

The use of genomics in European livestock genebank collections

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How to open the genetic reservoirs



Sequencing traditional breeds



Samples sequenced

Every sample 10x genome coverage:

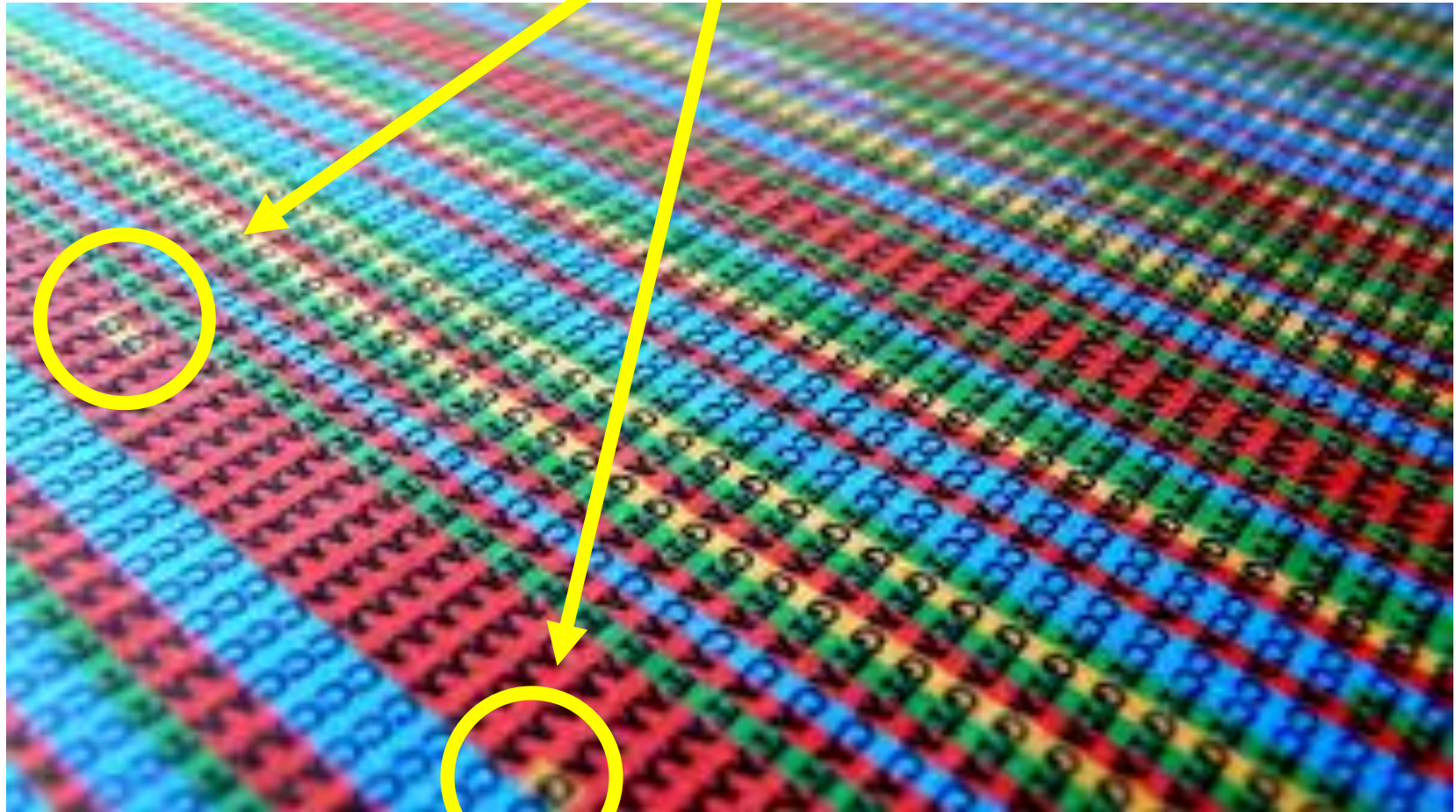
- 60 cattle (14 breeds)
- 296 chicken (131 breeds)
- 100 pigs (31 breeds)
- 100 sheep (67 breeds)

SNP pool:

