Commentary

Recent news on Single-Cell Identification and Quantification

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Single-cell technologies are revolutionizing biology but are today mainly limited to imaging and deep sequencing. However, proteins are the main drivers of cellular function and in-depth characterization of individual cells by mass spectrometry (MS)-based proteomics would thus be highly valuable and complementary.

The top20 highest differentially expressed genes were selected, but only the aforementioned ones were also identified in our data. This scoring method yields the average expression on the provided set of genes minus the average expression on a reference set of genes, for each cell. The reference set is chosen to mirror the average expression of the target gene set.