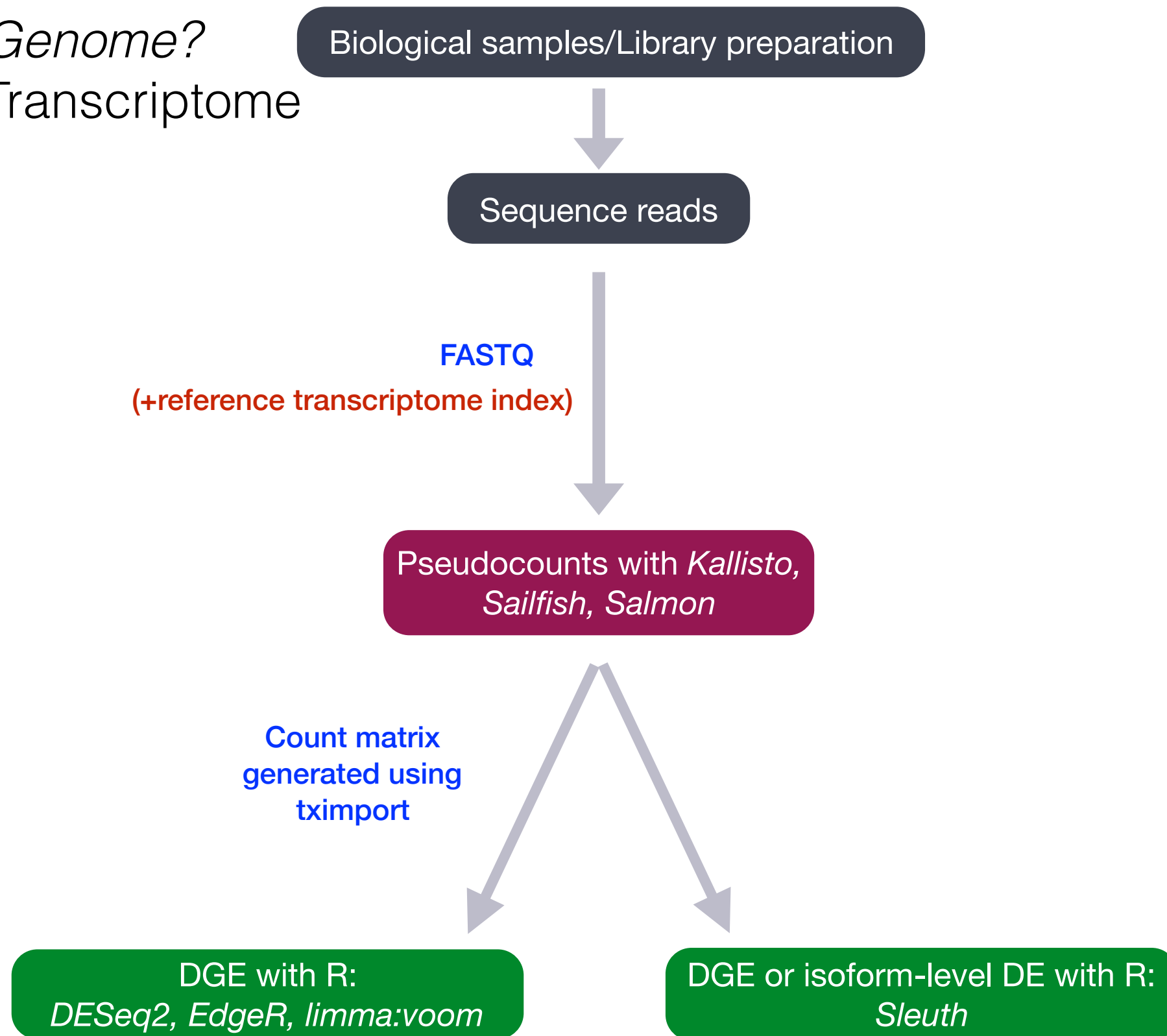


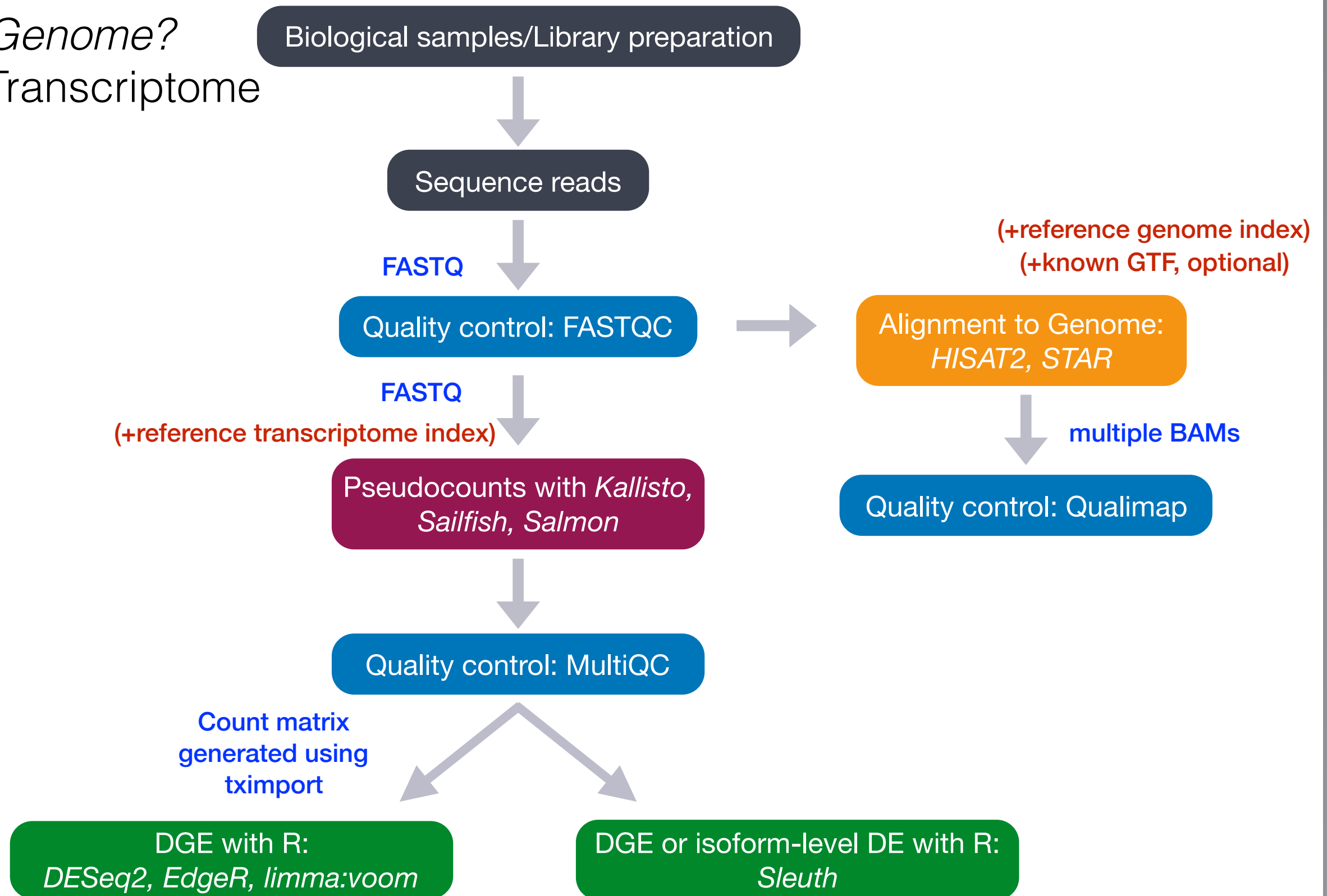
