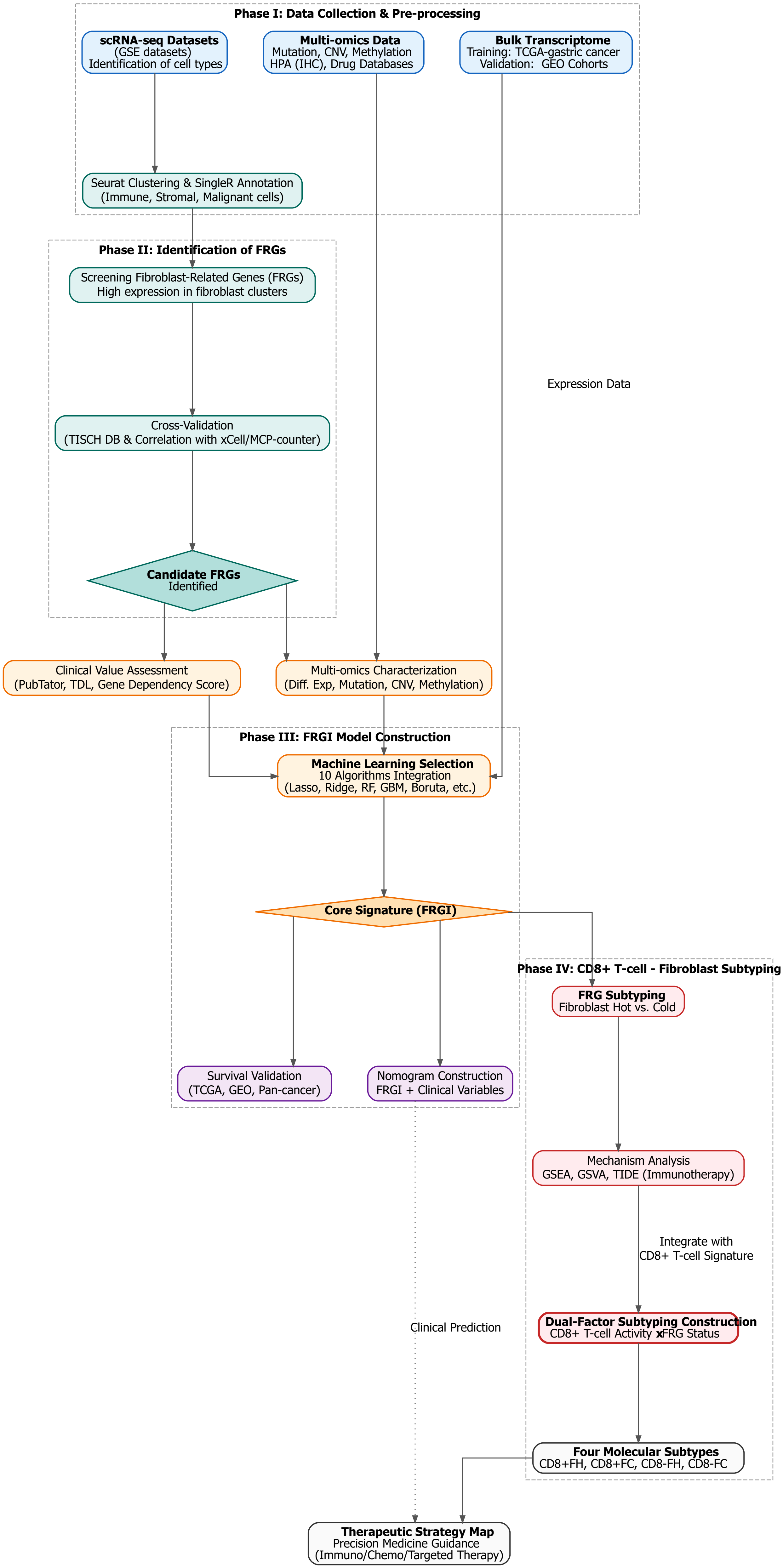
Phase I: Data Collection & Pre-processing
scRNA-seq Datasets
(GSE datasets)
Identification of cell types
Multi-omics Data
Mutation, CNV, Methylation
HPA (IHC), Drug Databases
Bulk Transcriptome
Training: TCGA-gastric cancer
Validation: GEO Cohorts
Seurat Clustering & SingleR Annotation
(Immune, Stromal, Malignant cells)
Phase II: Identification of FRGs
Screening Fibroblast-Related Genes (FRGs)
High expression in fibroblast clusters
Expression Data
Cross-Validation
(TISCH DB & Correlation with xCell/MCP-counter)
Candidate FRGs
Identified
Clinical Value Assessment
(PubTator, TDL, Gene Dependency Score)
Multi-omics Characterization
(Diff. Exp, Mutation, CNV, Methylation)
Phase III: FRGI Model Construction
Machine Learning Selection
10 Algorithms Integration
(Lasso, Ridge, RF, GBM, Boruta, etc.)
Core Signature (FRGI)
Phase IV: CD8+ T-cell - Fibroblast Subtyping
FRG Subtyping
Fibroblast Hot vs. Cold
Survival Validation
(TCGA, GEO, Pan-cancer)
Nomogram Construction
FRGI + Clinical Variables
Mechanism Analysis
GSEA, GSVA, TIDE (Immunotherapy)
Integrate with
CD8+ T-cell Signature
Clinical Prediction
Dual-Factor Subtyping Construction
CD8+ T-cell Activity xFRG Status
Four Molecular Subtypes
CD8+FH, CD8+FC, CD8-FH, CD8-FC
Therapeutic Strategy Map
Precision Medicine Guidance
(Immuno/Chemo/Targeted Therapy)