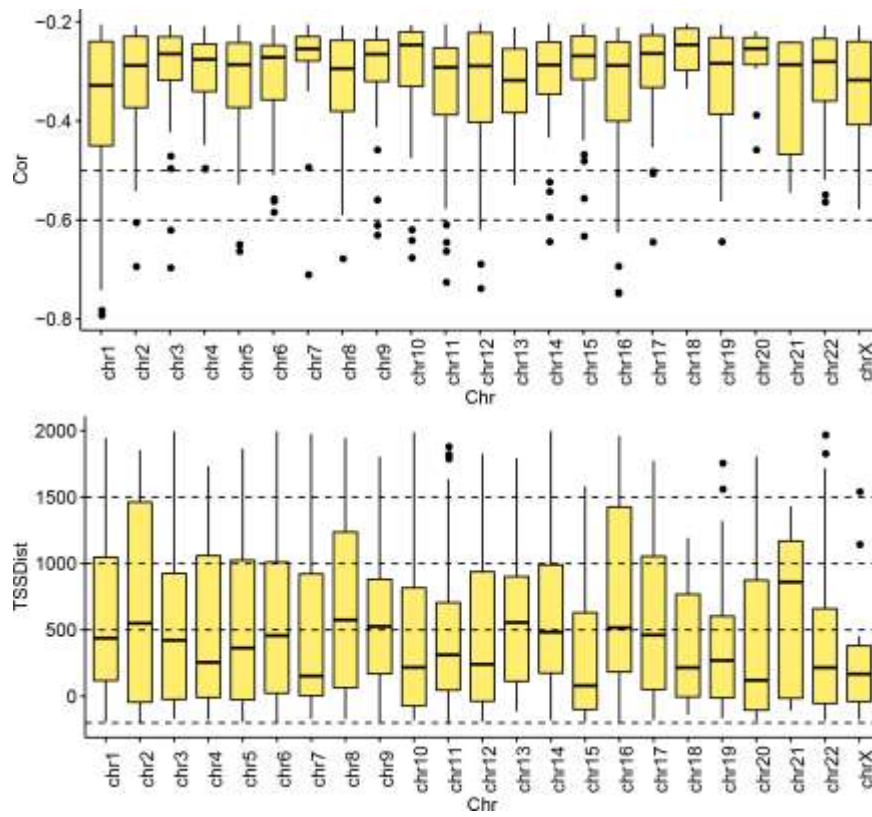
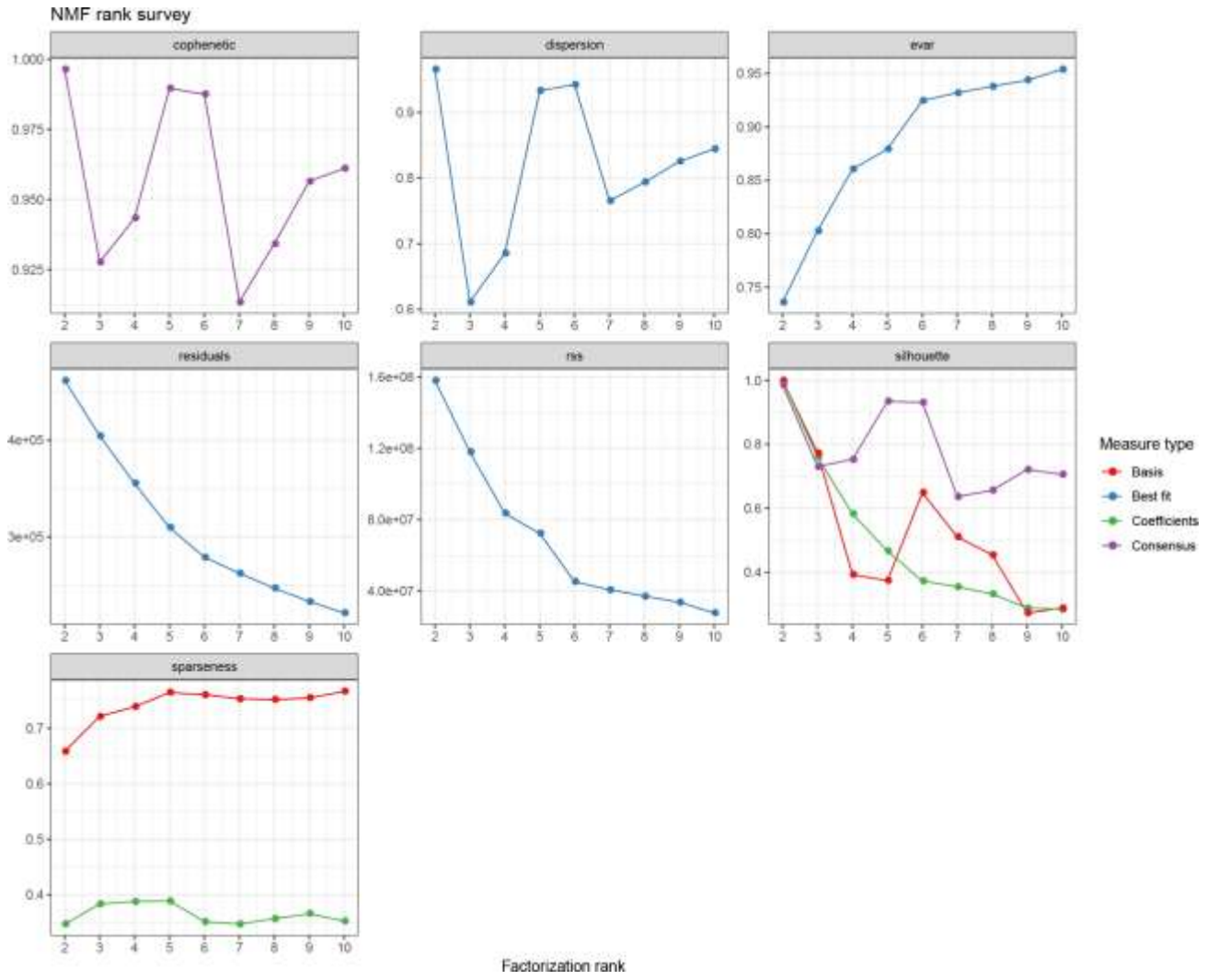


