Near-optimal probabilistic RNA-seq quantification

Bray and Pachter *et al.* Nature biotechnology(2016) doi:10.1038/nbt.3519

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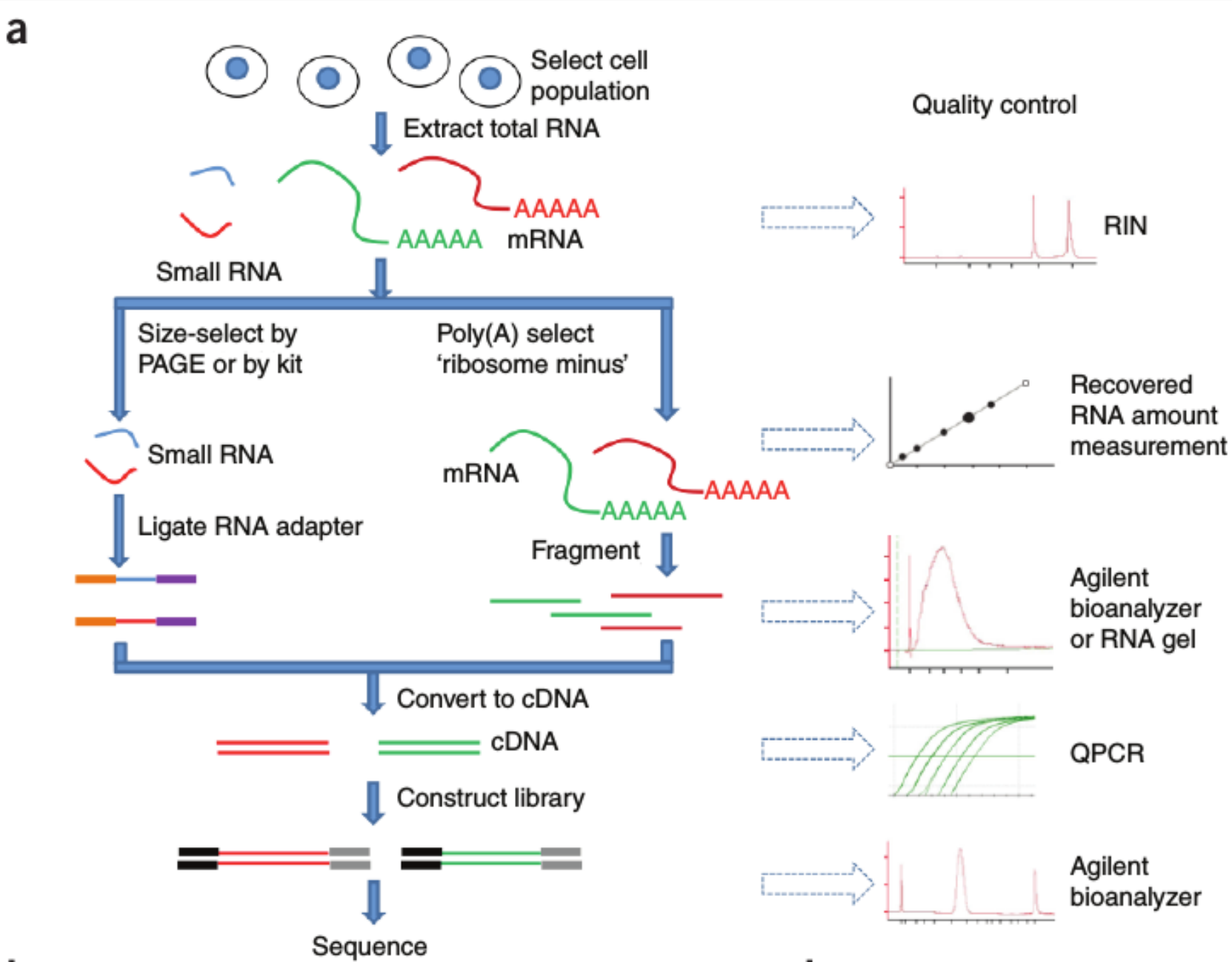
RNA-Seq Workflow



