A Large X-Chromosomal Haplotype is Associated with Small Body Size of Minipigs

C. Reimer[1], A.R. Sharifi, C.-J. Rubin[2], S. Weigend[3], K.-H. Waldmann[4], O. Distl[4], S.D. Pant[5], M. Fredholm[5], H. Simianer[1]

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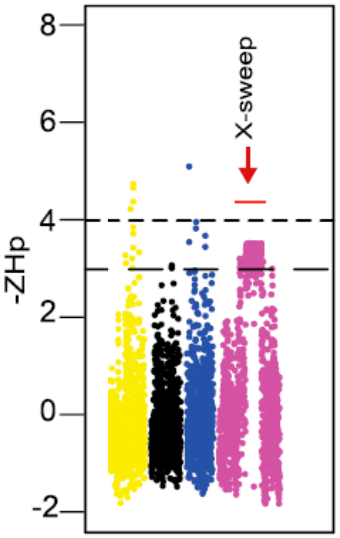

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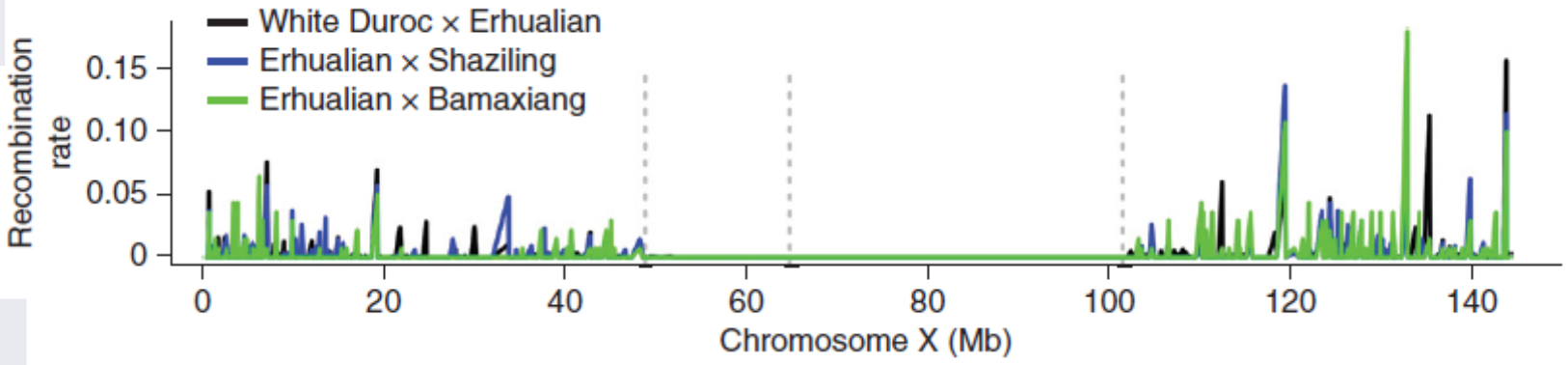

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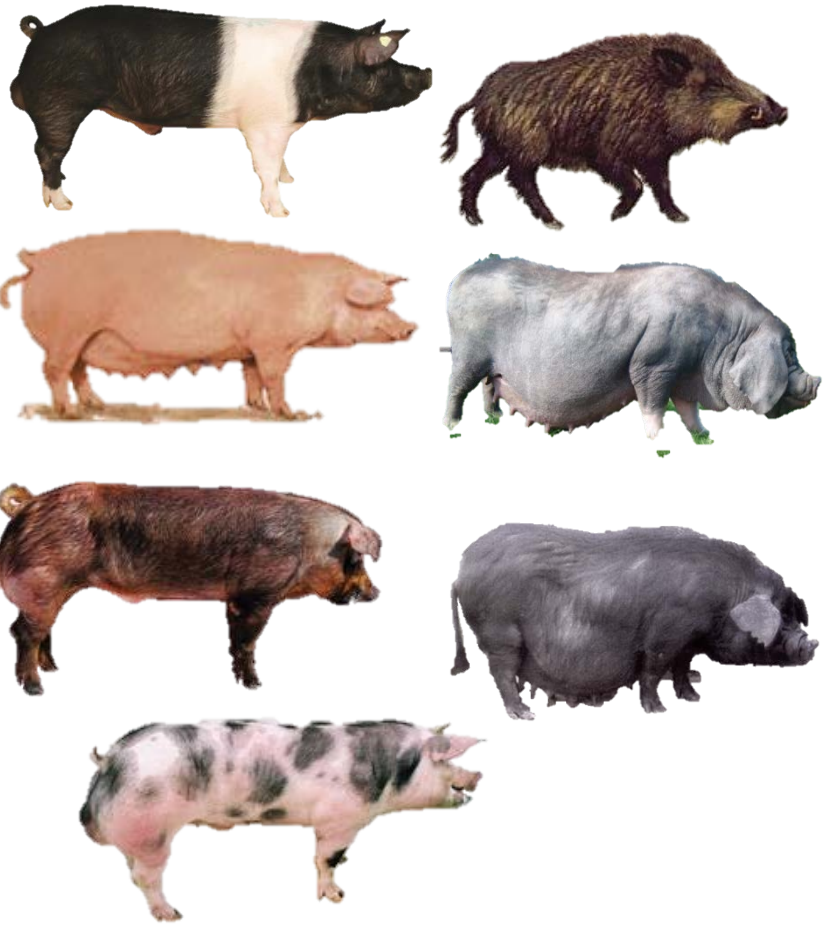

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A virtual pool of
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Filtering

- SNP call rate > 90%
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Statistical modelling

Linear model, Proc GLM, SAS (SAS Institute, Cary, NC)

	Mean	SD
Height at scanning	39.93	4.39
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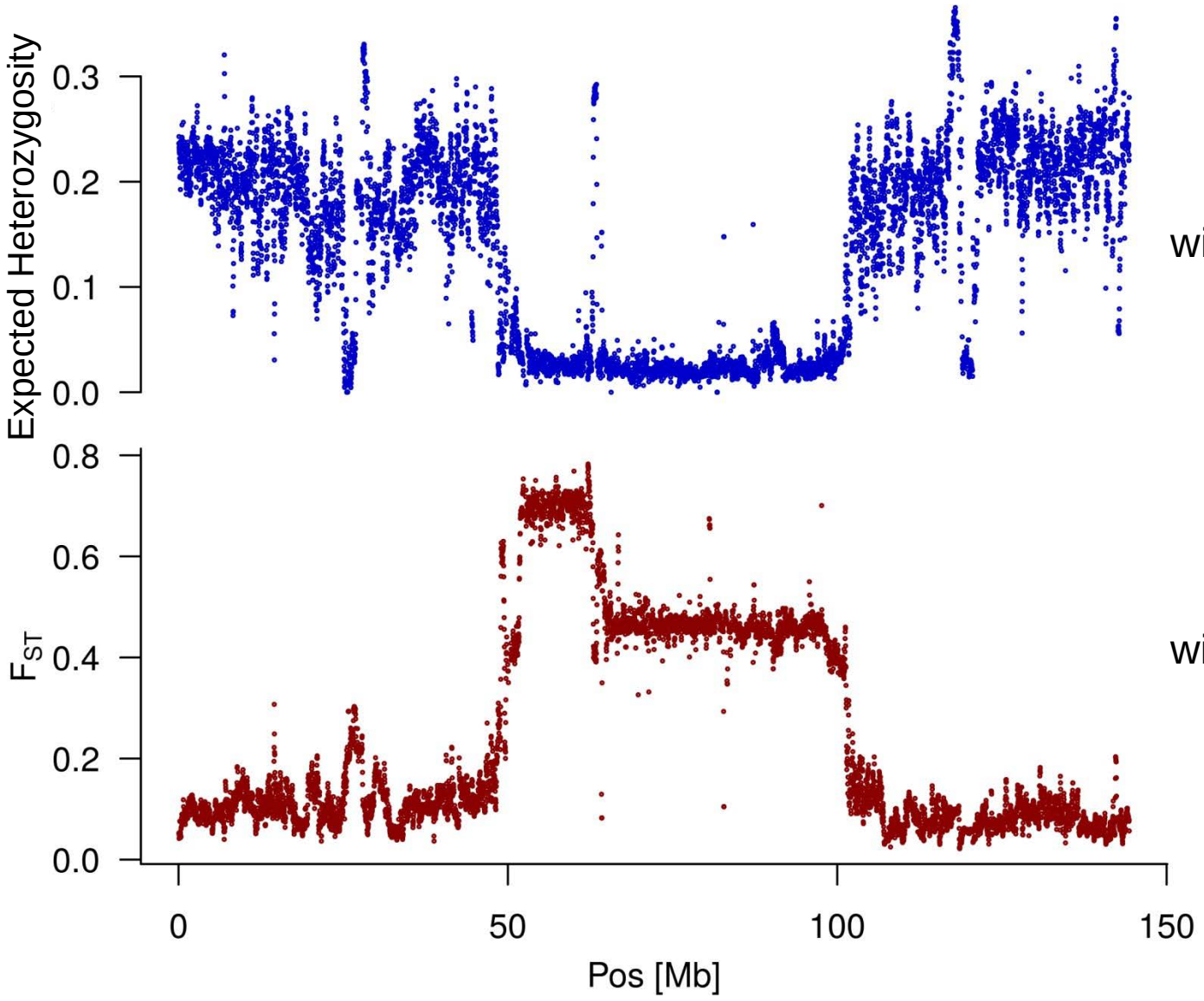

