

Genome Analysis 2021

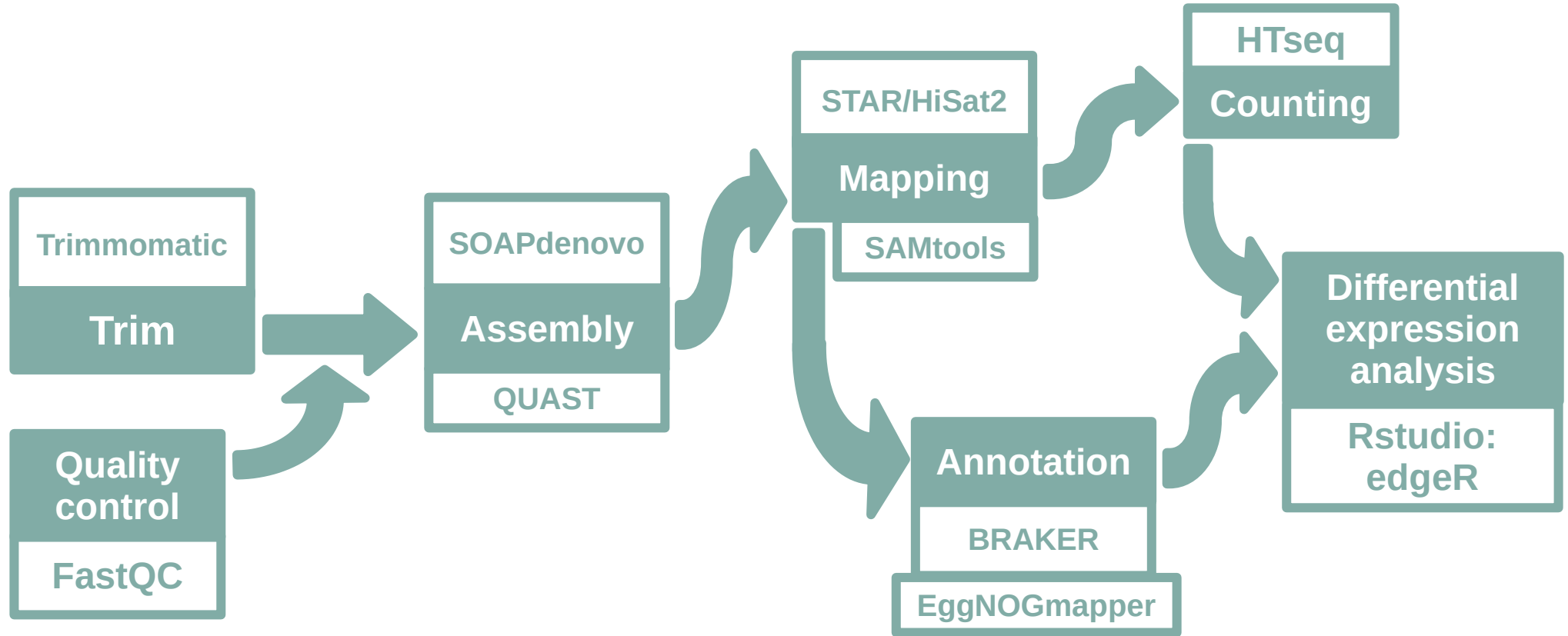
Paper II:

Transcriptomic and epigenomic characterization of the developing bat wing

Eckalbar et al.

