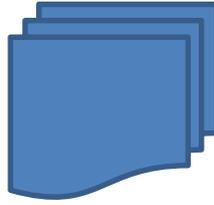# Lilly Rat miRNAs Atlas Processing Workflow

miRNA-Seq data
for tissues/organs

Preprocess Data

Trimming adaptors
Quality filtering
Elimination of short reads

miRDeep Alignment

miRBase v20

Filter mature miRs

Count > 10 in at least
one tissue/organ

Non-negative Matrix
Factorization

Rank = 14
# of runs = 20
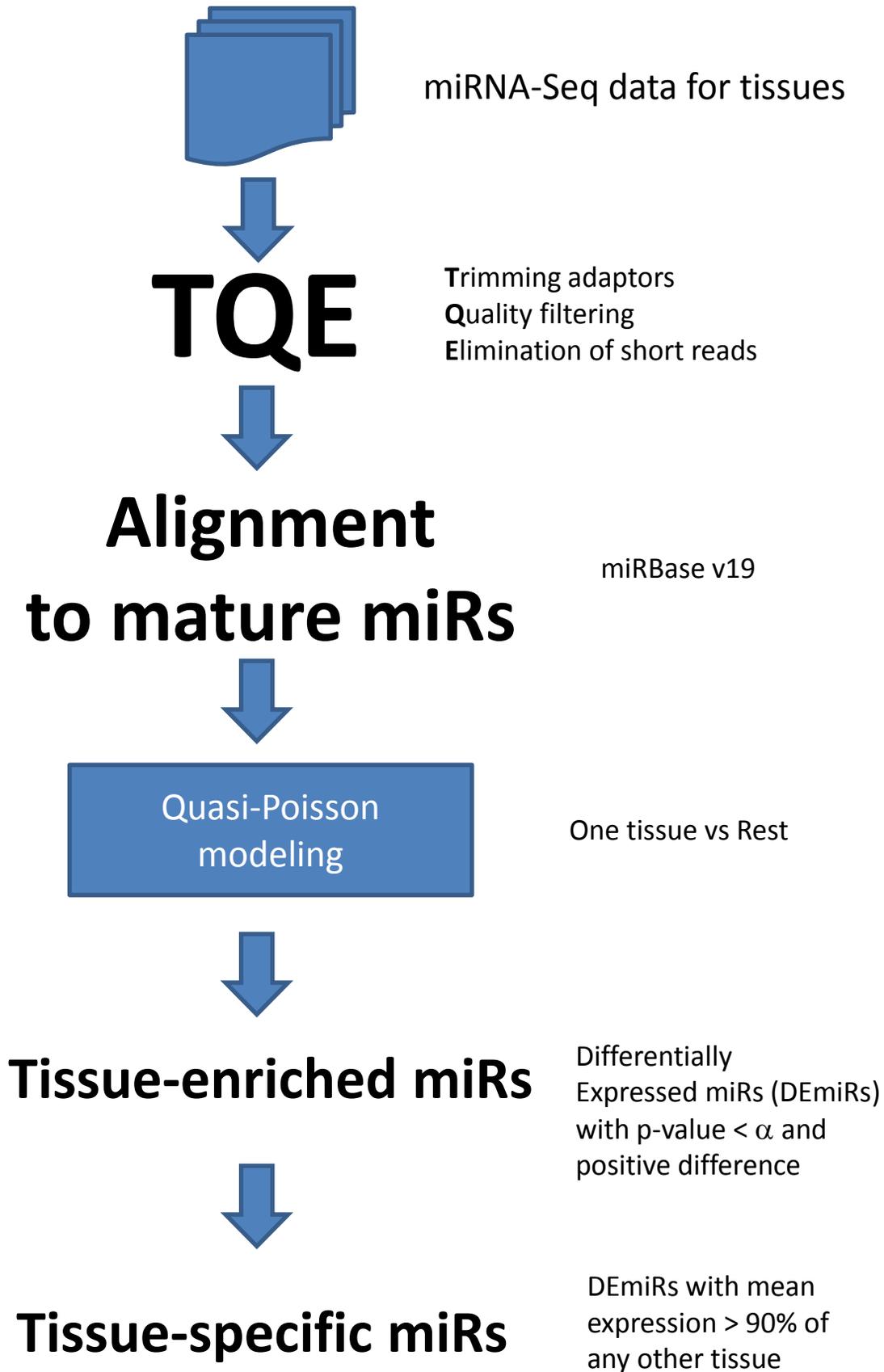
Extract & normalize
basis and coefficient matrix

Thresholding

One tissue vs others

Tissue-specific miRs

% > 80

NIEHS Rat miRNAs Atlas Processing Workflow

miRNA-Seq data for tissues

TQE

Trimming adaptors
Quality filtering
Elimination of short reads

Alignment to mature miRs

miRBase v19

Quasi-Poisson modeling

One tissue vs Rest

Tissue-enriched miRs

Differentially Expressed miRs (DEmiRs) with p-value < α and positive difference

Tissue-specific miRs

DEmiRs with mean expression > 90% of any other tissue

Maastricht Rat miRNAs Atlas Processing Workflow

miRNA-Seq data for tissues

Trim reads

miRDEEP2 alignment to rat genome

Ensembl v5.0.73

PatMaN alignment

predicted pre-miRs
known pre-miRs

miRBase v20

Scale counts

according to # of loci

mature miRs

TMM Normalization and filtering

Thresholding

One tissue vs others

Tissue-enriched miRs

% > 50

Tissue-specific miRs

% > 90