- IMAGE sequence effort
- Public available
- Partner input



variation

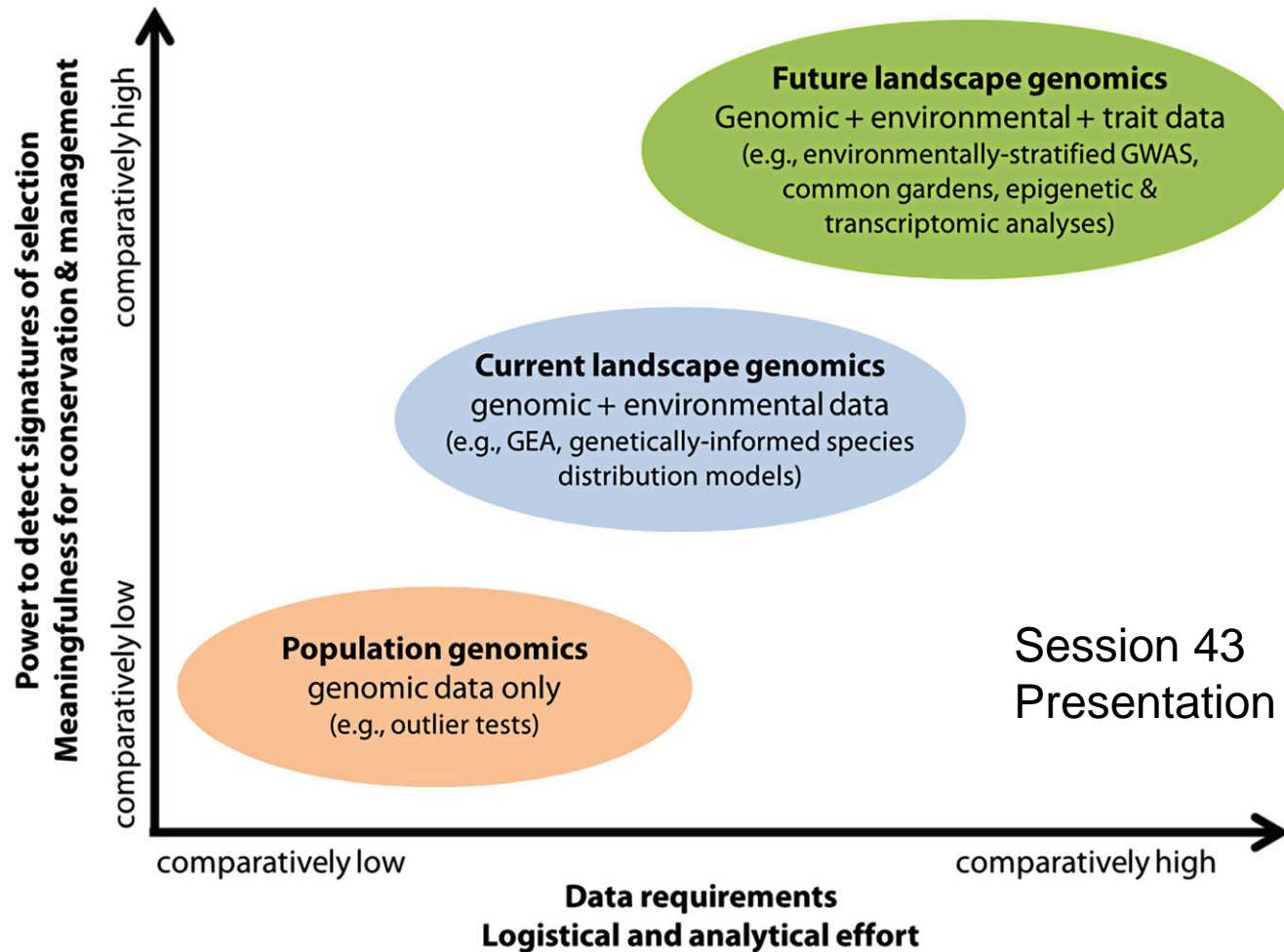


variation will be used in IMAGE for:

- Biodiversity measurements (Inbreeding, Heterozygosity, Admixture, Selective sweeps, ROH, Population management)
- Landscape genetics
 - Within breed: Cattle, HF
 - Over breeds: sheep
- Disentangle traits: example Bantam
- Multi-species SNP array: IMAGE001



Landscape genomics



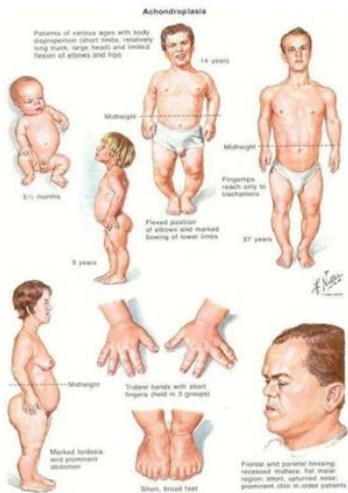
Session 43

Presentation of Paolo Marsan

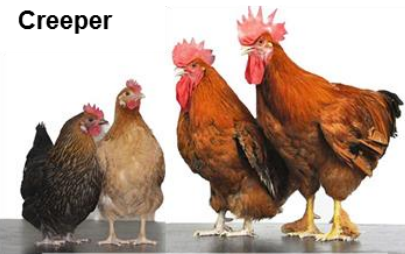
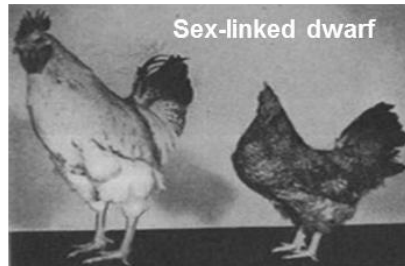


Disentangle dwarfism using DNA/RNA variation (example of a trait)

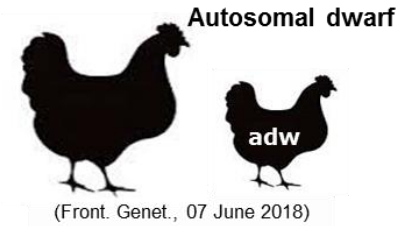
- ◆ Short stature
- ◆ Selection & Breeding
- ◆ Benefit & Ornamental



(Genetics. 2017 Feb;205(2):955-965.)



(Sci Rep.2016;6: 30172. (2016))



What type of data used

Traditional chicken breeds in the Netherlands

- 38 breeds: large fowls
neo-bantams
true-bantams
- 140 animals with WGS
- 450 animals with 60K genotyping



Clusters based on bantamization

Cluster 1 (Dutch Bantam)	Cluster 2 (Java_Sebright)	Cluster 3 (Sumatra)
Dutch Bantam	Java	Sumatra
Frisian Fowl	Sebright-gold	Schijndelaar
Groninger Mew	Sebright-silver	Barnevelder
Assendelft Fowl	Eikenburger	Twentse Fowl(Kraik)
Drenthe Fowl	Dutch Polish Bearded	Welsummer
	Dutch Polish non Bearded	North Holland Blue
	Brabanter	
	Kraienkoppe Fowl(BreFw)	
	Dutch Owl Bearded	
	Dutch Fowl	
	Lakenvelder	
N=34	N=66	N=36



