GEroNIMO and RUMIGEN Joint Final Event

Breeding the Future

Genomics, Epigenomics & Societal
Acceptability for Sustainability in Livestock

Integration of GEroNIMO omics data to reveal details about the genetic architecture behind efficiency-related traits

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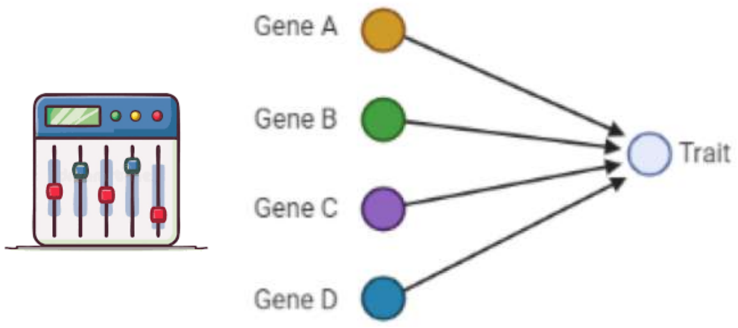
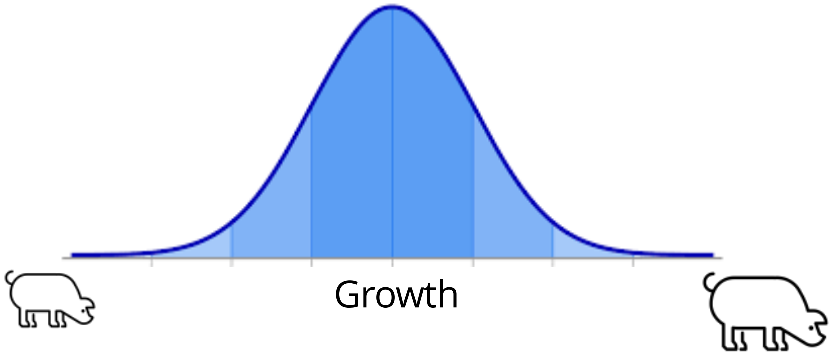
Efficient Livestock Production (ELP) traits

Sustainability ~ efficient use of resources

Most relevant traits for animal production, including growth, feed efficiency, and sustainability-related, are complex or polygenic.





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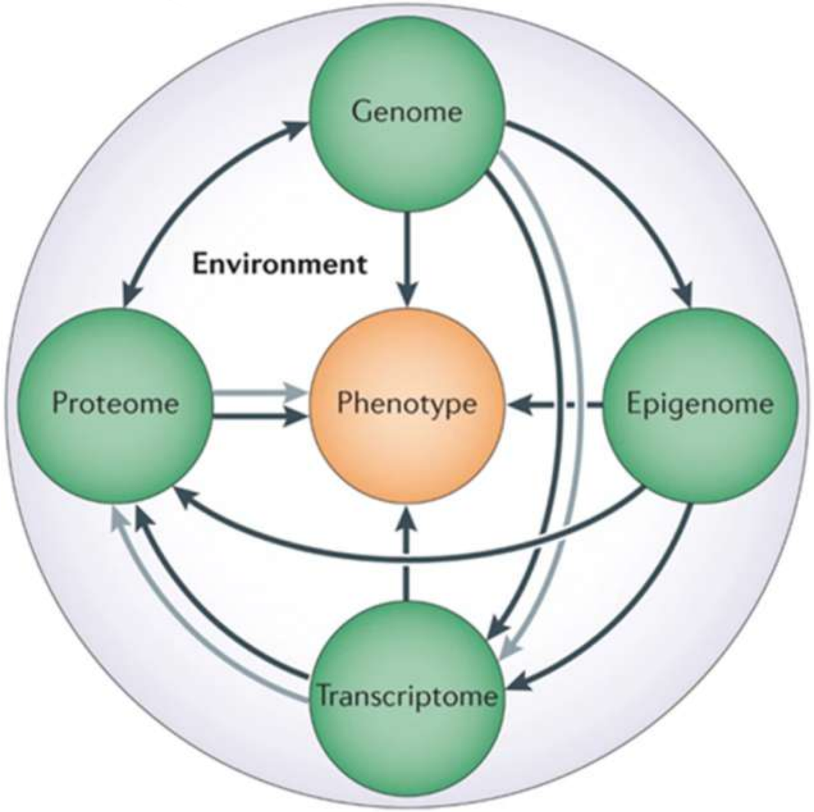

Ritchie, M. D. et al. (2015)

