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Single cell transcriptome analysis upon MCF-7 breast cancer

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Background

During cancer progression, the genome and epigenome of each cancer cell mutate constantly, leading to a diverse transcriptome in a cancer tissue. Such diversity results in variations in drug response among individual cancer cells and is responsible for poor prognosis. It is therefore important to reveal the diversity in the transcriptome profiles of single cancer cells, in order to further understand how the diversified cancer cells interplay to make a cancer cell population capable of escaping immune surveillance and respond poorly to drug treatment.

Materials and methods

Here, we adopt the recently published single cell transcriptome (SCT) analysis protocol and evaluate its reliability using RNA- seq approach on analysis of housekeeping (HK) gene expression as a control, and describe four SCT libraries and one 5,000-cell transcriptome library generated from MCF-7 breast cancer cells.

Results

The SCT libraries and the 5000-cell library mapped to 11,534, 12,053, 10,805, 12,533, and 13,032 known genes, respectively. Among the four SCT libraries, there were 61-85% and 76-91% overlaps at the exon and gene levels, respectively. Moreover, out of 143 HK genes previously selected by two independent groups, 140 were found to be consistently expressed and 1 was unexpressed in all five libraries, whereas the other 2 HK genes were expressed only in some single cells, suggesting a high sensitivity and reproducibility of the SCT approach.

Conclusions

Comparison between genes constitutively expressed in all libraries (14,429) and genes differentially expressed only in some libraries (7,068) revealed that most of the differentially expressed genes are either extracellular proteins, or proteins involved in synaptic activities or metabolism. Taken together, our data demonstrate a high degree of reproducibility of SCT analysis and suggest a plausible 'collaboration' between cancer cells on secretion, nerve development and metabolism.

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