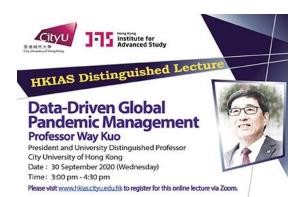
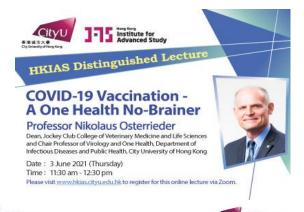
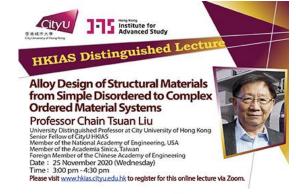
Institute for Advanced Study































Single Cell Analysis of Tumor Heterogeneity During Cancer Metastasis

Prof. Mengsu (Michael) Yang

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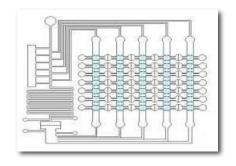
18 Feb 2022 Hong Kong Institute of Advanced Studies

Research Interests: Development of biochip technology and nanomedicine for cancer research and molecular diagnostics and therapeutic applications.



Biochip Technology

Biosensors & Microfluidics
Single Cell Analysis



Anal Biochem **2017**, 409, 2163-78.

Biosens Bioelec 2017, 89, 837-845.

Anal Chem 2018, 90, 1992-2000.

Anal Chim Acta, 2018, 1044, 29-65.

ACS Sensors 2020, 5, 870-878.

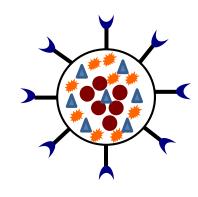
Biosens Bioelec 2021, 181, 113142.

Lab Chip **2021**, 21, 122-142.

iScience, 2022, in press

Nanomedicine

Bio-Nano Interactions
Targeted Cancer Therapy



Adv Healthcare Mat 2017, 1700185.

Nanotechnology 2018, 29, 365503.

Adv Materials 2019, 1904197.

Theranostics 2020, 10, 1181-1196.

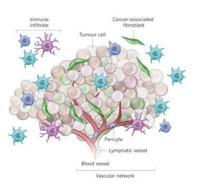
Adv Healthcare Mat 2021, 2001658.

Nanomedicine 2021, 16, 1411–1427.

Cancer Biology

Circulating Tumor Cells

Migration & Metastasis



Br J Pharm 2017, 174, 302-313.

Nat Comm 2018, 9, 2359 (15pp).

Oncotarget 2020, 11, 1017-1036.

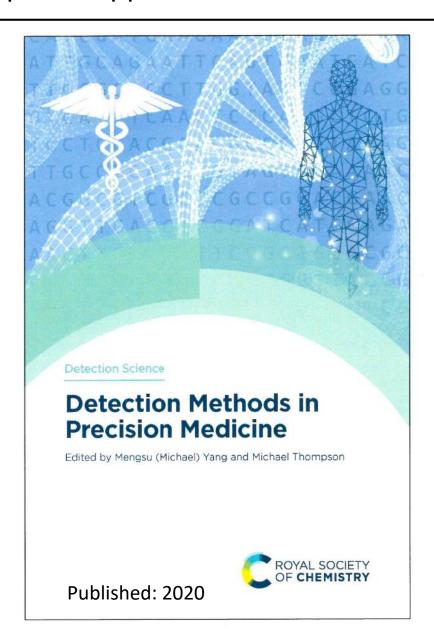
Cell Signalling 2020, 71, 109555.

Oncogene 2020, 39, 4227-4240.

Oncogene, 2021, 40, 1775-1791.

Nat Comm 2021, 12, 6103. (9pp)

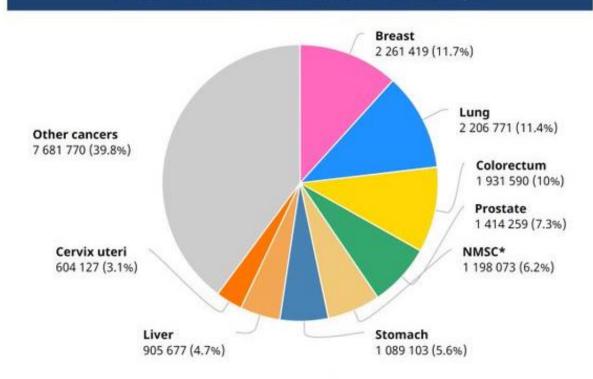
Oncogene, 2022, 41, 895-906.





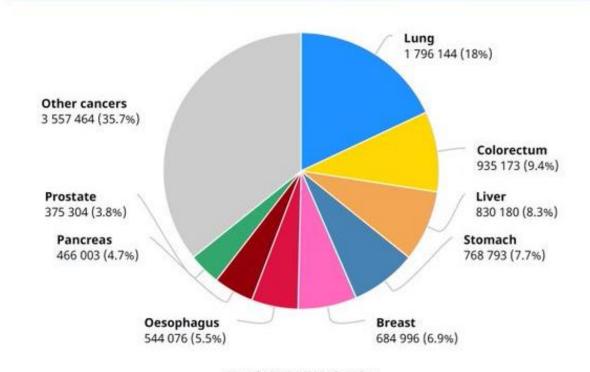
Cancer Incidence and Death: According to Globocan 2020, an estimated 19.3 million new cancer cases and 10 million cancer deaths occurred worldwide.

Number of new cases in 2020, both sexes, all ages



Total: 19 292 789 cases

Number of deaths in 2020, both sexes, all ages



Total: 9 958 133 deaths

International Agency for Research on Cancer







Alarming Numbers in China: 24% of newly diagnosed cases and 30% of the cancer-related deaths worldwide in 2020.