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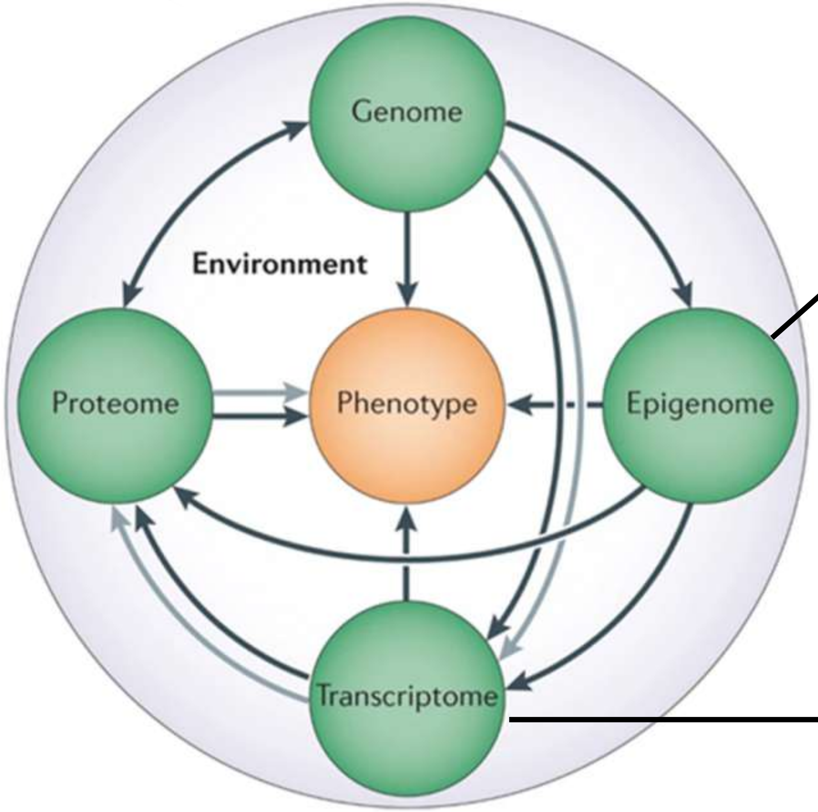
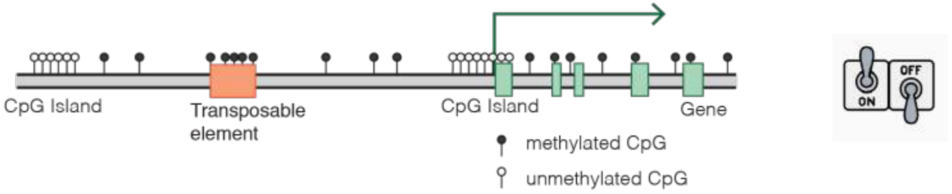


Ritchie, M. D. et al. (2015)

DNA methylation

Chemical tags attach to a particular location within DNA where they turn a gene on or off, thereby regulating the production of proteins that the gene encodes.



Messenger RNA (mRNA)

Single-stranded RNA is involved in protein synthesis. It is made from a DNA template during transcription.

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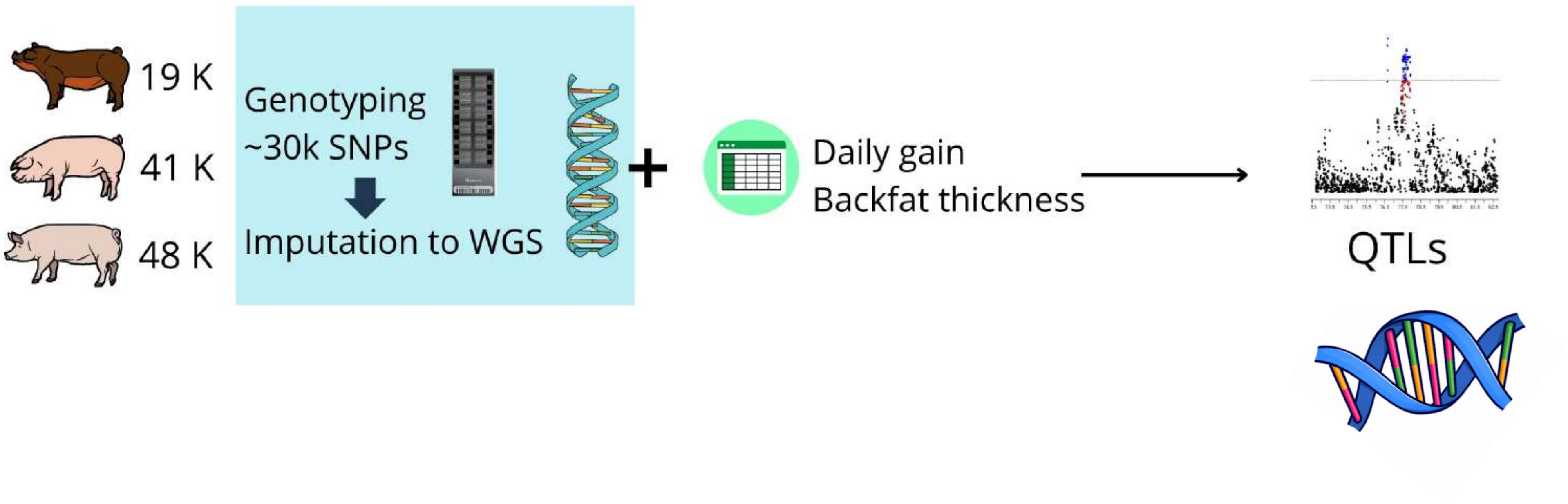
Genomic background of ELP traits

