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