevin R. Parker, Yanyan Qi, Ansuman T. Satpathy, Edward A. Stadtmauer, Jamie H.D. Cate, Justin Eyquem, Joseph A. Fraietta, Carl H. June, Howard Y. Chang, Chun Jimmie Ye, Jennifer A. Doudna, ***Cell***, 2023, "Mitigation of chromosome loss in clinical CRISPR-Cas9-engineered T cells" (**Engineered main plasmid vector system for this CRISPR screen**)
2. **Byungjin Hwang***, David S. Lee*, Whitney Tamaki, Yang Sun, Anton Ogorodnikov, George Hartoularos, Aidan Winters, Bertrand Yeung, Kristopher L. Nazor, Yun S. Song, Eric D. Chow, Matthew H. Spitzer, Chun Jimmie Ye, ***Nature Methods***, 2021, doi: 10.1038/s41592-021-01222-3, "SCITO-seq: single-cell combinatorial indexed cytometry sequencing".
3. **Byungjin Hwang***, Wookjae Lee*, Soo-Young Yum*, Yujin Jeon, Namjin Cho, Goo Jang, Duhee Bang; ***Nature Communications***, 2019, doi:10.1038/s41467-019-09203-z, "Lineage tracing using a Cas9-deaminase barcoding system targeting endogenous L1 elements".
4. Namjin Cho*, **Byungjin Hwang***, Jung-Ki Yoon*, Sangun Park*, Joongoo Lee*, Han Na Seo, Jeewon Lee, Sunghoon Huh, Jinsoo Chung, and Duhee Bang, ***Nature Communications***, 2015, DOI:10.1038/ncomms9351, "De novo assembly and next-generation sequencing to analyze full-length gene variants from codon-barcoded libraries".

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Introduction to single cell multiomics

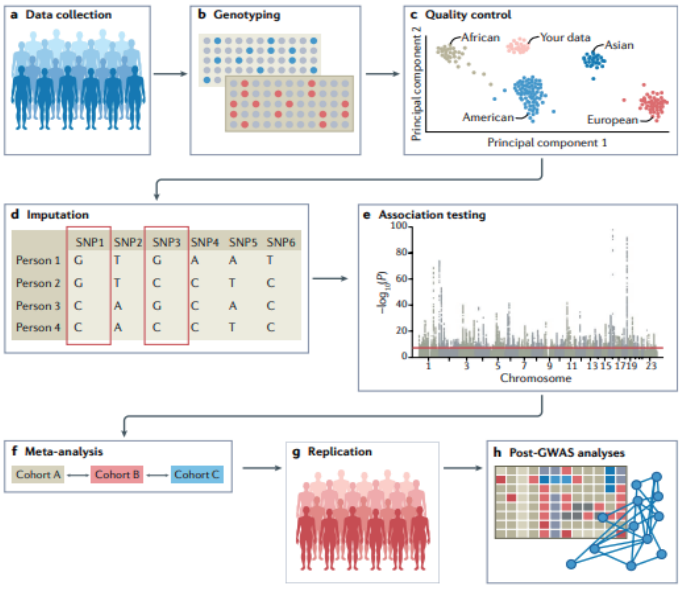
연세대학교 의과대학 황병진

Contents

1) GWAS to Now
2) From bulk to single cell technology
3) 단일세포 멀티오믹스 기술 I (Unimodal)
4) 단일세포 멀티오믹스 기술 II (multimodal)

What we learned from the GWAS

GWAS (Genome-wide association studies)



Fine mapping
SNP-to-Gene map
Gene-to-Function map
Pathway analysis
Gene-gene correlation

SNP (단일염기다형성) : 1,000개의 염기마다 하나씩 존재, 4,5백만/사람

From GWAS to Function

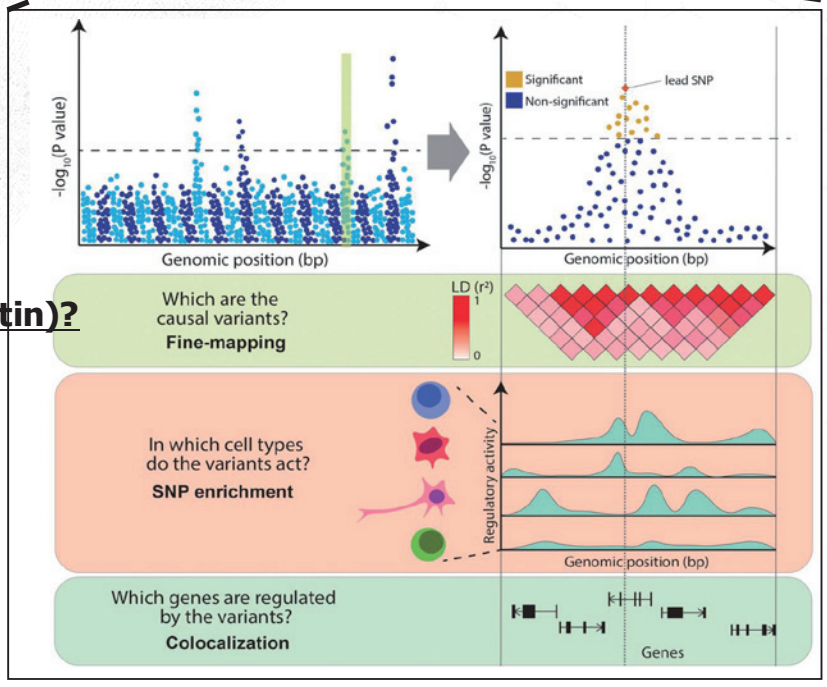
DNA -> RNA -> Protein -> **Phenotype**

SNP-to-Gene map
Most of them lie
Non-coding region

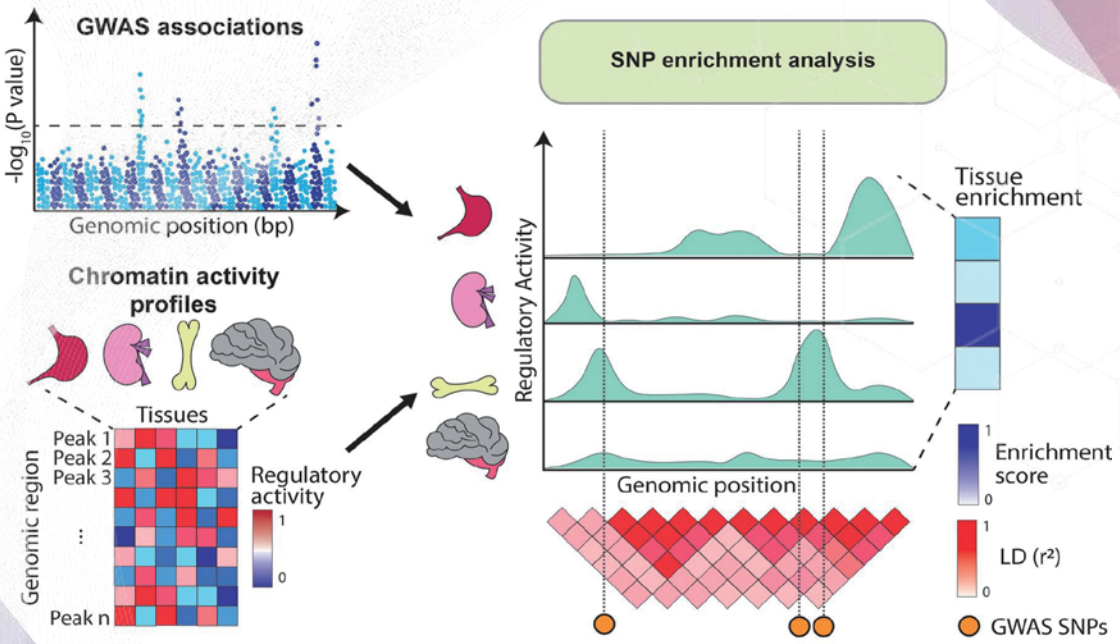
Regulatory(Chromatin)?

&

Cell-type specific?

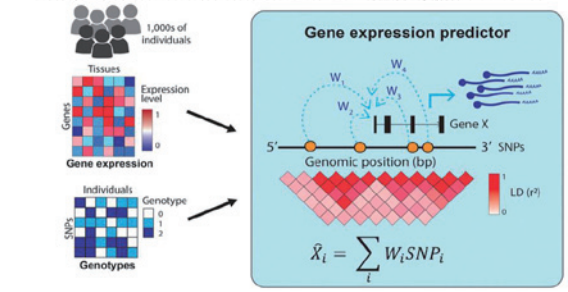


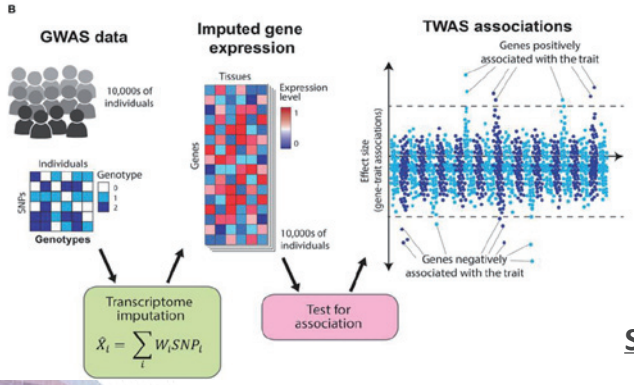
SNP enrichment and chromatin annotation



Chromatin activity : 염색체의 풀림정도 (openness)를 측정

Overview of transcriptome-wide association studies (TWAS)



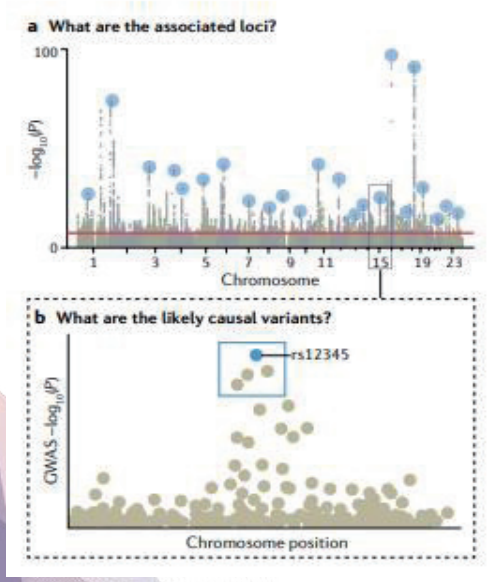


Gene level association
Vs
SNP level association

Less burden for testing size
(각 loci가 통계적으로 의미가 있는지)
3.3Gbp -> 20,000 genes

Statistical burden 을 줄여준 의미!

Functional follow-up of GWAS

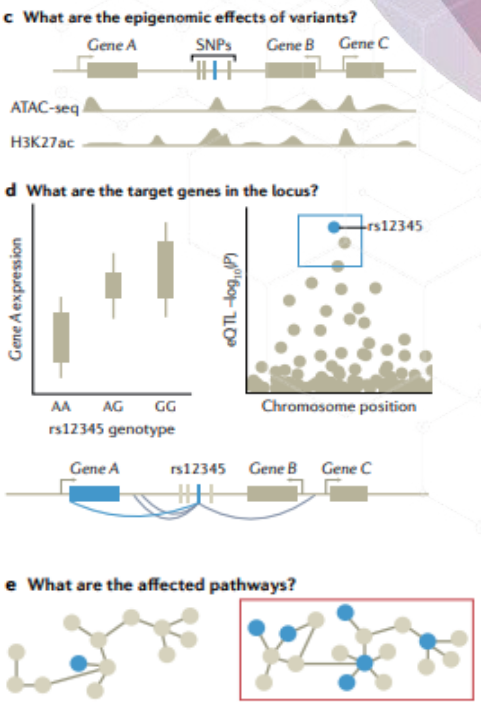


ATAC
Methylation

eQTL

3C, 4C, HiC

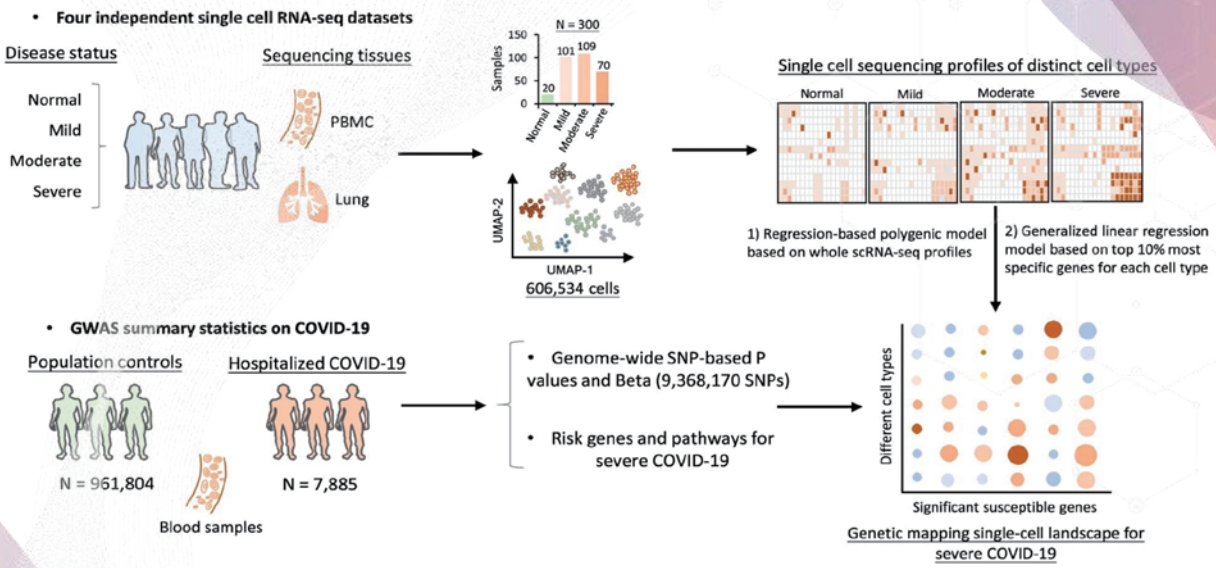
Pathway



Ex) IBD (inflammatory bowel disease) -> **12%** of risk loci as causal variant

(future +**CRISPR** data for Mechanism)

Integration of GWAS to scRNA-seq datasets



Cell type aware association is feasible to map DNA-RNA (genotype-phenotype) relationship

Moving the paradigm to phenotype cells better ?

- **Genotype -> Phenotype**
- ~15 years of GWAS (DNA) was not sufficient (explained variance <20% for complex diseases)

What GWAS did well

1. Thousands of risk loci
2. Strong statistical association (not mechanism)
3. Entry point for disease biology

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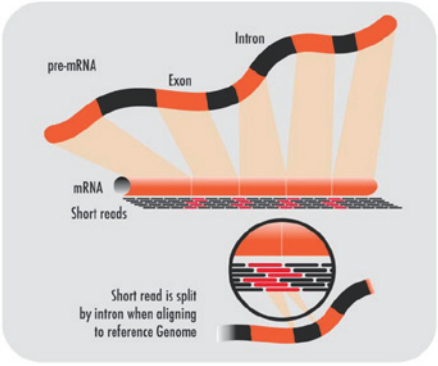
RNA-seq: a revolutionary tool for transcriptomics

- **For functional annotation, we measure 'Gene expression'**
- **Transcriptome** : The complete set of transcripts in a cell, and their quantity for a specific developmental stage or physiological condition

- Catalogue (mRNA, non-coding RNA and small RNAs), Structure (5' and 3' ands splicing patterns etc)



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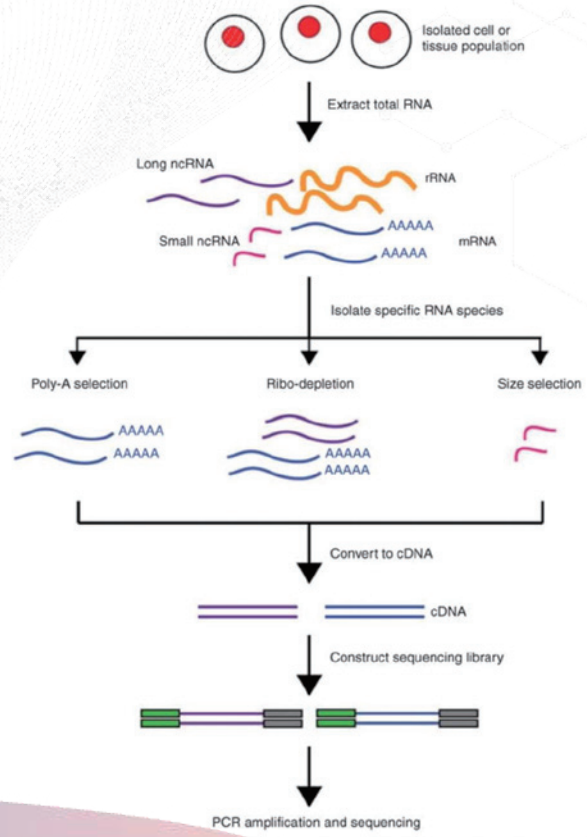
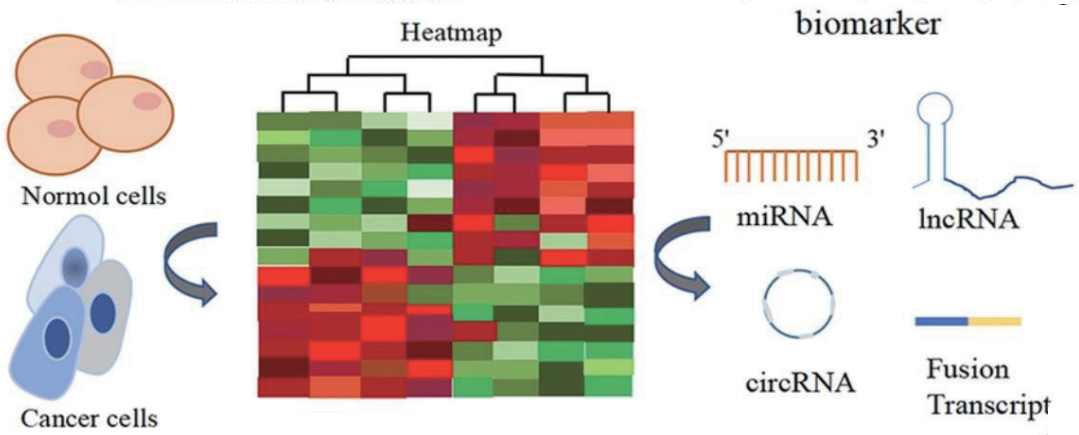
Overview of bulk RNA-seq



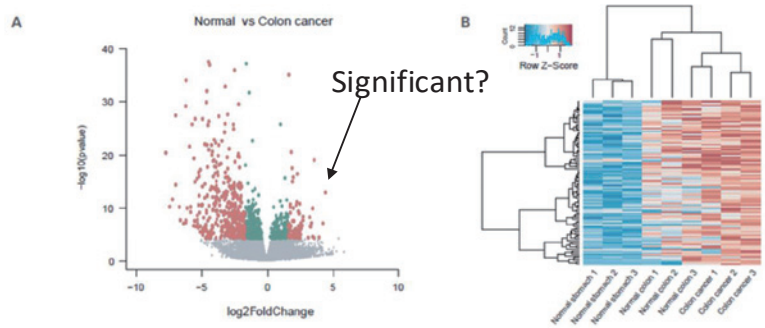
Various applications of bulk RNA-seq

1) Expression Profiling and **Differential expression (DE)** analysis



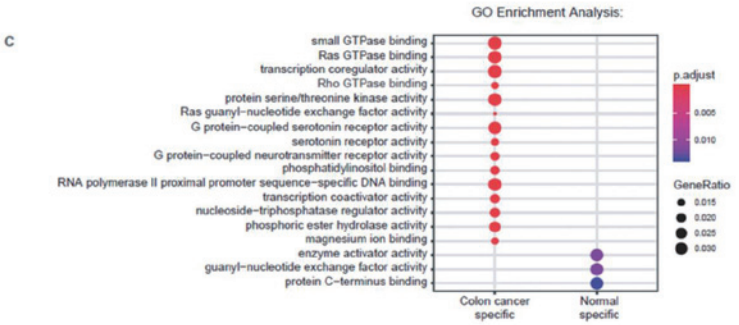
***(Differentially Expressed Gene, **DEG**) 차등 발현 유전자란 **두 실험 조건 하에서 샘플 집합의 유전자 발현량이 많이 차이나는 유전자**
→ 궁극적 질병 유전체 스터디의 목표

DE analysis of cancer vs normal



Fold-change volcano plot

Clustering heatmap



Gene set enrichment analysis

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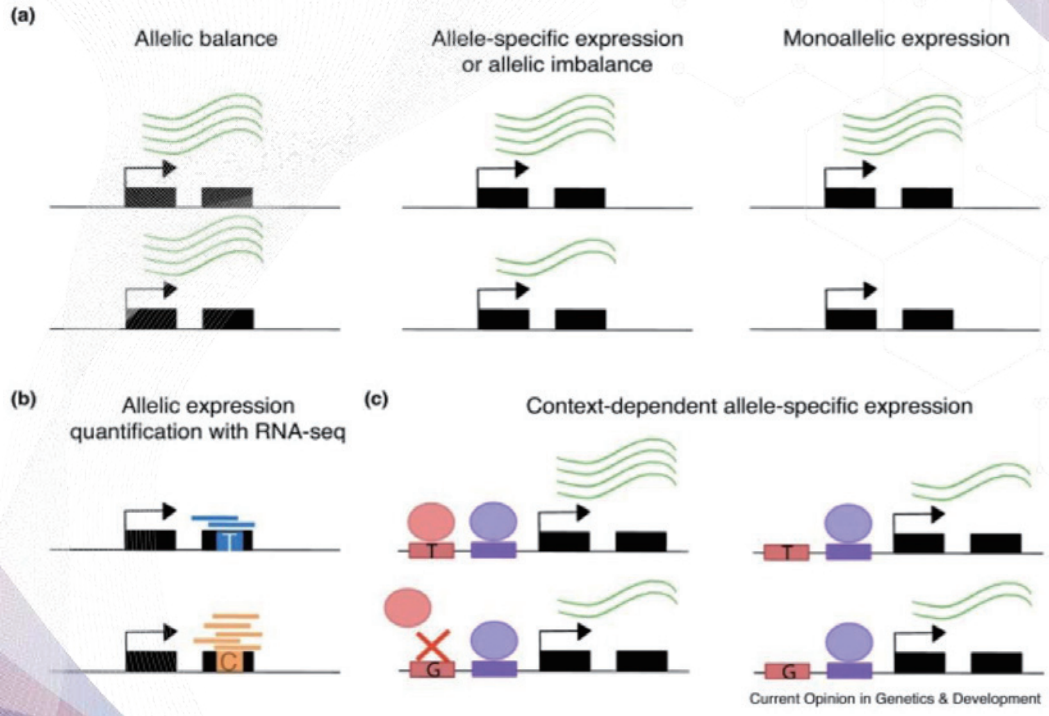
Allele-specific expression (ASE)



Current Opinion in Genetics & Development

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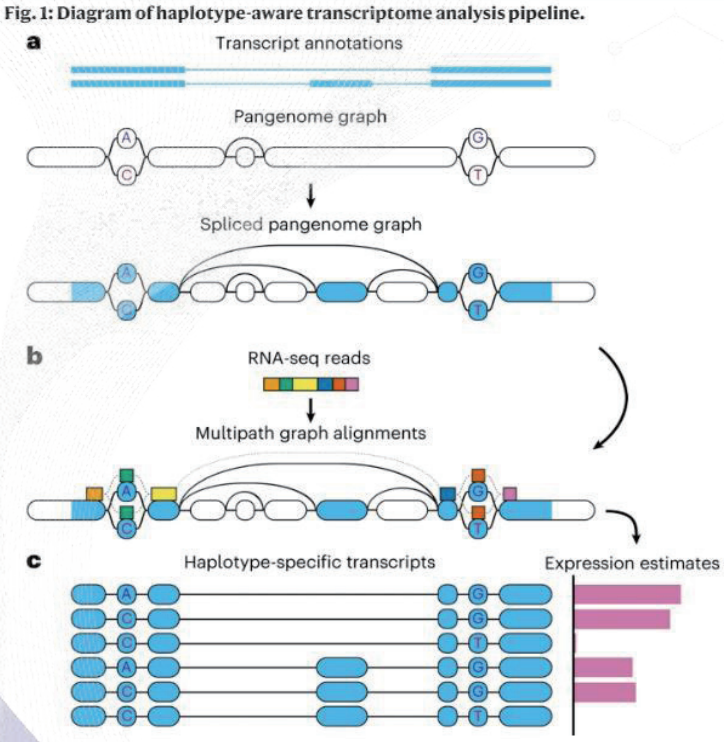
Haplotype-aware pantranscriptome



Pangenome -> 인류의 인종별 특징을 모두 취합한 reference genome임.

현재 phased variant (알려진 **haplotype block**) 에 대해서 분석됨

Long-read 시퀀싱 기술이 발전할수록 resolution증가

Splice구조가 haploid수준에서 규명되어야함.

