The solution is trivial.

▸ We have "standardised features" within every patient to build models

Log-ratio
Take the differences between log(gene A) and log(gene B)

Compare genewise means

ns

array
Corr = 0.631
iden−dist = 1.103

tcga
Corr = 0.747
iden−dist = 3.006

Corr = 0.552
iden−dist = 3.970

sweden
Corr = 0.699
iden−dist = 1.319

Corr = 0.735
iden−dist = 0.424

Corr = 0.622
iden−dist = 4.253

Compare log−ratio means

ns

array
Corr = 0.631
iden−dist = 0.849

tcga
Corr = 0.747
iden−dist = 0.732

Corr = 0.552
iden−dist = 0.749

sweden
Corr = 0.699
iden−dist = 0.783

Corr = 0.735
iden−dist = 0.574

Corr = 0.622
iden−dist = 0.598