

CROP-Seq Datasets to Train AI/ML-based Foundation Models of Human Cell Biology

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myllia.

- Myllia specializes in **single-cell CRISPR screens linked to scRNA-Seq (CROP-Seq)**
- **CROP-Seq datasets (transcriptomic perturbation data) enable the analysis of genetic perturbations in single cells**, augmenting drug-induced perturbation and helping to dissect the specific mechanism of action of drugs and the mechanism of disease phenotypes
- **CROP-Seq datasets can be used to train AI/ML-based models of human cell biology** which will be used to predict phenotypic changes across cellular backgrounds
- **Training datasets for such AI models need to achieve highest quality standards** and can fuel the creation of digital avatar cells to study drug-induced and/or gene-induced phenotypic consequences *in silico*
- **Myllia provides CROP-Seq datasets off-the-shelf (non-exclusive licensing) and conducts tailor-made CROP-Seq screens** to exactly meet the requirements of your experimental set-up, incl. cellular backgrounds, target gene lists and unbiased NGS read-outs
- **Contact Myllia to explore in-licensing of CROP-Seq data** and check out the proof-of-concept comparative CROP-Seq screens performed across 8 different cancer cell lines

A sizeable CROP-Seq screen performed across 8 human cell lines