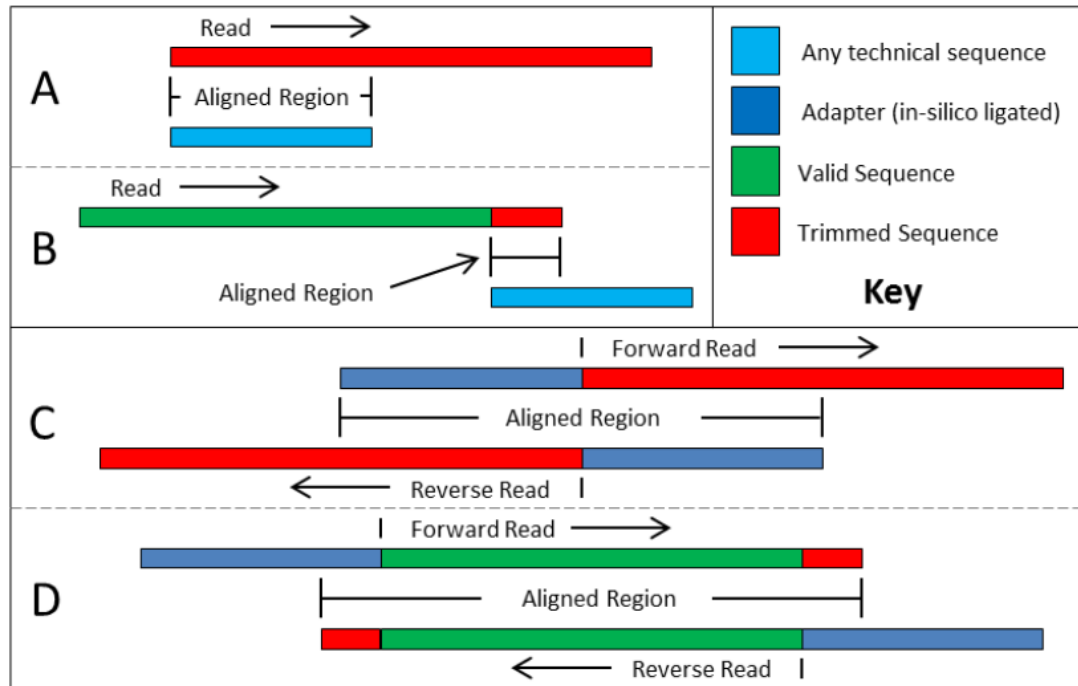
Milena Regina Trabert

Workflow



Trimmomatic & FastQC

ILLUMINA alignment parameters



Seed mismatches:..... **2**
palindrome clip threshold:..... **20**
simple clip threshold:..... **7**
minimum adapter length:..... **2**
keep both reads:..... **true**

LEADING & TRAILING:..... **17**
SLIDINGWINDOW: length..... **5**
min. avg. quality..... **20**
MINLEN:..... **20**

Assembly

SOAPdenovo

SOAPdenovo config file parameters

	Run 1	Run 2	Run 3
<code>reverse_seq</code>	0	1	1
<code>asm_flag</code>	3	3	1

`reverse_seq`: complementary reverse paired-end sequences (0=FR, 1=FF)

`asm_flag`: which parts of the reads are used (1=contig assembly, 3=contig and scaffold assembly)

Assembly

SOAPdenovo & QUAST

SOAPdenovo config file parameters

	Run 1	Run 2	Run 3
reverse_seq	0	1	1
asm_flag	3	3	1

Total length	141836091
Reference length	3990777
GC (%)	43.24
Reference GC (%)	36.99

reverse_seq: complementary reverse paired-end sequences (0=FR, 1=FF)

asm_flag: which parts of the reads are used (1=contig assembly, 3=contig and scaffold assembly)

Mapping

STAR (+ indexer)

Samtools functionality integrated

Unmapped: 69.41%

HiSat2 (+ indexer)

Samtools used separate (pipe)

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Gene content in scaffold 1?

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Gene content in scaffold 1?

