



ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA

Whole genome resequencing detects signature of selection in 23 European pig breeds and wild boars

Luca Fontanesi

***Department of Agricultural and
Food Sciences***

**University of Bologna
Bologna, Italy**

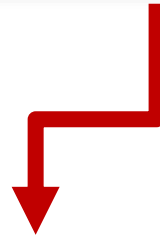
S. Bovo, G. Schiavo, A. Ribani, M. Muñoz,
V.J. Utzeri, M. Gallo, J. Riquet, G. Usai, R.
Charneca, J.P. Araujo, R. Quintanilla, V.
Razmaite, M. Candek-Potokar, A.
Fernandez, C. Ovilo, L. Fontanesi



Global description of genetic variability/diversity in European pig populations



Global description of genetic variability/diversity in European pig populations



**Extract interesting information:
Potential application**



9 European countries 20 autochthonous breeds

Schwäbisch-Hällisches



Senojis tipo Lietuvos baltosios



Lietuvos vietinis



Krškopoljski



Gascon



Basque

Bisaro



Portugal



Alentejano

Spain



Iberico



Negre Mallorquí



Mora Romagnola



Casertana



Nero Siciliano



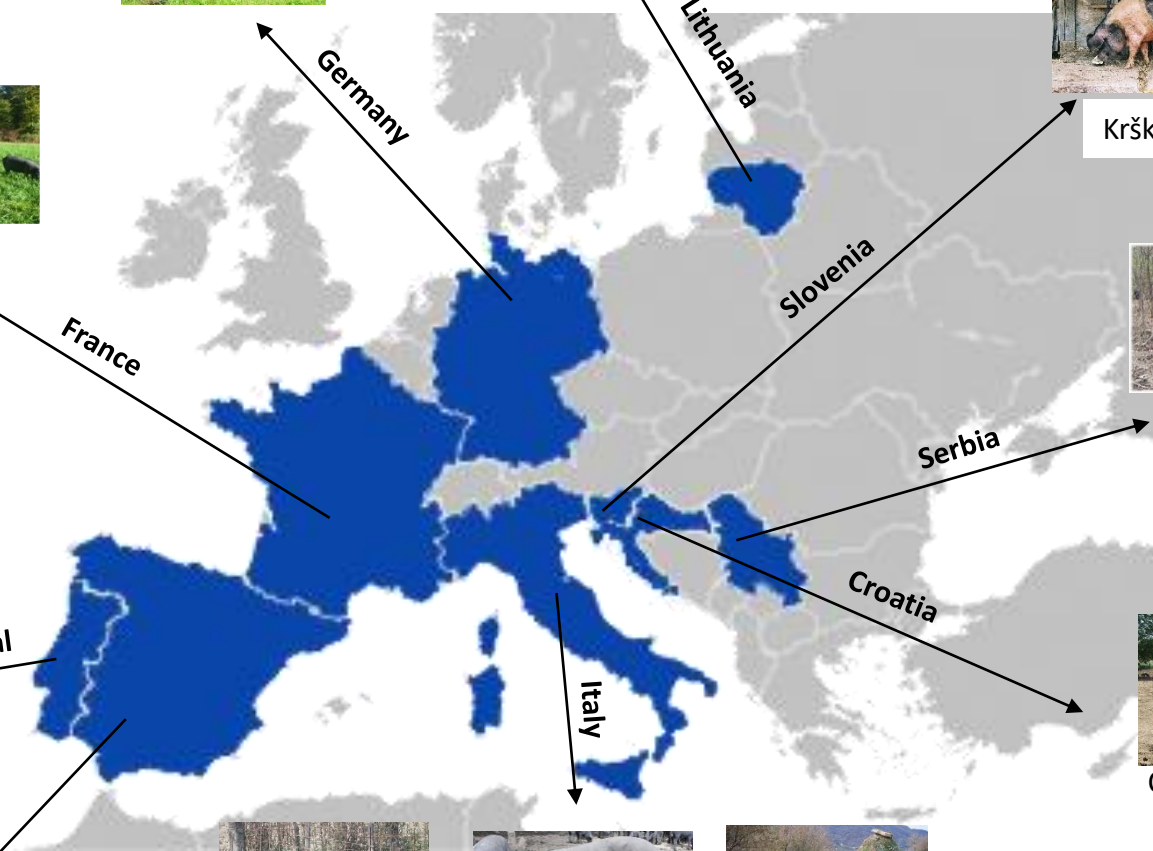
Cinta Senese



Apulo Calabrese



Sarda



Germany

France

Portugal

Spain

Italy

Lithuania

Slovenia

Serbia

Croatia

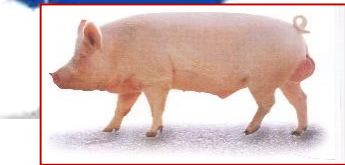
Mangulica

Moravka

Crna slavonska

Turopoljska

Italian Wild Boars



Italian Large White



Italian Landrace



Italian Duroc

Materials

Genotyping

- At least 48 animals x breed/population: genotyped with the GGP 70K SNP/60k Illumina chips.
- For some breeds – a larger number of pigs was genotyped

Sequencing

- 30-35 animals x breed/population: DNA-pools
- Whole genome sequencing of all DNA pools (40X – Illumina paired end)



Sequencing data

| Breed | No. of reads (in pairs) | No. of animals in pool |
|----------------------|-------------------------|------------------------|
| Cinta Senese | 422120850 | 35 |
| Alentejano | 419690476 | 35 |
| Apulo Calabrese | 418529727 | 35 |
| Mangalitsa | 416663891 | 35 |
| Black Slavonian | 405316112 | 35 |
| Casertana | 435598516 | 35 |
| Mora Romagnola | 411095541 | 35 |
| Nero Siciliano | 405812223 | 35 |
| Krskopolje | 404204144 | 35 |
| Duroc | 420384723 | 35 |
| Negre Mallorqui | 414314159 | 35 |
| Gascon | 408764207 | 30 |
| Basque | 407698128 | 30 |
| Bisaro | 415284437 | 35 |
| Lietuvos Baltosios | 405822217 | 35 |
| Lietuvos Vietines | 409935460 | 35 |
| Turopolje | 416663891 | 35 |
| Scwabisch Hallisches | 428982876 | 35 |
| Moravka | 413100992 | 35 |
| Sarda | 442035147 | 35 |
| Large White | 450673024 | 35 |
| Landrace | 442780637 | 35 |
| Wild boars | 184076376 | 35 |



| Databases/ items | Features | No. of SNPs | No. of INDELS |
|-----------------------------|---------------------------|--------------------|----------------------|
| dbSNP | | | |
| | Common* | 19,004,673 | 961,368 |
| | Rare[#] | 3,315,987 | 95,287 |
| | Fixed^{\$} | 5,295 | 9 |
| Novel | Common | 3,475,057 | 2,184,363 |
| | Rare | 1,423,002 | 445,019 |
| | Fixed | 4,871 | 358 |
| Total | | 27,228,885 | 3,686,404 |

*AF_{mean} ≥ 0.0143; #AF_{mean} < 0.0143; \$Fixed: only the ALT allele is present.



