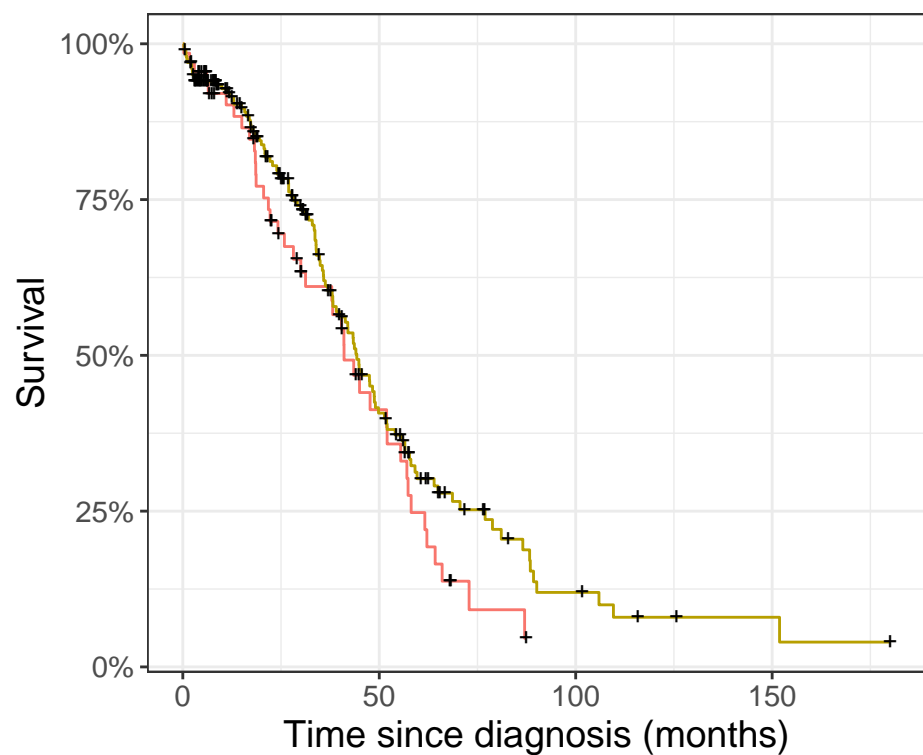


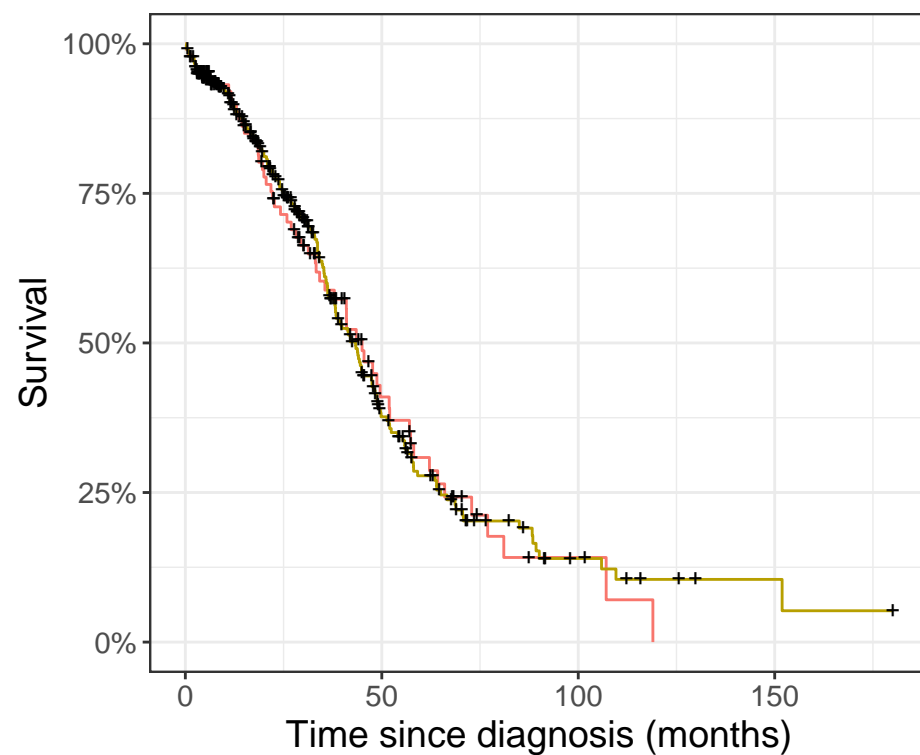
A

TCGA RNA-seq



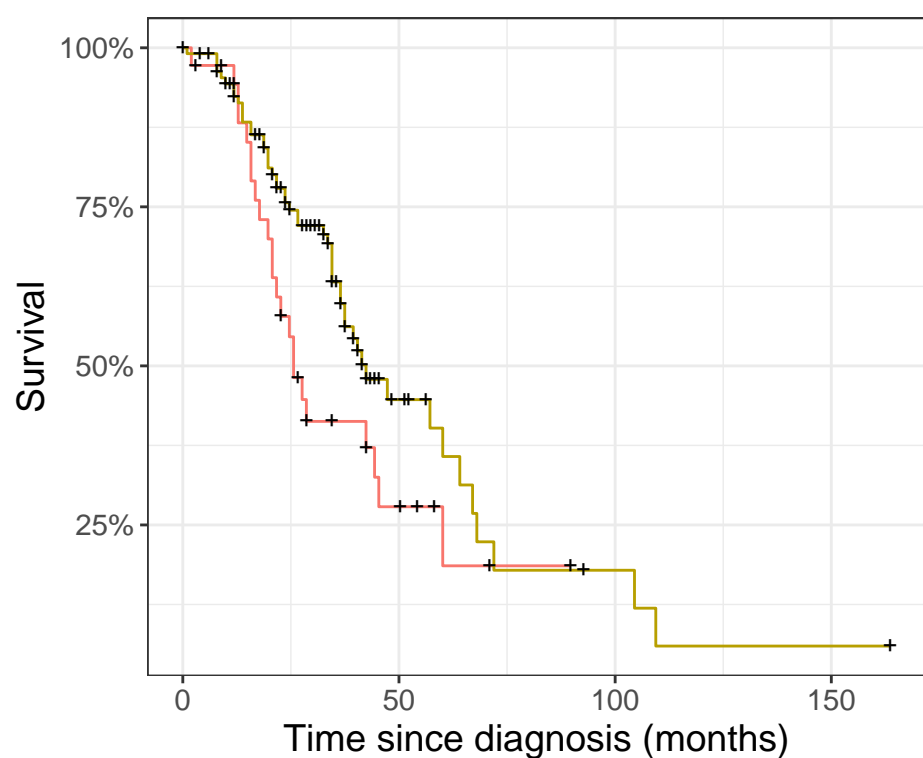
