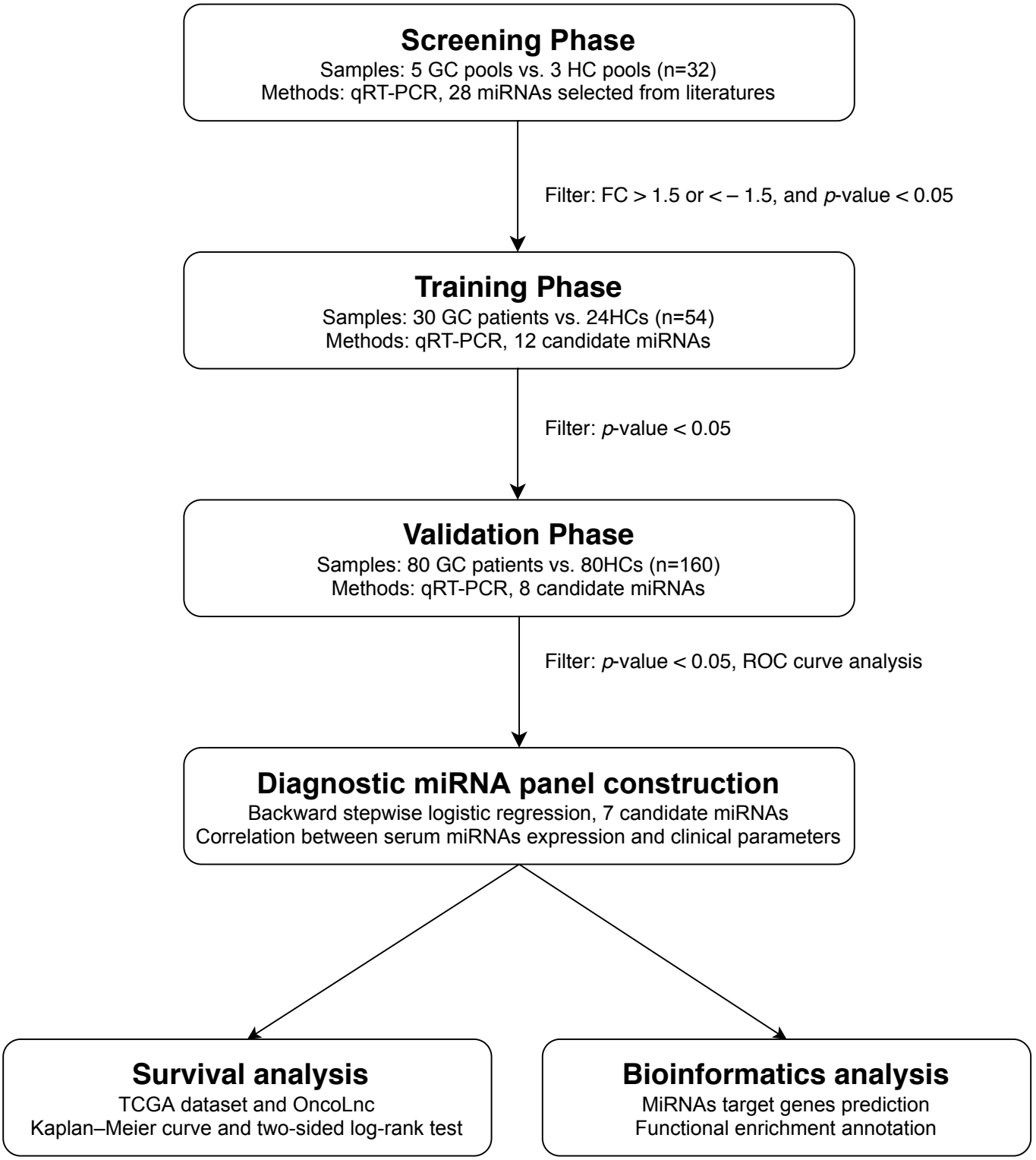
Screening Phase
Samples: 5 GC pools vs. 3 HC pools (n=32)
Methods: qRT-PCR, 28 miRNAs selected from literatures
Filter: FC > 1.5 or < – 1.5, and p-value < 0.05
Training Phase
Samples: 30 GC patients vs. 24HCs (n=54)
Methods: qRT-PCR, 12 candidate miRNAs
Filter: p-value < 0.05
Validation Phase
Samples: 80 GC patients vs. 80HCs (n=160)
Methods: qRT-PCR, 8 candidate miRNAs
Filter: p-value < 0.05, ROC curve analysis
Diagnostic miRNA panel construction
Backward stepwise logistic regression, 7 candidate miRNAs
Correlation between serum miRNAs expression and clinical parameters
Survival analysis
TCGA dataset and OncoLnc
Kaplan–Meier curve and two-sided log-rank test
Bioinformatics analysis
MiRNAs target genes prediction
Functional enrichment annotation