Genetic characterization of cattle populations for optimized performance in African ecosystems

Introduction to population genomics with WGS data from the OPTIBOV project

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Welcome

to

Introduction to population genomics with WGS data from the OPTIBOV project

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Why OPTIBOV

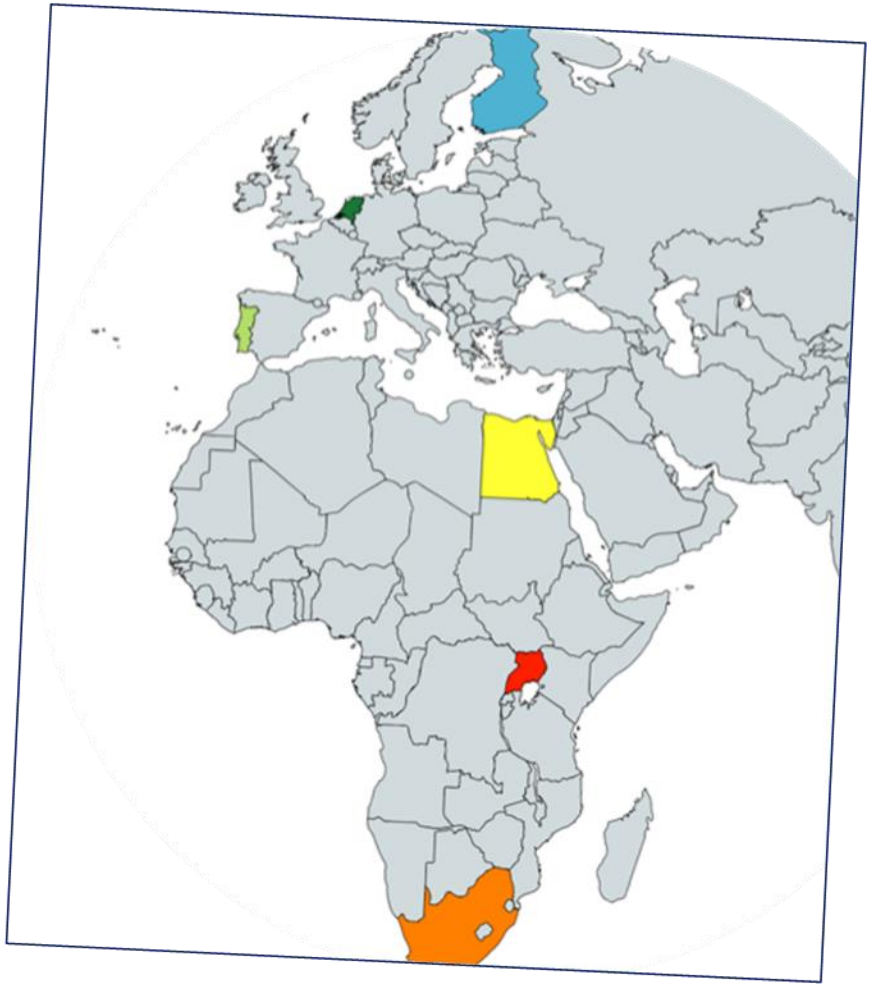
- Maintain traditional cattle breeds
- Capture genetic and genomic variation
- Use strength of these breed (adaptation)
- Use these breeds to find selective sweeps related to adaptation
- Use known variation in production to improve production (marker assistant selection)
- Train, educate and involve people to perform optimal breeding (longterm investment) (workshops, app, website)

Aim of the project: Adaptation!

- Improve production and survival of traditional breeds adapted to their local environment
  - Select local breeds
  - Collect phenotypes
  - Collect DNA
    - Estimate the amount of inbreeding
    - Find selection signals on the genome
    - Find genes and variant on the genome
    - How to improve adaptation and production

Partners (PI)

- Europe:
  - Prof Dr. J. Kantanen (FI:LUKE)
  - Dr. C. Ginja (PT:CIBIO/ICETA)
  - Dr. R. Crooijmans (NL: WUR) project leader
- Africa:
  - Dr. D. Kuganza (UG:MU-CAES)
  - Dr. M. Makgahlela (ZA:ARC)
  - Dr N. Ghanem (EG:CU)



Breeds

Eastern, northern and western Finn cattle

Groninger Whiteheaded Dutch belted, MRY, Deep Red, Dutch Friesian

Mirandesa, Barrosã and Mertolenga.

Menofi (Baladi) / Domiaty (Damietta) / Maryuti

Ankole, karamajong, Nganda Ntuuku, Nkedi

Nguni, Afrikaner, Tuli

EU: North Finland

EU: mid The Netherlands

EU: south Portugal

Africa: North Egypt

Africa: Mid Uganda

Africa: South South Africa

Potential traits:

-Climate, amount of rain, ecosystem

- Temperature-humidity index

Availability of water\food

- Food quality
- Amount of food available
- Type of food
- Disease recording
- Disease resistance
- Parasites infections (ticks, nematotes)
- Housing (outdoor-indoor)
- Production records
- Calving interval/total number of calves
- Age of first calf
- Treatments
- Biochemical measurements on blood
- Immune parameters (Ig)
- MHC haplotypes