Scaffold 1
576

Scaffold 2
2210

Scaffold 4
4933

Mapping

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Samtools functionality integrated

Unmapped: 69.41%

HiSat2 (+ indexer)

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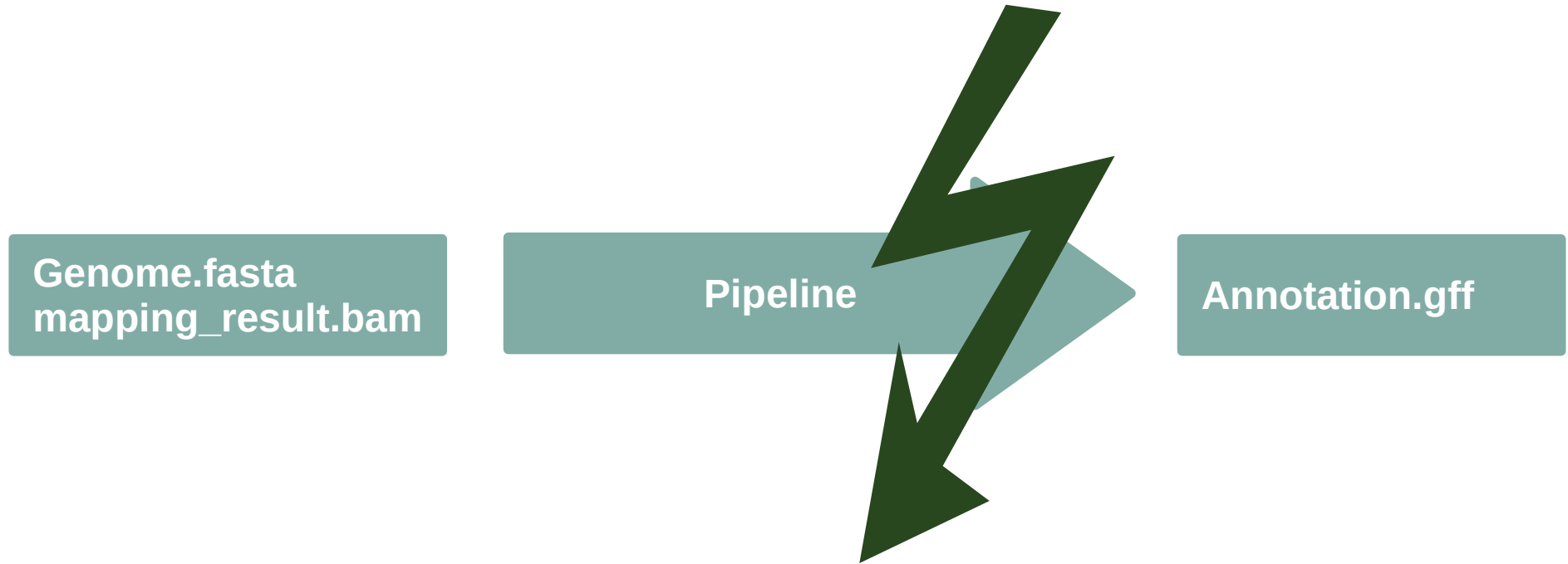
Mapping.bam