Breast

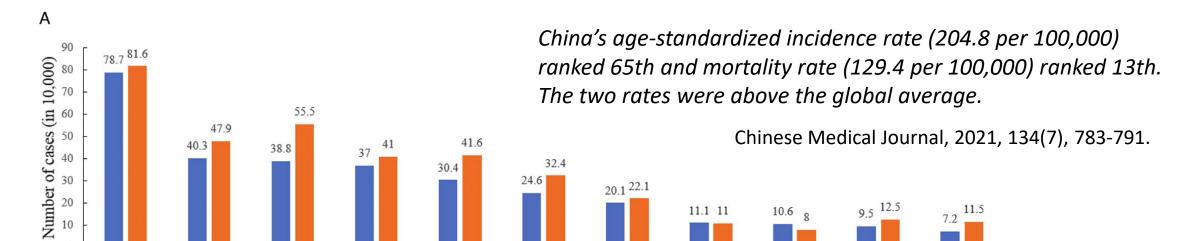
Colorectum

Stomach

Lung

Liver



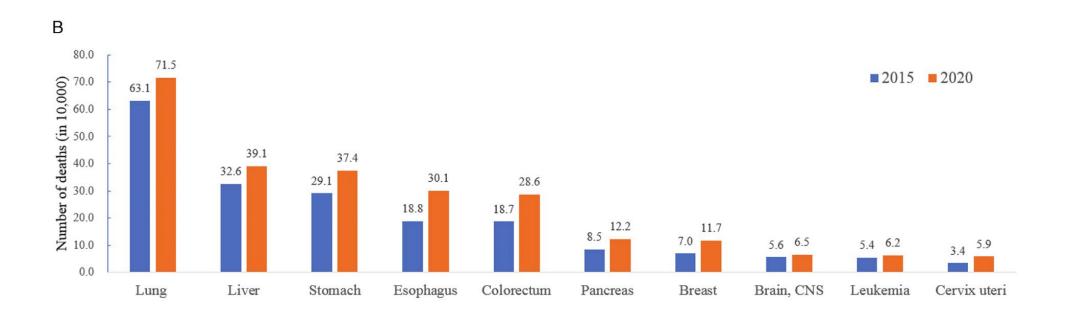


Thyroid

Cervix uteri Brain, CNS

Pancreas

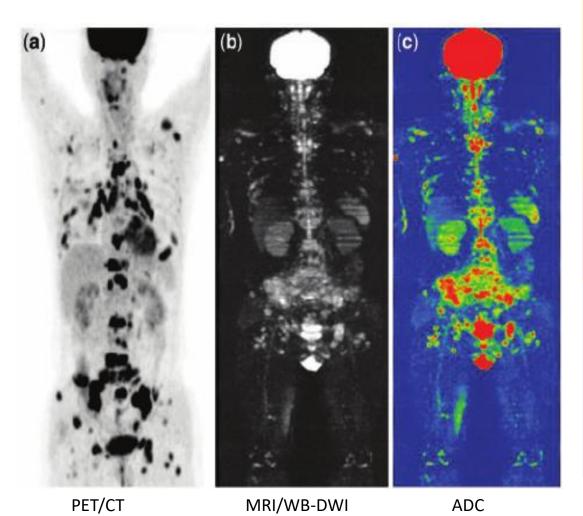
Prostate

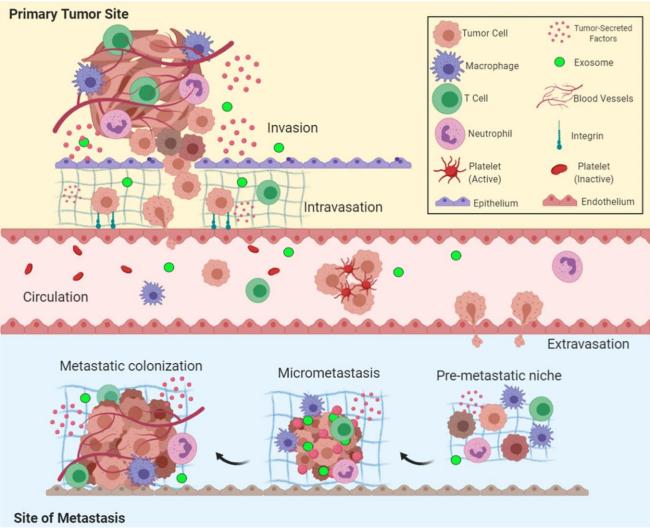


Esophagus



Cancer Metastasis: the primary cause of death for >90% of patients with cancer

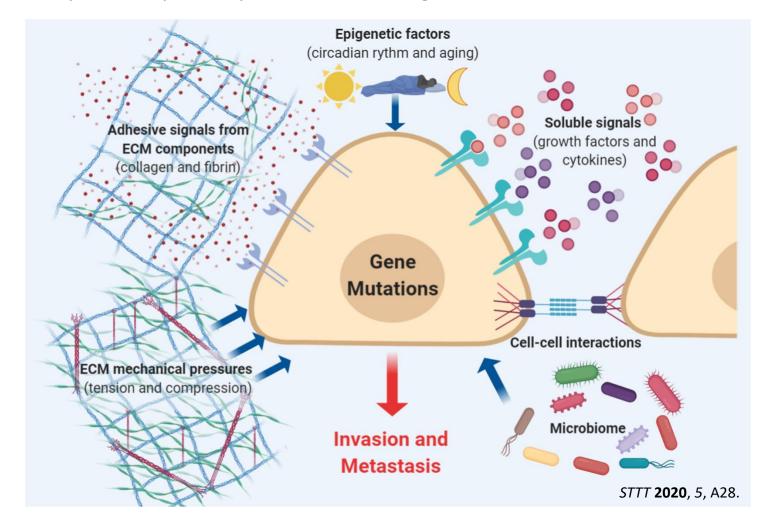




The metastatic cascade includes five key steps: invasion, intravasation, circulation, extravasation, and colonization

Determinants of Metastasis:

- CityU
- The activation of invasion and metastasis is triggered by genetic and epigenetic factors induced by multiple environmental stimuli, including biological and physicochemical signals.
- Understanding the dynamics of this process will help identify targets for molecular therapies that may halt or possibly reverse cancer growth and metastasis.



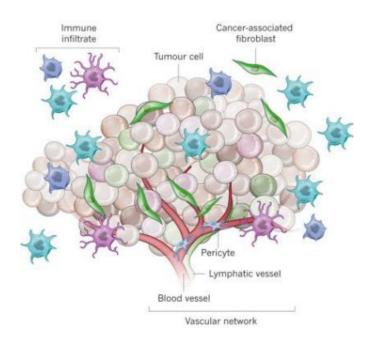
Research Challenges



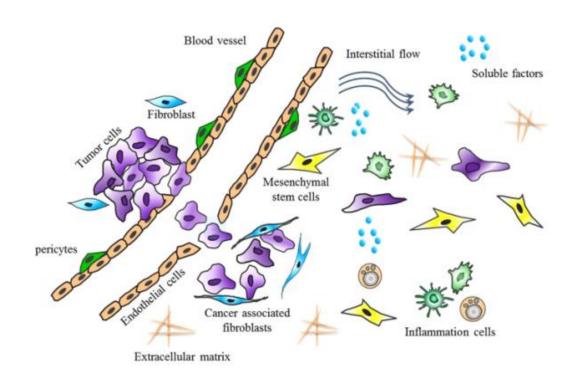
in vitro modeling and study of tumor heterogeneity and microenvironment

Tumor Heterogeneity:

- Tumors consist of cancer cells, cancer associated fibroblasts, infiltrated immune cells...
- Cancer cells within the same tumor are heterogeneous (clones, cancer stem cells)...



Microenvironment: including surrounding blood vessels, immune cells, fibroblasts and other cells, signaling molecules and extracellular matrix (ECM).



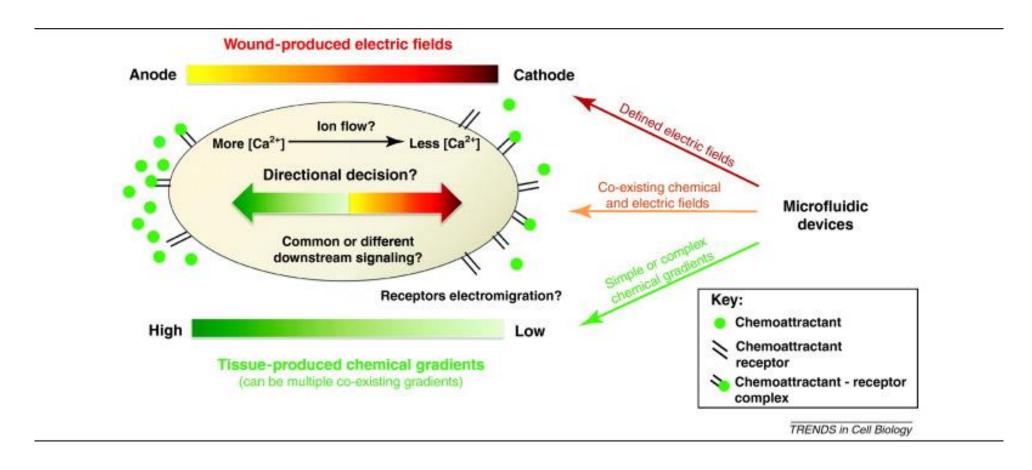
Heterogeneity

- Genetic
- Phenotypic
- Functional
- Microenvironmental

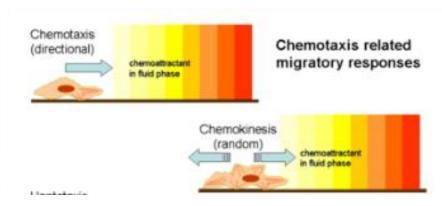
Cell Migration under Chemical/Electrical Gradients

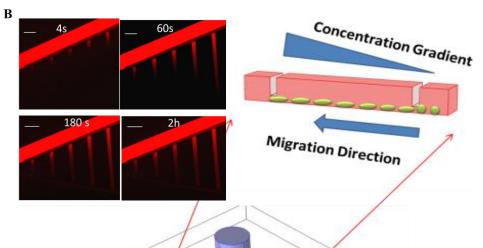


Chemotaxis/Electrotaxis plays an important role during embryogenesis, inflammation, wound healing, and tumour metastasis. However, the mechanisms at play are still poorly understood.



Cancer Cell Chemotaxis in Microfluidics



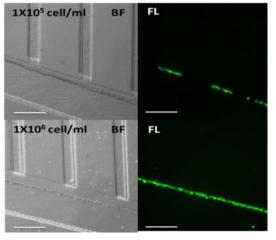


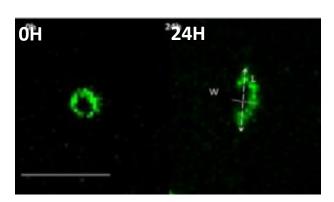
Microfluidics with gradient control and microchannels for single cell migration

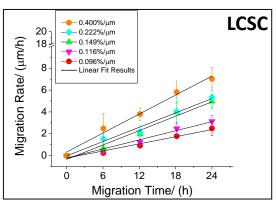
Migration, Cytoskeleton Change, and Metabolism

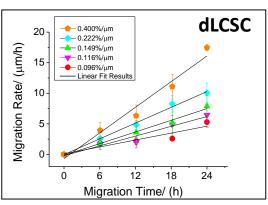


Quantitative model to study chemotaxis at single cell level









- Gradient-dependent migration, elongation and acceleration
- Association of migration rates with metabolism
- Chemotaxis mediated by Wnt/β-catenin signaling pathway

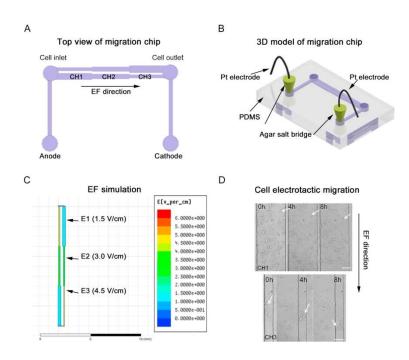
Zou Heng et al, *Anal. Chem.* **2015**, *87*, 7098-7108.