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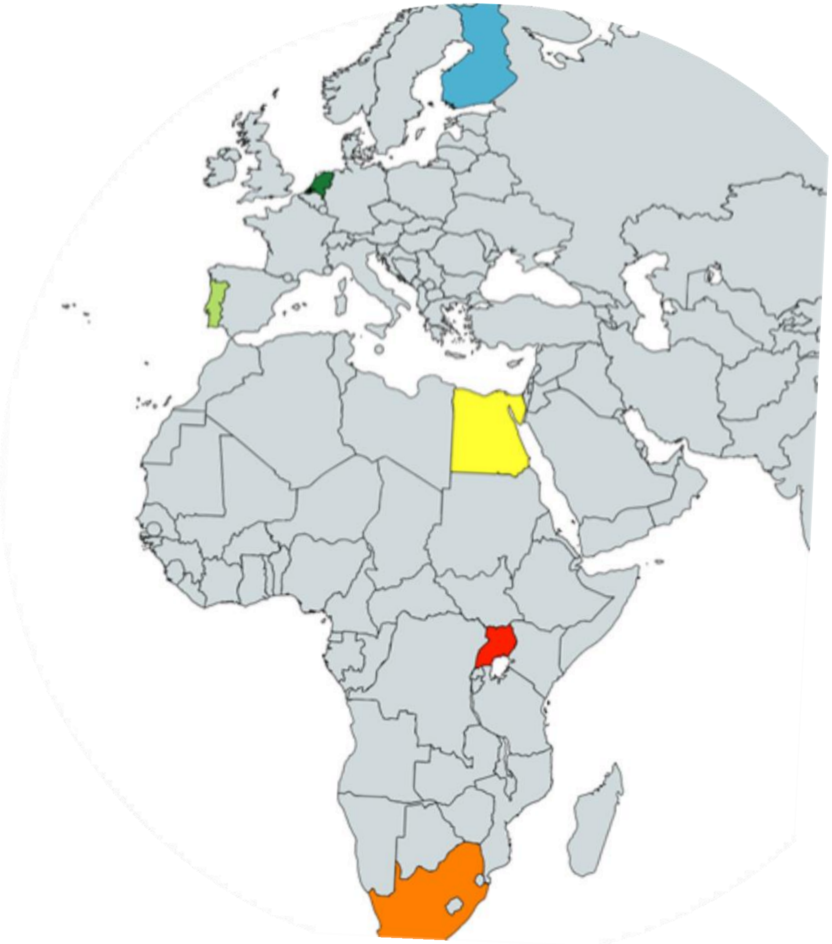
breeds

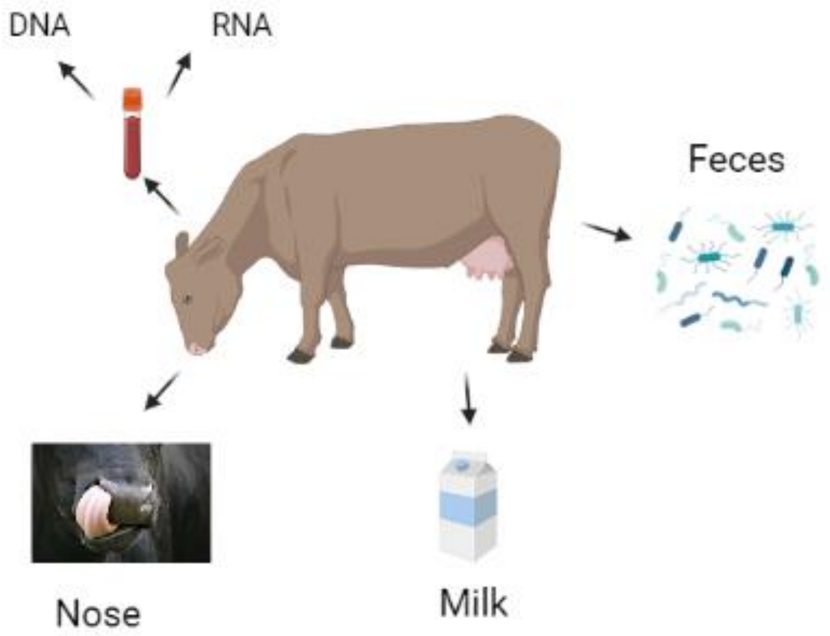

AFRIKAANSE WEERGAWE
NGUNI
Cattle Breeders' Society | Beestelersgenootskap
Maryuti
cow
Egypt
Pohjois-Suomalainen Karja
(PSK)
cow
Finland

OPTIBOV Project



- ☐ Characterize locally adapted cattle breeds
- ☐ Identify genetic variation related to adaptation and traits (selective sweep, RHOs , SV, SNPs ...)
- ☐ Use genetic variation to improve breeding schemes (production, longevity, disease resistance)

Sample collection from local breeds



Country	Breeds (Samples)	DNA	RNA	Feces	Milk	Environment
Finland	4 (80)	🟩	🟥	🟩	🟩	🟩
Netherlands	5 (120)	🟩	🟩	🟩	🟩	🟩
Portugal	3 (80)	🟩	🟥	🟩	🟥	🟩
South Africa	3 (60)	🟩	🟥	🟥	🟥	🟩
Uganda	3 (80)	🟥	🟥	🟥	🟩	🟩
Egypt	3 (80)	🟥	🟥	🟥	🟥	🟩
Total	21 (500)					

🟩 Completed
🟥 In progress

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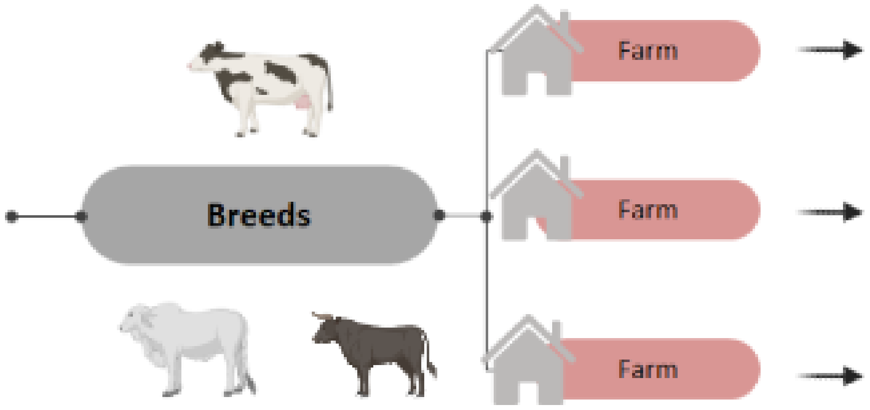
Data structure and information layers

Country

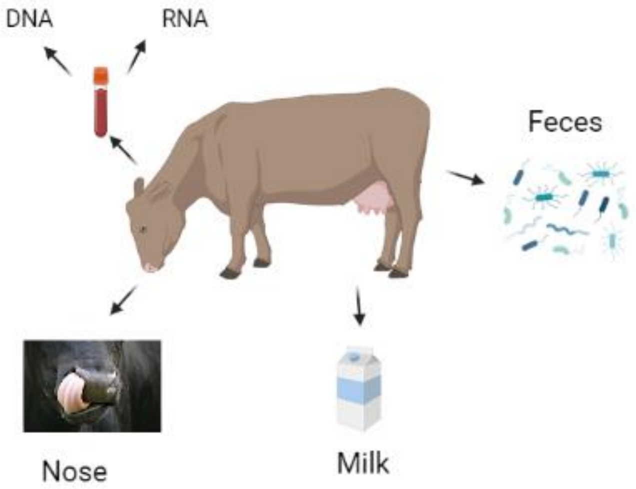
- ☐ Finland
- ☐ The Netherlands
- ☐ Portugal
- ☐ South Africa
- ☐ Uganda
- ☐ Egypt