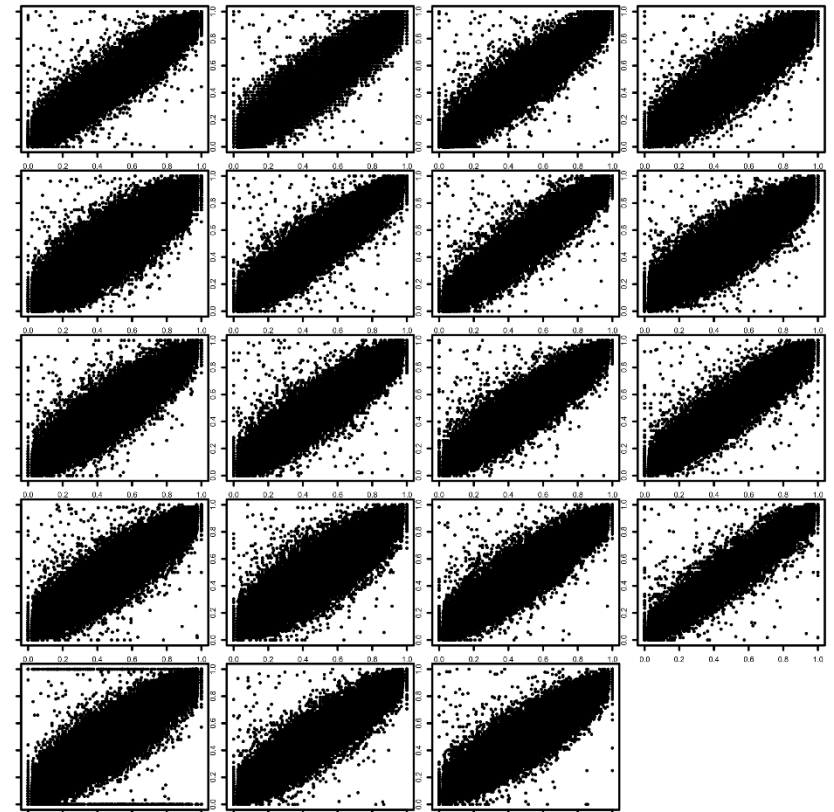
| Consequence | No. of SNPs |
|------------------------------------|--------------------|
| Intron variant | 27,723,666 |
| Intergenic variant | 15,604,676 |
| 3'-UTR variant | 469,853 |
| Non-coding transcript variant | 396,126 |
| Synonymous variant | 274,870 |
| Missense variant | 149,180 |
| 5'-UTR variant | 93,507 |
| Splice region variant | 52,788 |
| Non-coding transcript exon variant | 15,757 |
| Stop gained | 1,357 |
| Splice donor variant | 806 |
| Splice acceptor variant | 567 |
| Start lost | 376 |
| Stop lost | 201 |
| Stop retained variant | 144 |
| Coding sequence variant | 107 |
| Mature miRNA Variant | 48 |
| Total* | 44,784,029 |

- **SNPs impacting the gene at the protein level (i.e. start/stop gained/lost and missense SNPs) accounted only for 0.34%.**



Estimation of allele frequency: SNP-CHIP vs DNA Pool-Seq

| Breed | PCC | SNPs |
|------------------------------|-------------|---------------|
| Cinta Senese | 0.97 | 46,674 |
| Alentejano | 0.96 | 40,614 |
| Apulo Calabrese | 0.96 | 45,354 |
| Mangulica | 0.96 | 40,278 |
| Black Slavonian | 0.92 | 46,730 |
| Casertana | 0.96 | 44,813 |
| Mora Romagnola | 0.97 | 35,238 |
| Nero Siciliano | 0.93 | 47,283 |
| Krskopolje | 0.94 | 46,625 |
| Negre Mallorquí | 0.96 | 44,895 |
| Gascon | 0.96 | 42,319 |
| Basque | 0.97 | 37,531 |
| Bisaro | 0.93 | 46,948 |
| Lietuvos Baltosios | 0.93 | 45,163 |
| Lietuvos Vietines | 0.95 | 44,376 |
| Turopolje | 0.98 | 39,194 |
| Schwäbisch Hällisches | 0.91 | 46,946 |
| Moravka | 0.95 | 47,063 |
| Sarda | 0.92 | 47,540 |



