
Whole genome sequencing of livestock: insight in the genetics and molecular mechanisms underlying selection

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Domestication and breeding of livestock: 10,000 years of selection

- What changes have occurred in the genomes of these animals and what can we learn from it?



Today's talk: 1 million years of genetic change and selection in the pig (*Sus scrofa*)

European–Asian split ~ 1 Mya



Wild boar Europe



1 Mya



Wild boar Asia

Stronger bottleneck during last ice age in European wild boar



20 Kya

10 Kya

Independent domestication of *Sus scrofa* in Europe and Asia



Introggression of Asian haplotypes into European domestic breeds in the 18th and 19th century



Strong selection within specific breeding lines since 1950's



European domestic



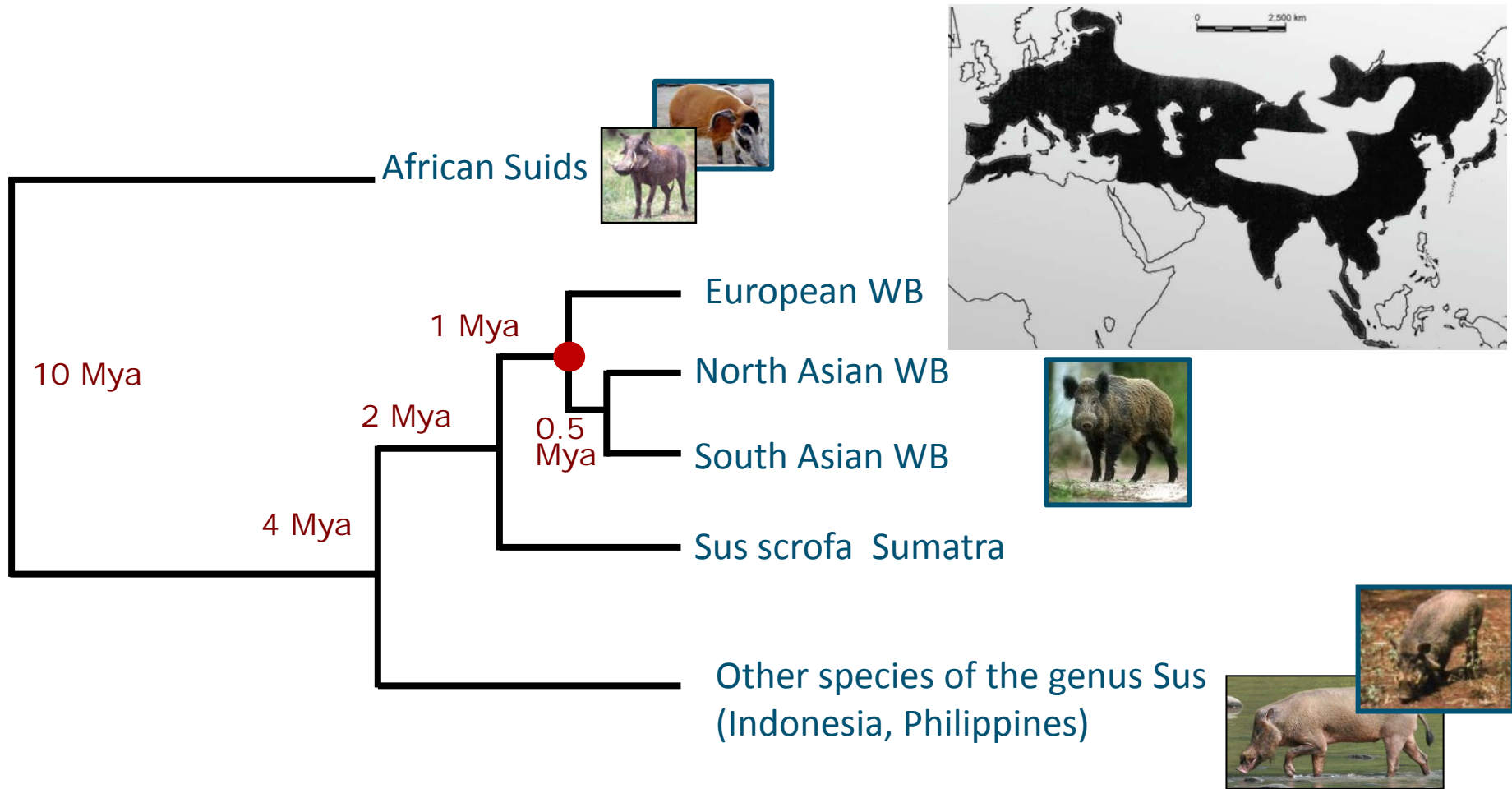
200 ya



Asian domestic



Split between European and Asian wild boar: Tree based on 1 million random SNPs



Frantz et al (2013) *Genome Biology*

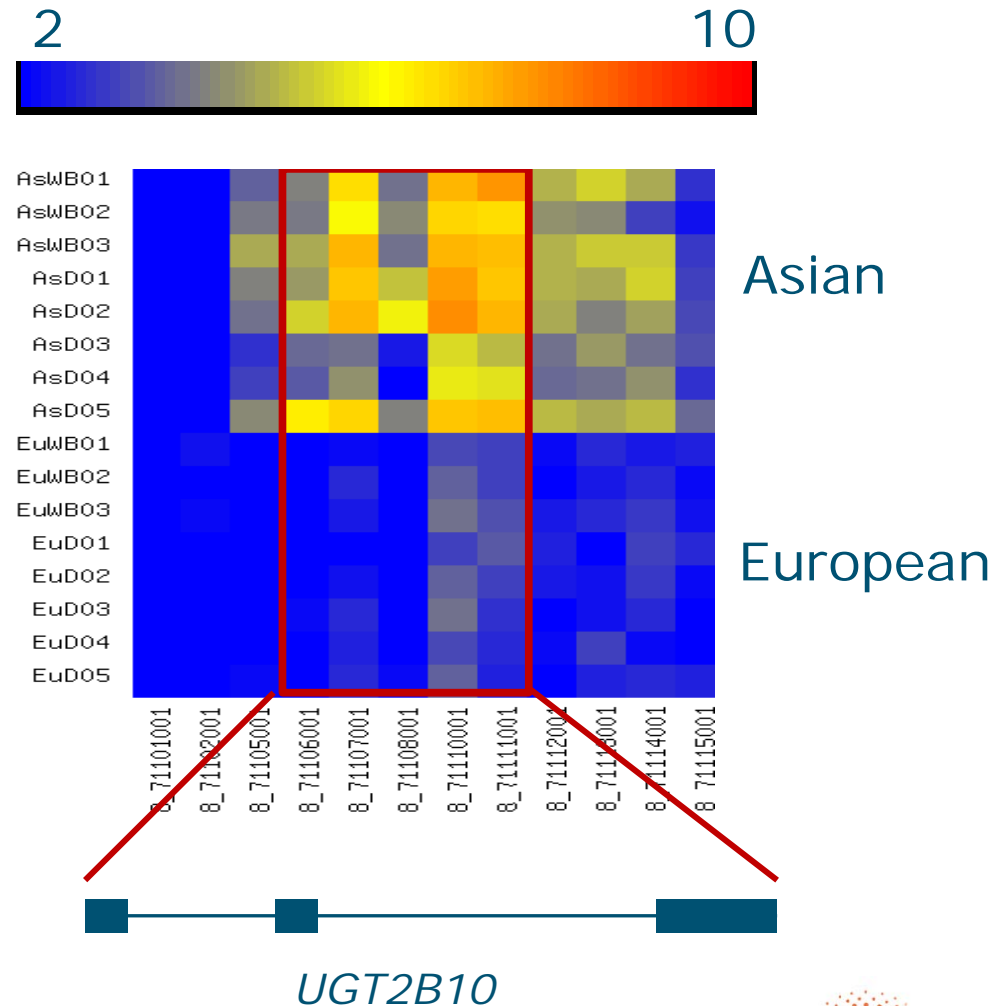
Differentiation of European and Asian wild boar

- More than 1.2 million fixed differences between the genomes of these pigs
- 5% of the genes (1191) code for different protein variants
- genes involved in sensory perception, immunity and host defense are among the most rapidly evolving genes
- Lower nucleotide diversity in European wild boar
- Fixed differences in copy number of specific genes



