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

Targeted single-cell transcriptomics for studying genotype-phenotype relationships



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Lies Van Horebeek¹, Klara Mallants¹, Nina Dedoncker¹, Suresh Poovathingal³, Bénédicte Dubois^{1,2}, An Goris¹

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 Bulk cDNA Reverse transcription Single-cell sample **GEM** generation within GEM amplification TS0 Chromium Next GEM Read 1 UMI Poly(dT)VN ead 1 10x UMI Poly(dT)VN Automated Chip G Barcode Poly(dT) Primer **cDNA** Amplification **Reverse Transcription** CCC Partitioning Oil 10x Barcoded Template Switch Oligo Priming Enzyme CCC Template Switch, Transcript Extension Standard library prep Targeted library prep* Sequencing & data analysis Read 1 UMI Poly(dT)VN Sequencing: Illumina Enzymatic Fragmentation Data analysis: Tailed PCR CellRanger End Repair, A-tailing, Ligation Tailed PCR Seurat ۲ Sample Index P7 Cleanup & Priming VarTrix (SC-GT) Sample Index PCR

* Similar to: Nam et al. Nature 2019

10x UMI Poly(dT)VN

Read 1

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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.

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CD8+ T cells of two timepoints

D. Clustering of CD8+ T lymphocytes Timepoint 1 Timepoint 2 Timepoi E. Genotypes based on standard methodology



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.