Washington University in St. Louis
Office of Technology Management

CELLTAGS: TRACKING INDIVIDUAL CELLS DURING CELL REPROGRAMMING

Morris, Samantha

Richards, Jennifer

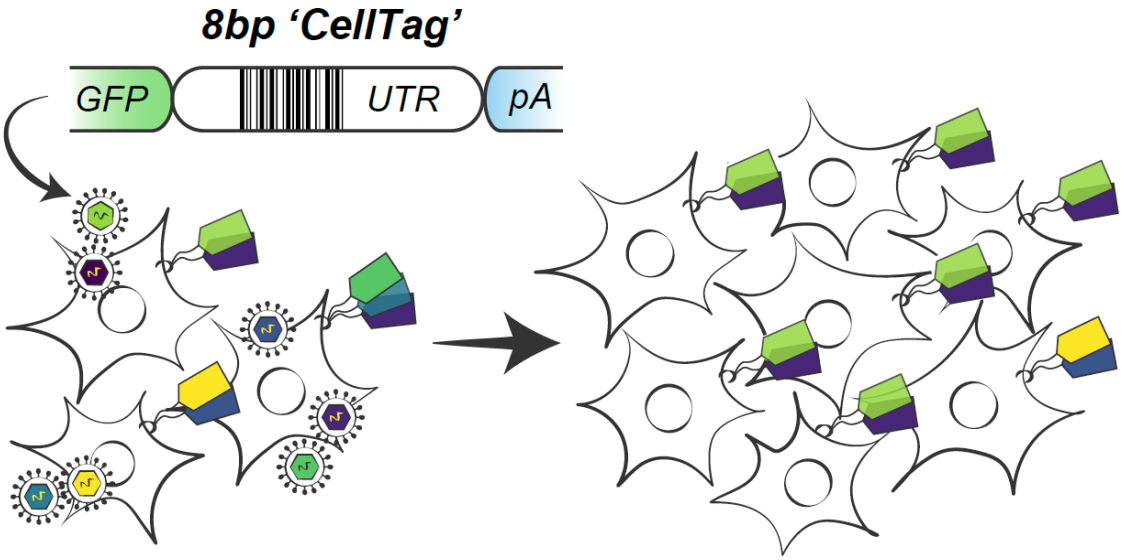
T-018555

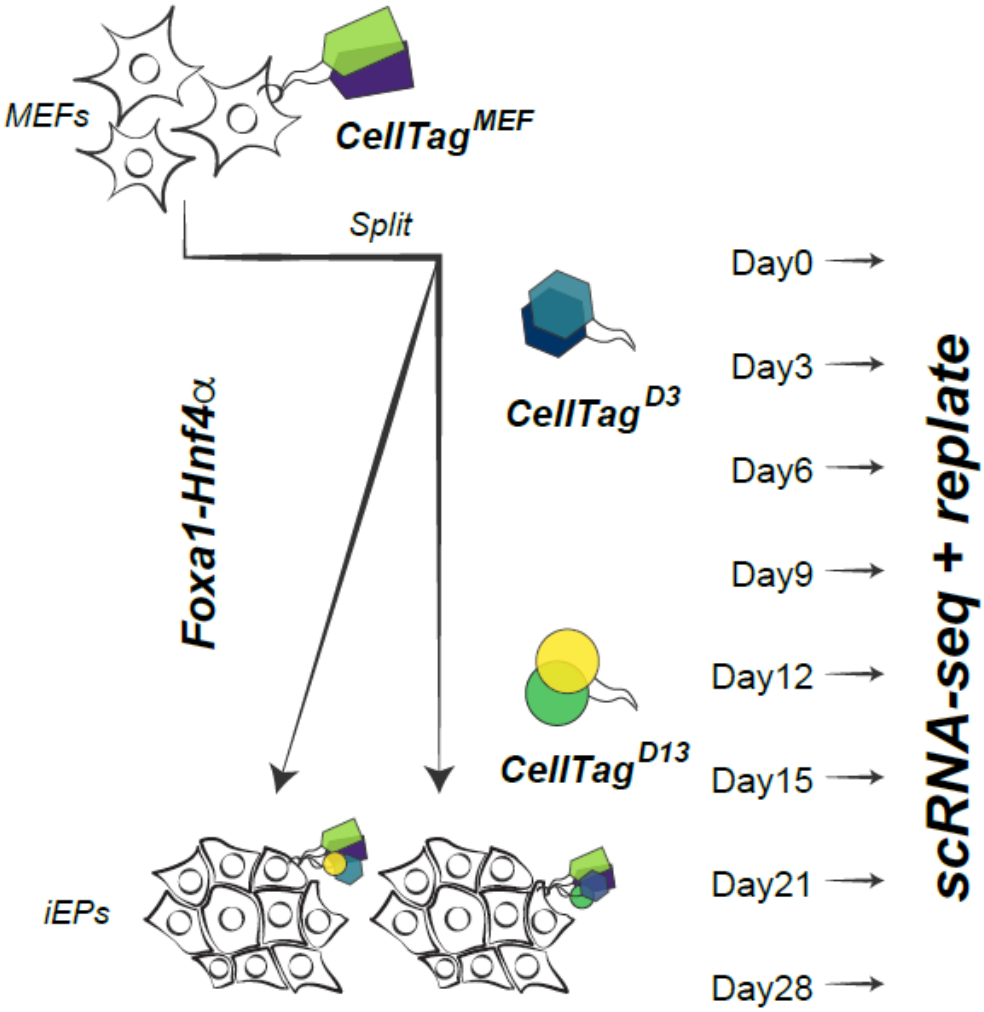
Background

Cell populations are quite heterogeneous yet are typically analyzed in bulk, masking unique behavioral features. This is particularly problematic in cell reprogramming, where in a given population of cells, only a small number complete reprogramming. Single-cell technologies address the issue above but information about lineage is often lost as a result of cell processing. Lineage information is critical in tracing the order of events leading to successful or unsuccessful reprogramming.

Technology Summary

A single-cell resolution lineage-tracing approach used in combination with high-throughput single-cell RNA-sequencing. Individual cells are labeled with genetic indexes, “CellTags”, by lentiviral transduction, in combination with a PolyA signal. The multiplicity of infection is around 5, ensuring that each cell is labeled with multiple CellTags. CellTags consist of unique 8 nucleotide sequences added into the 3’UTR of GFP, resulting in up to 64,000 unique CellTags. CellTags are stable and can be detected at least 11 weeks post-labeling in fibroblasts, kidney, and liver cells. Clonal relationships can be visualized in a correlation matrix and clones are identified using hierarchical clustering based on CellTag overlap.





CellTags and the software for de-multiplexing are both available for licensing.

Related Publications

Biddy et al, 2017 *bioRxiv*

Guo et al, 2018 *bioRxiv*

Patent

Pending