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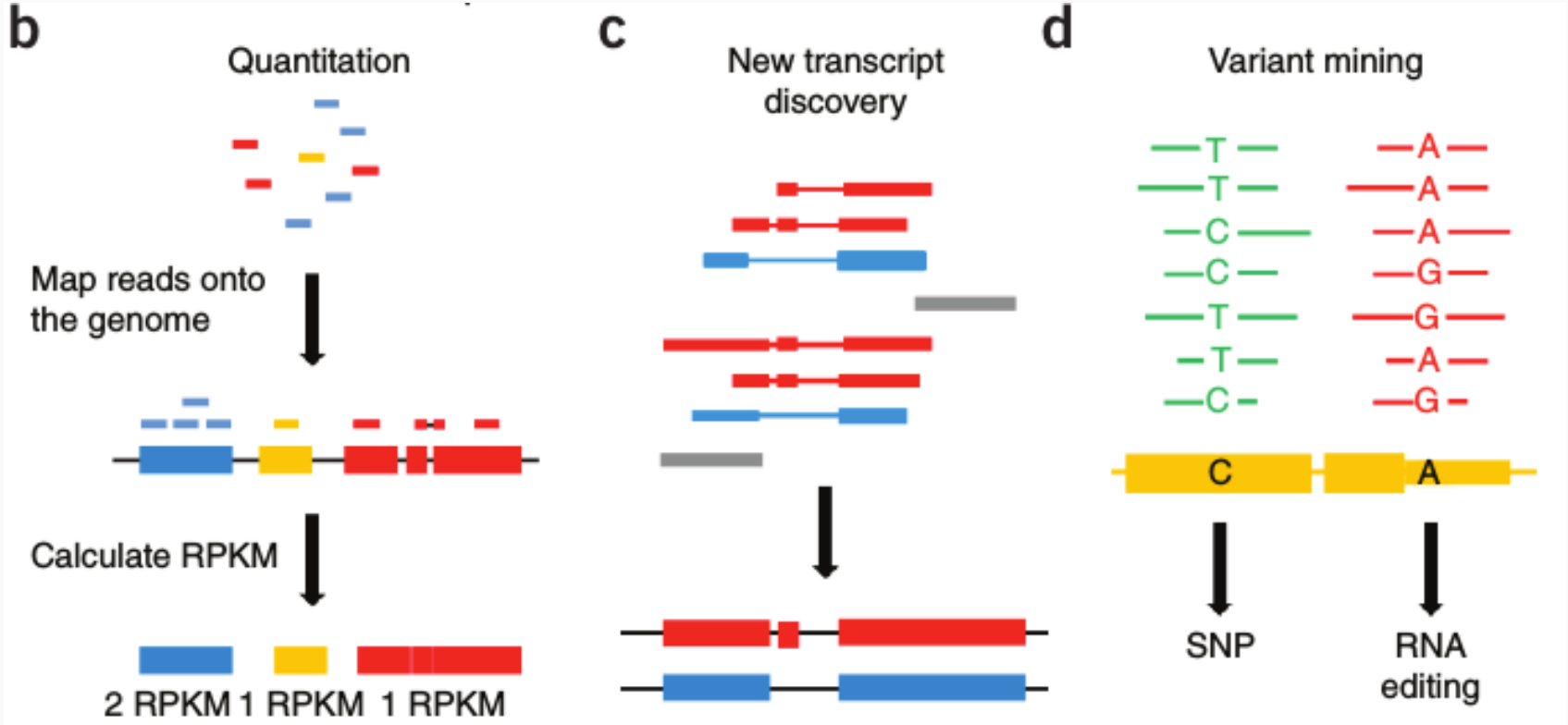

Zheng and Mortazavi(2012)

Motivation

- First two steps in typical RNA-Seq processing pipeline:

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  - Quantification
- Alignments are slow and probably not so important

It’s all about compatible transcripts

- Circumvent alignment step – Use information from $k-mers$
- Pseudoalignment: Find *compatible* transcripts for a read, without pinpointing where exactly it aligns