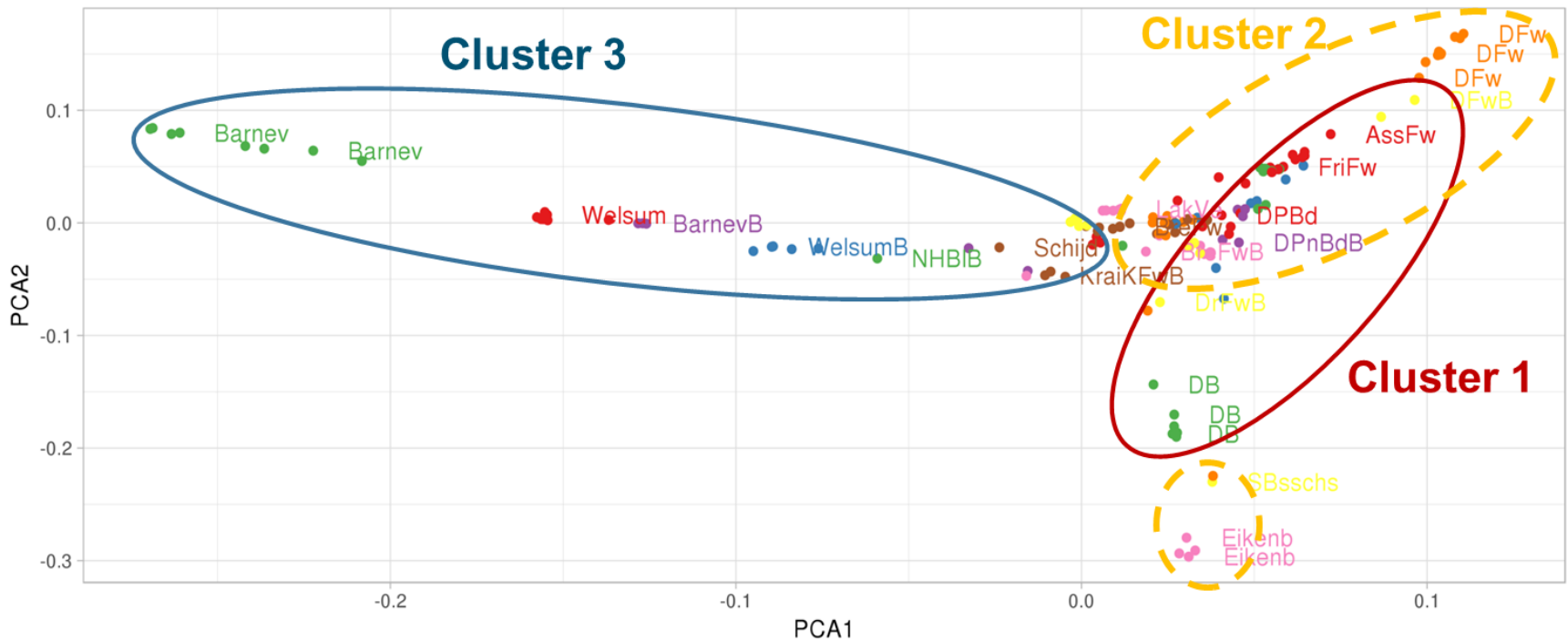
- Whole Genome Sequence data
- **136** individuals from **38** breeds

***Traditional breeds with small counterparts**



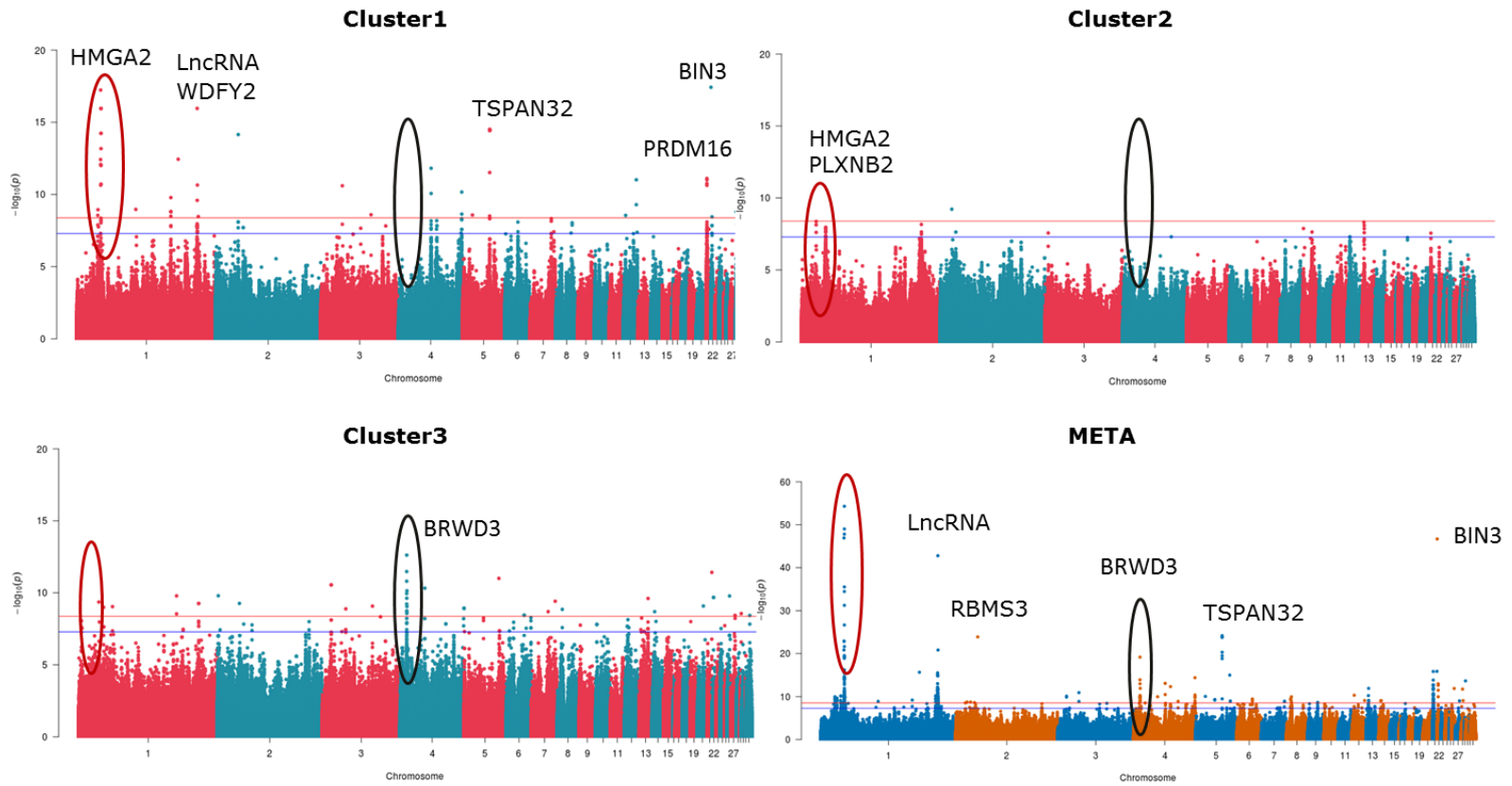
Principal component analysis

- Individuals from the same breed distinguished by PCs
- Large & neo-bantam clustered together