# RNA-seq: Analysis options

- ✓ *Genome?*
- ✓ Transcriptome



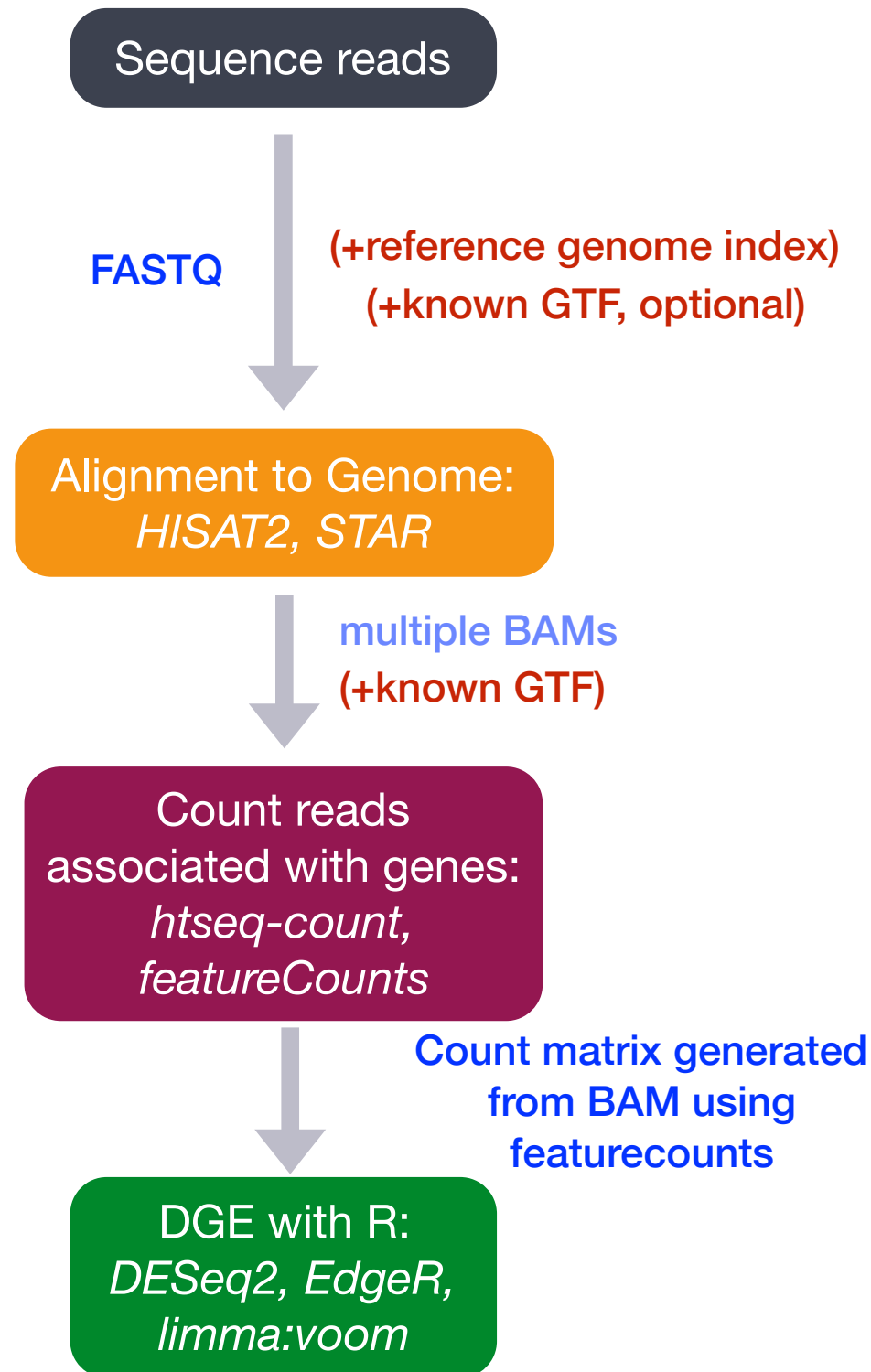
## Differential Expression Analysis Workflow #1