Minipig
without Wushizhan

Minipig
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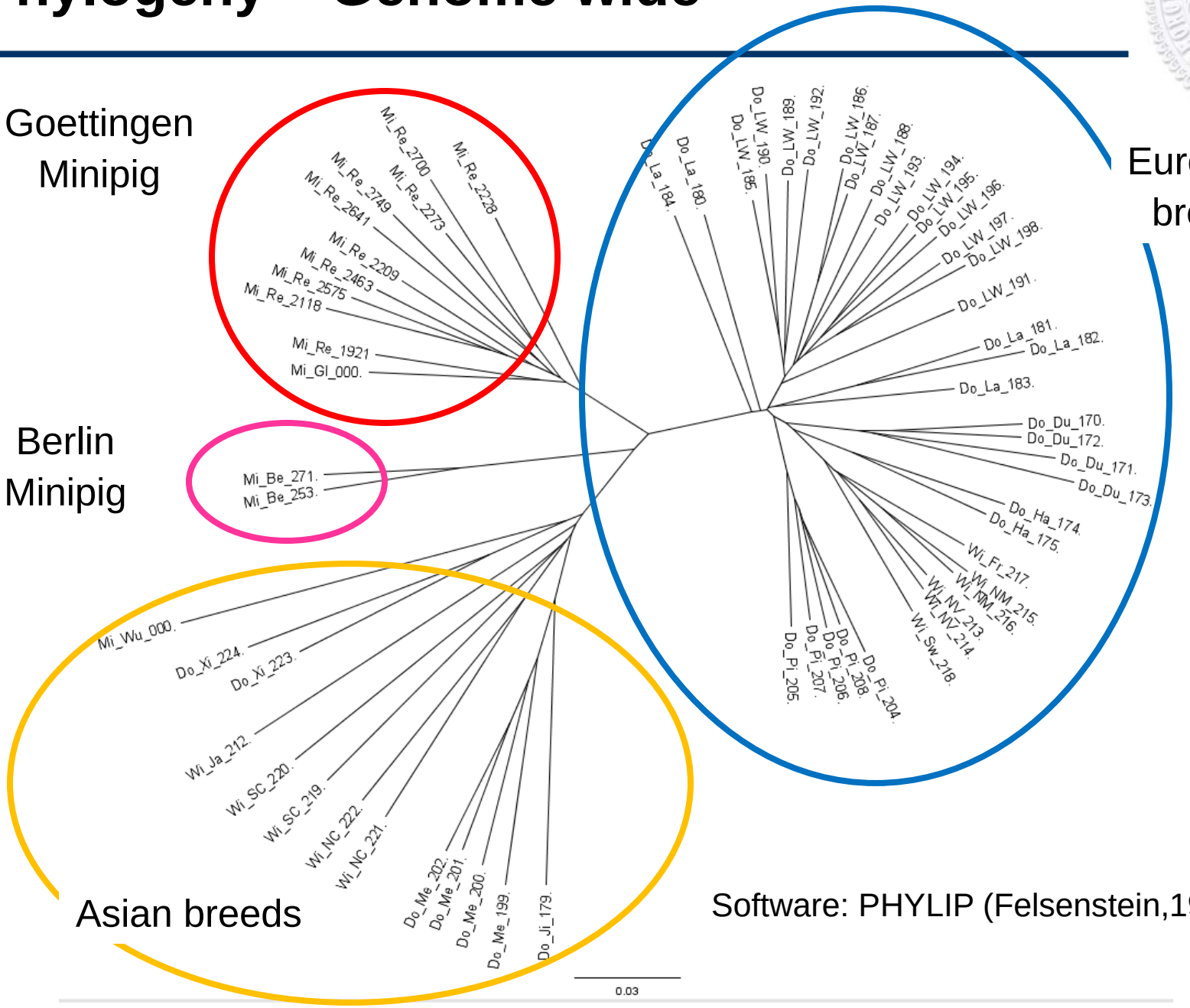
Phylogeny – Genome wide

Goettingen Minipig

Berlin Minipig

European breeds

Asian breeds



Software: PHYLIP (Felsenstein,1989)

Phylogenie – X:53-61

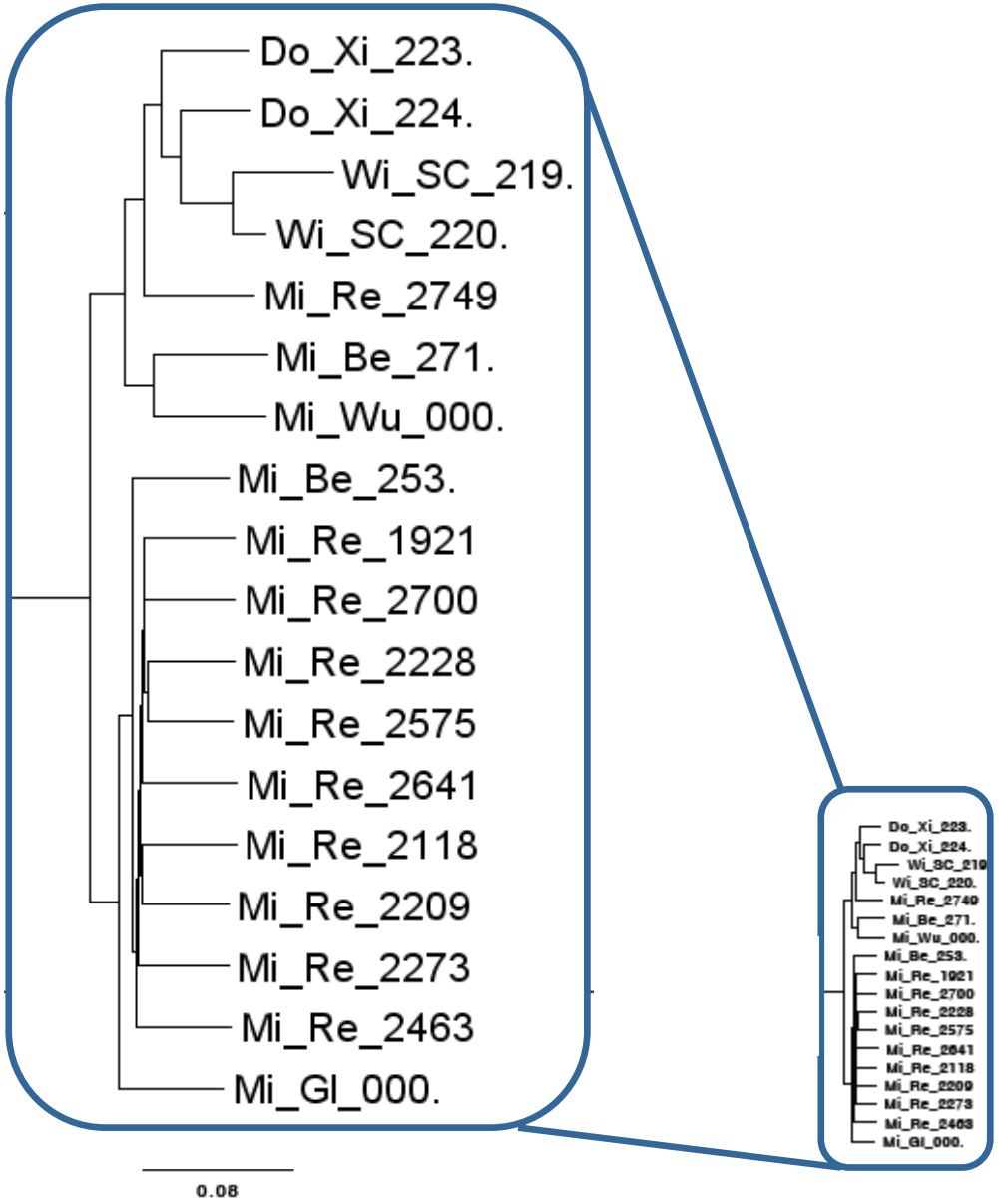
Xiang

South-chinese wild boar

Wushizhan

Berlin Minipig

Goettingen Minipig



SNPs and haplotypes

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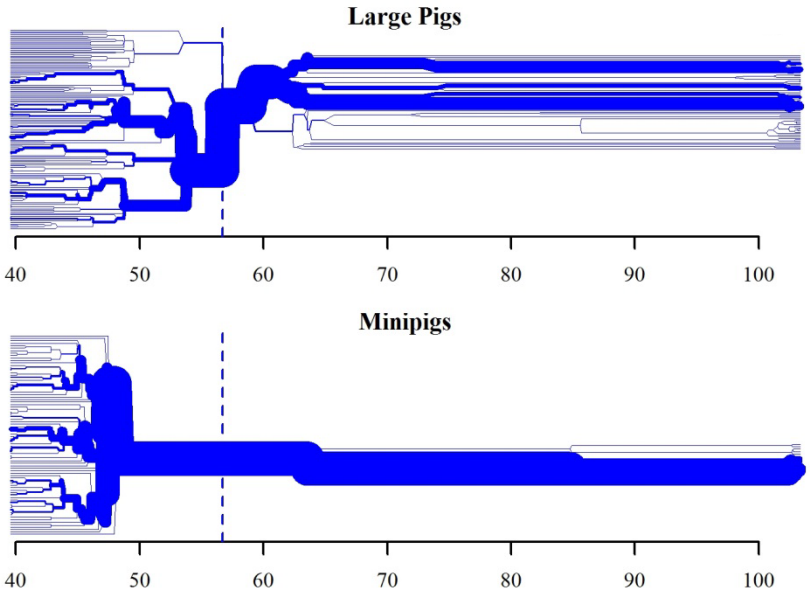
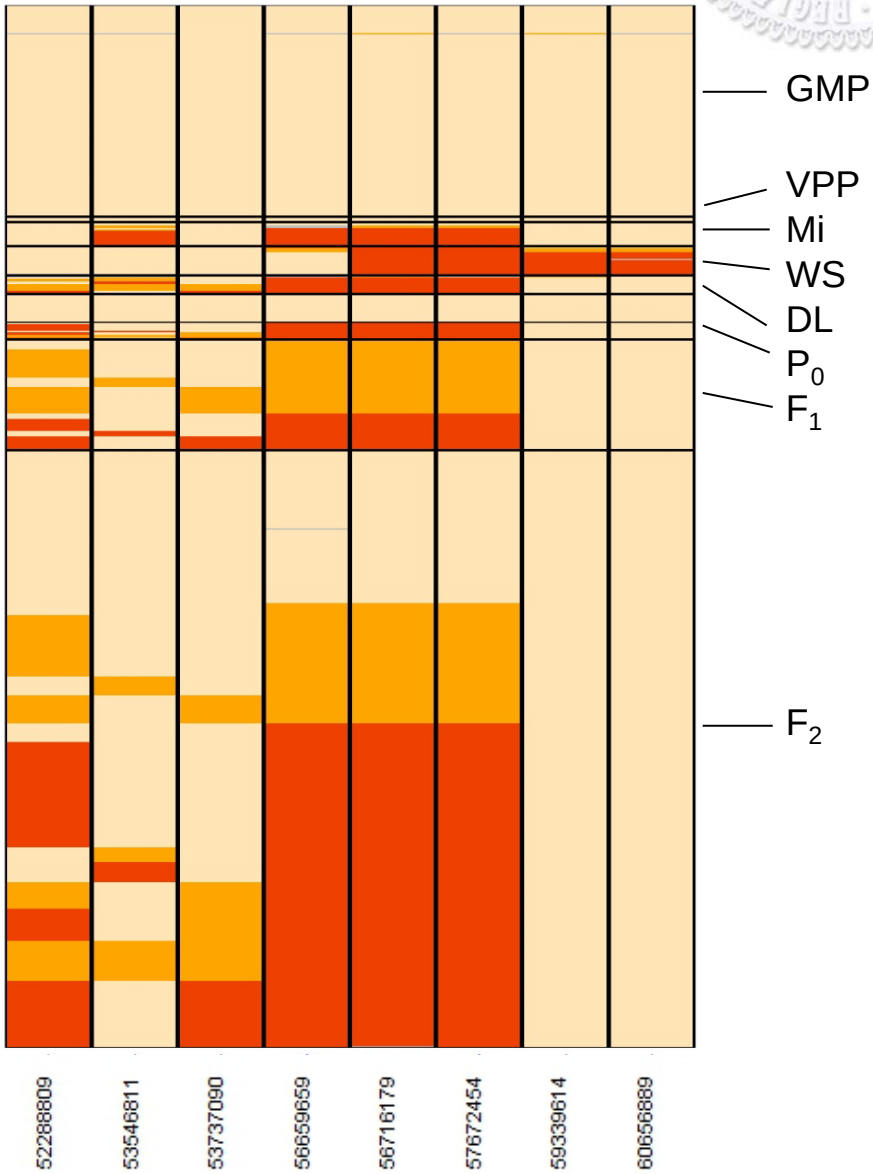
3 SNPs clearly linked to size groups





