

Strategies for Bulk RNA-seq Analysis



Genome Mapping

Transcriptome Mapping

Assembly

Reads

Reads

Reads

*STAR,
HISAT2*

*RSEM,
Kallisto,
Sailfish,
Salmon*

*Trinity,
Scripture,
Stringtie*

Splice-aware
Genome mapping

Transcript mapping
and quantification

Assembly into
transcripts

*htseq-count,
featureCounts*

StringTie

Trinotate

Gene
counting

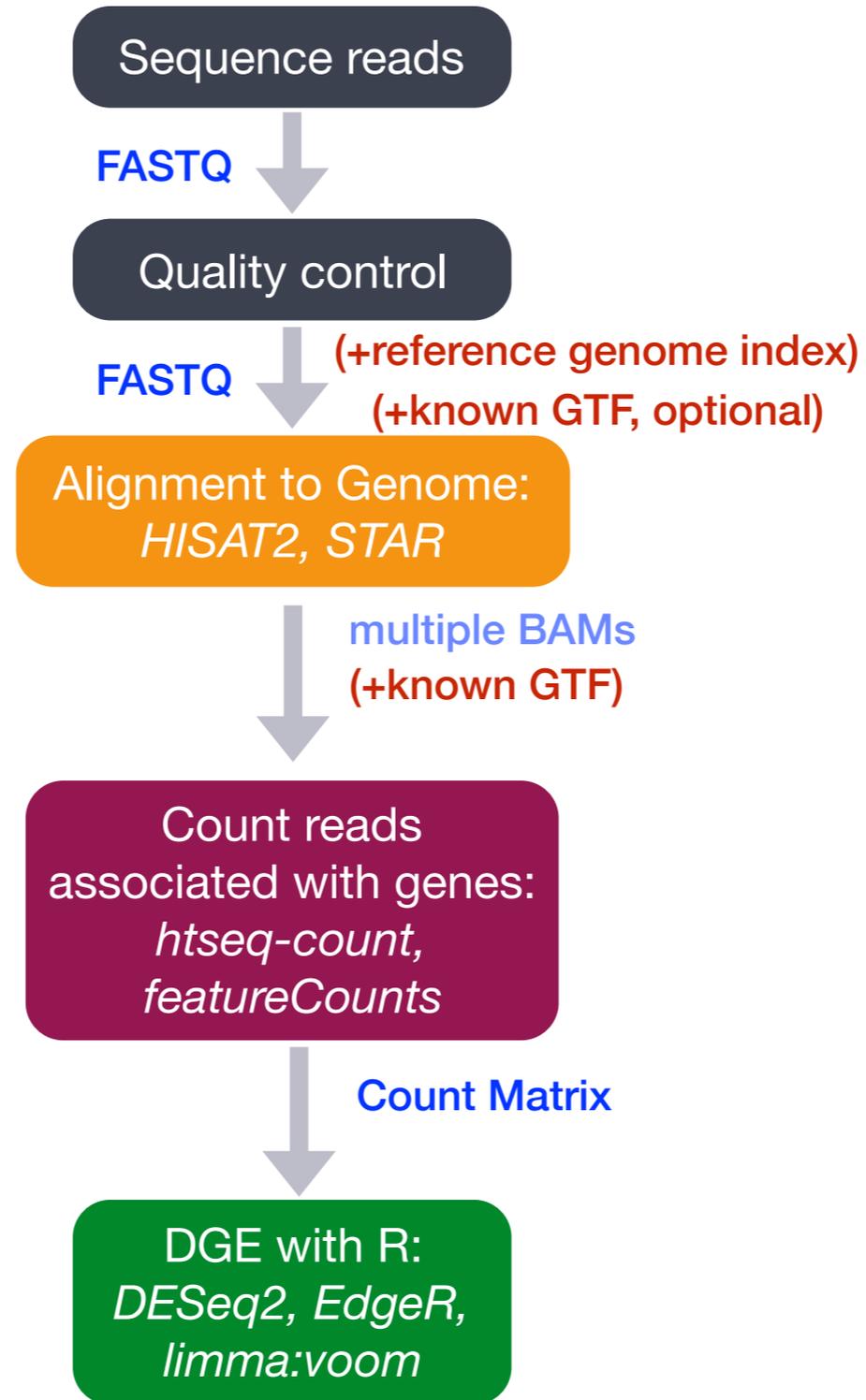
Transcript
discovery &
