Our lab is looking for a postdoc with single-cell experience.
Interested? Mail to An.Goris@kuleuven.be

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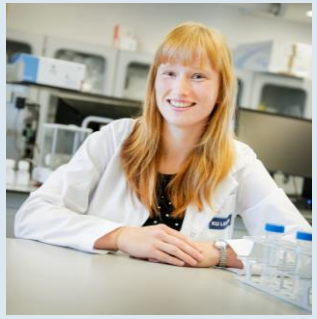
Targeted single-cell transcriptomics for studying genotype-phenotype relationships

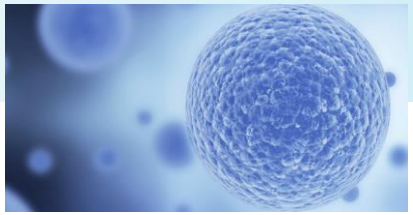


Lies Van Horebeek[1], Klara Mallants[1], Nina Dedoncker[1], Suresh Poovathingal[3], Bénédicte Dubois[1,2], An Goris[1]

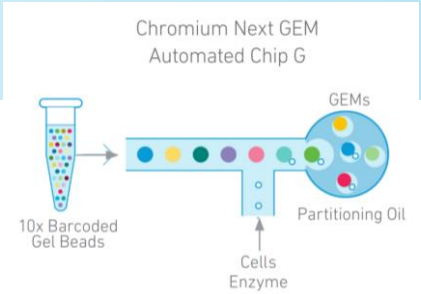
[1] Laboratory for Neuroimmunology, KU Leuven, BE; [2] University Hospitals Leuven, BE; [3] Laboratory of Computational Biology, VIB - KU Leuven, BE

Method: standard 10x + targeted library prep

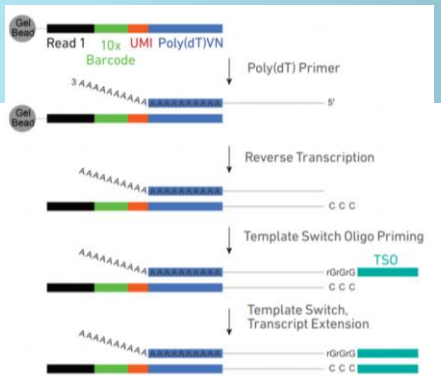
Single-cell sample



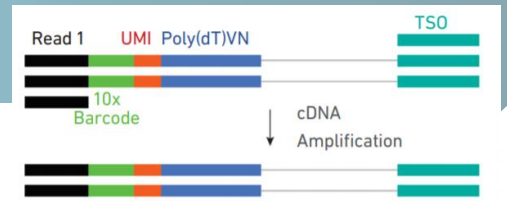
GEM generation



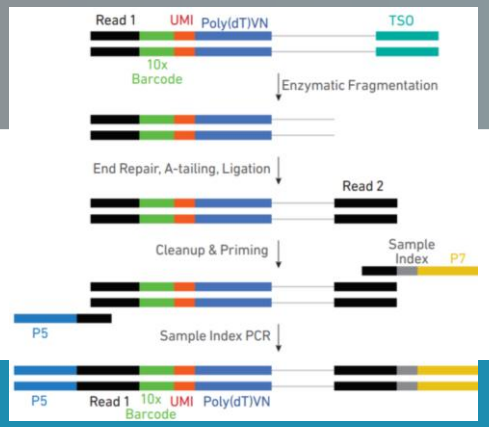
Reverse transcription within GEM



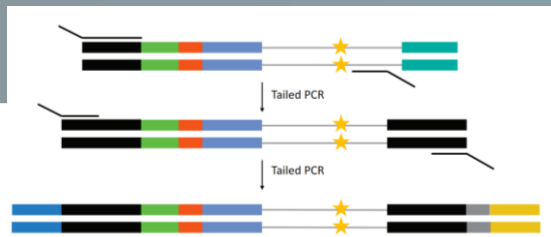
Bulk cDNA amplification



Standard library prep



Targeted library prep*



Sequencing & data analysis

Sequencing: Illumina
Data analysis:

- CellRanger
- Seurat
- VarTrix (SC-GT)