MAX correlation

MIN correlation

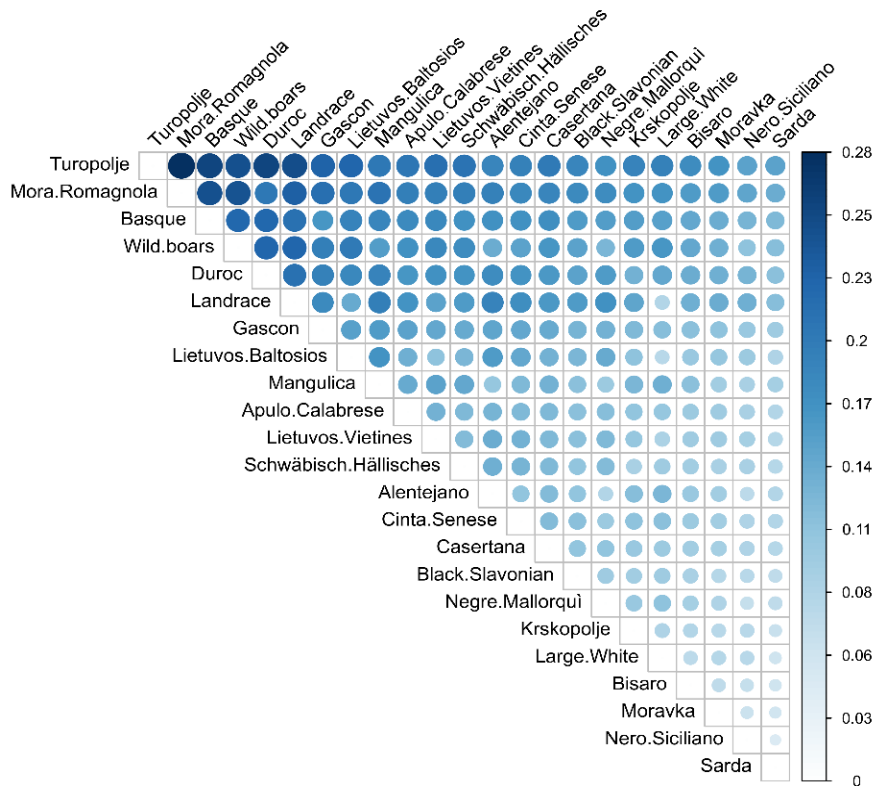


Whole genome sequencing data

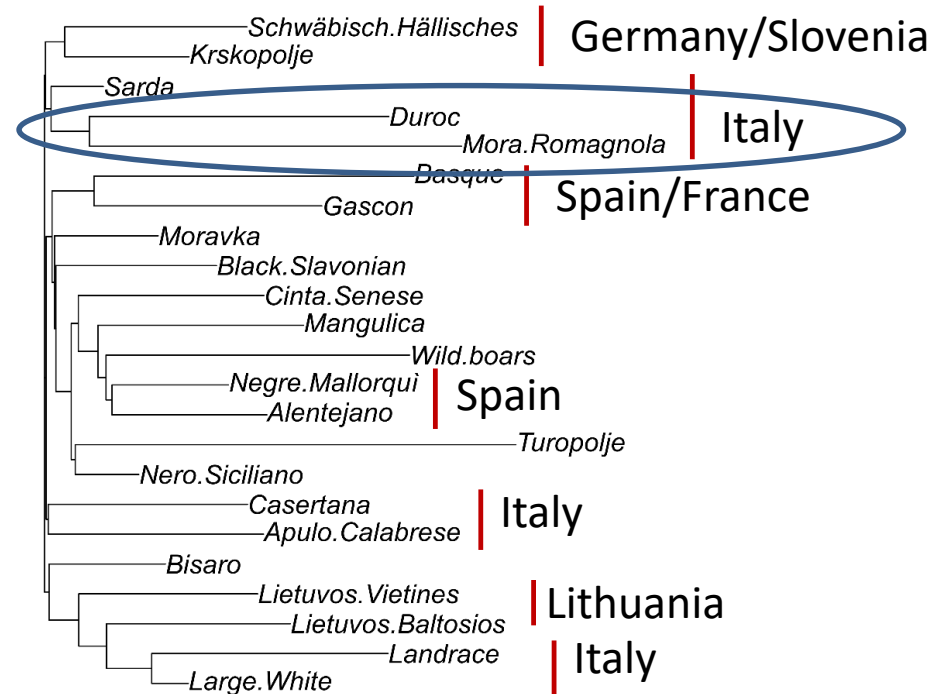


Genetic similarity between populations

Heatmap plot of Fst distances



Fst based Neighbour-Joining tree

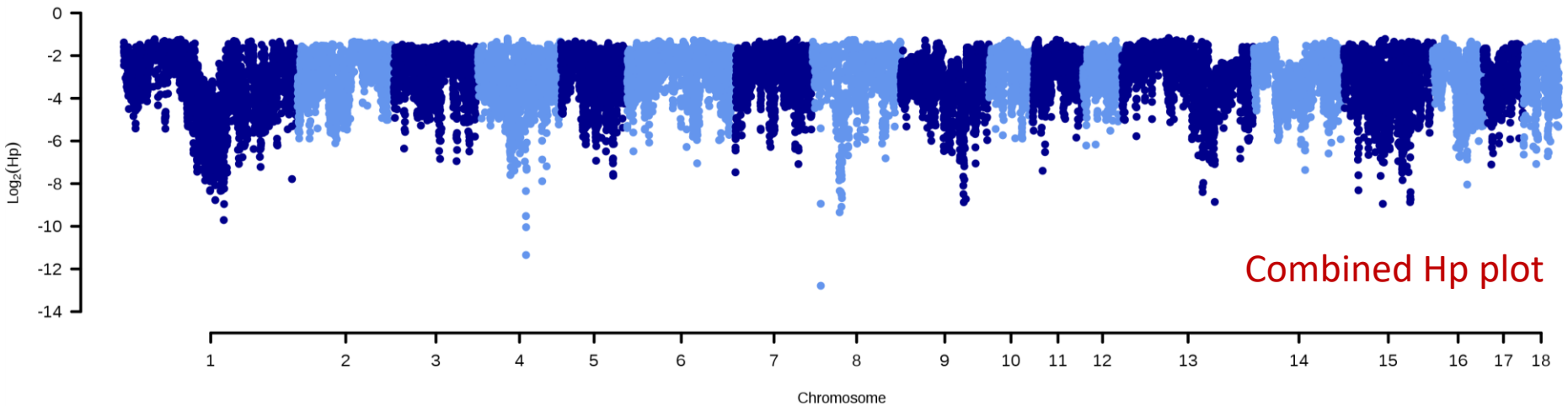


1

Pooled heterozygosity

Identified genome windows

- A total of 276 outliers windows identified across the 23 populations
- 68 genome windows shared among two or more populations.
- 9 genome windows were shared by four to seven populations.



