HENDRIX GENETICS

Exploring the genetic architecture of larval body weight in Black Soldier Fly

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Context of the study

Black Soldier Fly *Hermetia Illucens*

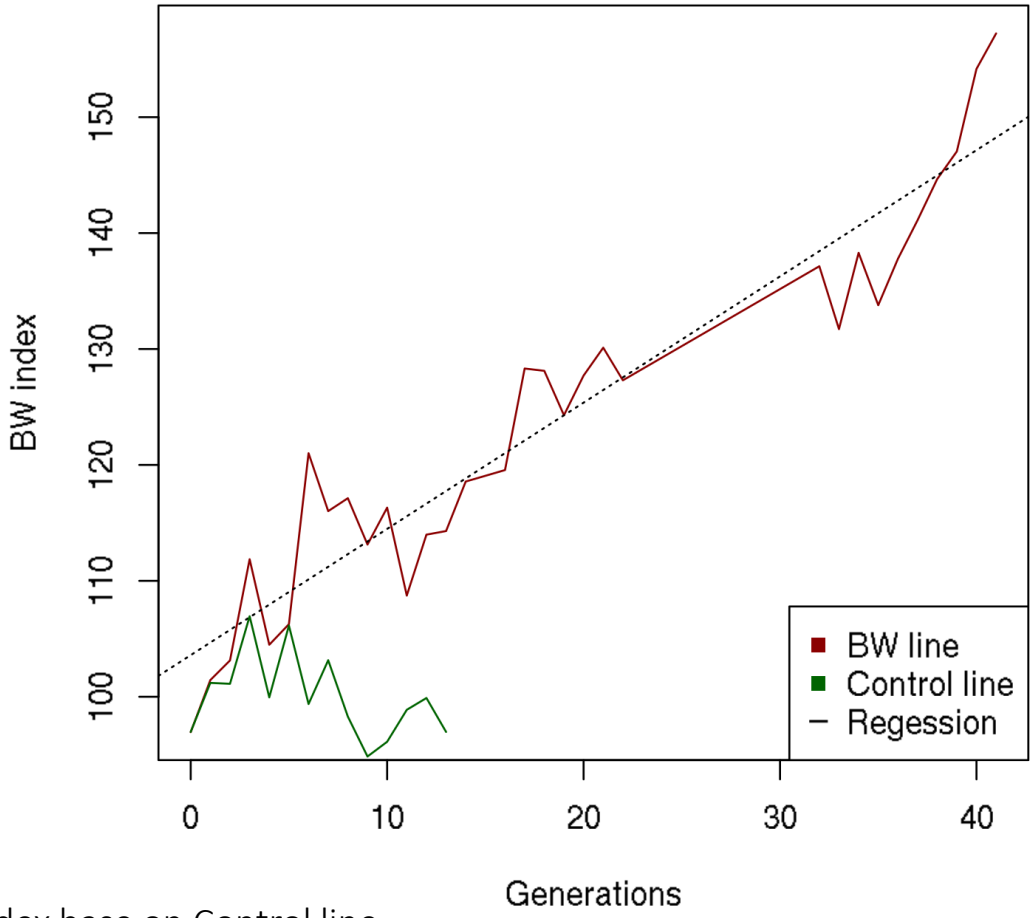
Relatively new species kept for protein production

Known for its waste recycling capacity
(“*Best Sustainable Friend*”)

Remarkable genetic improvement of body weight (BW)
(Facchini et al. 2019)
Currently + 5 standard deviations in 40 generations
(6 week generation interval)

Little is known on the genetic architecture of BW

Evolution of BW index over generations



BW index base on Control line
average 100
standard deviation 10
Gain per generation : + 1.09