Genome-wide association study



19 K

41 K

48 K

Genotyping
~30k SNPs

Imputation to WGS

+

Daily gain
Backfat thickness

QTLs

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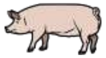
Genomic background of ELP traits

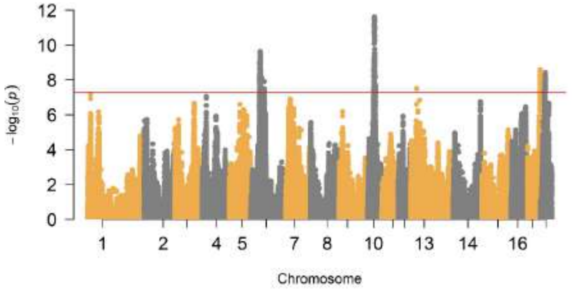
DUROC (n= 19K)

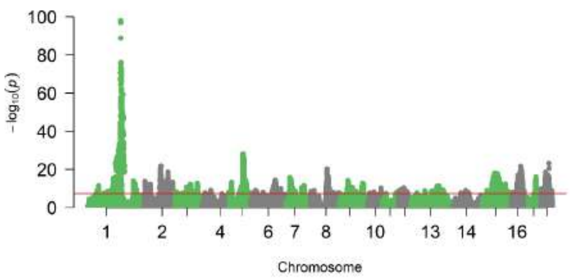
LANDRACE (n= 41 K)

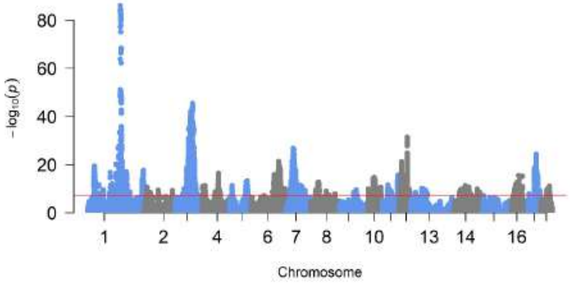


YORKSHIRE (n= 48K)