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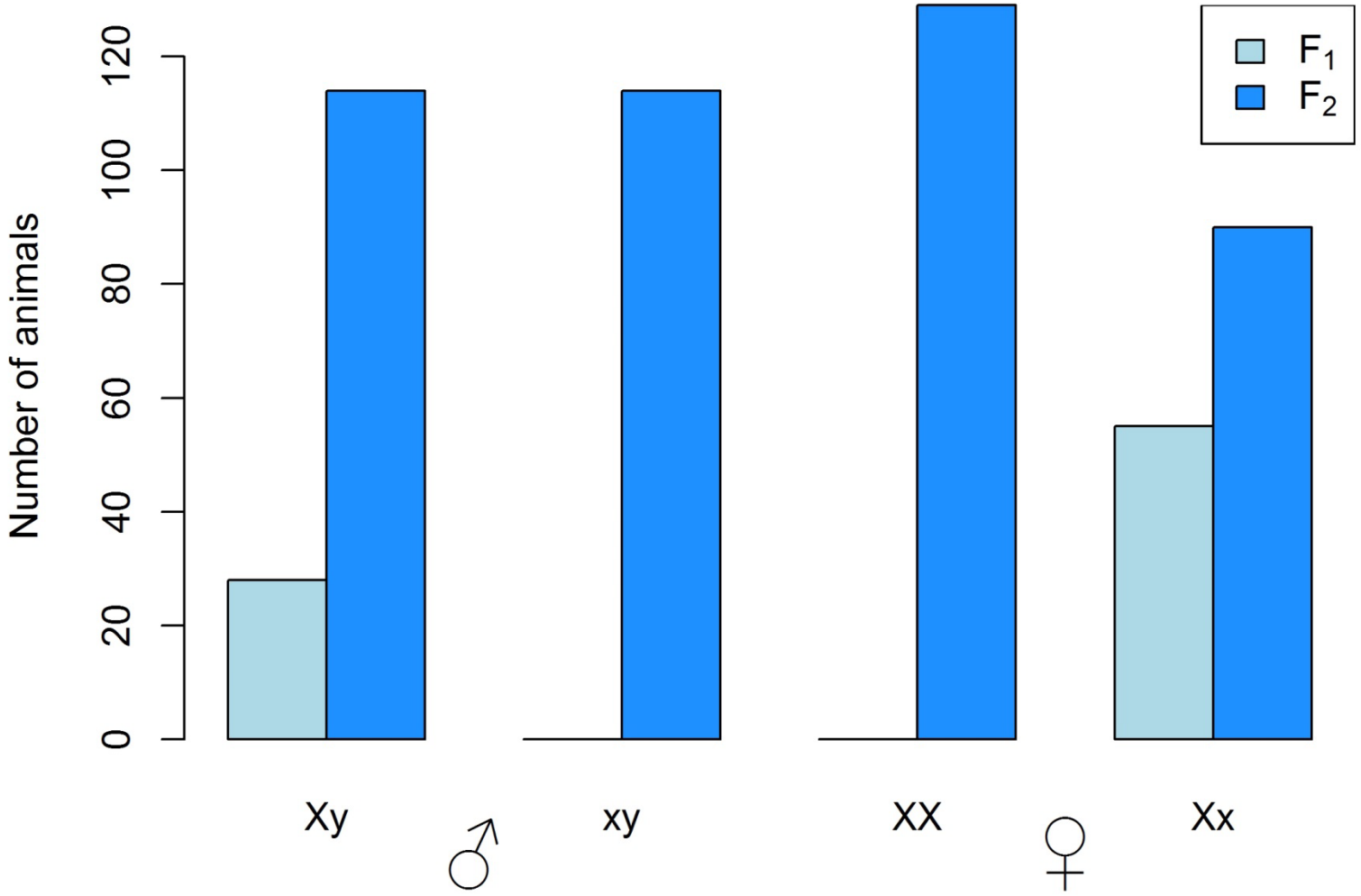

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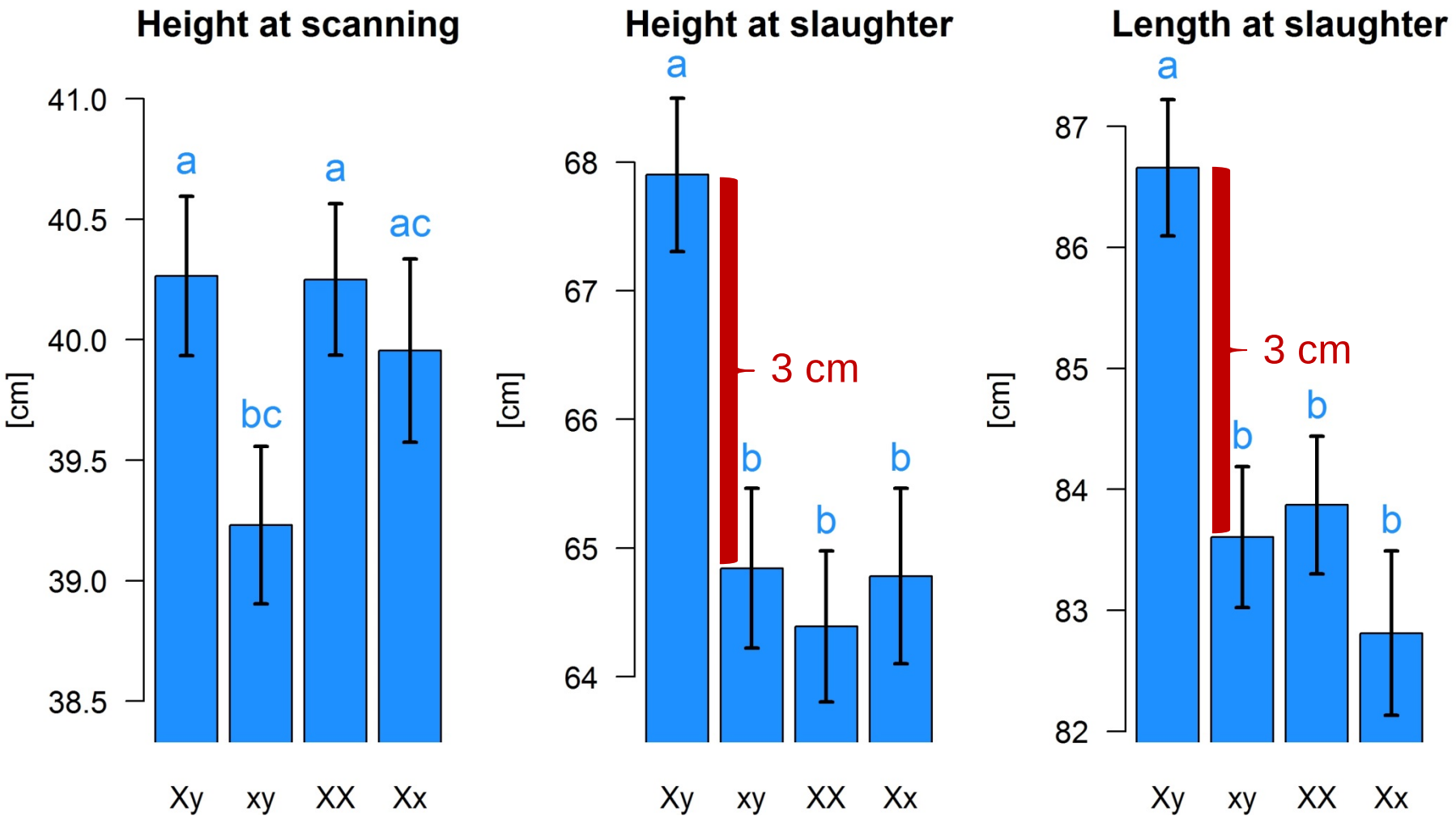

Conclusion

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- Female cross-breds can carry both haplotypes

- Boars carrying the minipig haplotype are significantly smaller than boars carrying the large pig haplotype (3% shorter and 3% less high)

➔ **The X-chromosomal sweep region explains a considerable part of the total variability of body size**

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References

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Filtering with GATK

- Sequencing depth lower 90 X or higher 840 X
- BaseQualityRS lower -5.5 or higher 5.5
- MappingQualityRS lower -11 or higher11
- ReadPositionRankSum lower -6
- FisherStrand higher 45
- Mapping Quality lower 30
- SNP Clusters with more than 5 SNP within 20 Basepairs

- Individual filtering
  - Genotyping Quality lower 20
  - Depth higher lower 5

Used Samples

Breed	Individual sequence		DNA pool sequence	
Duroc	4	6X		
Hampshire	2	6.5X		
Jiangquhai	1	8.2X		
Large White	14	6.5X		
Landrace	5	6.4X		
Meishan	4	6.8X		
Pietrain	5	5.6X		
European Wildboar	6	6.4X		
Asian Wildboar	5	6.3X		
Göttingen Minipig	11	12.8X		
Berlin Minipig	2	13.9X	1 (10)	13.1X