- ✓ *Genome?*
- ✓ Transcriptome



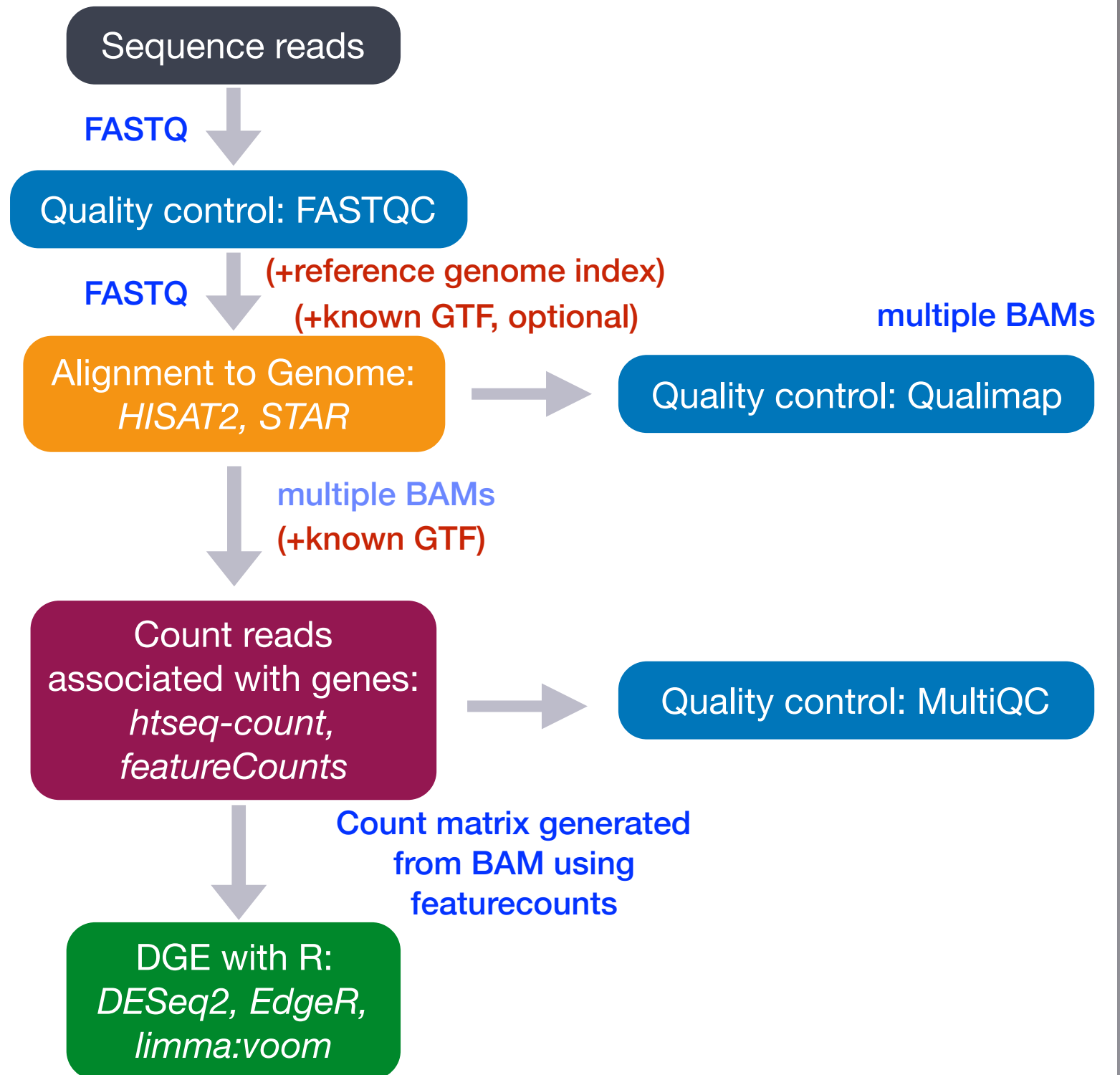
## Differential Expression Analysis Workflow #1

- ✓ Genome
- ✓ GTF annotation file (transcriptome)



## Differential Expression Analysis Workflow #2

- ✓ Genome
- ✓ GTF annotation file (transcriptome)

