

1-2. Construct a correlation network from 26 TMA markers to identify “WGCNA patient groups”



3. Relate WGCNA groups to clinical variables



4. Identify a subset of markers that approximate the WGCNA groups = “WGCNA* patient groups”



5. Conduct a conventional Cox regression analysis of the 26 TMA markers = “COX patient groups”



6. Compare WGCNA, WGCNA* and COX groups to clinical variables in bivariate and multivariate models



7. Validate WGCNA* and COX groups in independent gene expression data sets