B

TCGA Microarray



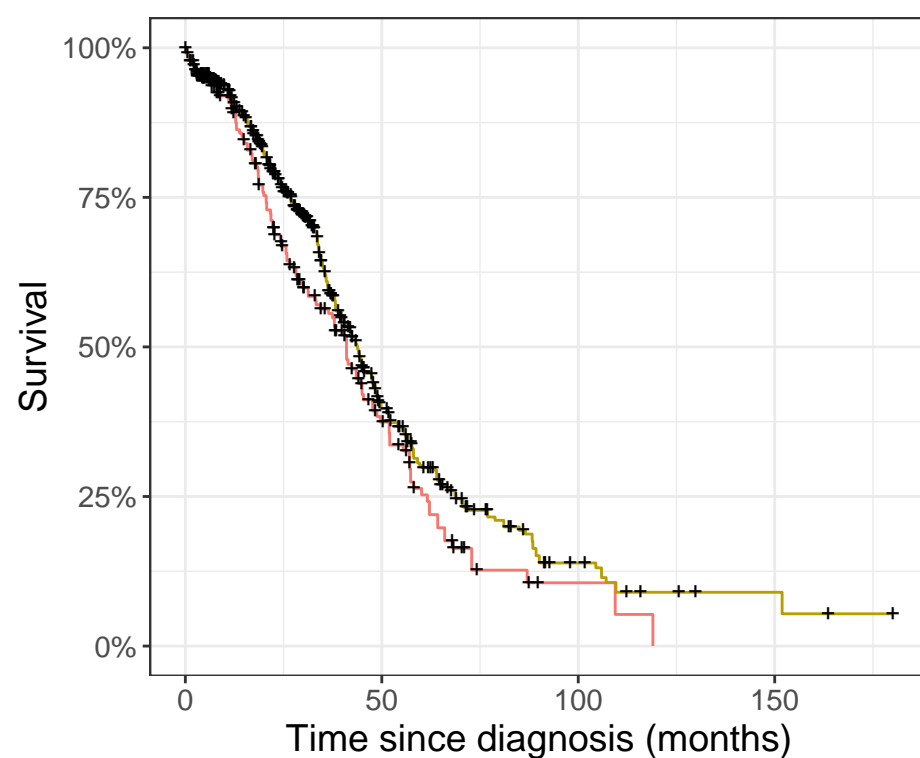
C

Tothill



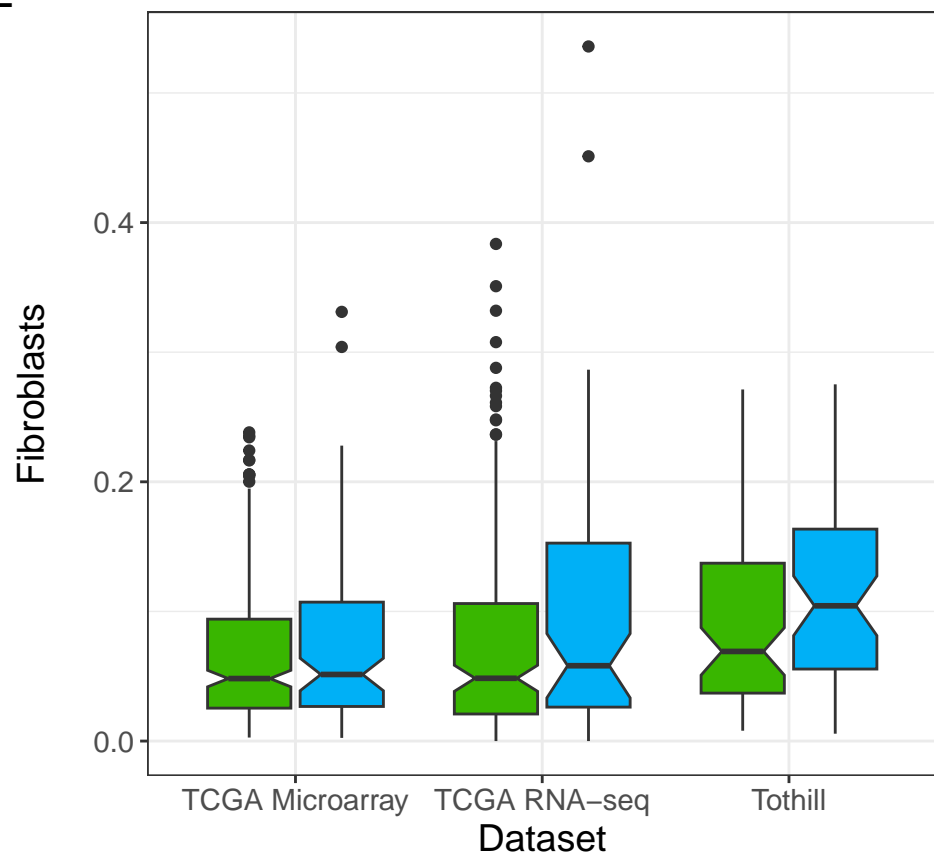
D