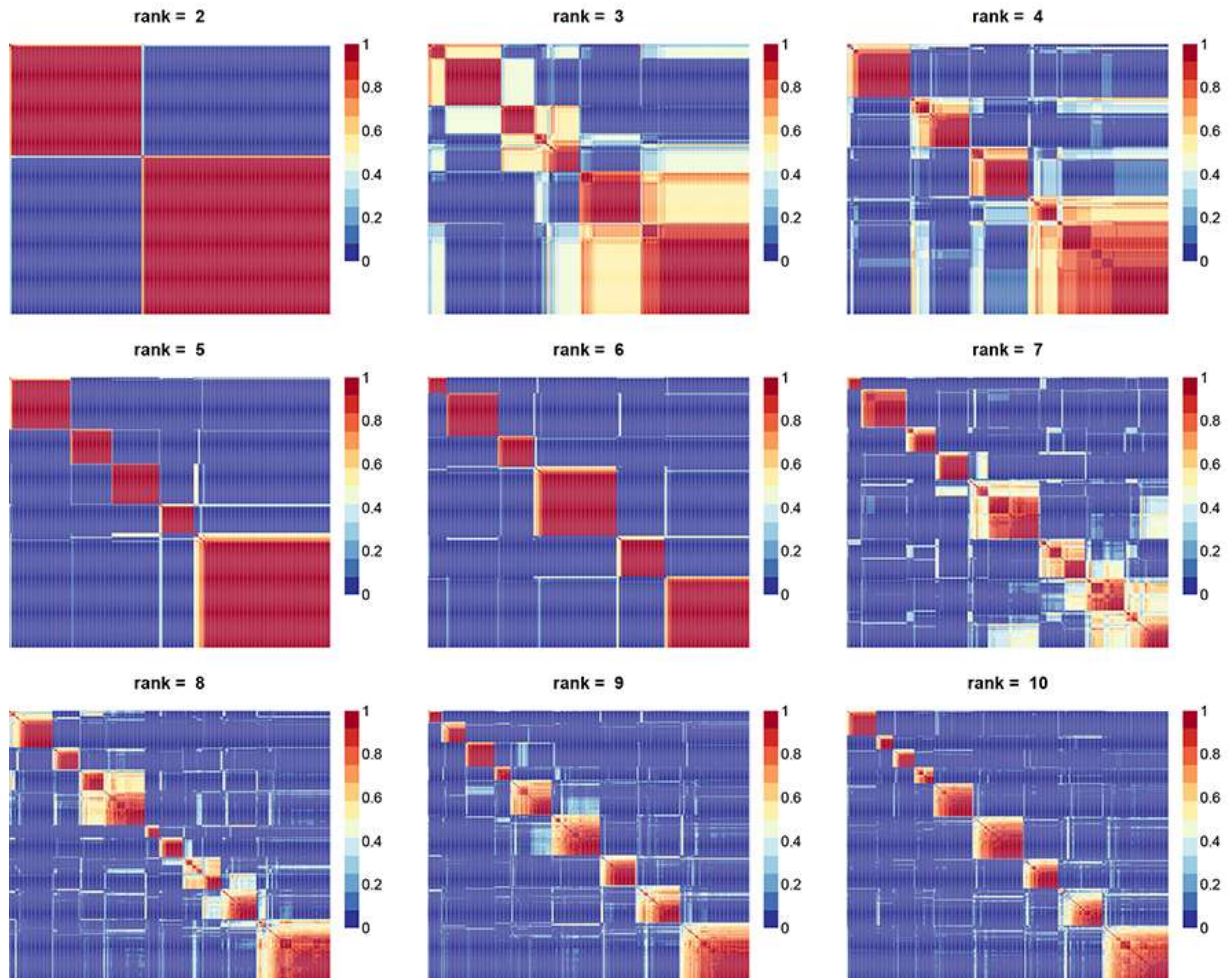
## SUPPLEMENTARY FIGURES



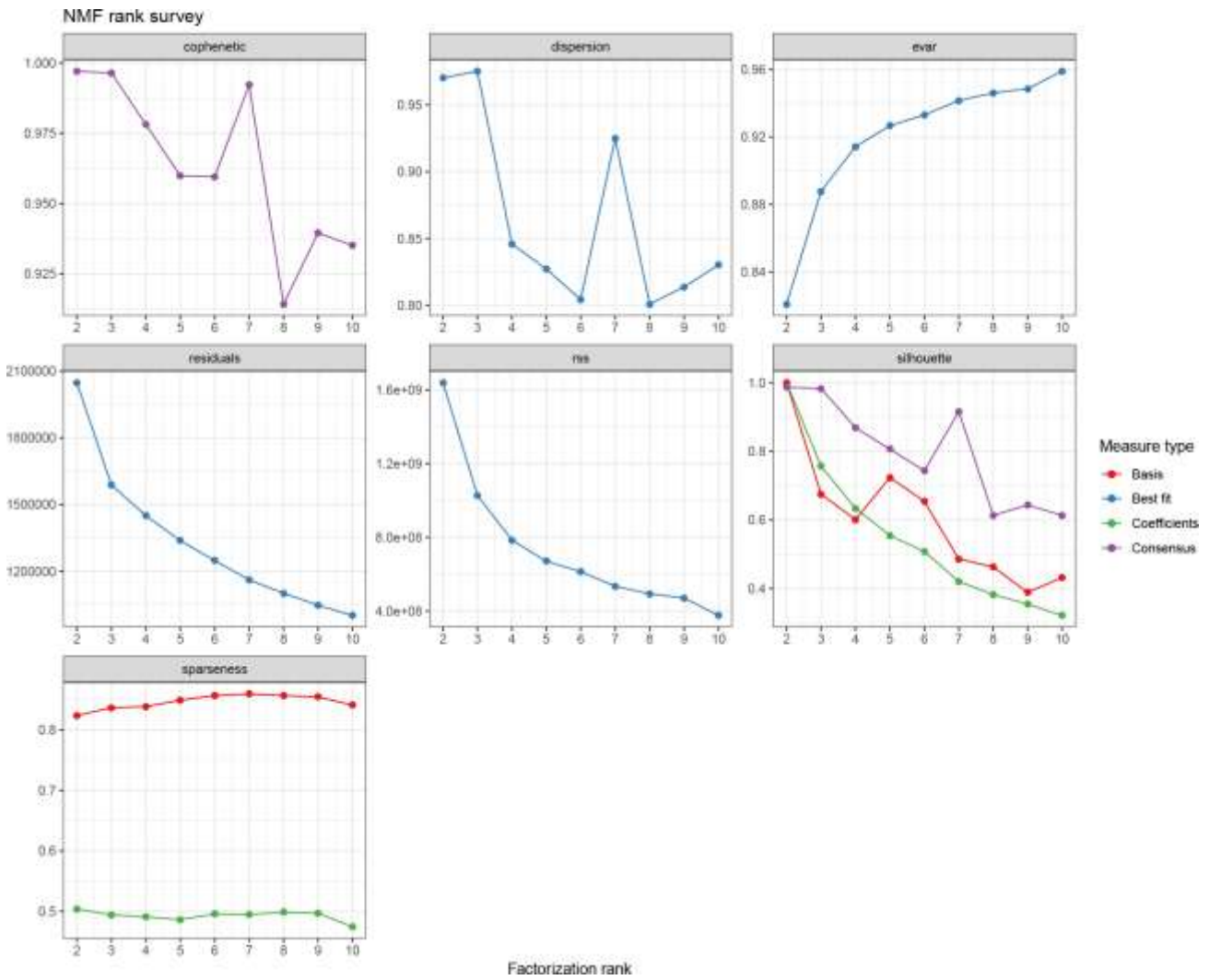
Supplementary Figure 1. The METCor genes' distribution on the genome.