Cancer Cell Electrotaxis

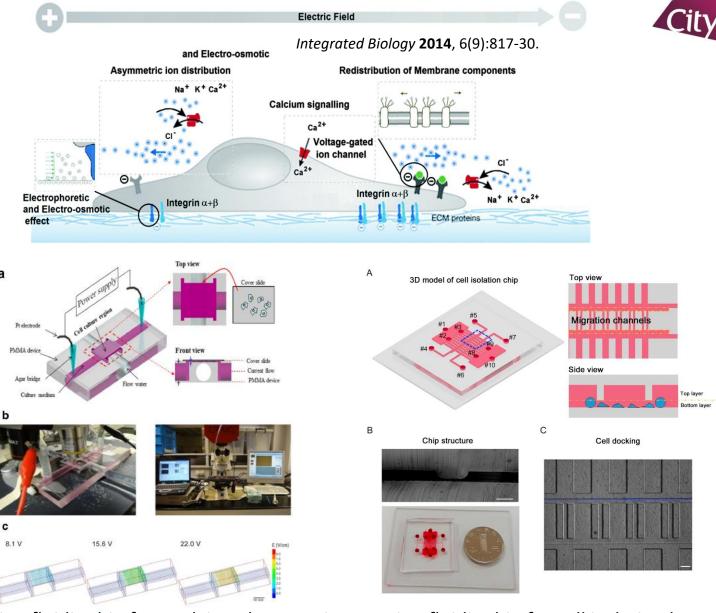
Microfluidics for electrotaxis-based cell migration

Li Yaping, Xu Tao et al

Biosens Bioelec **2017**, 89, 837–845. Anal Bioanal Chem **2017**, 409, 2163–2178. Bioelectrochem **2018**, 124, 80–92.

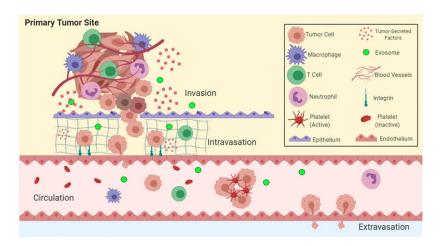


Microfluidic chip for <u>electric field gradient</u> generation and electrotactic migration of cells.

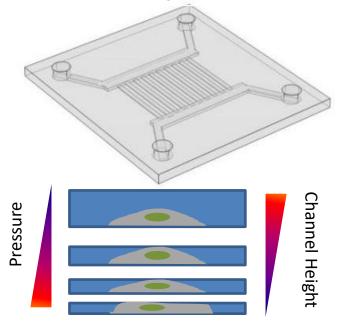


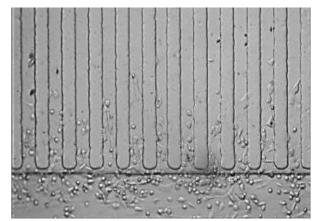
Microfluidic chip for studying electrotaxis- Microfluidic chip for <u>cell isolation</u> based based <u>cell heterogeneity</u> on migratory ability.

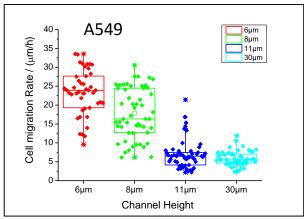
Mechanical Stress and Cell Migration

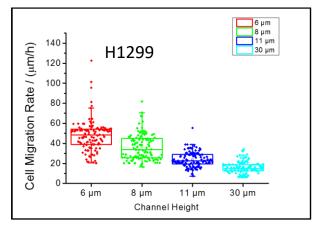


Microfluidics with controlled confined space for cell migration under stress





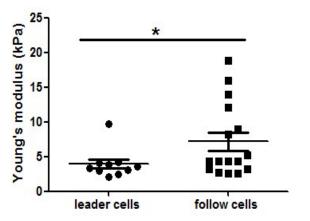


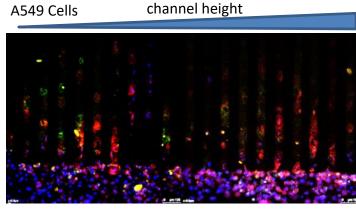




Cancer cell plasticity:

- mechanical plasticity elasticity/stiffness
- biological plasticity phenotypic changes





Green: N-cadherin; Red: E-cadherin; Blue: Nucleus

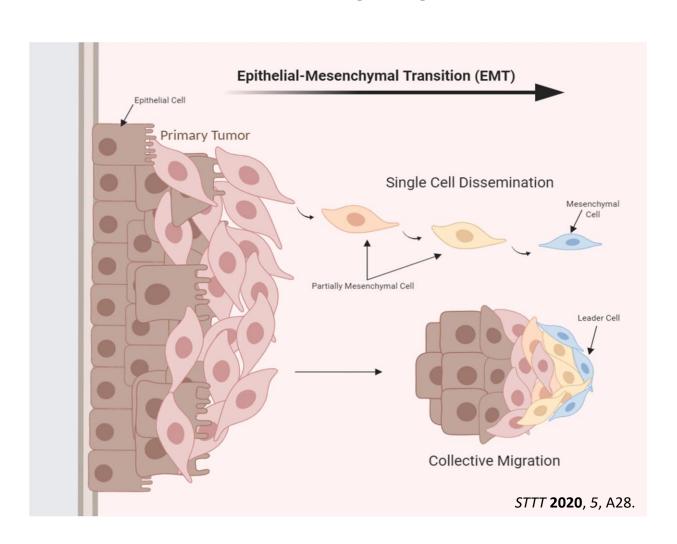
Migration rate in confined channels is associated with cell elasticity and EMT.

Zou Heng et al, Anal. Chim. Acta, 2018, 1044, 29-65.

Epithelial–Mesenchymal Transition (EMT)



EMT occurs through single-cell dissemination or through collective migration.



Single-cell dissemination:

- Random or by selection?
- EMT: before or after?

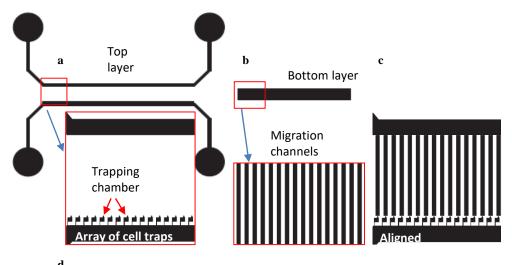
Collective migration:

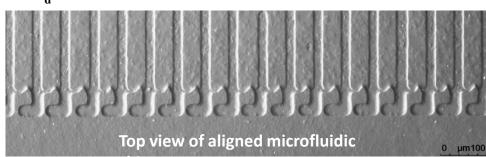
- Heterogeneity among the migrating cells?
- Plasticity: leaders vs. followers?

Heterogeneity of Cancer Cells Migrating into Confined Space

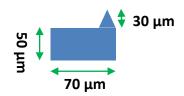


Microfluidic platform for single cell migration analysis





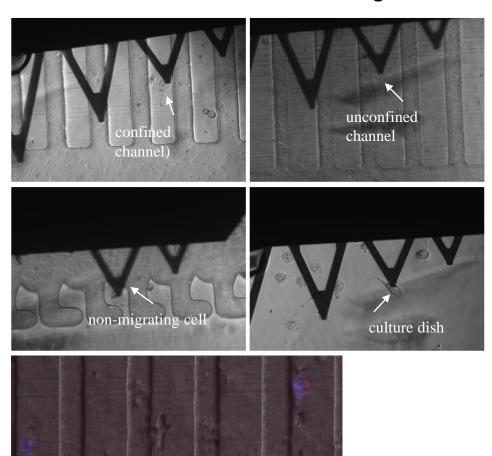
Cell trapping chambers

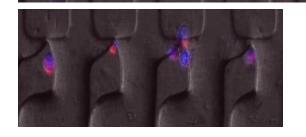


Migration channel heights

- 6 µm ≈ confined channels
- 13 μm ≈ Semi-confined channels
- 24 μm ≈ Unconfined channels

AFM-based stiffness measurement of single cells





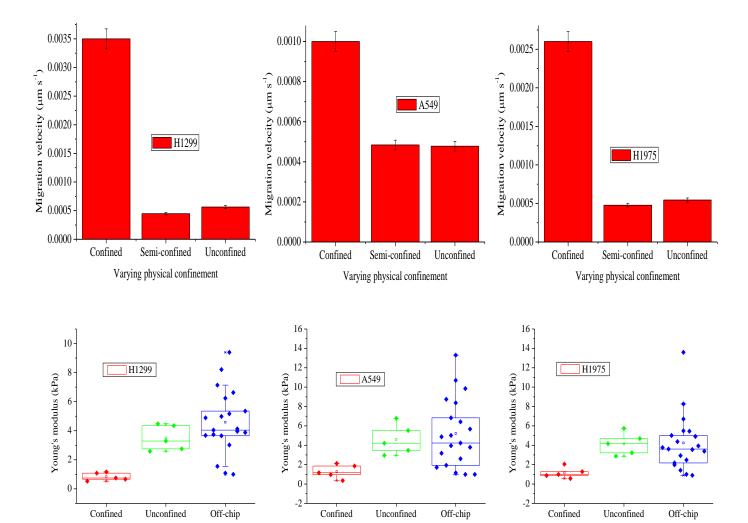
EMT-related markers staining Single cell elasticity profiling Single cell EMT gene profiling

Kowsar Alam et al, unpublished.