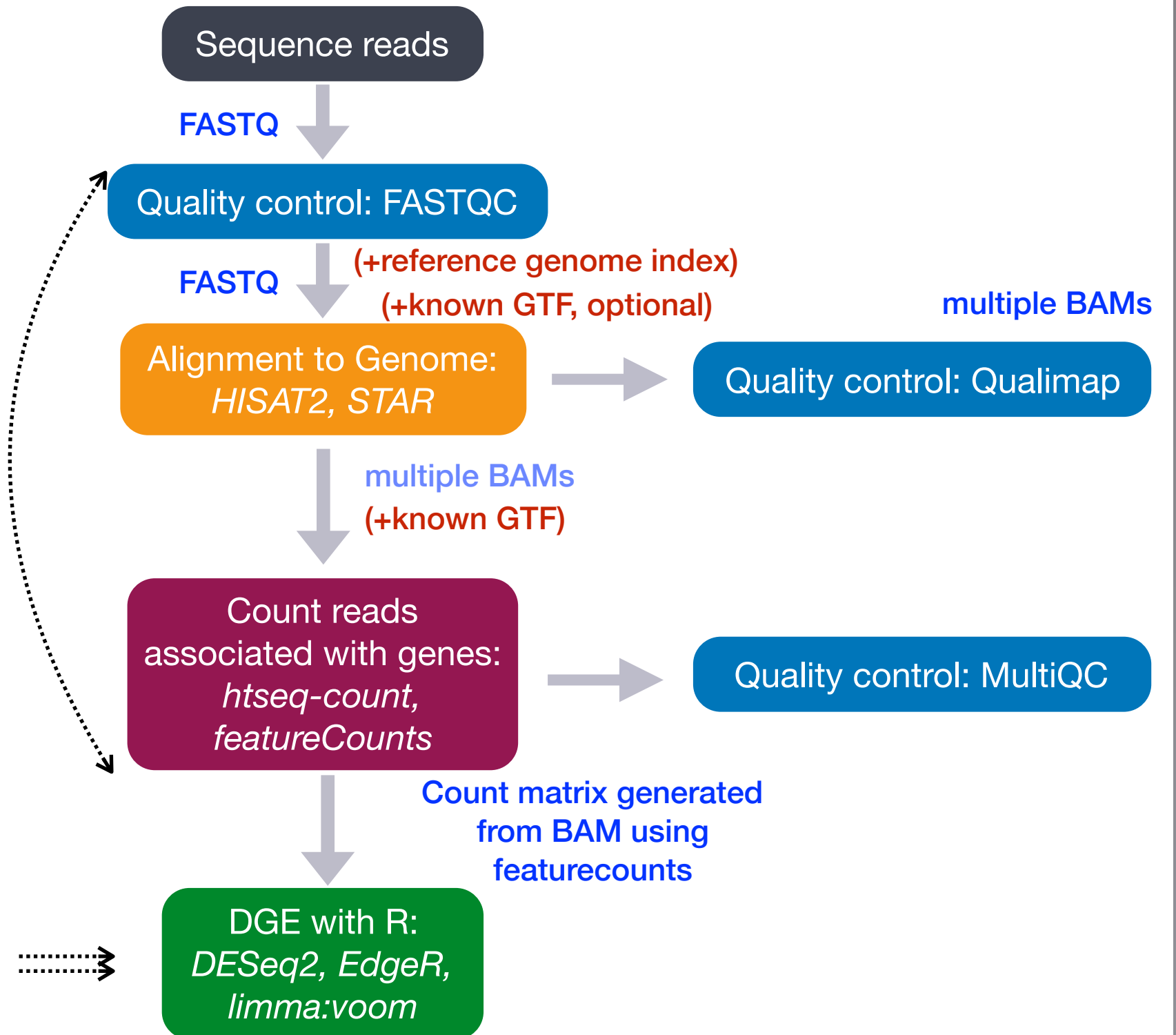


## Differential Expression Analysis Workflow #2

- ✓ Genome
- ✓ GTF annotation file (transcriptome)

[https://  
hbctraining.github.io/  
Intro-to-rnaseq-hpc-O2/](https://hbctraining.github.io/Intro-to-rnaseq-hpc-O2/)

[https://  
hbctraining.github.io/  
DGE\\_workshop/](https://hbctraining.github.io/DGE_workshop/)



## Differential Expression Analysis Workflow #2

# Alternative methods: transcriptome assembly

## Reference-based assembly

- Genome is known

# Alternative methods: transcriptome assembly

## Reference-based assembly

- Genome is known
- Transcriptome not available or is not good enough



# Alternative methods: transcriptome assembly

## Reference-based assembly

- Genome is known
- Transcriptome not available or is not good enough
- [Cufflinks](#) and [Scripture](#) are two reference-based transcriptome assemblers

# Alternative methods: transcriptome assembly

## Reference-based assembly

- Genome is known
- Transcriptome not available or is not good enough
- [Cufflinks](#) and [Scripture](#) are two reference-based transcriptome assemblers
- Additional annotation of any newly-discovered genes or isoforms will need to be generated

