Read the paragraphs below, read the method and try to create a stepwise protocol based on the paper description. Once you finish, discuss with the person next to you and make a small bullet list of what is missing to become a real, complete and reproducible protocol.

1. “The resulting emulsion was collected in aliquots of 50 μL total volume and thermocycled according to the RT program (42°C for 90 min, 11 cycles of [50°C for 2 min, 42°C for 2 min], 85°C for 5 min, followed by a final hold on 4°C). 125 μL of recovery agent (20% PFO in HFE), 55 μL of GITC Buffer (5 M GITC, 25 mM EDTA, 50 mM Tris-HCl pH 7.4) and 5 μL of 1 M DTT was added to each separate aliquot of 50 μL thermocycled emulsion and incubated on ice for 5 min.”
2. Barcode reads were trimmed to exclude the intersub-barcode linear amplification adapters using a mawk script. Reads were then mapped and cell-demultiplexed using STARsolo ([Kaminow et al., 2021](https://elifesciences.org/articles/73971#bib16)) in CB\_UMI\_Complex mode. The resulting STARsolo-filtered count matrices were further analyzed using Scanpy ([Wolf et al., 2018](https://elifesciences.org/articles/73971#bib45)). ~~In short, cells were filtered on expression of a maximum of 4000 genes, and a maximum of 1% UMIs from mitochondrial genes. Genes were filtered on expression in a minimum of three cells. Potential cell doublets were filtered out using a Scrublet (~~[~~Wolock et al., 2019~~](https://elifesciences.org/articles/73971#bib46)~~) threshold of 0.25.~~
3. The [real protocol](https://www.protocols.io/view/hydrop-rna-v1-0-dm6gpwqjjlzp/v2?step=5) can be found in this link so you can take a look together.
4. The [real protocol](https://github.com/aertslab/hydrop_data_analysis/blob/main/HyDrop-RNA_publicdata_comparison/3b_indrop_1_naive_mapping.ipynb) can be found in this link so you can take a look together.