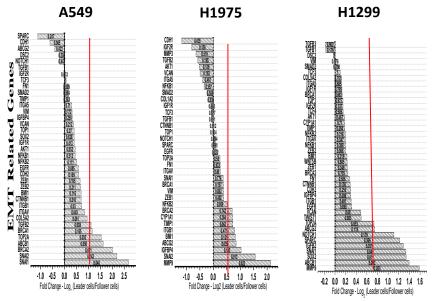
Single Cell Migration in Confined Space



Cells with more elasticity entered the confined channels and migrated faster under mechanical stress...



...with significant upregulation of EMT-related genes



Single-cell dissemination:

- Random or by selection? Cells with greater elasticity are preferred to migrate into confined space.
- EMT: before or after? Partial EMT before and continue to undergo EMT during the migration under confined space.

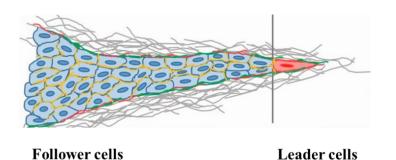
Single Cell Transcriptional Profiling of Collectively Migrating Cells



TGFB

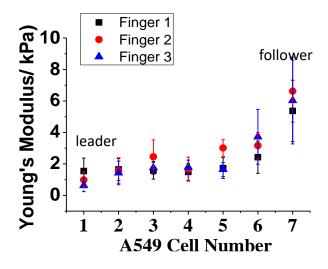
H1299

NFKB1



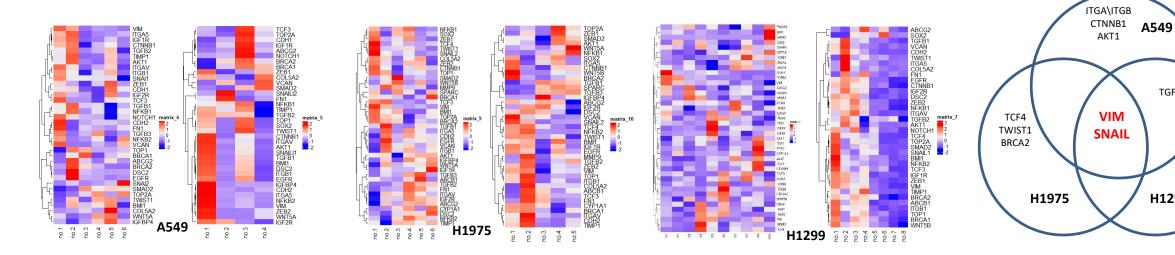
- Collective migration during metastasis
- Single-cell analysis of the migration front
- Spatial resolution of EMT-profiles

Elasticity of Fingers in Collective Migration



Single cell elasticity profiling with spatial resolution

Single cell EMT transcription profiling with spatial resolution

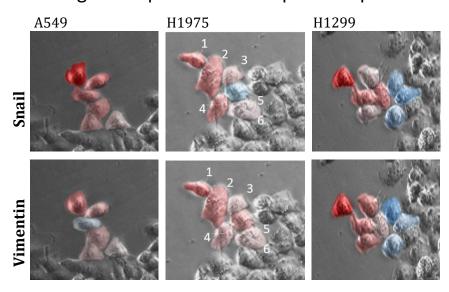


Zou Heng, Yang Zihang, et al iScience, 2022, in press.

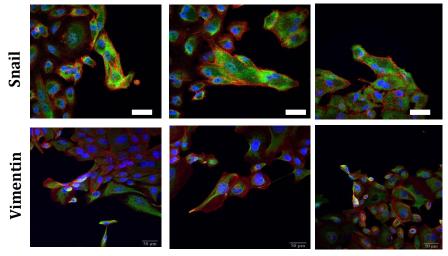
Single Cell Transcriptional and Elastic Profiles of Collectively Migrating Cells



Single cell qPCR - mRNA expression pattern

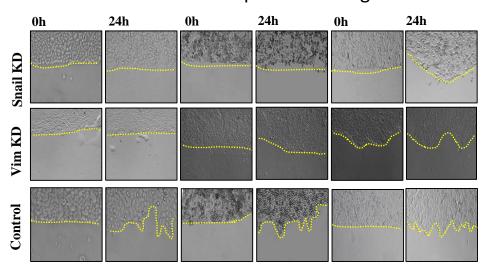


Immunofluorescence - protein expression pattern



Scale: 20 µm

Inhibition of Snail & Vimetin prevented finger formation



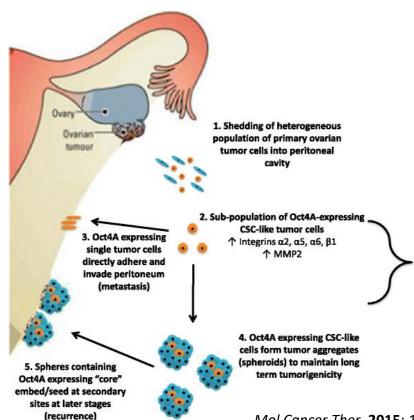
Collective migration:

- Heterogeneity among the migrating cells?
 - Yes, spatially-dependent transcription and stiffness profiles among the cells.
- Plasticity: leaders vs. followers?
 - continuous increase of phenotypic plasticity (EMT) and mechanical plasticity from follower to leader cells.

Single-cell EMT-related Transcriptional Analysis of Epithelial Ovarian Cancer Ascites

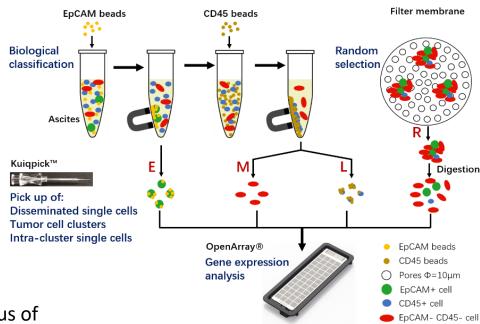
CityU

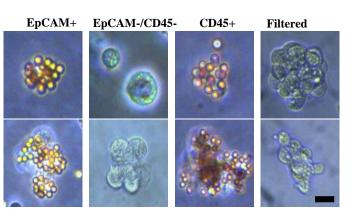
- ➤ Ascites are tumor cells or cell clusters disseminated from the primary ovarian cancer into peritoneal cavity.
- ➤ The presence of ascites correlates with the OC peritoneal metastasis and is associated with poor prognosis.



Questions:

- ➤ EMT gene expression status of disseminated cells and cell clusters in ascites of EOC?
- Classification of cells based on EMT gene expression profile?
- Components in cell clusters? Intracluster and inter-cluster heterogeneity?



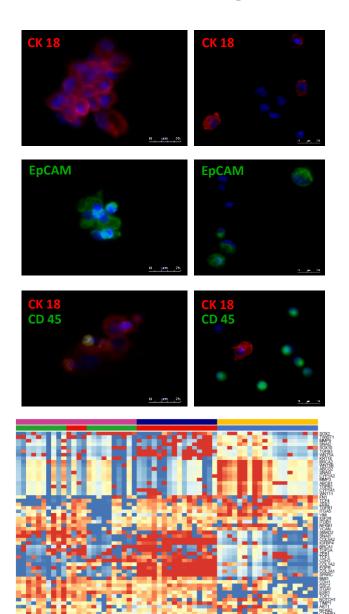


Mol Cancer Ther. 2015; 14, 747-756.

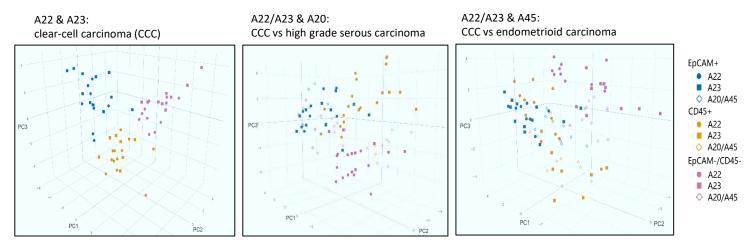
Kan TT et al, Oncogene, 2020, 39(21), 4227-4240.