Breeds

Farm



Animal

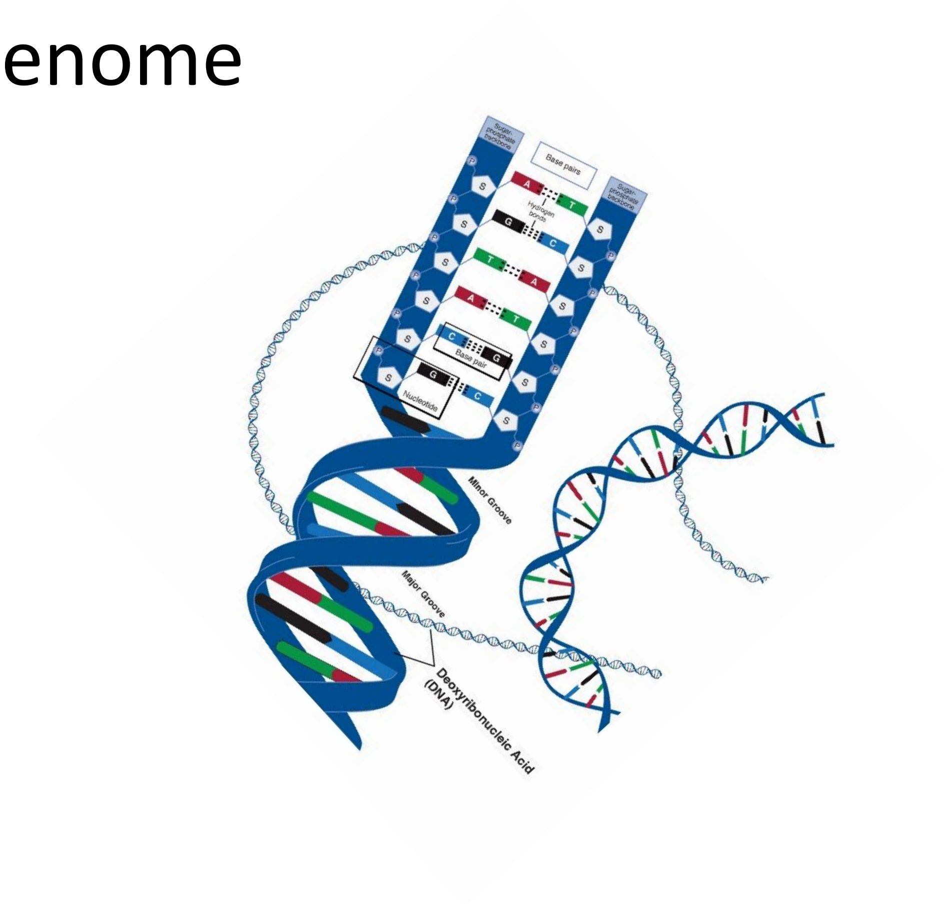


https://www.optibov.com/

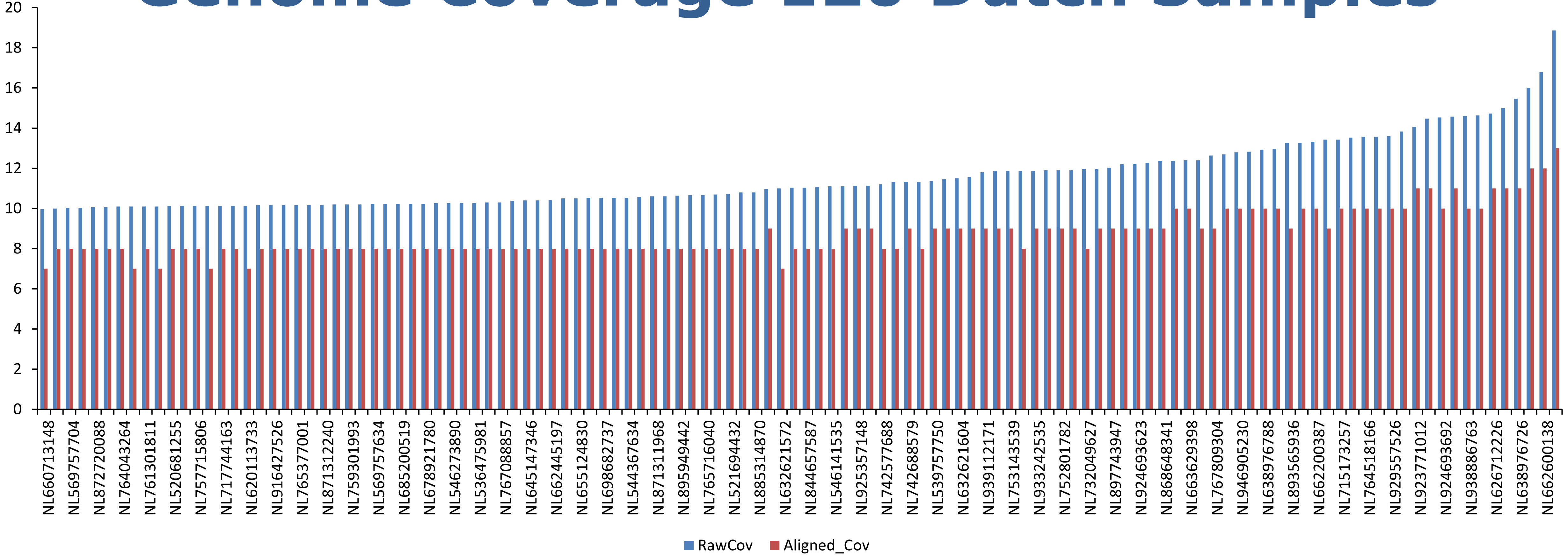
WGS data analysis

- ✓ Sequence alignment to the reference genome
  - Sequences which do align
    - Variation detection
      - SNPs
      - INDELs
      - CNV