Re-sequenced breeds

Whole genome re-sequencing (Illumina HiSeq2000)

	Large pigs	Minipigs
Wild boars	European Wild boars Asian Wild boars	
Hausschweine	Land Race Hampshire Duroc Pietrain Jiangquhai Large White Meishan	Goettingen Minipig (GMP) MiniLEWE (Berlin) Xiang Wuzhishan MiniLEWE-Pool
	46 Individuals	16 Individuals 1 DNA Pool of 10

Publically available WGS data:
Rubin et al., 2012; Fang et al., 2012; Vamathevan et al., 2013

Distribution of haplotypes in cross-breds

- Distribution of F_1 and F_2 follow expectation

F_1	Sum	Boars	Sows	Sex / Haplotype	Boars	Sows	Sum	F_2
	28	28		XX,Xy	114	129	243	
	55		55	xX	0	90	90	
				xy	114	0	114	
	83	28	55	Sum	228	219	447	

	Mean	SD	min	max
Height at scan	39.93	4.39	24.00	55.00
Height at slaughter	65.3	5.05	45.0	79.0
Length at scan	48.56	5.91	34.50	69.00
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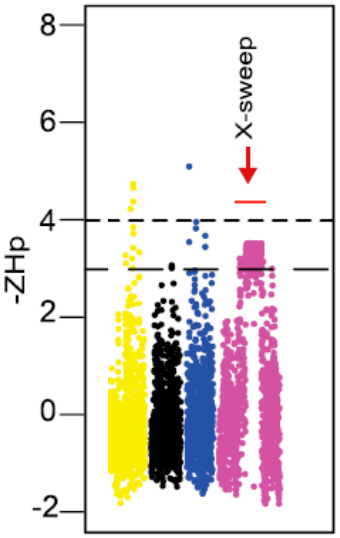

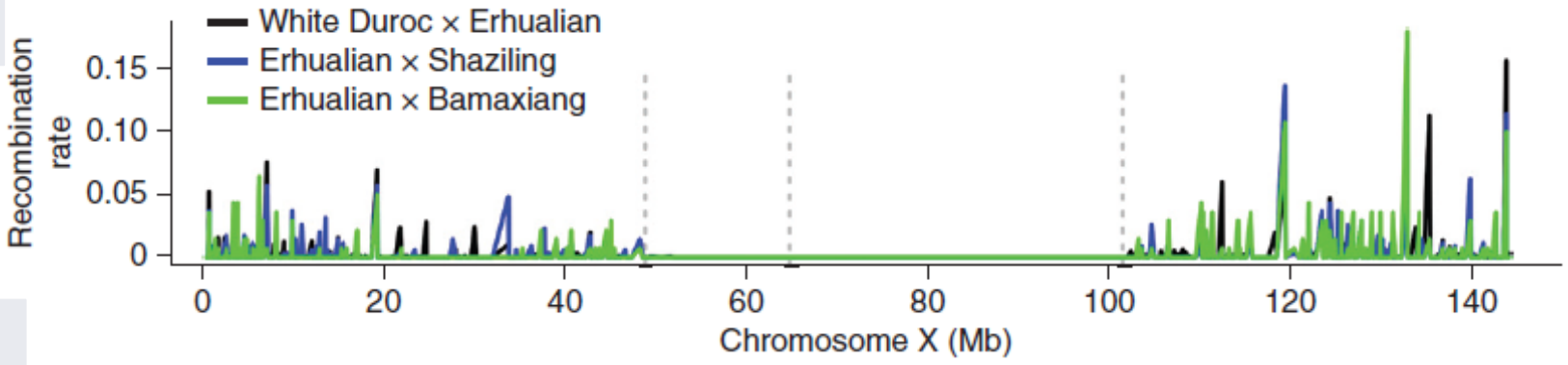

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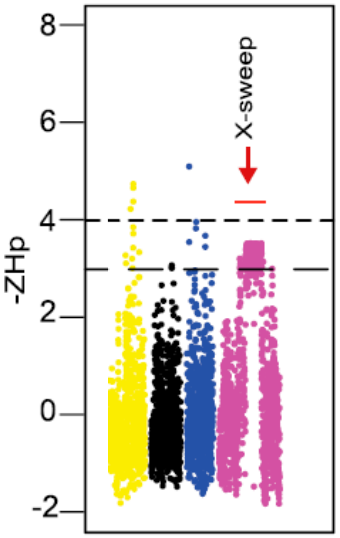

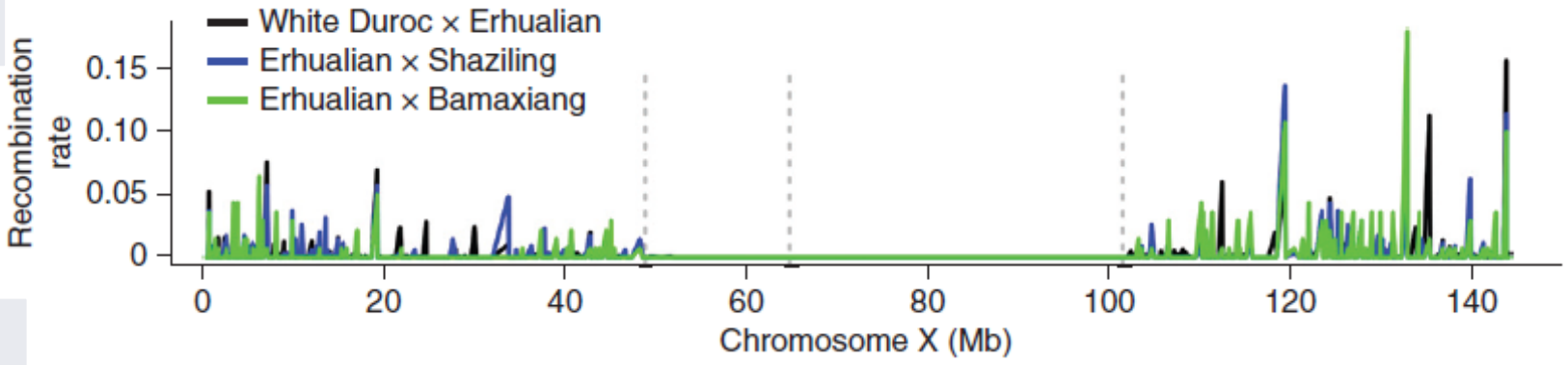

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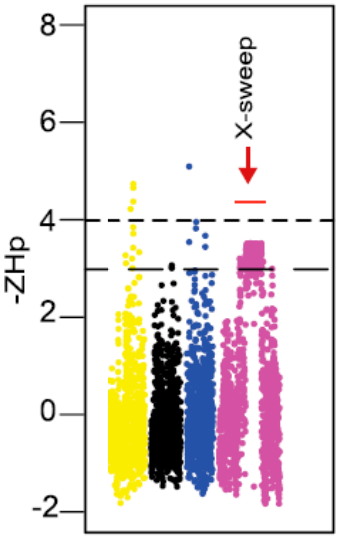

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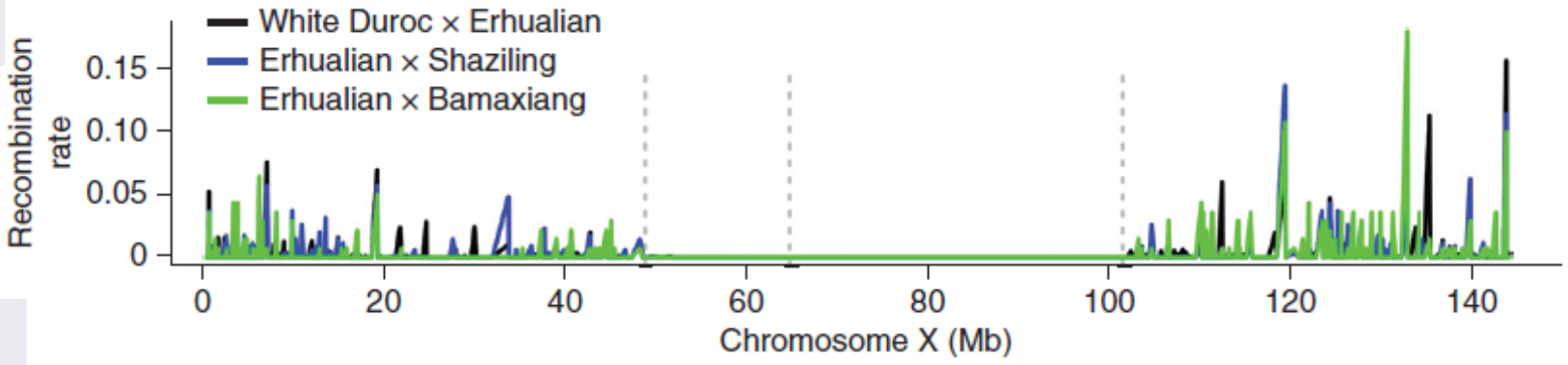

