Chimeric Antigen Receptor T (CAR-T) cells are cell-based therapies that have quickly shown great potential to manipulate the immune system and regulatory agencies are starting to approve them to treat diseases such as large B-cell lymphoma. However, understanding the variability of sample preparation and establishing critical quality attributes and parameters (CQAs, CPPs) that are predictive of potency, safety, and consistency for manufacturing purposes are still challenging issues. Hence, the overall goal for this project within the NSF-funded ERC for Cell Manufacturing Technologies is to develop a data-driven modeling pipeline for relating CAR-T cellular phenotype to multi-omics information. To achieve this, we focused on assessing the effect of different culture conditions on quality measures. Also, it aims to evaluate the correlation of these quality measures to omics information (e.g. non-targeted metabolomics) and phenotype output responses (e.g. memory) through an integrative computational pipeline. Several experiments culturing and expanding T cells across different process parameters (e.g. media type) have been conducted. These included synchronized multi-omics measurements (i.e. metabolomics, secretomics) across different laboratories from media samples at early time points and from cell pellets at the end of the expansion process. These were used to collect information regarding cell quality (e.g. memory). The computational tool incorporates the implementation of models such as Random Forest, Gradient Boosted Trees, Support Vector Machines, and Symbolic Regression. These models showed high prediction performance ($R^2$:75%-95%) and strong feature consensus (e.g. IL2R, IL21, MIF) when modeling CD4 memory fraction. Many other growth and memory responses were investigated to characterize T-cells.