All Datasets

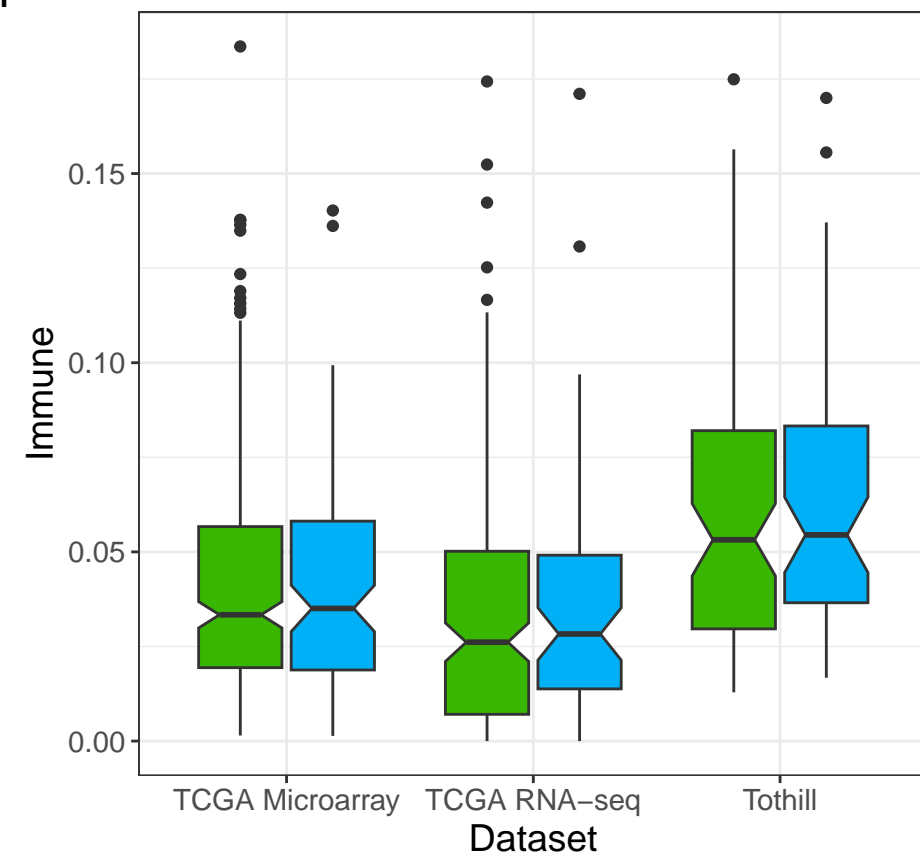


— High fibroblast
— Other

E



F



Debulking status
■ Optimal
■ Suboptimal