counting

Novel transcript
annotation

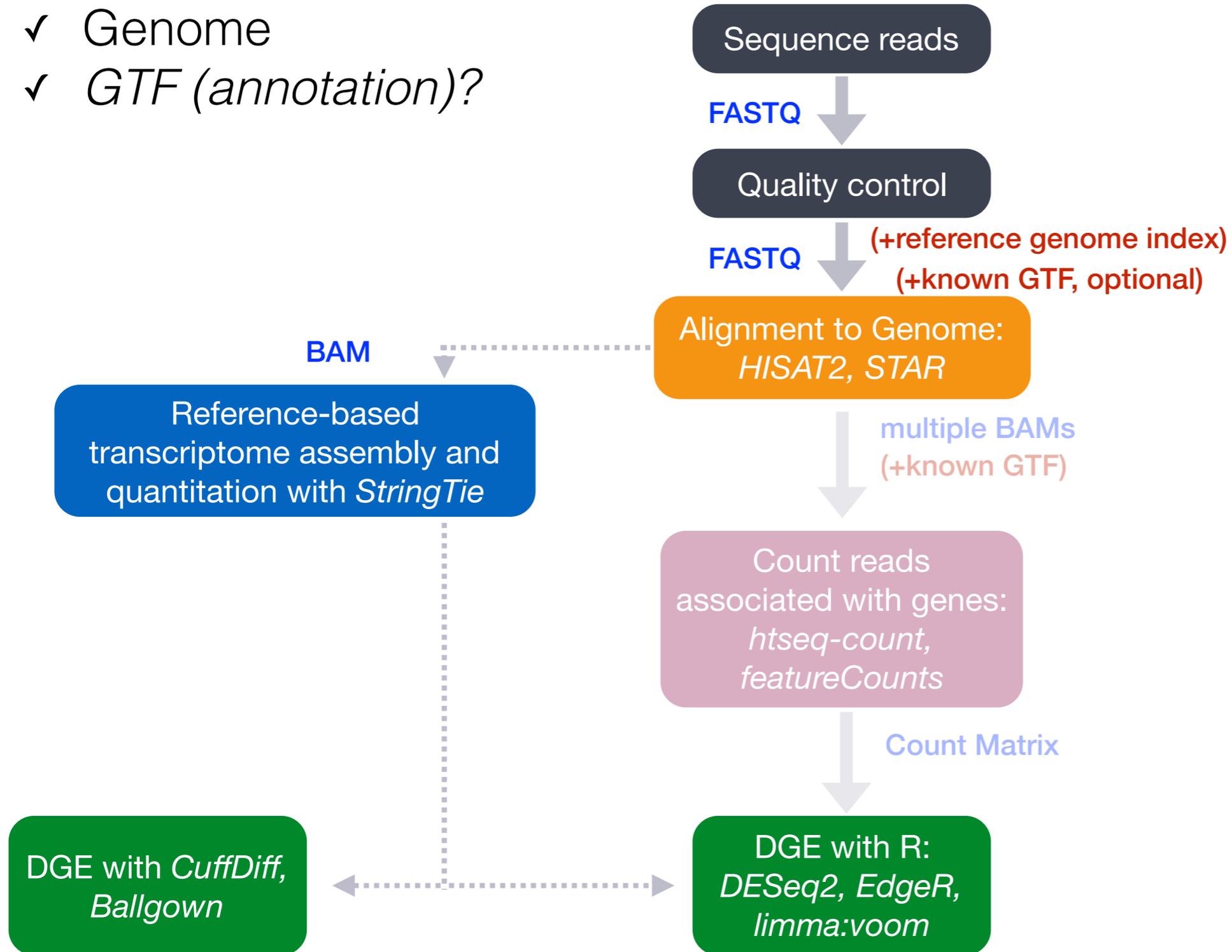
*Homology-based
BLAST2GO*

Novel transcript
annotation

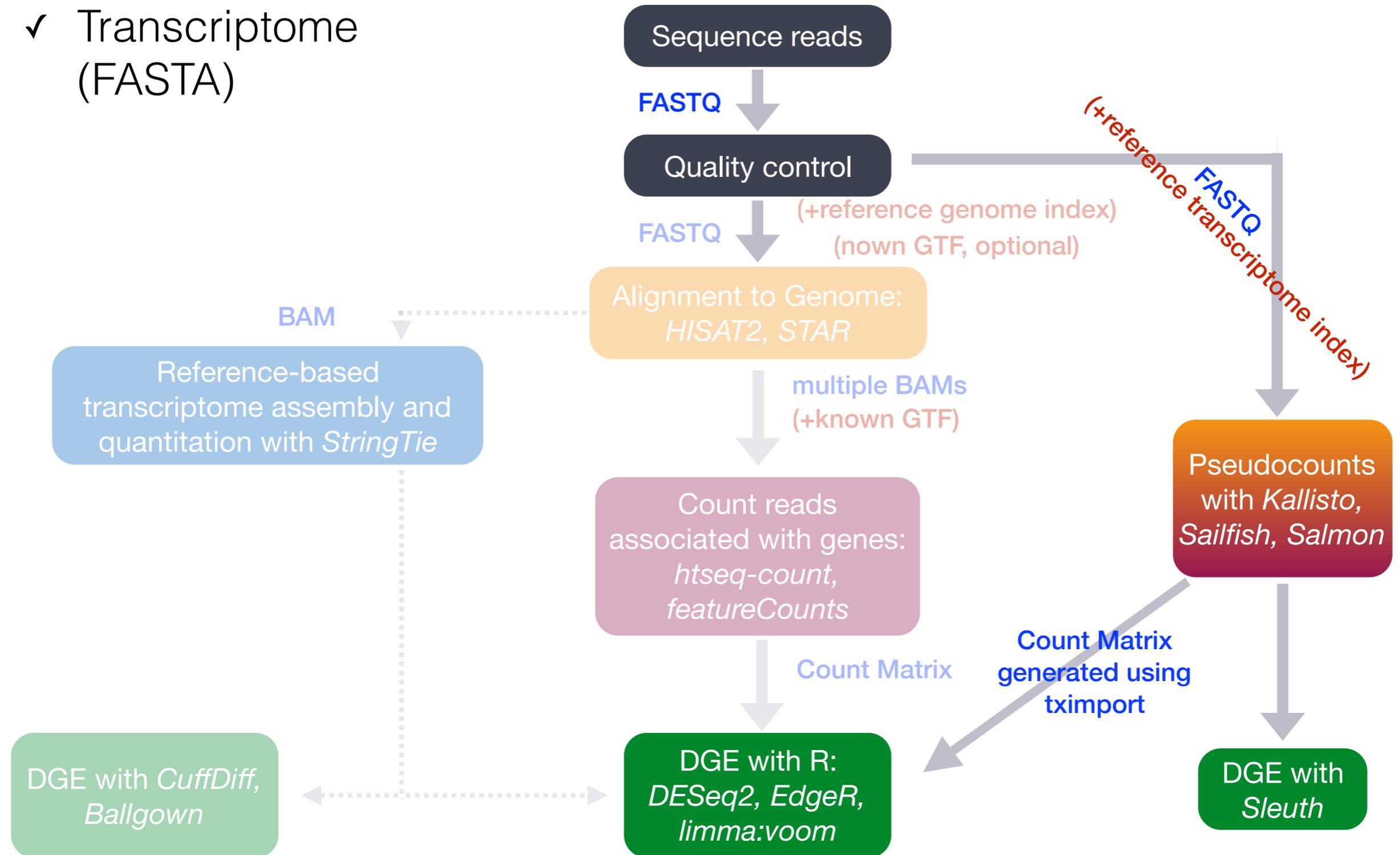
- ✓ Genome
- ✓ GTF (annotation)



