# Technical Workflow of the CD48 Multi-omics Study in Cervical Cancer

## Stage 1 | Samples

### Sample & Data Acquisition

1. TCGA-CESC cohort (n = 296)
2. GSE168652 single-cell data
3. CTD / GeneCards cervical cancer genes
4. Data preprocessing & QC

## Stage 2 | Analysis

### Bulk Transcriptomic Analysis

1. WGCNA co-expression
2. xCell immune infiltration
3. ML consensus genes (LASSO / RF / SVM-RFE)
4. Cox + timeROC + nomogram

### Single-cell Transcriptomic Analysis

1. Seurat clustering (10 cell types)
2. CellChat communication
3. Pseudotime trajectory (Slingshot / CytoTRACE)
4. scTenifoldKnk knockout

## Stage 3 | Validation

### Functional Validation & Immune Regulation

1. CD48 core protective gene (HR = 0.498)
2. Checkpoint consensus (CD48/CTLA4/HAVCR2/CD86)
3. TIDE immune evasion + drug sensitivity (oncoPredict)
4. CD48-2B4 axis + NKG7 / GZMA effectors

**Legend**

- Data source
- Bulk analysis
- Single-cell analysis
- Validation & immune regulation