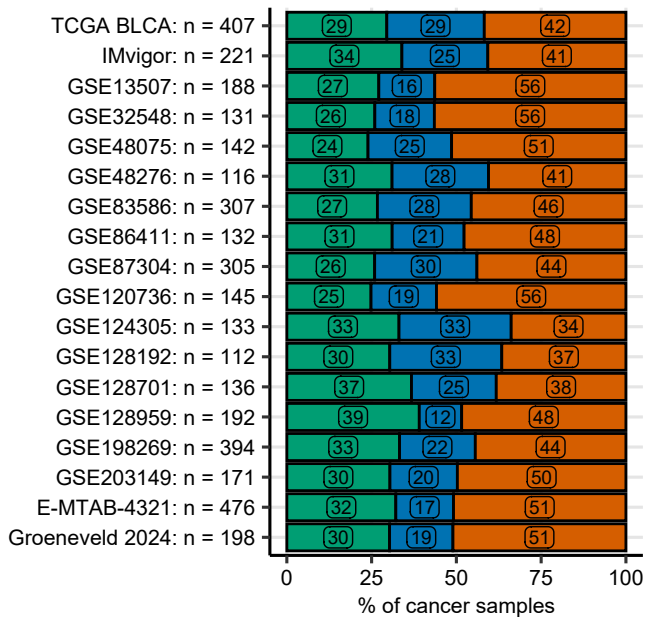
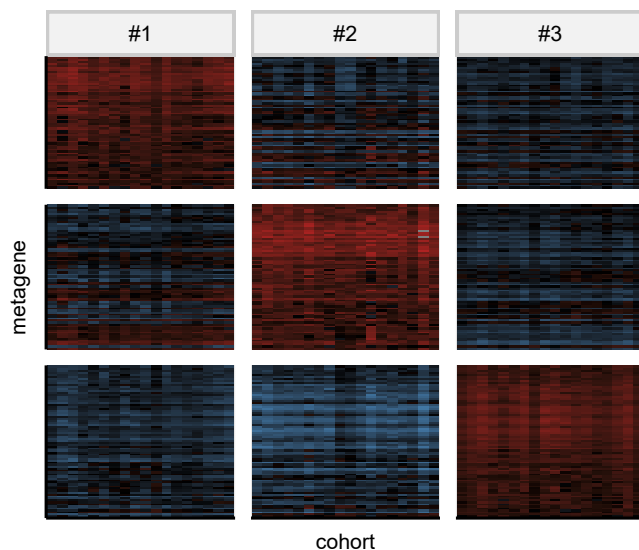
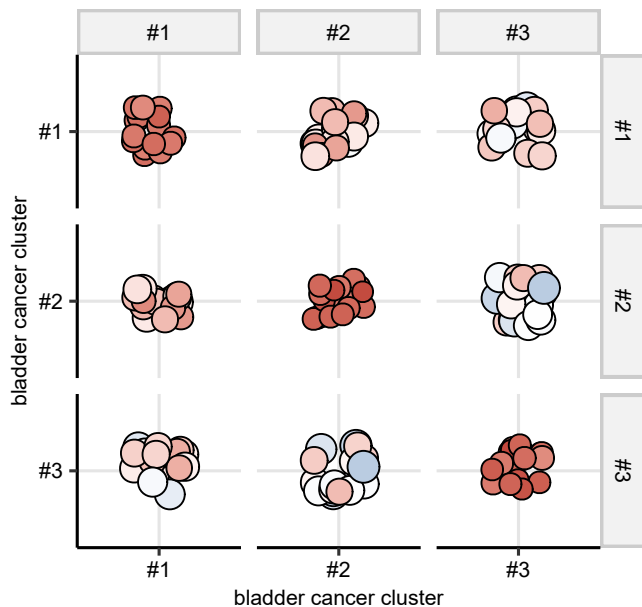


A**Cluster sizes, transcriptome cohorts****B****Significant metagenes, bulk transcriptome cohorts**total metagenes: n = 256, significant in ≥ 10 cohorts: 213

average
 ssGSEA
 score -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5

C**Cluster separation, transcriptome cohorts**

Euclidean²
 distance 800 700 600 500 400 300 200

D**Similarity to TCGA BLCA, bulk transcriptome cohorts**