Genome windows, suggestive for selective sweeps, shared by four or more pig breeds

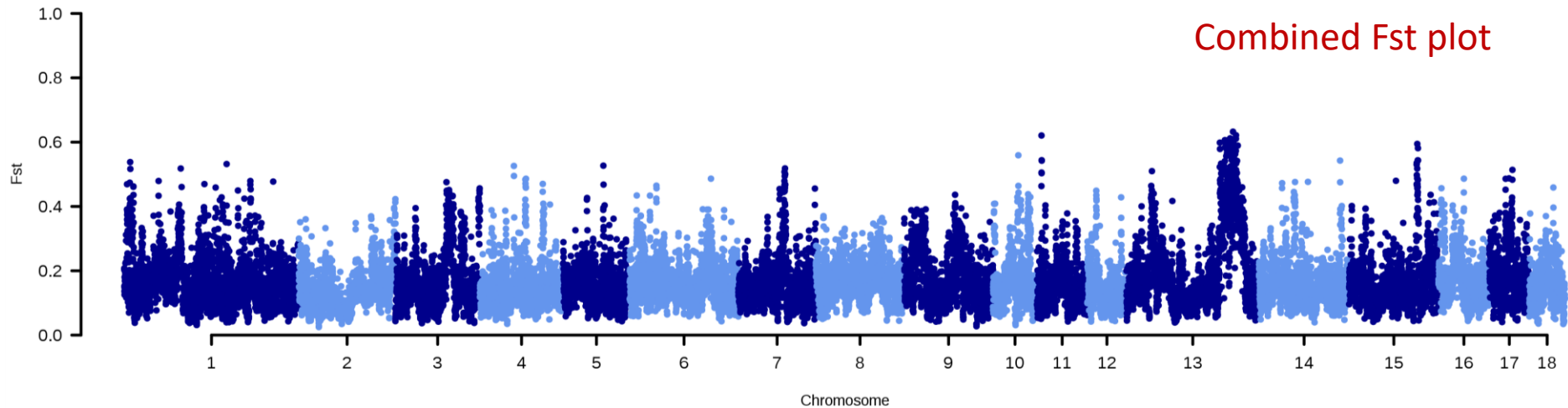
| Genome Windows (SSC:start-end)* | Breeds | No. of SNPs | Annotated genes (± 200 - kb)* |
|------------------------------------|---|----------------|--|
| 1:170,300,001:170,400,001 | Apulo Calabrese, Casertana Krskopolje, Negre Mallorquì | 829 | na |
| 4:42,900,001:43,000,001 | Black Slavonian, Nero Siciliano Krskopolje, Gascon | 683 | TMEM67; PDP1 ; FAM92A; RBM12B |
| 4:75,500,001:75,900,001 | Cinta Senese, Apulo Calabrese Krskopolje, Lietuvos Baltosios, Sarda Large White, Landrace | 2356 | CHCHD7; SDR16C5; MOS; PENK; TMEM68; LOC100626876; TGS1; LYN; LOC106510084; PLAG1 ; XKR4 |
| 8:12,900,001:13,000001 | Bisaro, Schwäbisch Hällisches, Large White, Landrace, Negre Mallorquì | 1067 | NCAPG ; CAF16; FAM184B; LCORL |
| 8:42,600,001:42,700,001 | Bisaro, Lietuvos Baltosios, Large White, Landrace | 683 | LOC102162630; LOC100526059; TLL1; LOC100620475 |
| 8:45,500,001:45,600,001 | Bisaro, Lietuvos Baltosios, Large White, Landrace | 1482 | PDGFC LOC102162630 LOC100526059 MAP9 TLL1 LOC100620475 |

2

Fst analysis of single breeds

Fst values

- Fst ranged from 0.0878 (Sarda) to 0.2016 (Turopolje)
- The average Fst value was 0.1347 in agreement with a previous study