  - Sequences which do not align
    - Which species



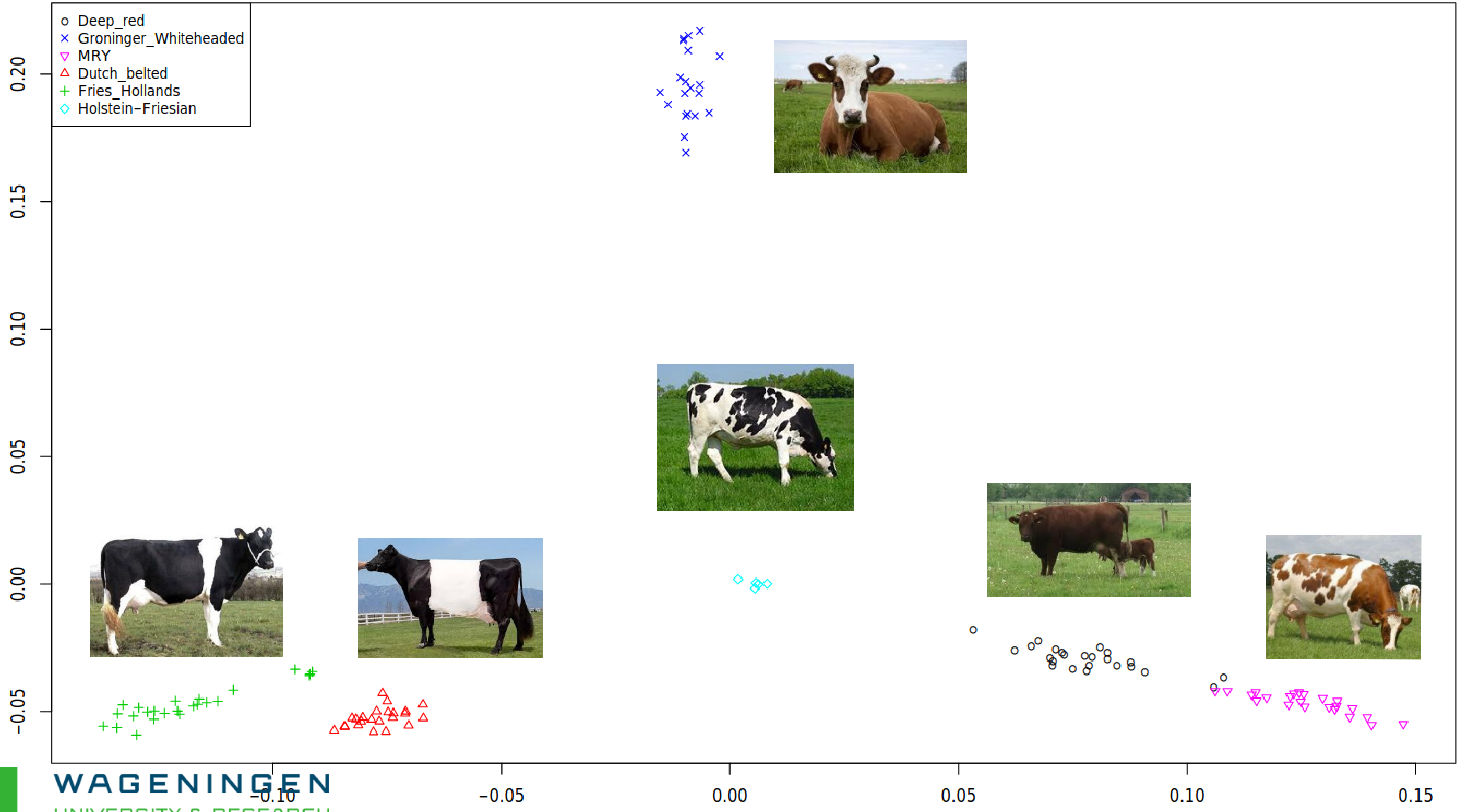
Genome Coverage 120 Dutch Samples



Raw data 4172.1 G

	Average	min	max	Average
Raw	**11.58**	**9.97**	**18.87**	**11.03**
Mapping	**8.72**	**7**	**13**	**8**
Difference	2.86	1.97	5.87	2.7

MDS of IBS distances for local Breeds



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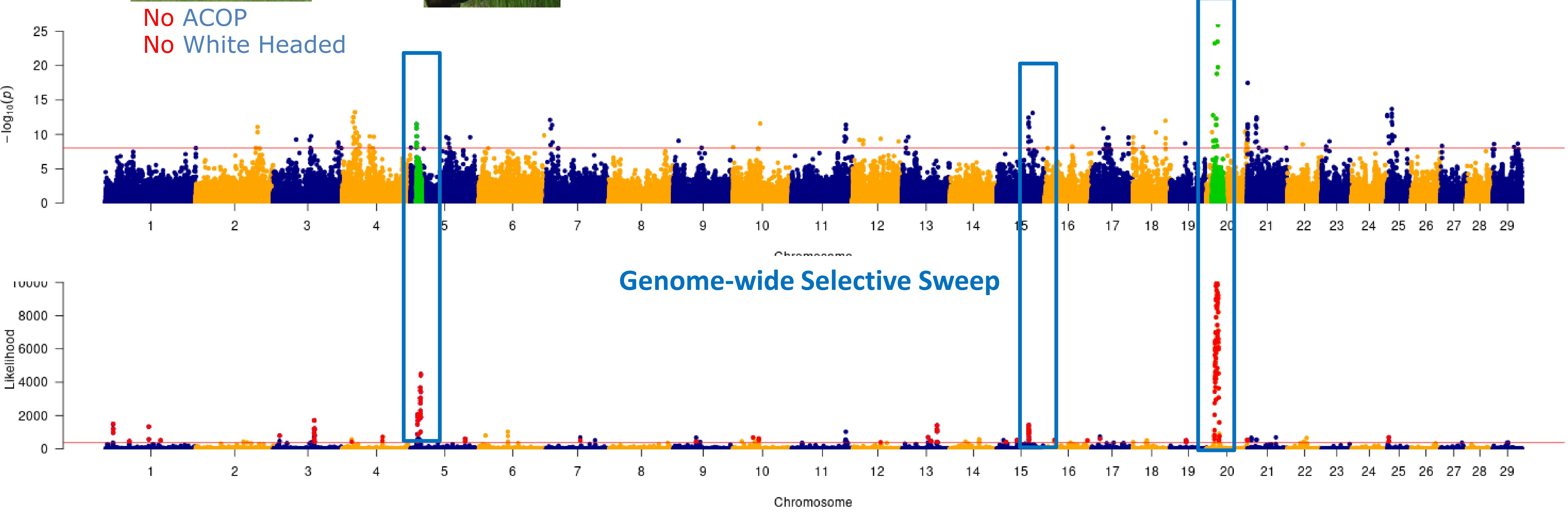
Co-localization between QTLs and specific SS