* Similar to: Nam *et al*. *Nature* 2019

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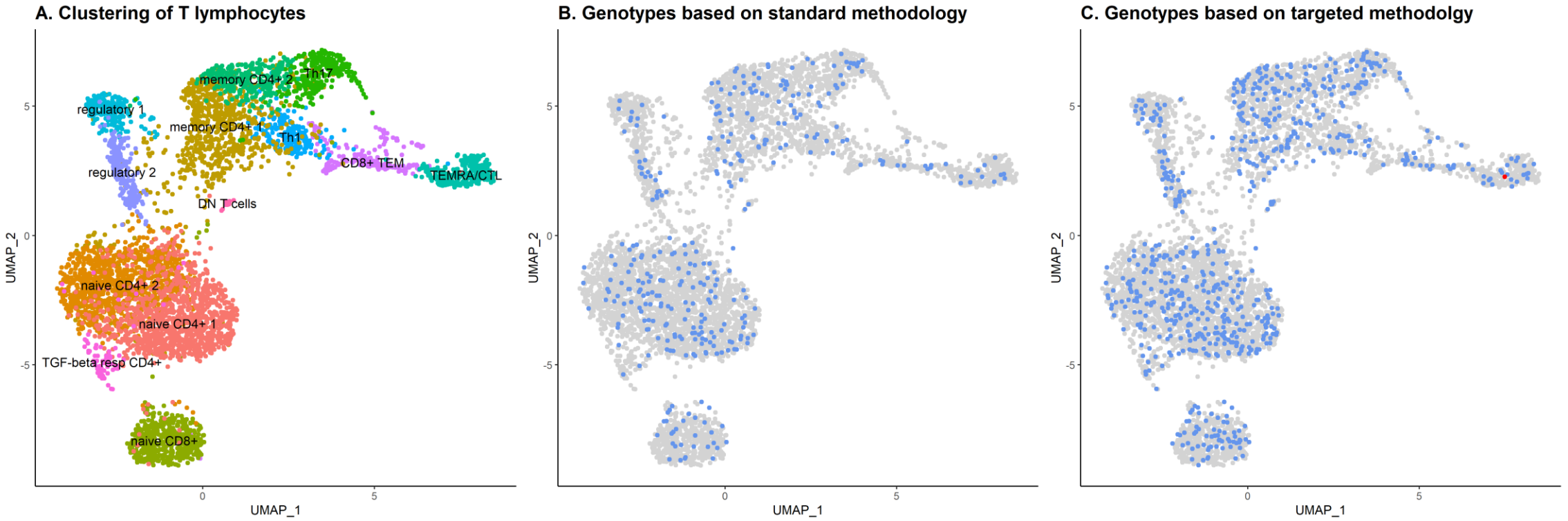
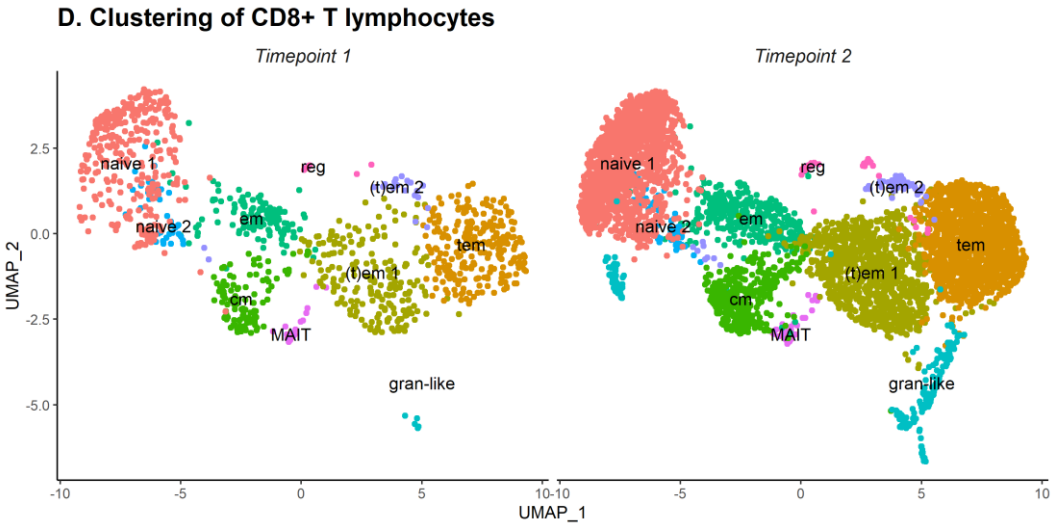
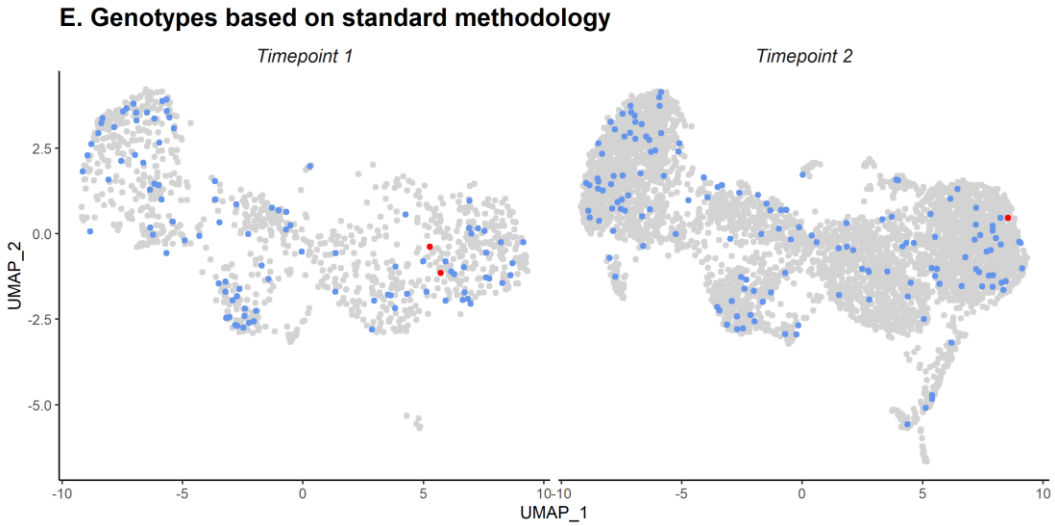
Applied to somatic *TREX1* variant in MS patient

