

scRNA-seq Analysis



Integrate Sc-RNA datasets
GSE148071 (n=42),
GSE131907(n=58)

First-level
clustering (10 cells)

Second-level
clustering (28 cells)

Cell communication
analysis with iTAKL

Pseudotime trajectory
analysis of Neutrophil
differentiation status
by Monocle

GSEA explores functional
in different
differentiation states

Integrate TCGA-LUAD (n=585),
TCGA-LUSC (n=550)
Bulk-RNA cohort

CIBERSORT
annotates the
TCGA cohort

NDRGs obtained
between different
differentiation states

NDRGs mutational
landscape analysis

Bulk RNA-seq Analysis

TCGA cohort 7:3 split
into training set and
internal validation set

GSE81089 as
external validation set

DEGs obtained
from tumor and
normal subgroups

Intersection genes of
NDRGs and DEGs

6 NDRGs associated
with prognosis

Construction of prognostic
risk model based on NDRGs /
reference genes rate by Elastic
Net Regression and
Multivariate Cox

Exploring immune
infiltration in
prognostic risk models

Mock Low-xpression
or Overexpression

Screening small molecule
compounds that
help fight tumors

ROC, nomogram, and KM
verify the performance of
the prognostic model

Exploring the clinical
application value of
prognostic models

GSEA explores pathway
changes after
dysregulation of NDRGs

AutoDock realizes
docking of NDRGs
and compounds