Single-cell CRISPR screens in primary human T cells identify regulators of Th2 cell skewing

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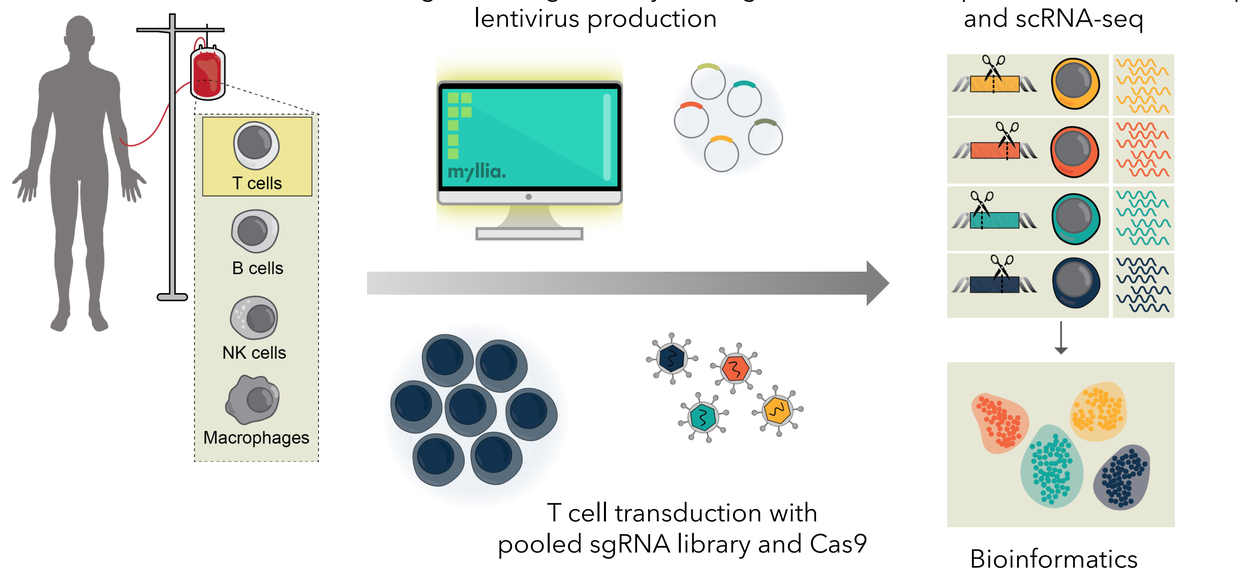
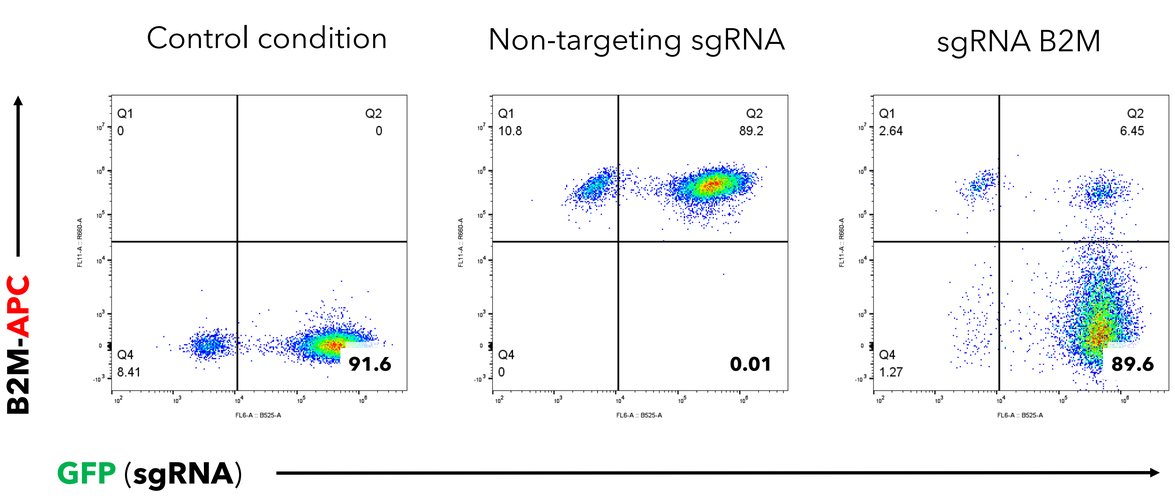
About Myllia Biotechnology

Myllia Biotechnology combines CRISPR screening with single-cell RNA sequencing, leveraging two powerful technologies to enable detailed analysis of complex phenotypes. Using CROP-Seq alongside other high-content screening technologies, we systematically investigate the effects of thousands of genetic perturbations in primary human cells. Our platform delivers a comprehensive view of transcriptomic changes at single-cell resolution, revealing how genetic perturbations shape cellular behaviour and disease mechanisms. This innovative approach supports a wide range of applications, including the discovery of novel drug targets, elucidating the mechanism of action of drugs, and understanding genetic variants linked to disease risk.

