SynEcoSys: a standardized scRNAseq database for clinical translation

Singleron

From Single Cell Multi-omics to Precision Medicine

Introduction

The rapid growth of single cell RNA sequencing led to the generation of massive number of datasets covering most tissues in both healthy and disease states. SynEcoSys® offers a comprehensive single cell sequencing data repository that gathers and analyses all these datasets using a standard pipeline.

Testing hypothesis in larger cohorts allows for more robust conclusions. In the case of breast cancer, SynEcoSys® allowed for validation of drug targets and study of mechanisms with multiple published datasets.

SynEcoSys ® a standardized database of scRNAseq data

SynEcoSys ® is an online database providing an extensive collection of single-cell sequencing data from published studies. Datasets are processed with uniform standards of data analysis and cell type annotation to ensure precision and inter-comparability.

For disease-related datasets, all available clinical information associated with the single-cell are collected as sample metadata, such as patient disease stages and disease subtypes. The inclusion of meticulous clinical information highlights SynEcoSys ® as the first-in-the-field single cell sequencing database capable of clinical translations.

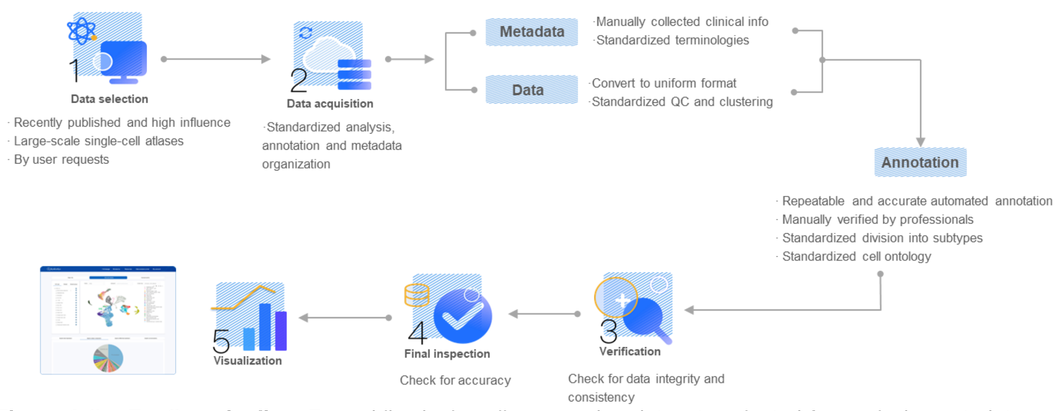


Figure 1 SynEcoSys pipeline. For public single cell sequencing datasets selected for analysis, metadata are collected for each sample presented in the study. Data are analyzed using a standard pipeline and only datasets that meet the quality standards are added to the database. Cells are first automatically annotated, and the annotations are then manually verified. Multiple analysis and visualization modules are available for the exploration of each dataset.

Exploring potential targets in larger cohorts

SynEcoSys® makes it possible to explore gene expression patterns in a lager breast cancer cohort. A core dataset is available for breast cancer that integrates data from six publications (Fig.3A).