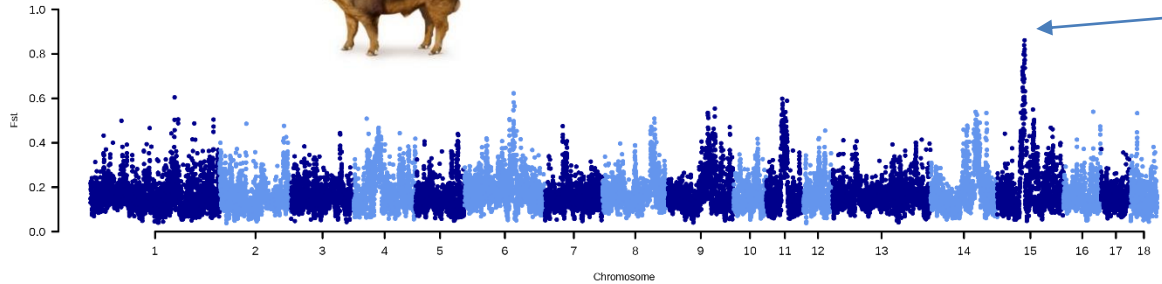


2

F_{st} analysis of single breeds

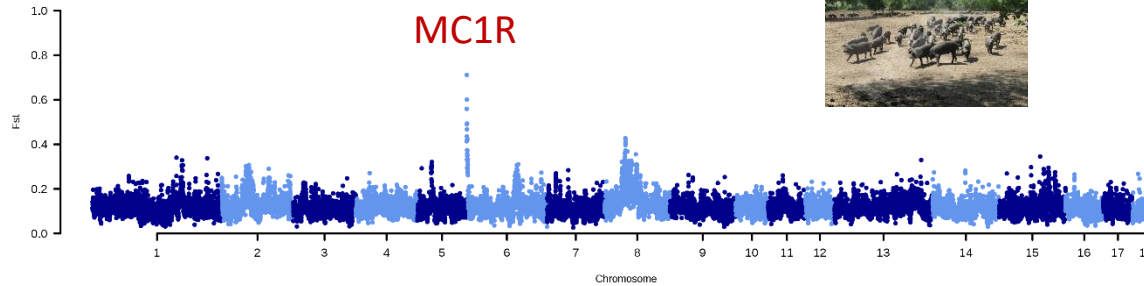


Italian Duroc

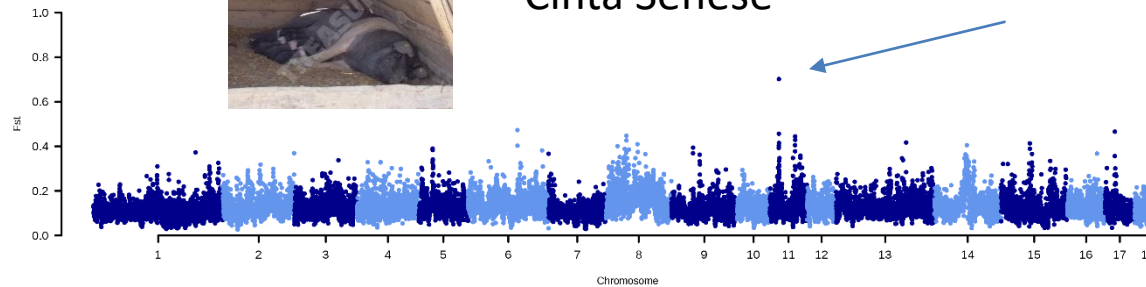


Black Slavonian

MC1R



Cinta Senese



3

F_{ST} analyses of breed groups

Belted and Spotted

Cinta Senese vs All others
Cinta Senese vs solid
Cinta Senese vs Black
Cinta Senese vs spotted
Cinta Senese vs White

Belted vs all Others
Belted vs solid
Belted vs Black
Belted vs Spotted
Belted vs White

Belted non Cinta vs Cinta Senese
Belted non Cinta vs All (no Cinta Senese)
Belted non Cinta vs solid
Belted non Cinta vs Black
Belted non Cinta vs Spotted
Belted non Cinta vs White

Spotted vs Black
Spotted vs White

Colored

White vs Black
White vs Red
Gray vs Black
Gray vs White

Red vs ALL
Duroc vs Mora

Wild boar

Wild boars vs Mora Romagnola
wild Boar vs Mangalitza
wild boar vs All
wild boar vs All (no mangalitza)
Wild boar vs non commercial
Wild boar vs non commercial (no Mangalitza)
Wild boar vs commercial