Method I

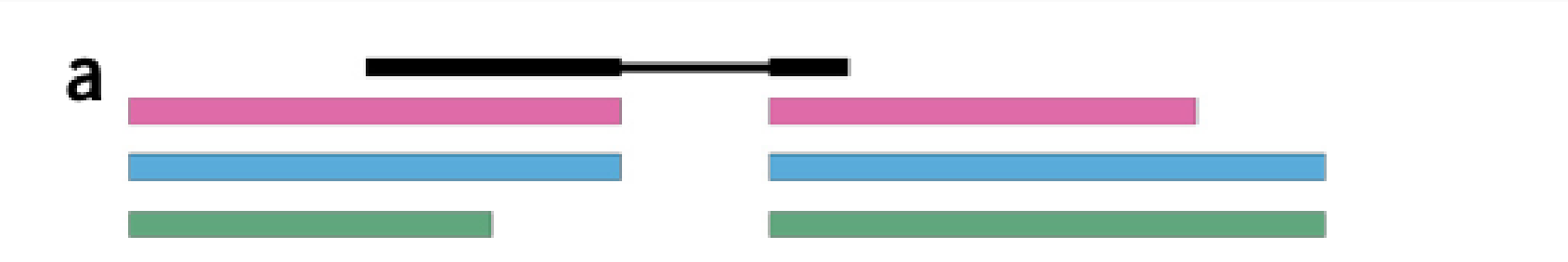

Figure 1: Reads and overlapping transcripts

Method II

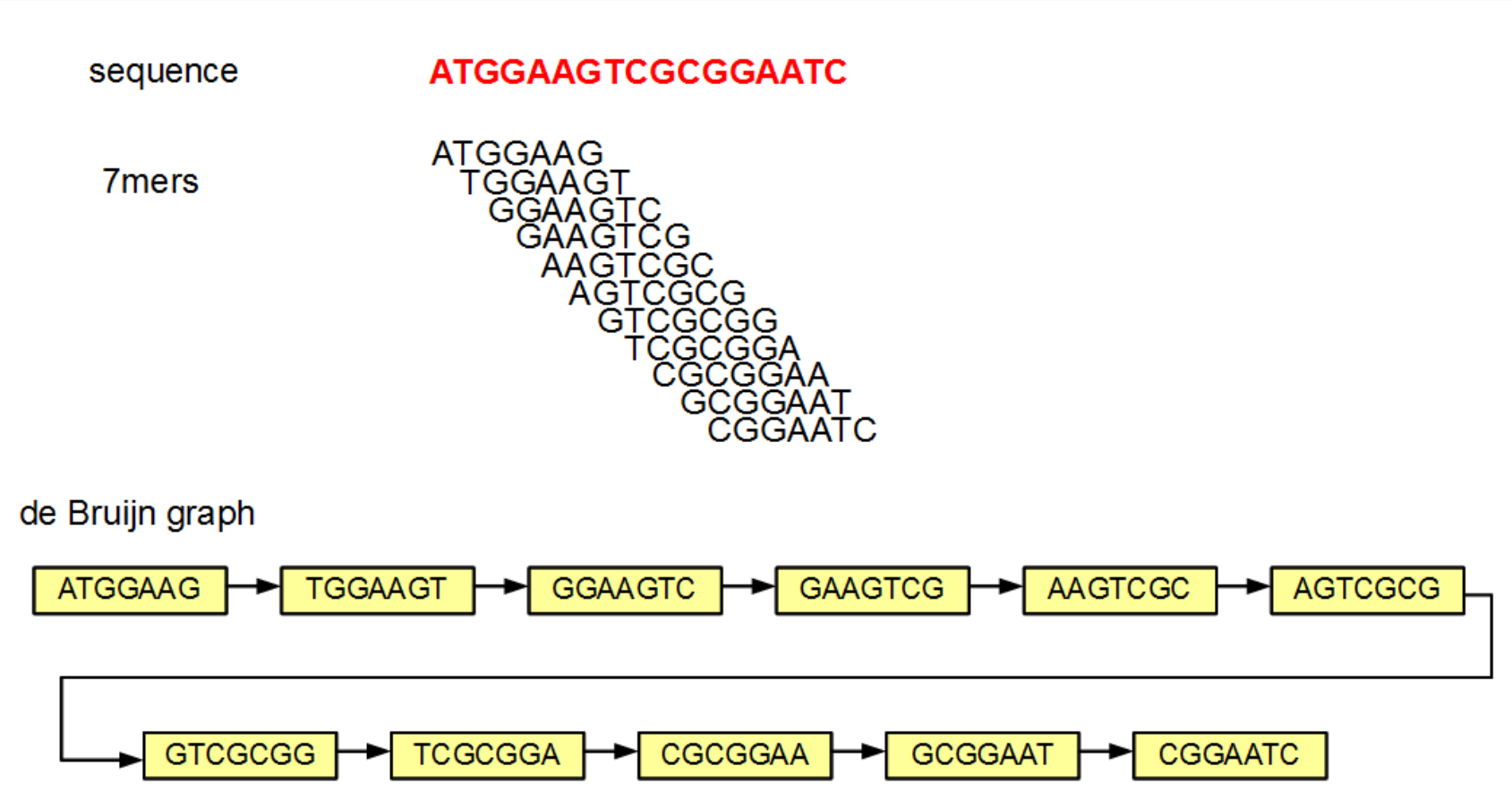

Figure 2: de Bruijn Graph

Method III

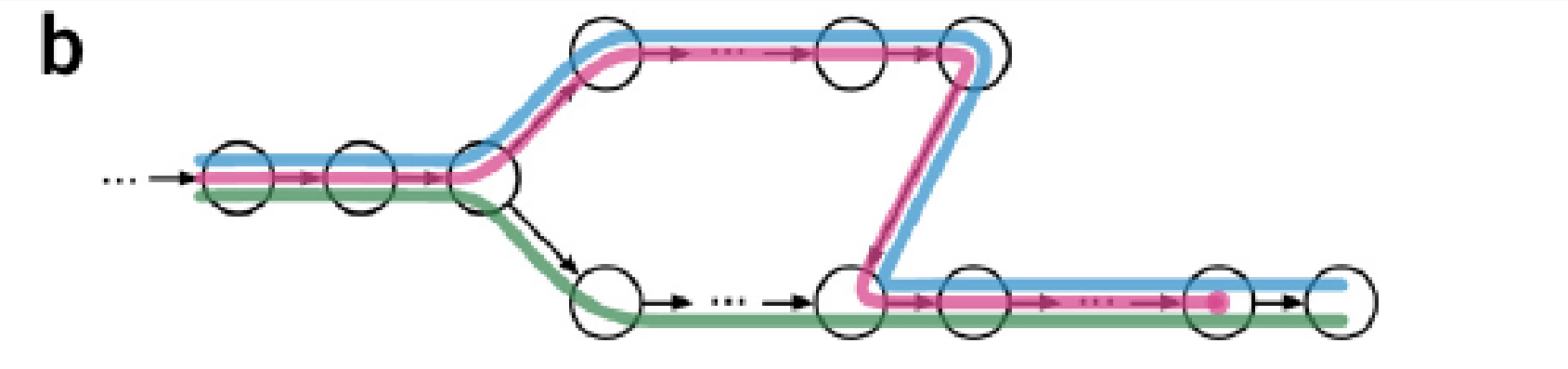