# Alternative methods: transcriptome assembly

## De novo assembly

- Genome is not known, or is of poor quality

# Alternative methods: transcriptome assembly

## De novo assembly

- Genome is not known, or is of poor quality
- Amount of data needed is greater than for a reference-based assembly

# Alternative methods: transcriptome assembly

## De novo assembly

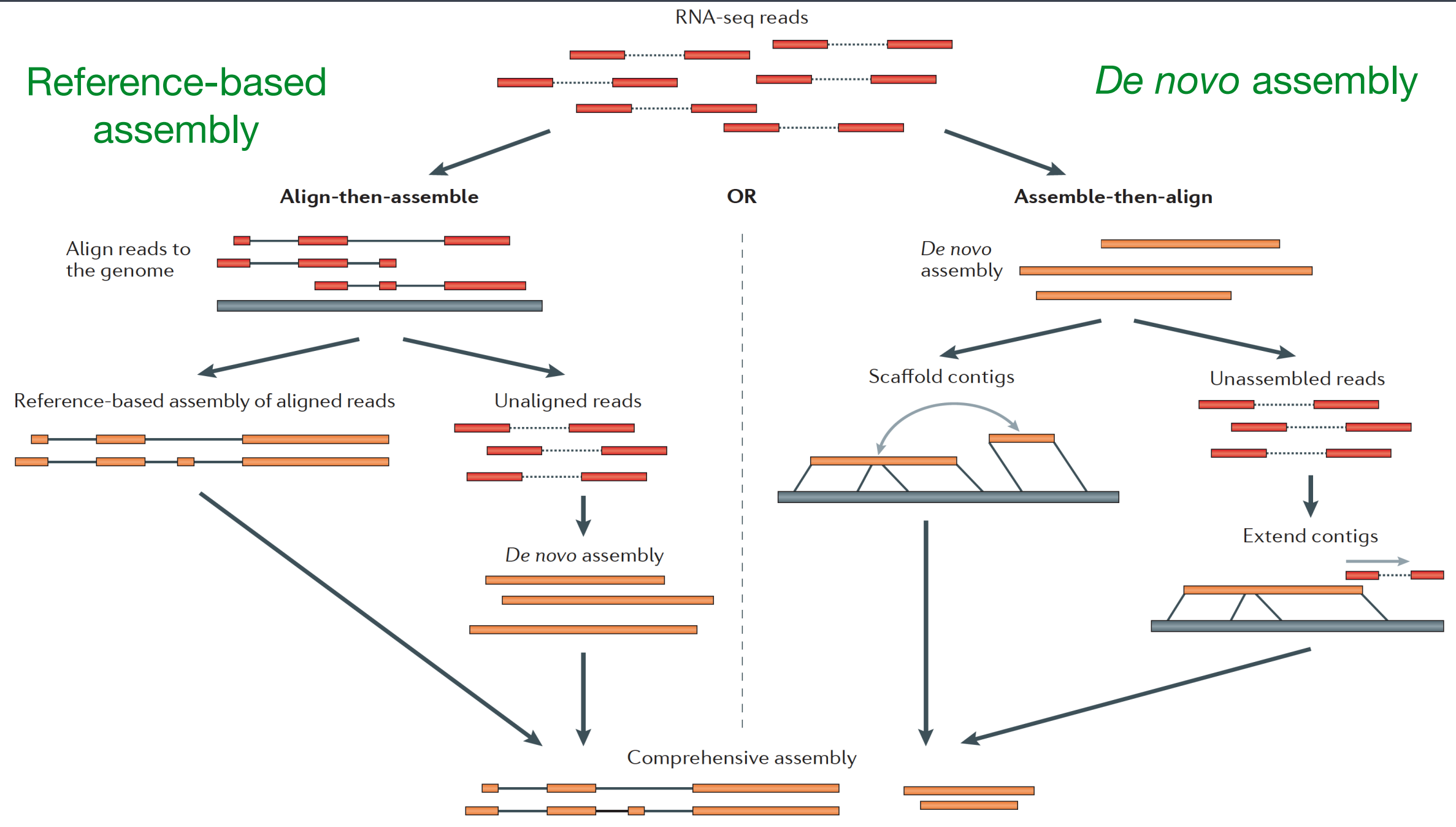
- Genome is not known, or is of poor quality
- Amount of data needed is greater than for a reference-based assembly
- [Oases](#), [TransABySS](#), [Trinity](#) are examples of well-regarded transcriptome assemblers, especially Trinity