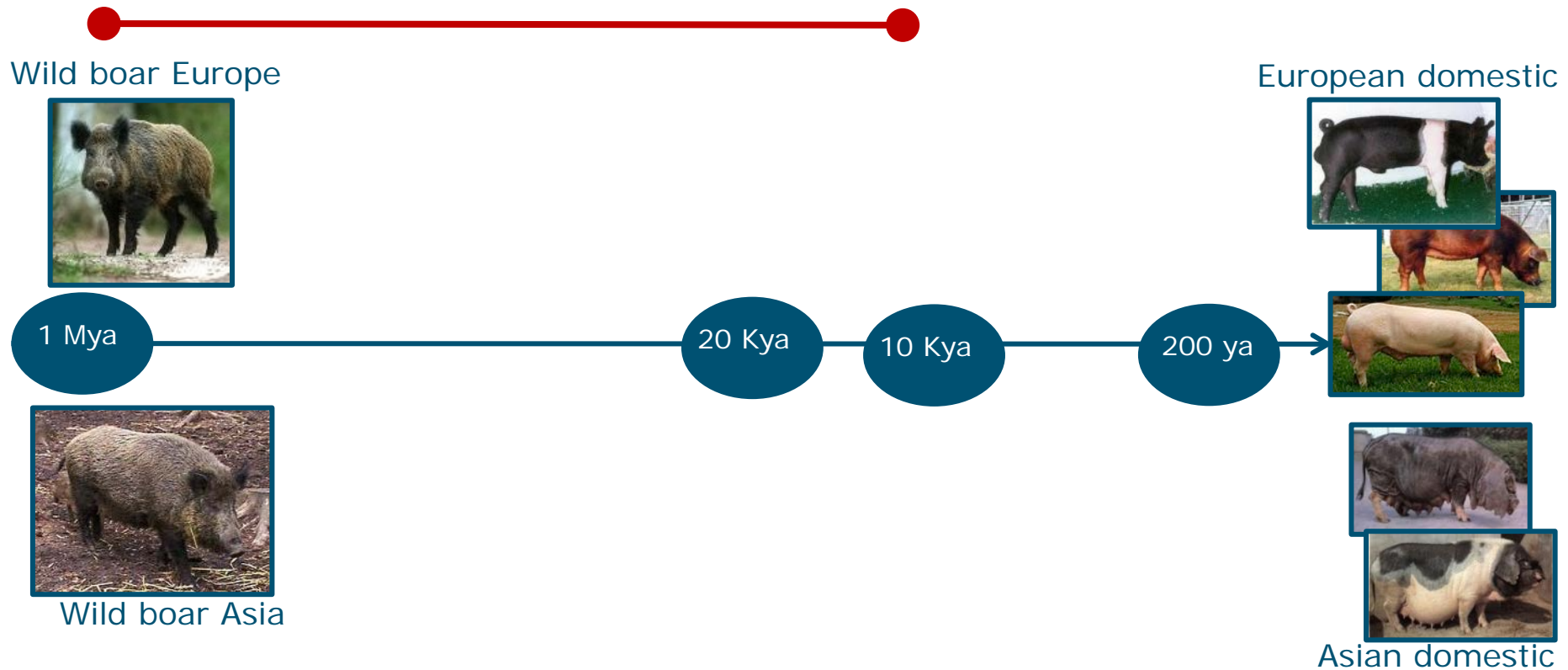
Fixed differences in copy number of specific genes

- Fixed duplication of the *UGT2B10* gene in Asian wild boar
- UDP glucuronosyltransferase is a hepatic enzyme involved in detoxification
- Differences in diet

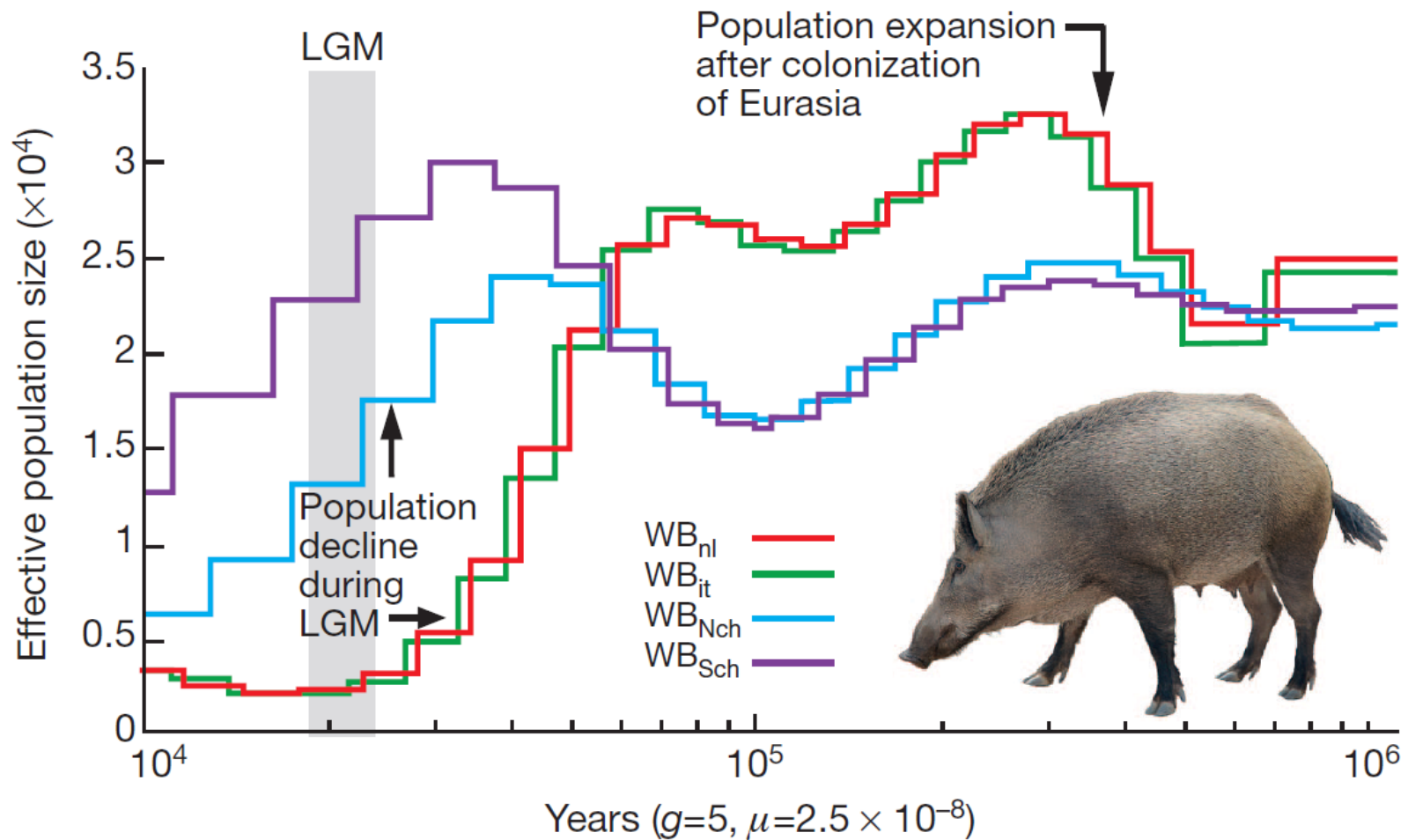


Inference of demographic history of wild boars

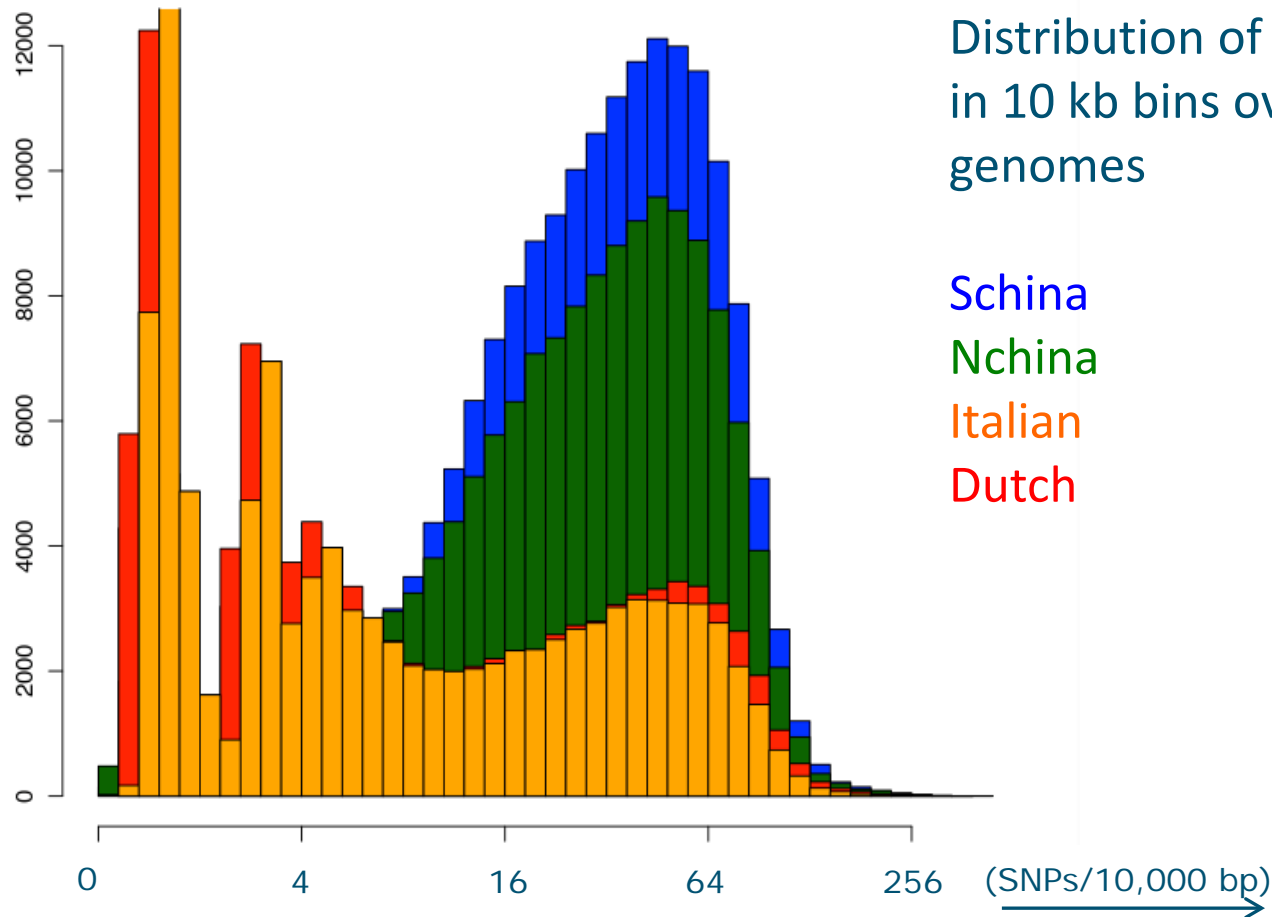
Changes in effective population size between Eu-Asia divergence and domestication of WB in Europe and Asia