Material available

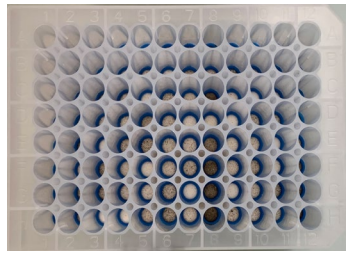
96 flies sampled per generation

DNA extraction on membrane

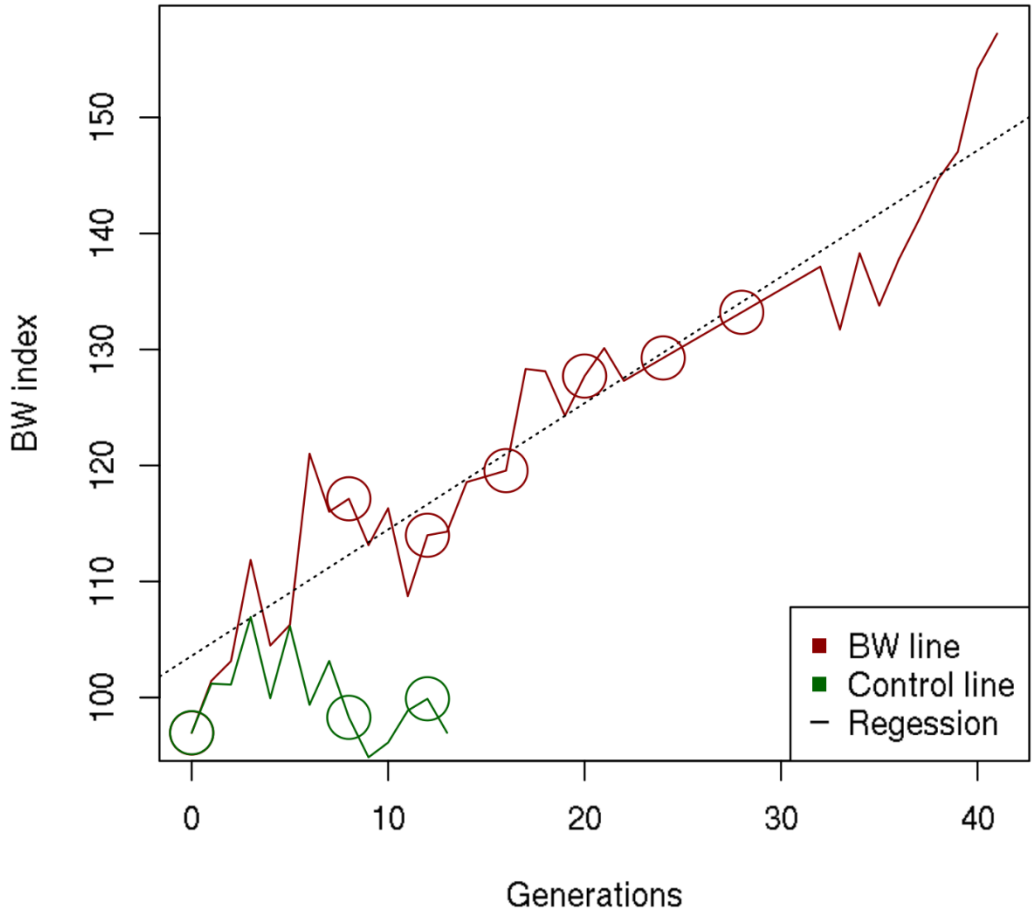
Check DNA quality (concentration / absorbance ratio)

Normalization and pooling (best 90 DNA)

Pool-sequencing 150 bp paired-end on NovaSeq X



Evolution of BW index over generations



◯ Generation sampled (9)

Bioinformatic pipeline

Run on high-performance computer

Sequence quality control

Alignment on reference genome

GCF_905115235.1_iHerIll2.2.curated.20191125

Variant calling (3 software)

Selection of SNP overlap

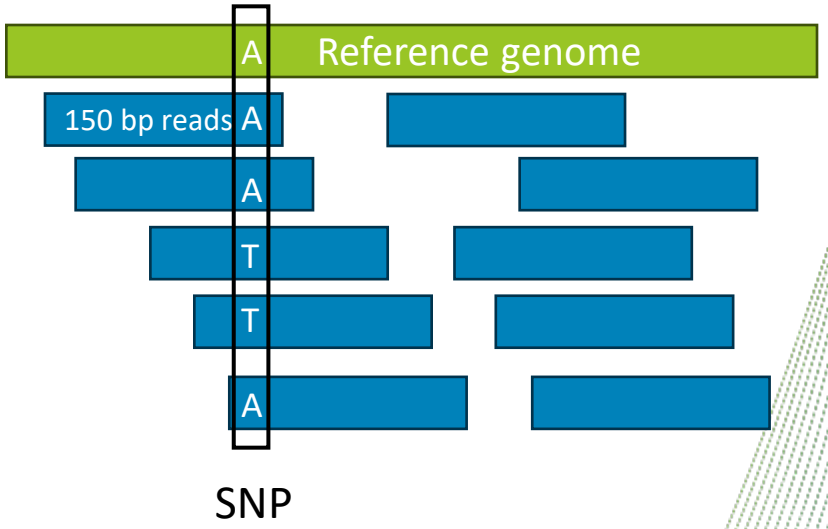
18 M SNP

VCF production

Popoolation2 toolkit

.sync file

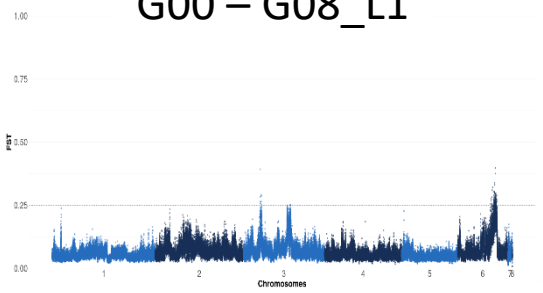
Population allelic frequencies



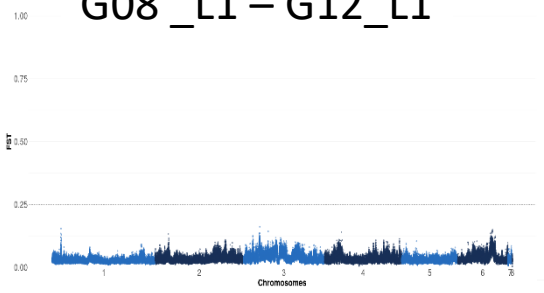
F_{ST} analysis

- **Wright's Fixation index:** the proportion of the total genetic variance contained in a subpopulation relative to the total genetic variance
- Main regions detected based on 12 first generations presented at EAAP 2023
- 1 vs 1 for 9 populations (3 control line, 6 BW line) makes 36 analyses…

