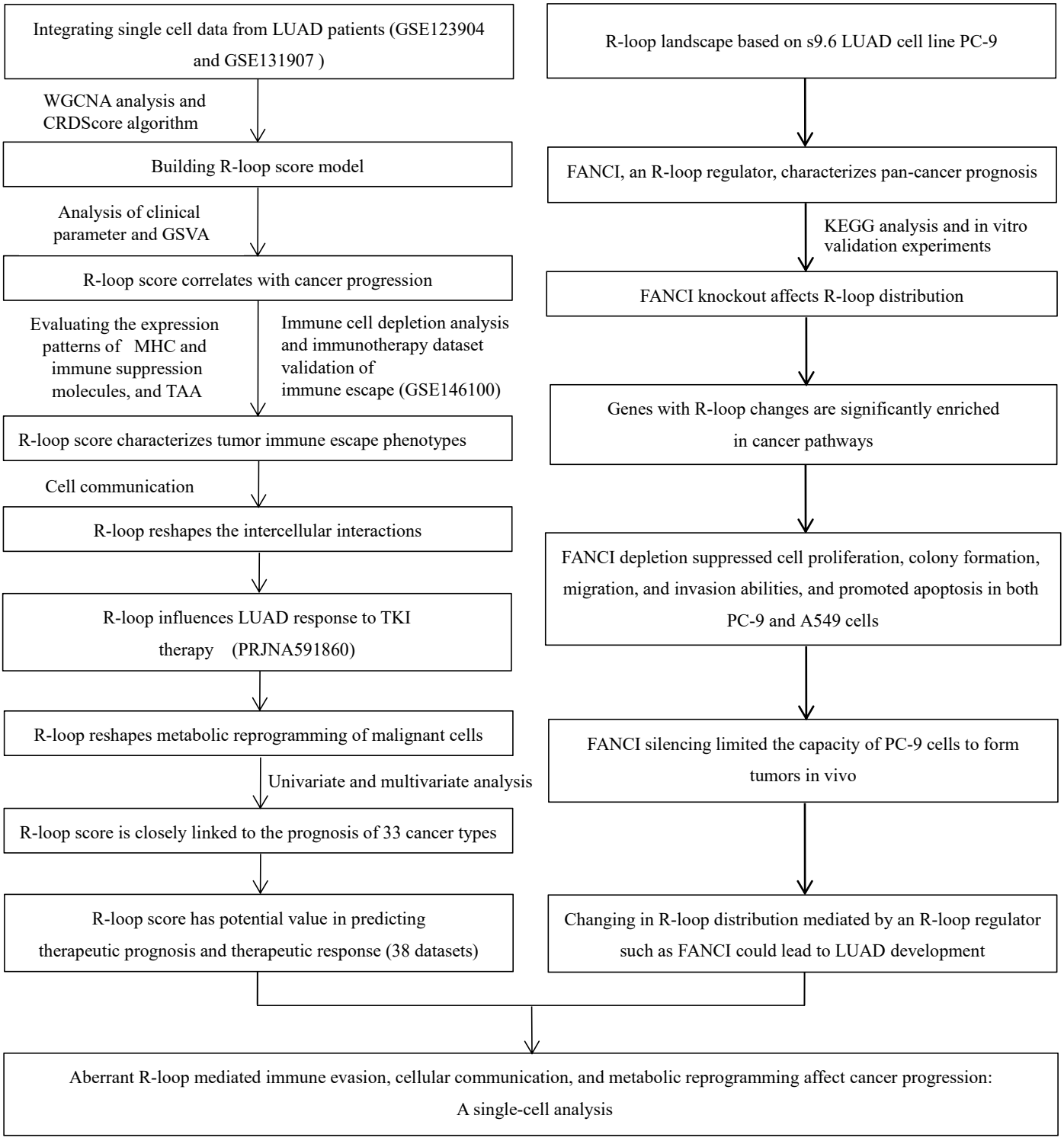
Integrating single cell data from LUAD patients (GSE123904 and GSE131907)
WGCNA analysis and CRDScore algorithm
Building R-loop score model
Analysis of clinical parameter and GSVA
R-loop score correlates with cancer progression
Evaluating the expression patterns of MHC and immune suppression molecules, and TAA
Immune cell depletion analysis and immunotherapy dataset validation of immune escape (GSE146100)
R-loop score characterizes tumor immune escape phenotypes
Cell communication
R-loop reshapes the intercellular interactions
R-loop influences LUAD response to TKI therapy (PRJNA591860)
R-loop reshapes metabolic reprogramming of malignant cells
Univariate and multivariate analysis
R-loop score is closely linked to the prognosis of 33 cancer types
R-loop score has potential value in predicting therapeutic prognosis and therapeutic response (38 datasets)
R-loop landscape based on s9.6 LUAD cell line PC-9
FANCI, an R-loop regulator, characterizes pan-cancer prognosis
KEGG analysis and in vitro validation experiments
FANCI knockout affects R-loop distribution
Genes with R-loop changes are significantly enriched in cancer pathways
FANCI depletion suppressed cell proliferation, colony formation, migration, and invasion abilities, and promoted apoptosis in both PC-9 and A549 cells
FANCI silencing limited the capacity of PC-9 cells to form tumors in vivo
Changing in R-loop distribution mediated by an R-loop regulator such as FANCI could lead to LUAD development
Aberrant R-loop mediated immune evasion, cellular communication, and metabolic reprogramming affect cancer progression: A single-cell analysis