Stronger bottleneck in European wild boar during last ice age



Stronger bottleneck in European wild boar: Higher SNP variation in Asian populations

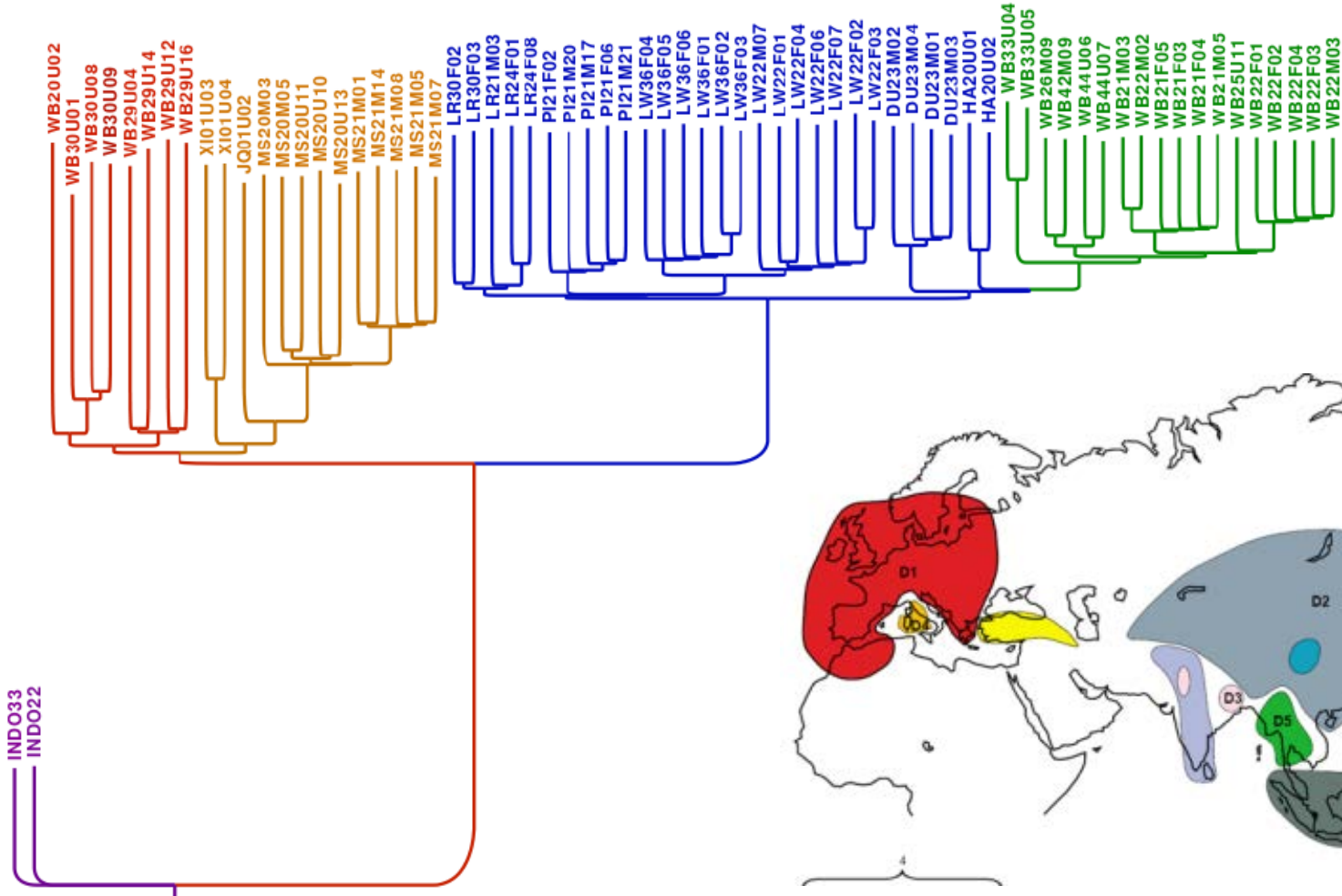


Independant domestication in Asia and Europe

Asia wild boar Asian domestic

European domestic

European wild boar



Distinct differences during the domestication process in Asia and Europe

- Europe:**
- Until the late middle ages use of pannage where pigs were freely roaming the forest and fed on mast
 - Selection on similar features as wild boar
 - interbreeding with wild boar
 - For a long time domestic pigs still showed many characteristics of wild boar

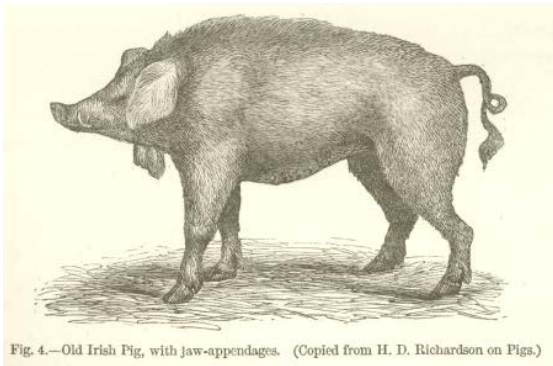


Fig. 4.—Old Irish Pig, with jaw-appendages. (Copied from H. D. Richardson on Pigs.)

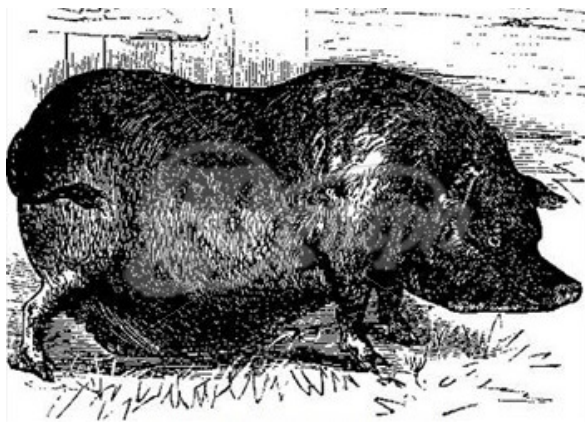
Illustration from Charles Darwin's book "The Variation of Animals and Plants under Domestication" (1868)



Illustration from 15th-century French manuscript Les Très Riches Heures du duc de Berry

Distinct differences during the domestication process in Asia and Europe

- Asia:**
- Housed in enclosures
 - Fed on human scraps and refuse
 - Selection on rapid growth and prolific breeding
 - Round, pot-bellied, small, short legs, highly prolific



From the Memorial Edition of Thomas Bewick's Works, vol III: A general History of Quadrupeds (Newcastle-upon-Tyne: Bernard Quatich, 1885)

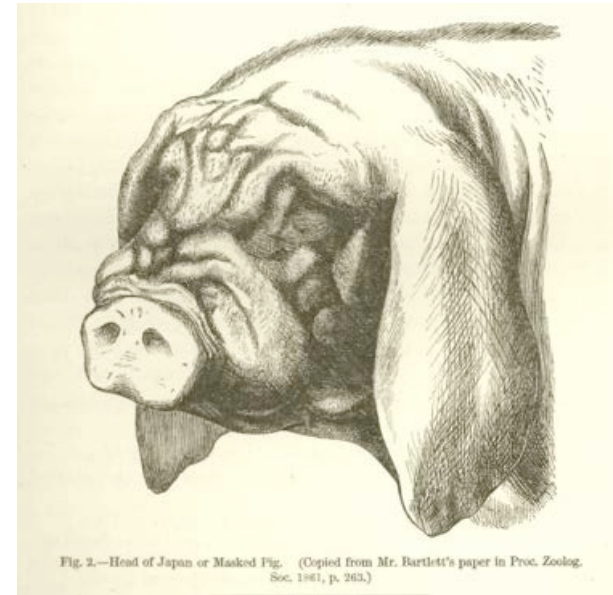
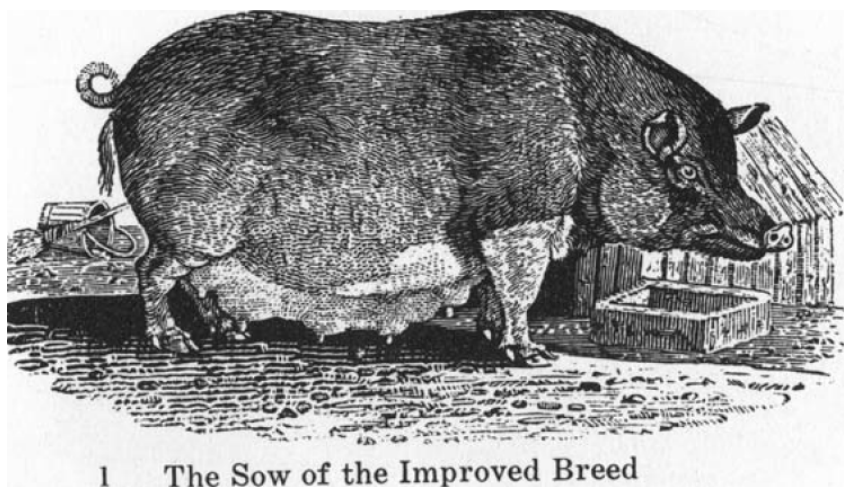