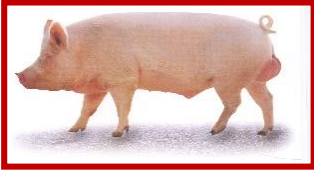
Size

Medium vs Big
Small vs Medium + Big
Small vs Medium
Small vs Big

Commercial

Commercial_ITA vs All
Commercial_ITA vs
Non_Commercial_ITA

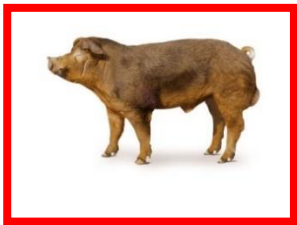




Italian Large White



Italian Landrace



Italian Duroc



Mora Romagnola



Cinta Senese



Casertana



Sarda



Apulo Calabrese

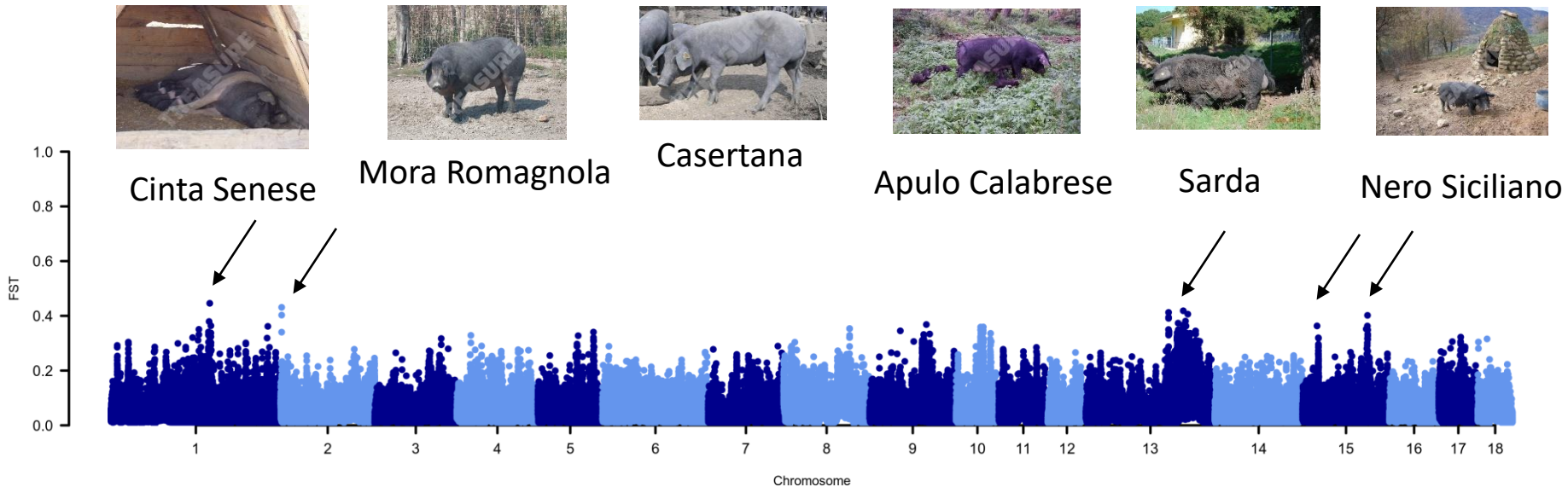


Nero Siciliano

3

F_{ST} analyses of breed groups

Italian autochthonous breeds



Italian cosmopolitan-derived breeds



Italian Large White



Italian Landrace

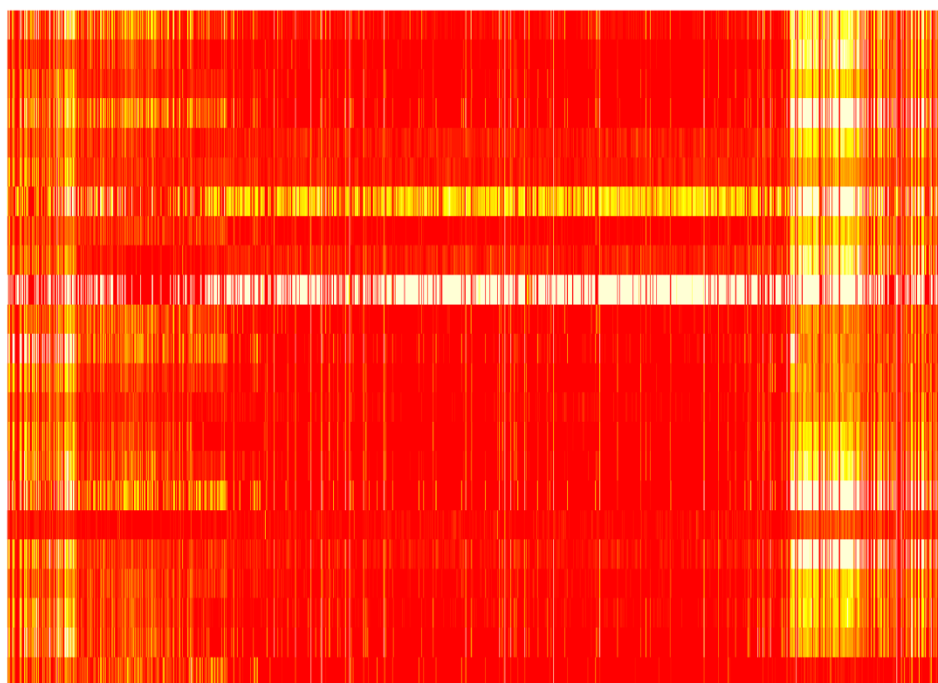


Italian Duroc



Red breeds (Italian Duroc + Mora Romagnola) vs all other breeds

Allele frequency of the alternative allele

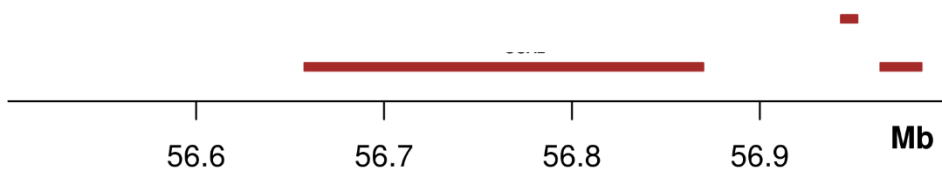


- Cinta Se
- Alentejar
- Apulo C2
- Mangulic
- Black Si
- Casertar
- Mora Ro
- Nero Sic
- Krskopol
- Duroc
- Negre M
- Gascon
- Basque
- Bisaro
- Lietuvos
- Lietuvos
- Turopolje
- Schwäbi
- Moravka
- Sarda
- Large W
- Landrace
- Wild boa