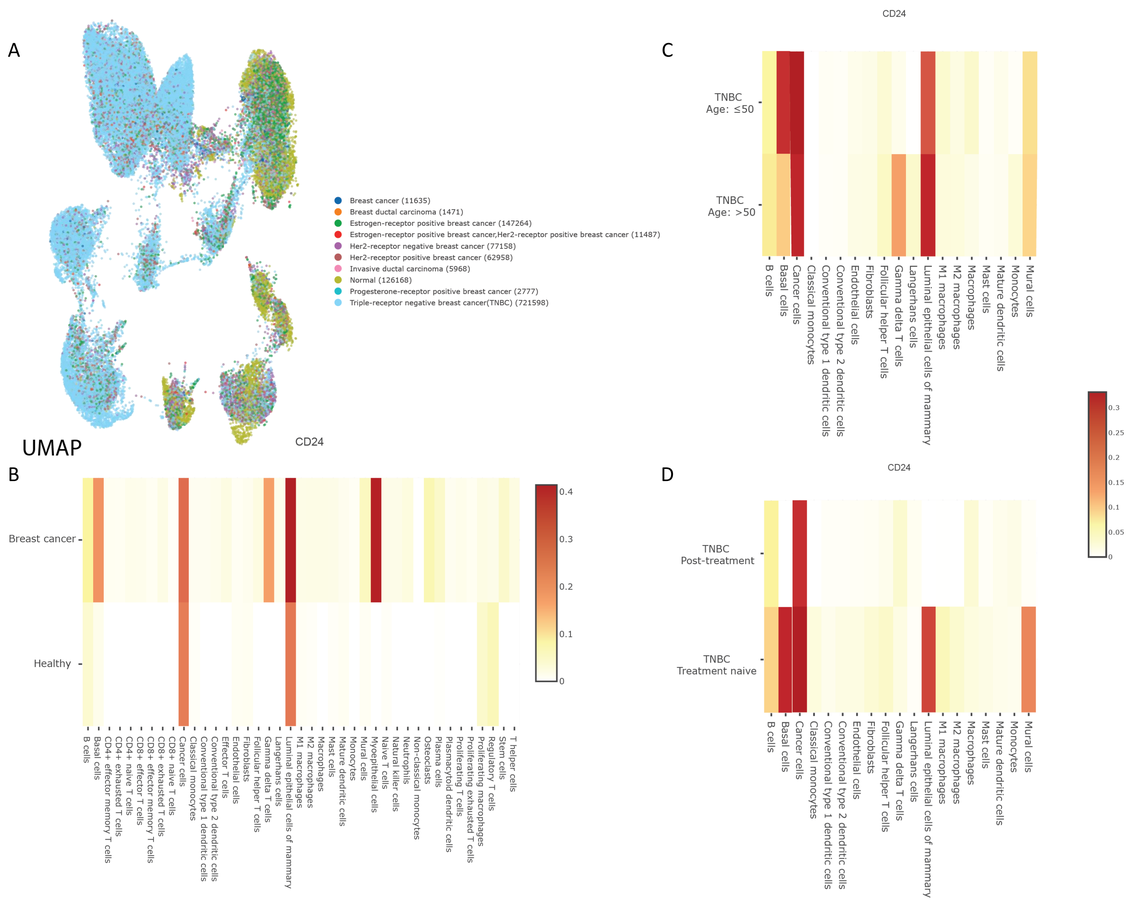
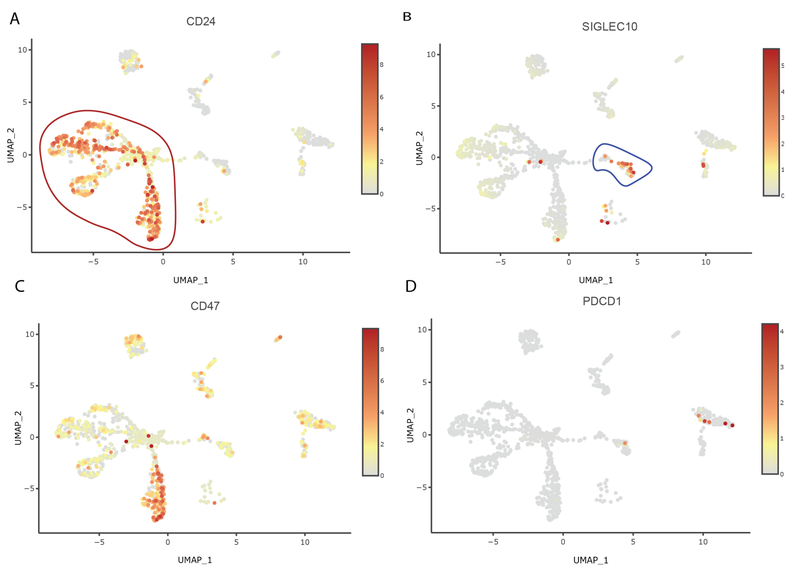


Figure 3 Validating findings in different breast cancer datasets. (A) UMAP representation of breast cancer dataset labeled by disease subtype (SynEcoSys breast breast cancer core dataset of 270 samples covering seven subtypes and normal tissue). (B) CD24 is not only expressed in cancer cells, but also in other cell types both in cancer and healthy samples (C) Expression of CD24 changes with age, more cell types express CD24 in older patients (D) Expression of CD24 changes with treatment, post-treatment CD24 expression becomes restricted to cancer cells.

Expression of CD24 is not exclusive to cancer cells (Fig.3B); Expression of CD24 in other cell types changes with age and treatment (Fig.3C/D).

Breast Cancer – Validation of published results

Cancer cells inhibit the immune function of macrophages using anti-phagocytic signals (Fig.2 C/D,[1,2]), which could potentially compromise the efficacy of immunotherapy for those patients .



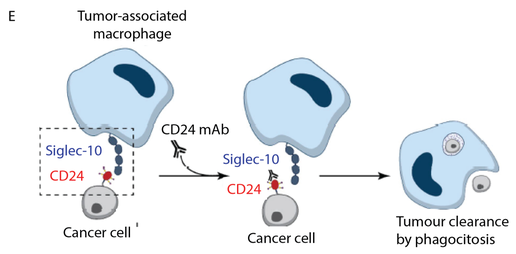


Figure 2 Expression of antiphagocytic signals in TNBC. (A) Expression of CD24 is restricted to cancer cells (red circle). (B) Siglec-10 is exclusively expressed in Tumor associated macrophages (blue circle). (C) Expression of CD47 and (D) PDCD1 is not restricted to any cellular population. (E) Schematic of the interaction between CD24 in the tumor cells and Siglec-10 in the macrophages, the interaction between these proteins inhibits phagocytosis, the blockade of CD24 by a monoclonal antibody prevents these proteins from interacting and the macrophages can perform tumor clearance by phagocytosis (adapted from Barkal, AA *et al*, Nature 2019).

The specificity of CD24 expression in cancer cells along with the restricted expression of Siglec-10 in TAMs, indicates that this interaction is a potential target for immunotherapy.

SynEcoSys Capabilities

SynEcoSys offers a fast-growing scRNAseq database that can be mined for clinical and biological insights.

Every dataset is comprehensively annotated with the clinical and prognostic metadata available for each sample. These annotations can be used for data analysis and visualization using the **CeleLens™** and **CeleViz™** modules.

CeleViz™ is the visualization module and is divided into 5 groups of analysis:

- Gene expression
- Cellular Composition
- Differential Expression
- Cellular Interactions
- Trajectory Analysis

SynEcoSys® is the single cell sequencing data platform to use for clinical translation to easily validate results and find new insights with a few clicks.

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