Fig. 2.—Head of Japan or Masked Pig. (Copied from Mr. Bartlett's paper in Proc. Zool. Soc. 1861, p. 263.)

Illustration from Charles Darwin's book "The Variation of Animals and Plants under Domestication" (1868)

Improved pig breeds by introgression of Asian breeds in the 18th and 19th century



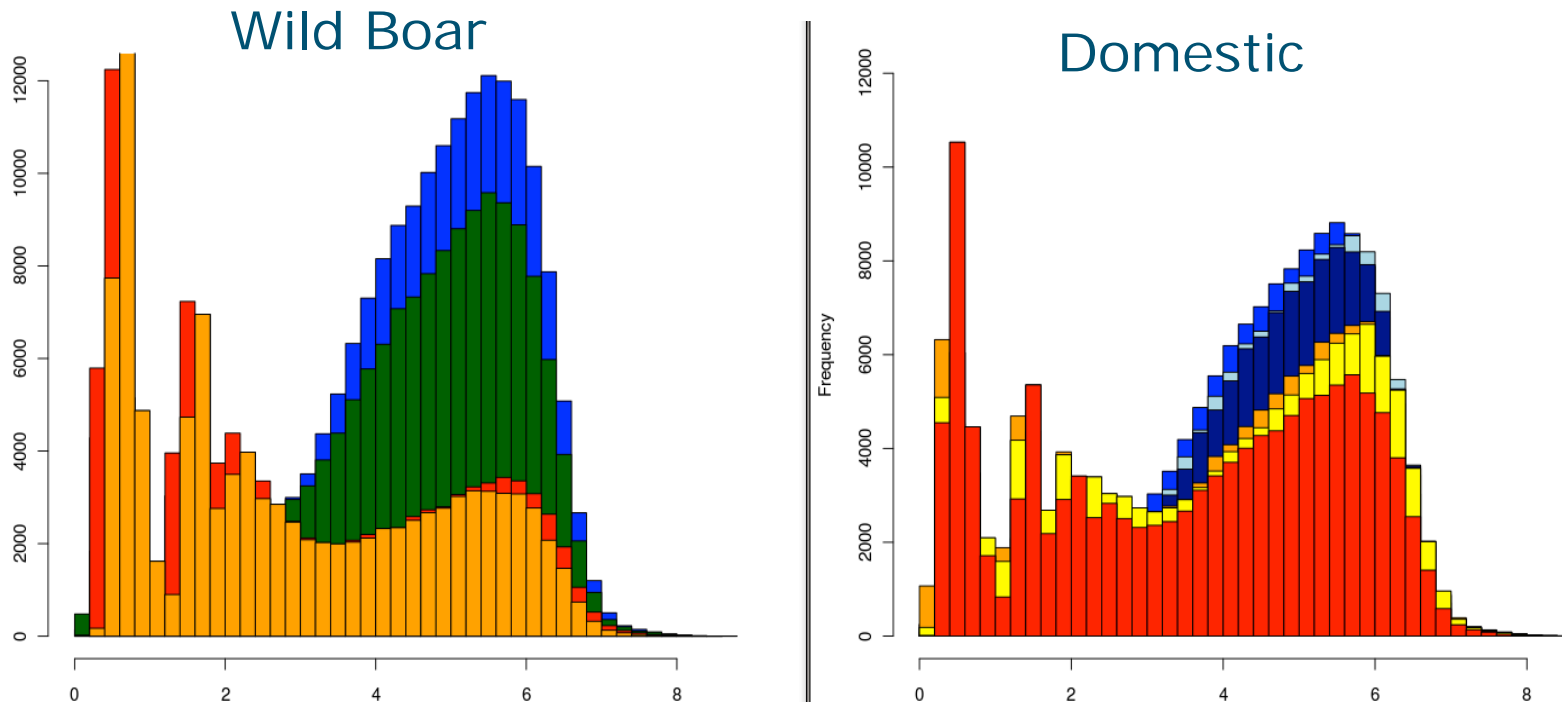
1 The Sow of the Improved Breed



Gloucester Old Spot. Painting by John Miles 1834

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Increased SNP variation in European breeds as a result of Asian introgression

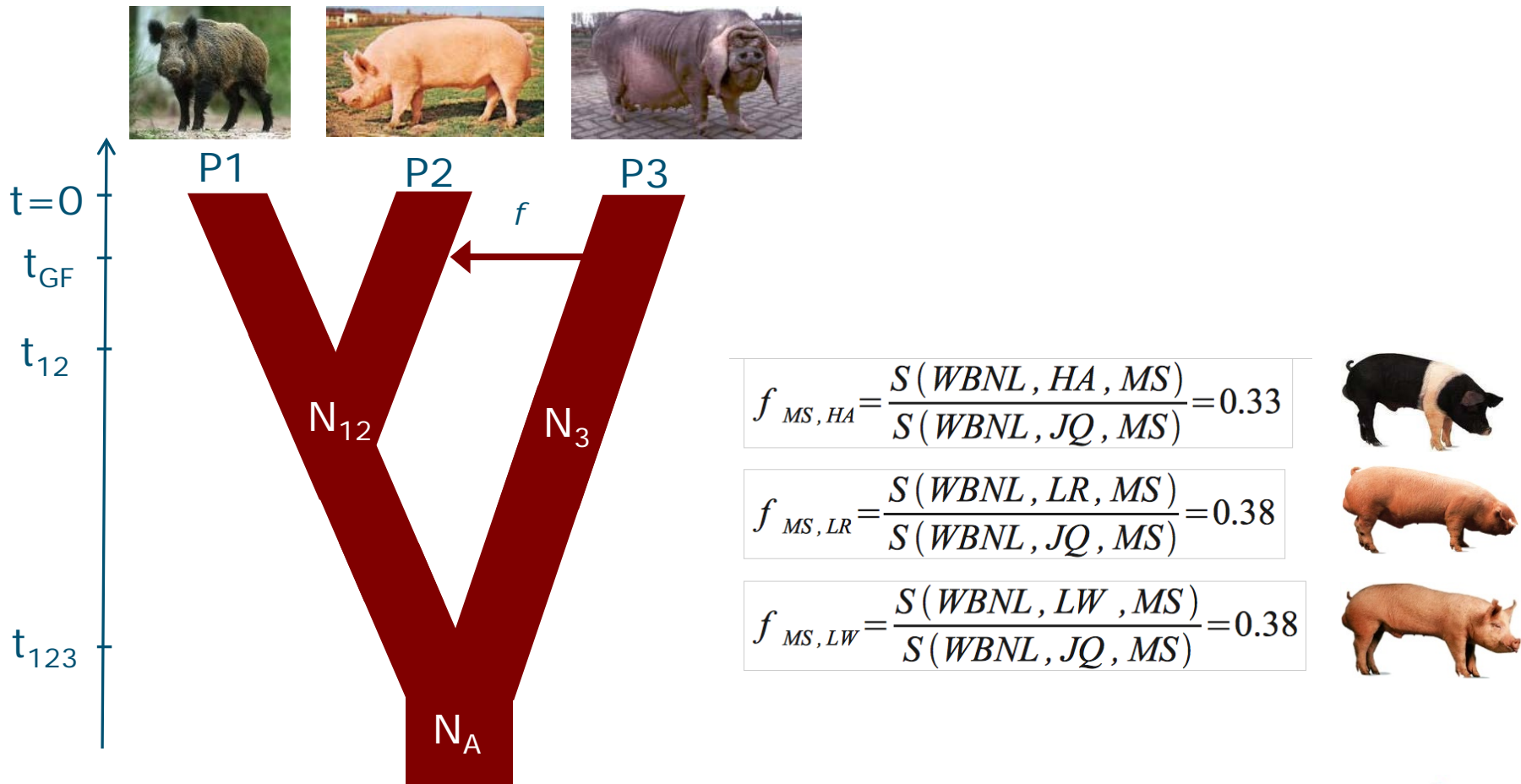


Distribution of heterozygosity ($\log_2(\text{SNPs})$ per 10kbin) over individual genomes

A: Wild Boar: SChina, NChina, Italian, Dutch

B: Breeds: blue=Chinese breeds, red-yellow=European breeds

D-statistics suggest introgression of ~ 35% Asian sequence into European breeds



- Results presented so far show how WGS data provides insight in European and Asian *Sus scrofa* evolution, population demography and admixture
- What does WGS data tell us about selection for specific genes related to specific traits during domestication and more recent pig breeding?