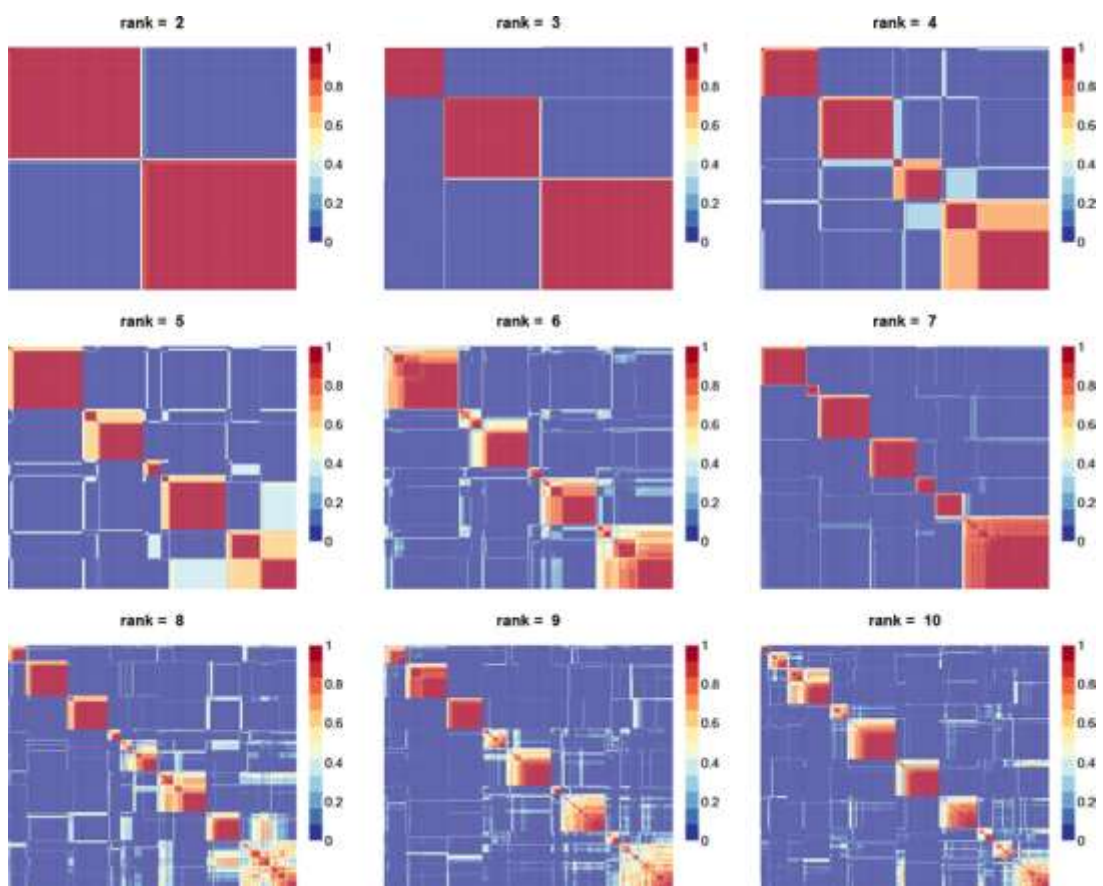
Supplementary Figure 2. NMF rank survey for CNVcor gene set. NMF: non-negative matrix factorization.