DEG 분석의 패러다임도 알려진**transcriptome 뿐만 아니라 새로운 것들에 대한 재정의 필요해질 것임.**

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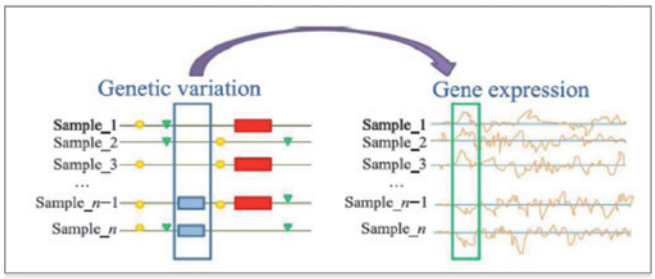
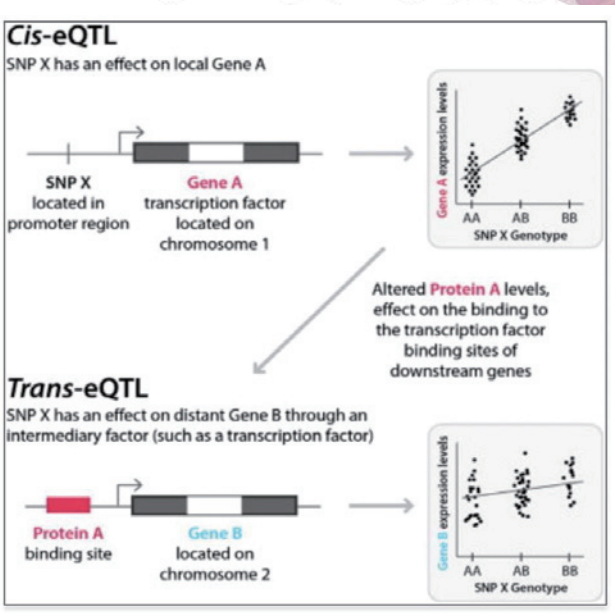
Expression quantitative trait loci (eQTL)



그동안의 많은 **GWAS** (genome-wide association study, DNA 염기서열의 변이 (SNP) 와 질병 유/무의 상관성 분석된 Hit들이 **non-coding SNP (코딩 영역x 해석 어려움) ->**

이 중 일부가 유전자 발현에 영향을 미칠 수 있다 (not protein), 새로운 질병/형질 연구의 가능성



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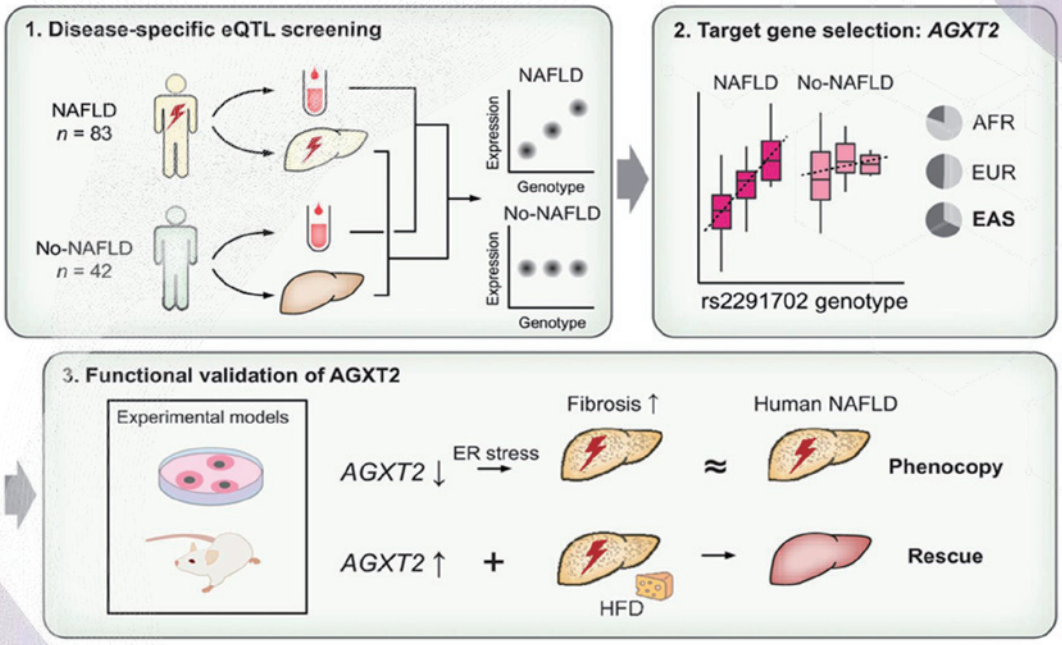
eQTL in liver disease



NAFLD (Non Alcoholic Fatty Liver Disease, 비알코올성지방간)

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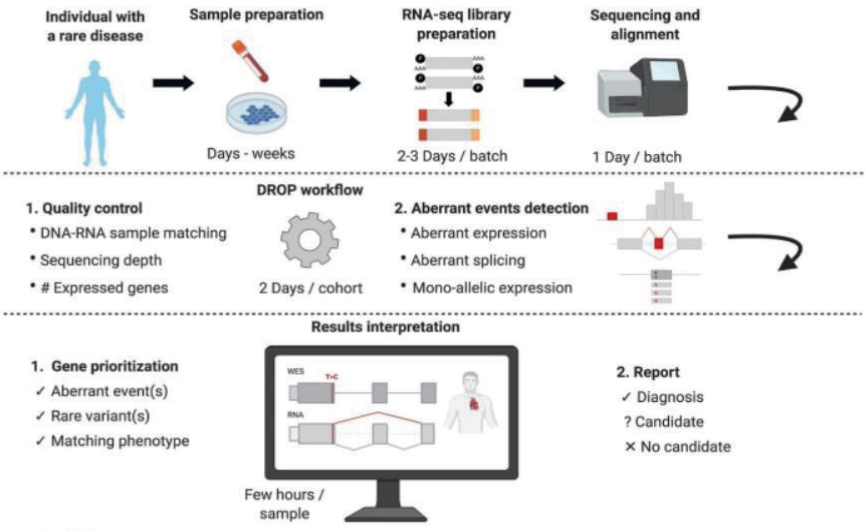
Clinical diagnostics of Mendalian diseases using RNA-seq

WES/RNA-seq of 303 people with Mendalian disease
(**rare**: 3~5% population, **80% of them are driven by genetic cause**)



Able to genetically diagnosed **16% of inconclusive case from WES**

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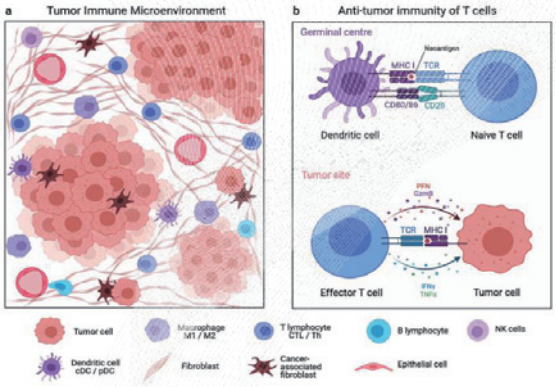
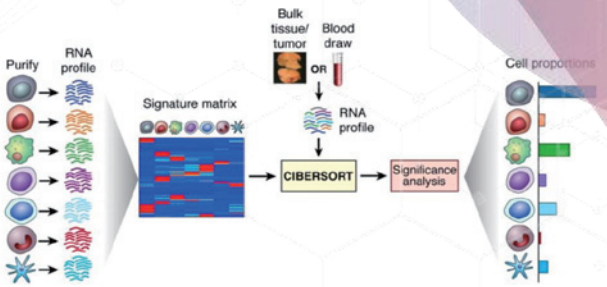
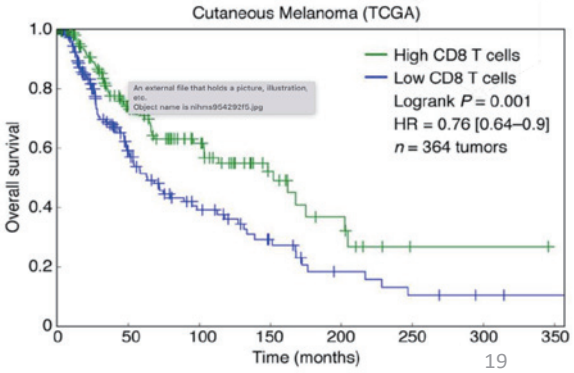
Tumor-immune-composition (Mixed cell)



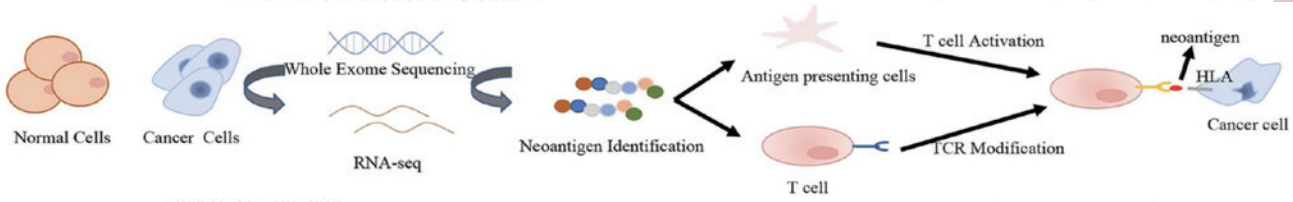


Input Sample									
		0.108	0.186			0.000	0.569	0.822
		0.07	0.068	0.029		0.000	0.497	1.028
		0.206	0.143			0.000	0.432	0.907
				0.051		0.000	0.419	0.914
				0.016	0.165	0.000	0.397	0.925
	0.099	0.191		0.019		0.000	0.366	1.069
	0.051			0.048		0.000	0.365	1.044
	0.078		0.162	0.02		0.000	0.358	1.114
				0.031		0.000	0.354	0.964
	0.056			0.026		0.000	0.353	1.022
		0.144	0.13		0.193	0.000	0.348	0.969
		0.068	0.068	0.062		0.000	0.348	1.140
	0.069			0.063		0.000	0.346	1.017
				0.032		0.000	0.342	0.968
						0.000	0.342	1.129



19

Neoantigen profiling by RNA-seq and TCR modification targeted neoantigens



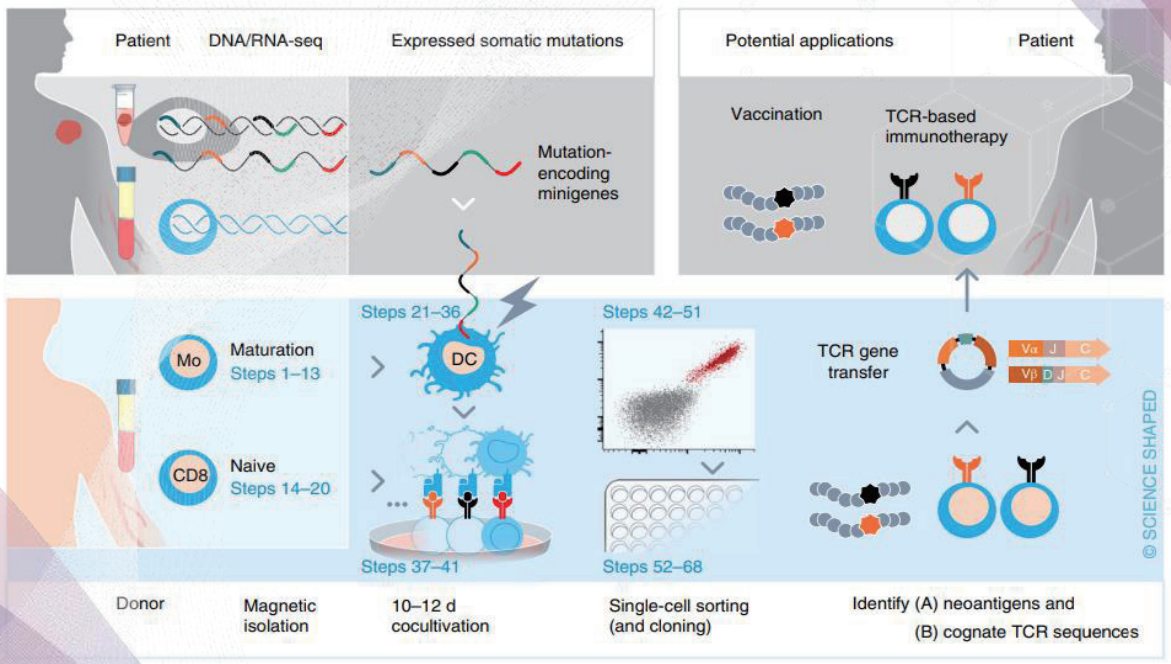
1.**Whole exome sequencing to identify the mutations** by using different computational and mutation calling tools

2.**RNA-seq analysis to focus specifically on the expressed mutations** and identification of neoepitopes (신항원) in silico with computational algorithms for MHC class I and class II binding

Which T cells are responsible for this? -> Single-cell

20

Identifying neoantigen reactive T cells



유전자 편집 기술(ex CRISPR)의 발달로 allogenic donor에서 CAR-T, TCR-T같은 세포치료제가 획기적으로 발달하고 있다.

21

We need better resolution for phenotyping cells

?

- Genotype -> **RNA -> Phenotype**
- Bullk RNA-seq is adopted in clinical labs along with GWAS (DNA) information
- Cancer **heterogeneity** not solved due to mixed signal (TME)

단일세포 오믹스의 필요성!!!

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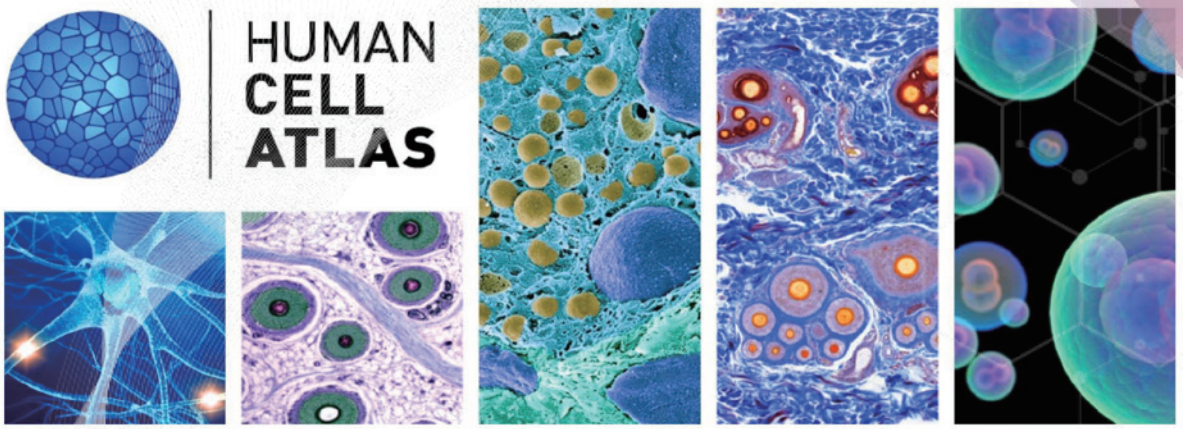
Human Cell Atlas (HCA) project



Bulk studies -> Single Cell Genomics (Catalogue of all cell types in the body from healthy and diseased individuals)

2016 결성, 초기목표: 모든 **단일세포의 전사체 (Transcriptome) 지도**

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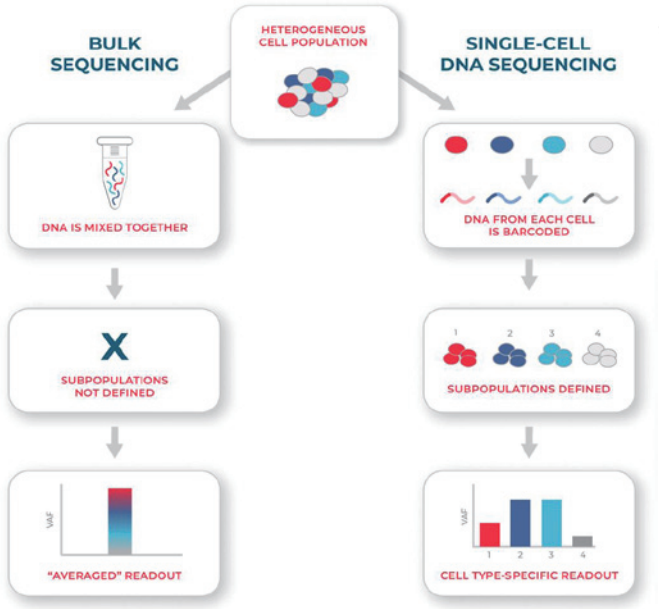
Why we care about single cell?



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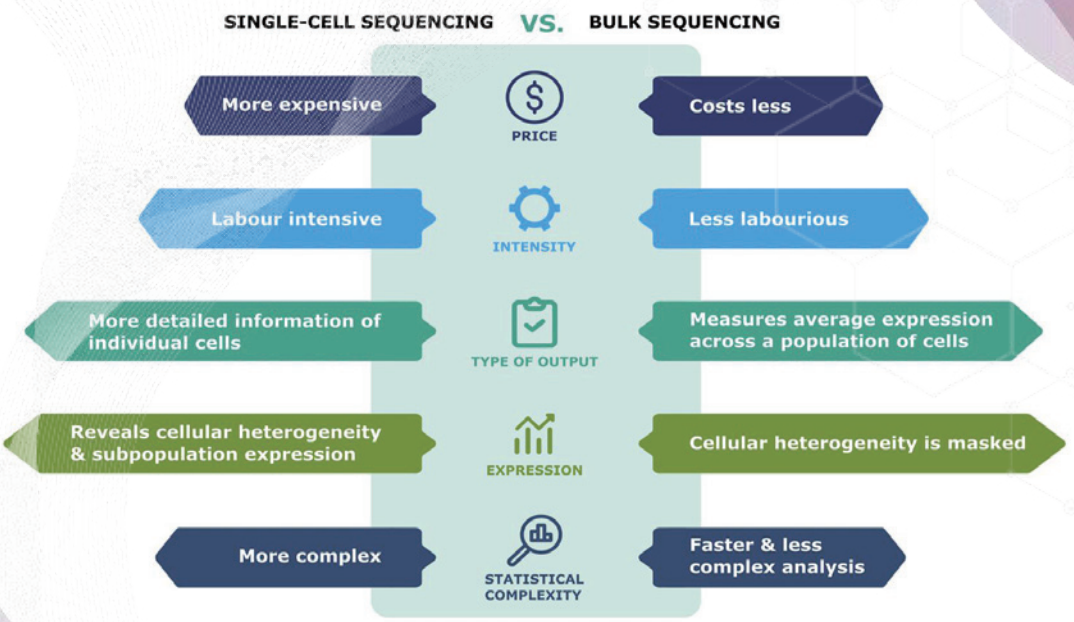
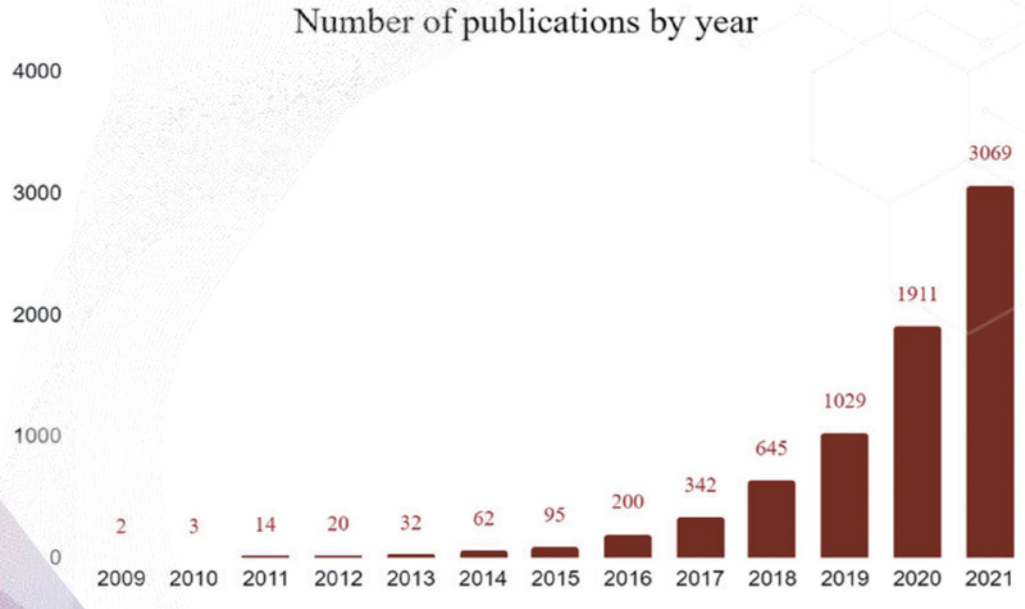
Bulk vs Single cell sequencing



Heterogeneity : 이질성, 단일세포에서 중요한 개념임

25

Increasing popularity of single cell RNA sequencing (scRNA-seq)



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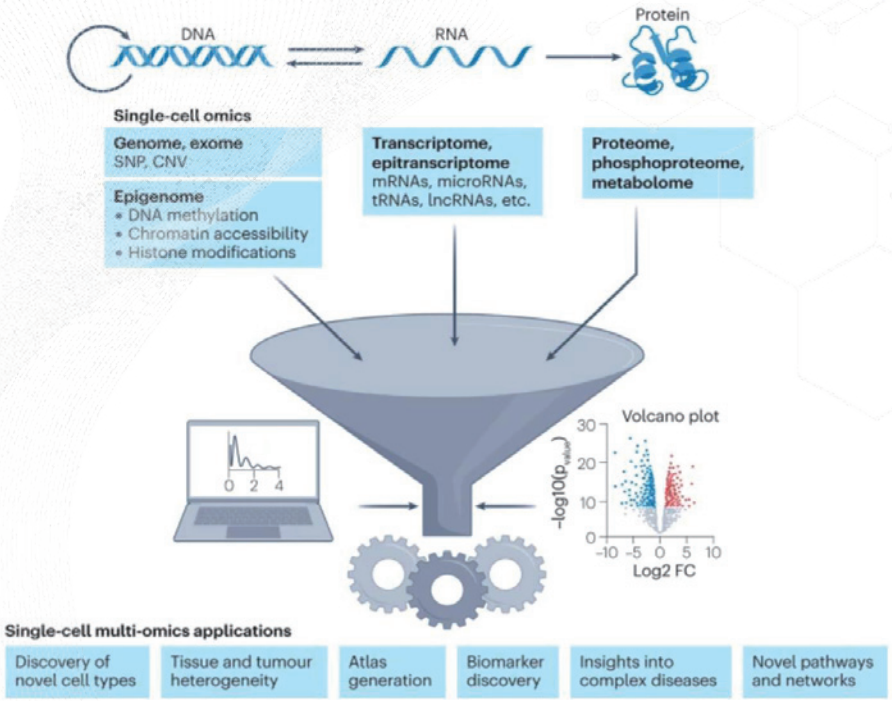
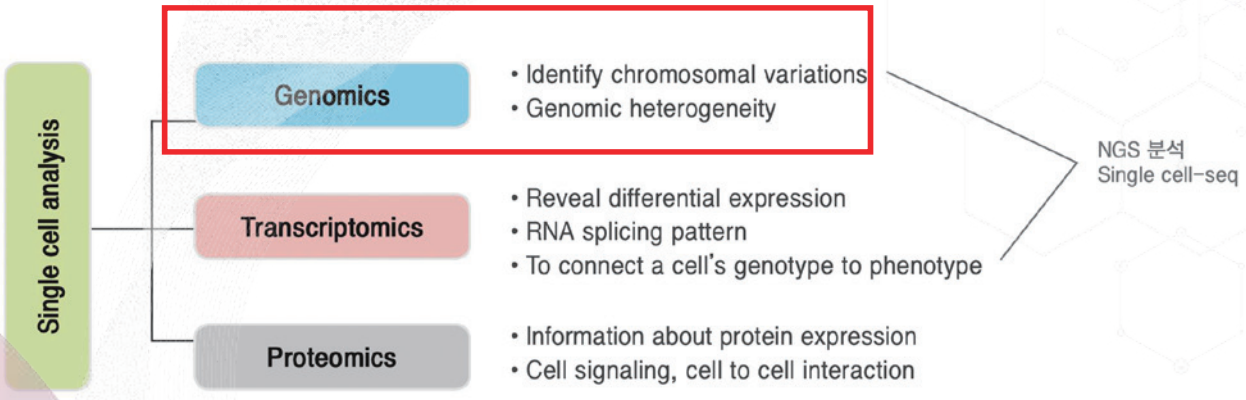
Single-omics to multi-omics

