Read the paragraphs below, adapted from the original paper, and try to share all the information with your colleague. Your partner is going to ask you a few questions and, without double checking in the text, you should try to give the most complete description about the information on Study level:

| **Hydrop enables droplet-based single-cell ATAC-seq and**  **single-cell RNA-seq using dissolvable hydrogel beads**  Florian V De Rop , Joy N Ismail , Carmen Bravo González-Blas , Gert J Hulselmans , Christopher Campbell Flerin, Jasper Janssens , Koen Theunis , Valerie M Christiaens , Jasper Wouters , Gabriele Marcassa , Joris de Wit , Suresh Poovathingal , Stein Aerts  **In order to increase the sensitivity and user-friendliness of open-source microfluidic protocols, and to provide a more flexible and open platform, we developed HyDrop, a new hydrogel-based droplet microfluidic method for high-throughput scRNA-seq or scATAC-seq encompassing three protocols. The first protocol involves creating dissolvable hydrogel beads with custom oligos that can be released in the droplets, for that we adapted inDrop’s original isothermal extension bead barcoding protocol (Zilionis et al., 2017) to a linear amplification workflow to generate more uniformly barcoded beads. In the second protocol, we applied a custom hydrogel bead production process similar to a recently published protocol (Wang et al., 2020) to generate dissolvable beads, improving barcoded primer release and diffusion. In the third protocol, we adapt both the reaction chemistry and the capture sequence of the barcoded hydrogel bead to capture mRNA, and demonstrate a significant improvement in throughput and sensitivity compared to previous open-source droplet-based scRNA-seq assays (Drop-seq and inDrop). We optimized Drop-seq’s pooled template-switching reverse transcription strategy for application inside the cell/bead emulsion, and optimized the assay’s sensitivity by testing several different cDNA library preparation strategies.**  **Similarly, we applied HyDrop-RNA to flash-frozen mouse cortex and generated 9508 single-cell transcriptomes closely matching reference single-cell gene expression data. Finally, we leveraged HyDrop-RNA's high capture rate to analyze a small population of fluorescence-activated cell sorted neurons from the Drosophila brain, confirming the protocol's applicability to low input samples and small cells. HyDrop is currently capable of generating single-cell data in high throughput and at a reduced cost compared to commercial methods, and we envision that HyDrop can be further developed to be compatible with novel (multi) omics protocols.**  **The data have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO Series accession number GSE175684 ) and on SCope (https://scope.aertslab.org/#/HyDrop/\*/welcome). Source data files have been provided for Figures 2a, 3a, 3b, 3c and 3i, and can be regenerated data analysis tutorials for HyDrop.**   | **FUNDING** |  | | --- | --- | | **H2020 European Research Council (724226\_cis- CONTROL)**  **KU Leuven (C14/18/092)**  **Fonds Wetenschappelijk Onderzoek (G0B5619N)**  **Michael J. Fox Foundation for Parkinson's Research (ASAP-000430)**  **Aligning Science Across Parkinson's (ASAP-000430)** | **Foundation Against Cancer (2016-070)**  **Stichting Tegen Kanker**  **Belgian Cancer Society**  **Fonds Wetenschappelijk Onderzoek**  **VIB Tech Watch** |   **The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.** |
| --- | --- | --- | --- | --- |

**Question to make to your partner:**

1. What is the Title of the project?
2. Can you give me a Summary of the study (project)?
3. What are the aims?
4. Can you tell me the authors?
5. What were the funds for this project?
6. What methods were used to achieve the desired results?
7. Can you tell me the licence and id for data sets?
8. What was the documentation structure, such as folder structure and file naming?