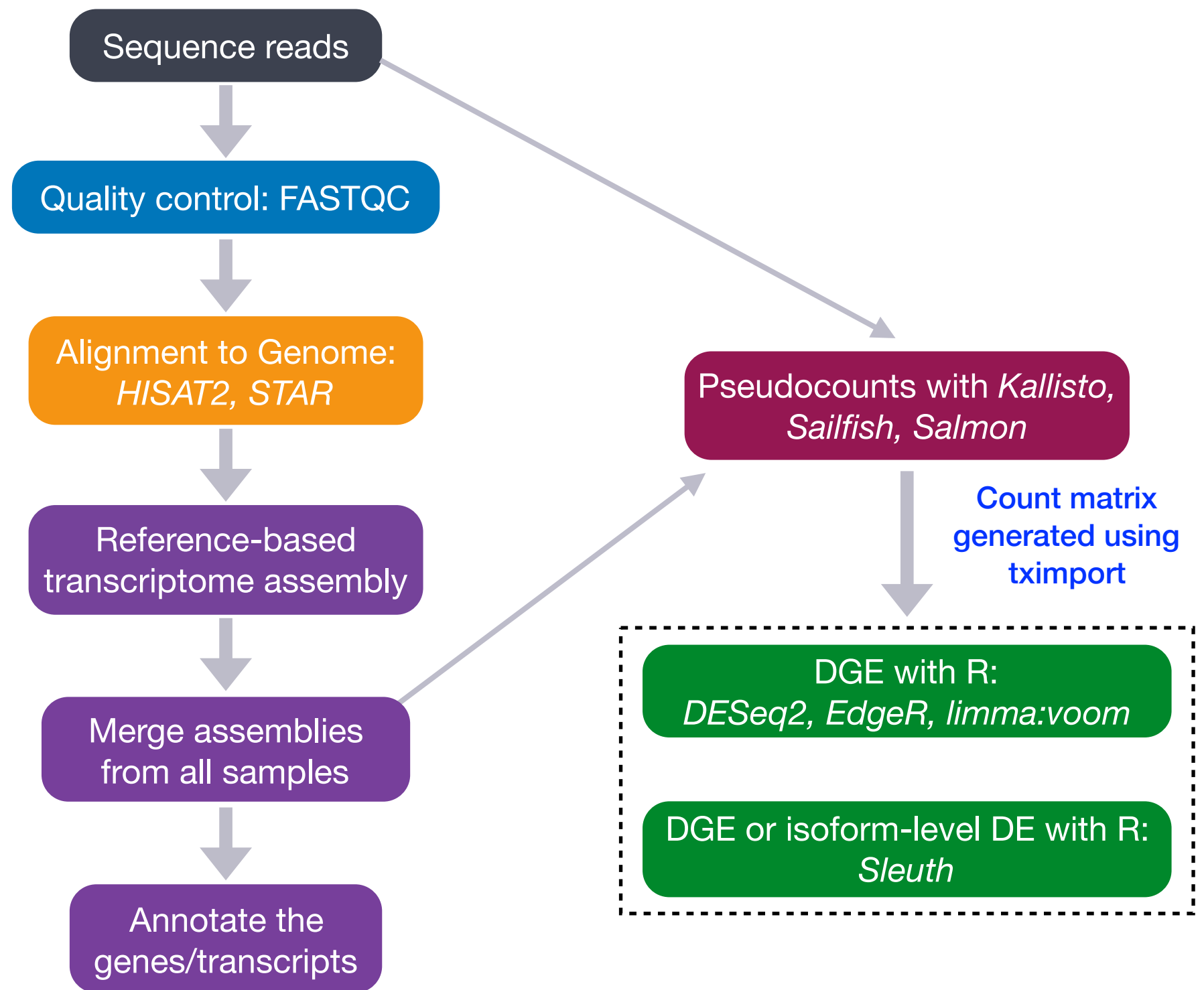
# Alternative methods: transcriptome assembly