vs

No ACOP
No White Headed

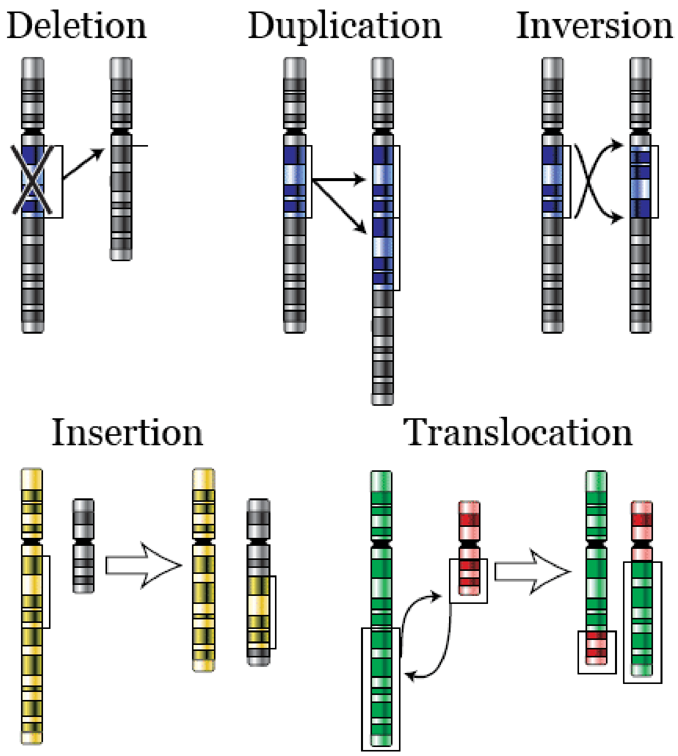


Genome-wide Selective Sweep

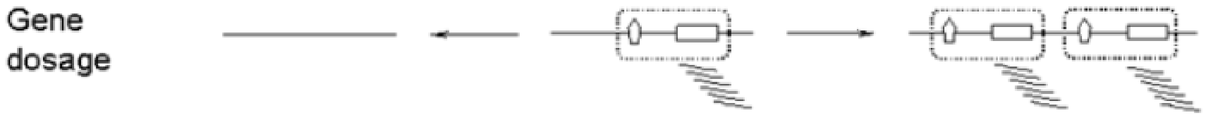
- Genomic regions on **BTA5 (10.0-13.6Mb), BTA15 (55.6-59.7Mb) and BTA20 (10.9-19.5 Mb)** confirmed by Specific selective sweep and GWAS

Structural Variations

Types structural variations



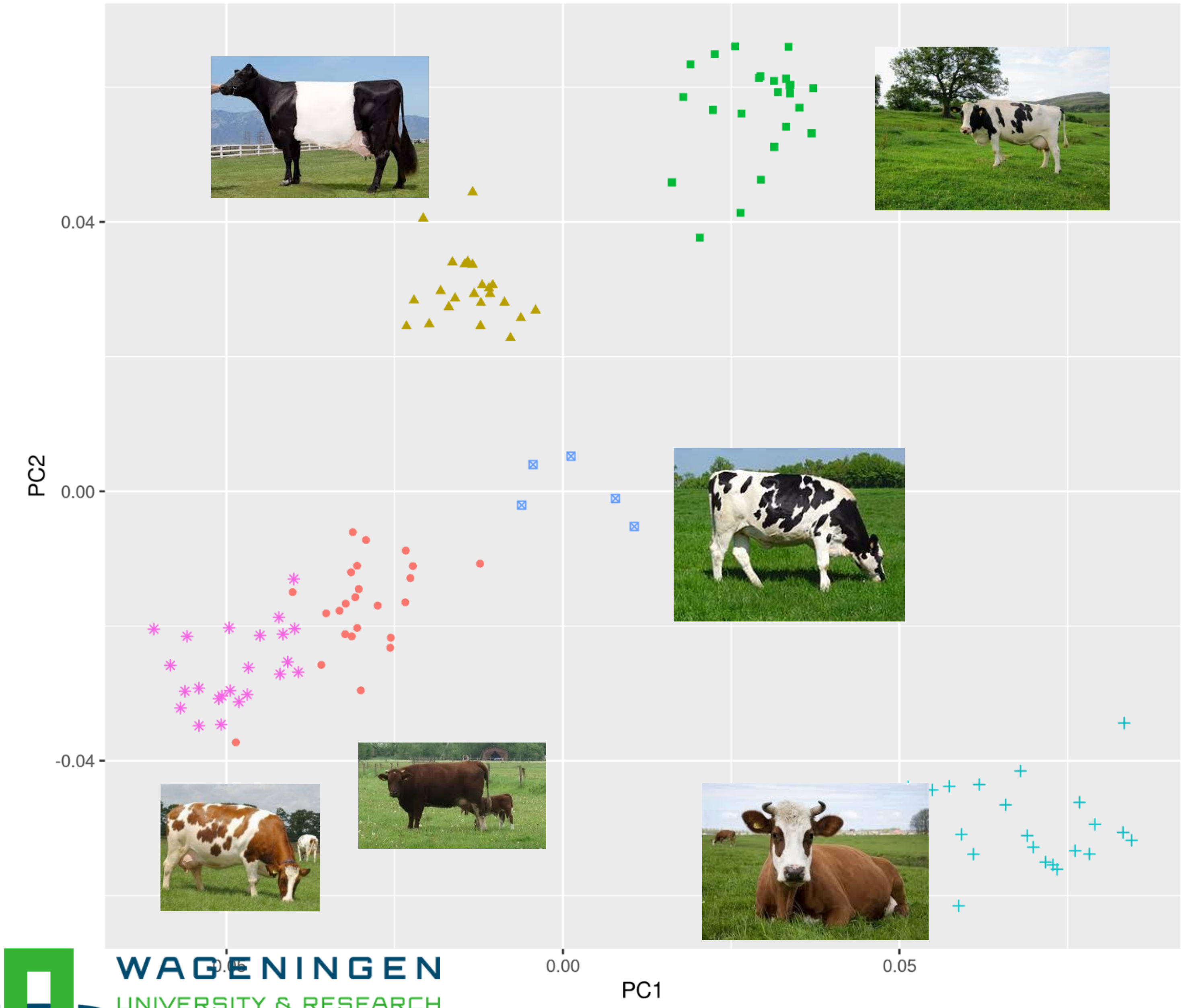
Copy Number Variation (CNV):
large-scale deletions or gains of DNA fragments