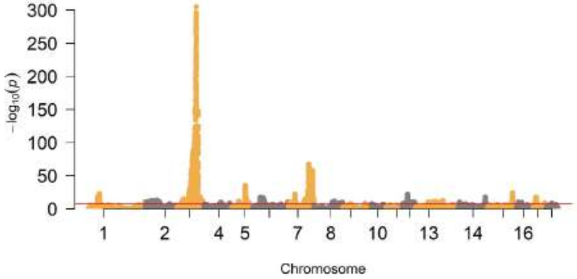
Daily gain

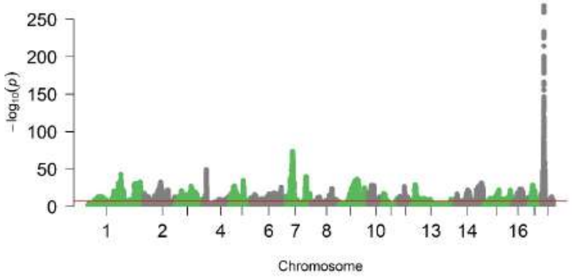


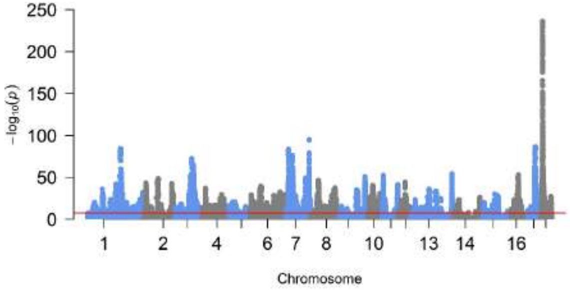




Backfat thickness







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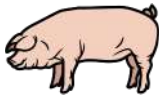
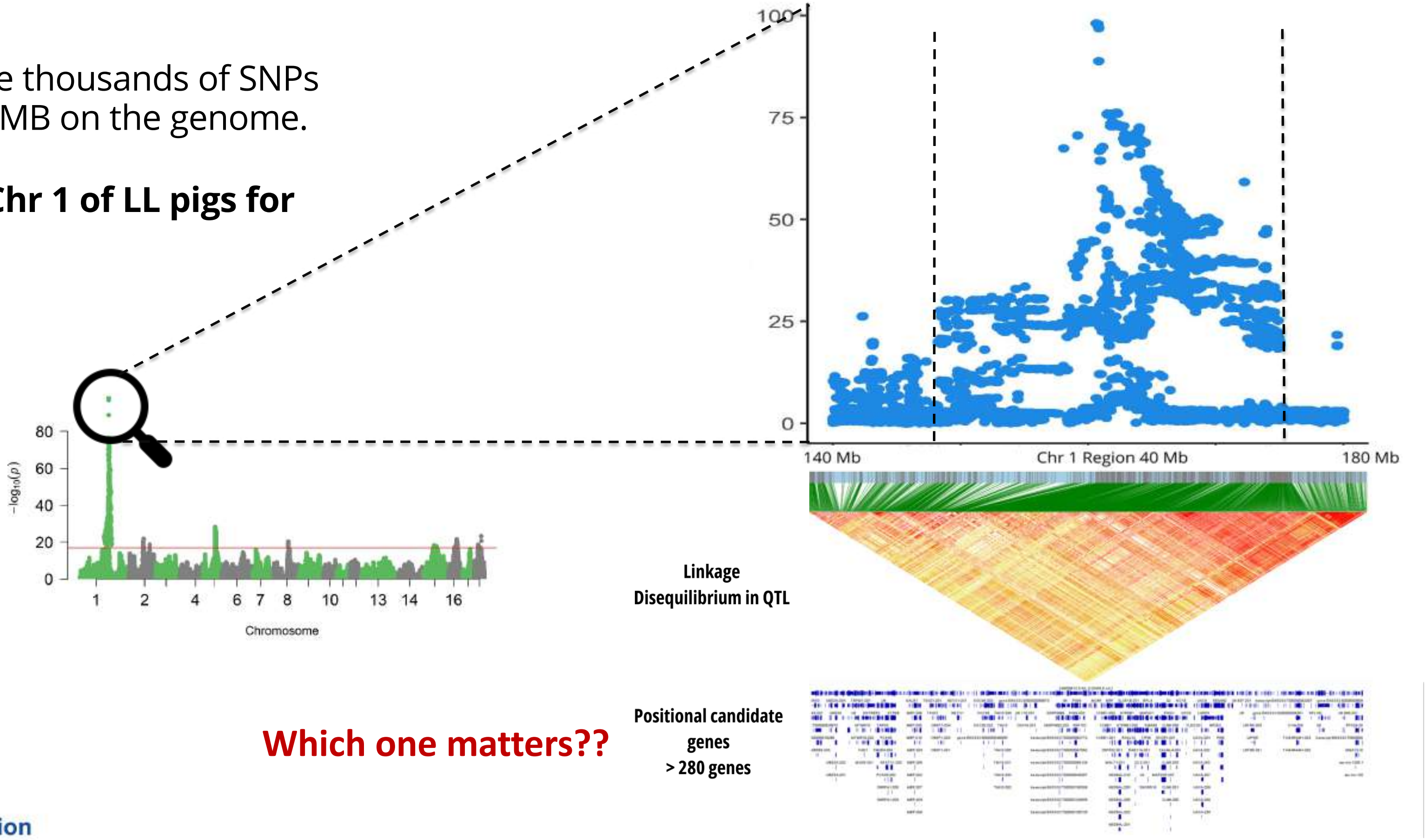
Genomic background of ELP traits

Most QTLs include thousands of SNPs spanning several MB on the genome.

Example **QTL in Chr 1 of LL pigs for daily gain**:



Daily gain



Linkage Disequilibrium in QTL

Positional candidate genes > 280 genes

Which one matters??