Single-cell EMT-related Transcriptional Analysis of EOC Ascites

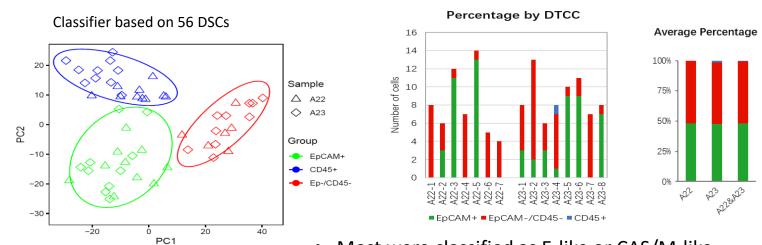




Intra-pathological Similarity and Inter-pathological Difference



Intra-cluster and Inter-cluster Heterogeneity of DTCCs in Ascites



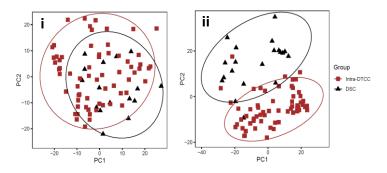
- Most were classified as E-like or CAS/M-like
- Difference between population and individual clusters

Single-cell EMT-related Transcriptional Analysis of EOC Ascites



DTCCs are more metastatic than DTCs

Similarity between DSCs and single cells from DSCCs



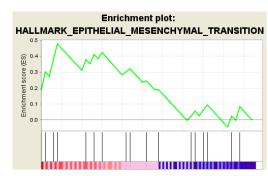
- i. CSA/M-like cells (EpCAM-/CD45-): similar
- ii. E-like tumor cells (EpCAM+): different

GSEA: Difference between E-like and CAS/M-like cells in DTCCs



Up-regulation of **ECM-related genes** (COL5A2, 3A1 and 1A2) in CAS/M-like cells - **enabled strong cell-cell connection and prevent anoikis**

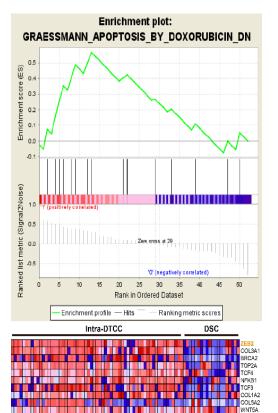
GSEA: Difference in E-like cells between DSCs and DTCCs

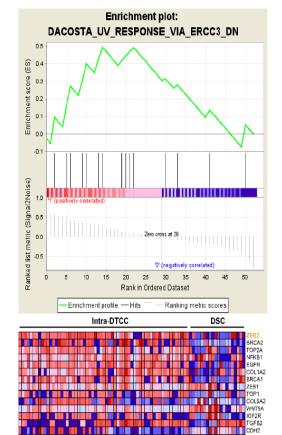


Up-regulation of **EMT-related genes** in E-like cells from DTCCs - **higher migration and invasion abilities**

EMT activation is related to chemo-resistance and DNA damage repair

GSEA: Difference in E-like cells between DSCs and DTCCs



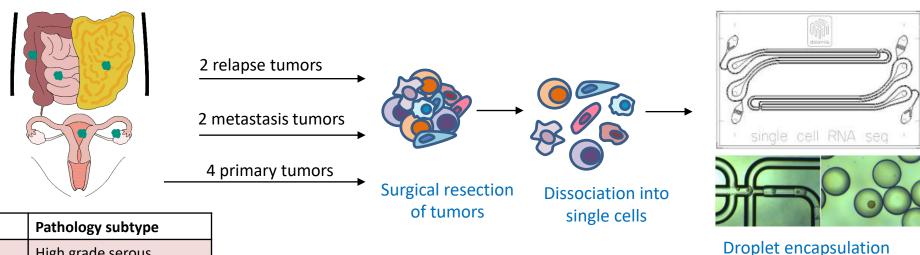


Activation of chemo-resistance and DNA damage repair programs E-like cells in the DTCCs may be better protected from
chemotherapy and radiotherapy Kan TT et al, Oncogene, 2020

Single-cell RNA-seq identified tumor subpopulation as progenitor of epithelial ovarian cancer recurrence



- Identify the initiation population of tumor cells in primary/relapsed/metastatic tumors;
- Roles of stromal cells in tumor microenvironment in relapse/metastasis;
- Biomarkers for prognosis and prediction of recurrence.



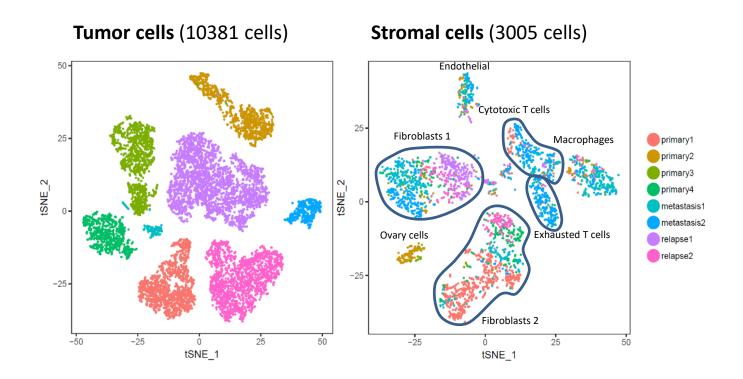
Sample Primary-1 High grade serous Primary-2 Endometrioid Primary-3 Low grade serous Primary-4 Low grade serous Metastasis-1 High grade serous Metastasis-2 Low grade serous Relapse-1 Serous Relapse-2 Low grade serous

- Metastasis tumors: EOC patients were diagnosed with peritoneal metastasis before chemotherapy;
- Relapse tumors: recurrence of cancer several years after EOC surgery and chemotherapy.

and single cell RNA-seq

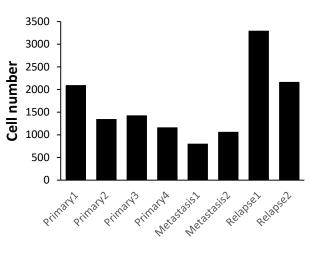


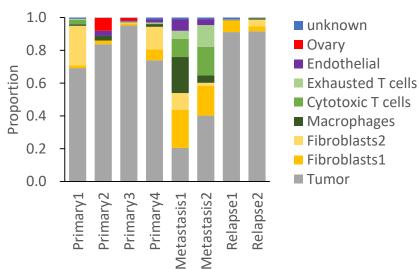
Tumors are different, microenvironments are similar



- For tumor cells, the cells were clustered according to their tumor of origin;
- For the stromal cells, each cell population contained cells from all patients, no matter primary, metastasis or relapse tumors.
- Fibroblast was the dominate cell population of tumor microenvironment;
- Metastatic tumors contained more immune cells and less tumor cells than the other tumor types.