**Supplementary Figure 3. NMF clustering analysis for CNVcor gene set.** NMF: non-negative matrix factorization.

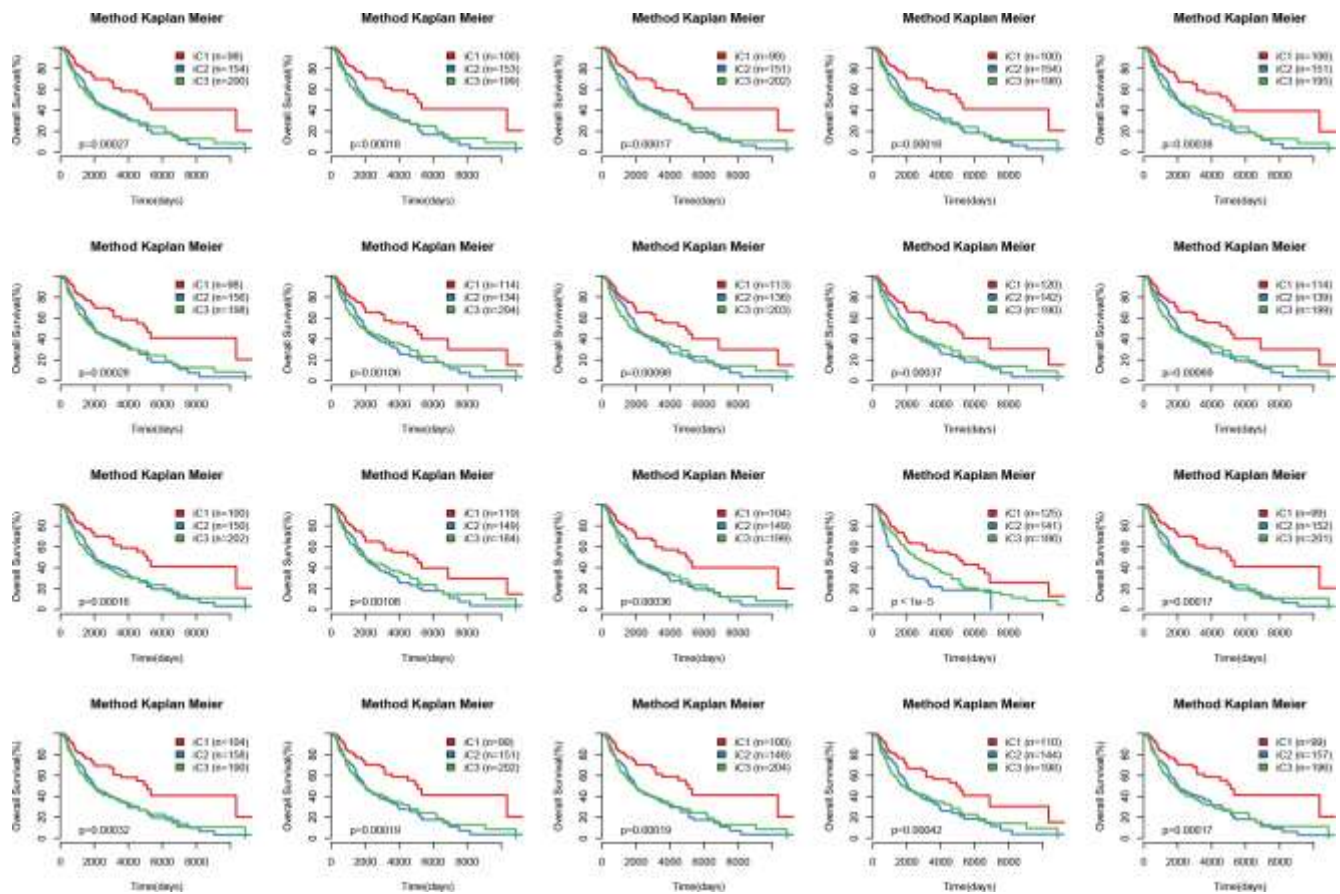


Supplementary Figure 4. NMF rank survey for METcor gene set. NMF: non-negative matrix factorization.

