

TCGA-SARC RNA-seq and Clinical Data Acquisition

262 Patients (108 Old Age [OA - ≥ 65 yrs], 154 Young Age [YA - 18-65 yrs])

Data Normalization and Filtration using
TCGAbiolinks R package

Differential Gene Expression Analysis (DGEA) using
TCGAbiolinks R package

Significant Differentially regulated genes (sig-DEGs)
Criteria for selection - $(|\log FC|) > 1.5$ and $p \text{ value} < 0.005$
733 sig-DEGs (197 upregulated and 536 downregulated genes)

Functional Enrichment
Analysis (FEA)

Pathways enriched with
dysregulated genes

Transcription Factor
Enrichment analysis

Significant Transcription
Factors (sig-TF's)

Gene-Specific
Survival Analysis

Clinically significant
prognostic markers

Protein Protein
Interaction Network

Significant Hub genes