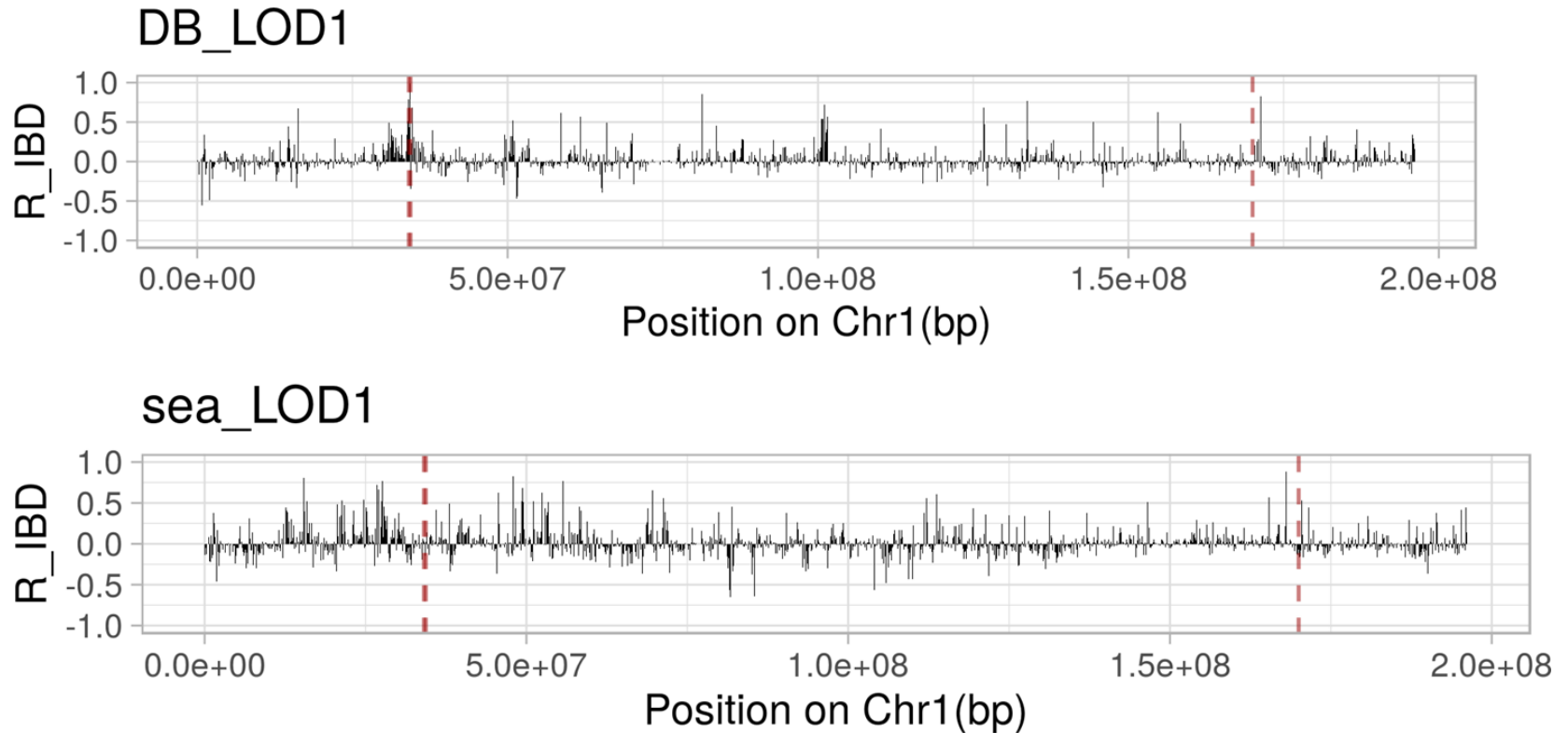


GWAS

- Multiple peaks in different clusters
- Different Bantam genes/mechanisms among clusters