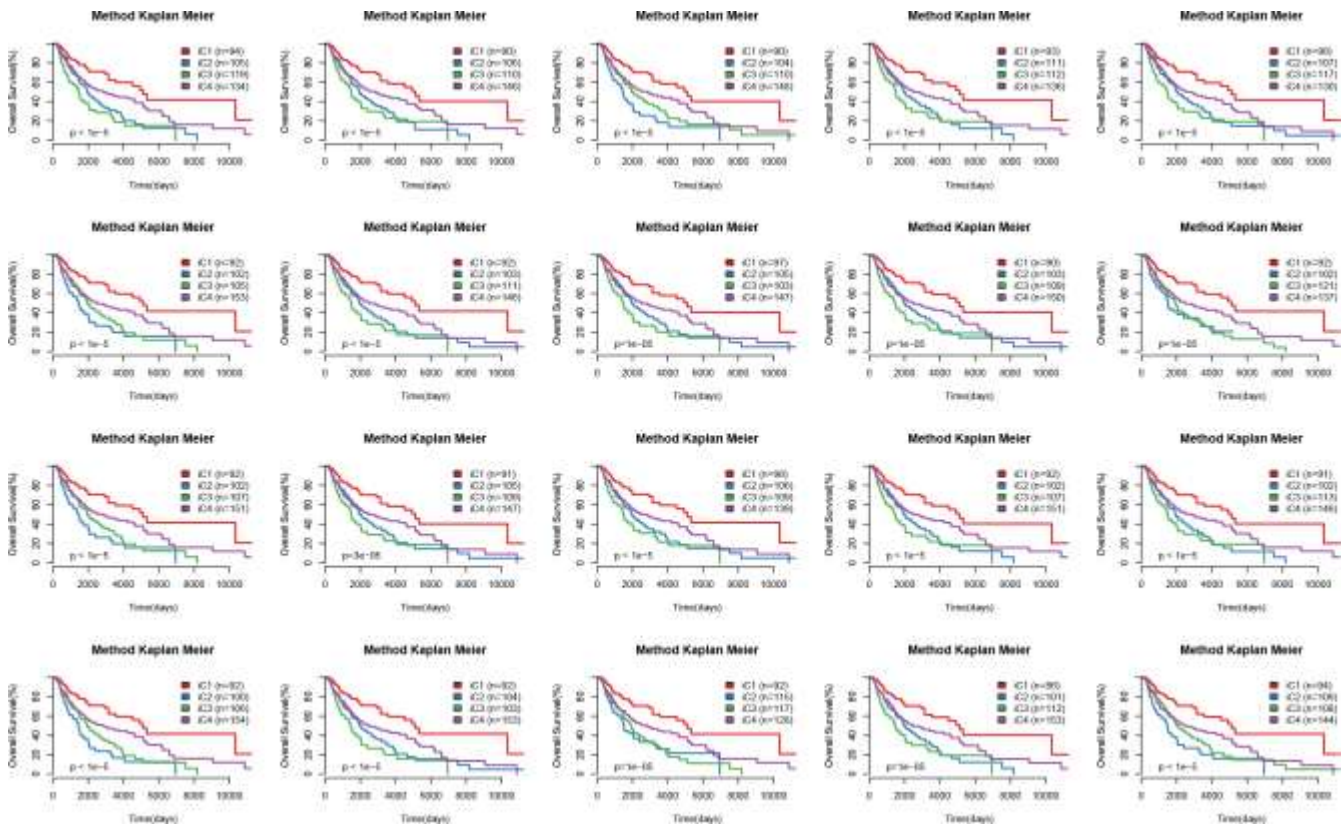


Supplementary Figure 5. NMF clustering analysis for METcor gene set. NMF: non-negative matrix factorization.