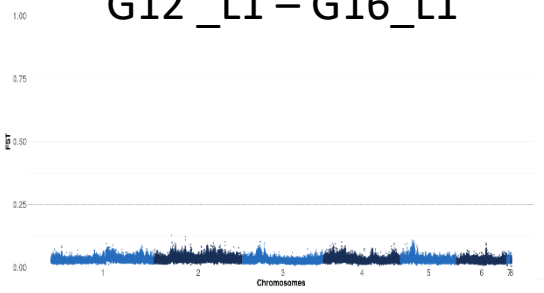
G00 – G08_L1



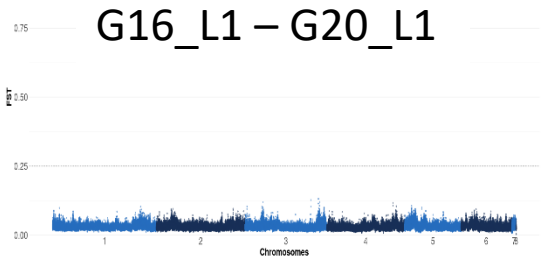
G08 _L1 – G12_L1



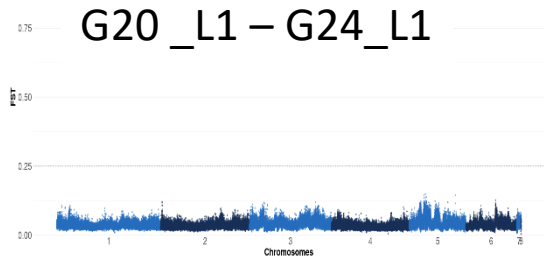
G12 _L1 – G16_L1



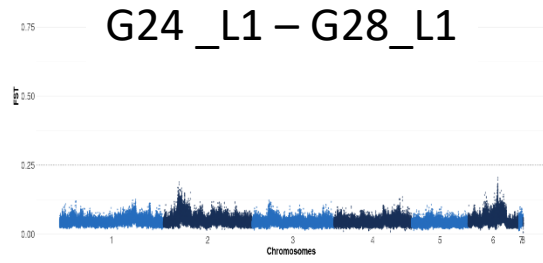
G16_L1 – G20_L1

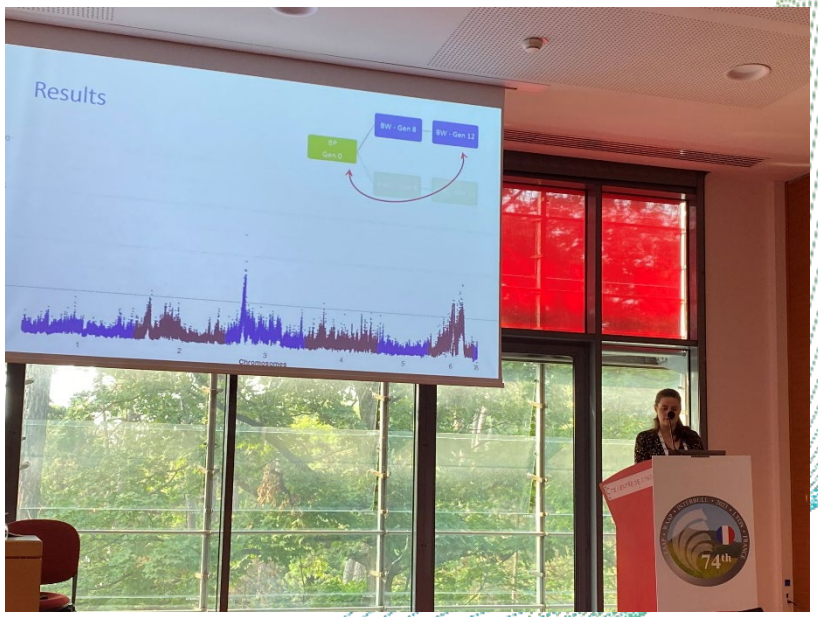


G20 _L1 – G24_L1



G24 _L1 – G28_L1



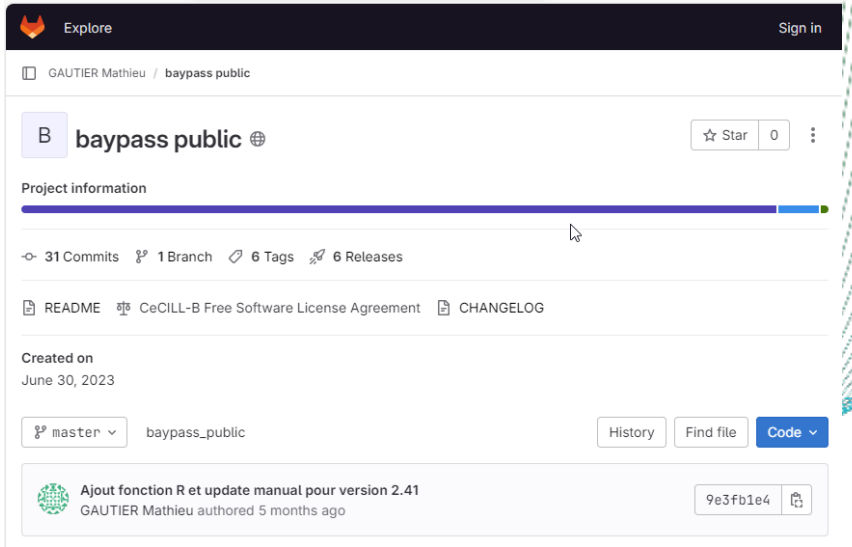


BayPass approach

- Population genomics software package
- Works with pooled sequences (frequency estimates of SNP)
- Includes multiple populations in one single analysis
- Accounts for covariance structure among population allele frequencies (resulting from the shared history of populations)

Gautier (2015). Genetics. Genome-Wide Scan for Adaptive Differentiation and Association Analysis with population-specific covariables.