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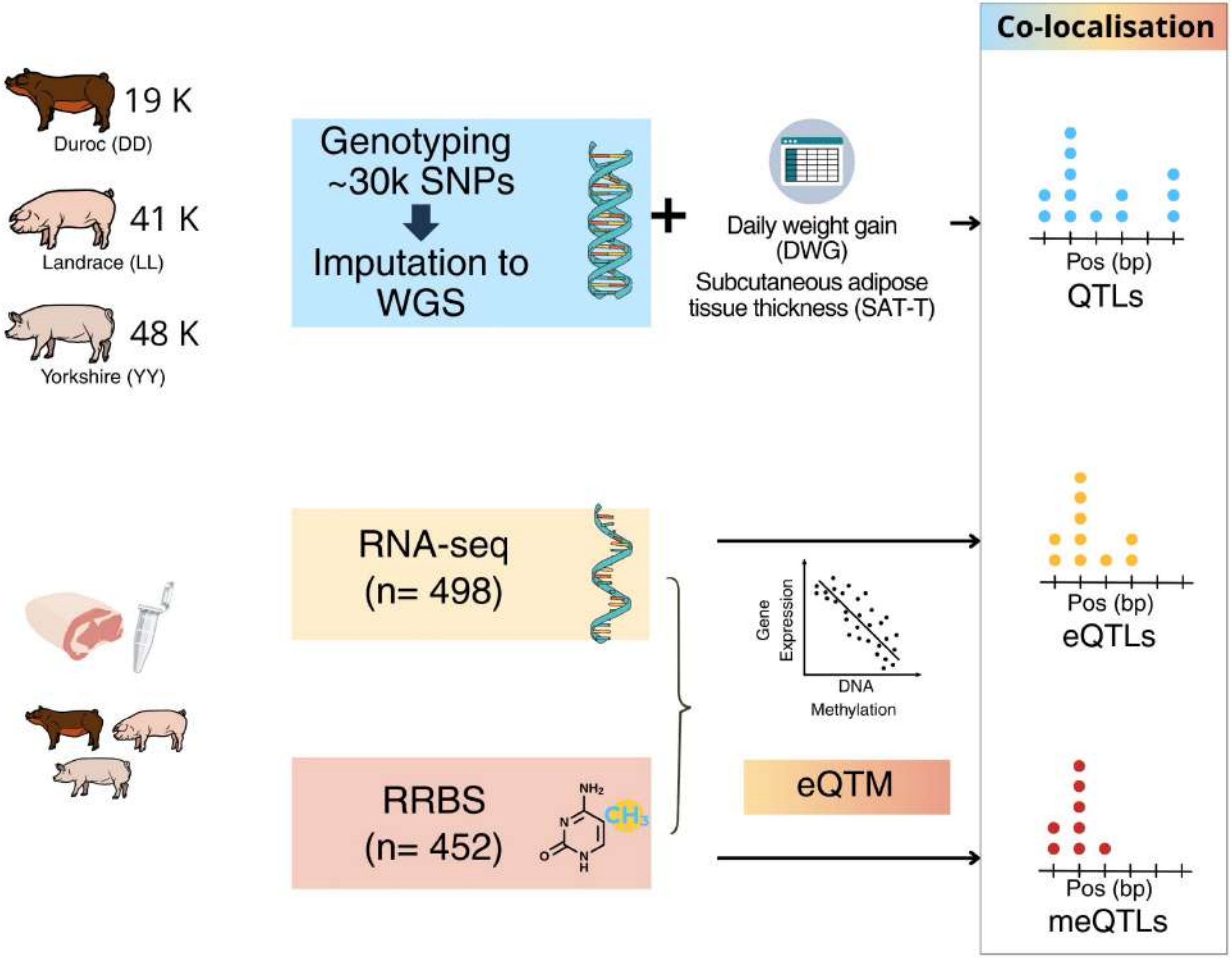
We integrated additional molecular data to better understand the biology of ELP traits

(Identify the buttons)

(Find out how they are adjusted)



19 K
Duroc (DD)

41 K
Landrace (LL)

48 K
Yorkshire (YY)

Genotyping
~30k SNPs
Imputation to
WGS

+

Daily weight gain
(DWG)
Subcutaneous adipose
tissue thickness (SAT-T)

RNA-seq
(n= 498)

RRBS
(n= 452)