Signatures of selection and introgression in the genome of domestic pigs

- Medium-high density SNP genotyping in combination with genome sequencing
Wilkinson et al. (2013) PLoS genetics
- Sequencing pools of different breeds
Rubin et al. (2012) PNAS
- Whole genome sequencing of individual pigs
Bosse et al (2013) in preparation

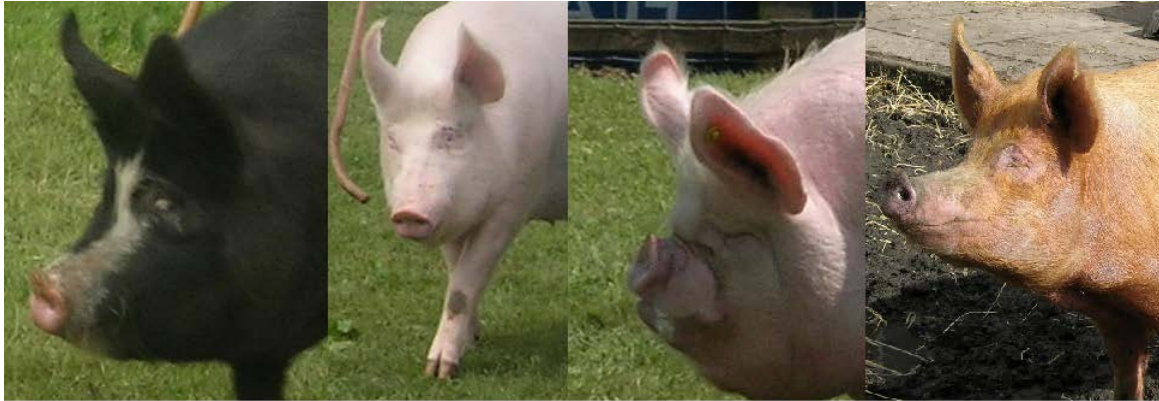


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Differences in coat colour, facial and ear morfologie:



Berkshire

Large White

Middle White

Tamworth

Prick eared breeds



Flat eared breeds

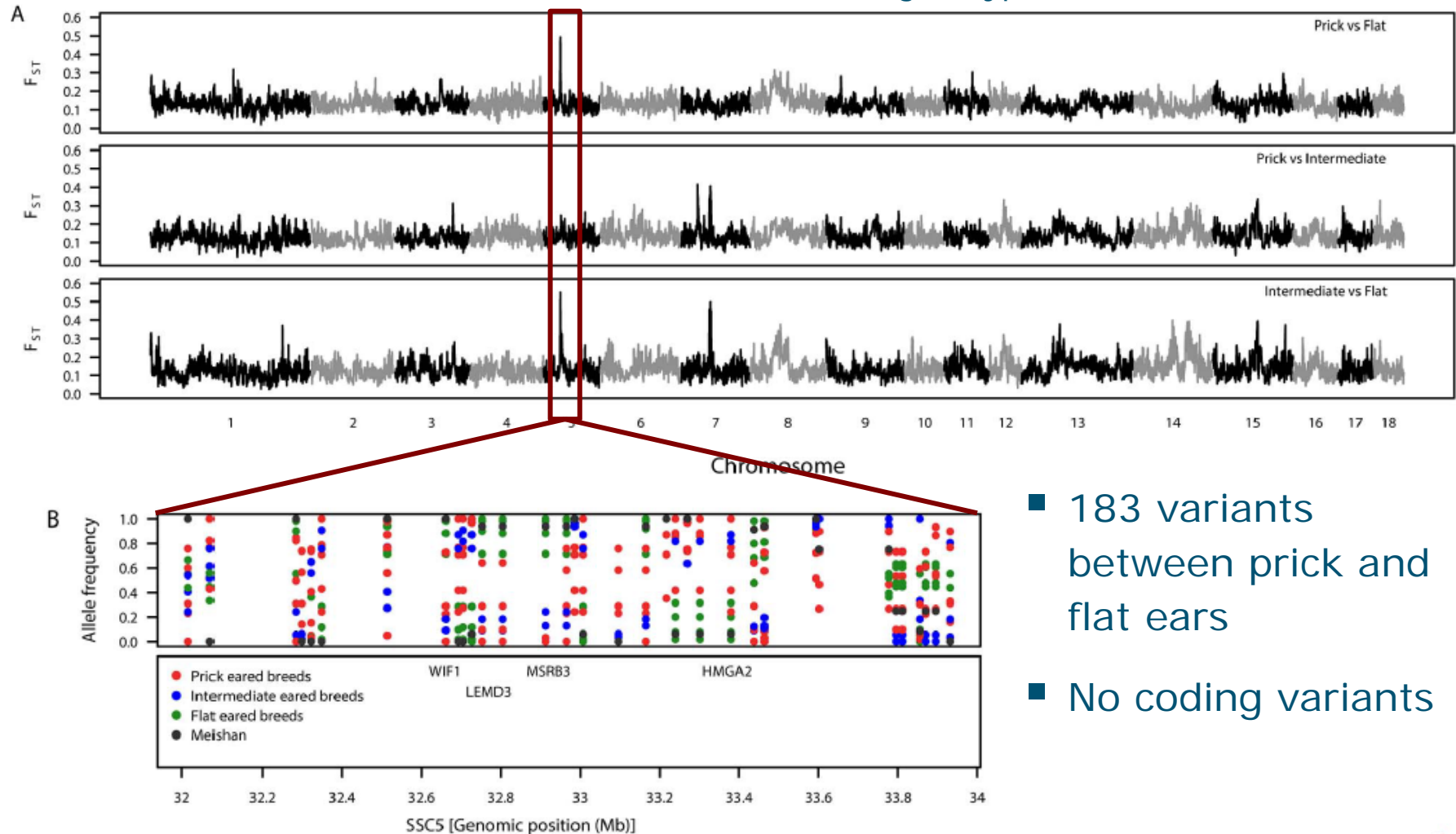
British Saddleback

Gloucestershire
Old spots

Large Black

Genetic variation associated with ear phenotypes

F_{ST} based on Illumina 60K genotype data



- 183 variants between prick and flat ears
- No coding variants

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Groenen et al (2012) Nature 491:393-398
Bosse et al (2012) PLoS genetics 9:
Bosse et al (2013) submitted