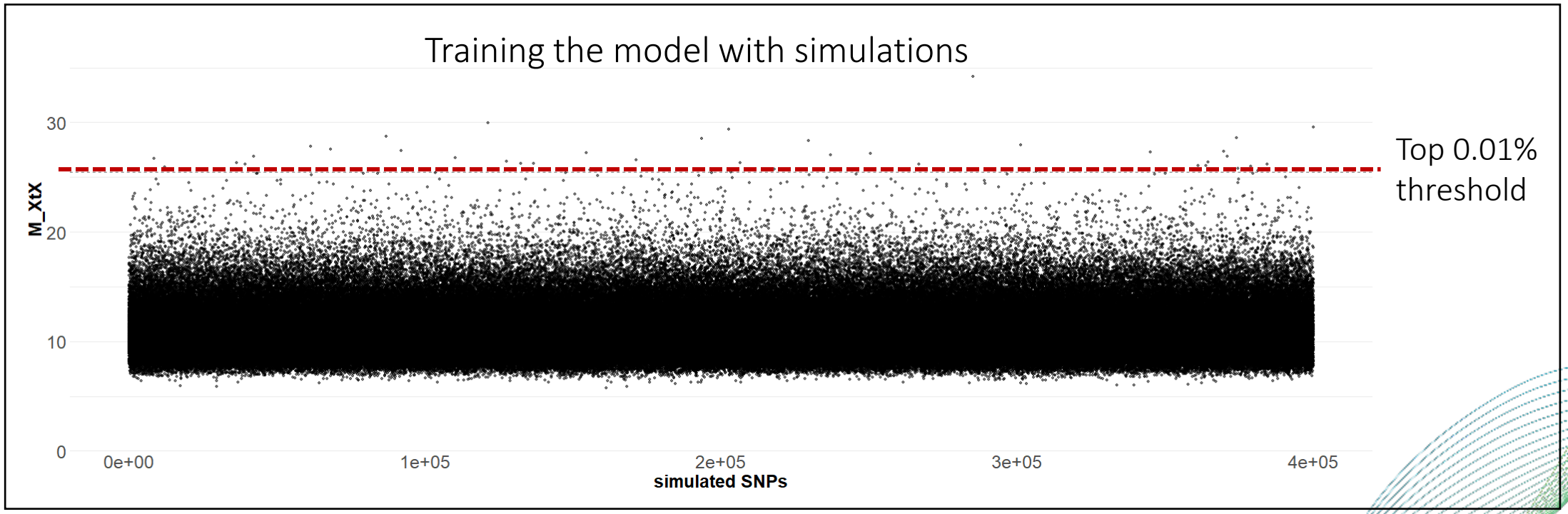
⇒ Applied to 600 K SNP located in genes



BayPass threshold definition

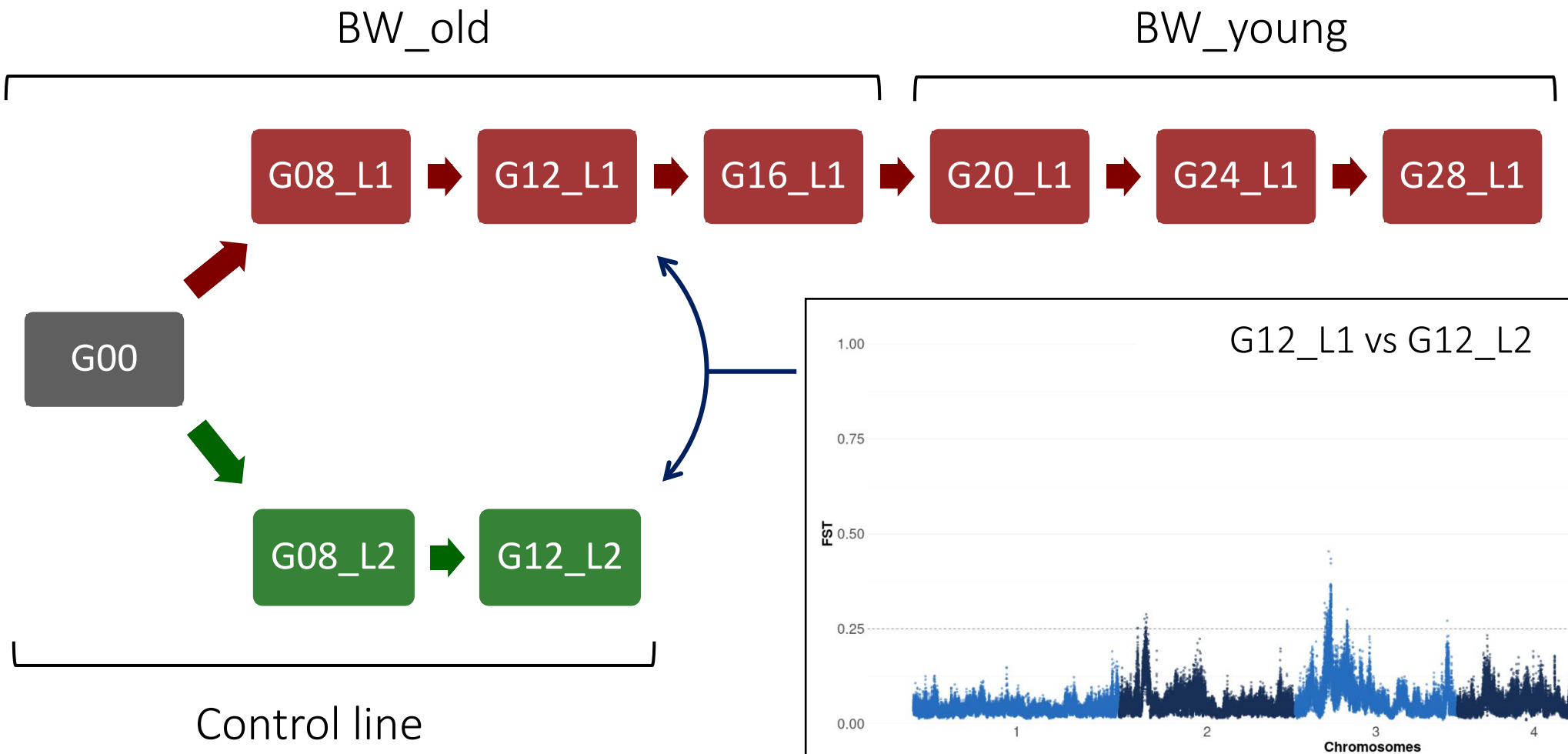
Gunther and Coop (2013). Genetics. Robust identification of local adaptation from allele frequencies