Figure 3: Transcriptome - de Bruijn Graph. Node = k — *mers*, Path = Transcript

Method IV

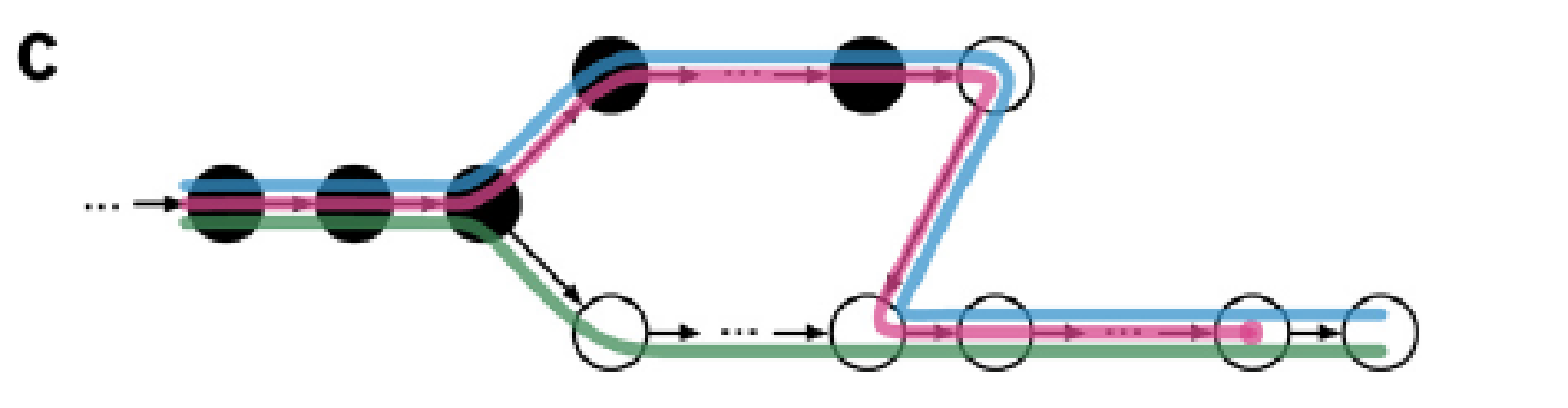

Figure 4: *k — mers* in read = black nodes

Method V

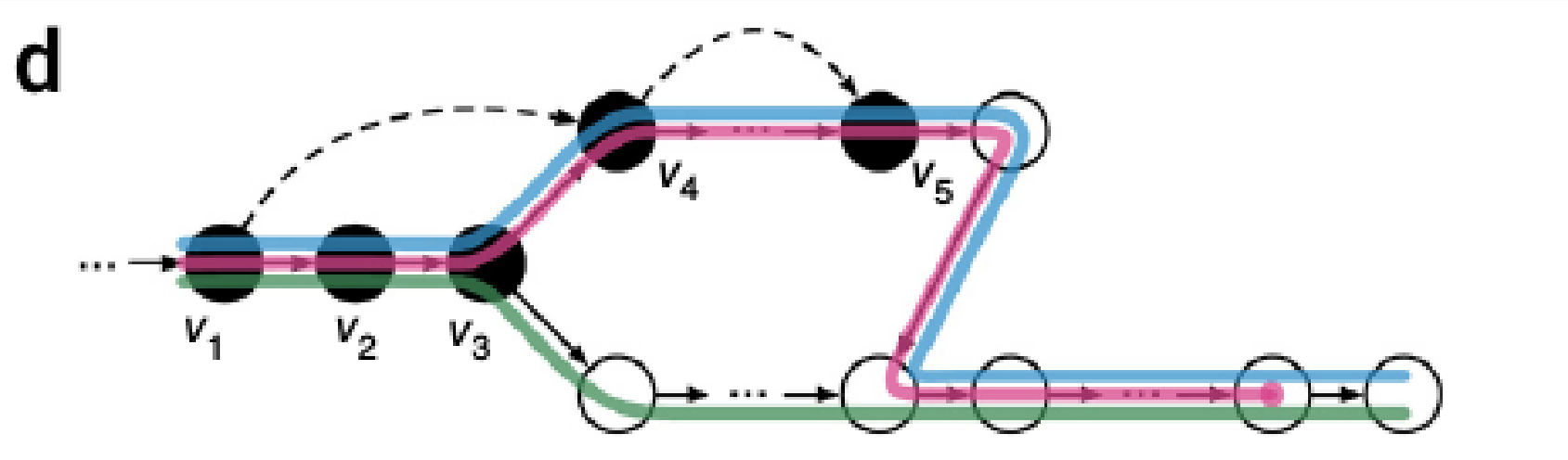