For centuries man has selected coat colour in pigs

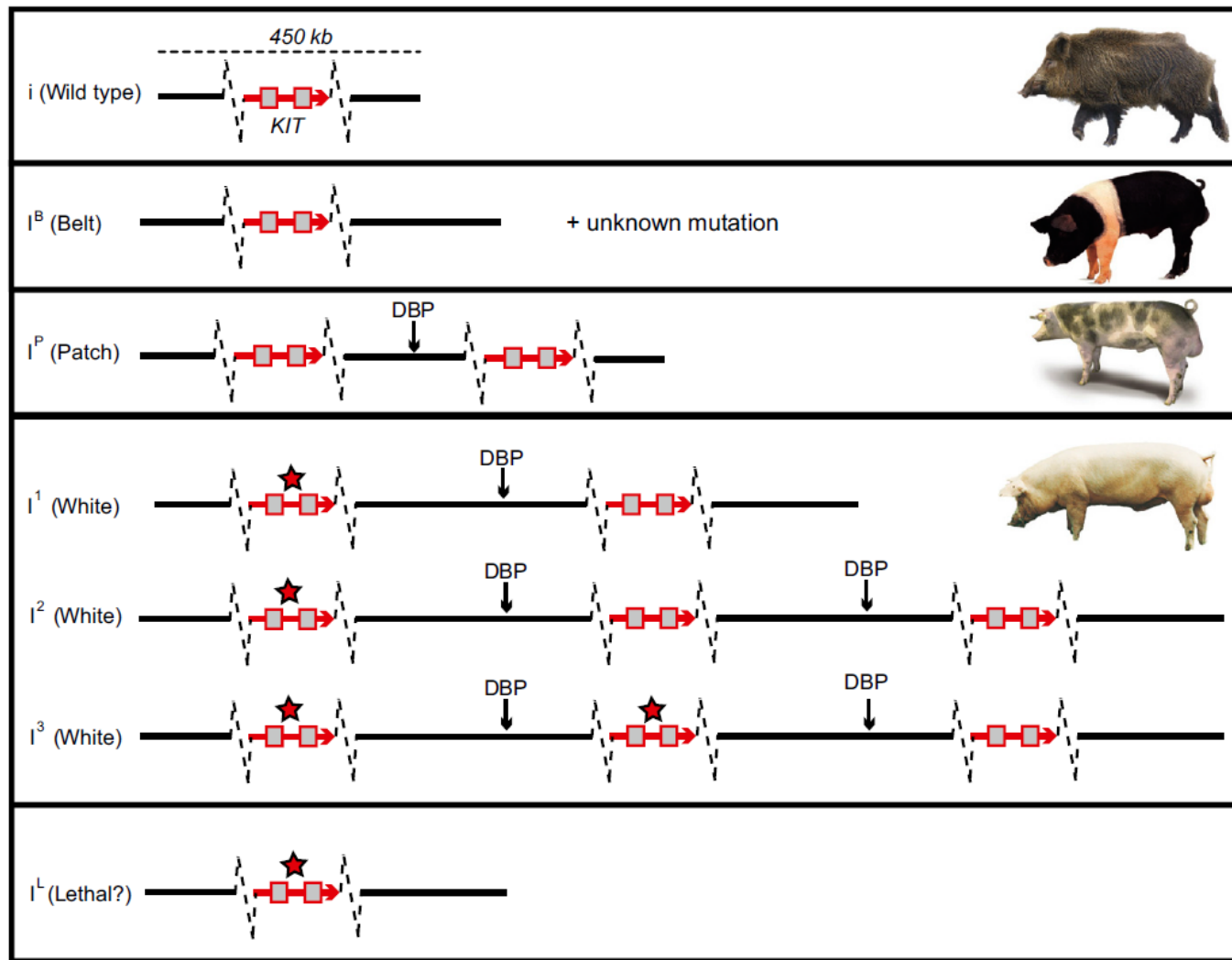


Detail of the fresco *Effetti del Buongoverno in Campagna* in the Palazzo Pubblico in Siena, Italy painted by Ambrogio Lorenzetti in 1337 showing a white belted pig

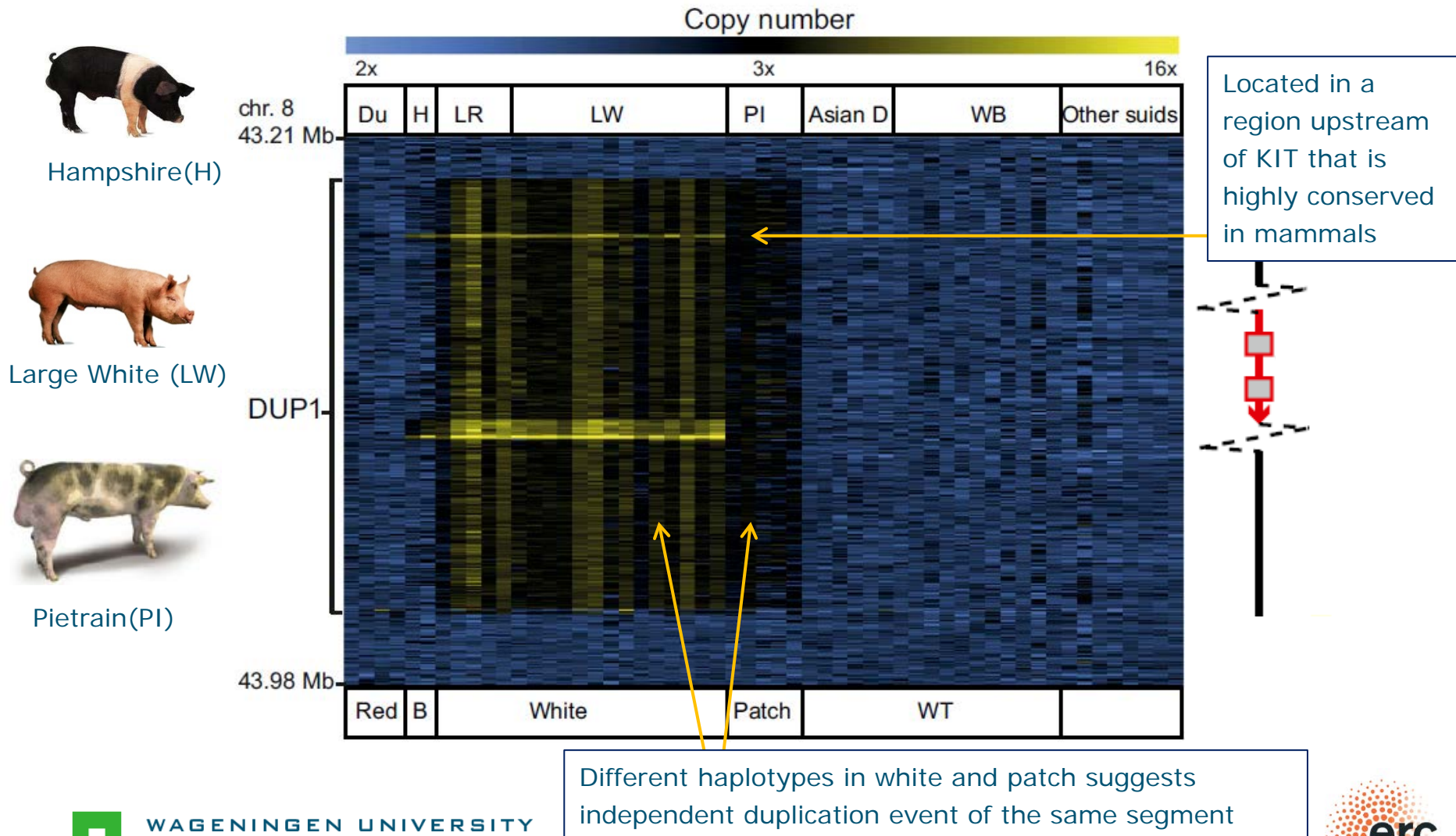


image of a spotted pig from the fourteenth-century *Luttrell Psalter*

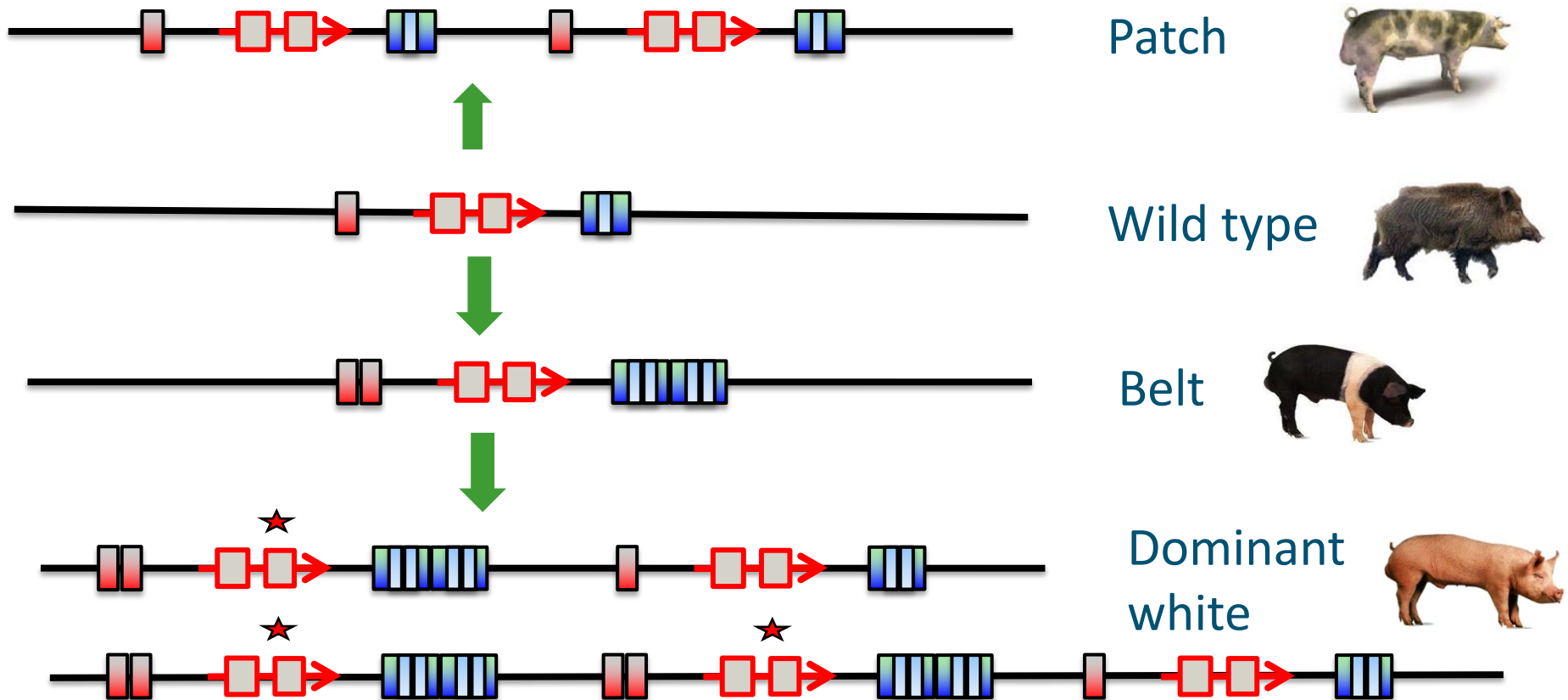
Duplication of KIT gene affects coat colour