Mora Romagnola



Italian Duroc



Combined SNP genotyping and whole genome sequencing data





Casertana

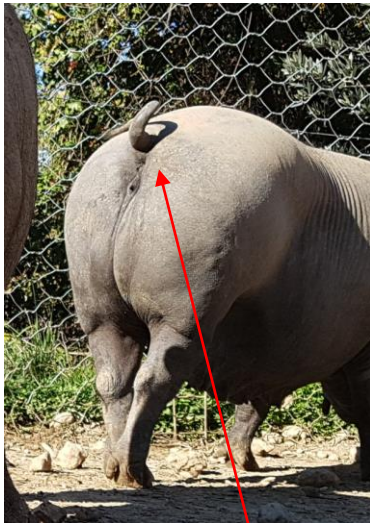


Phenotypic heterogeneity in Casertana

Hairless



Hairy



Curly tail

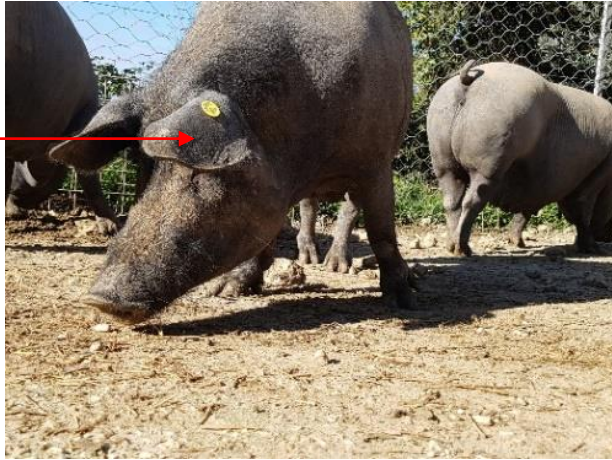


Straight tail

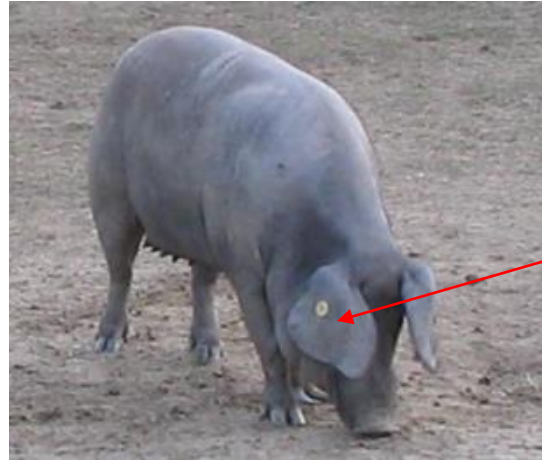


Phenotypic heterogeneity in Casertana

Small-
forward
ears



Large-
floppy
ears



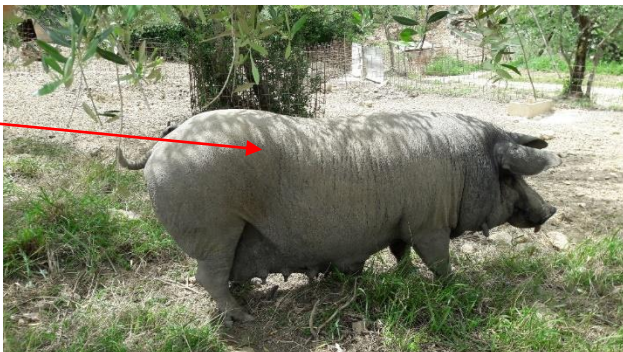
Presence
of wattles



Absence
of wattles



Slate-
grey coat
colour



Black
coat
colour



SNP chip data

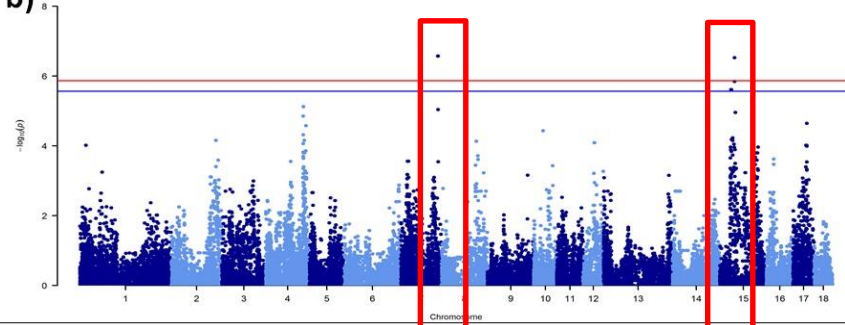


Genome Wide Association Study

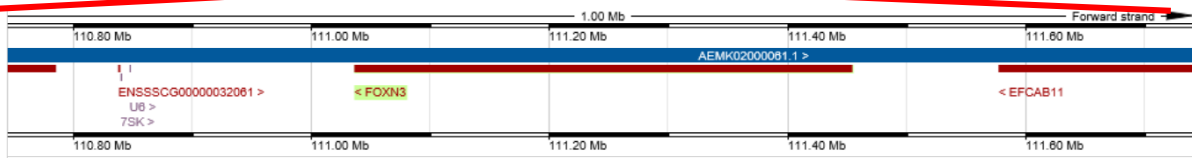
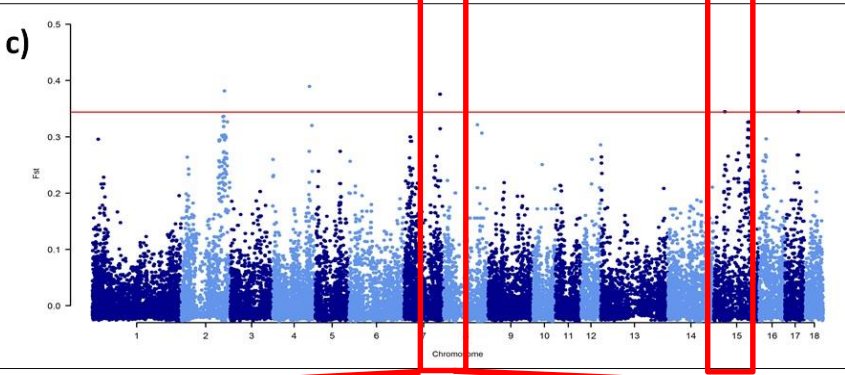
a)



b)



c)



ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics
 SHORT COMMUNICATION doi: 10.1111/age.12665

Taking advantage from phenotype variability in a local animal genetic resource: identification of genomic regions associated with the hairless phenotype in Casertana pigs

G. Schiavo¹, F. Berolini^{1,2}, V. J. Utzeri³, A. Ribani⁴, C. Geraci⁵, L. Santoro⁶, C. Ovílo⁷, A. I. Fernández⁸, M. Gallo⁹ and L. Fontanesi^{1*}

¹Division of Animal Sciences, Department of Agricultural and Food Sciences, University of Bologna, Viale Fanin 46, 40127 Bologna, Italy; ²Department of Animal Science, Iowa State University, 2255 Kildee Hall, 50011 Ames, IA, USA; ³Department of Bio and Health Informatics, Technical University of Denmark, Kemitorvet, Building 208, Room 007, 2800 Kongens Lyngby, Denmark; ⁴CarSDABI - National Focal Point Italiano IFAO, Contrada Piano Cappelle, 02100 Bevegnate, Italy; ⁵Departamento de Mejora Genética Animal, Instituto Nacional de Tecnología Agraria y Alimentaria (INIA), Cta. de la Coruña km. 7.5, 28040 Madrid, Spain; ⁶Associazione Nazionale Allevatori Suini, Via Nizza 53, 00198 Roma, Italy.