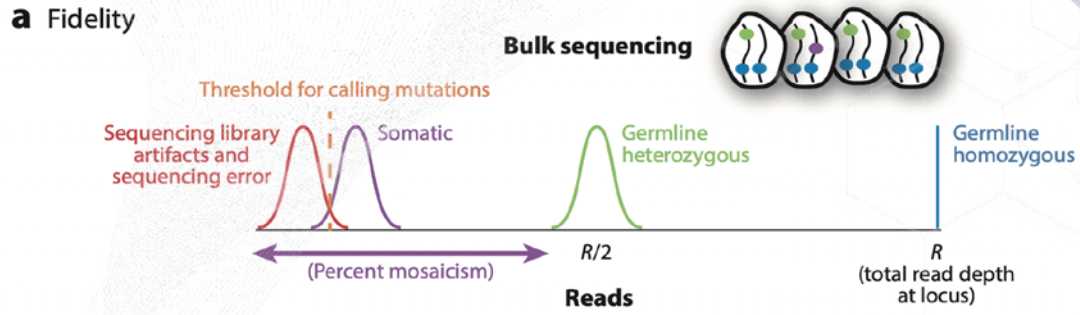


Single-cell analysis platforms

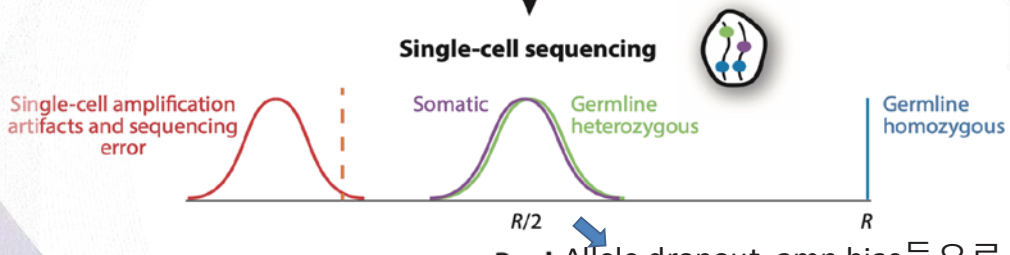


Fidelity of single cell genomics

Fidelity: 진짜 생물학적 변이를 얼마나 잘 구분할 수 있느냐?



bulk에서는 threshold를 정해서somatic mutation과 error를 비교적 안정적으로 구분



Allele dropout, amp bias등으로 분산이 더 큼

싱글셀 DNA분석: 변이를 진짜 가진 세포 없는 세포 구분이 용이

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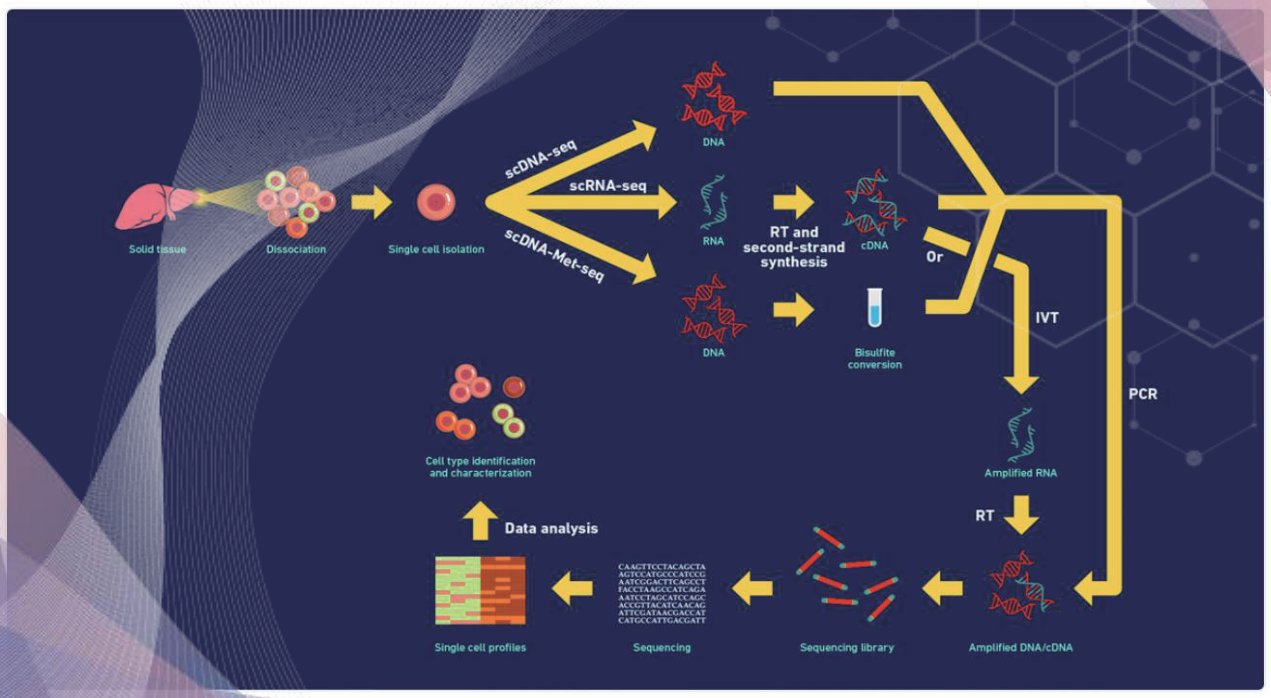
Single cell sequencing workflow



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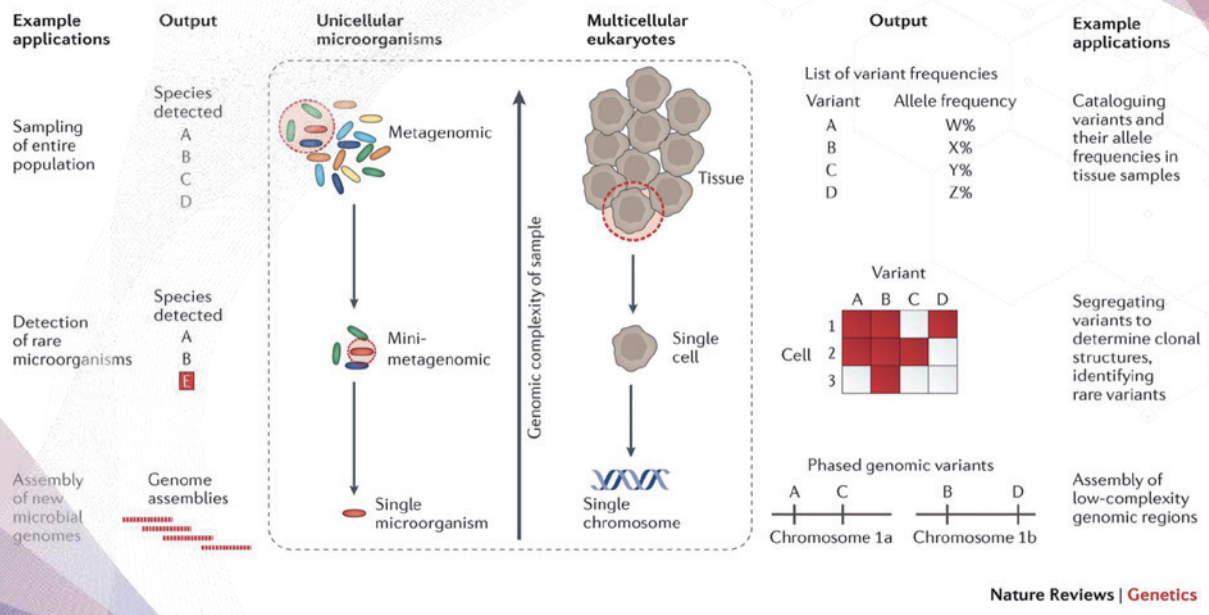
Opportunities enabled by single-cell genome sequencing



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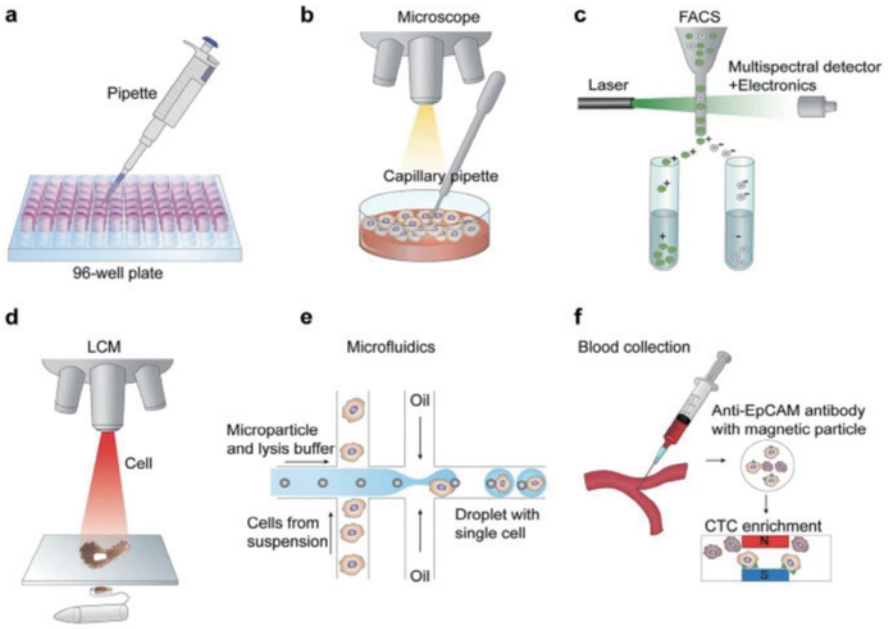
Single-cell isolation methods



a. Limiting dilution b. tweezers c. FACS d. LCM
e. Microfluidics f. Bead based capture

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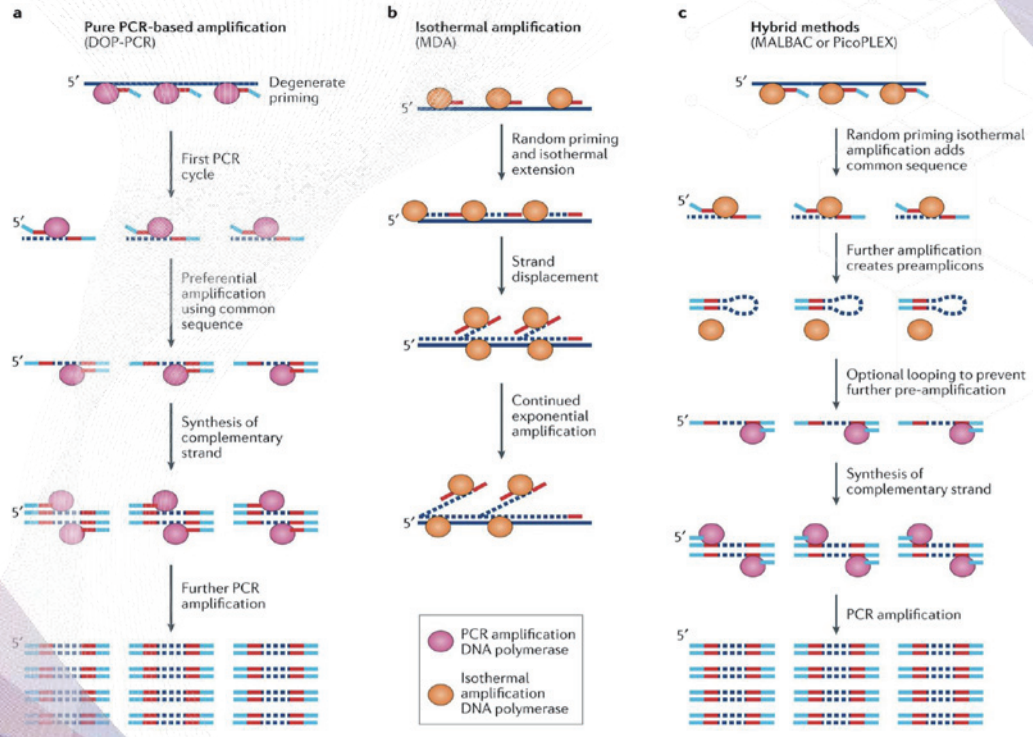
How to amplify single-cell genomes?

- 10 yrs of progress for **WGA** (whole genome amplification) to reduce artefacts, amplification bias
- Merely 6pg in diploid DNA
- Needs to be amplified >100 times to generate sequencing library and analysis
- Cover as much of the genome (3 Billion) as possible without bias

33

Three main WGA methods



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Pros and Cons

	PCR-based (DOP-PCR)	Isothermal (MDA)	Hybrid (MALBAC or PicoPLEX)
False-negative rate (coverage and allelic dropout)	High	Low	Intermediate
Non-uniformity	Low	High	Low
False-positive rate (amplification error rate)	High	Low	Intermediate

DOP-PCR: Degenerate oligonucleotide Primed

MALBAC : Multiple annealing and looping-based amplification cycles

MDA : Multiple displacement amplification
(등온이라 비특이적 결합 잘되고, stochastic증폭)

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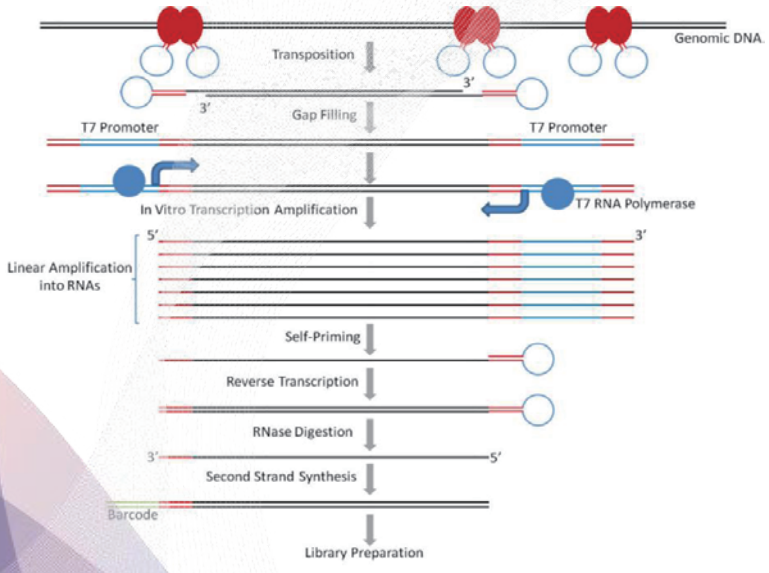
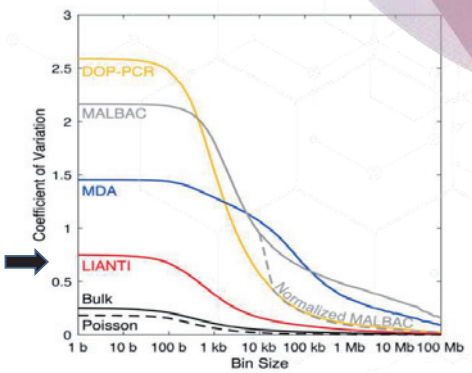
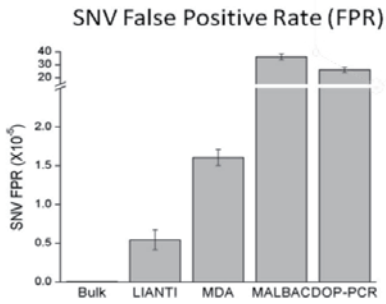
LIANTI (LInear AmplicatioN via Transposon Insertion)

에러를 최대한 낮춰 FP줄이는게 관건







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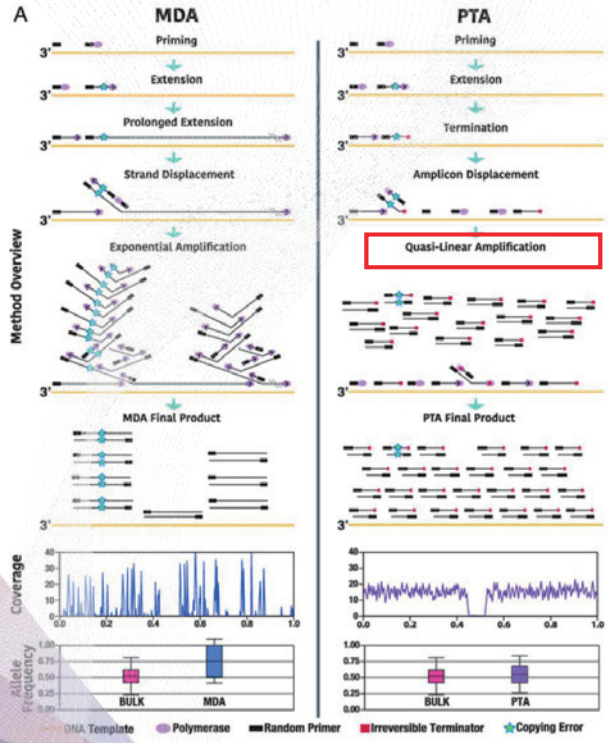
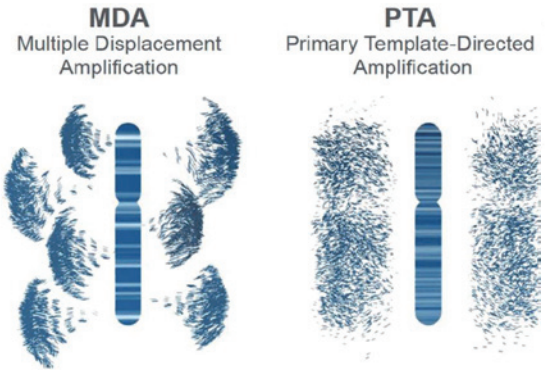
PTA (Primary Template directed Amplification)





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Future directions

- Long-read sequencing in scDNA-seq
  - Resolve haplotype structure
  - CNV+SV detection
- More efficient droplet-based WGA needed
  - Now cost prohibitive (~only few hundred cells)

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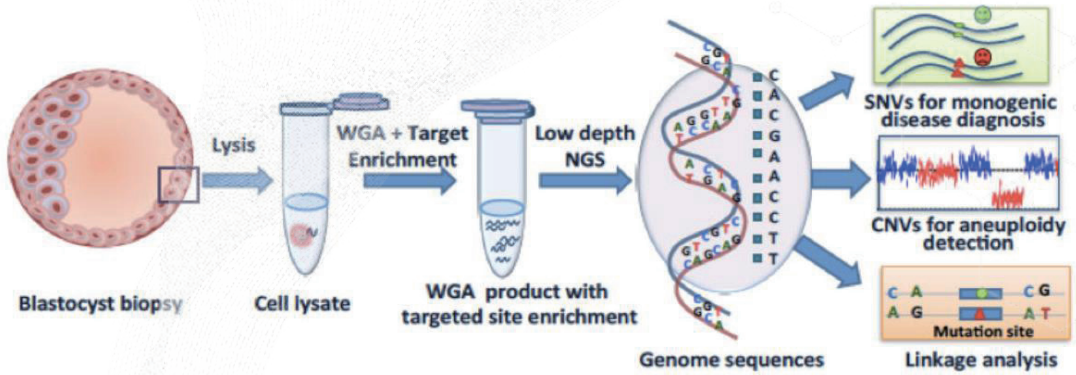
MALBAC Babies (not gene engineering)



In vitro fertilization (IVF) - **플랫폼**

preimplantation genetic screening (PGS) / diagnosis (PGD)

외배엽생검(장차 태반)-> WGA 분석(copy, single gene)-> 착상

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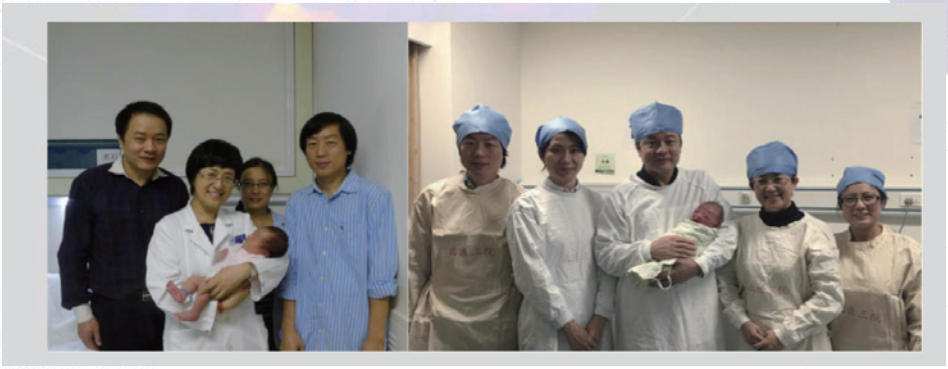
New opportunity for are genetic disorders



The first IVF baby from Sunny Xie's (Peking University)

Case 1. Monogenic disease (husband, autosomal dominant disorder,hereditary multiple exostoses (HME, 유전적 다발성 외골증), c.233delC (frameshift point mutation in EXT2 gene)

Case 2. Monogenic disease (wife, X-linked disorder, hypohidrotic ectodermal dysplasia (HED, 외배엽이형성증), c.T1085G at EDA1 gene)

→ No mutation or no copy number variation cells were selected for transfer (**배아 선별**)

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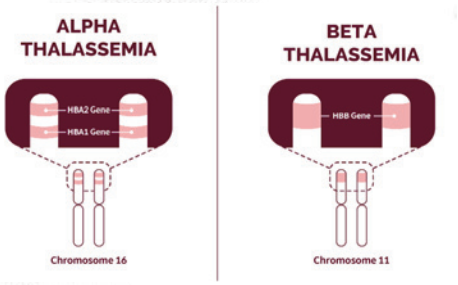
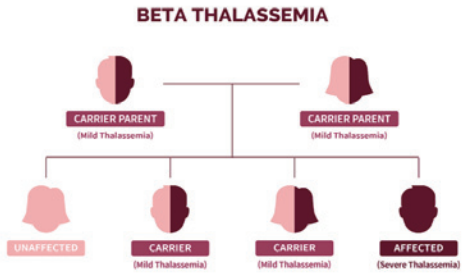
지중해빈혈 (Thalassemia)

- 헤모글로빈 폴리펩타이드 사슬 합성저하로 산소운반 혈색소감소
- 상염색체 열성 (beta형: HBB유전자, alph형: HBA1/2유전자)
- 2500명당 1명꼴





- PGD 앞에서 언급된 방법론을 활용한 임상적 성공케이스.
- **질환은 germline BUT 배아는 somatic mosaicism → scWGS은 유용**

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Single cell Whole genome vs exome

- **Whole-genome** :
  - More uniform amplification, suitable for detecting **SNV** (단일염기변이, single nucleotide variant), **CNV** (염색체 수 이상, copy number variation), **SV**(구조이상변이)
  - 30-fold more expensive than exome (only ~2% of the genome)
- **아직까지 WGS 가격이 hurdle임**
- **Droplet기반 고처리량 기술은 아직 not mature**

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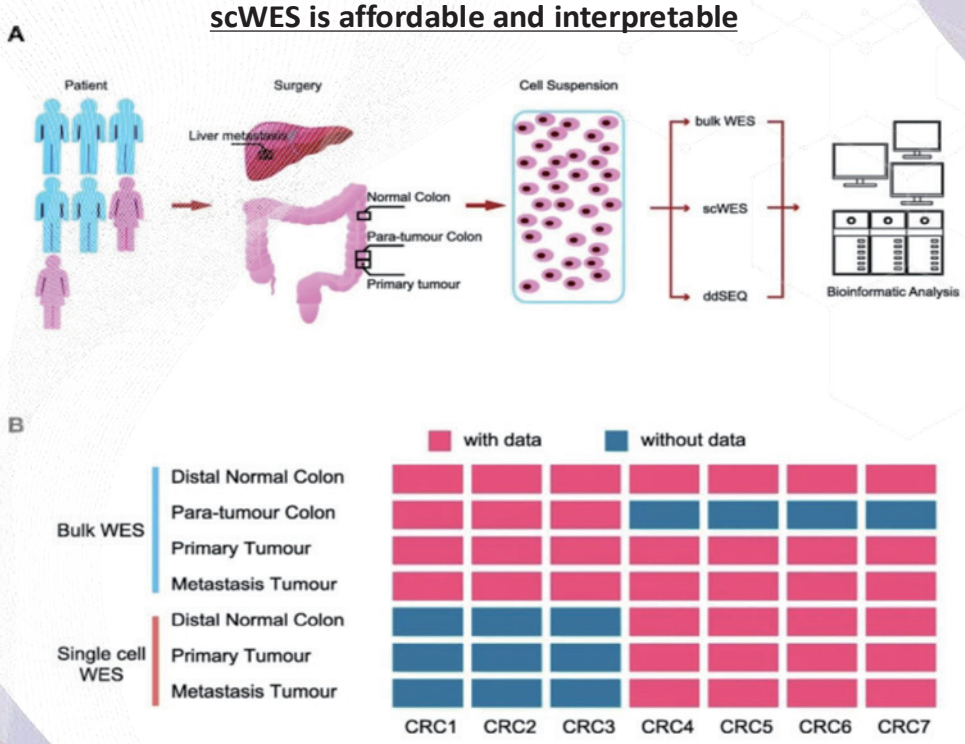
Single cell Whole-exome seq for cancer

scWES is affordable and interpretable



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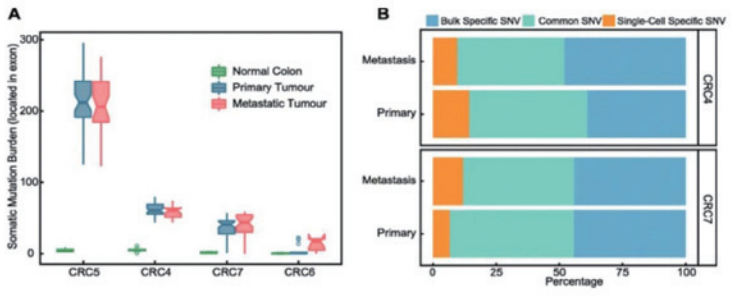
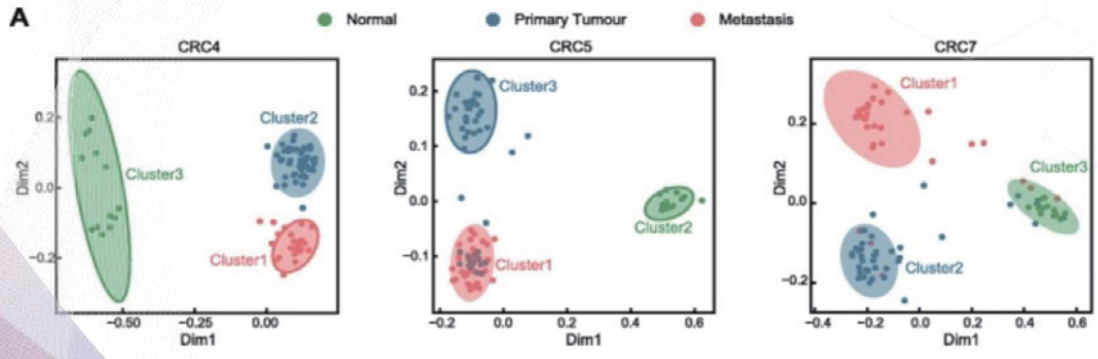
Mutation burden detection and clustering