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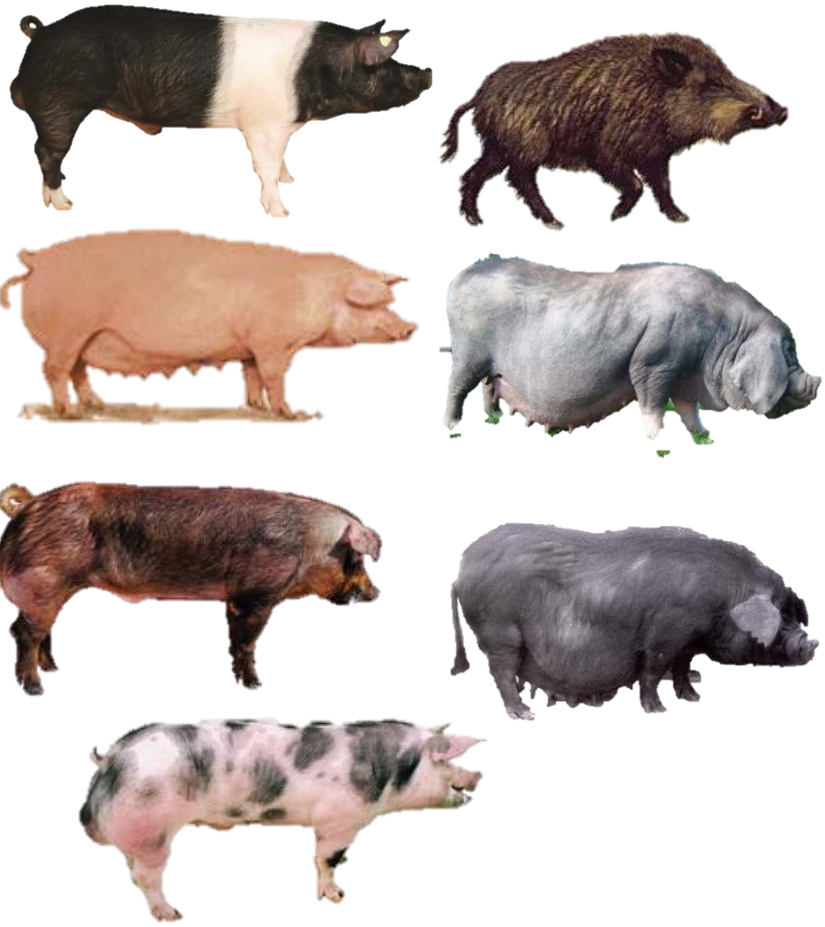

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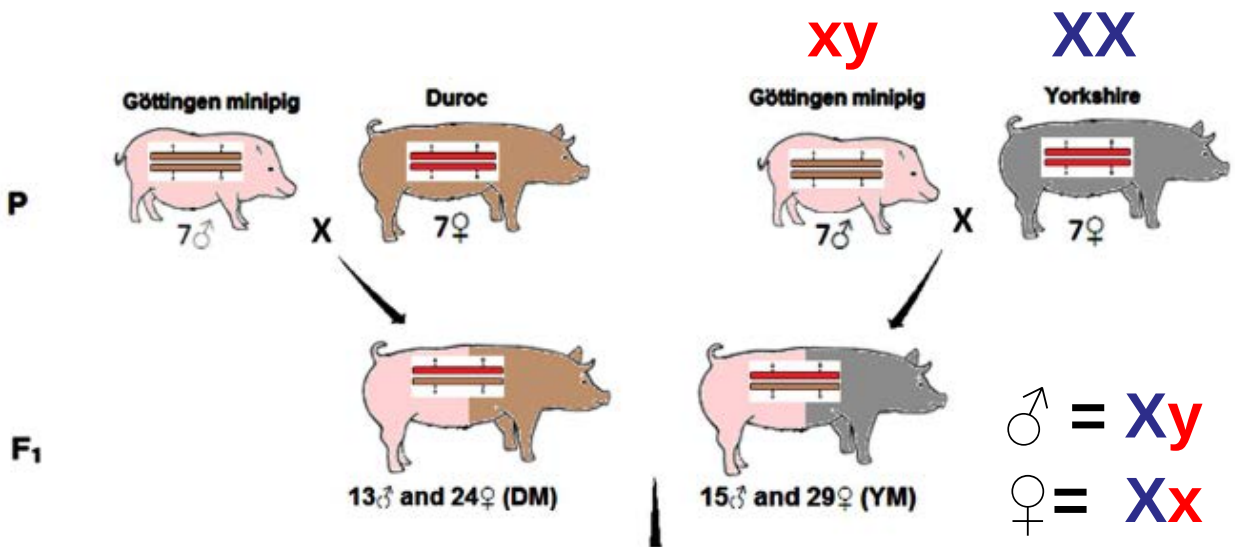

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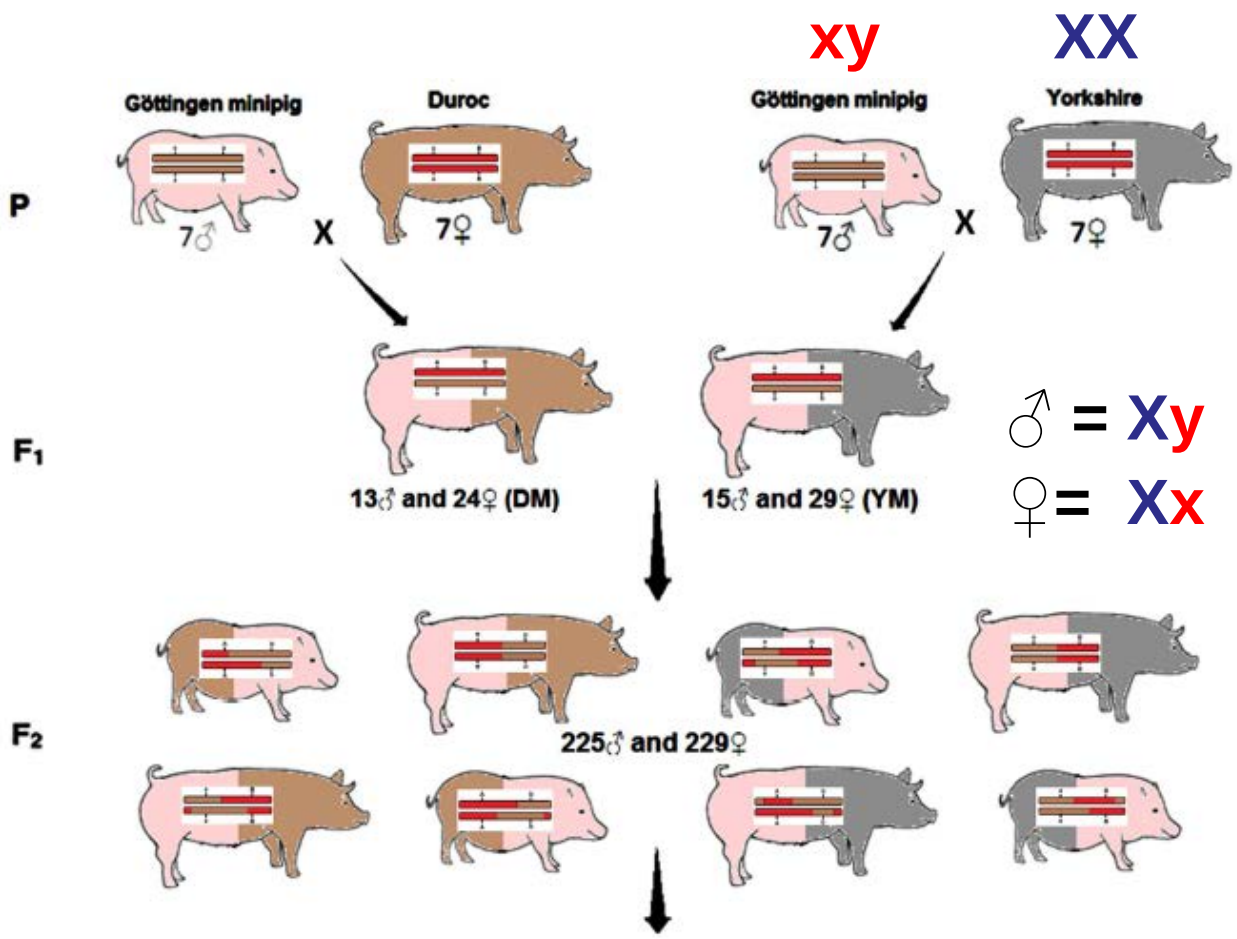

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Determination of the haplotypic state of F_2 animals

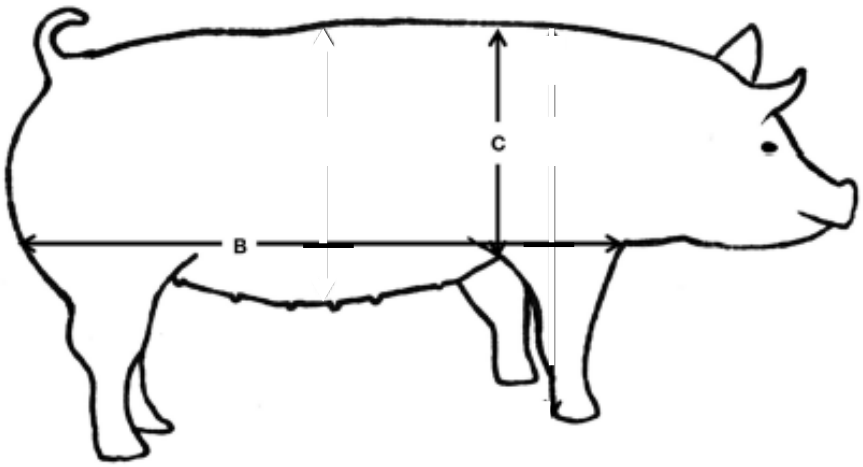
➔ **XX,Xy = 1; Xx = 2; xy = 3**

Statistical modelling

Linear model, Proc GLM, SAS (SAS Institute, Cary, NC)

$$y_{ijk} = B_i + S_j + b_1(A_{ij}) + b_2(A_{ij}{}^2) + H_k(S_j) + B_i * S_j + b_3(B_i * A_{ij}) + b_4(B_i * A_{ij}^2) + e_{ijk}$$

y_{ijk}	Body length/ height
B_i	Breed of dam in P_0
S_j	Sex
A_{ij}	Age at recording
H_k	Haplotype state
b_x	Regression coefficients