Figure 5: Nodes can be skipped if $k - mers$ did arise from blue transcript

Method VI

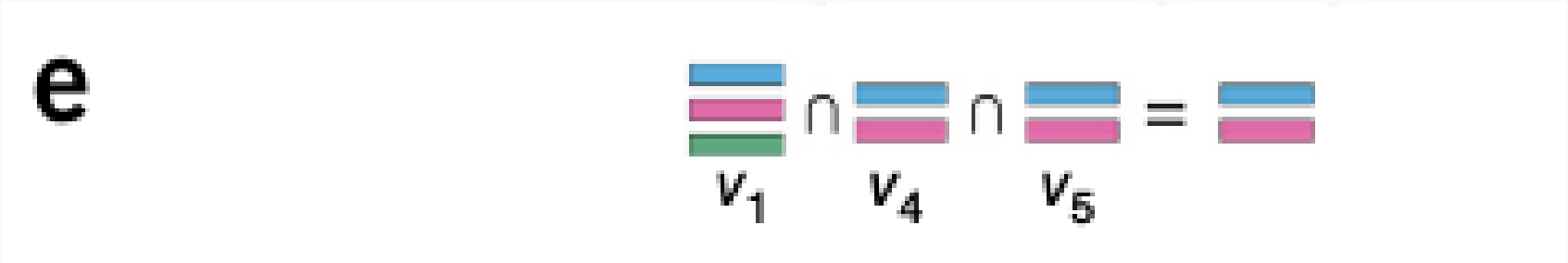

Figure 6: Intersection of k-compatibility class

Method VII