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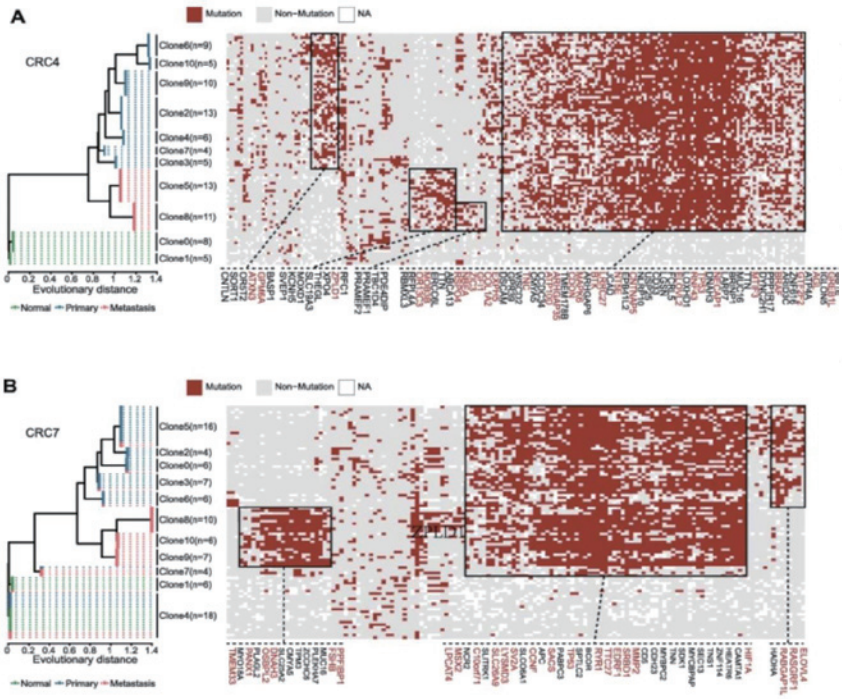
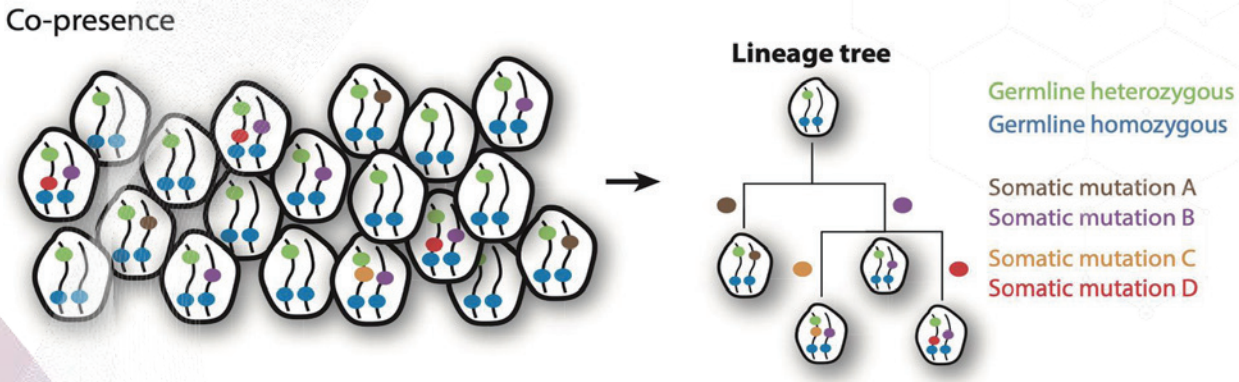
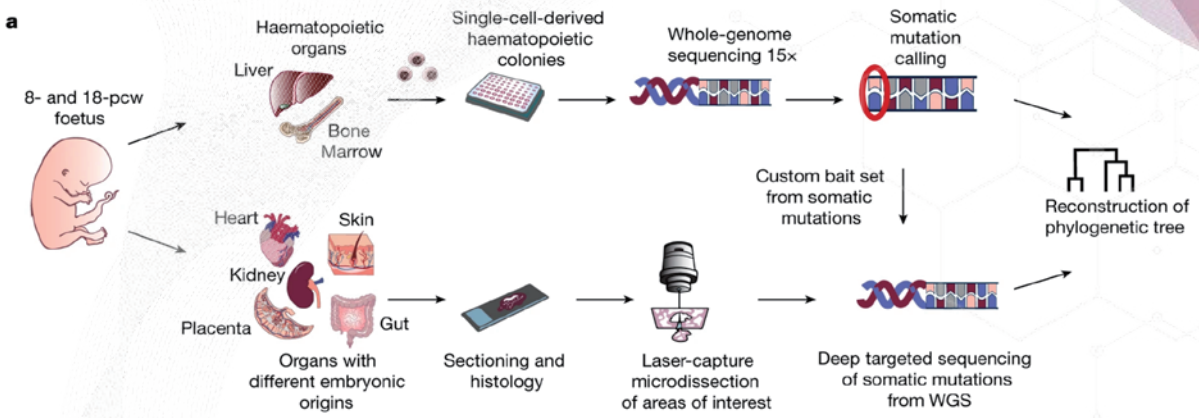
Sub-clonal analysis using single cell SNVs



Lineage tracing of human development through somatic mutations



Lineage tracing experimental workflow



원시 조혈모세포의 유래?

최초의 조혈모세포 AGM에서 유래 -> 간에서 크게 증식 -> 출생 전 골수에 정착

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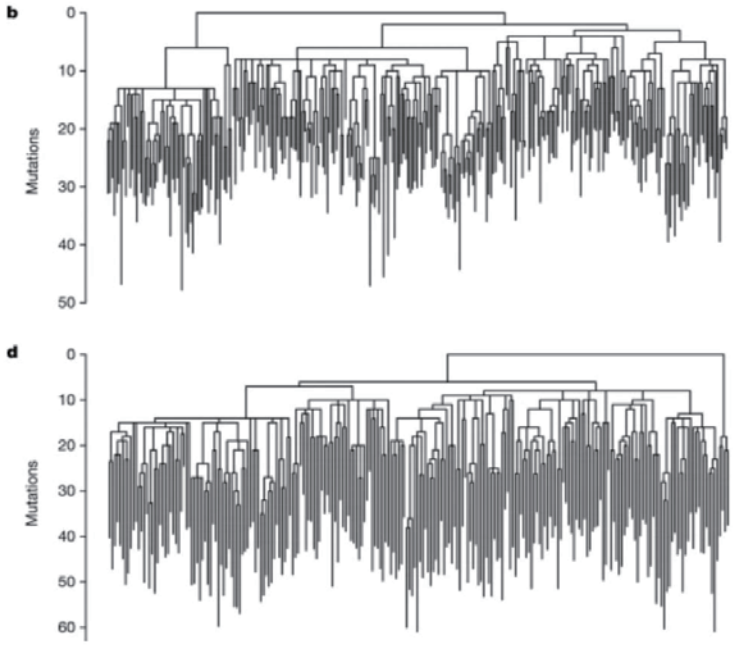
Phylogeny of 277 single cell 8-pcs liver HSPC



Pcw: post conception week

HSPC : haematopoetic stem and progenitor cell (조혈 줄기/전구 세포)

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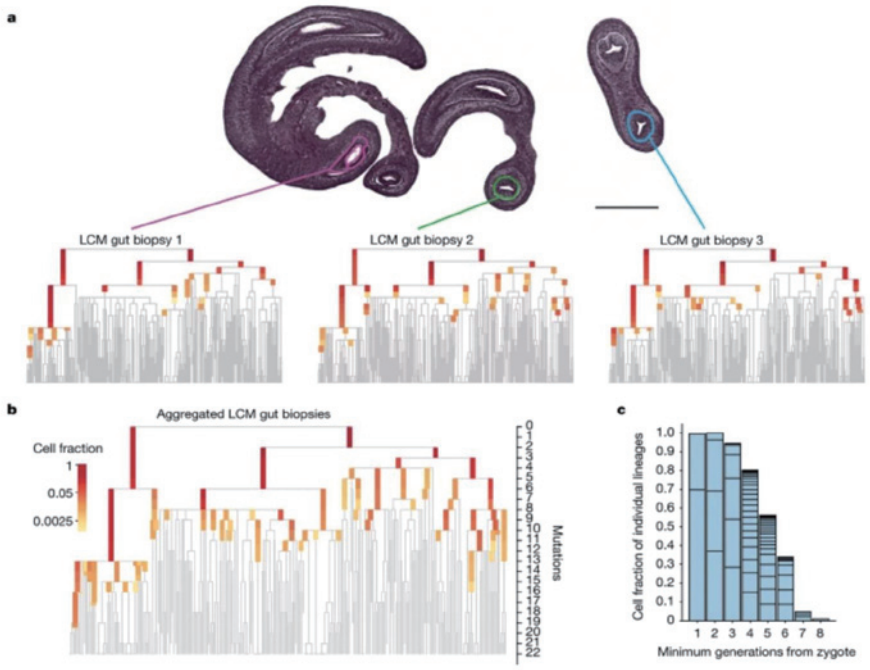
Reconstructing lineage divergence



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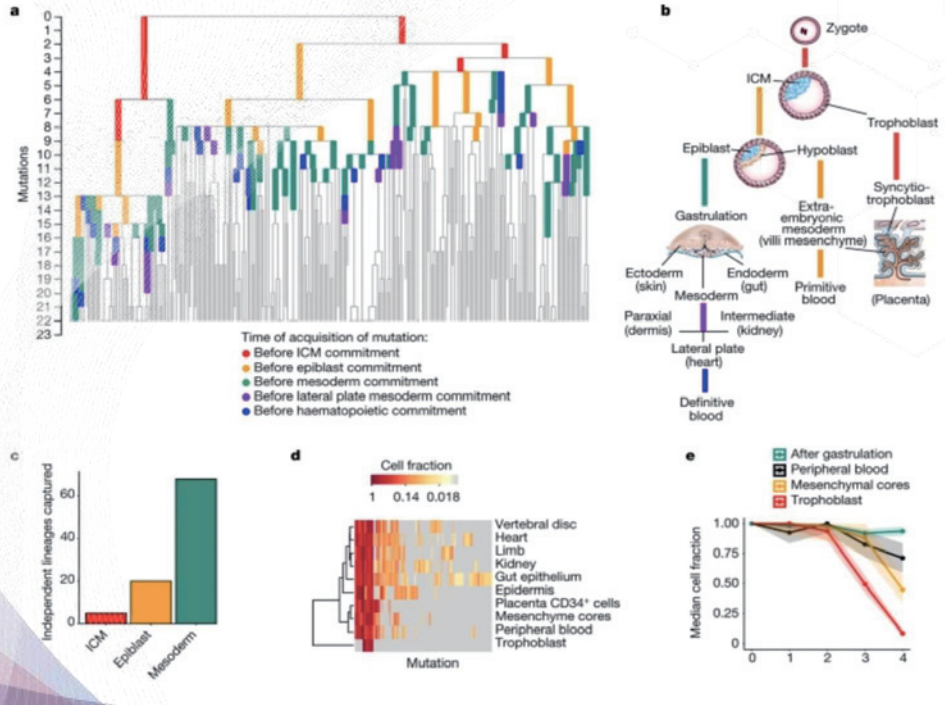
Timing of divergence of lineages during development



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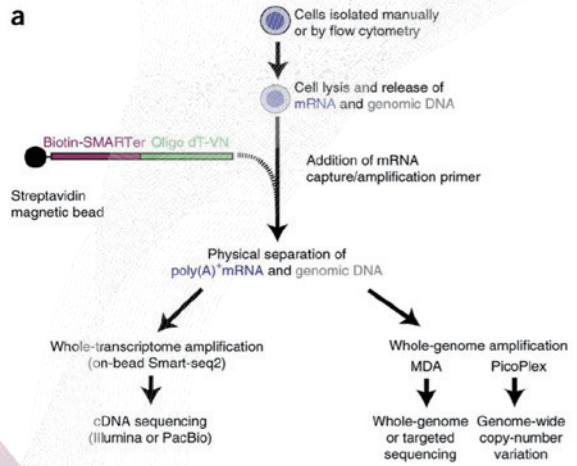
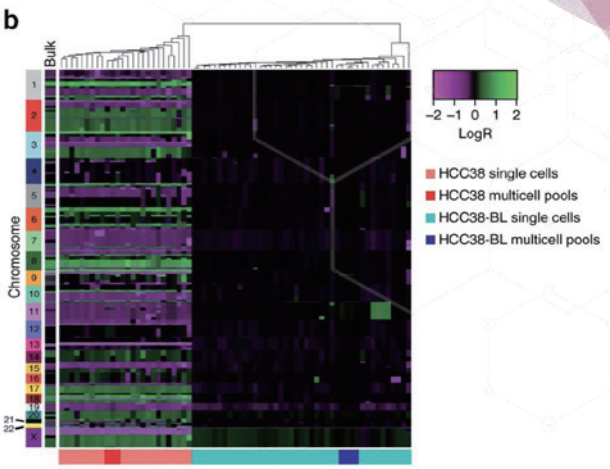
Phenotype association

Somatic mutations	Cell type
●	Cell type 1
●	Progenitor of cell types 2 and 3
● + ●	Cell type 2
● + ●	Cell type 3

How do we associate DNA & RNA (phenotype) information?

Single cell genome and transcriptome sequencing (G&T-seq)

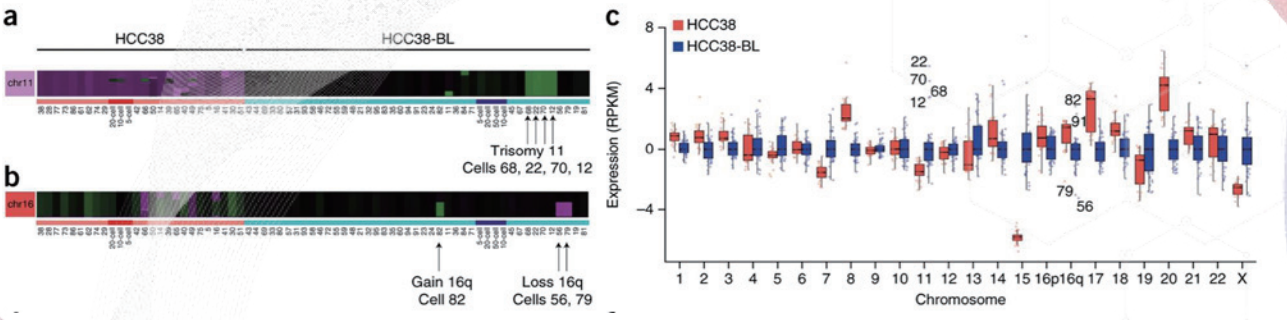




싱글셀 / bulk behavior안에 포함되어 있음.

Physical isolation of DNA & RNA within a same **'single-cell'**

Simultaneous detection of chromosomal aneuploidy and gene expression



These data show that (sub)chromosomal copy number in a single cell is mostly positively correlated with gene expression in that cell.

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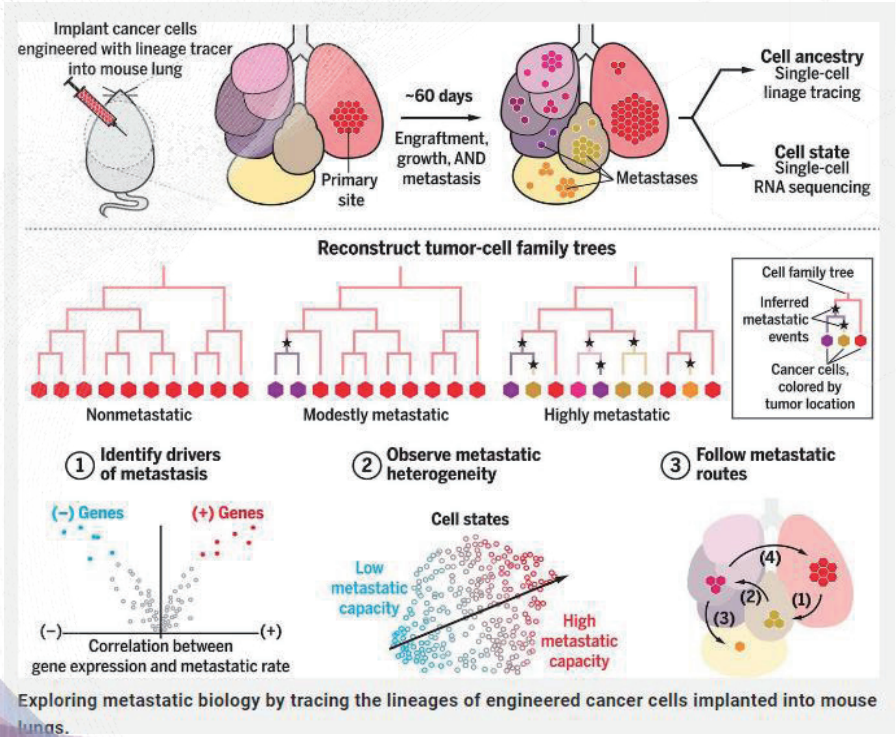
Lineage tracing in engineered cancer cells



Exploring metastatic biology by tracing the lineages of engineered cancer cells implanted into mouse lungs.

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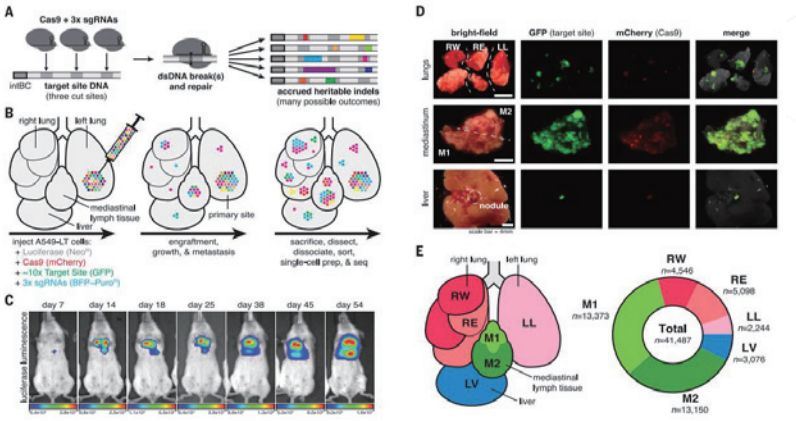
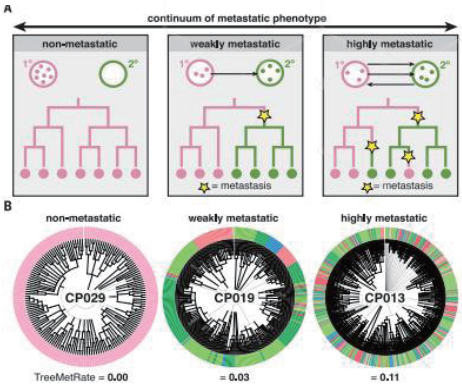
CRISPR edited lineage tracing



A549 cell line engineered to express :
CRISPR, guide, target site(**record lineage**)

Target site+transcript (lineage DNA + RNA)
information to construct lineage tree



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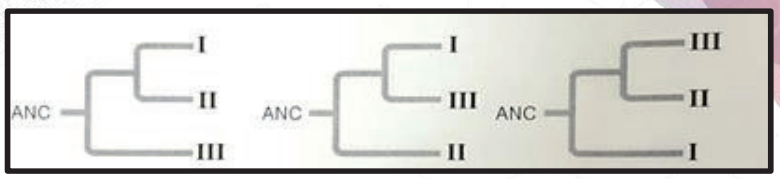
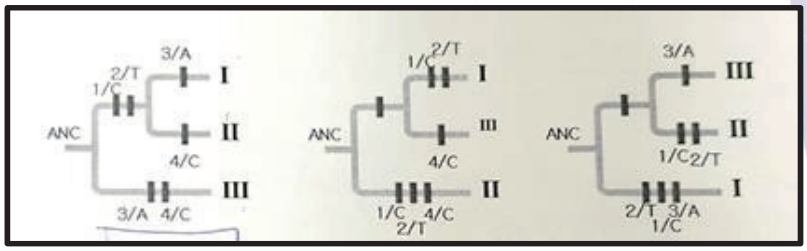
Maximum parsimony

	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral state	A	G	T	T





진화가 항상 변화 단계의 수를 최소화하는 방향으로 일어난다는 가정 하에 수행
계통 분류학에서 많이 쓰이며 evolutionary tree를 적용하는 모든 케이스에 사용

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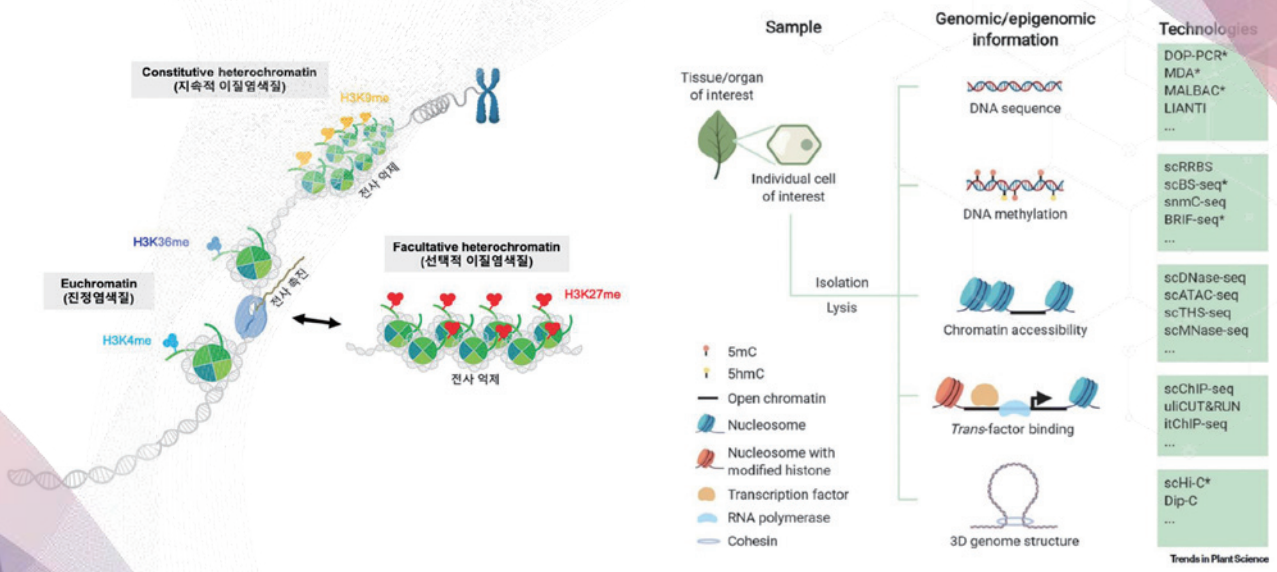
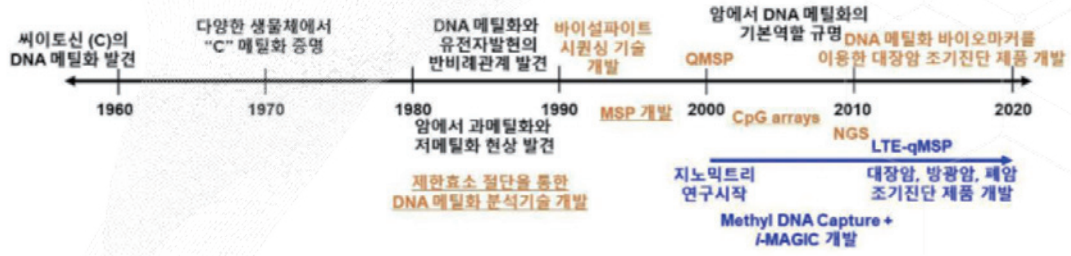
Epigenetics in single-cell genomics