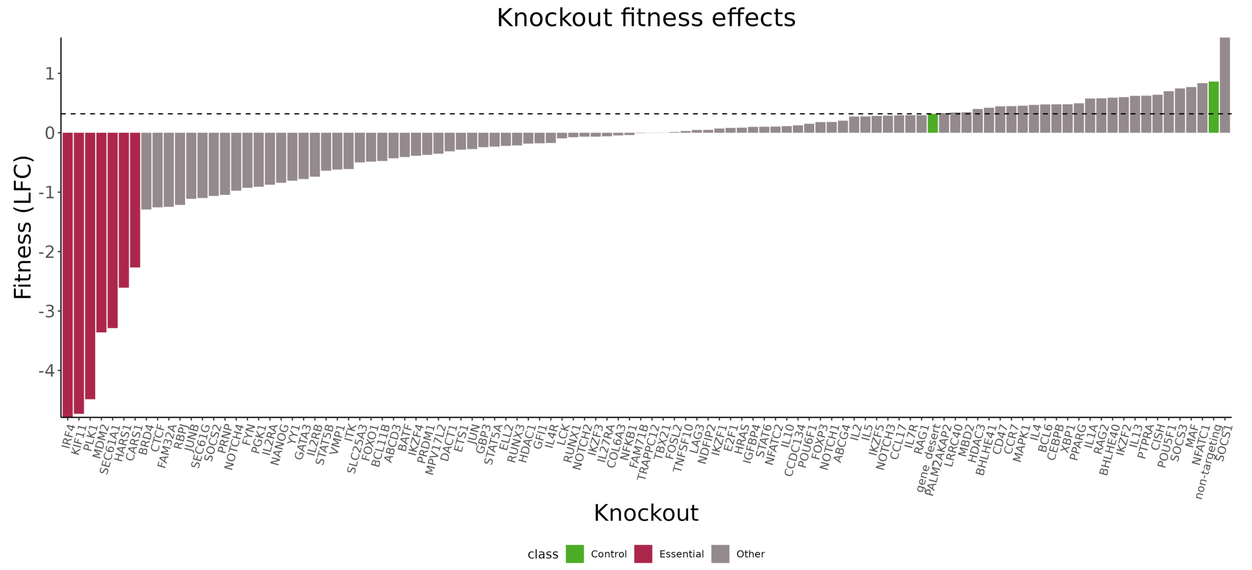
1 CROP-Seq screens in primary human T cells



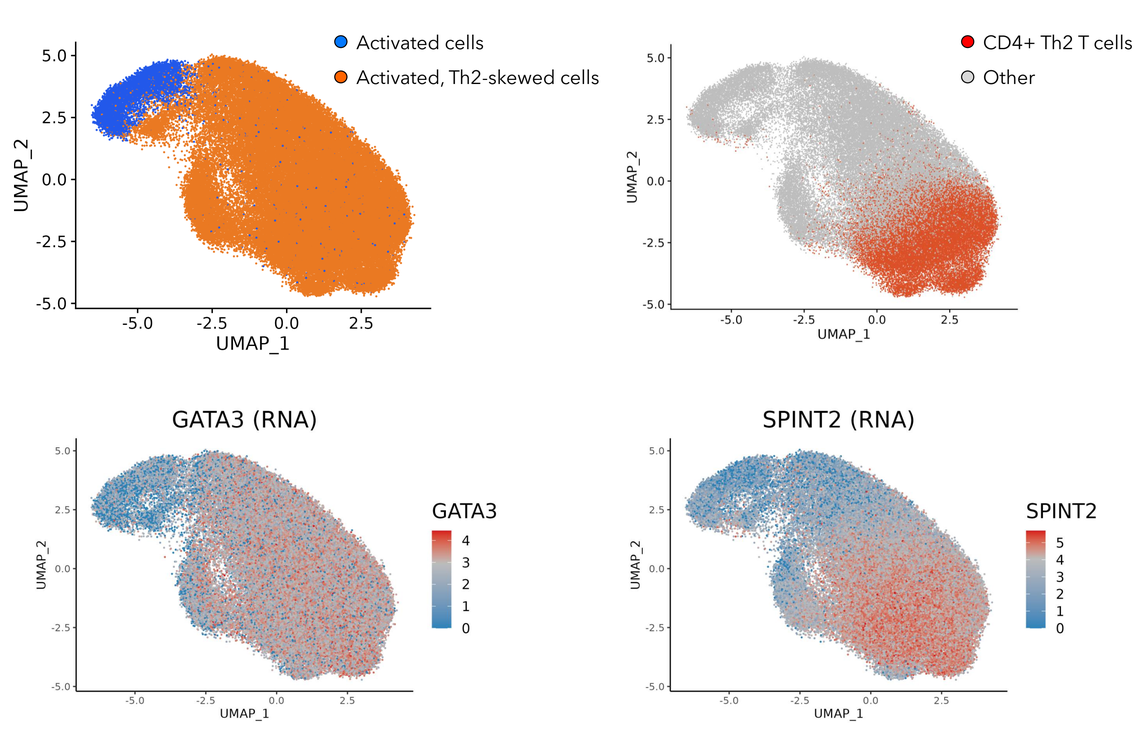
2 Use of CRISPR/ Cas9 in primary T cells