- Criteria: XtX statistics (Gunther and Coop)
- XtX is "*SNP-specific F_{ST} explicitly corrected for the scaled covariance of population allele frequencies*" as defined by Gautier
- Simulation runs provides threshold levels for detection from empirical distribution

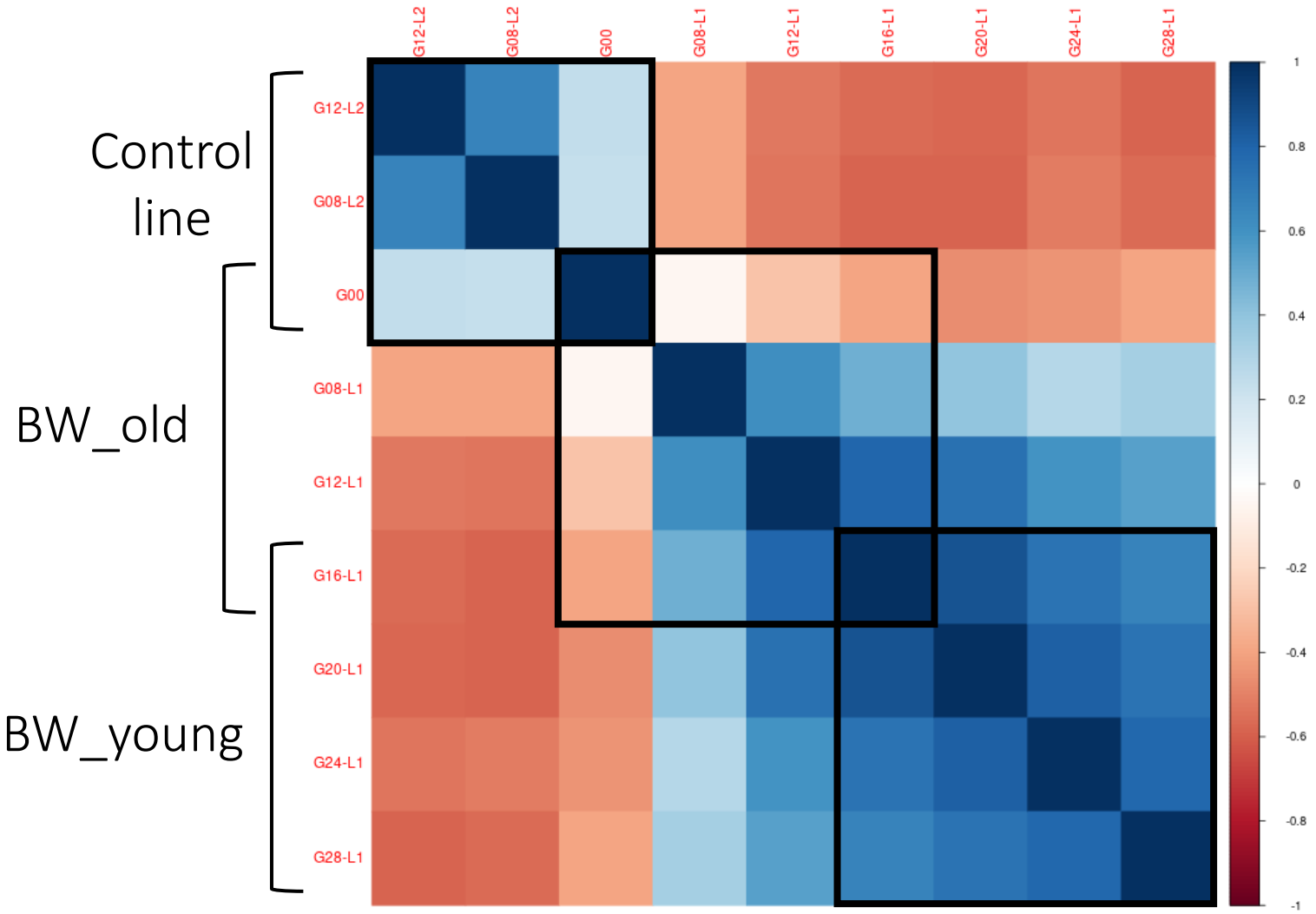


Population split

- F_{ST} showed 3 main blocks of differentiation split in the analysis



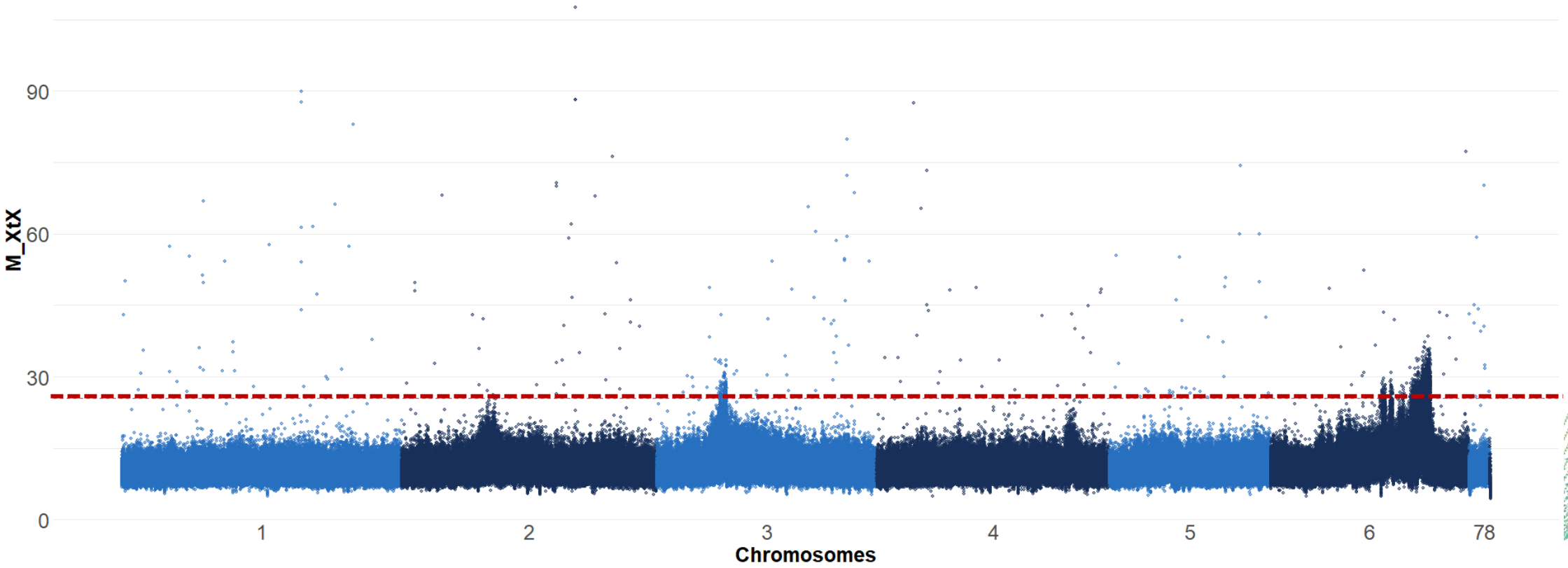
Population split



- Considered in Ω matrix for scaling reasons

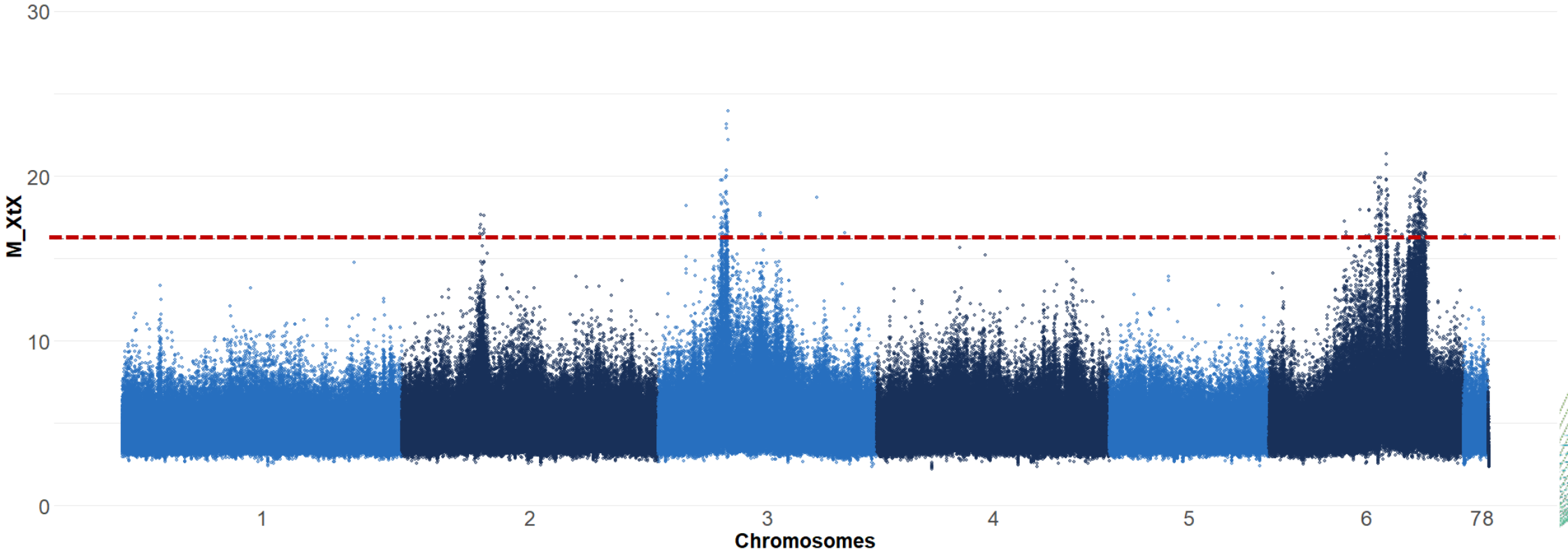