후성유전(Epigenetics)은 **DNA 염기서열의 변화가 아닌** DNA의 메틸화, RNA의 메틸화 그리고 히스톤 단백질의 번역 후 변형(Post-translational modification; PTM) 에 의한 유전자 발현의 변화를 의미

DNA methylation and cancer diagnosis

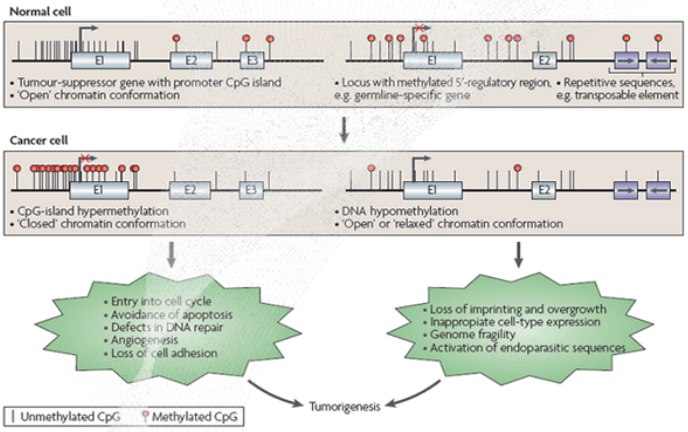


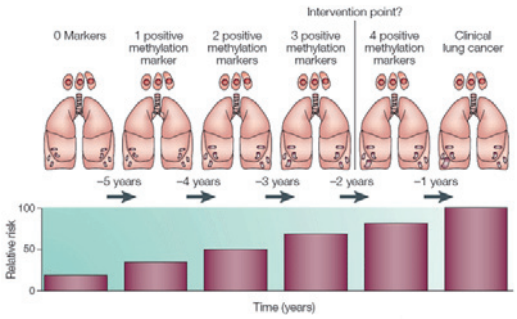
- 바이설파이트 시퀀싱: 1992, Frommer
- Methylation-specific PCR (MSP): 1996, Herman
- QMSP: 실시간 MSP 기술, 2000
- CpG array: DNA microarray를 이용한 메틸화 분석 기술, 2006, Pfeifer
- 차세대시퀀싱 (NGS)를 이용한 메틸화 분석기술 개발: 2009, Smith

[DNA 메틸화 기술 개발 및 암 조기진단 기술 개발의 역사]

1979 robin holiday의해 메틸화가 암 연관있다는 것을 처음 증명
암후성유전체에서 가장 많이 연구된 것이 "메틸화" 임

DNA methylation and cancer





정상세포 대부분 CpG는 메틸화, **프로모터 CpG는 주로 비메틸화**(발현위해)
Tumor-suppressr 프로모터 de novo메틸화 문제 →유전자 발현 억제
암세포 전반 저메틸화 → 염색체이상, translocation문제야기
이벤트는 **'초기 ' 에 일어나는것으로** 알려져 있어 진단이 시급함

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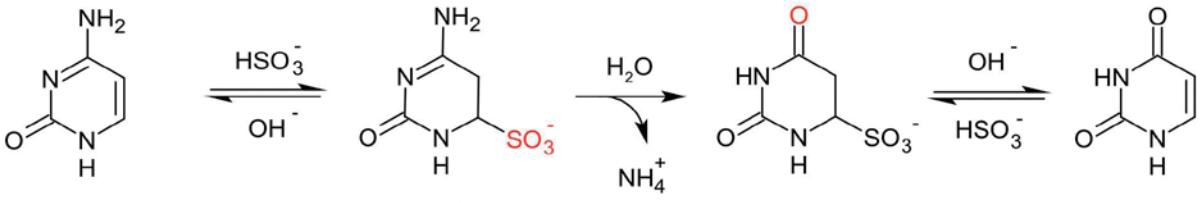
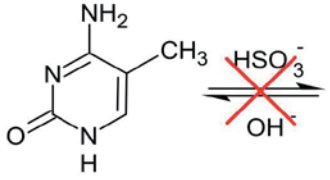
Bisulfite chemistry





5-methylcytosine

In animals it predominantly involves the addition of a methyl group to the carbon-5 position of cytosine residues of the dinucleotide CpG, and is implicated in repression of transcriptional activity.

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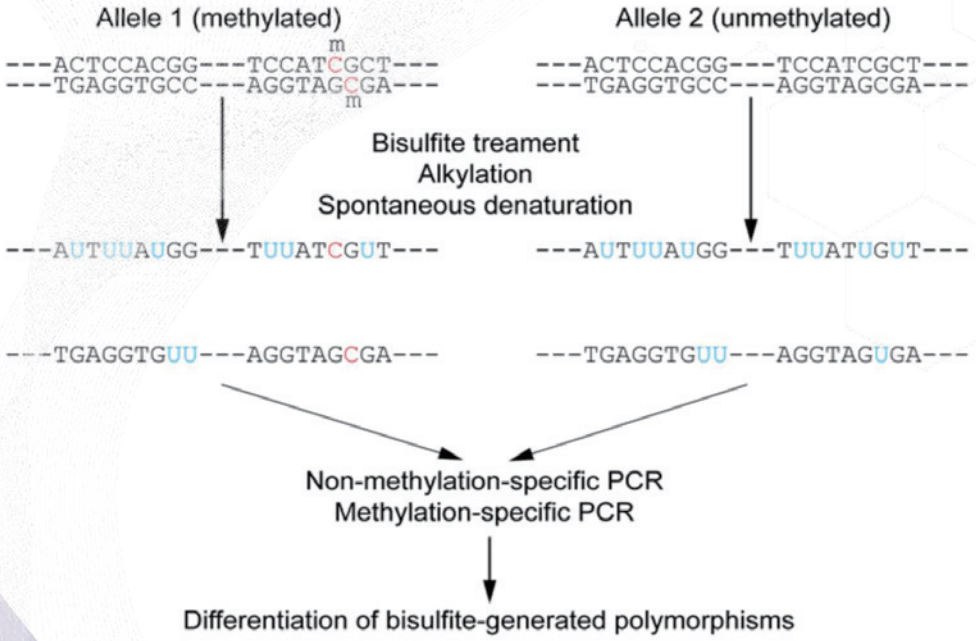
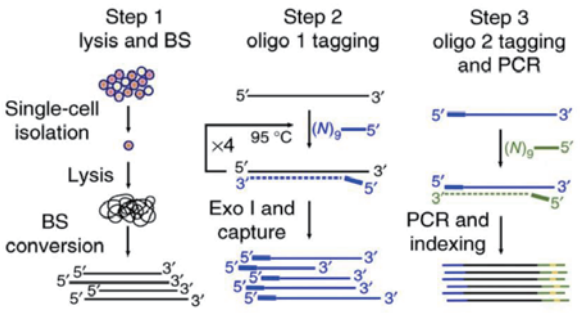
How bisulfite conversion works



***5-methylcytosine (5mC), 5-hydroxymethylcytosine (5hmC) both read as 'C'

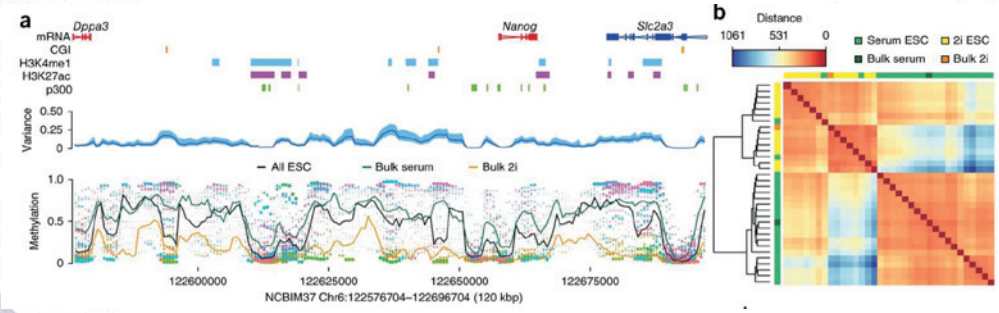
scBS-seq (single cell bisulfite sequencing)



DNA degradation during **harsh chemical** treatment

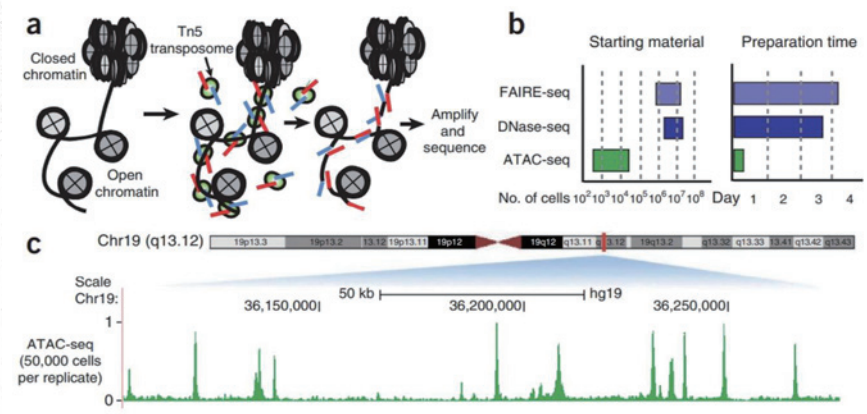
Severe loss in single-cell applications

High input DNA requirement (>100ng)



ATAC-seq
(Assays for Transposase Accessible Chromatin)

Chromatin accessibility (염색체 접근도)



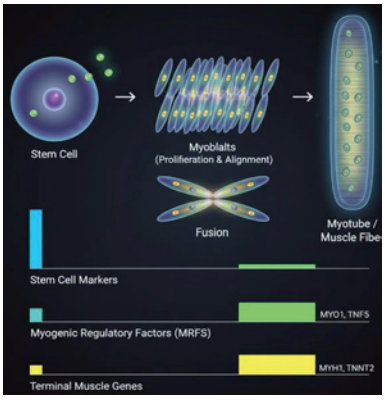
(적은 세포) 로 짧은 시간에 정확한 분석이 가능
열린 DNA영역만 분석 가능!

scATAC-seq

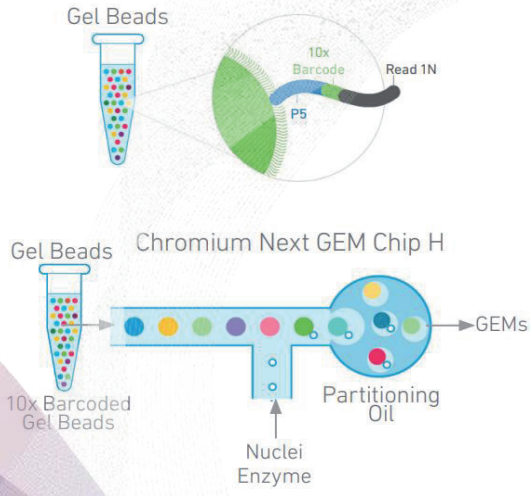
Chromatin accessibility (염색체 접근성)왜 중요?

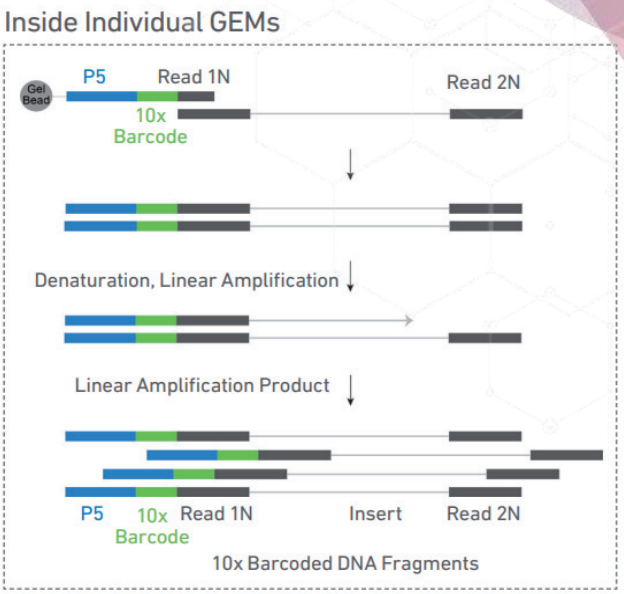
Ex) 줄기세포 -> 근육세포로 분화

1. **줄기세포**: 다양한 운명 결정 유전자 주변 염색체가 열려있는 '준비'
2. **분화 신호초기**: 근육 발달 핵심 MyoD같은 유전자 주변이 열림
3. **분화중기**: 근육관련 유전자들 모두 열려있고, 피부/신경 등 다른 부분 다 닫히기 시작함
4. **최종**: 근육 기능 필수 유전자들이 열려있고 다른종류가 모두 닫힌 안정적/정체성이 확립된 세포



Commercialized scATAC-seq





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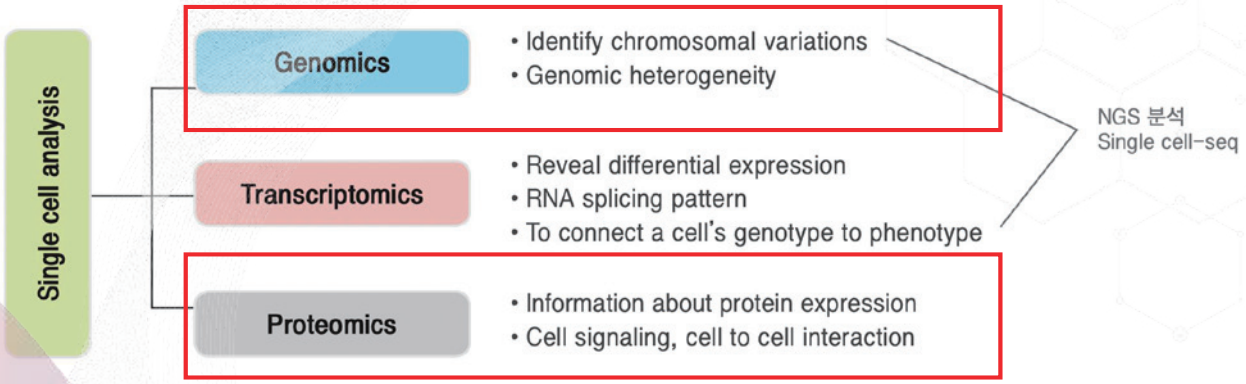
Single-cell analysis platforms
→ Multiome (DNA+Protein)



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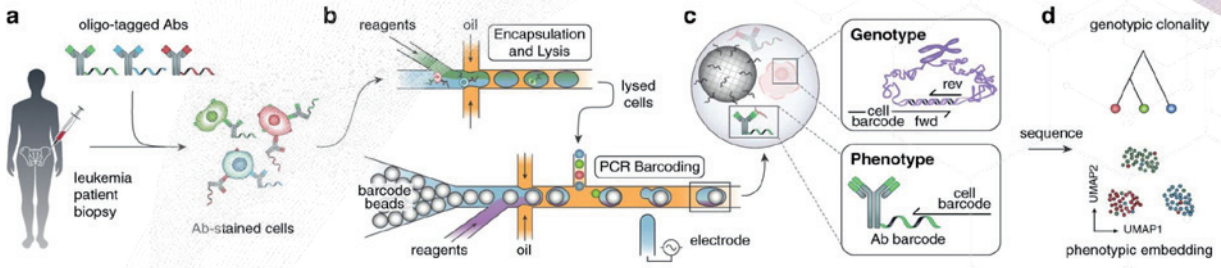
Joint profiling of DNA+Protein



Dab-seq workflow

혈액암(AML)의 진단은 주로 Flow cytometry나 DNA mutation분석을 통해하지만 동시에 한세포에서 진단하는 방법론은 없었음.

1.**Mission Bio's Tapestri** platform을 modify하였음
2.Oligo conjugated Antibody를 활용하여 custom하게 실험이 가능함.
3.TotlaSeq-D(biolegend회사) 가 타겟 항체패널을 개발함.

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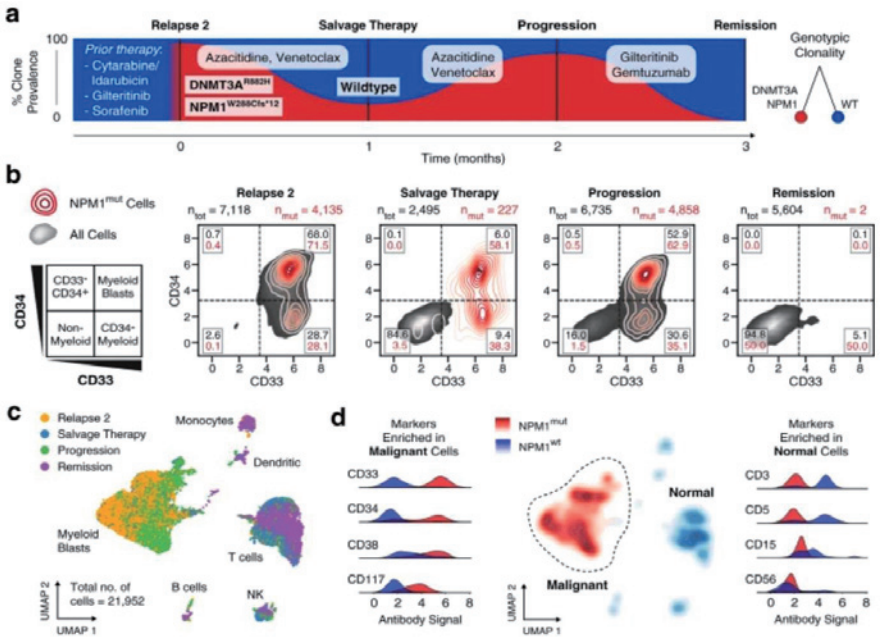
Multiomics profiling of patient dynamics



혈액암 유전형-표현형 동시 진단 가능
암환자 CD19 (특정단백질 예) 소실시 CNV/mut의 문제인지 판별

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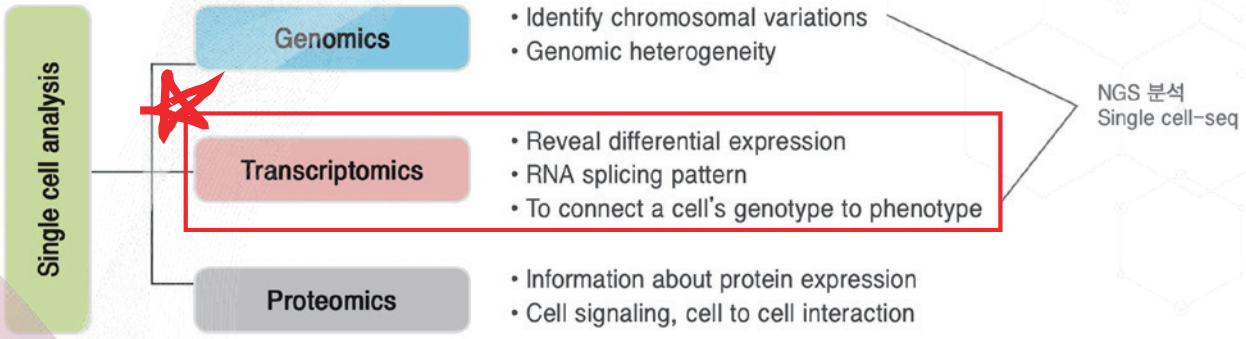
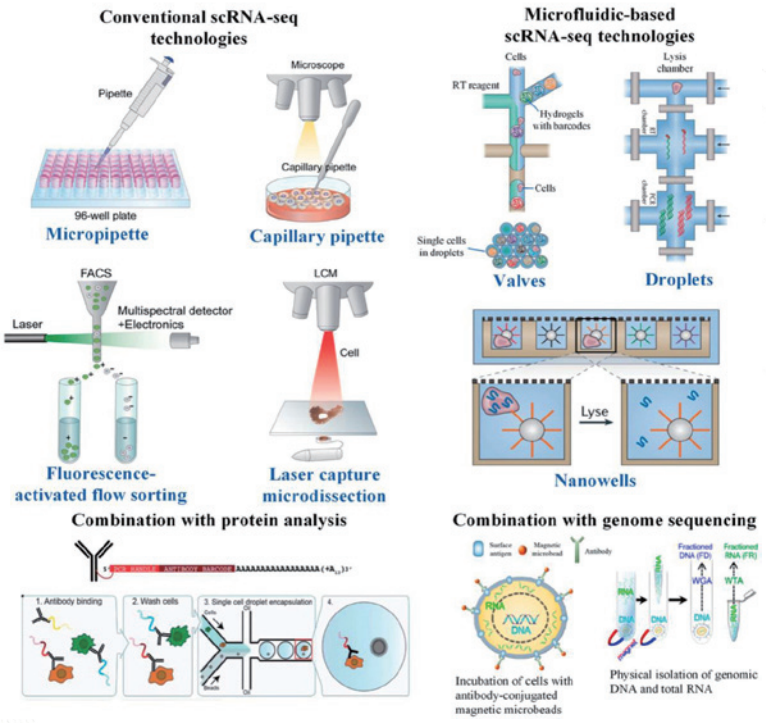
Single-cell analysis platforms



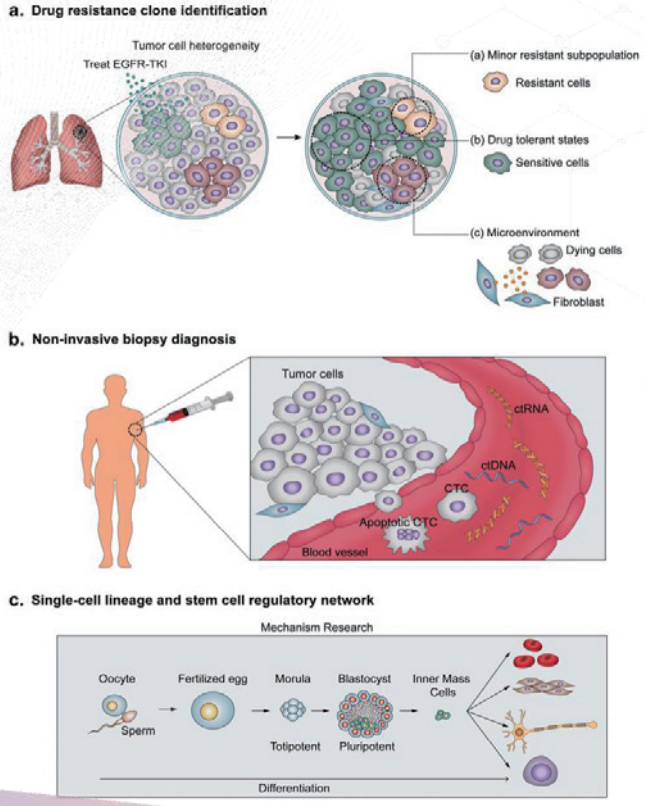
Single-cell RNA sequencing (scRNA-seq)



RNA+protein

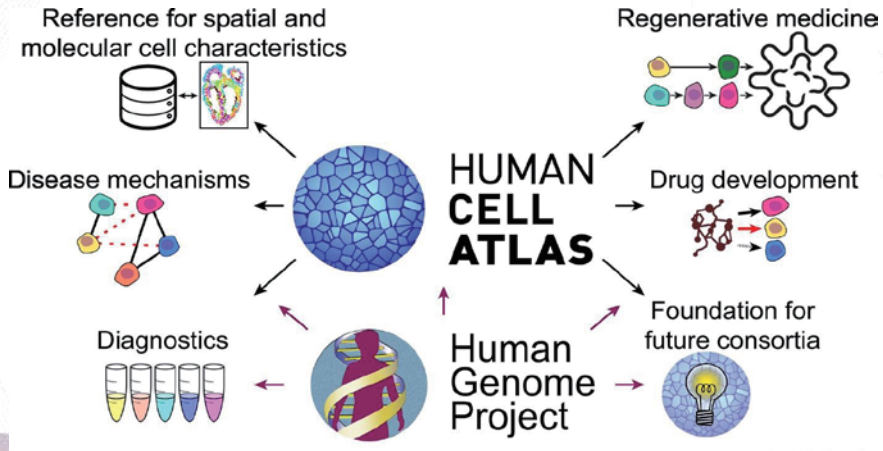
DNA+RNA

Applications of scRNA-seq



Towards a Human Cell Atlas (HCA)

- Inspirations from HGP (human genome project) as a collaborative project
  - Impact is illustrated by world-wide collaboration w/COVID-19
- 39million cells from 15 organs
- Healthy people의 단일세포 전사체 맵 (scRNA-seq) → disease



Google Maps of human cells is a milestone

- HCA Portal Site: https://data.humancellatlas.org/
- 하버드/MIT 브로드 연구소: https://singlecell.broadinstitute.org/single_cell
- 유럽연합 생물정보 연구소: https://www.ebi.ac.uk/gxa/sc/home