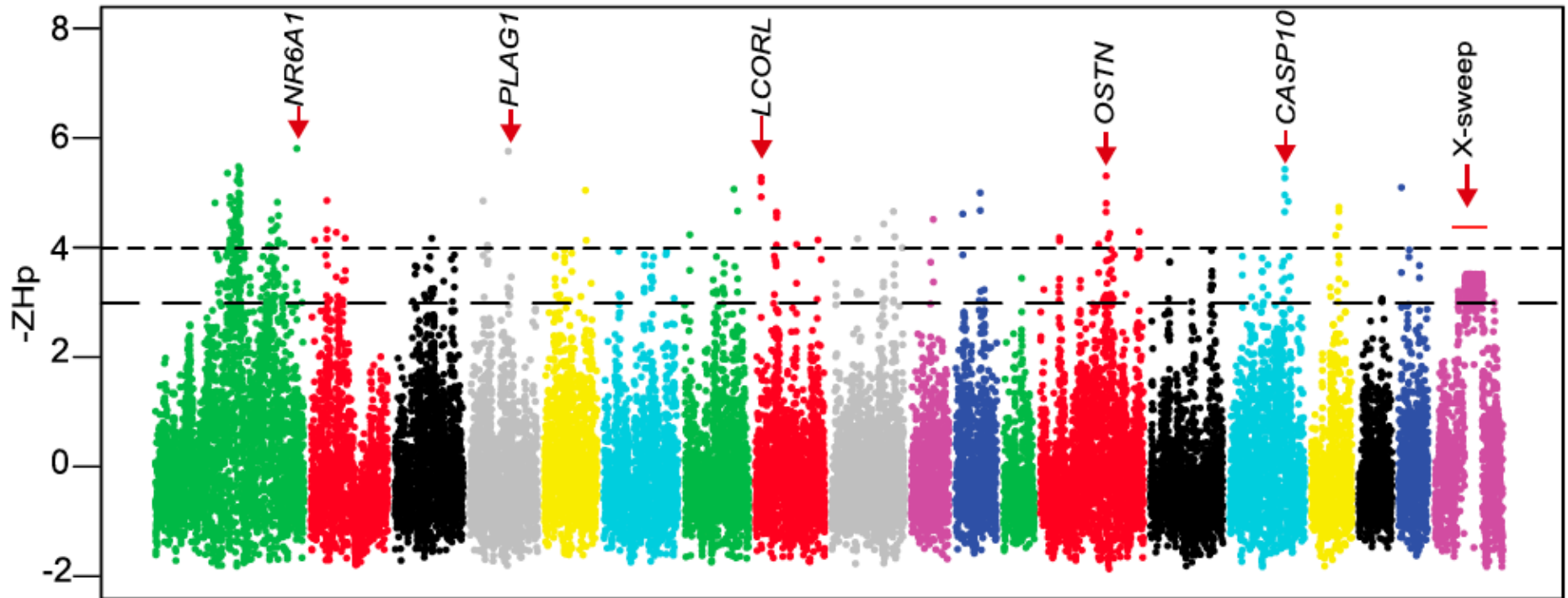
Identification of belted allele using a NGS read depth CNV analysis



KIT alleles: Complex organization resulting from multiple independent duplications



Selective sweeps in European domestic pigs



Windows ordered along pig chromosomes (1-18 and X)

↑
QTL for number of vertebrae

↖ ↗
QTL for body length

wild boar



Domestic pig

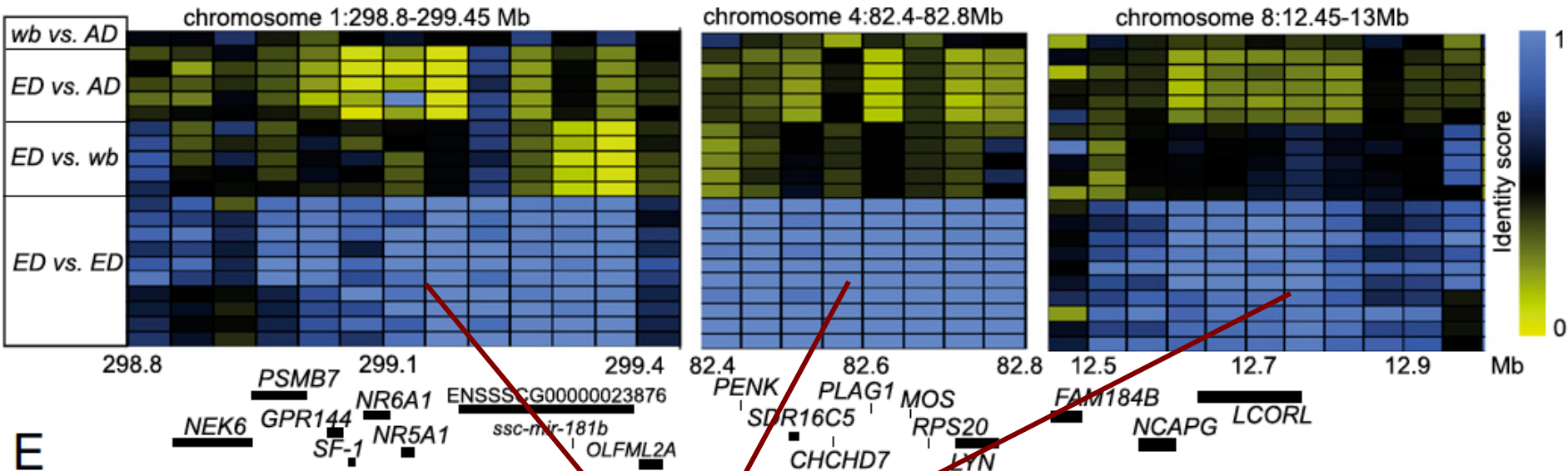


Haplotype sharing in European domestic pigs

NR6A1

PLAG1

LCORL



E

Haplotypes in European breeds for all three regions are of European origin

wild boar

Domestic pig



Rubin et al. (2012) PNAS



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WAGENINGEN UR



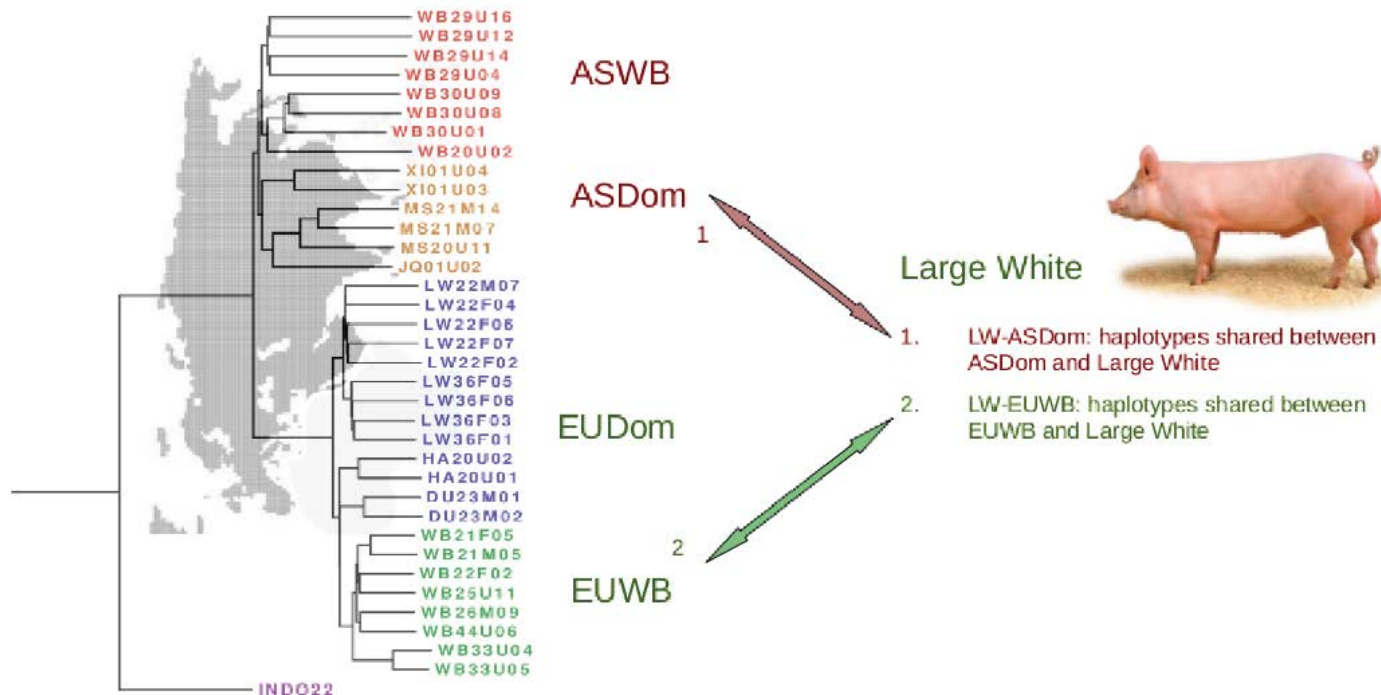
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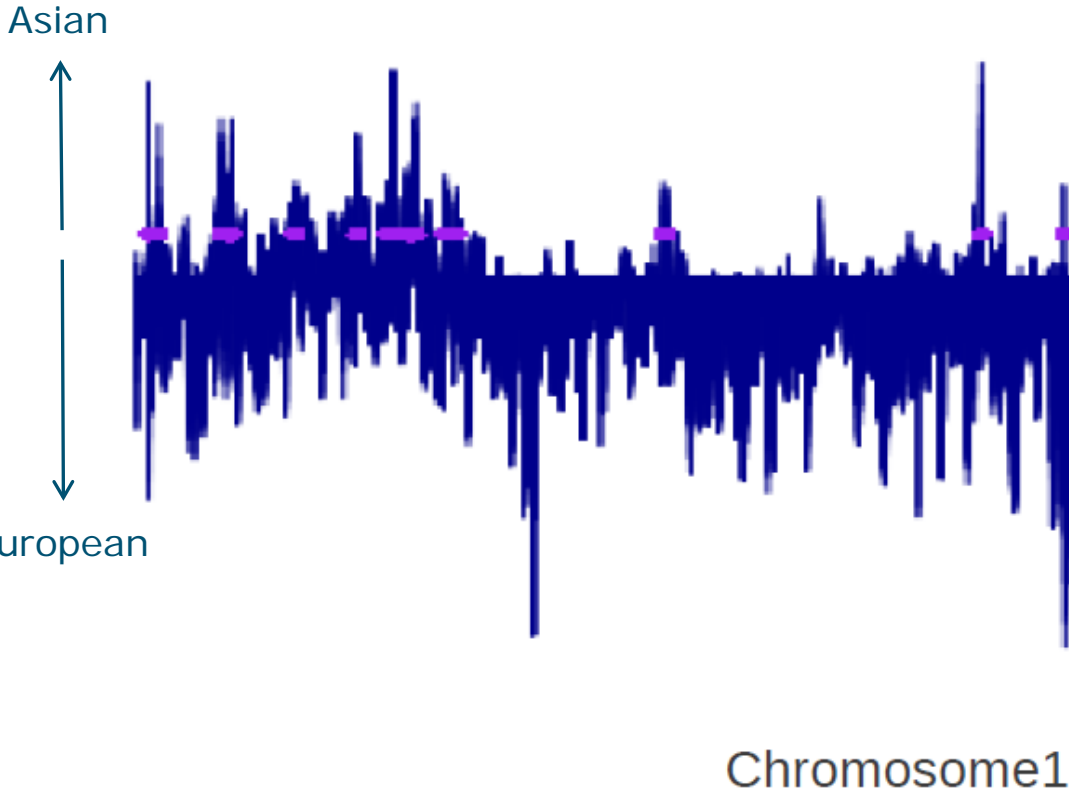