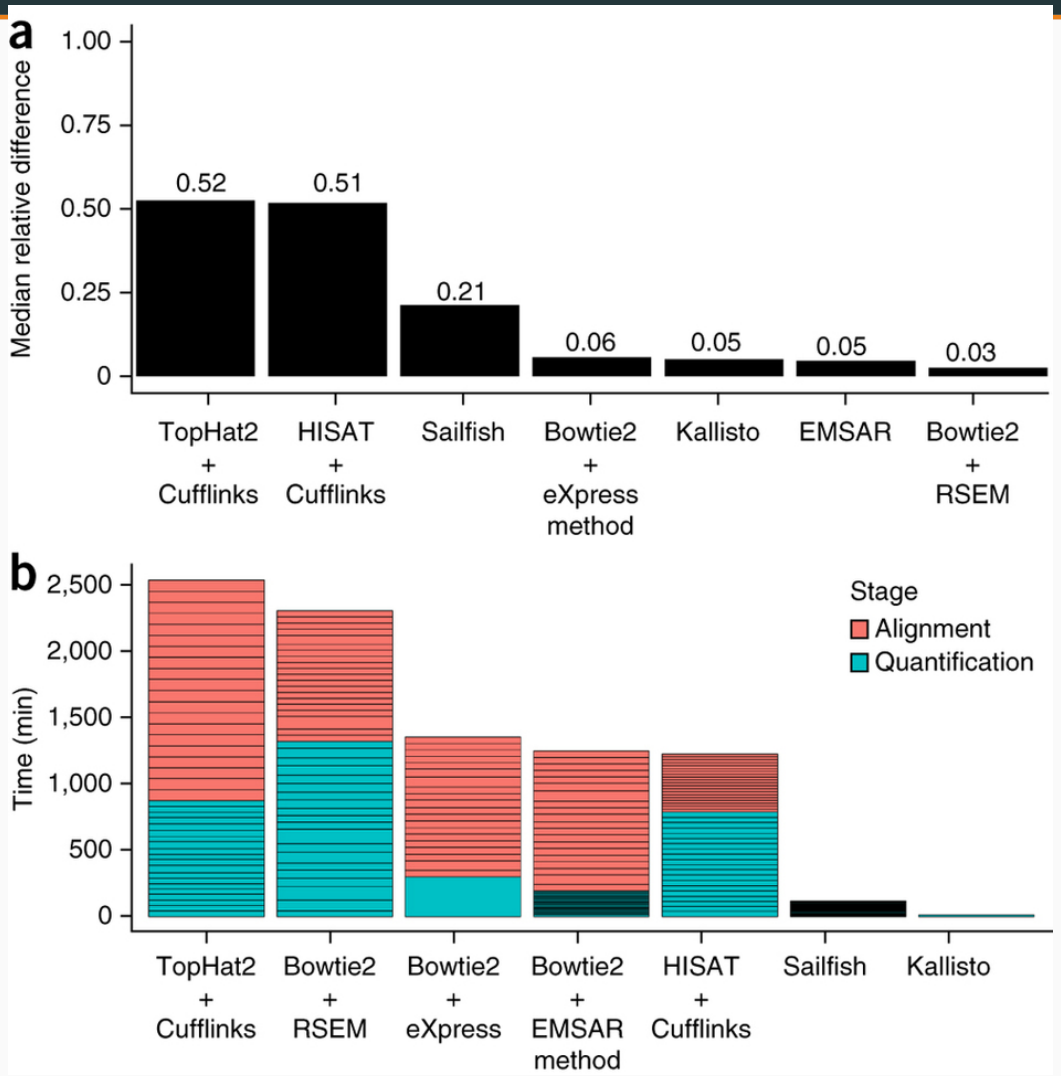

Figure 7: Quantification over a cup of coffee

Questions?

notes

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- Hash table stores mapping of each k-mer to the contig it is contained in