Cellular proportion of each tumor



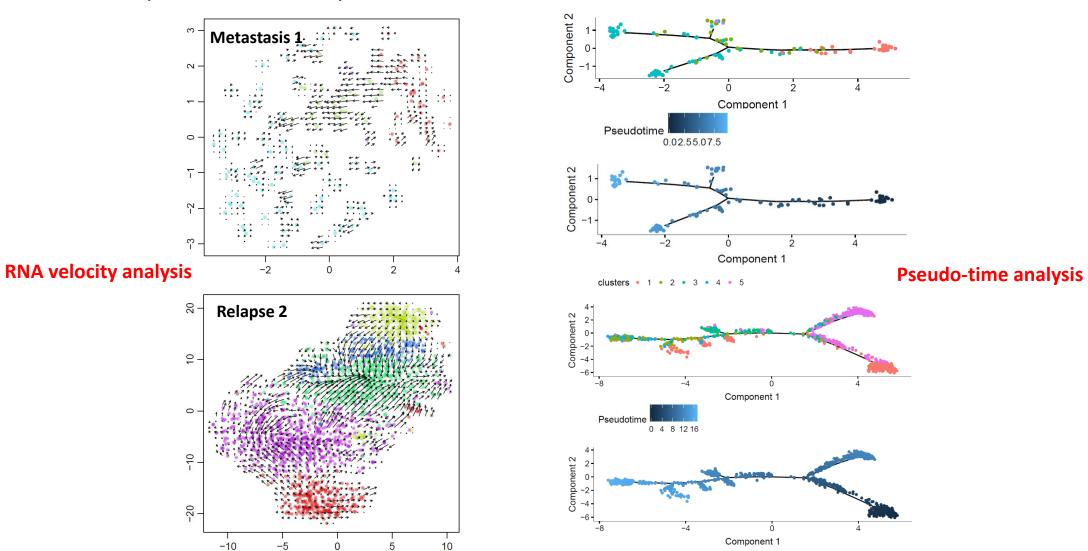


The initiation cell population of metastatic/relapsed tumors



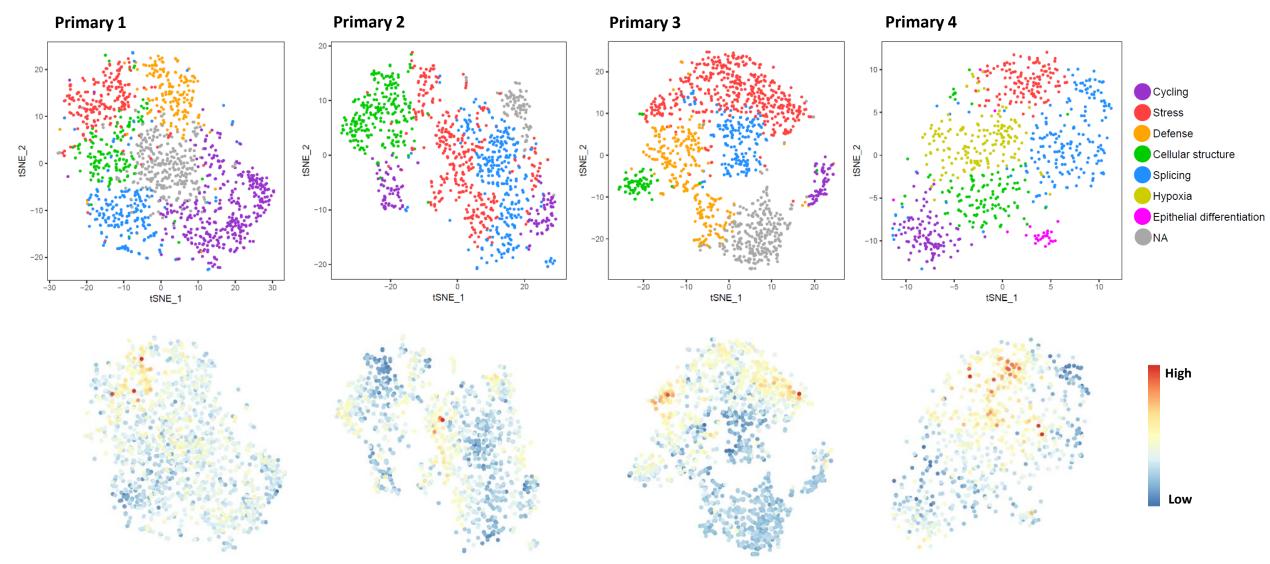
The earliest cell population were identified by the combination of the RNA velocity

and pseudo-time analysis:



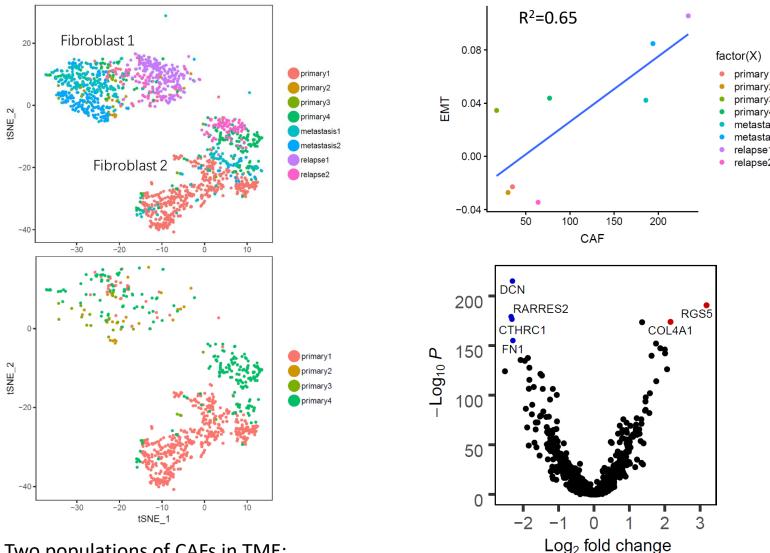


The initiation subpopulation in relapsed tumors was found in primary tumors – cancer cells with enhanced stress program



A subpopulation of cancer-associated fibroblasts (CAF) contributed to tumor metastasis with enhanced EMT program



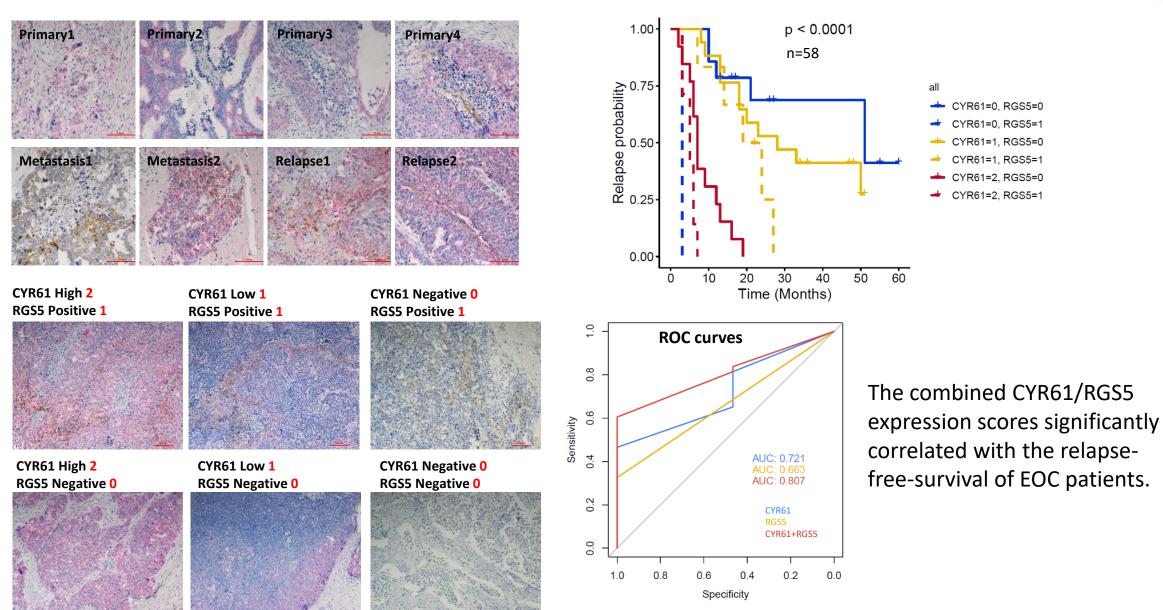


- Two populations of CAFs in TME;
- CAF1 metastatic; CAF2 primary.