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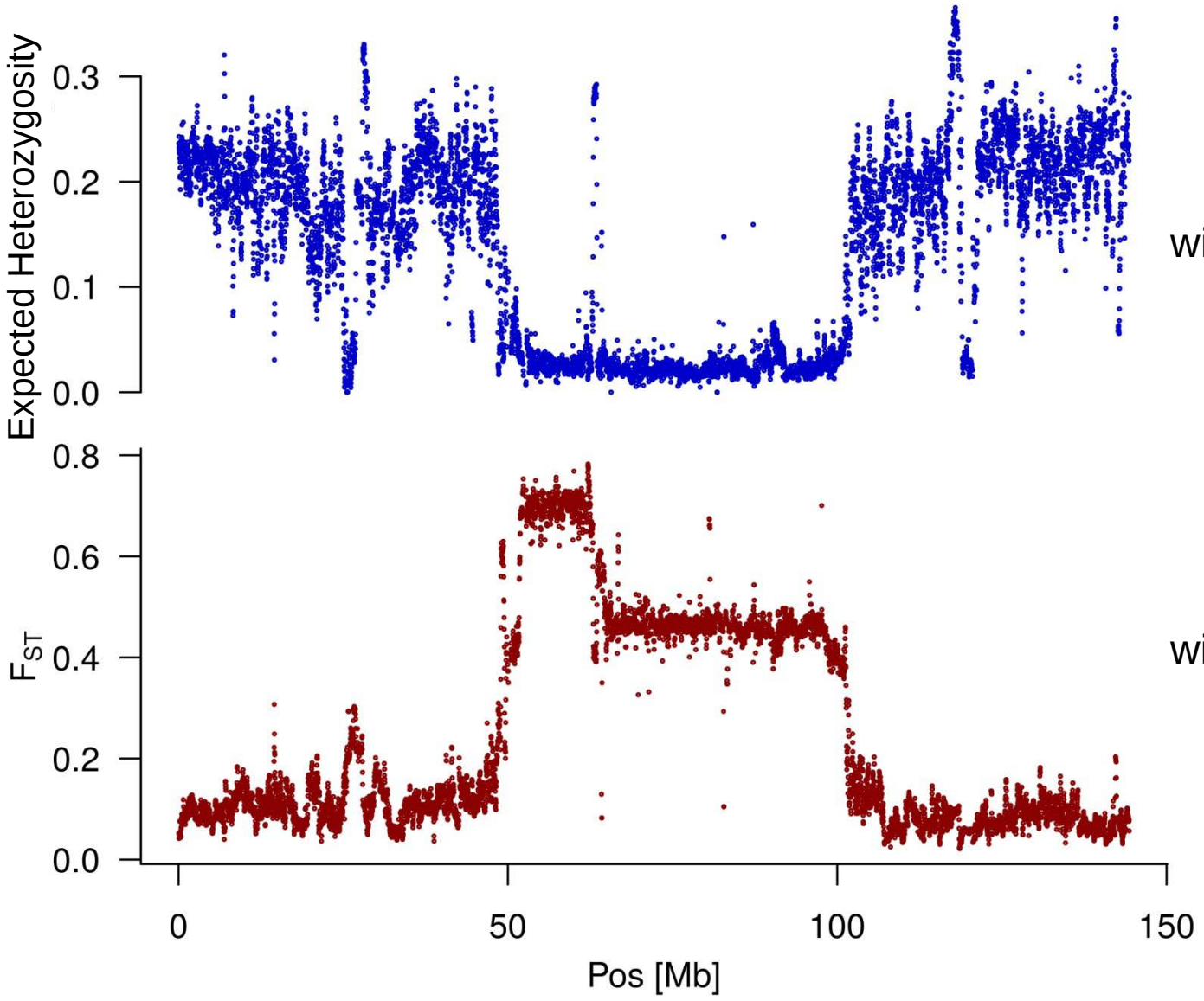

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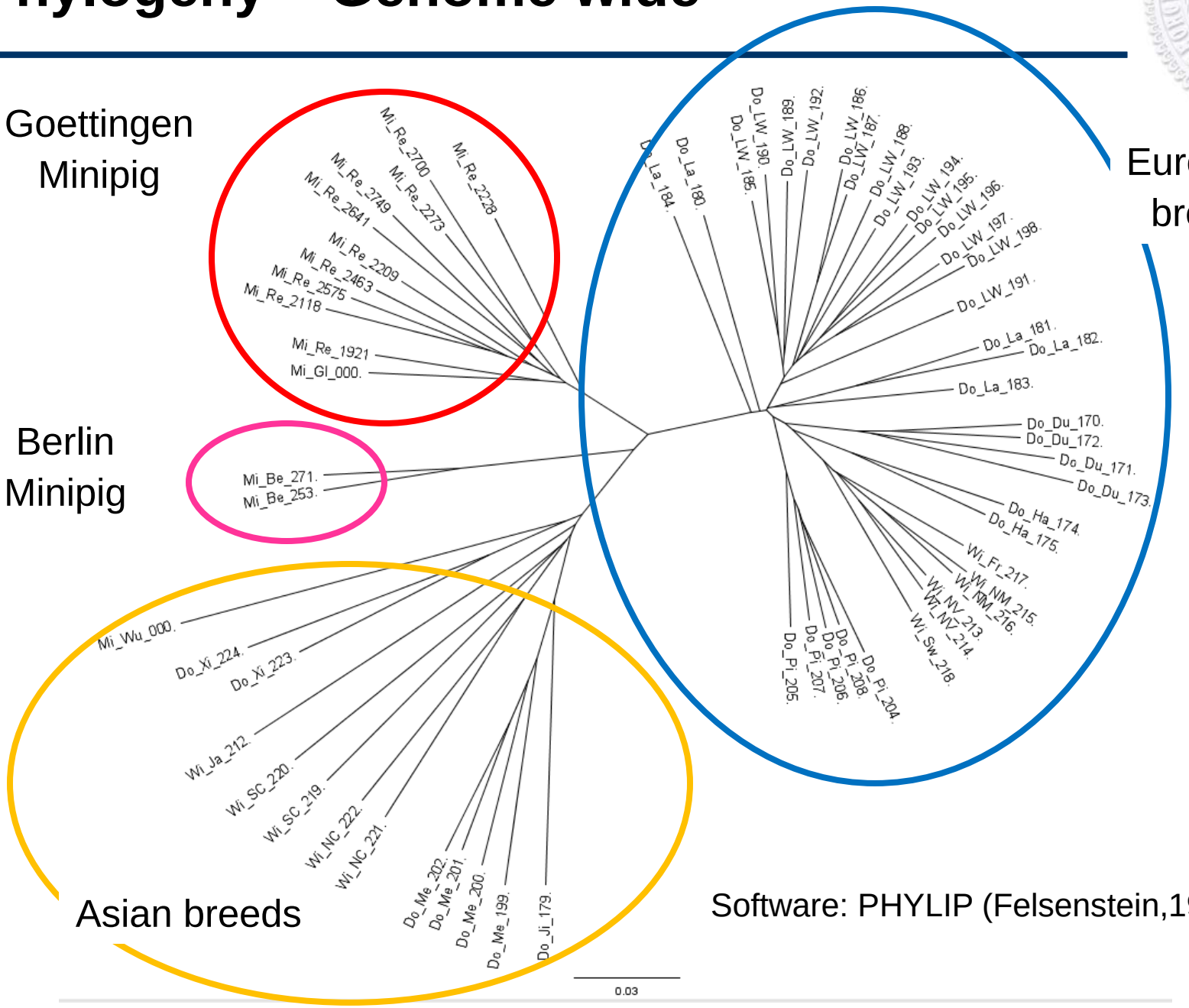

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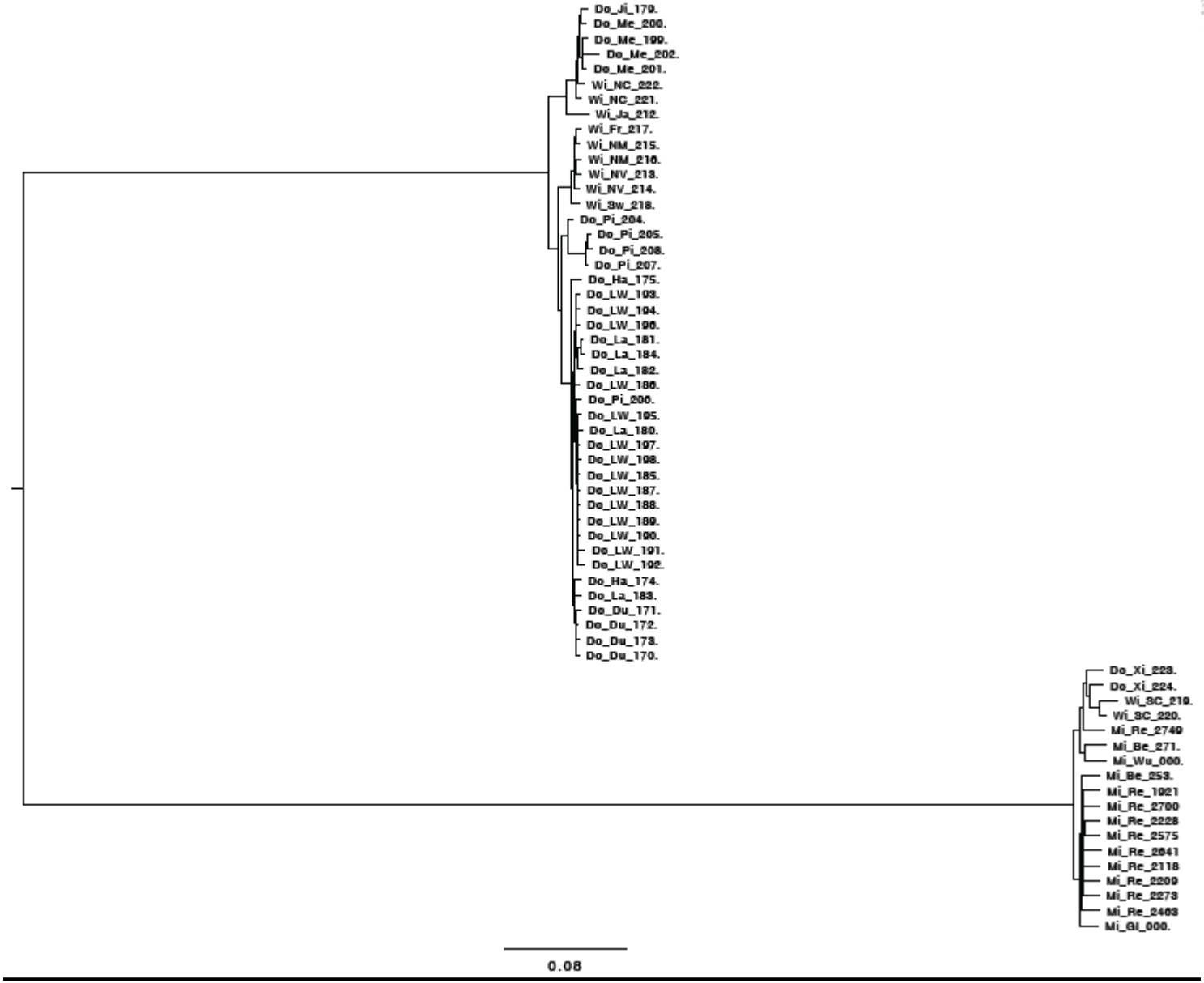