European vs Asian origin of haplotypes across the genome

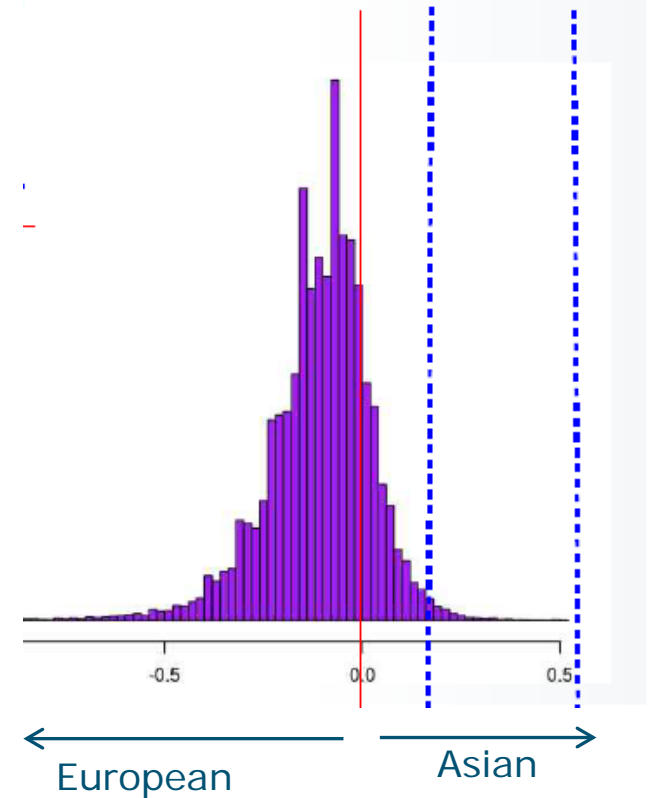
- SNPs identified from individually sequenced genomes
- Reconstruct haplotypes with Beagle



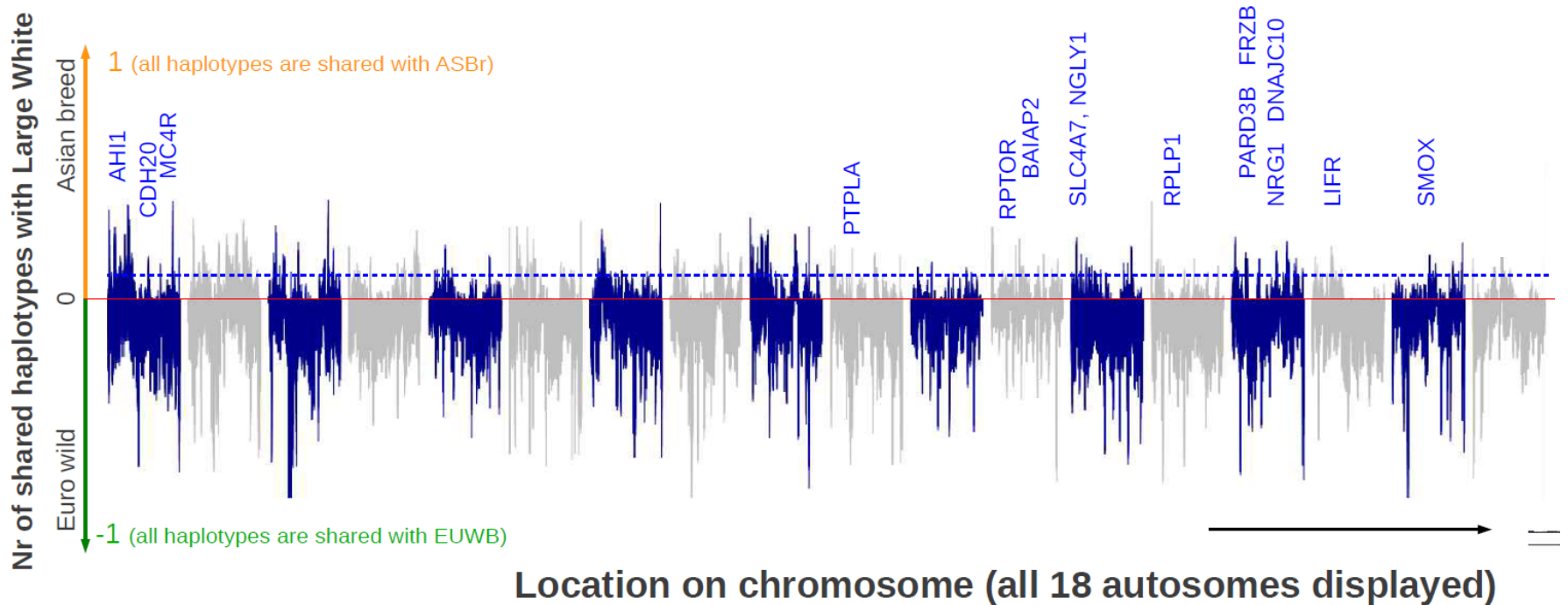
Comparison LW shared haplotypes with Asian and European wild boar



Genes in top 0.5% shared haplotypes



Genes in top 0.5% shared Asian haplotypes



- Identified non-synonymous mutations under selection
- Tested in GWAS study (fertility)
- Results show selection on fertility after introgression of Asian haplotypes

Take home messages

- WGS data of a few individuals provides detailed insight into evolution, population history and demography
- WGS data of defined populations provides powerful data for the identification of selective sweeps
- Variation in phenotypes result from single nucleotide variation as well as from complex genome rearrangements
- Well defined phenotypes are essential



Acknowledgements

- Wageningen University, NL
 - Hendrik-Jan Megens
 - Richard Crooijmans
 - Ole Madsen
 - Bert Dibbits
 - Mirte Bosse
 - Yogesh Paudel
 - Laurent Frantz
- University of Illinois, USA
 - Larry Schook
 - Laurie Rund
- University of California, Berkeley, USA
 - Joshua Schraiber
 - Montgomery Slatkin
- CAU, Beijing, China
 - Ning Li
- Roslin Institute, UK
 - Alan Archibald
 - Pam Wiener
 - Samantha Wilkinson
- Durham University, UK
 - Greger Larson
- Uppsala University, Sweden
 - Leif Andersson
 - Calle Rubin
- University of Copenhagen, Denmark
 - Merete Fredholm
- Topigs, Beuningen, NL
 - Barbara Harlizus
 - Egbert Knol