- ✓ Genome
- ✓ *GTF (annotation)?*

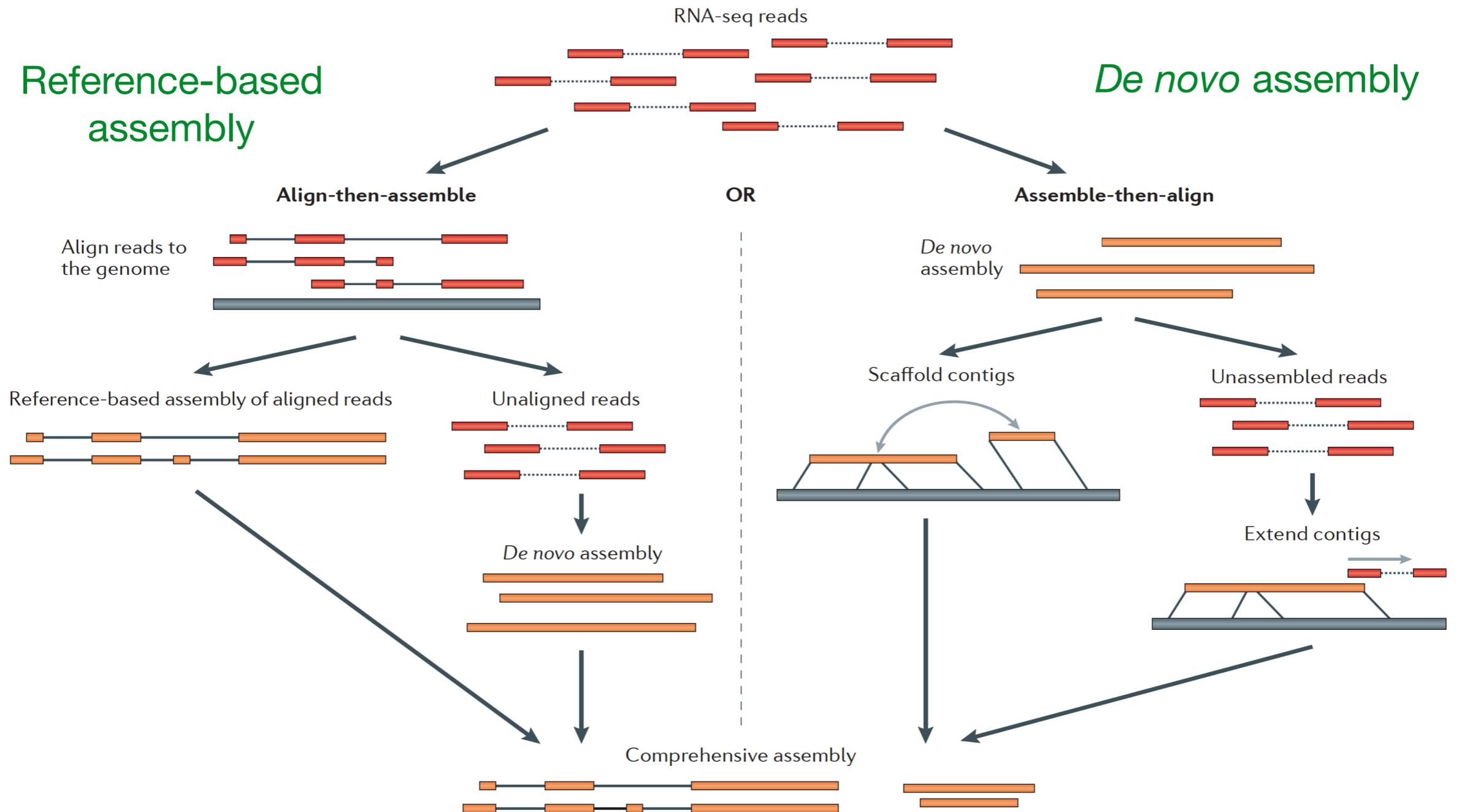


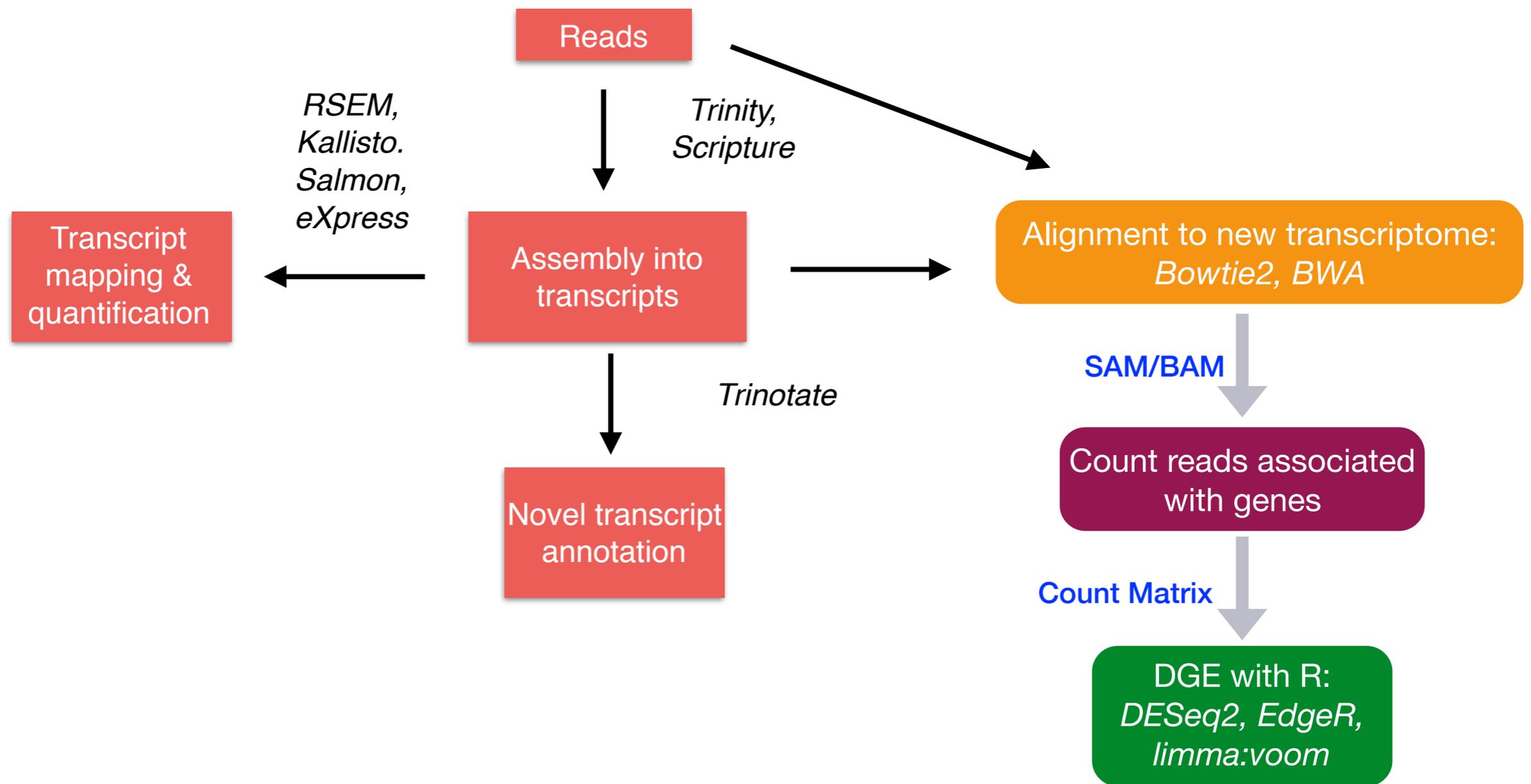
✓ Transcriptome (FASTA)



- ✓ Genome
- ✓ *GTF (annotation)?*

- ✓ *Genome?*
- ✓ *GTF (annotation)?*





Quantitation from assembled reads

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