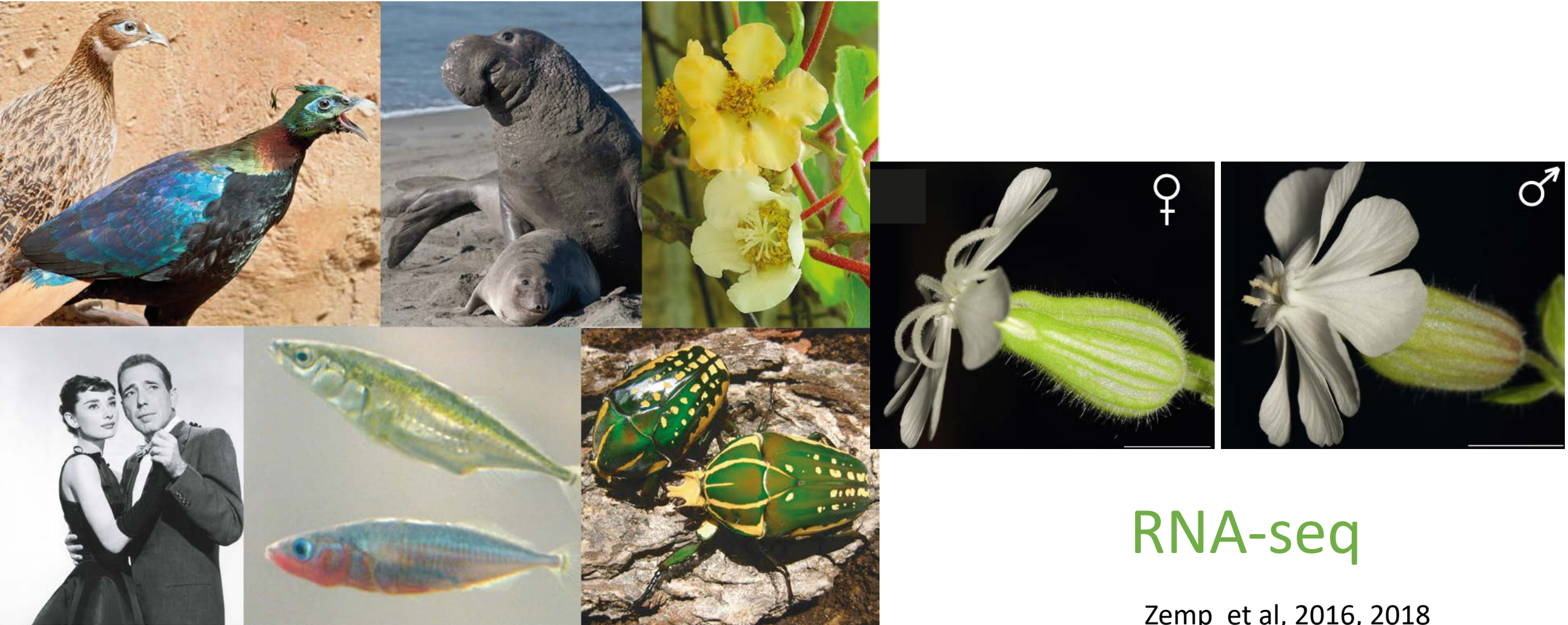# NextGenerationSequencing
Transcriptomics

Niklaus Zemp

June 2020

Bioinformatics

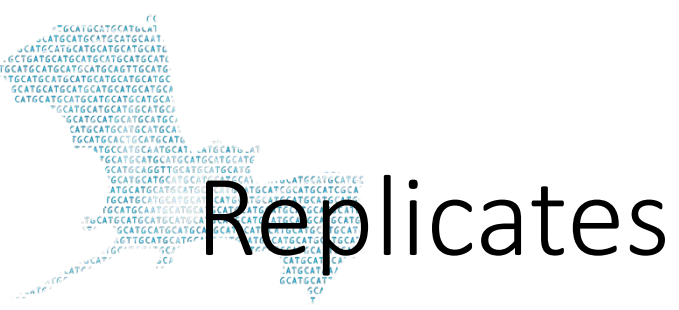Genetic Diversity Centre (GDC)

ETH Zurich

How important are sex chromosomes to express differences between females and males?