Haplotype sharing

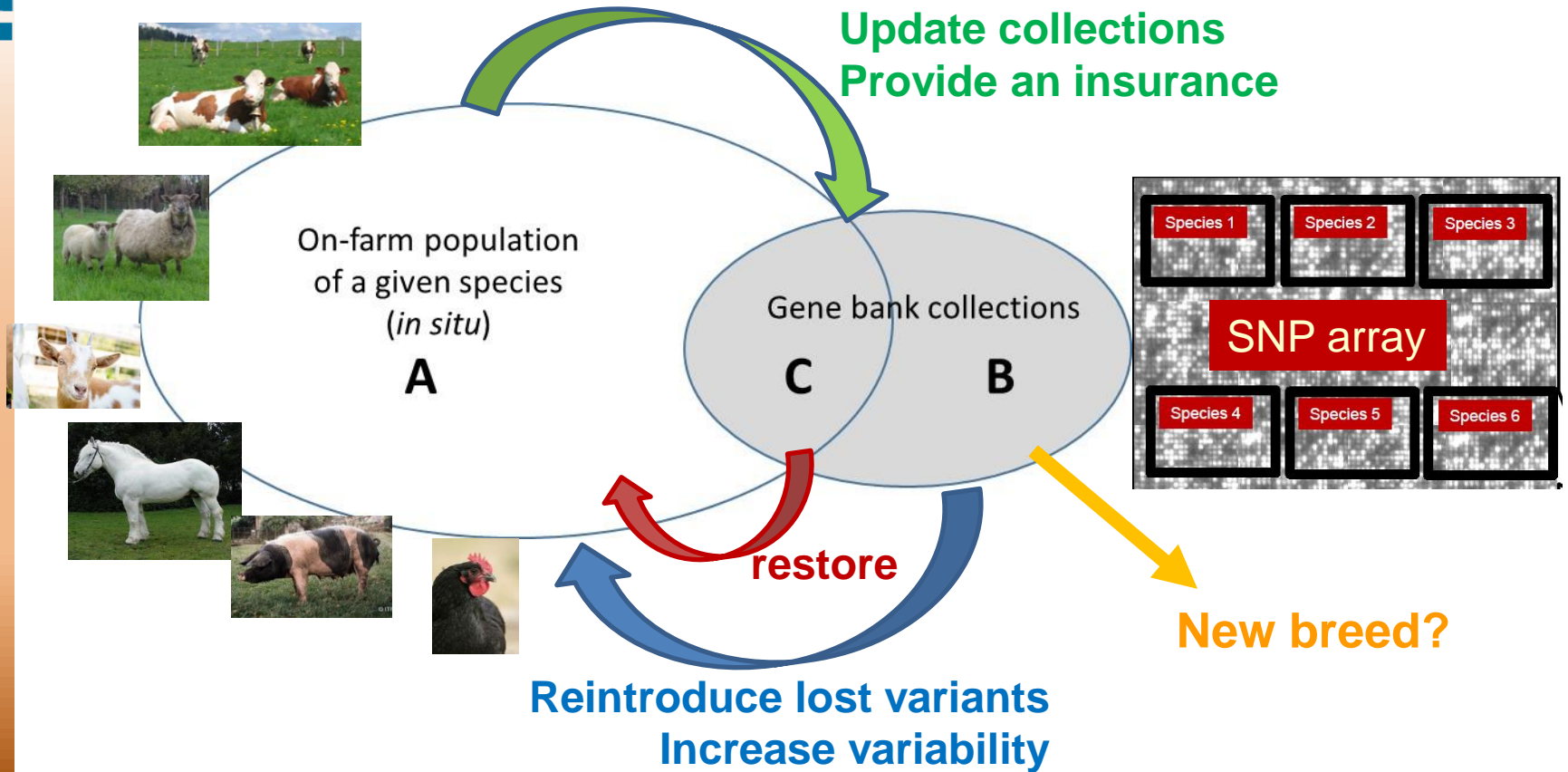


Follow up: Haplotype analysis

- GWAS-regions
 - Genotyping additional samples for specific SNPS/
use of 60K SNP data
- RNA-seq of 84 samples
 - Samples of each cluster included
 - Two time points (E5 and E13)
 - 3 replicates per breed per time point



Why a multi species SNP array



A multi-species SNP array

- 10K SNP per species
- Cost below \$20.00 (including genotyping)
- At least 10 species
- Accessible worldwide
- Public available
- No restrictions



Multi species SNP array:

IMAGE001

- Cattle
- Pig
- Chicken
- Goat
- Sheep
- Horse

IMAGE002

- Water Buffalo
- Duck
- Camel
- Bee
- Rabbit
- Quail

IMAGE003



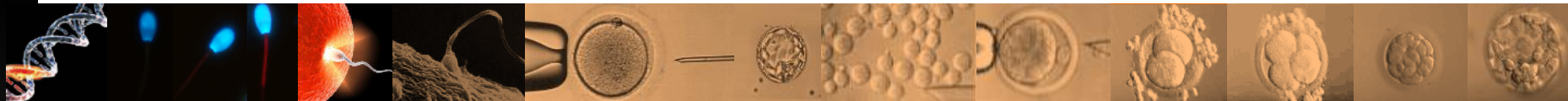
TBD

TBD



SNP selection

- **8000 'neutral'** markers for population structure and differentiation
- **1000 'functional'** markers, to be chosen from IMAGE results and known genetic defects
- **1000 'ancestral'** markers, chosen in the available data on wild ancestor or because of informativeness in a large range of populations



Multi species array: Pig

Objective: Select 10k SNPs reported in pigs to include in multi species chip

Common

Ancestral

Literature

Y chromosomal

Mitochondrial

	breeds	individuals
Asia_breed	11	348
Asia_WB	2	20
Europe_breed	24	580
Europe_WB	12	298

Dwarfism	PRRS
Muscle	Development
Boar taint	Von Willebrand Disease
Meat quality	Health
Color	Immune system / SLA
Behaviour	myopathy
Immune response	Vertebrae / Teats
Growth	Feed efficiency
Reproduction	Hairlessness
Production	Leg weakness
Stress	

2 Duroc
 3 Yorkshire
 11 Landrace
 14 European
 (wild&domesticated)
 14 Asian (wild&domesticated)

6,933 + 538
(Chr. X) SNPs
 chr. 1-18: MAF >
 0.44
 chr. X: MAF > 0.3

1,963 SNPs
 top 500 per
 'set'