Genes detected for all populations

- 416 genes detected
- Some regions missed because of scaling



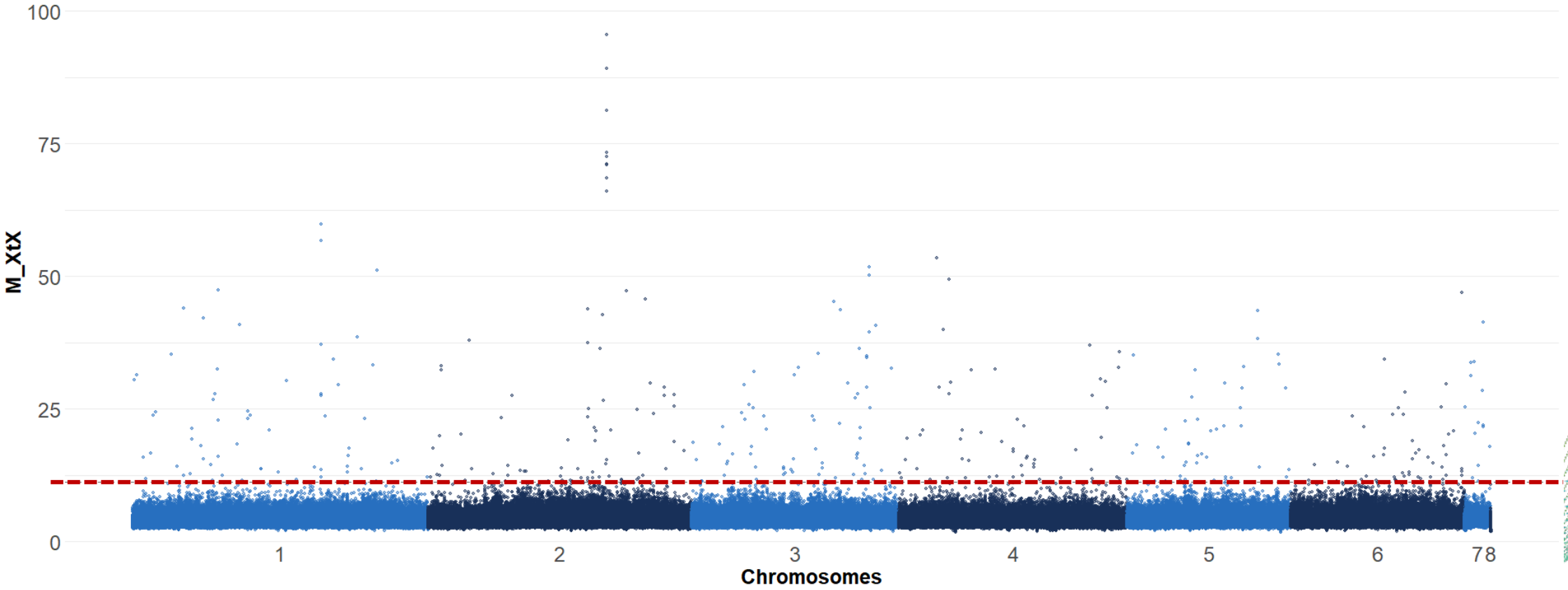
Genes detected for BW_old

- 158 genes detected



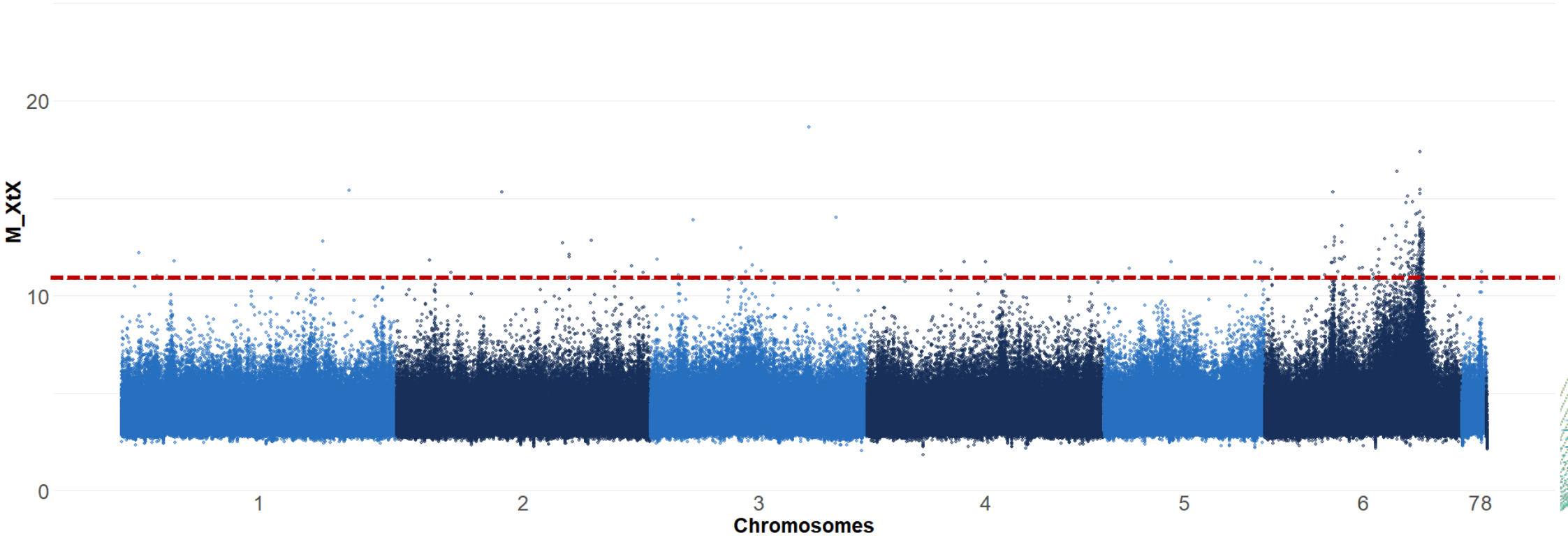
Genes detected for BW_young

- 312 genes detected
- More polygenic



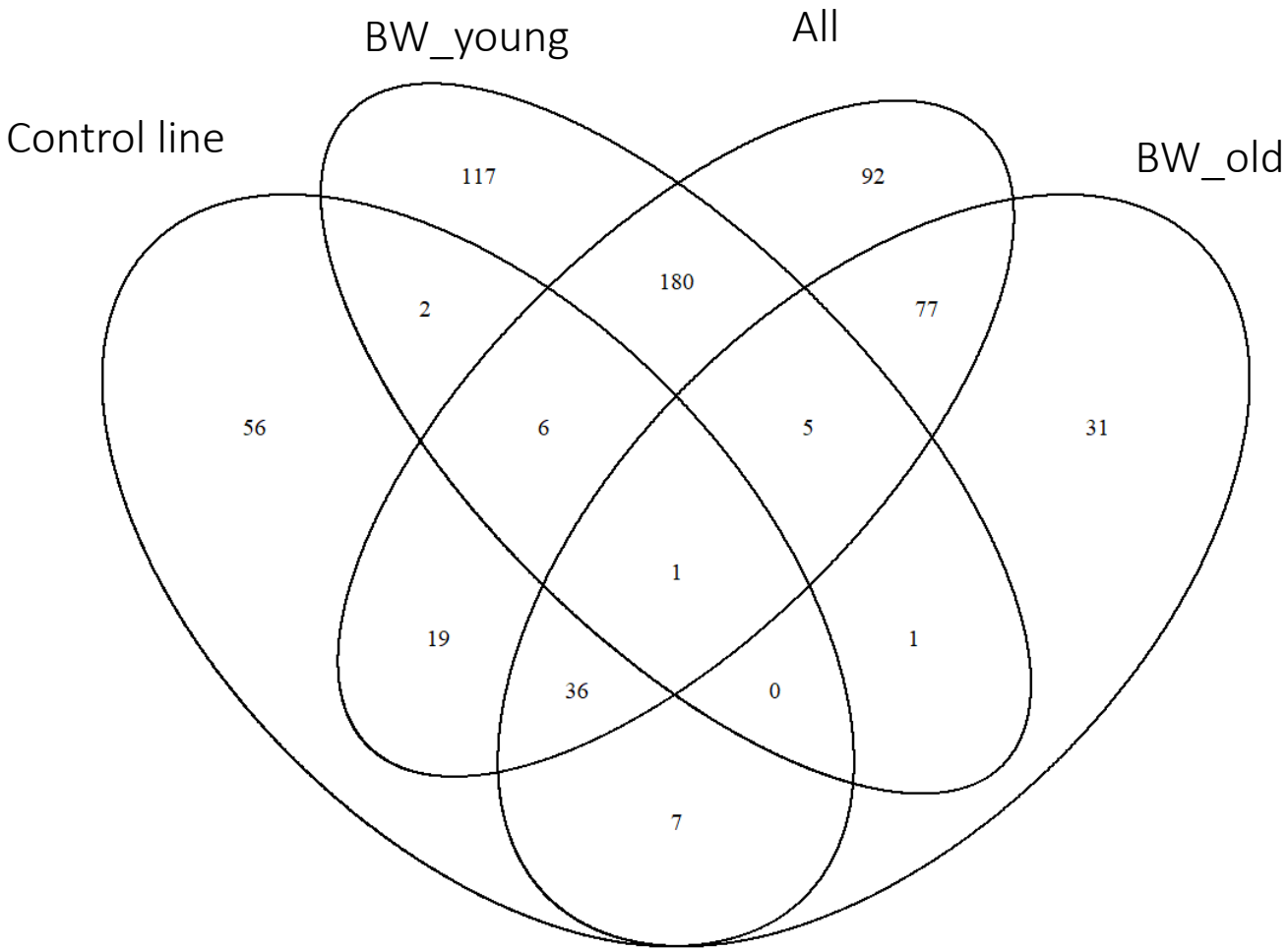
Genes detected for Control Line

- 127 genes detected
- Adaptation to the R&D environment conditions



Combination of results

- Total of 630 unique genes detected



=> Used for gene ontology enrichment analysis

Extra knowledge from orthologs

- Genes in a different species evolved from a common ancestral gene
- Drosophila melanogaster (fruit fly) has better defined genes in databases
- Several interesting genes detected having impact on **growth** and **development**

Key-messages

- Strong evolution of the genome of Black Soldier Fly when **genetic selection** is applied
- Gene ontology enrichment analysis based on molecular function highlighted some groups of genes, more precision from orthoglogs
- Better knowledge of the genome of the species help a **better monitoring of the selection applied**, and follow selection signatures

Acknowledgements

- Protix Team for data record
- HG lab in Ploufragan (France) for DNA extraction
- HG Research &Technology Center, and in particular Margot Slagboom, for advice

Announcement

Geneticist within the
global genotyping team

We are hiring!

Geneticist with a focus
on **Insect Genetics**

Thanks for your attention

Better Breeding Today. Brighter Life Tomorrow.

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