Gene Expression
DNA Methylation

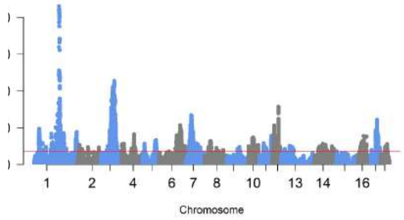
eQTM

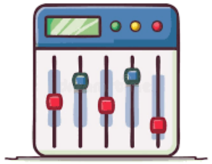
Co-localisation

Pos (bp)
QTLs

Pos (bp)
eQTLs

Pos (bp)
meQTLs





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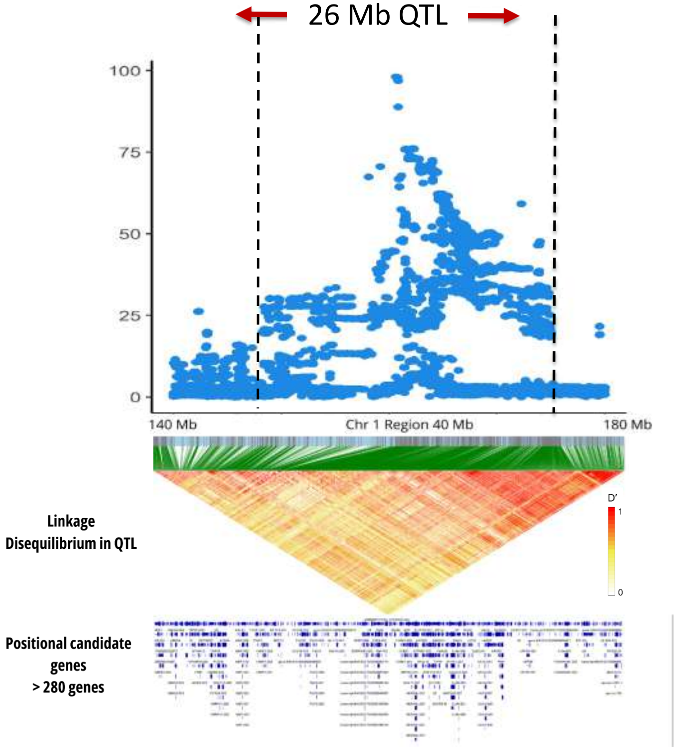
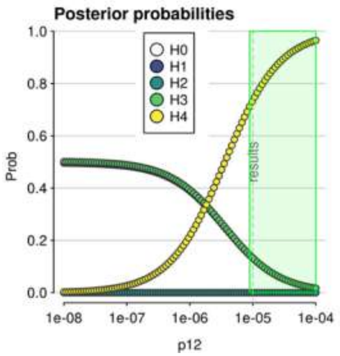
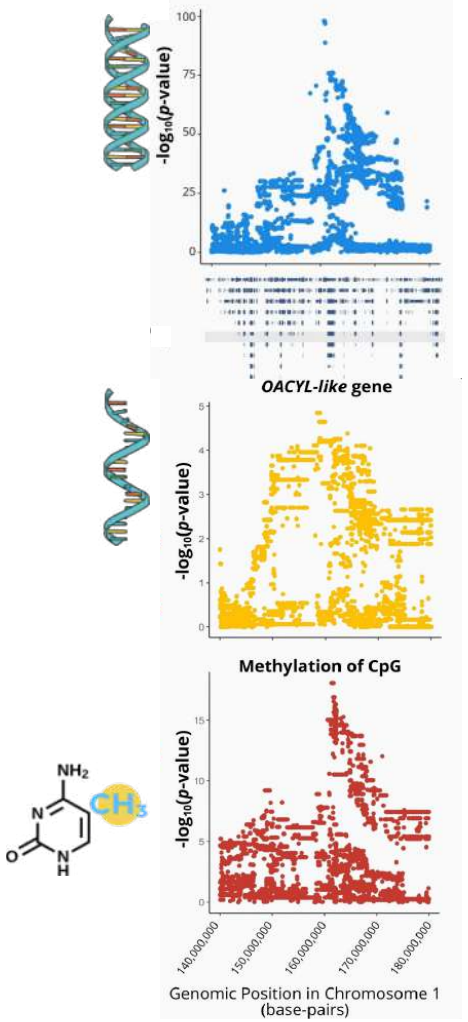


Co-localisation QTL with cis- eGenes / cis- eCpGs



Small set of Genes / CpGs colocalising with the trait with supportive molecular information