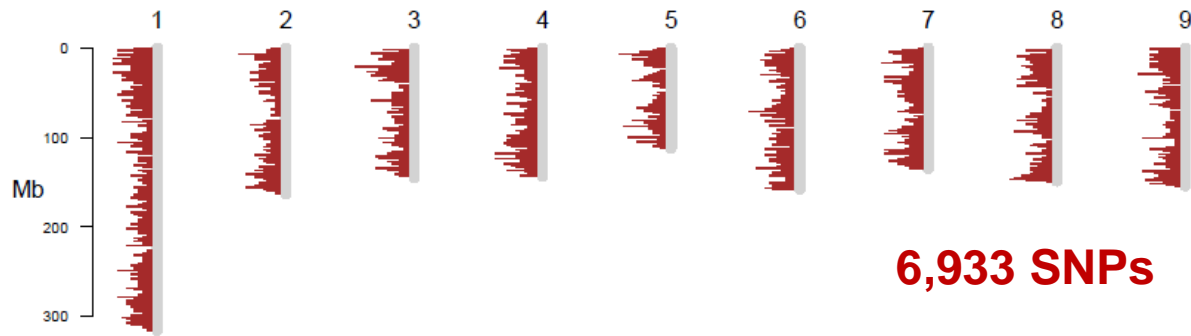
143 SNPs
 related to traits

44 SNPs

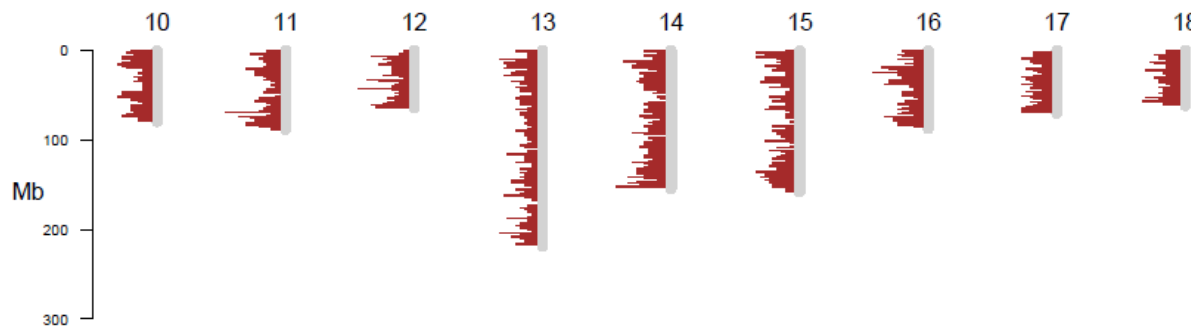
39 SNPs



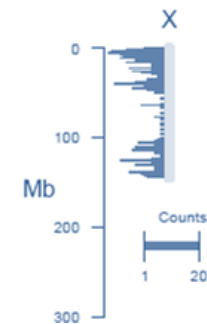
Distribution of common SNPs on pig genome



