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**THE CHINESE UNIVERSITY OF HONG KONG
FACULTY OF MEDICINE
SCHOOL OF BIOMEDICAL SCIENCES**

Dr. Joaquim Vong

Scientific Officer
School of Biomedical Sciences
Faculty of Medicine
The Chinese University of Hong Kong

will present a seminar entitled

***“Launch of the Spatial Omics services by
Single Cell & Spatial Omics Core (SCSOC)”***

on

11 September 2024, Wednesday, 10:00 – 11:00a.m.

via ZOOM platform

Registration at:



***** ALL INTERESTED ARE WELCOME *****

Topic: Launch of the Spatial Omics services by Single Cell & Spatial Omics Core (SCSOC)

Speaker: Dr. Joaquim Vong, Scientific Officer, School of Biomedical Sciences, The Chinese University of Hong Kong

Abstract:

The emergence of Single Cell technologies has greatly enhanced the development of biomedical research, especially in the areas of genomics, transcriptomics, epigenomics, proteomics and metabolomics. The Single Cell Omics Core (SCOC) was officially launched in May 2021 by the School of Biomedical Sciences (SBS) at the Chinese University of Hong Kong with a long-term mission to provide a technical platform for researchers to stay at the forefront of omics research. More recently, the “multi-omics” approach aims to targeting and integrating datasets at different levels, addressing biological questions in multiple perspectives.

Despite the robustness and versatility of the conventional single-cell modalities, spatial information of primary samples is absent in most single-cell Omics dataset. This is due to the inclusion of dissociation procedures during single cells preparation from the native tissue. Recently, “**Method of the Year 2020: spatially resolved transcriptomics**” by Nature Methods has highlighted breakthroughs in overcoming this hurdle. For instance, spatial transcriptomics, which targets the transcriptomic profiling of a tissue at single-cell level together with spatially resolved information of the same tissue. This is particularly important in multi-disciplinary research, such as integration of histopathology with sequencing dataset. Adoption of the latest spatial technology is crucial for the development of biomedical research and biotechnology industry in Hong Kong.

With the support of the CRF equipment grant (Ref.: C4062-22EF), SCOC is now renamed as “**Single Cell & Spatial Omics Core (SCSOC)**” at SBS. Based on the existing single-cell omics services, SCSOC aims to provide a streamlined, sample-to-data full service package for spatial omics. In this seminar, an outlook of the service packages will be introduced, including service type, sample requirement, spatial assay area and resolution, depending on the actual experimental needs. The proposed spatial transcriptomics service package includes initial sample QC (RNA), followed by an evaluation of overall quality of sample for fitness to continue run. A final QC is performed on the final sequencing library to ensure sound quality for massively-parallel sequencing. Finally, recommendations such as precautions and requirements of samples preparation are listed.

Besides service providing, the SCSOC welcomes interested PIs for experimental troubleshooting, intellectual advice as well as project discussions / collaborations.

About the speaker: Dr. Vong is currently a Scientific Officer and the Deputy Managing Director of Core Laboratories in the School of Biomedical Sciences (SBS), CUHK. Joaquim is now person-in-charge of the Single Cell Omics Core (SCOC) as well as the Genomics Core (Sequencing), which aims to provide single-cell omics solutions to users.

Webpage:

<https://www2.sbs.cuhk.edu.hk/en-gb/research/core-laboratories/single-cell-omics-core>

Service details:

1a. NanoString in-situ Spatial Transcriptomics Profiling

- A. Service item: NanoString CosMx Spatial Transcriptomics assay
- B. Format: Package, from sample to data, **NO** sequencing needed
- C. Sample input: Sample sections (FFPE/FF) on glass slide (with specific limitation)
- D. Assay area: 15mm x 20mm
- E. Assay resolution: 0.5 μ m
- F. RNA capture: Partial transcriptome (6k genes for human; 1k genes for mouse)
- G. Species supported: Human, mouse
- H. Items included: Spatial transcriptomics assay, default data run on AtoMx pipeline, all consumables inclusive
- I. Service duration: 5-10 full working days

1b. Service workflow (NanoString CosMx):

- A. Sample preparation on slide (to be done by users)
- B. Sample quality control (separately in tubes)
- C. Spatial RNA probe hybridization and cell segmentation
- D. Field of view (FOV) selection
- E. Sample imaging and data acquisition

2a. 10x Visium Spatial Transcriptomics

- A. Service item: Visium Spatial Transcriptomics (10X Genomics)
- B. Format: Package, from sample to sequencing library, sequencing*
- C. Sample input: Sample sections (FFPE/FF) on glass slide (with specific limitation)
- D. Assay area: 6.5mm x 6.5mm (standard/HD); 11mm x 11mm (standard)
- E. Assay resolution: 55 μ m (standard); 2-8 μ m (HD)
- F. RNA capture: Whole transcriptome (WTA)
- G. Species supported: Human, mouse, others (special order)
- H. Items included: Spatial transcriptomics assay, cDNA cleanup, sequencing library prep and QC, all consumables inclusive
- I. Order quantity: in every 2 reactions
- J. Price: \$15,000-30,000 HKD per reaction (assay dependent)
- K. Service duration: 3 full working days

*Sequencing **CAN BE** included as an optional item in this package*

2b. Service workflow (10x Visium):

- A. Sample preparation on slide (to be done by users)
- B. Sample quality control (separately in tubes)

- C. Spatial RNA capture and barcode labelling
- D. cDNA cleanup and PCR amplification
- E. cDNA quality control
- F. Sequencing library preparation
- G. Library quality control and sequencing

Precautions:

- A. User of this service are required to fill in the “Sample Submission Form” provided by the Core Laboratories, SBS.
- B. All users **MUST** declare the nature of sample(s) submitted to SCSOC **FREE** of any bio-hazardous material.
- C. An initial assessment of cell quality will be conducted for the generation of data with optimal quality. Users may take the risk of sub-optimal data quality if the initial sample quality check fails.
- D. Upon service booking, a copy of the confirmed service form will be forwarded to both the end user as well as the corresponding PI.
- E. Initial sample submission evaluation (sample quality, amount, etc) is recommended to optimize sample quality, depending on the sample nature. Potential experimental discussion(s) might be arranged prior to samples submission.
- F. The complete workflow takes approximately 3-7 full working days. As only limited number of samples can be performed per week, users are encouraged to optimize their sample quality before submission. Service bookings are arranged on a first-come-first-serve basis.

Equipment in SCSOC:

- Automated Cell Counter (Cell viability check and counting)
- Light Microscope / Hemocytometer (Manuel cell counting)
- Compact cooling centrifuge
- 10X Chromium iX Controller (Single cell encapsulation)
- PCR workstation
- PCRs, thermomixer, vortex, plate centrifuge
- Qubit 4 Fluorometer (DNA/RNA quantification)
- 10X CytAssist (Spatial omics)
- NanoString CosMx Spatial Molecular Imager
- Slide RapidFISH hybridizer

Equipment in Genomics Core (Sequencing):

- Illumina NextSeq 2000
- Tapestation 4200 (cDNA & sequencing library QC)
- SpeedVac vacuum concentrator