RNA-seq

Zemp et al, 2016, 2018
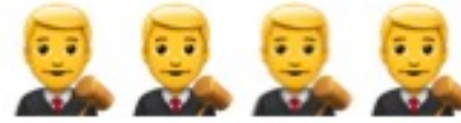
Replicates

Group 1   Group 2

A

B

C

D

Transcriptomics in non model organisms

1) Transcriptome: Short paired-end reads from a full-sib family and normalized 454 reads, develop a method to infer sex-linkage based on crosses

Option: Genome, PacBio or ONT to get full length transcripts

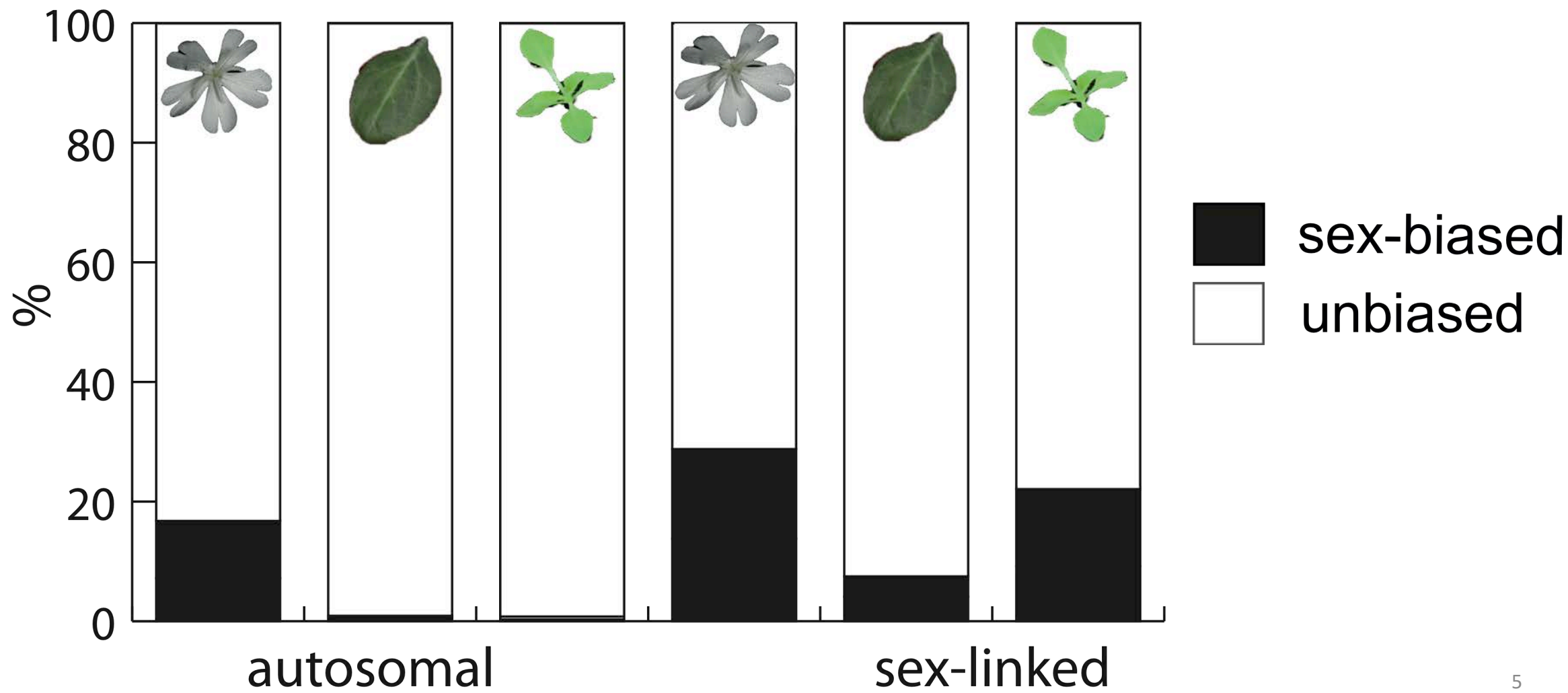**2) Counts:** Short single/paired-end reads for detecting differentially expressed genes

Method: Differentially expressed genes

U10_37 X Leuk_144.1

4 males (3 flower buds without calyx)
4 females (3 flower buds without calyx)

Distribution of genes with sex-biased expression

Validation