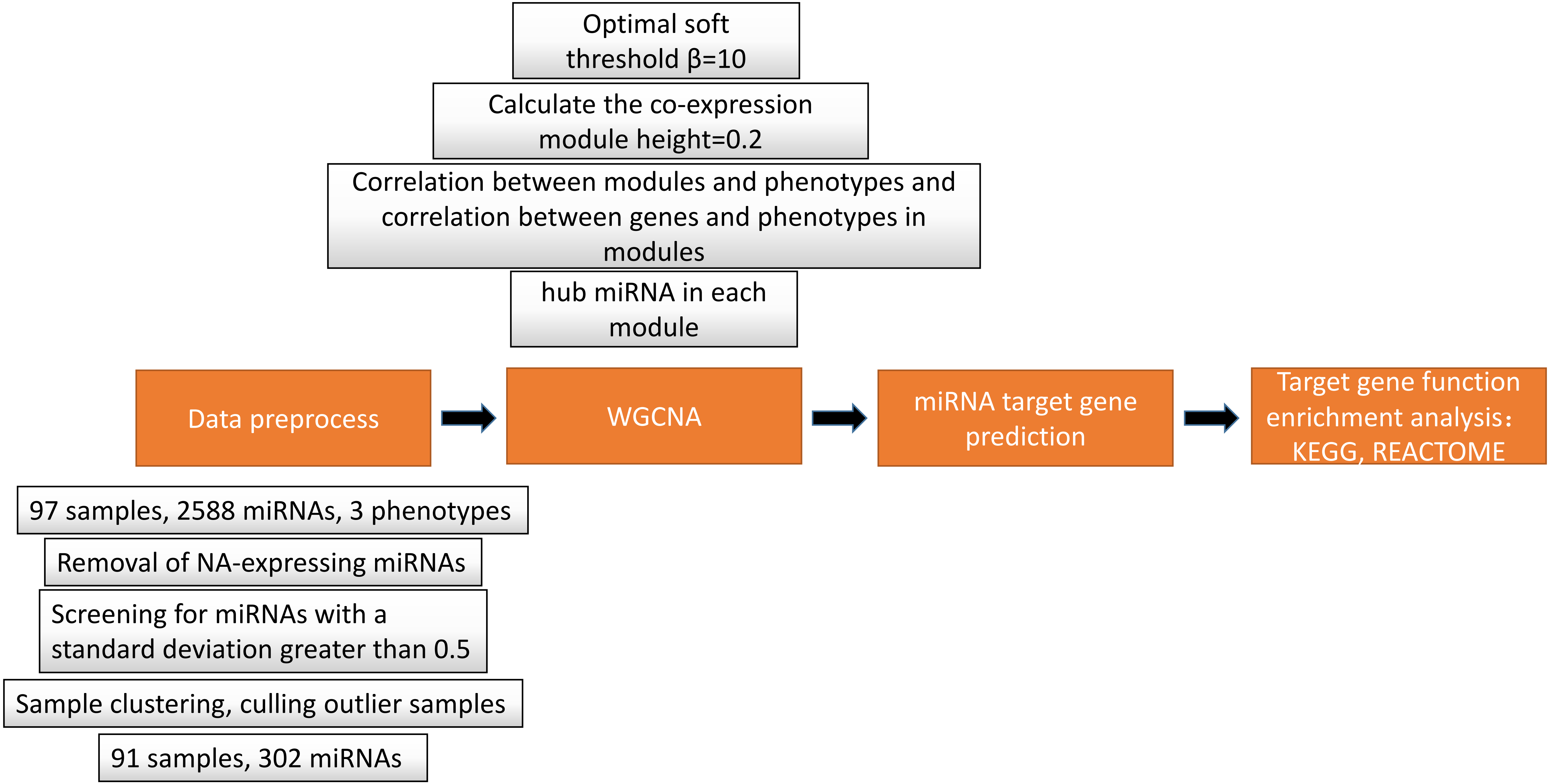

Optimal soft threshold β=10

Calculate the co-expression module height=0.2

Correlation between modules and phenotypes and correlation between genes and phenotypes in modules

hub miRNA in each module

Data preprocess → WGCNA → miRNA target gene prediction → Target gene function enrichment analysis：KEGG, REACTOME

97 samples, 2588 miRNAs, 3 phenotypes

Removal of NA-expressing miRNAs

Screening for miRNAs with a standard deviation greater than 0.5

Sample clustering, culling outlier samples

91 samples, 302 miRNAs