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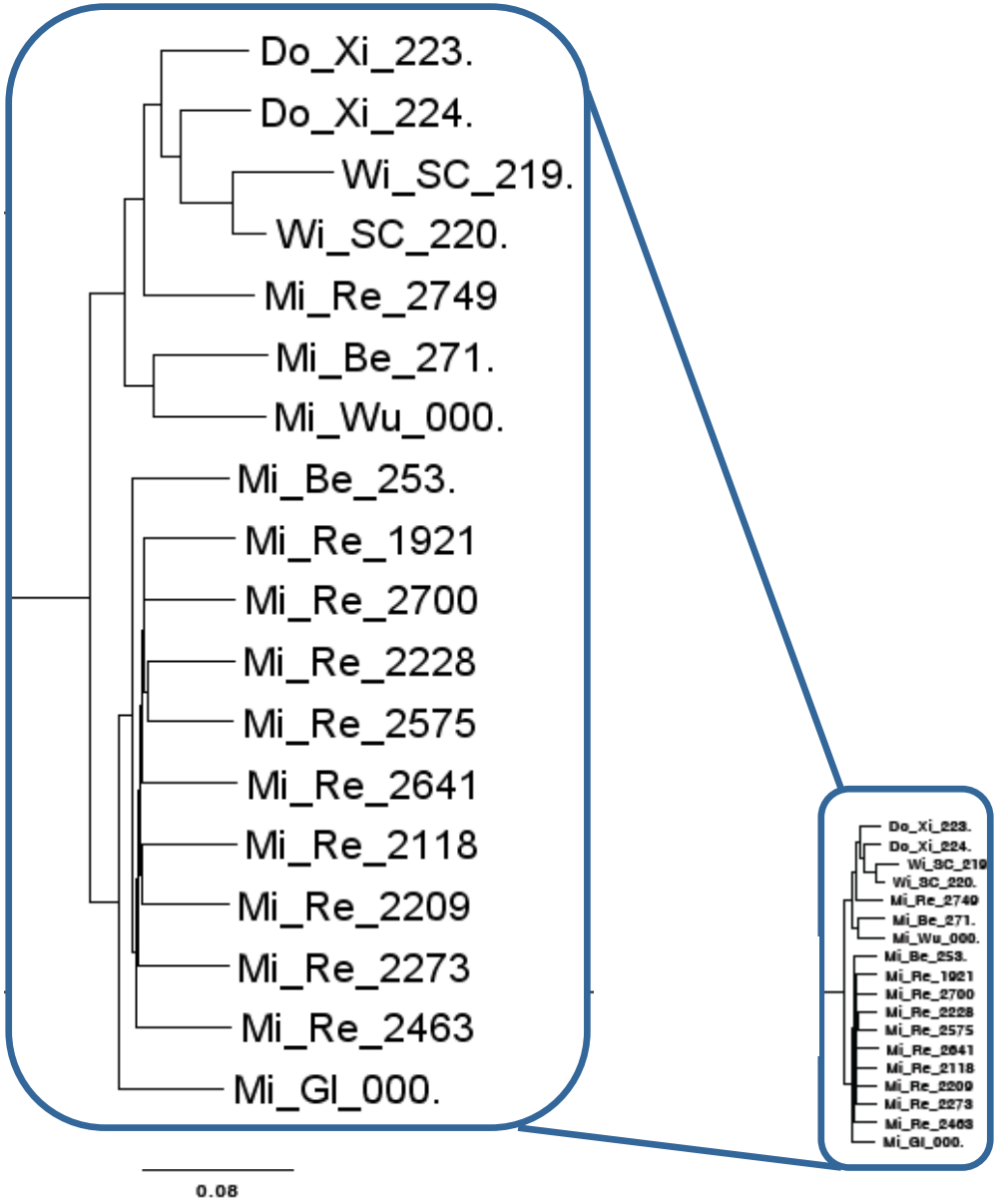

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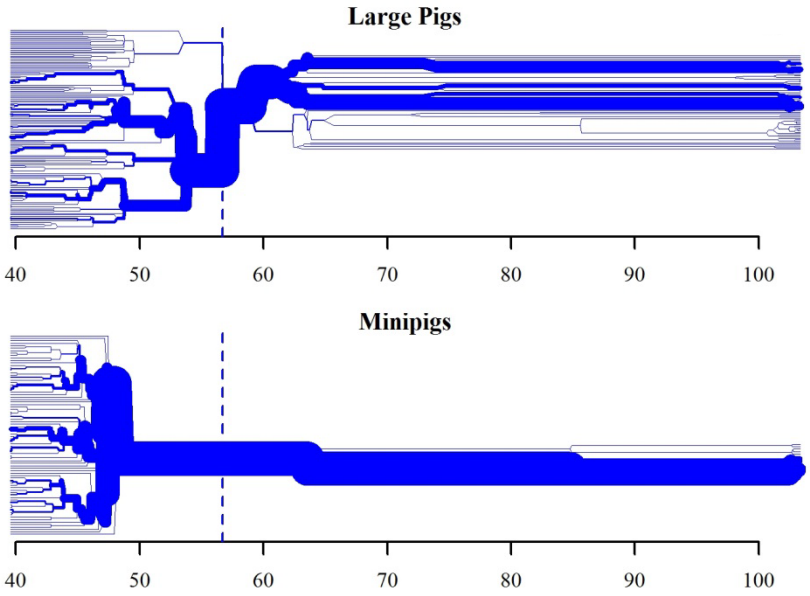