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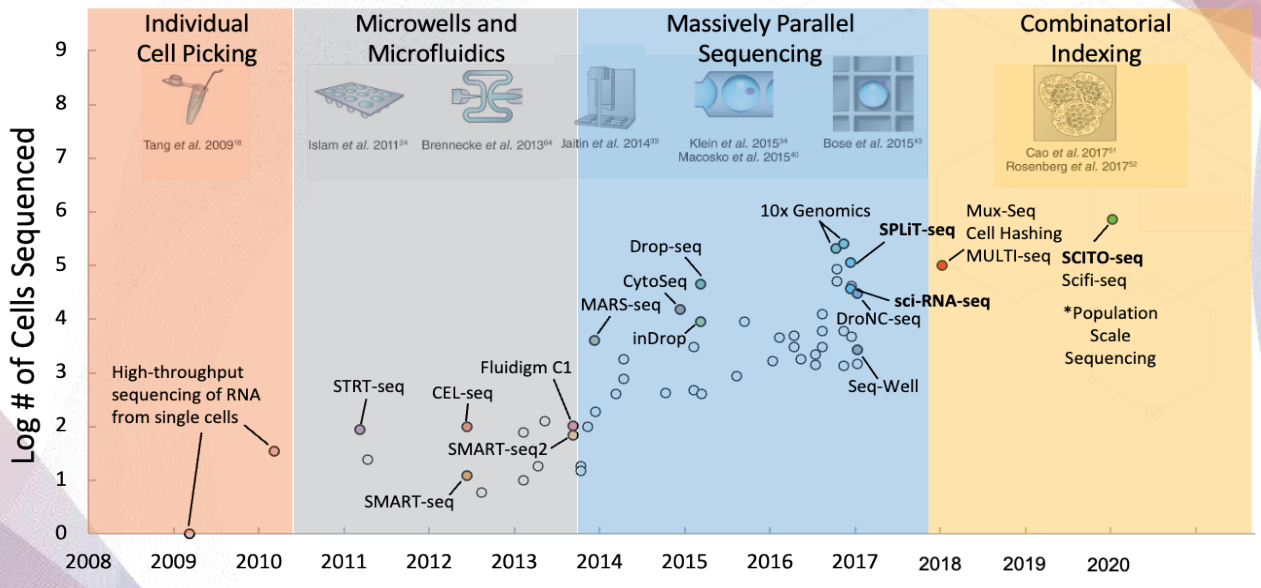
Exponential increase in scRNA-seq throughput



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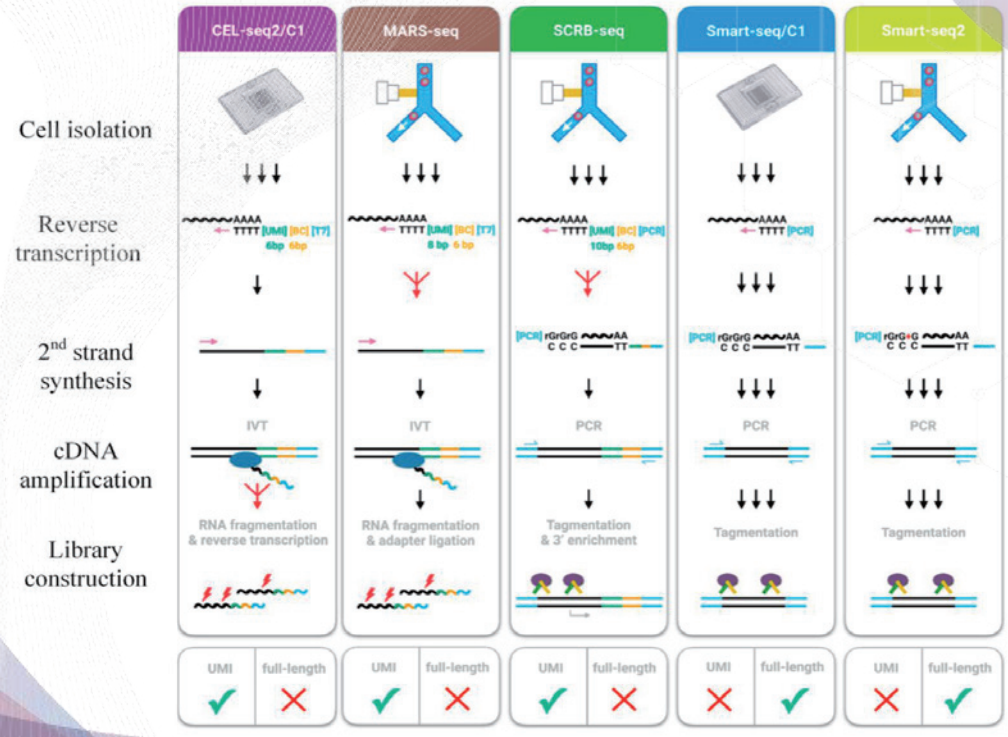
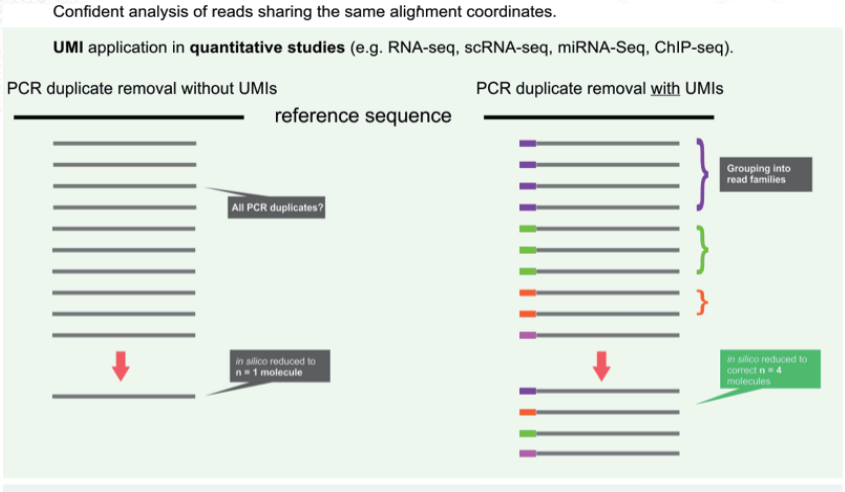
Initial phase of scRNA-seq technologies

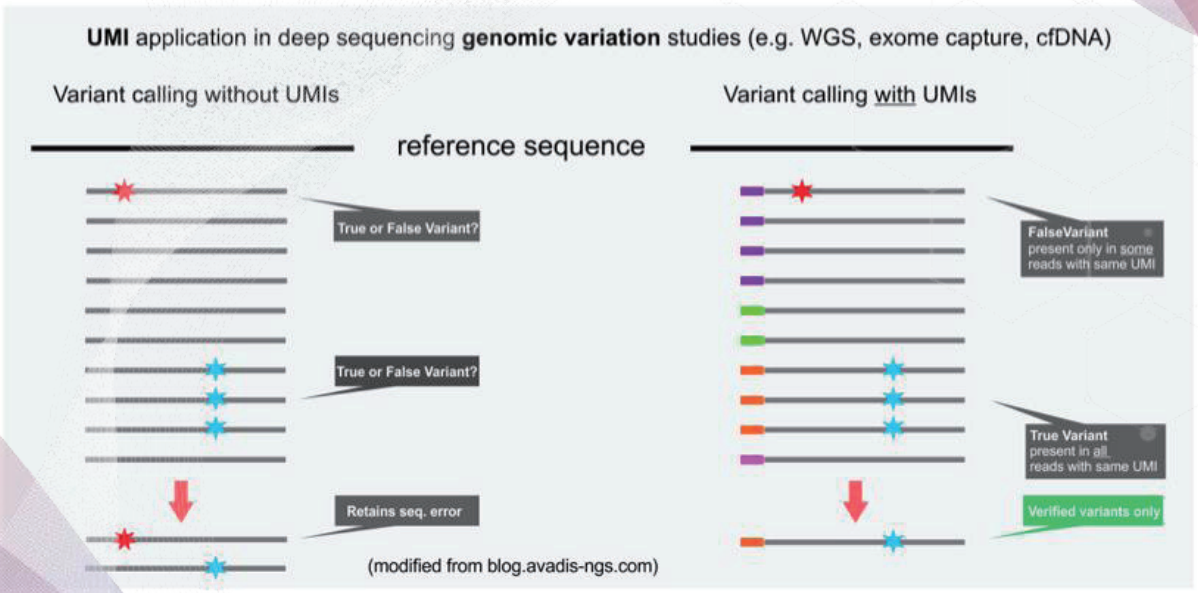


Unique Molecular Identifier (UMI) – Quantification (정량)

- Known as **Molecular Barcodes** (random 'N' 염기서열)
- Complex DNA sequences added to reduce PCR amplification bias

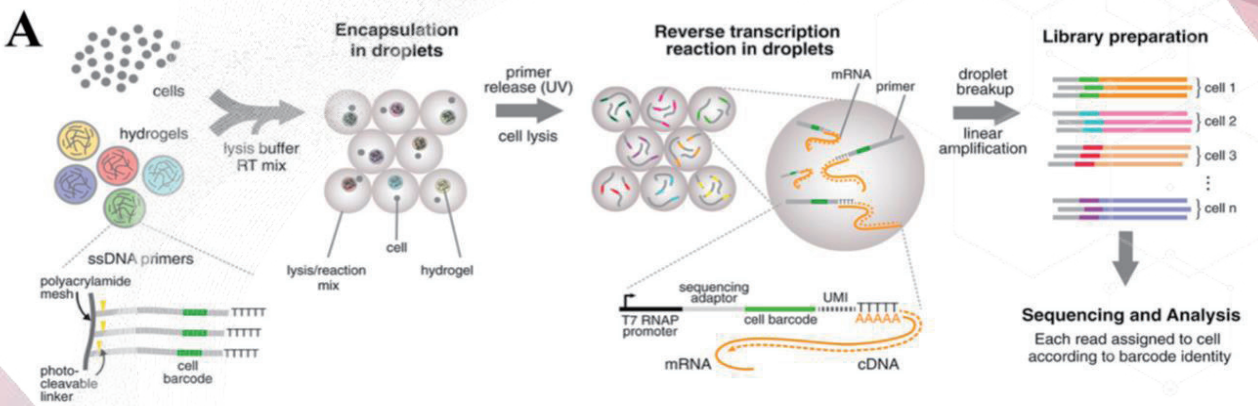


Unique Molecular Identifier (UMI) – Variant detection (변이 감지)



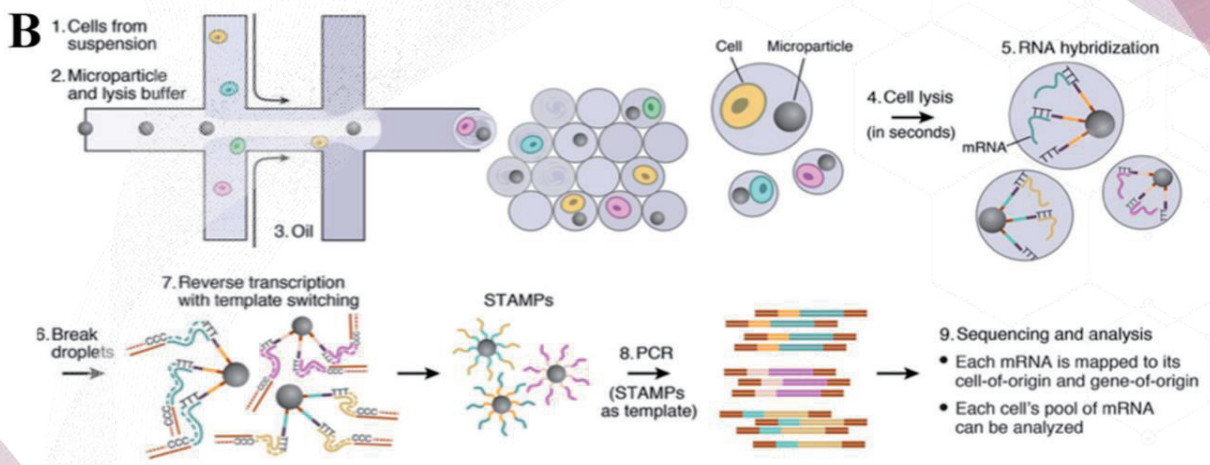
History of popular droplet-based scRNA-seq

- Droplet-based scRNA-seq



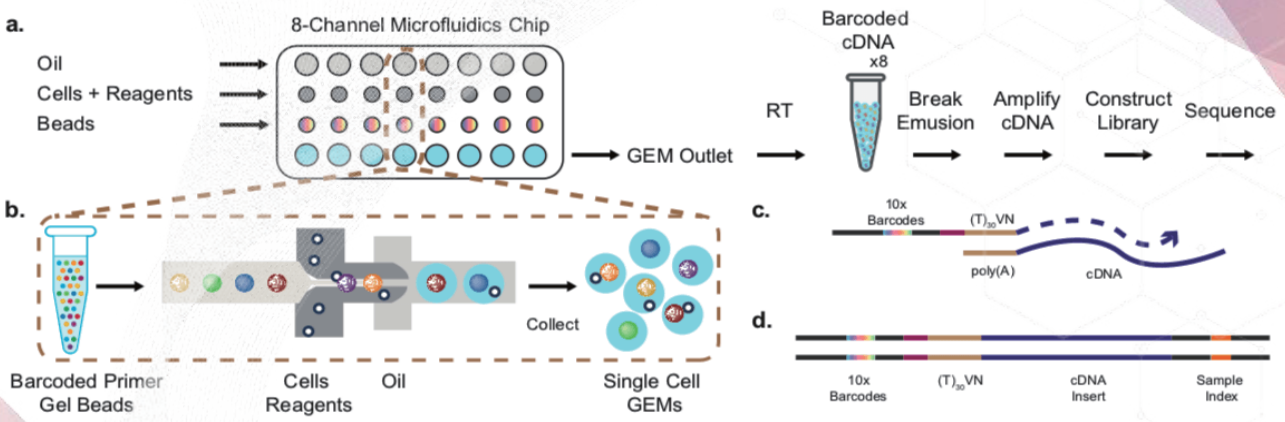
1. 초기 InDrop technology: low cell capture (~7%)
2. 20-50 copies/cell transcripts captured only

Drop-seq



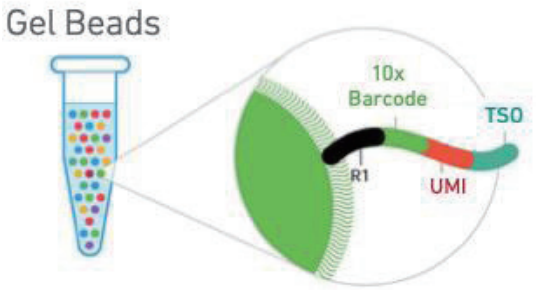
1.Use Barcoded Beads instead of hydrogel (InDrop)
2.Cell capture efficiency (~12.8%)
3.Captures 3' terminal fragments similar to In-Drop

10x Genomics (commercial)

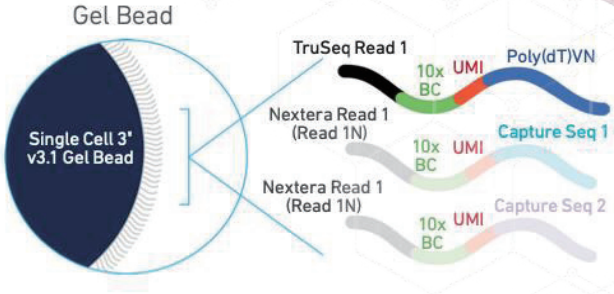


Uses Gel bead emulsion (GEM)
~50% Cell capture efficiency (Currently dominating the market!)

This can capture both 5’ and 3’ side of RNA



5’ GEM structure



3’ GEM structure

- They capture different parts of the transcript and show similar efficiency of capture
- Maybe limited to discovering alternative spliced transcripts (isoforms)
- 5’ technology can capture TCR (T-cell receptor) and BCR

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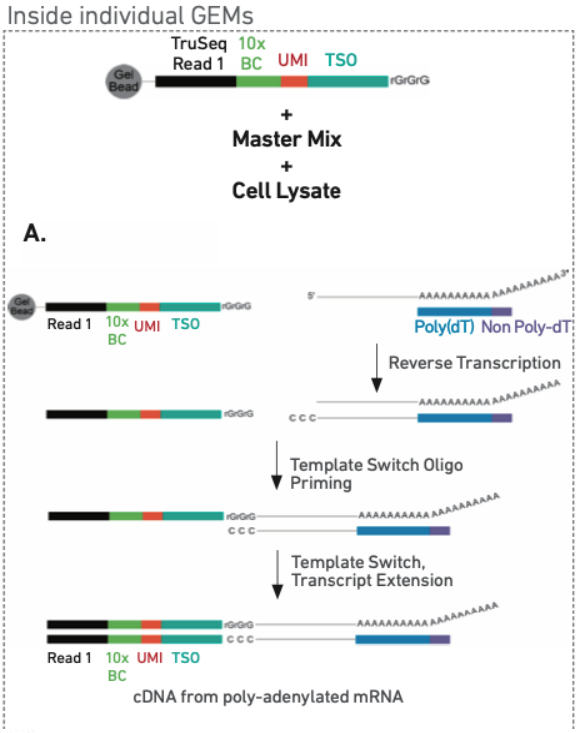
How do you capture 5’ side?



TSO : template switching oligonucleotide

BC : barcode (random ‘N’ 염기 서열)

UMI : unique molecular identifier

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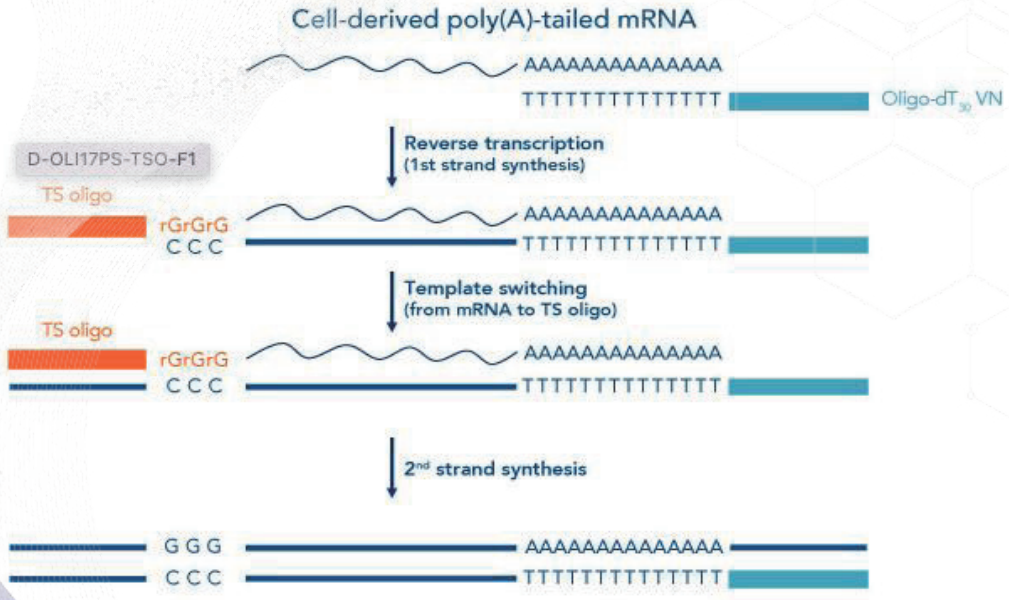
Template switching mechanism (RNA->cDNA)

- 1st cDNA 합성과정에서 cDNA 양 말단에 특정 서열을 삽입하는 획기적인 기술
  - 주로 Moloney Murine Leukemia Virus에서 유래한 MMLV RTase 라는 역전사 효소를 사용

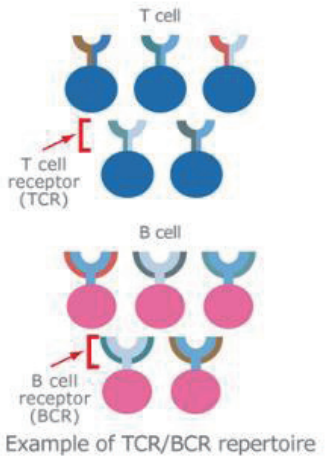
- 말단전이활성(Terminal transferase activity)
  - 역전사효소를 사용 mRNA 5'말단에 이르렀을때 일부 염기를 부가하는 능력

- 주형전환활성(Template switching activity)
  - 새로운 주형(template)으로 바꾸어 DNA를 합성하는 활성

Template switching schematic



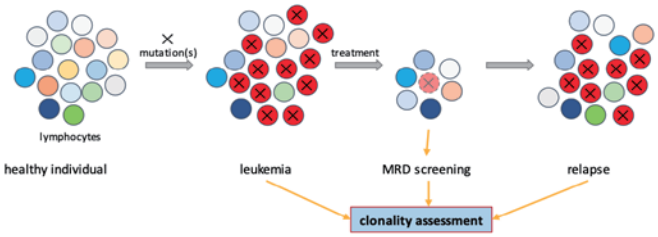
Why TCR and BCR sequencing is important



Main types of lymphocytes (T and B cells)
~10^12 diversity in DNA sequences

They recognize antigens

Malignant clones ~ 0.001%
→ **Need to sample many cells!**



Detection of minimal residual disease (MRD)

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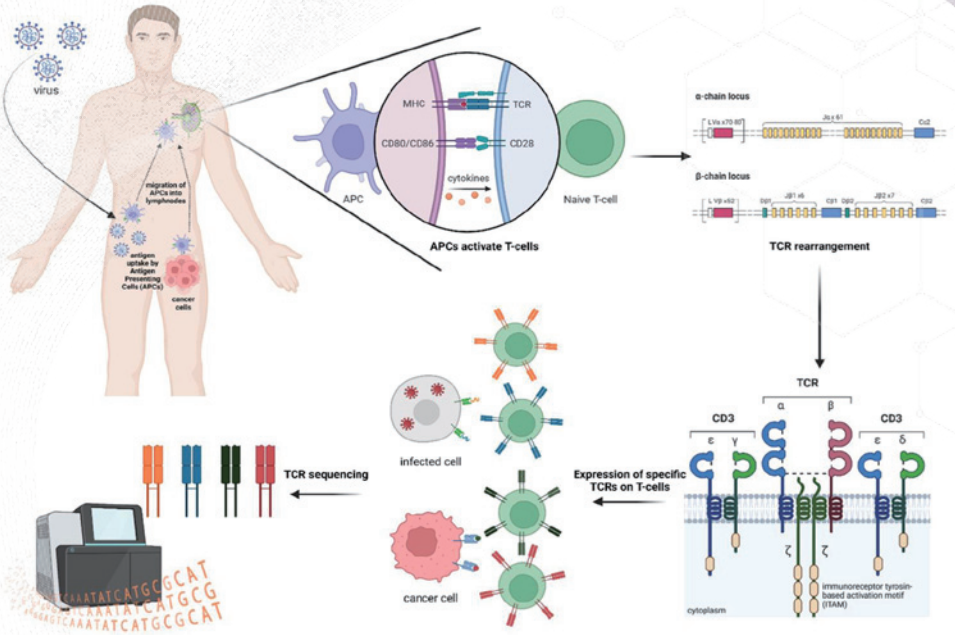
TCR and HLA



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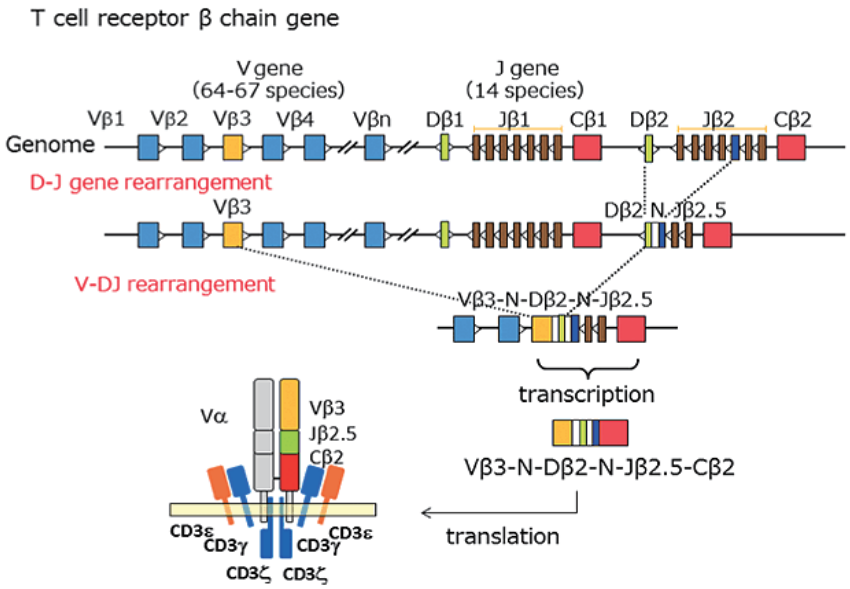
Gene arrangement in the T cell receptor beta chain gene



CDR3 is important for binding and determines 'Clonotype'

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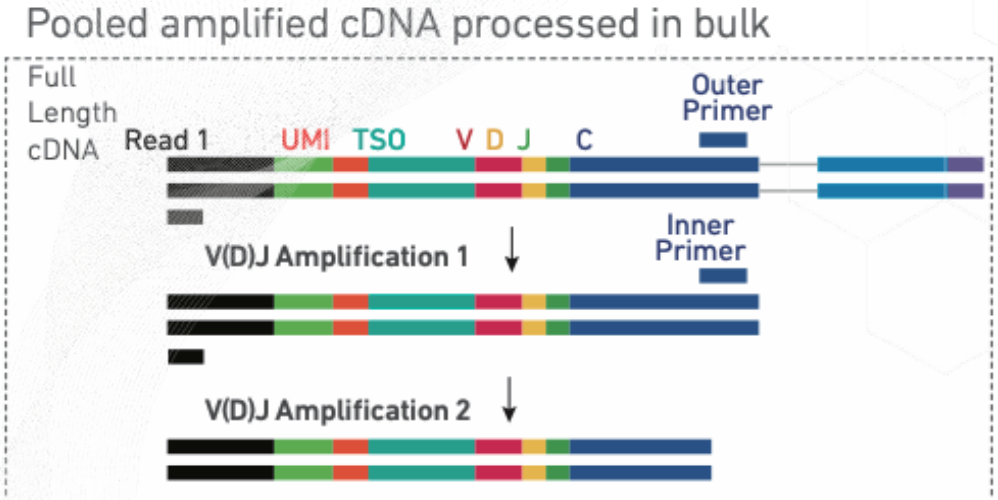
VDJ amplification from 5' captured cDNA



TCR/BCR gene은 Constant region에 specific 한 primer로 증폭이 쉽게 가능
Outer + Inner primer 두 step의 Nested PCR이라는 방법으로 specificity높임

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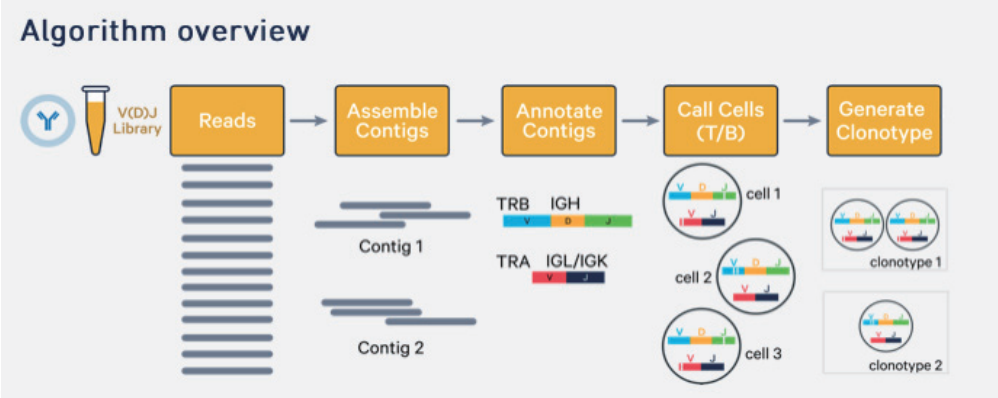
V(D)J sequence from assembly



시퀀싱 서열분석을 한 결과는 ~150bp로 짧아 전체 TCR의 reconstruct (~800bp) 하기 위해 조각들을 이어붙이는 assembly를 진행한다.

