THE ROLE OF SINGLE-CELL GENOMICS IN HUMAN GENETICS

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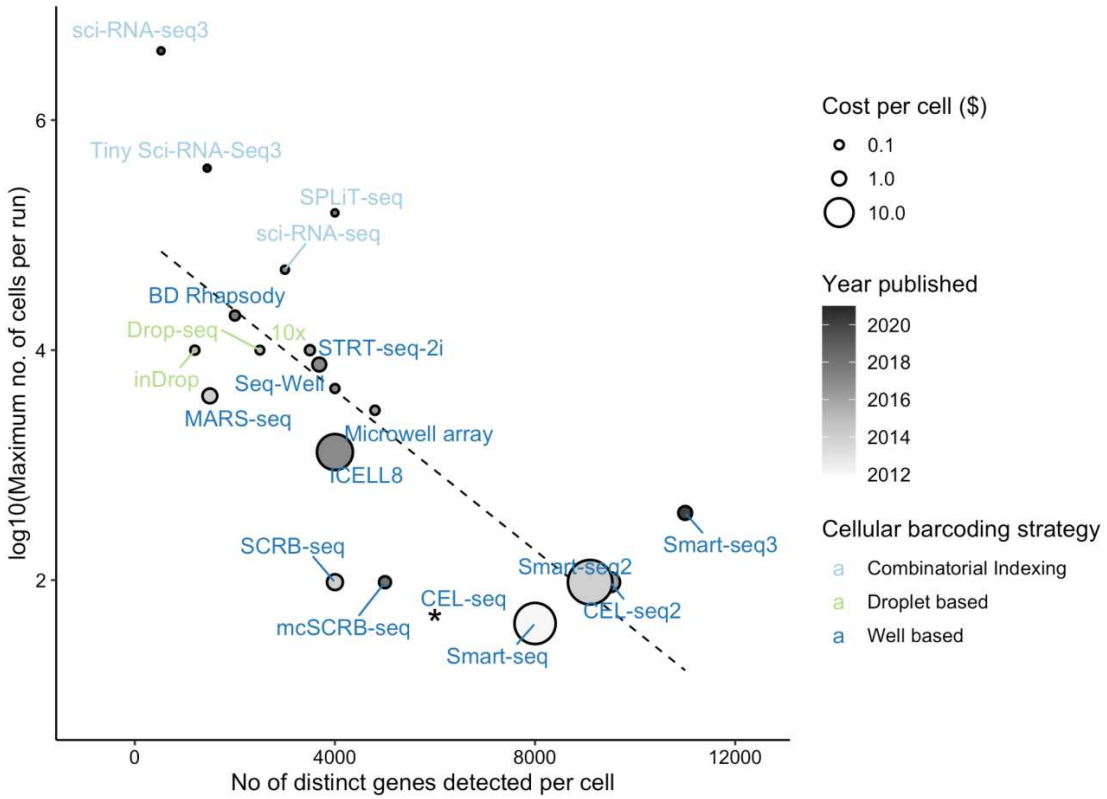
SUPPLEMENTARY FIGURE



Supplementary Figure 1. Comparison of sc-transcriptome-seq technologies. The various commercial and non-commercial sc-transcriptome-seq technologies are compared based on the maximum number of cells sequenced, the number of genes detected per cell, the year of publication (or the launch of the commercial product), and the cellular barcoding strategy. The displayed information is based on the first publication of the technology, whenever available; otherwise data was collected from comparative studies[1, 2]. The cellular throughput of most of the well based methods can at least theoretically be higher by using larger plates (e.g., 384- or 1536- instead of 96-well plates), which in general also reduces the cost per cell. The cost is for library preparation and excludes sequencing. The dashed black line is a linear fit to the log10-transformed data. In general, the technologies above the line tend to be superior. * Cost not available in the publication or in comparative studies.

REFERENCES

1 Comparative Analysis of Droplet-Based Ultra-High-Throughput Single-Cell RNA-Seq Systems. *Mol Cell* 2019;**73**:130–42.e5.

2 Ziegenhain C, Vieth B, Parekh S, Reinius B, Smets M, Leonhardt H, Hellmann I, Enard W. Comparative Analysis of Single-Cell RNA Sequencing Methods. doi:10.1101/035758