- An additional copy of a gene (**duplication**) increases the corresponding mRNA

- The loss of a regulatory element (**deletion**) may cancel the expression of the corresponding mRNA

MDS Representation of CNVR



CNVR in BTA3 in Dutch Belted

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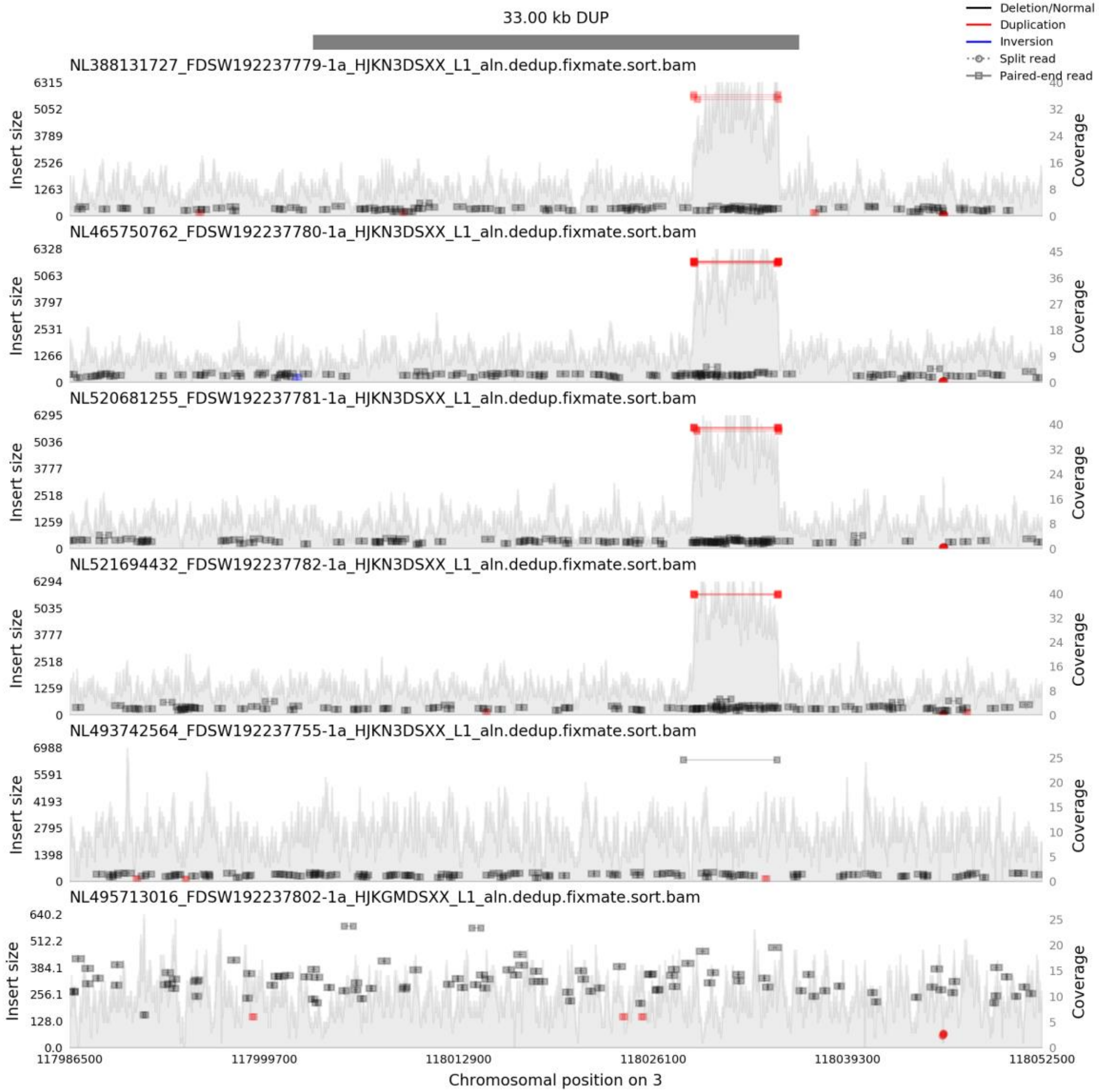
❑ Duplication 5,000 pb



- ❑ Circular belt of **Unpigmented hair and skin around their midsection**
- ❑ It is inherited as a **monogenic autosomal dominant trait**