Clonotype (클론형) : 특정 항원에 반응하는 TCR/BCR의 염기서열 조합

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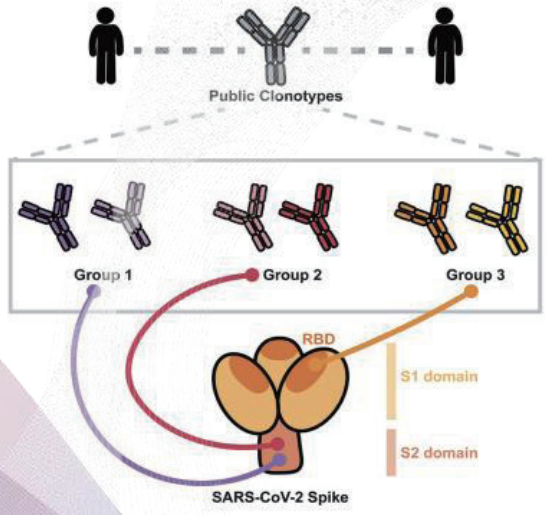
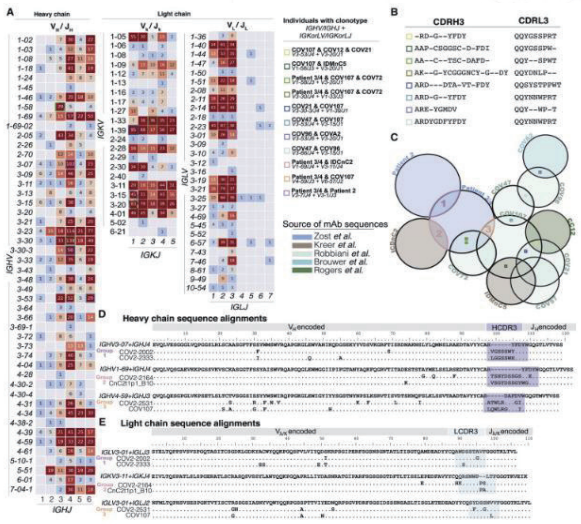
Convergent antibody response to the SARS-CoV-2 spike protein in convalescent and vaccinated individuals





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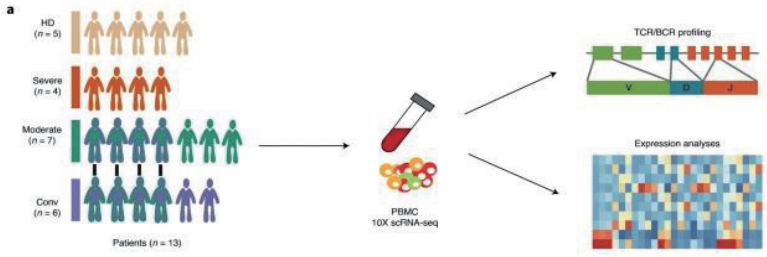
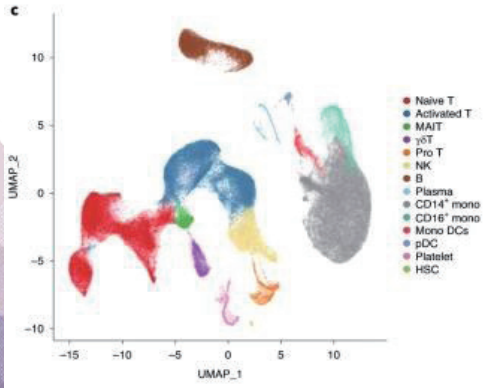
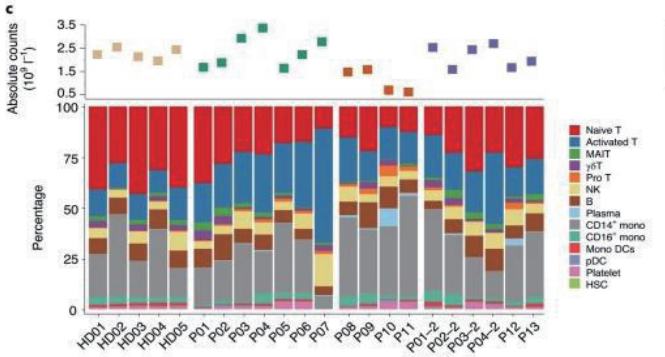
Case study with COVID-19

환자 sub-group의 단일세포 분석/차이 규명
→ 왜 특정환자가 더 취약한가? Genetic이유?







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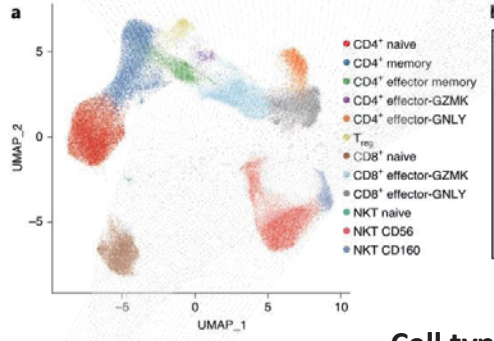
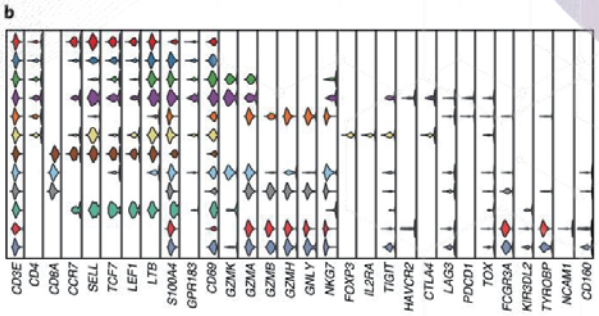
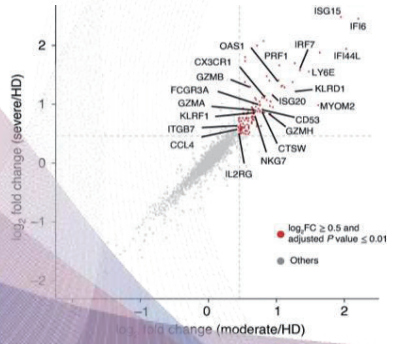
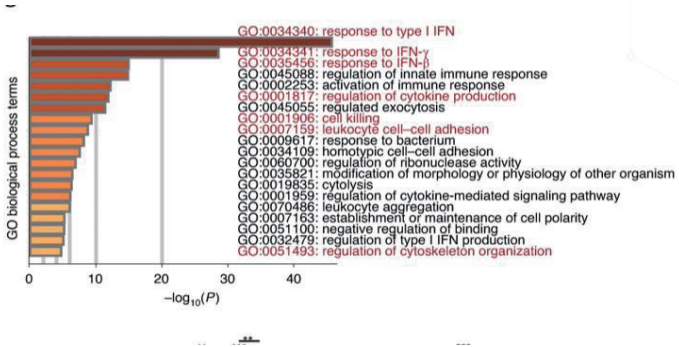
Immunological feature of T cells





Cell type specific and Pathway specific features?





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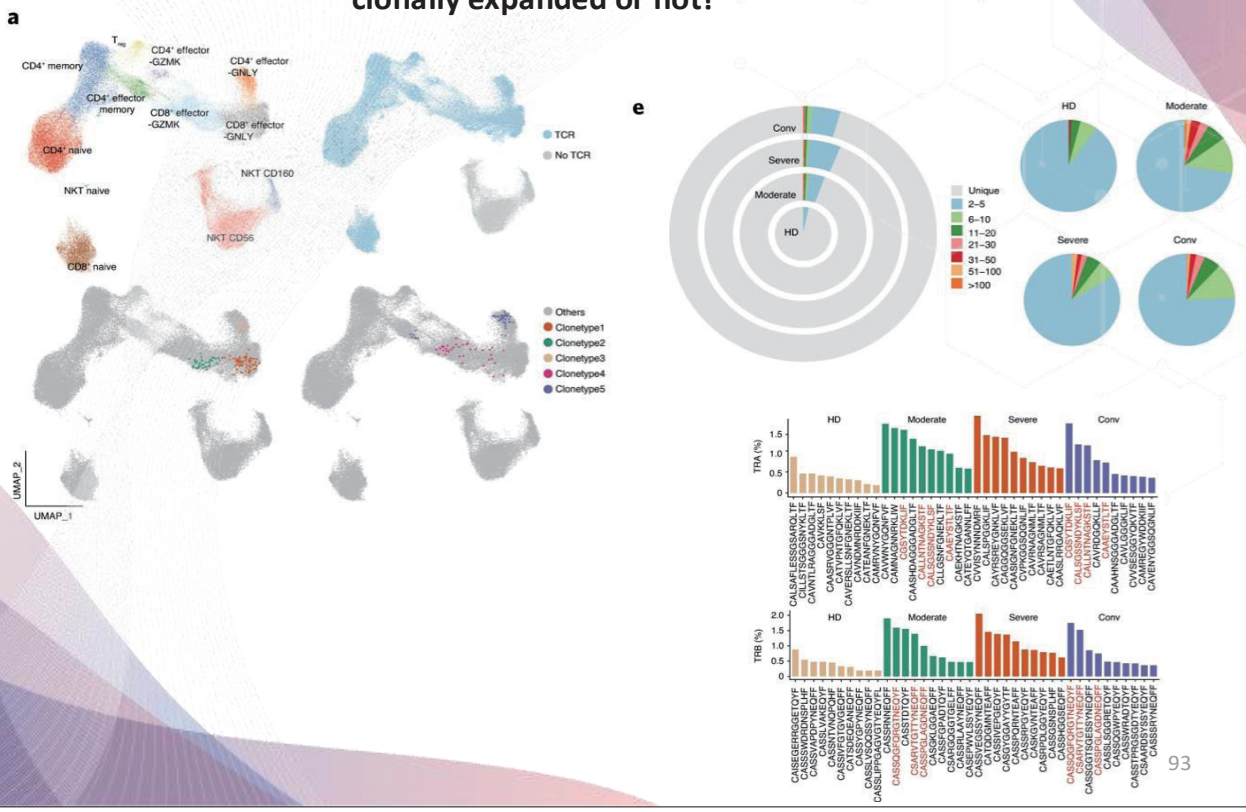
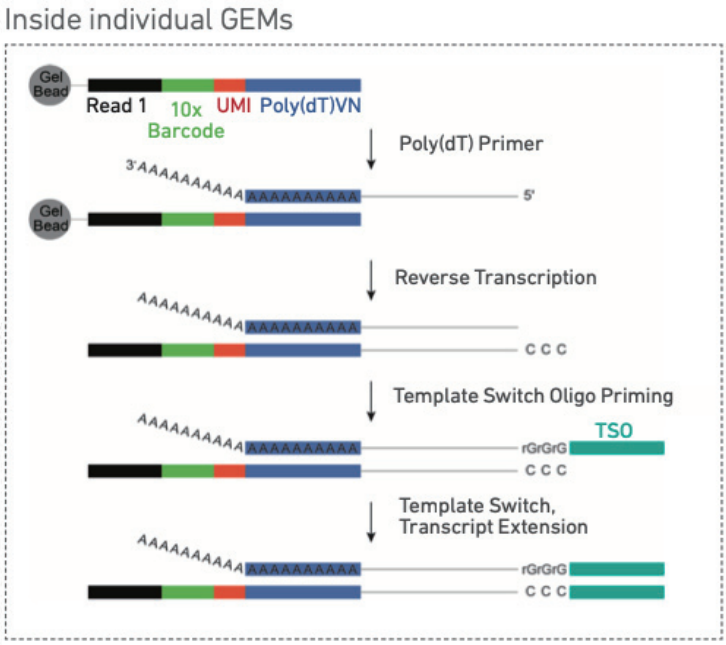
Expanded TCR clones and selective usage of V(D)J genes

Antigen pressure → CDR3 patterns → are they clonally expanded or not?



How do you capture 3' side of RNA?

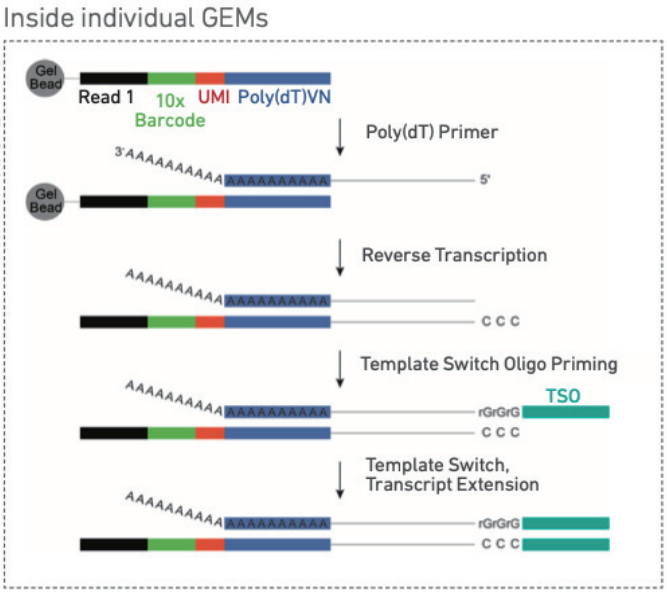


TSO : template switching oligonucleotide

BC : barcode
(random 'N' 염기 서열)

UMI : unique molecular identifier

Challenge: why 5' capture strategy is better to see V(D)J genes?



You will need many primers to target all Variable genes for 3' side!
Compare to 5' capture where you need 1 or 2 constant primers

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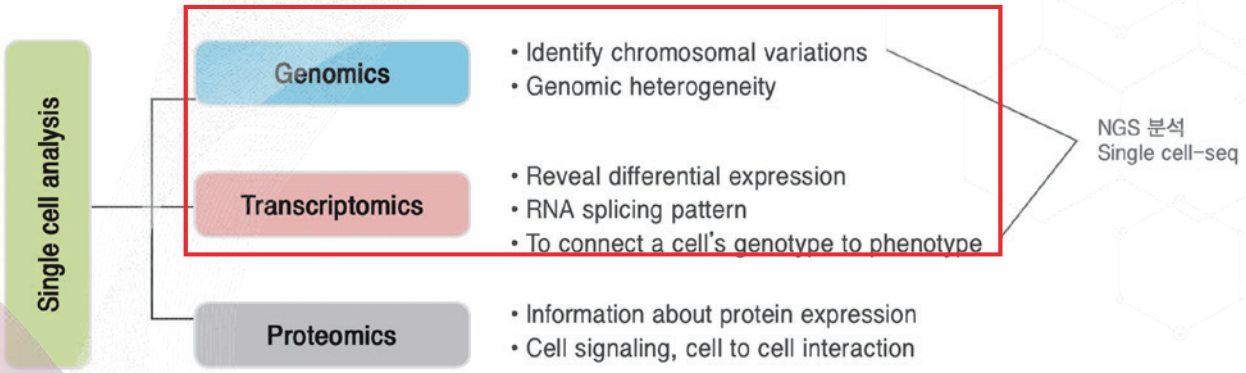
Single-cell analysis platforms Multiome (DNA+RNA)



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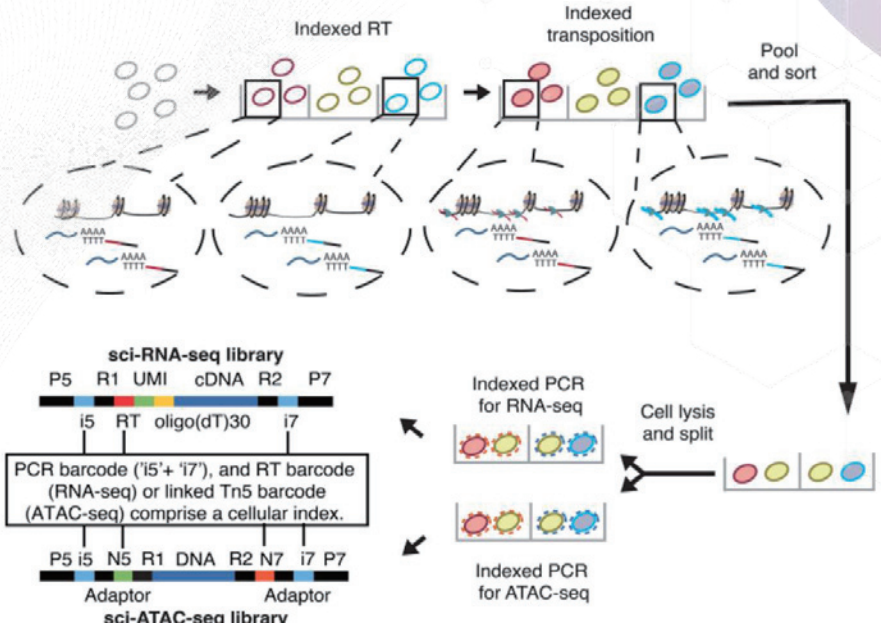
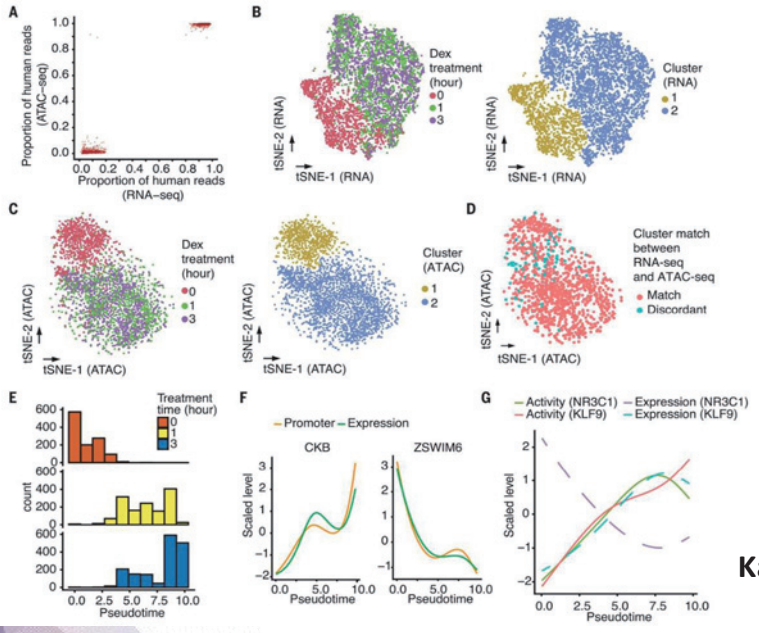
Joint profiling of RNA+ATAC (sci-CAR)



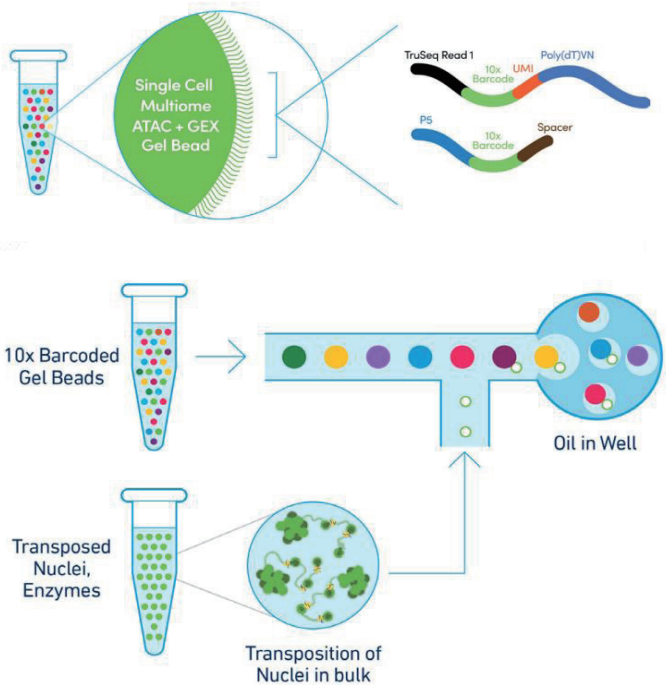
Different primer combinations for different modality amplification

Gene regulation dynamics (open chromatin + RNA)

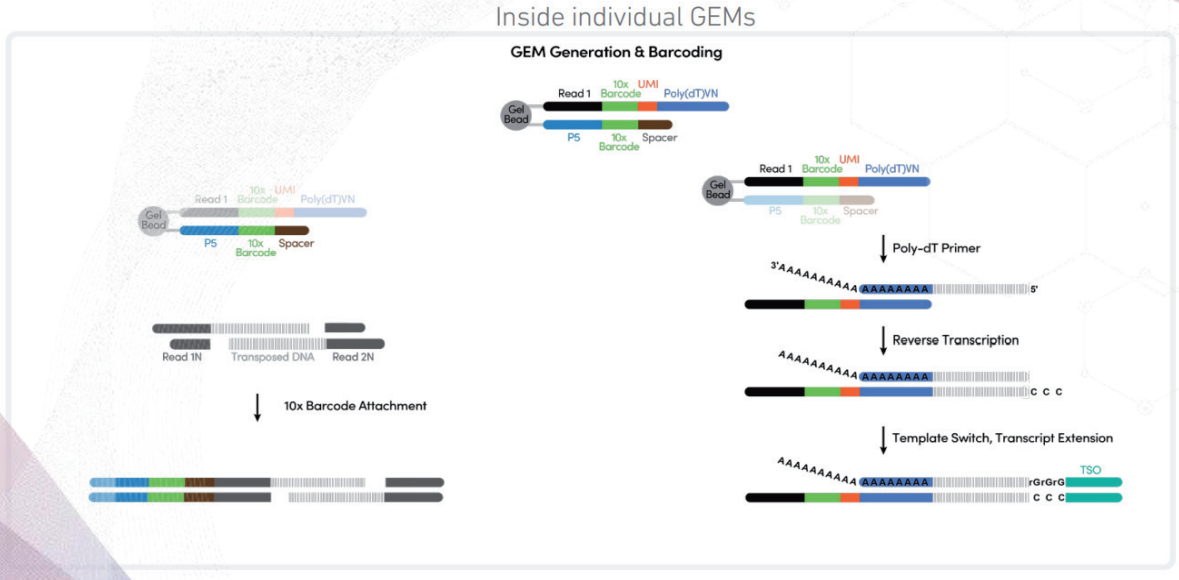


Kaggle Challenge for multiome datasets!