Candidate molecular signatures



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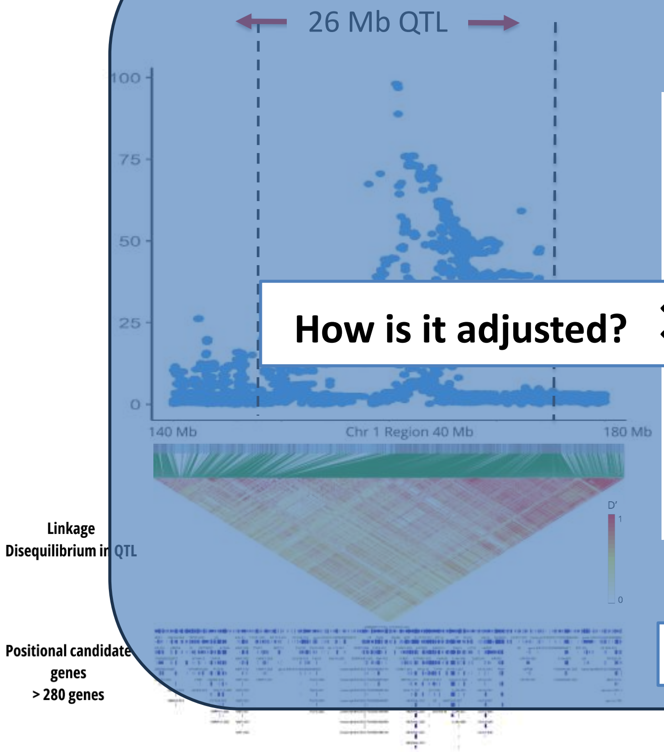
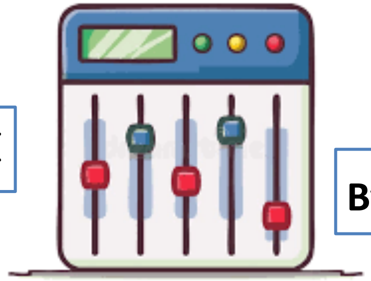
Candidate molecular signatures



Co-localisation QTL with
- eCpGs

The button



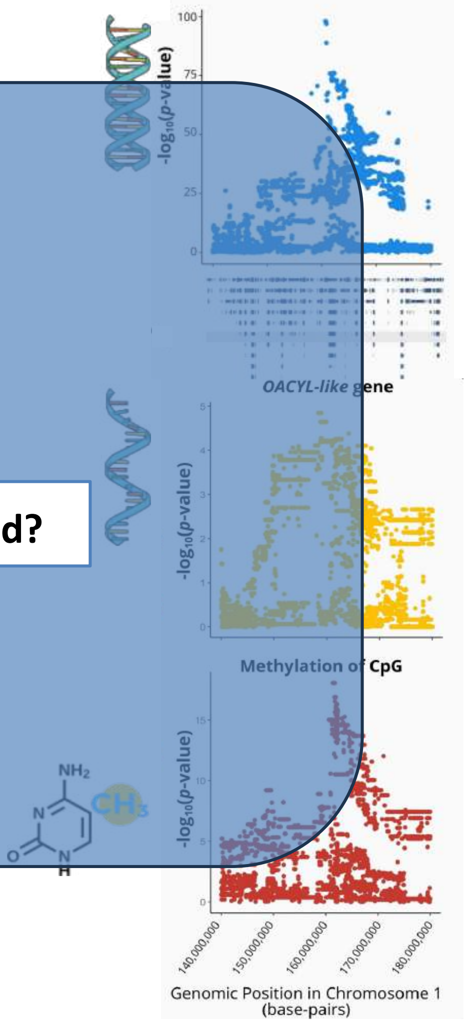
OACYL-like gene

How is it adjusted? ↕

By what is it adjusted?