6,933 SNPs



538 SNPs



Counts

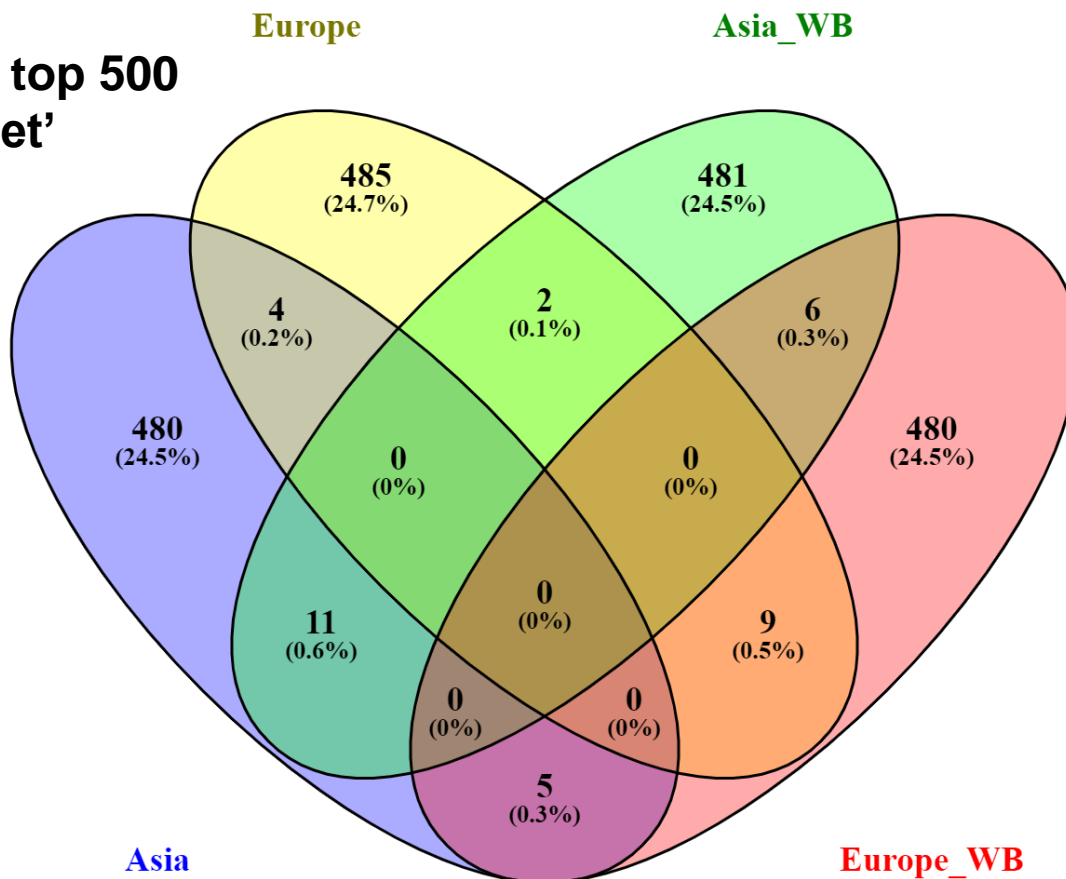
1 20



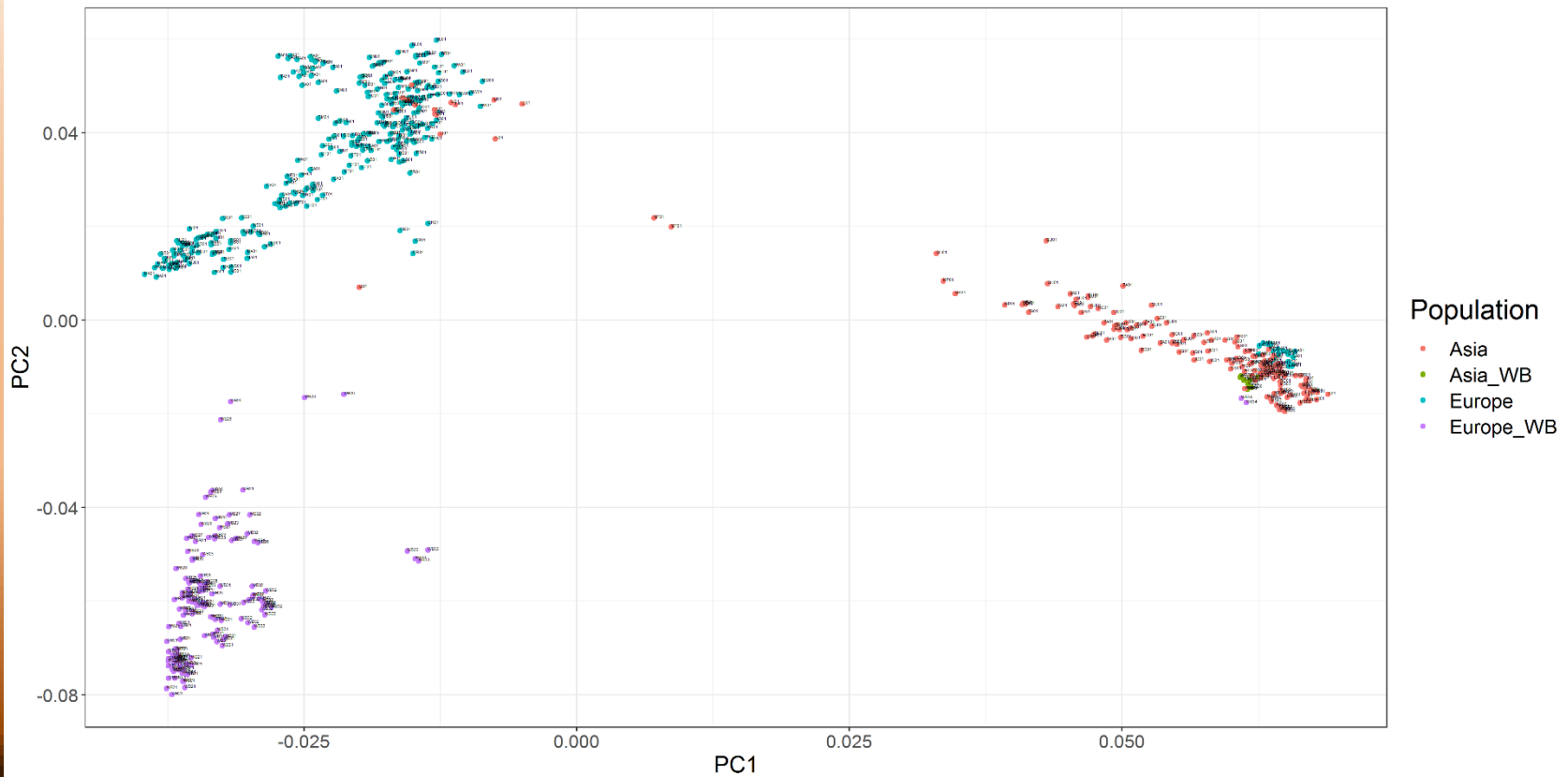
Ancestral-specific SNPs

NOTE:

Compared top 500 for each 'set'



PCA plot based on all SNPs (Asia+Europe)



Draft multispecies array: Horse

Objective: Select 10,000 SNPs reported in horse to include in multi species array



10 Population with 560 Dutch Horses

Array 50k and 70k

Selected **8k** with

- MAF >0.38
- Genotype Rate >0.9



OMIA dataBase



64 SNPs related traits



Major histocompatibility complex (MHC)



From SNPs in 10 genes

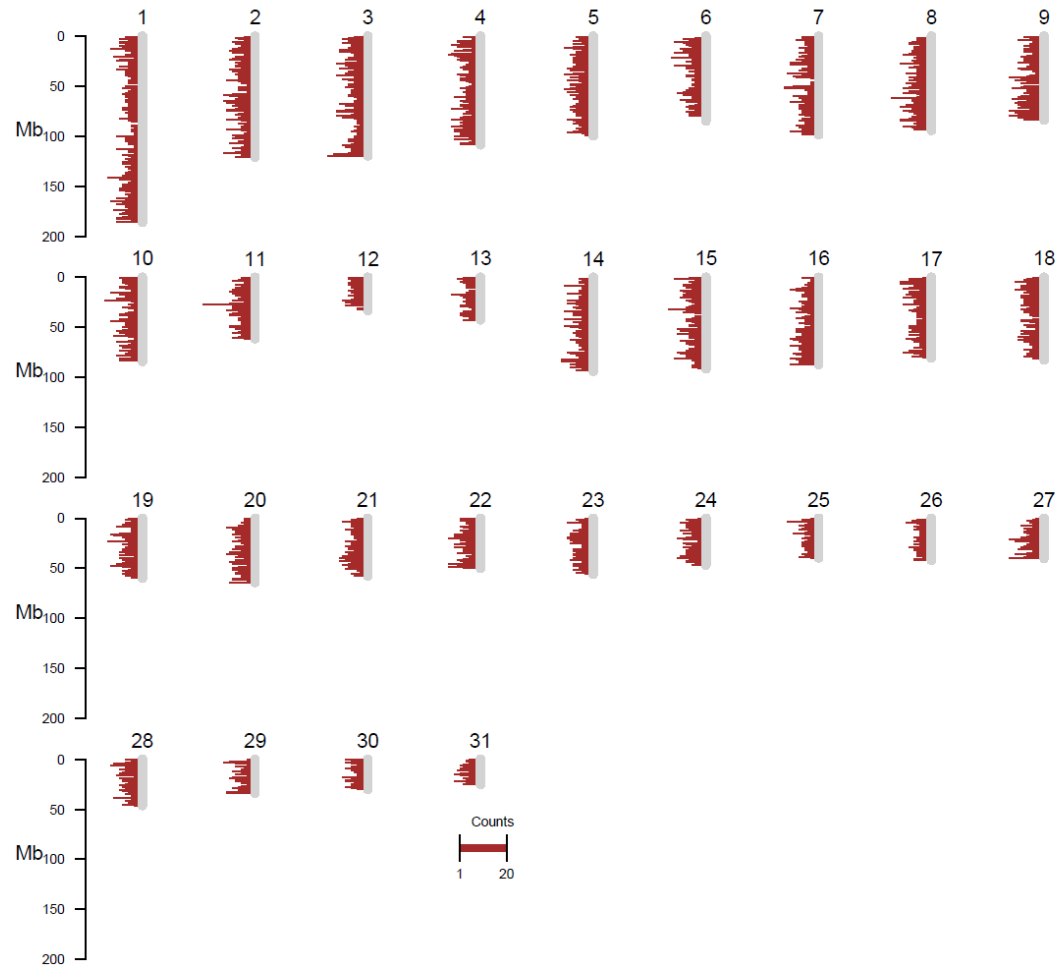
- SNPs in 5' and 3' UTR regions
- Mutations Synonims or missense
- Splice regions
- With values in SIFT



