SERS-based single cell phenotype profiling on a microfluidic chip

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Isolating and follow-up characterizing circulating tumor cells (CTCs) is critical but still challenging in diagnosis and treatment of cancers, not only because of their rarity in the blood but highly heterogeneity in the phenotype[1]. Herein, we report an on-chip single cell phenotype profiling strategy based on multiplexed surface enhanced Raman scattering (SERS) signals. CTCs deriving from three different breast cancer cell lines were flowed and trapped by a narrow-gap array in a microfluidic chip. The gap size was designed to efficiently hold up CTCs but allow blood cells to pass through. Then, cocktails of three distinct SERS-labelled aptamer-vectors were flowed into the chip, which are able to specifically recognize three surface biomarkers on breast cancer cells. Due to the phenotypic difference of cellular subgroups, the SERS spectra gathered from each cell lines show distinct patterns in accordance with the expression level of surface biomarkers[2]. Using multivariate analysis method, we analyzed the three surface biomarkers of three breast cancer subtypes with a single cell resolution.

Fig.1 shows the workflow of the SERS-based cell phenotype profiling strategy. Fig.1c displays the distinct typical spectra measured from single captured breast cancer cell that treated by a cocktail of SERS vectors. Owing to the variant biomarkers expression level on the surface of cells, the corresponding SERS signature shows different intensity. We clearly observed the spectral pattern difference among the three cell subpopulations and separate them utilizing multivariate analysis method (Fig.1d).

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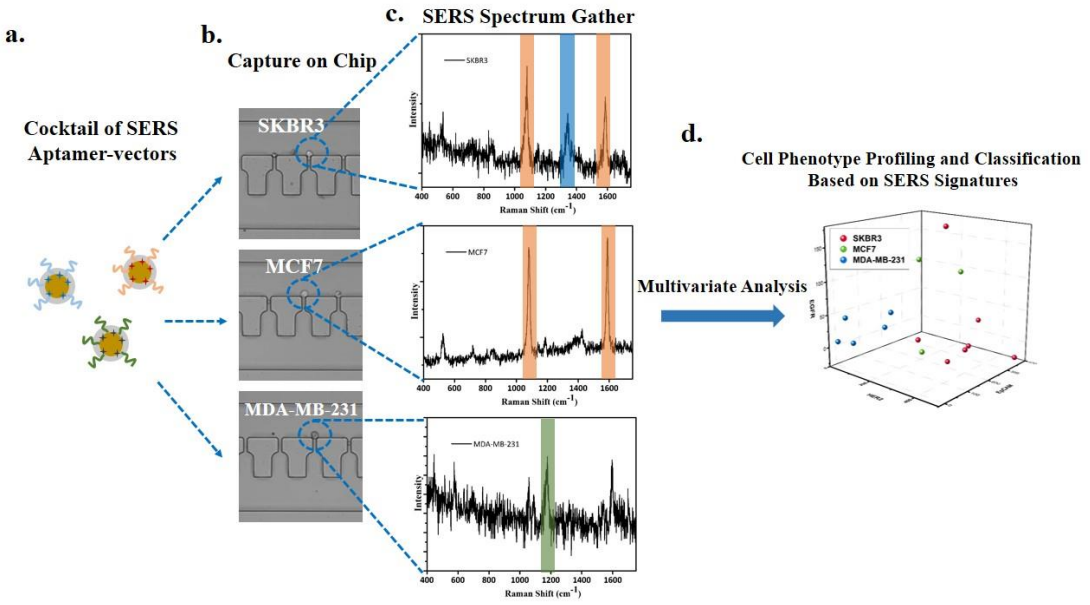

Fig. 1 The workflow of the SERS-based cell phenotype profiling strategy. CTCs were captured using a narrow-gap array in a microfluidic chip (b). Three distinct SERS labeled aptamer vectors (a) were fabricated and injected into the chip for cell phenotype profiling. The overall SERS spectrum (c) was gathered from each single cell on the chip. Finally, the collected SERS spectra were analyzed by multivariate analysis method and output the cellular phenotype information.

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