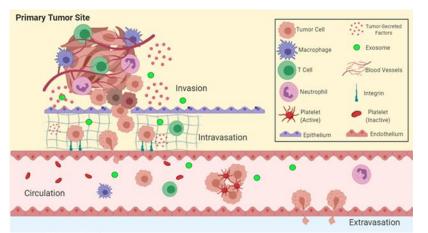
Volcano plot of DE genes in CAF1

Prognosis according to biomarkers on cancer cells and CAF cells

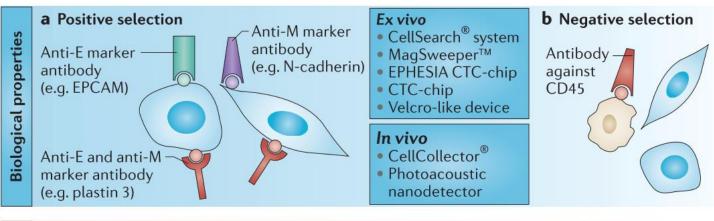


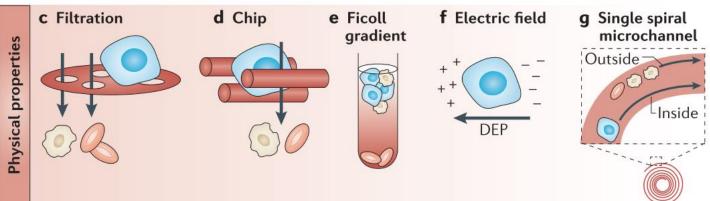


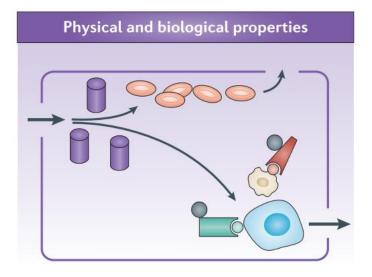


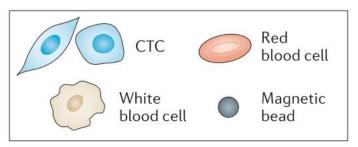


Circulating Tumor Cells and Techniques for CTC enrichment and isolation



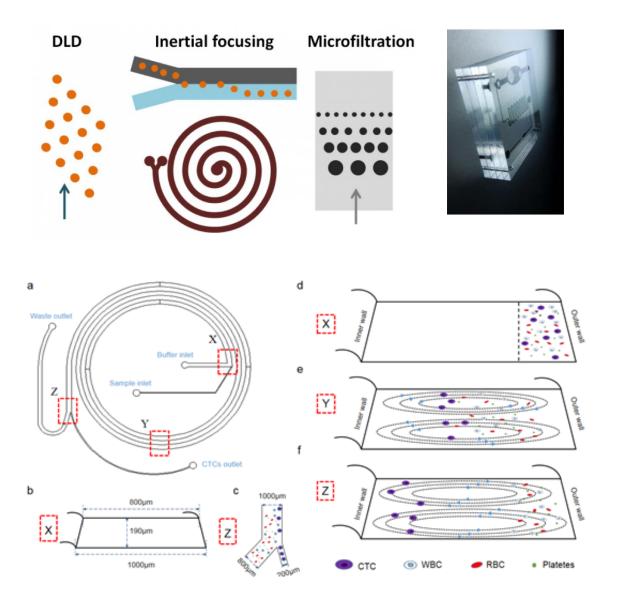




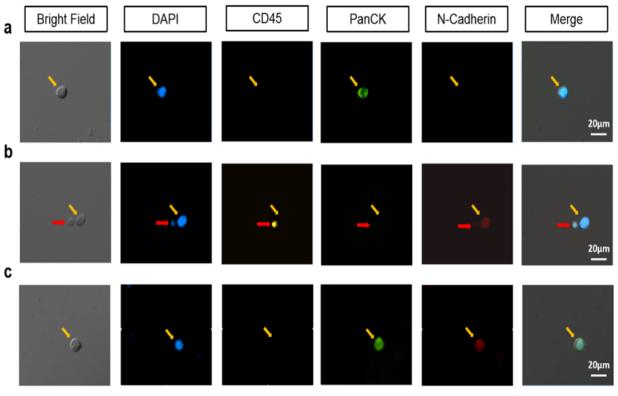


A microfluidic platform for CTC enrichment, isolation and characterization



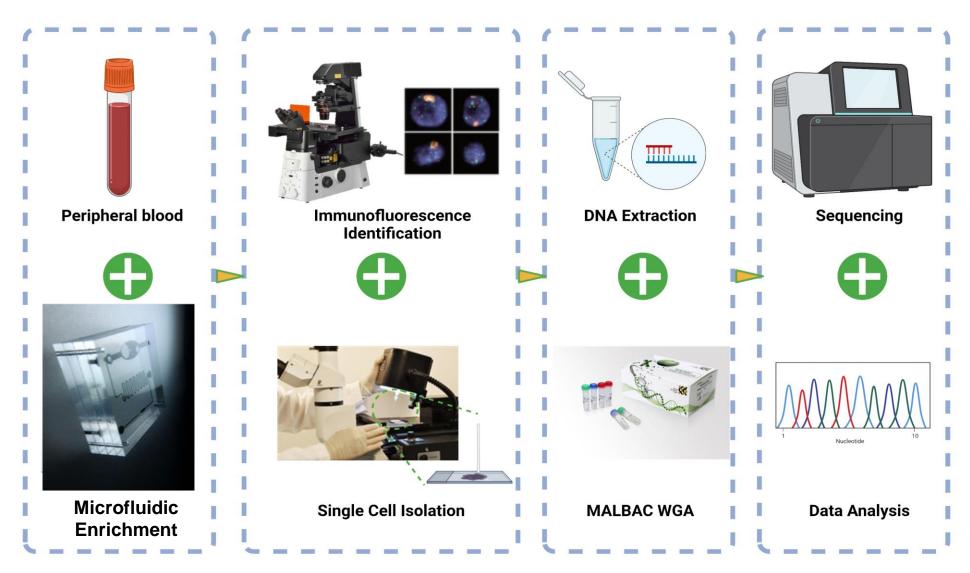


- Combined size-based separation with E/M markers.
- Capture and isolate CTCs alive for subsequent culturing





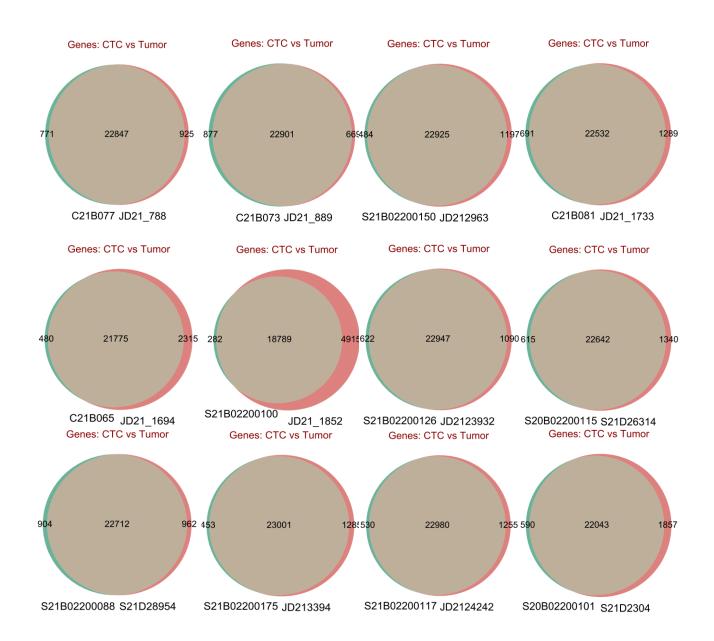
Whole-genome single cell sequencing of circulating tumor cells



- Concordance with primary tumor?
- CTC-specific mutations?
- Novel CTC marker?





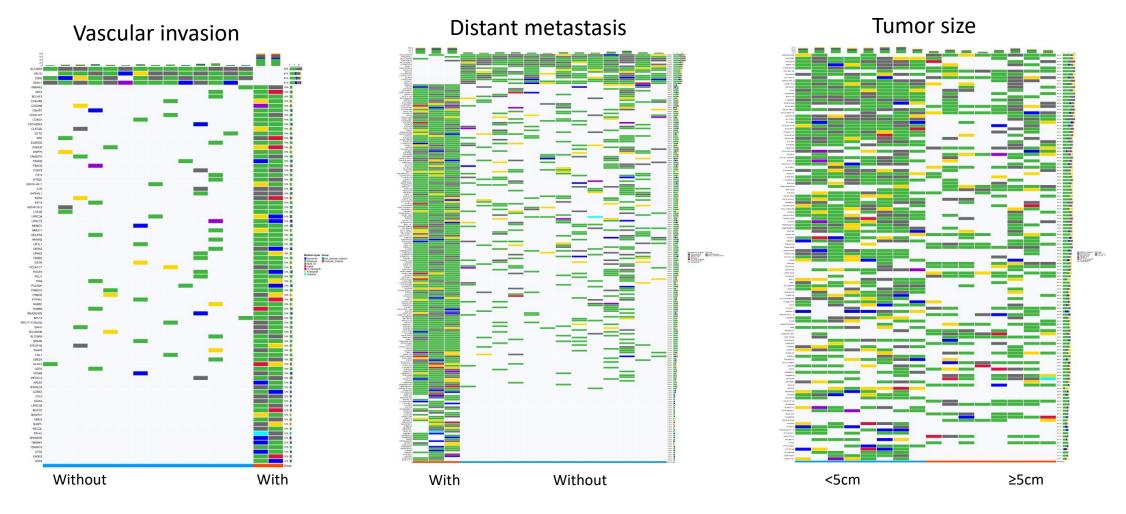


Patient NO.	CTC SNV	Overlap	Tumor snv	Concordance
1	771	22847	925	96.10886758
2	877	22901	669	97.16164616
3	484	22925	1197	95.0377249
4	691	22532	1289	94.58880819
5	480	21775	2315	90.3902034
6	282	18729	4915	79.2124852
7	622	22947	1090	95.46532429
8	615	22642	1340	94.41247602
9	904	22712	962	95.93647039
10	453	23001	1285	94.70888578
11	530	22980	1255	94.8215391
12	590	22043	1857	92.23012552
				02 22054629

93.33954638

Somatic mutated genes that are associated with tumor stage

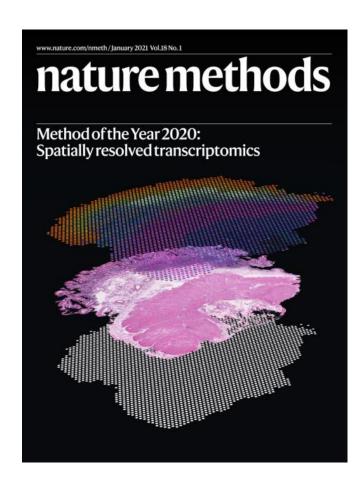




- The mutated genes in CTCs are highly consistent with primary HCC, indicating CTCs can be used to reveal genomic features of tumor when biopsy is not accessible.
- WGS of CTCs could reveal novel mechanism of metastasis.