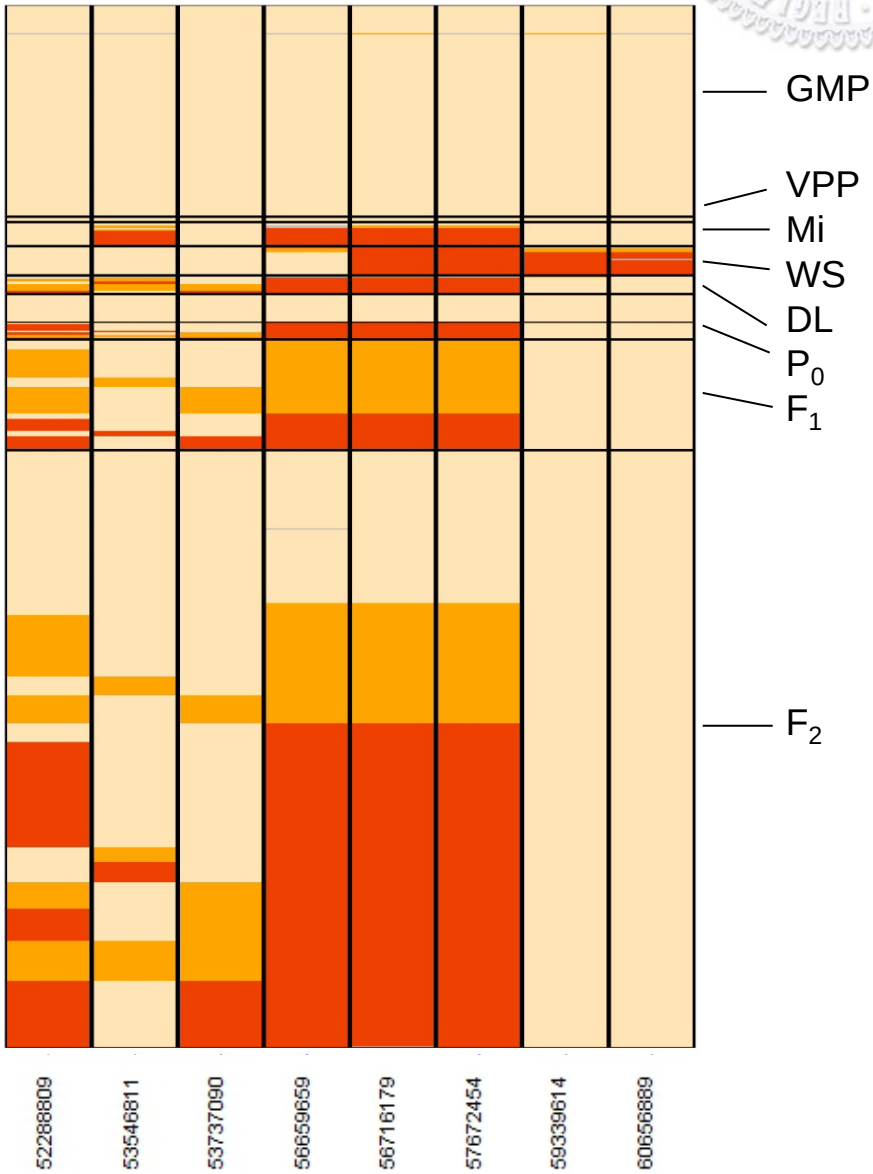

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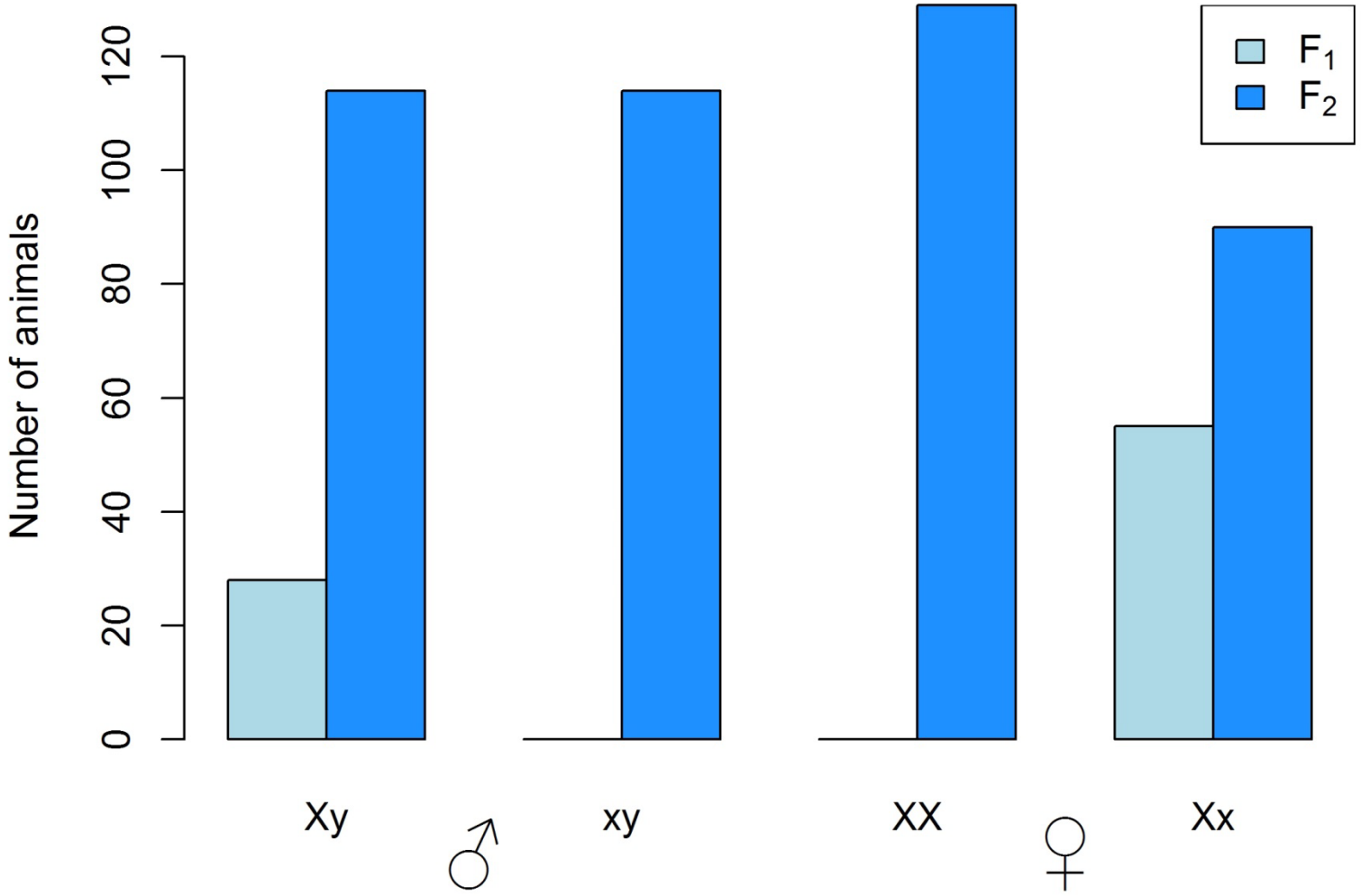

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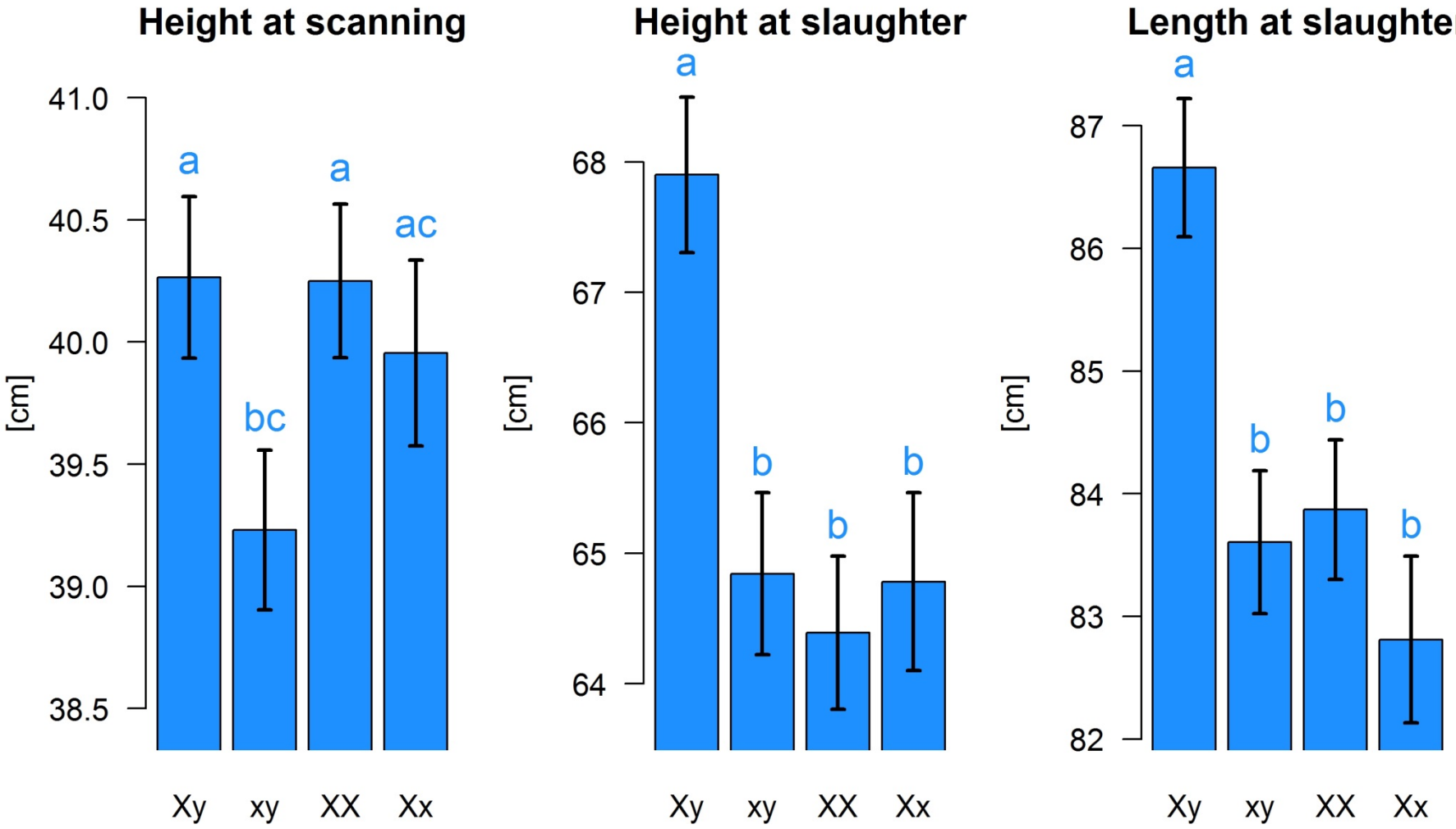

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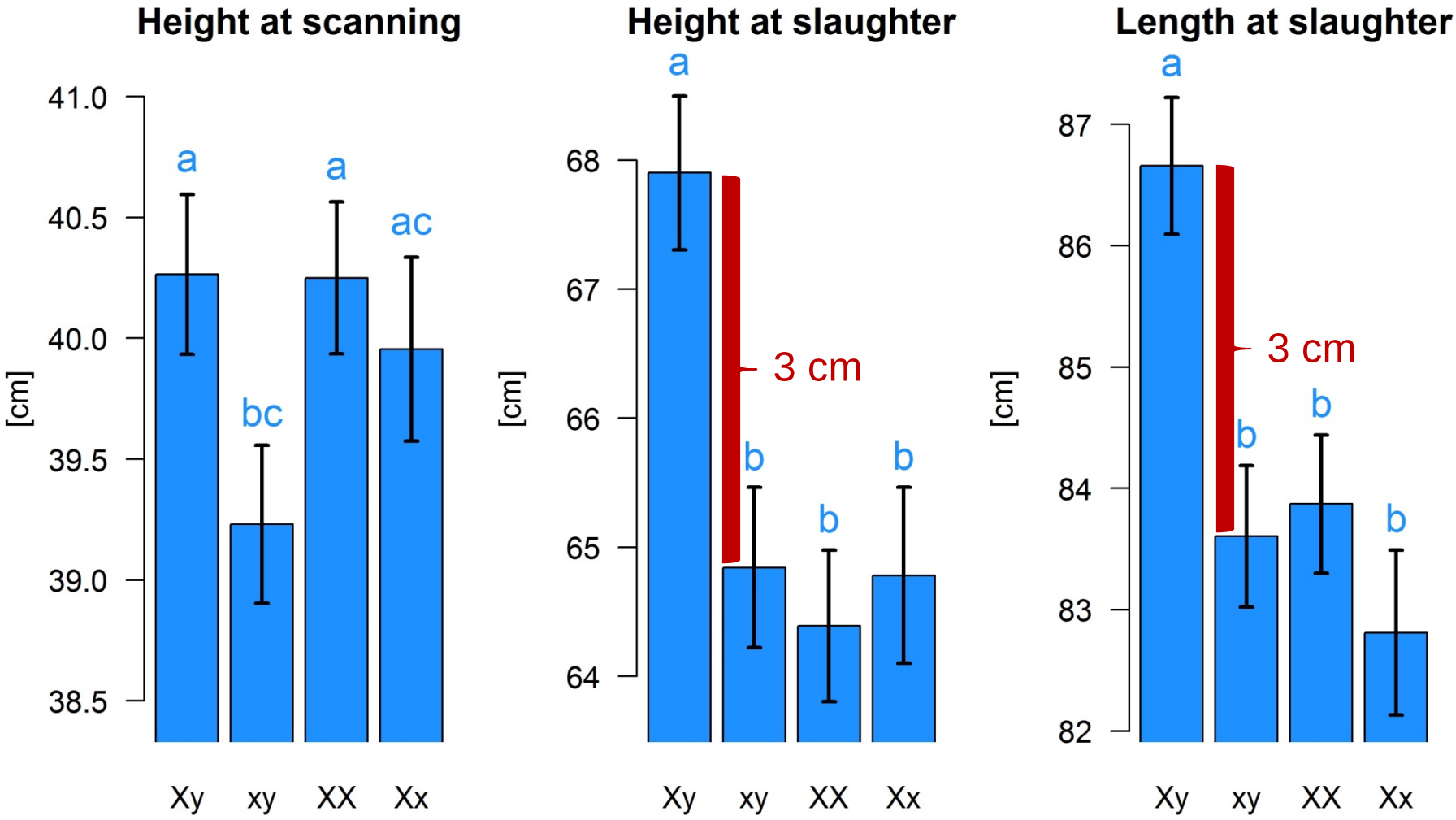

Conclusion

- All minipigs carry the same X-chromosomal haplotype

- Female cross-breds can carry both haplotypes

- Boars carrying the minipig haplotype are significantly smaller than boars carrying the large pig haplotype (3% shorter and 3% less high)

➔ **The X-chromosomal sweep region explains a considerable part of the total variability of body size**

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Thank you for your attention!

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