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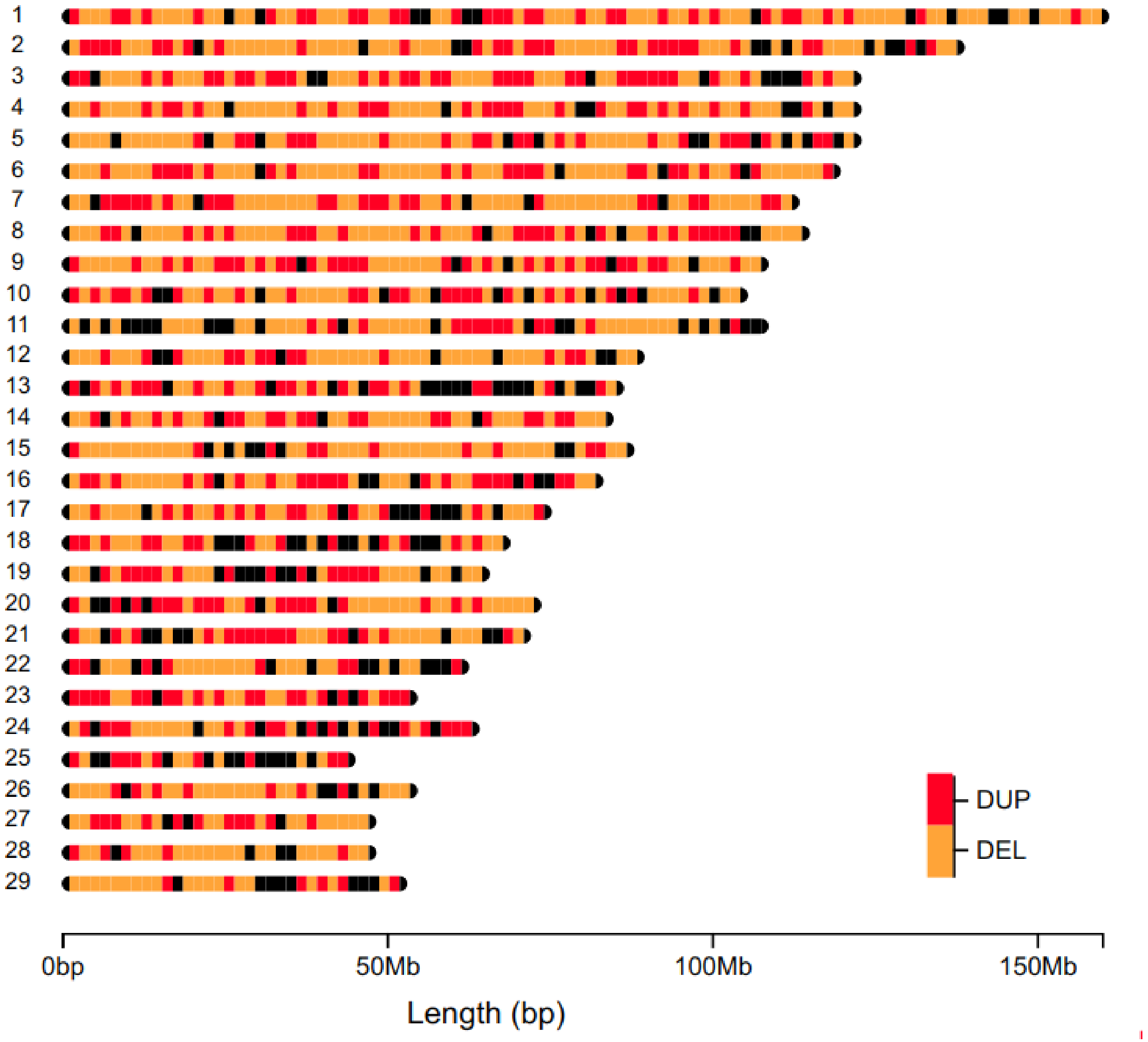
Distribution of CNV on cattle genome



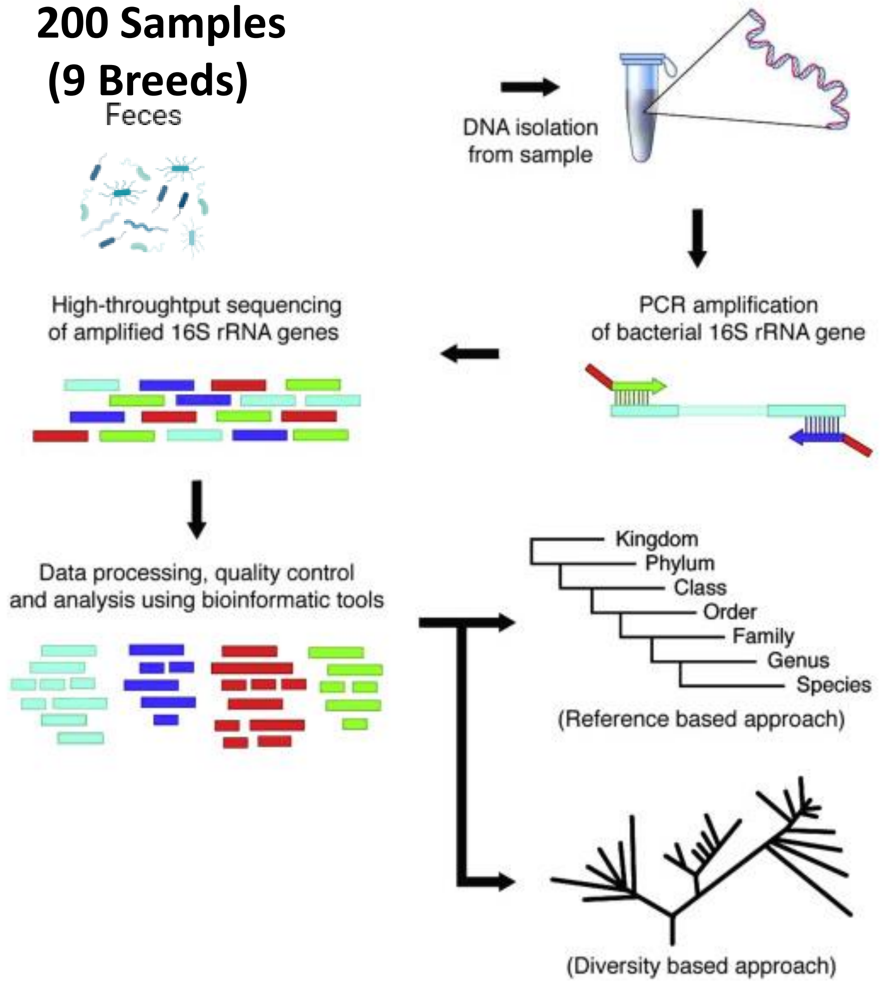
- ☐ **CNVs: 63,320**
- ☐ **Size:** 1,8Mb - 7.7 Mb
- ☐ **Deletions (DEL):** 60% (38,033)
- ☐ **Duplication (DUP):** 40% (25,287)

