

Data Selection & Preprocessing

TCGA colon adenocarcinoma
samples (n = 524)



Filter out normal and metastasis
samples (n = 481)



Filter out samples
with missing clinical data
(n = 475: 225F, 250M)



Normalization
and filtering



Differential Expression Analysis

327 DEGs
(122 Down, 205 Up)



Survival analysis
(CoxPH & KM)

Functional enrichment
analysis



Identification of clinically significant
prognostic Markers