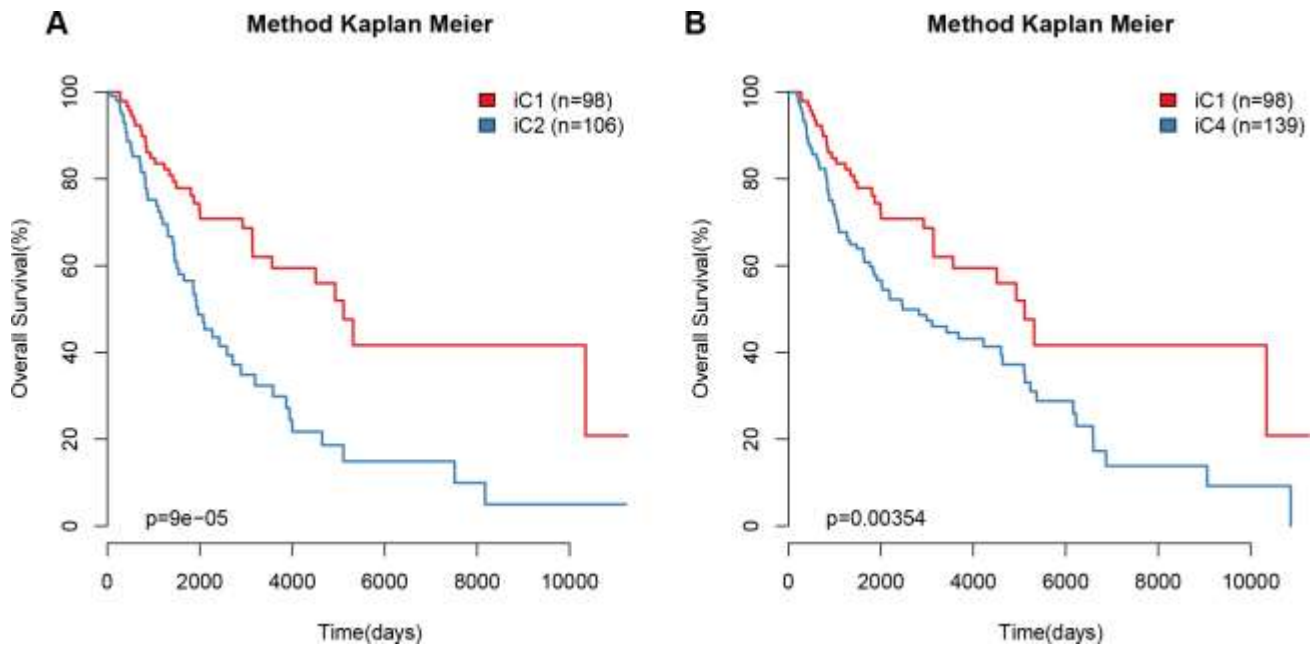




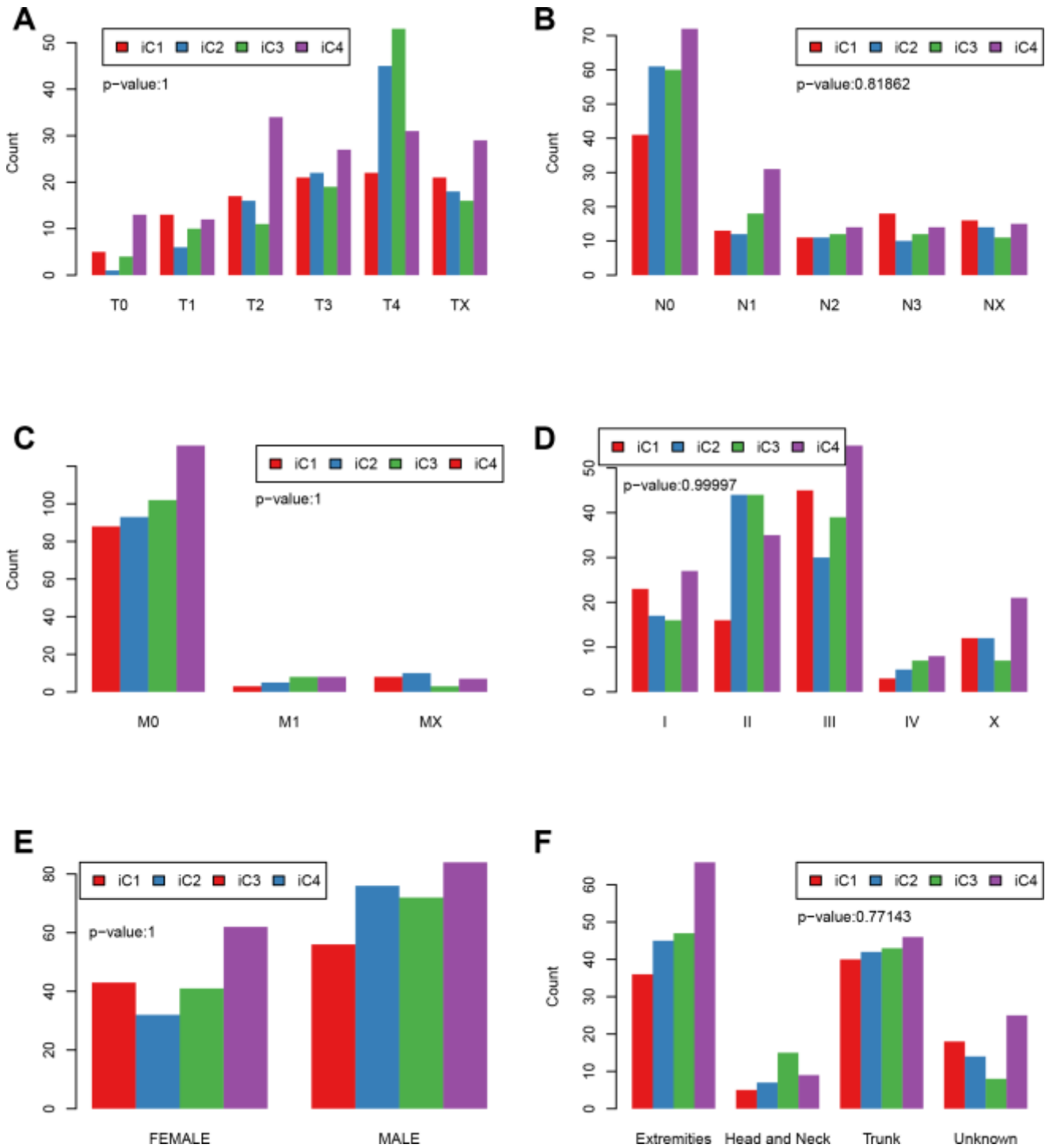
Supplementary Figure 6. iCluster multi-omics clustering result (K = 2, iC1-3).