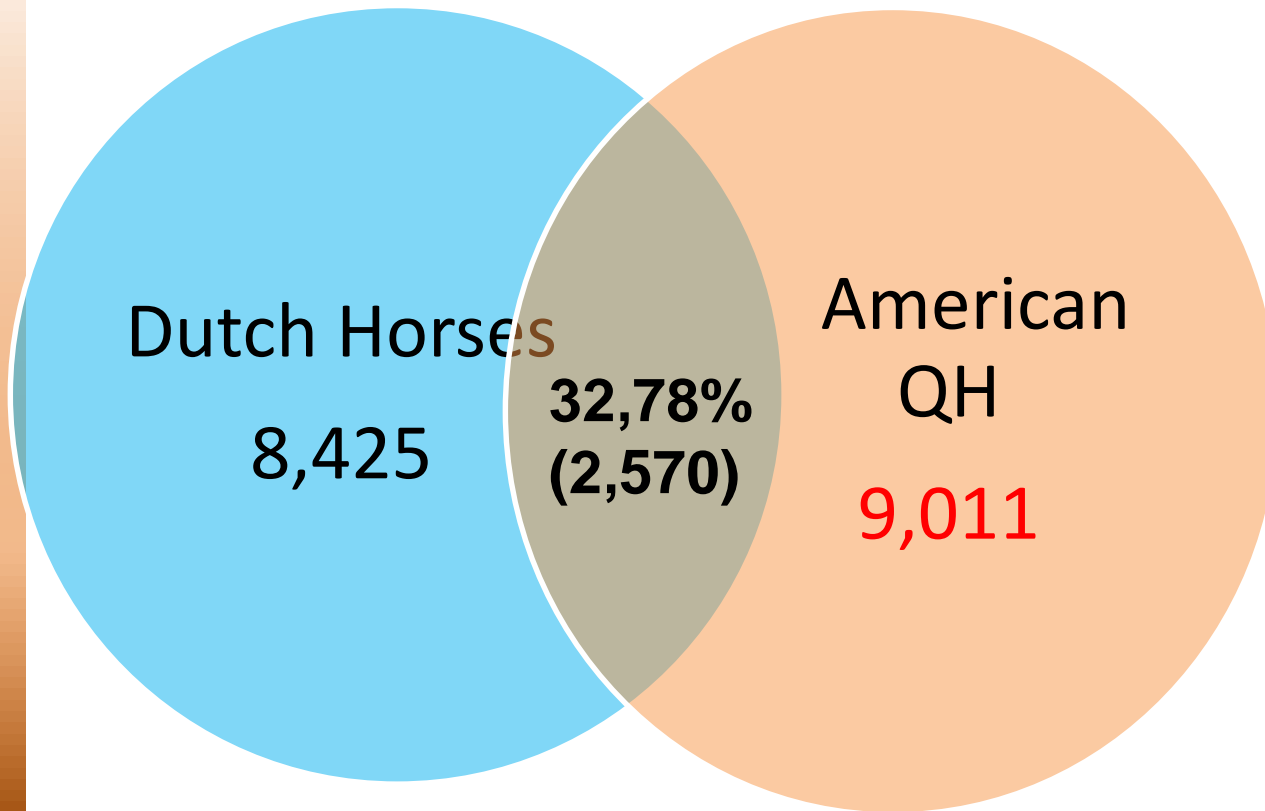
370 SNPs



Distribution of SNPs on horse genome



Common population-specific SNPs



137 American QH



Selected **9k**
with

- MAF >0.38
- Genotype Rate >0.9

<https://www.animalgenome.org/repository/horse/>



Draft multispecies array: Bovine

Objective: Select 10k SNPs reported in cattle to include in multi species chip

7K SNPs

- Autosomes
- Chrom X/Y
- MT-haplotypes
- **7,597 SNPs** from 7k are present in 40K SNPs
- **800 SNPs** on ChrX/Y not in 7k

OMIA dataBase

154 SNPs
related to traits

Major histocompatibility complex

- From SNPs in 7 genes annotated in ensemble
- SNPs reported in others populations and with frequency

340 SNPs



Validation and testing: IMAGE001

Array will be tested with 1920 samples derived from:

- Centres of genetic resources
 - Inventory and follow-up: Paul Boettcher and Sipke-Joost Hiemstra and Richard Crooijmans
- 6 species (340 animals per species)
- Covering >250 breeds



Acknowledgements



- **Chicken**-team: Chiara Bortoluzzi, Zhou Wu, Maria Bernard, Steffen Weigend, Michele Boichard, Richard Crooijmans
- **Pig**-team: Dirk-Jan Schokker, Martijn Derks, Hendrik-Jan Megens, Richard Crooijmans
- **Horse**-team: Rayner Gonzalez Prendez, Barbara Wallner and Molly McCue, Richard Crooijmans
- **Cattle**-team: Rayner Gonzalez Prendez, Richard Crooijmans
- **Goat**-team: Gwenola Tosser, Paola Ajmone-Marsan, Licia Colli, Alessandra Stella, Gabor Meszaros
- **Sheep**-team: Paola Ajmone-Marsan, Licia Colli, Alessandra Stella

- **Thermo Fisher Scientific**: support team : Fabian Grandke and Harry Veerman

- Overall coordination IMAGE001 array: Richard Crooijmans and Michelle Tixier Bochard