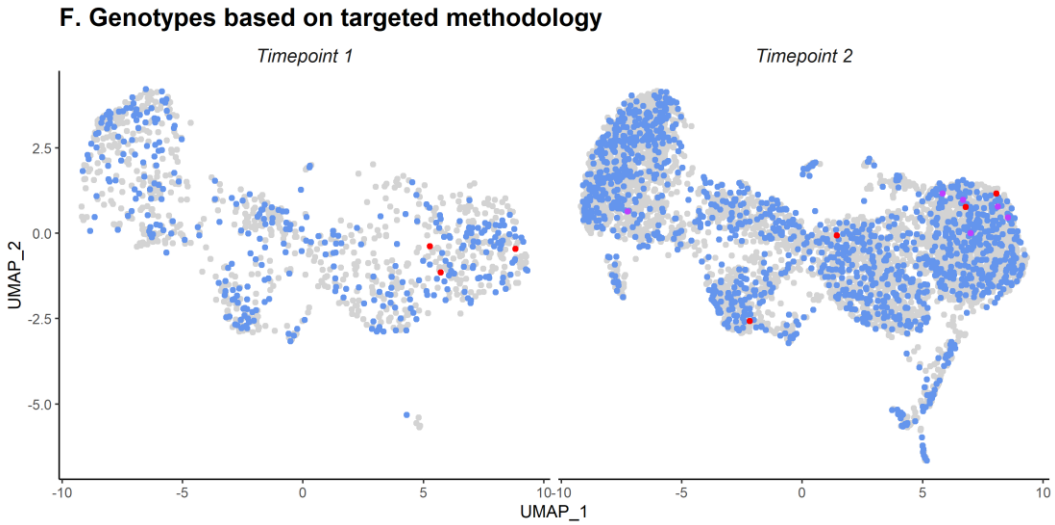


A. Clusters of T lymphocytes, based on gene expression data.
B and C. Genotypes of cells for the somatic *TREX1* variant based on the standard 10x methodology (B) or the targeted methodology (C). Blue: reference allele only, red: alternate allele only, purple: reference and alternate allele, grey: no coverage of variant region.

CD8+ T cells of two timepoints







D. Clusters of CD8⁺ T lymphocytes, based on gene expression data. E and F. Genotypes of cells for the somatic *TREX1* variant based on the standard 10x methodology (E) or the targeted methodology (F).
Blue: reference allele only, red: alternate allele only, purple: reference and alternate allele, grey: no/insufficient coverage of variant region.