Spatially-resolved transcriptomics: single-cell RNA seq in situ



Spatial transcriptomic, a combination of on-chip hybridization and single cell RNA-seq, allows for study of tumor heterogeneity in situ.

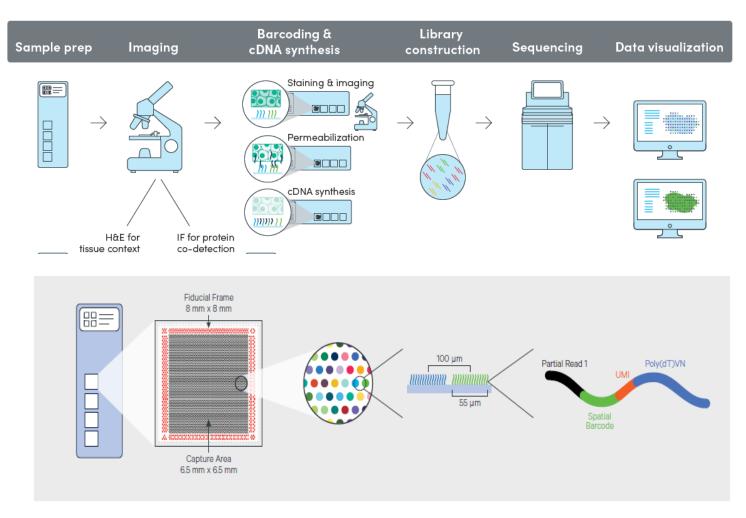


Figure 1. Composition of Visium Spatial Gene Expression Slide. Each slide can contain either two or four Capture Areas with approximately 5,000 barcoded spots, containing millions of spatially barcoded capture oligos. Released tissue mRNA binds to these oligos, enabling capture of gene expression information.

Spatially-resolved transcriptomics of liver tumor sections to reveal novel metastasis-related genes



Case 1: Tumor center



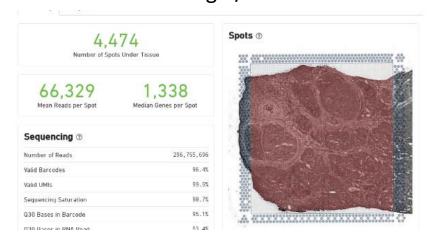
Case 1: Tumor margin/frontier



Case 2: Tumor center



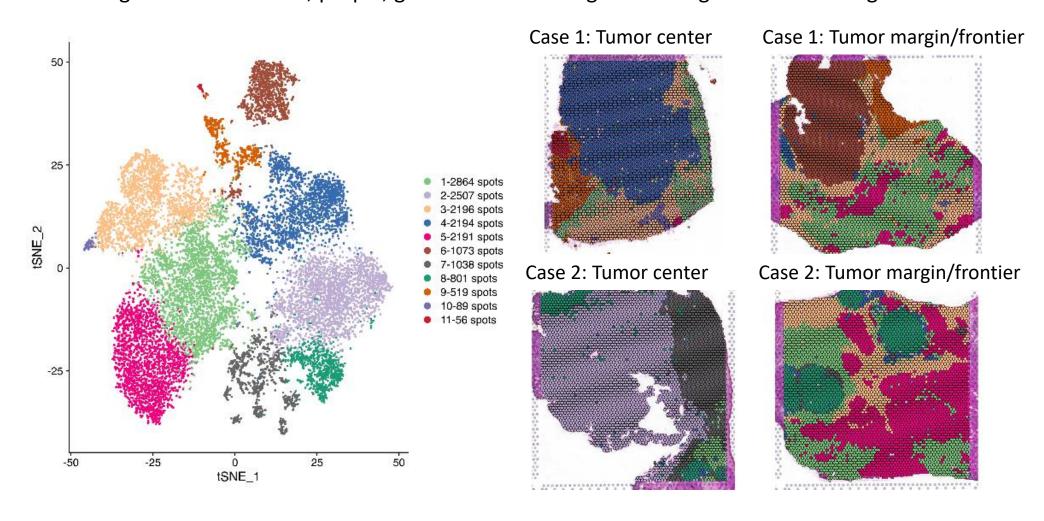
Case 2: Tumor margin/frontier



Cell clusters are spatially mapped to tissue sections to reveal heterogeneity



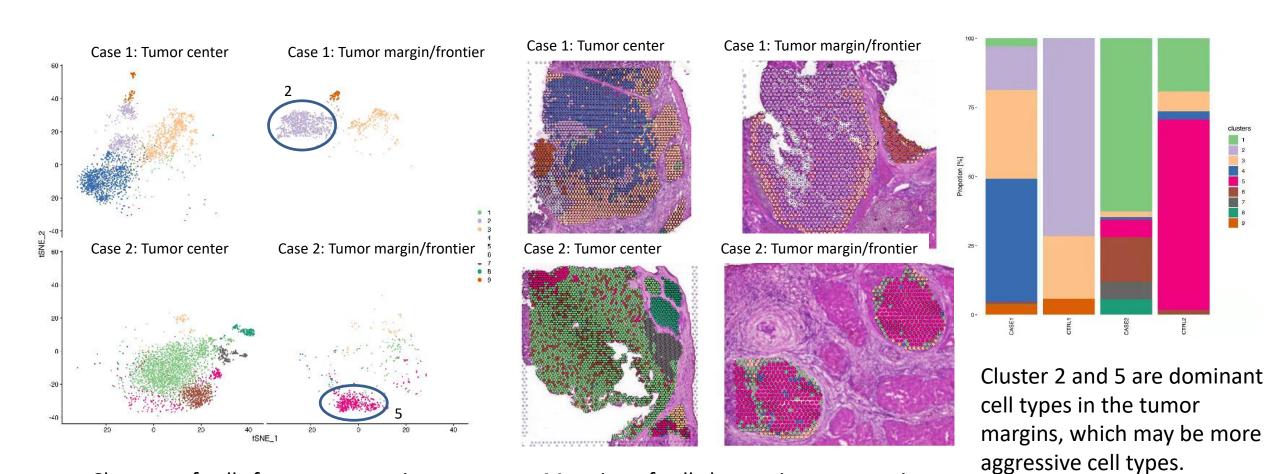
The samples are comprised of 11 clusters. More heterogenous in surrounding tissue than tumor. HE staining confirms the blue, purple, green and brown regions belong to the tumor regions.





Differentiation of dominant cell types in tumor centers and margins

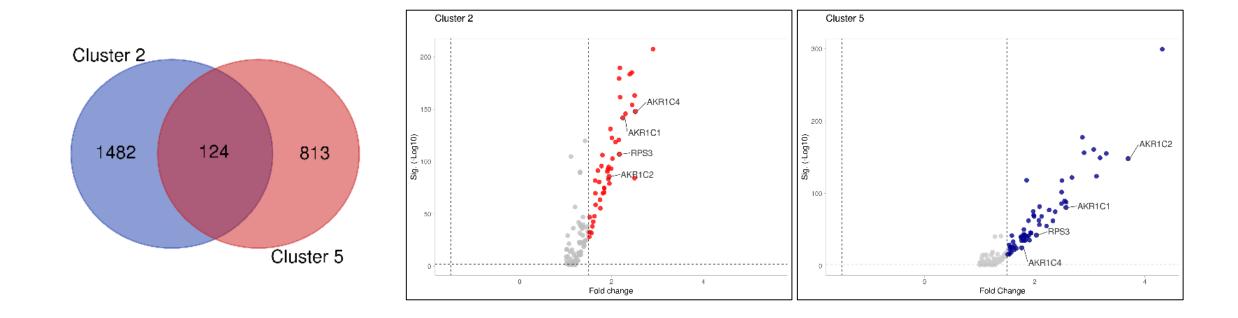
Clusters of cells from tumor regions



Mapping of cell clusters in tumor regions



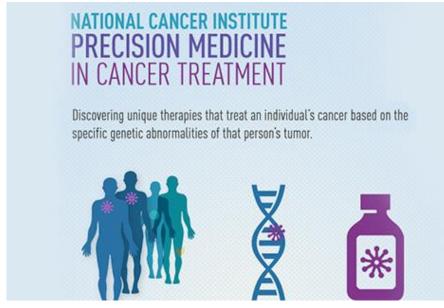
Upregulated genes found in cluster 2/5 may be drivers of metastasis



A number of upregulated gene families were identified in both Clusters 2 and 5, related to cell metabolism and ribosome biogenesis.

Winning the War on Cancer Together











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