Breed effect in the microbiota composition

Data generated by 16s rRNA Illumina Sequencing

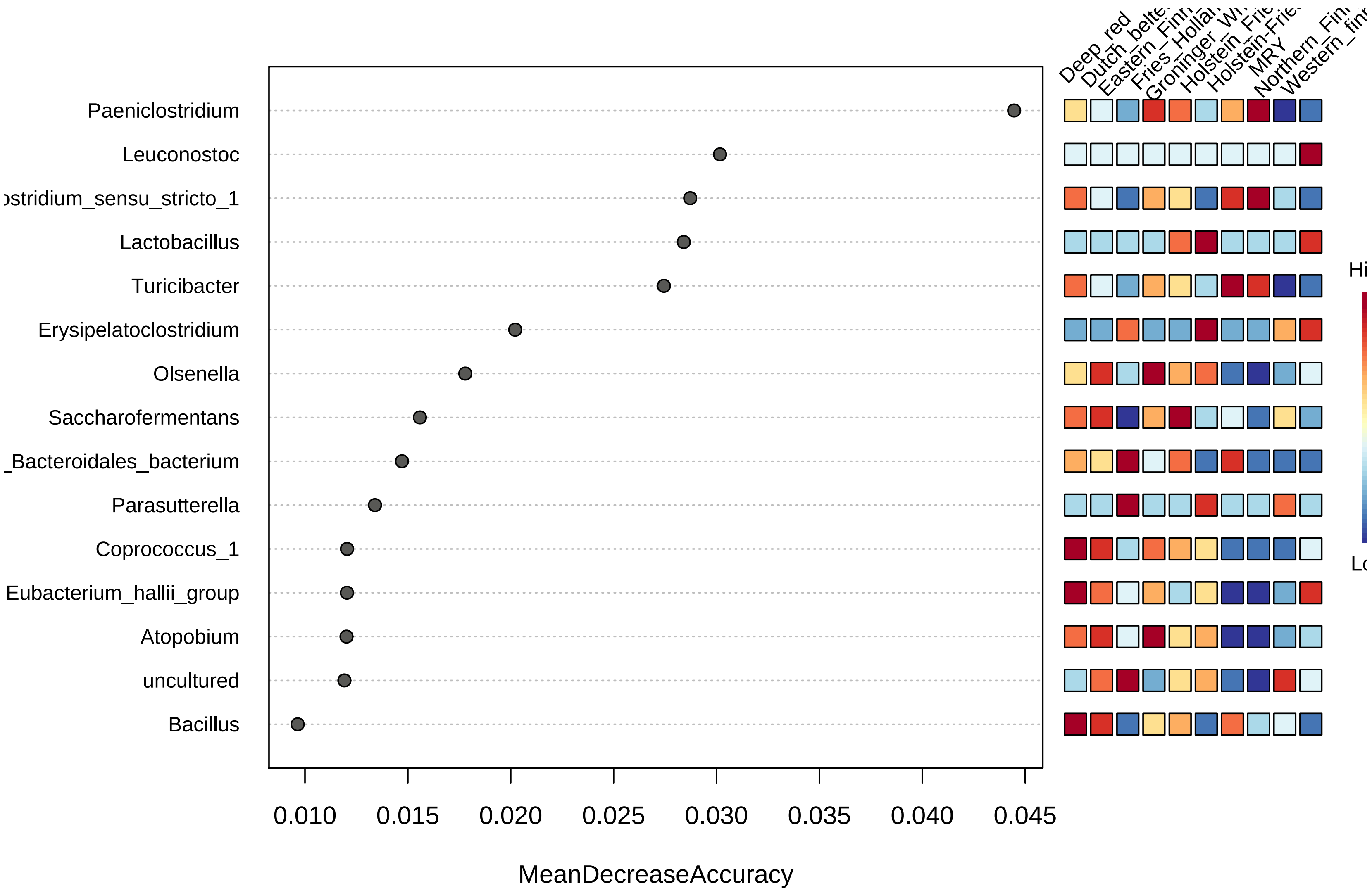
- Diversity indexes (Chao1[60] and Shannon[61])
- Between-sample (beta) diversity unweighted and weighted(UniFrac[62] distances and Bray-Curtis[63] dissimilarities)

200 Samples (9 Breeds)



J Invest Dermatol 2016 136e23-e27DOI: (10.1016/j.jid.2016.01.005)

Bacteria that can discriminate between breeds



Thank You

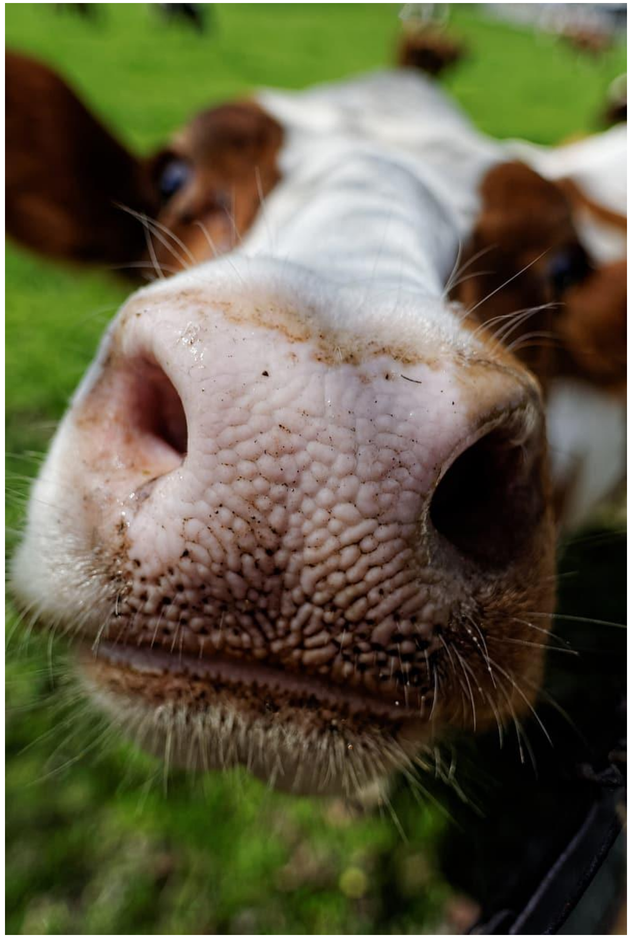
- ☐ Course organisers
  - Catarina Ginja
  - Rayner Gonzalez Prendes
  - Daniel Gaspar

OPTIBOV members

- ☐ Breeds Associations

- ☐ Funding:

LEAP-Agri/local funding agencies



LEAP-Agri

A Long term EU-Africa research and innovation Partnership on food and nutrition security and sustainable Agriculture

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