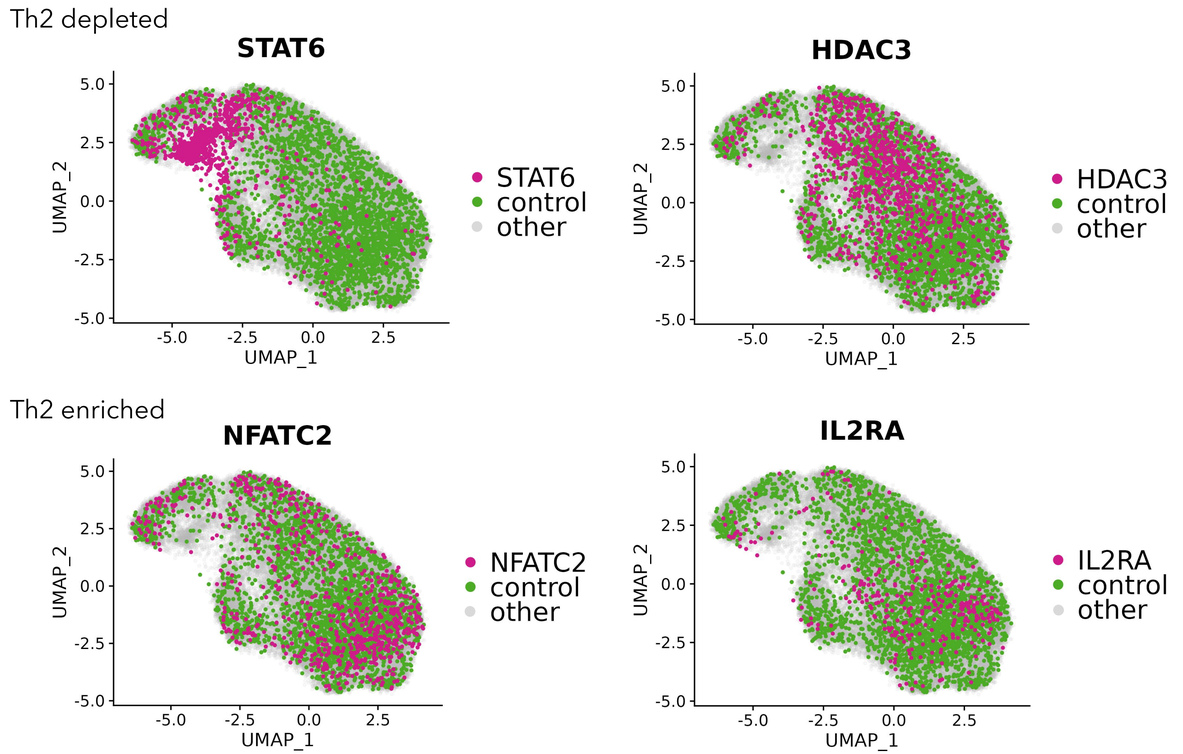
3 Fitness phenotypes of gene KOs in T cells



4 Th2 cell annotation using single-cell RNA-Seq



5 KOs depleted/ enriched in Th2 cells



Conclusions and Outlook

- CROP-Seq combines CRISPR perturbation with single-cell RNA sequencing
- Myllia's pipeline incorporates primary T cell gene editing and differentiation in a single-cell RNA sequencing workflow including custom assay development and bioinformatics
- T cell fate choices can be annotated via transcriptomic signatures and CROP-Seq reveals genetic perturbations which affect Th2 cell differentiation

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