## De novo assembly

- Genome is not known, or is of poor quality
- Amount of data needed is greater than for a reference-based assembly
- [Oases](#), [TransABySS](#), [Trinity](#) are examples of well-regarded transcriptome assemblers, especially Trinity
- Newly-discovered genes or isoforms will need to be annotated using homolog-based and other methodologies

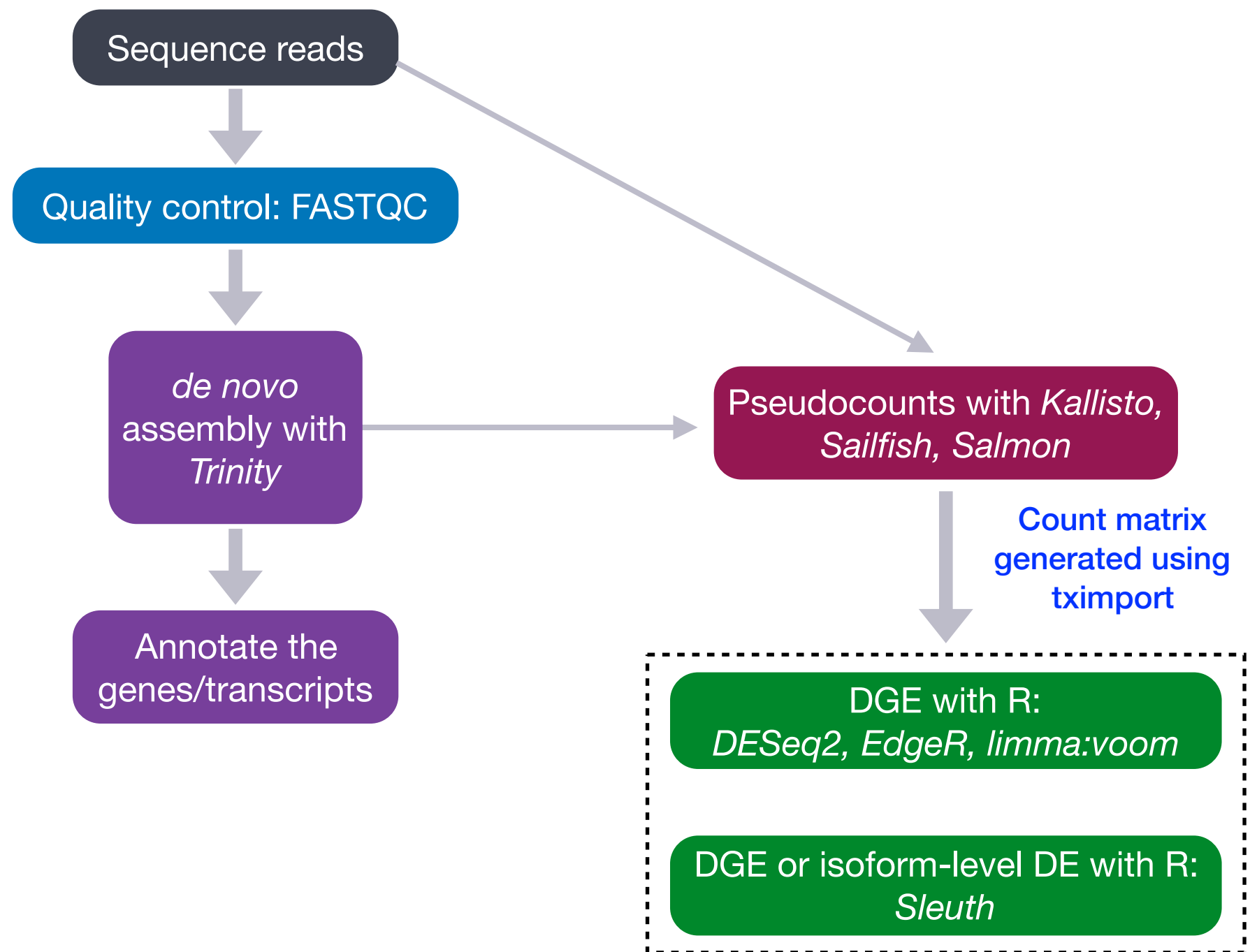
# Transcriptome Assembly





## Differential Expression Analysis Workflow #3





## Differential Expression Analysis Workflow #4

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