GWAS plot

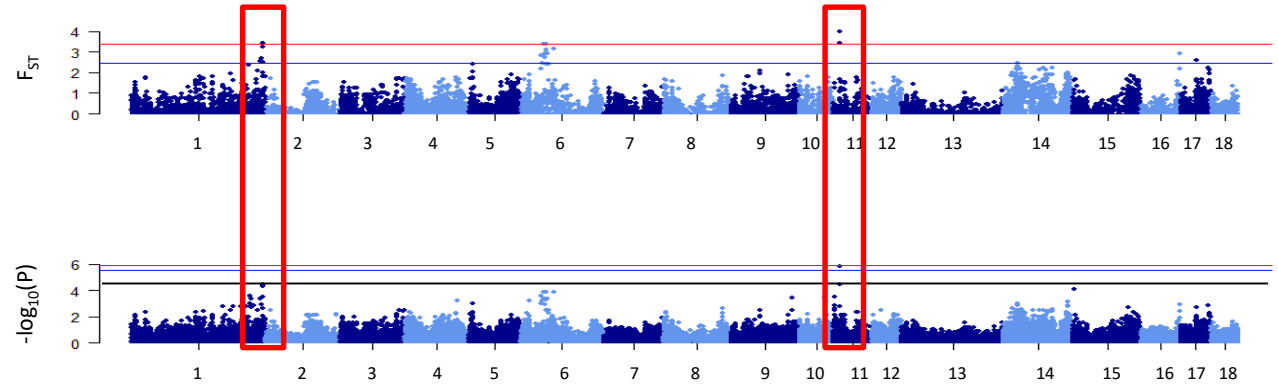
Fst plot



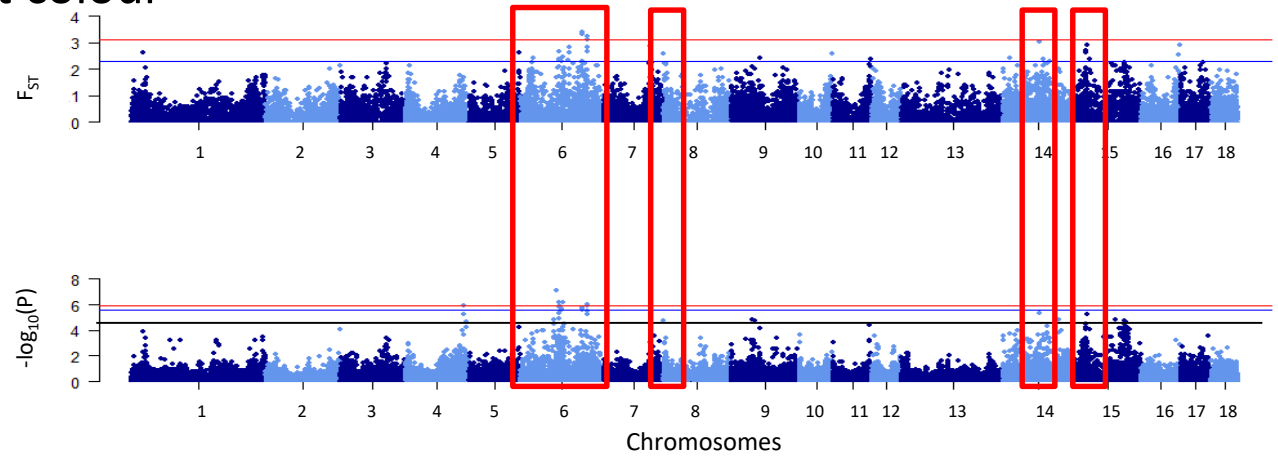
SNP chip data



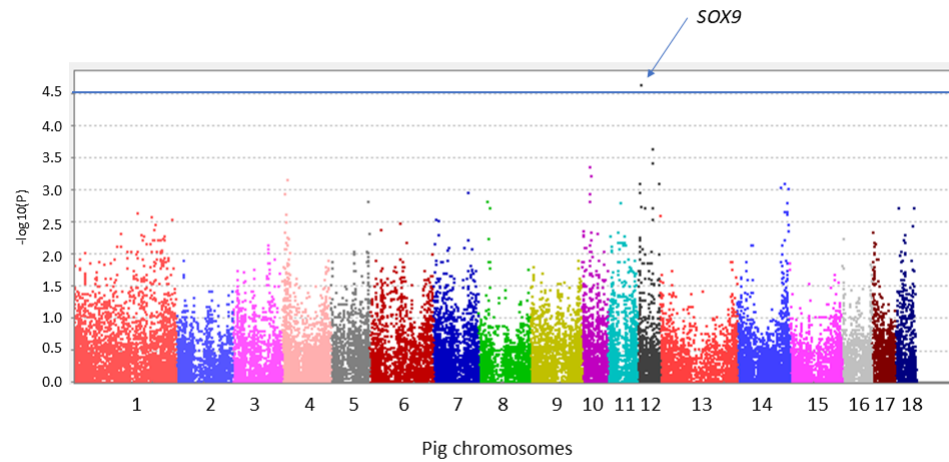
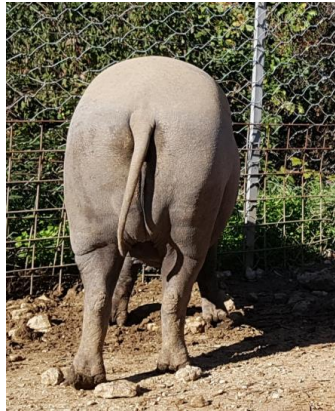
Presence/absence of wattles



Slate-grey vs black coat colour



SNP chip data



Exploiting phenotype diversity in a local animal genetic resource:
Identification of a single nucleotide polymorphism associated with the tail
shape phenotype in the autochthonous Casertana pig breed



Francesca Bertolini^{a,b,1}, Giuseppina Schiavo^{a,1}, Silvia Tinarelli^{b,c}, Laura Santoro^d,
Valerio Joe Utzeri^a, Stefania Dall'Olio^a, Leonardo Nanni Costa^a, Maurizio Gallo^c,
Luca Fontanesi^{b,*}



Conclusions

- We have characterized genetic variability in European pig breeds
- The large number of comparisons made it possible to detect hundreds of selection signatures
- We are moving from the description to the use of genetic variability in pigs





Funded by European Union
Horizon 2020
Grant agreement No 634476



ALMA MATER STUDIORUM A.D. 1088

UNIVERSITÀ DI BOLOGNA



Instituto Nacional de Investigación
y Tecnología Agraria y Alimentaria



associazione nazionale allevatori suini



ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA



UNIVERSITÀ DI BOLOGNA



University of Novi Sad



ConSDABI - National Focal Point Italiano FAO



ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA

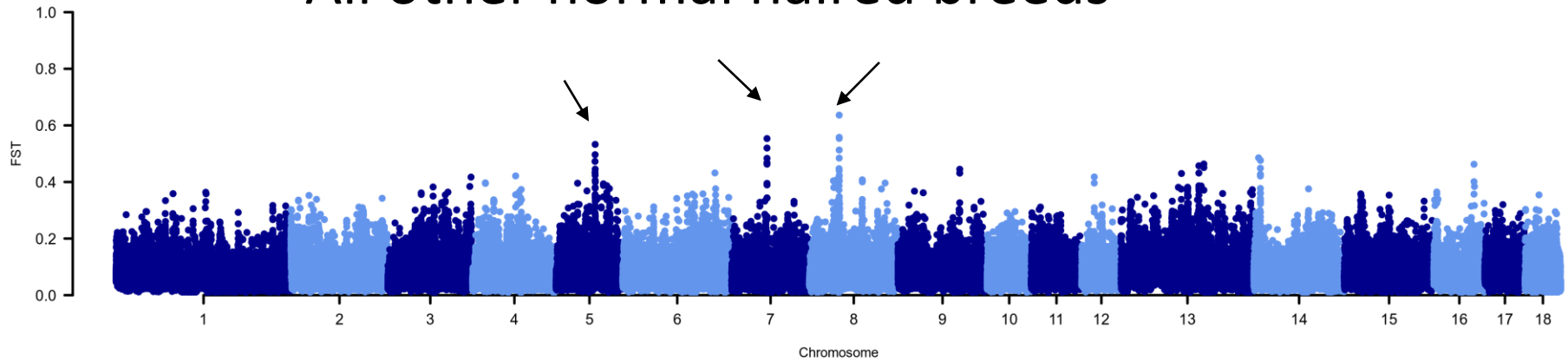


ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA

3

F_{ST} analyses of breed groups

All other normal haired breeds



Long-curly haired



Mangulica



Turopolje