Read counting

HTSeq

Structural Annotation

BRAKER



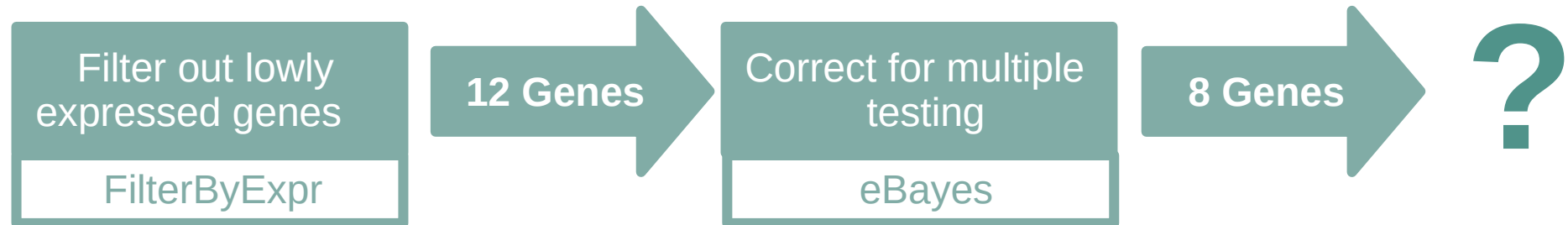
Functional Annotation

EggNOGmapper



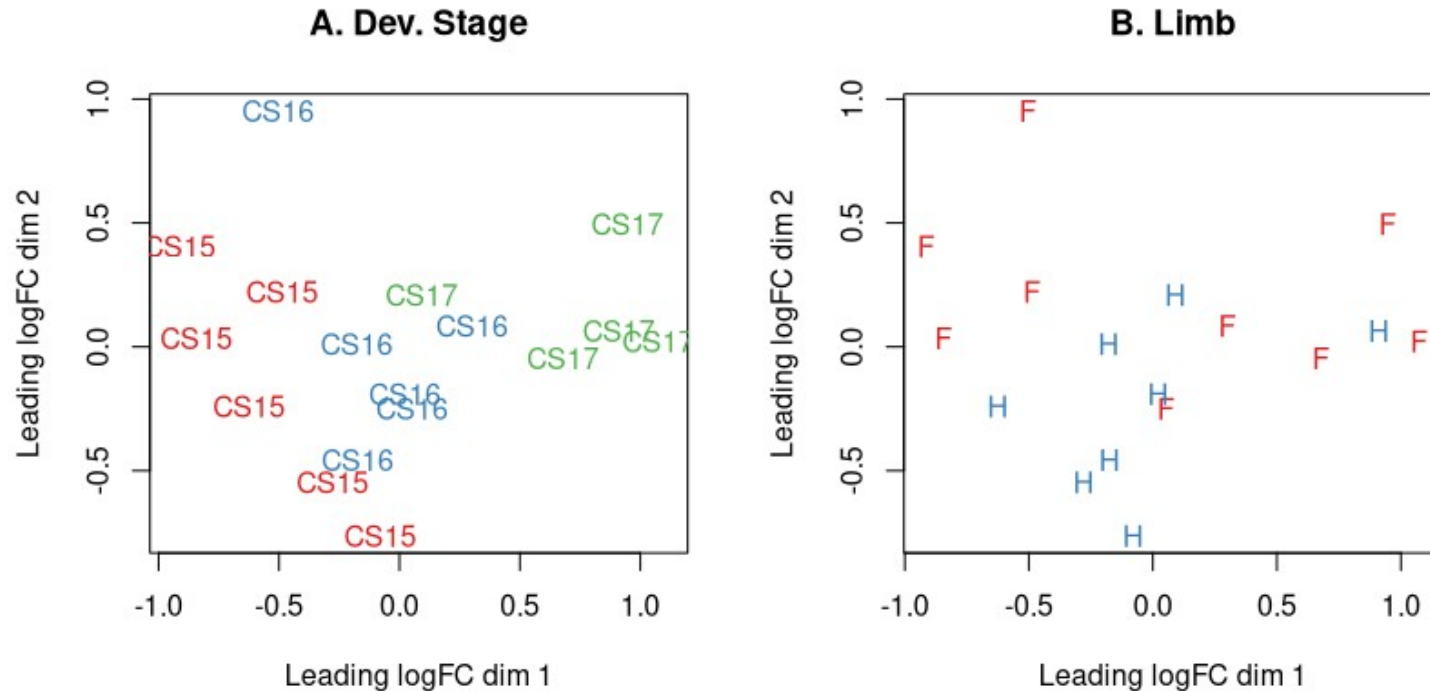
Differential expression analysis

Rstudio, edgeR



Differential expression analysis

Multidimensional scaling



Differential expression analysis

PCA, clustering, Heatmap

Paper: PC1: 47.9%, PC2 13.3%
Me: PC1: 89%, PC2: 6%