Supplementary Figure 7. iCluster multi-omics clustering result (K = 3, iC1-4).

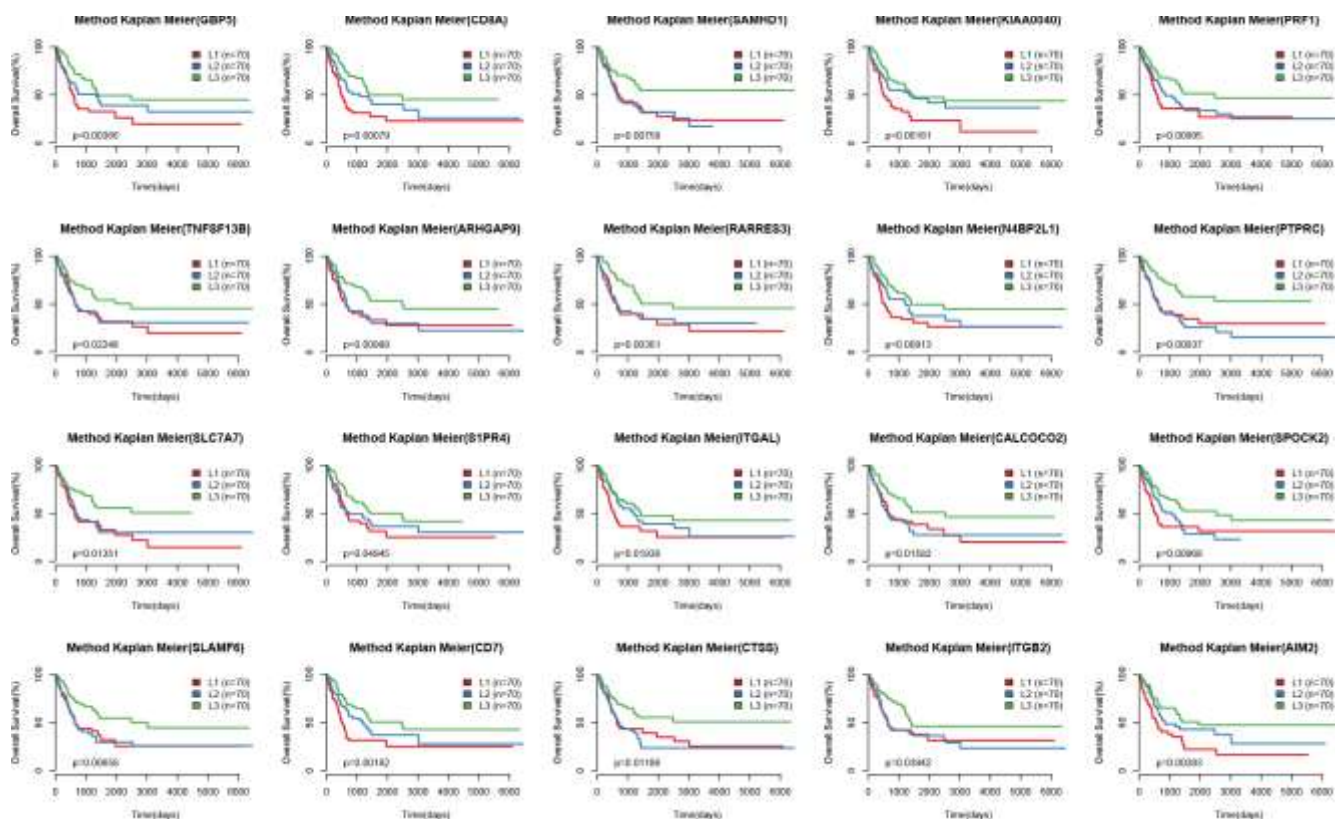


Supplementary Figure 8. Differences in prognosis between iC1 and iC2 / iC1 and iC4.



Supplementary Figure 9. Clinical characteristics (TNM, Stage, Gender, Primary site) differences between iC1-4.





Supplementary Figure 10. Survival curves for the top 20 differential genes in the GEO validation data.