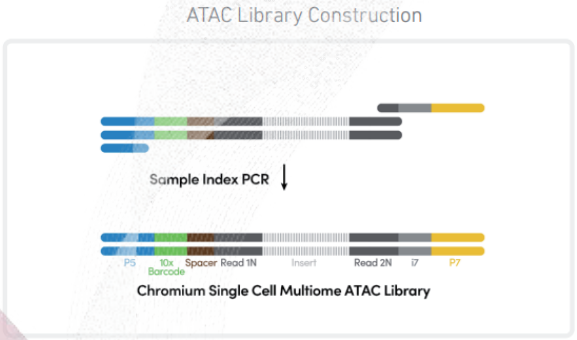
Multiome RNA+ATAC (Commercial)

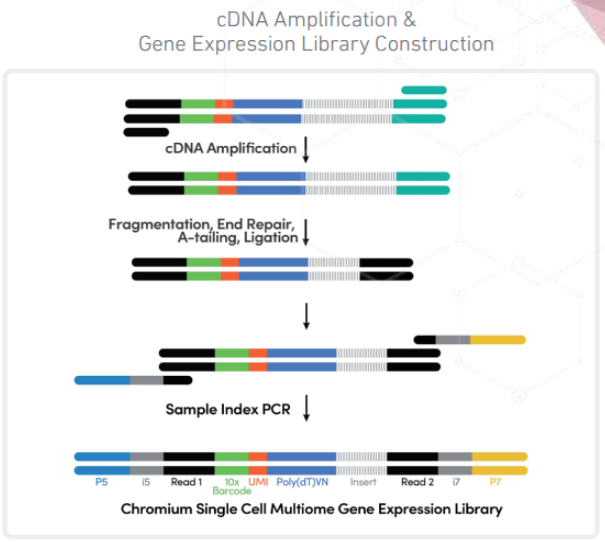


Split DNA and RNA reaction



ATAC / RNA library preparation





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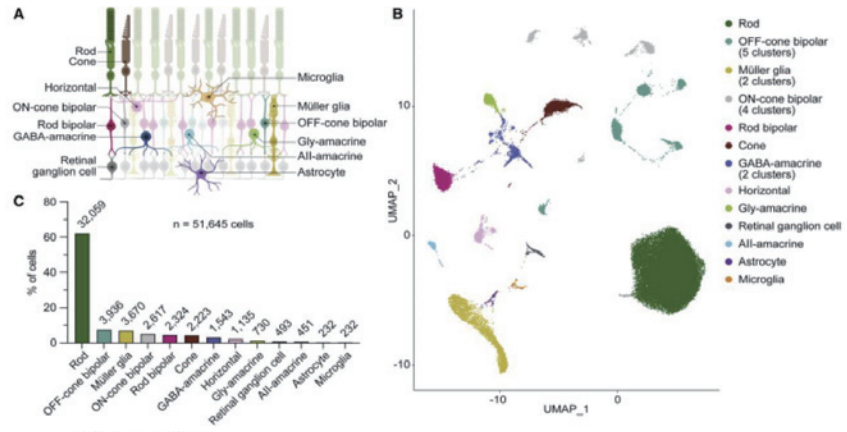
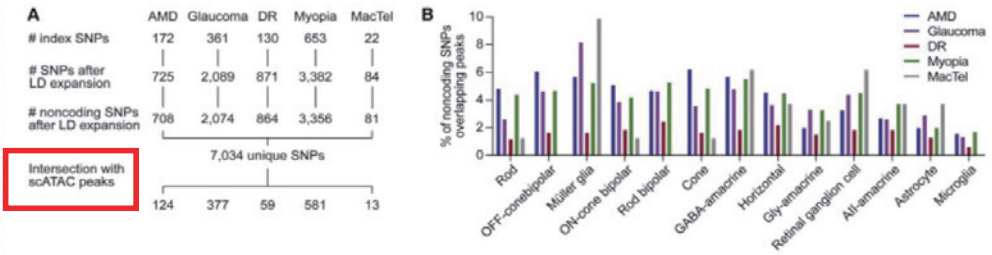
Multiome in retina cells





Prioritize cell-type specific ATAC peaks from GWAS datasets

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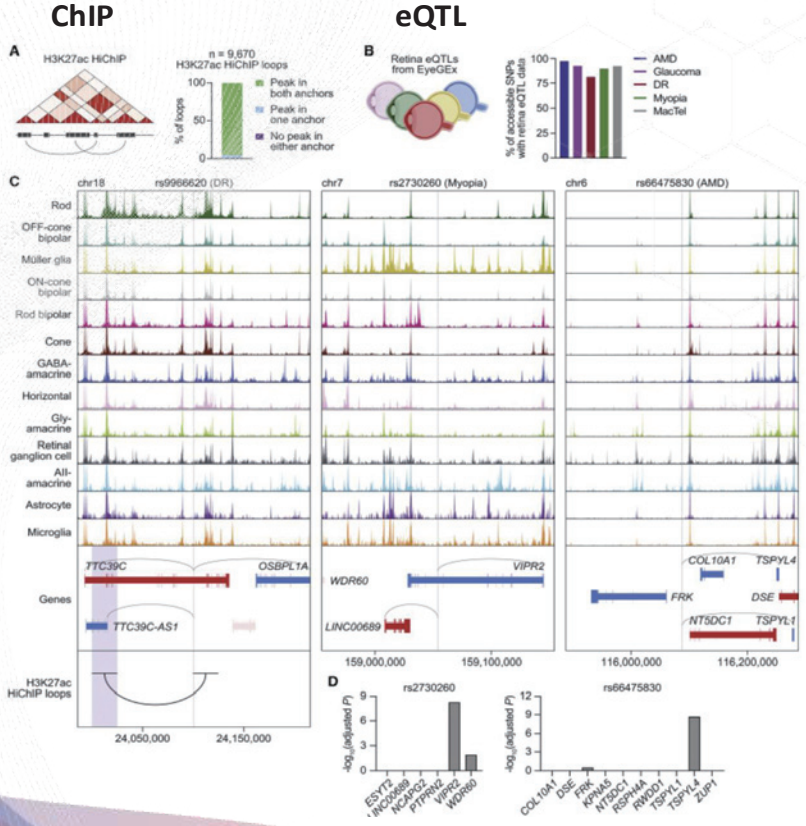
Multiome + public data integration

Multiple DB Comparison and Interpretation gets more complex



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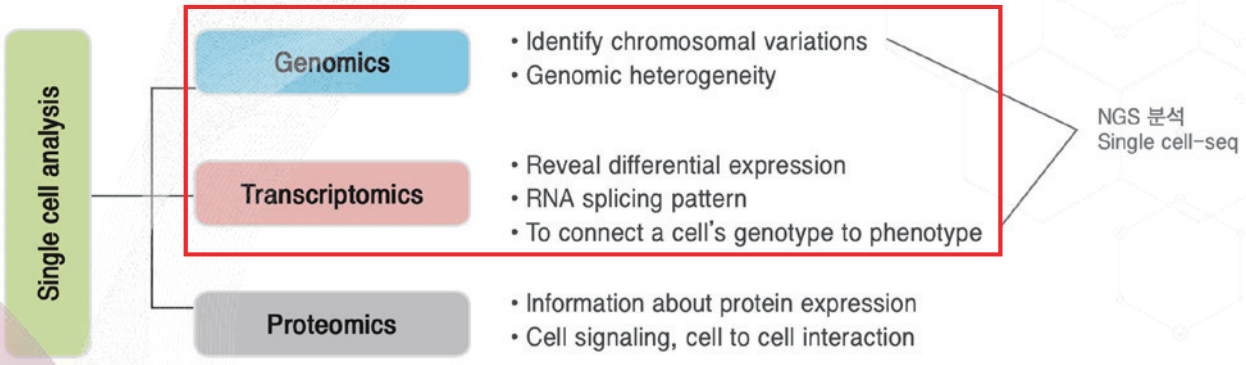
Single-cell analysis platforms



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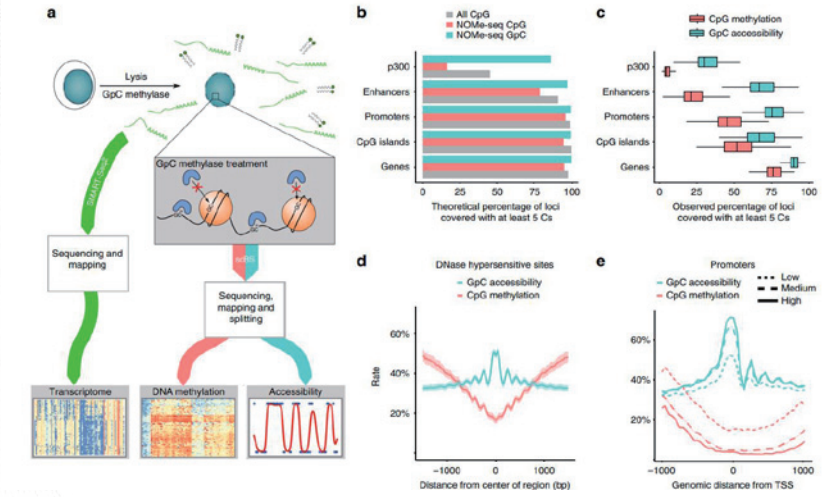
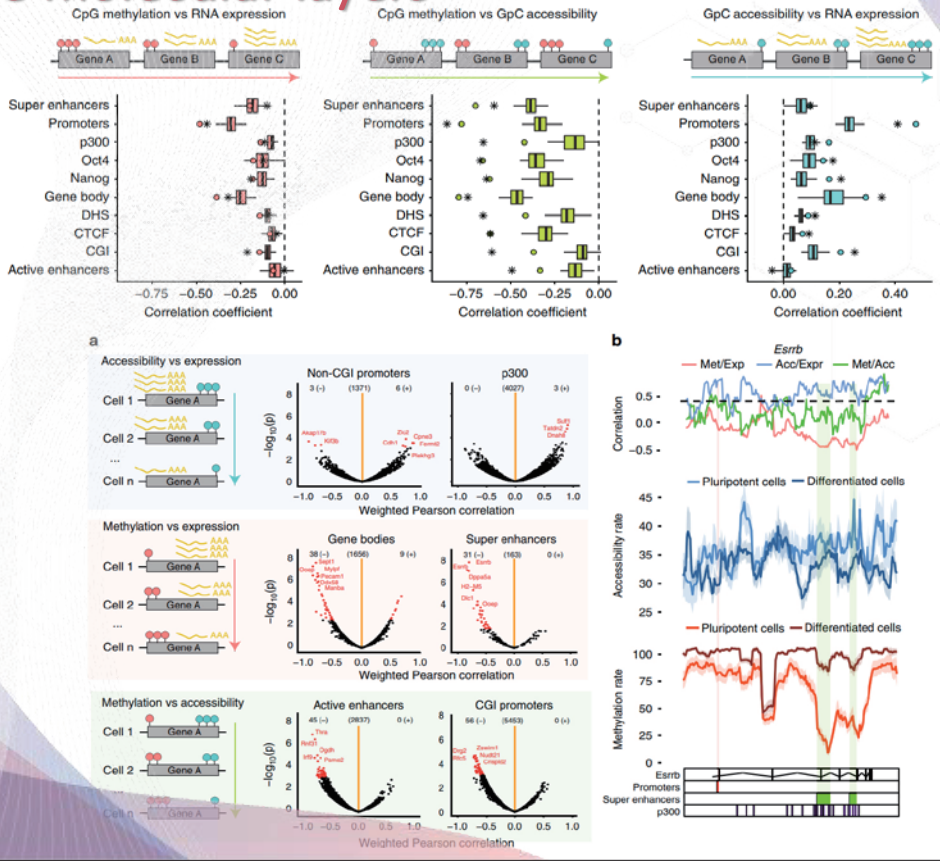
Joint profiling of methyl+chromatin+RNA

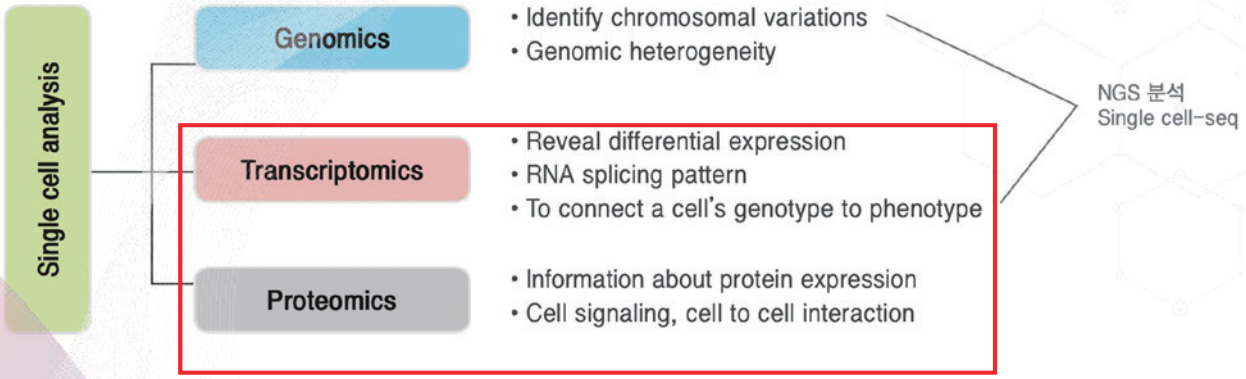
- scM&Tseq (methylation+RNA)
- NOMe-seq (nucleosome occupancy and methylation)
  - **Methyltransferase** (advantage over count based ATAC, DNase-seq methods)
  - **Frequency estimates** of CpG methylation doesn't suffer technical variation



Known/novel association between three molecular layers



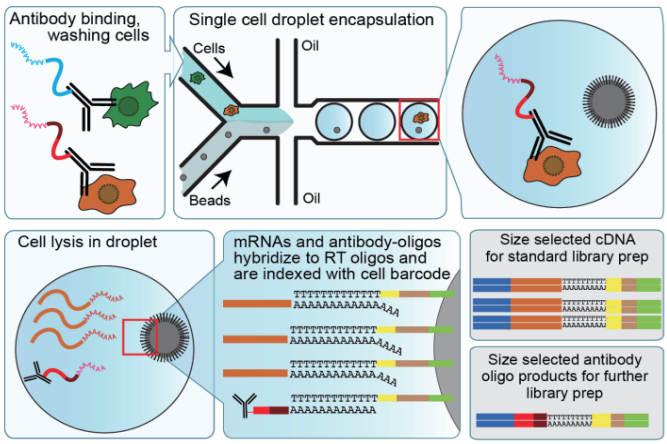
Single-cell analysis platforms



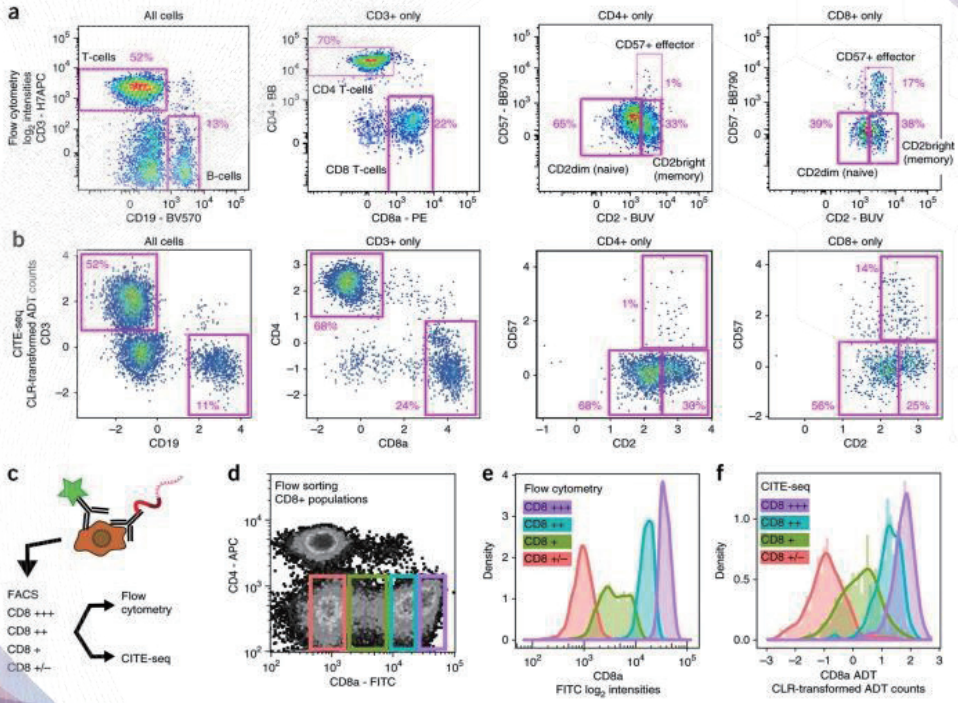
scRNA-seq + Surface protein

- **CITE-seq** (Cellular Indexing of Transcriptome and Epitopes by Sequencing)

CITE-seq uses DNA-barcoded antibodies to convert detection of proteins into a quantitative, sequenceable readout. Antibody-bound oligos act as synthetic transcripts that are captured during most large-scale oligodT-based scRNA-seq library preparation protocols (e.g. 10x Genomics, Drop-seq, ddSeq).

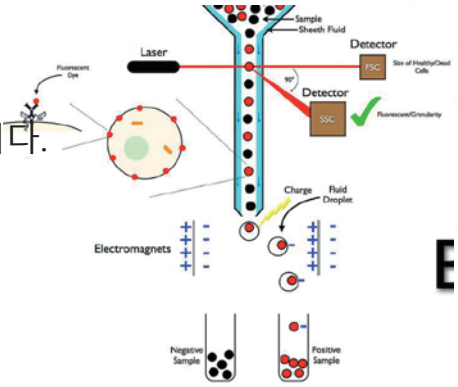


Comparison to FACS (fluorescence activated cell sorting)



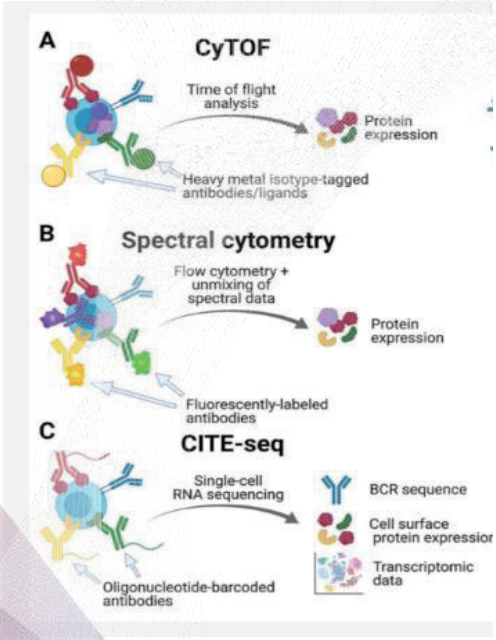
FACS (유세포 형광 분석기)

- 세포표현형을 분석하는 golden standard
- 세포 **표면마커**에 기반함.



FACS는 유세포 분석기의 분화한 타입이다.
이것은 **이질적으로 혼합된 세포들을 각각의 특정한 광산란과 형광 특징들에 기반하여 분류하는 방법**

What is the advantage of CITE-seq?



자연계에 존재하는 heavy metal동위원소 개수의 한계 존재 (~50)

Spectral overlap해결이 어려움

Use of oligo sequence as a readout Is unlimited !!!

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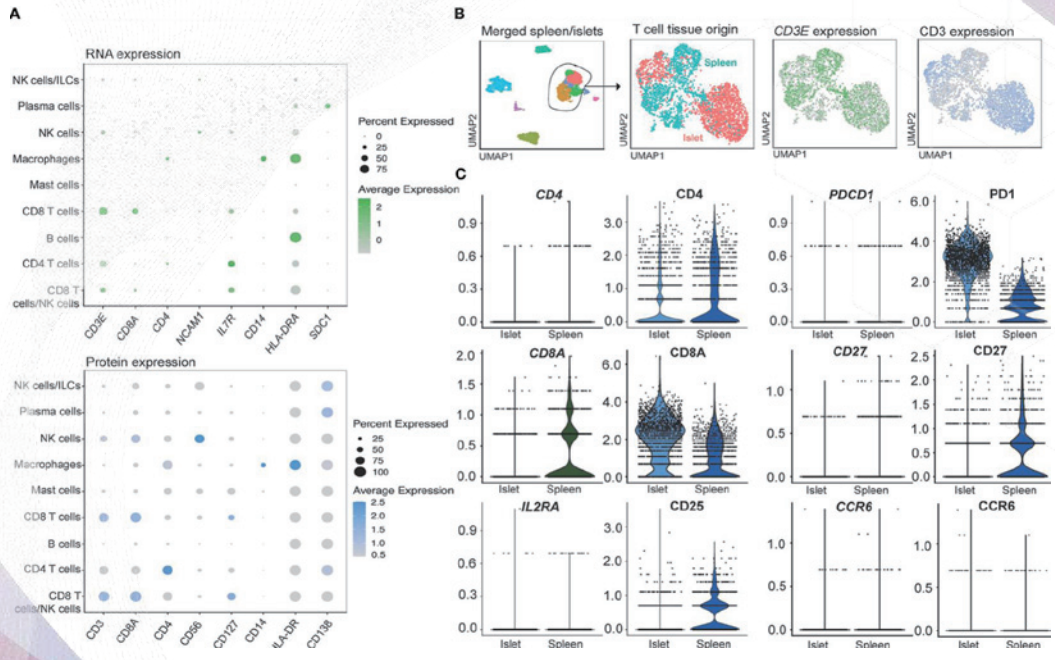
Both modalities are necessary to define clusters



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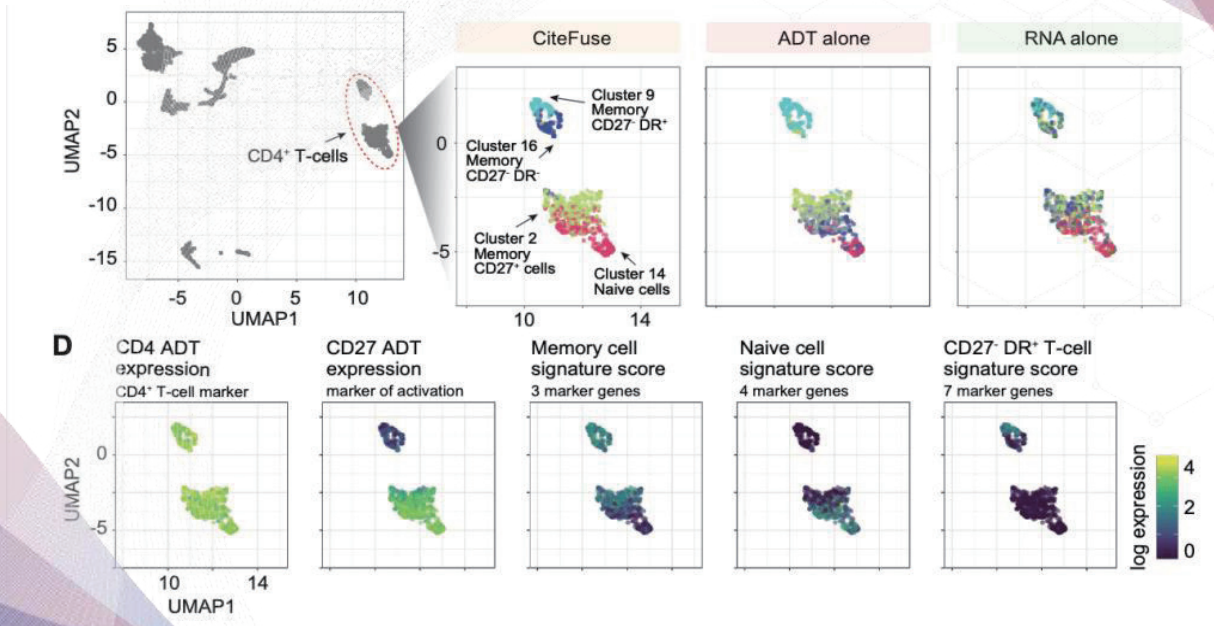
CITE-seq enables novel cell type discovery



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Future

- Ultra high-throughput multiomics technologies

(ex: SCITO-seq, scifi-RNA-seq, UDA-seq etc)

- Trimodalities (ex: RNA+protein+ATAC..)
- Integration with public dataset (batch effect removal) + interpretation will be the key!
- Foundation models (complex AI) to learn massive datasets for FUN ☺

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Closing

Thank you~!

Further readings:
Single-cell overview reading (Easy):
https://www.nature.com/articles/s12276-018-0071-8

Single-cell multiomics (Intermediate):
https://www.nature.com/articles/s41580-023-00615-w

If you have any questions or inquiry about collaboration opportunity:
bjhwang113@yuhs.ac

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