Daily growth

nes /
CpGs colocalising with
the trait with supportive
nation



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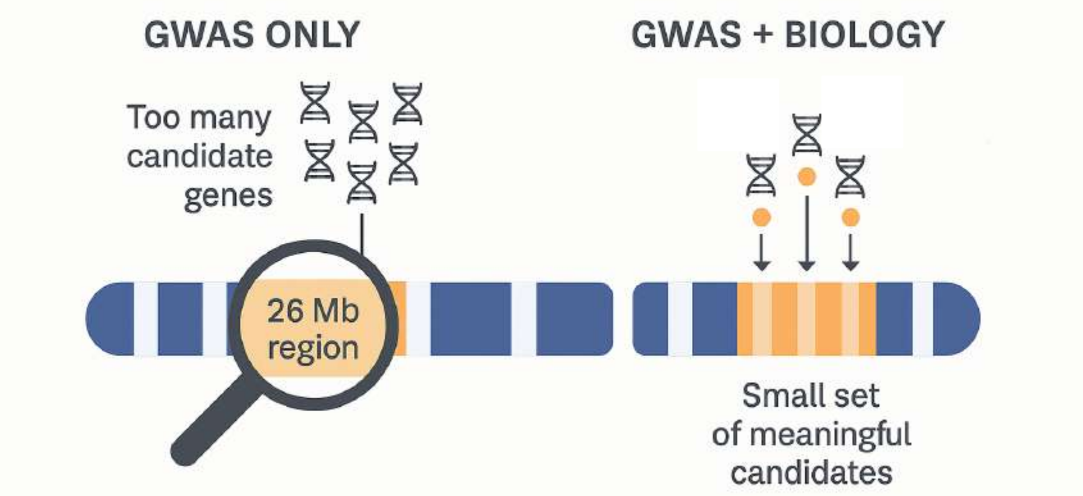
Key Takeaways

- GWAS for production traits in highly selected **livestock** species often identifies **broad QTL regions with many candidate genes**.
- **Multi-omics** integration (eQTLs, meQTLs, etc.) adds **functional and regulatory context**.
- **Colocalization** analyses help identify **variants affecting both molecular** traits and **production** traits.
- Broad **QTLs** are **reduced to a small**, biologically supported **set of genes and variants**.
- Enables better fine mapping, targeted functional validation, and more **informed and biologically supported breeding decisions**.
- Establishes a pipeline **for associating traits with molecular changes**, which, for management-related traits, can be **useful to tailor and adapt management practices in livestock production to improve ELP traits**.



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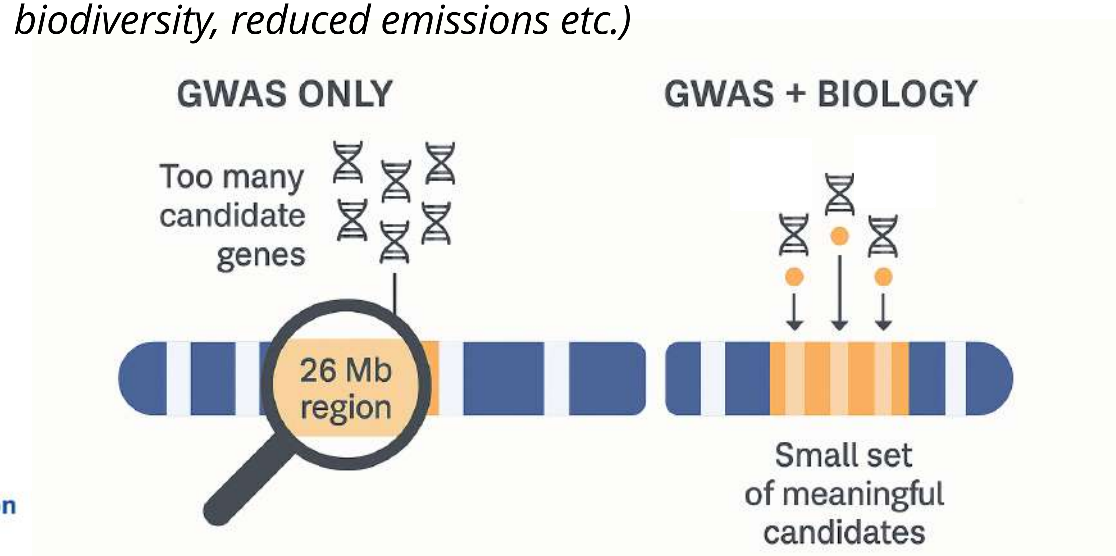
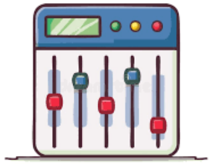
The next thing to do

- Now we know
  - some of the buttons and how they are regulated
  - there are more buttons and genetic architecture to discover

- Two tasks:
  - Continue exploration
  - Start exploitation → this knowledge can help us breed the animals for a future of ethically responsible animal production within planetary boundaries *(animal health & welfare, scale of production, efficient resource use, biodiversity, reduced emissions etc.)*





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THANK YOU

Rumigen

TOWARDS IMPROVEMENT OF **RUMI**NANT BREEDING THROUGH **GEN**OMIC AND EPIGENOMIC APPROACHES

GERONIMO

GENOME AND EPIGENOME ENABLED BREEDING IN MONOGASTRICS

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