

Imputation from 60K SNP data to whole-genome level in Danish Landrace and Duroc pigs

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Imputation
whole-genome
Landrace



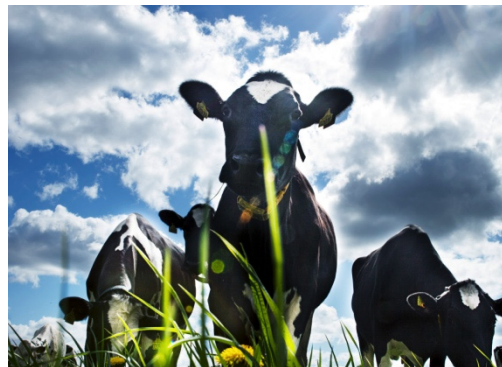
IP data to
Danish
pigs

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Whole-genome sequencing of Danish Landrace and Duroc pigs

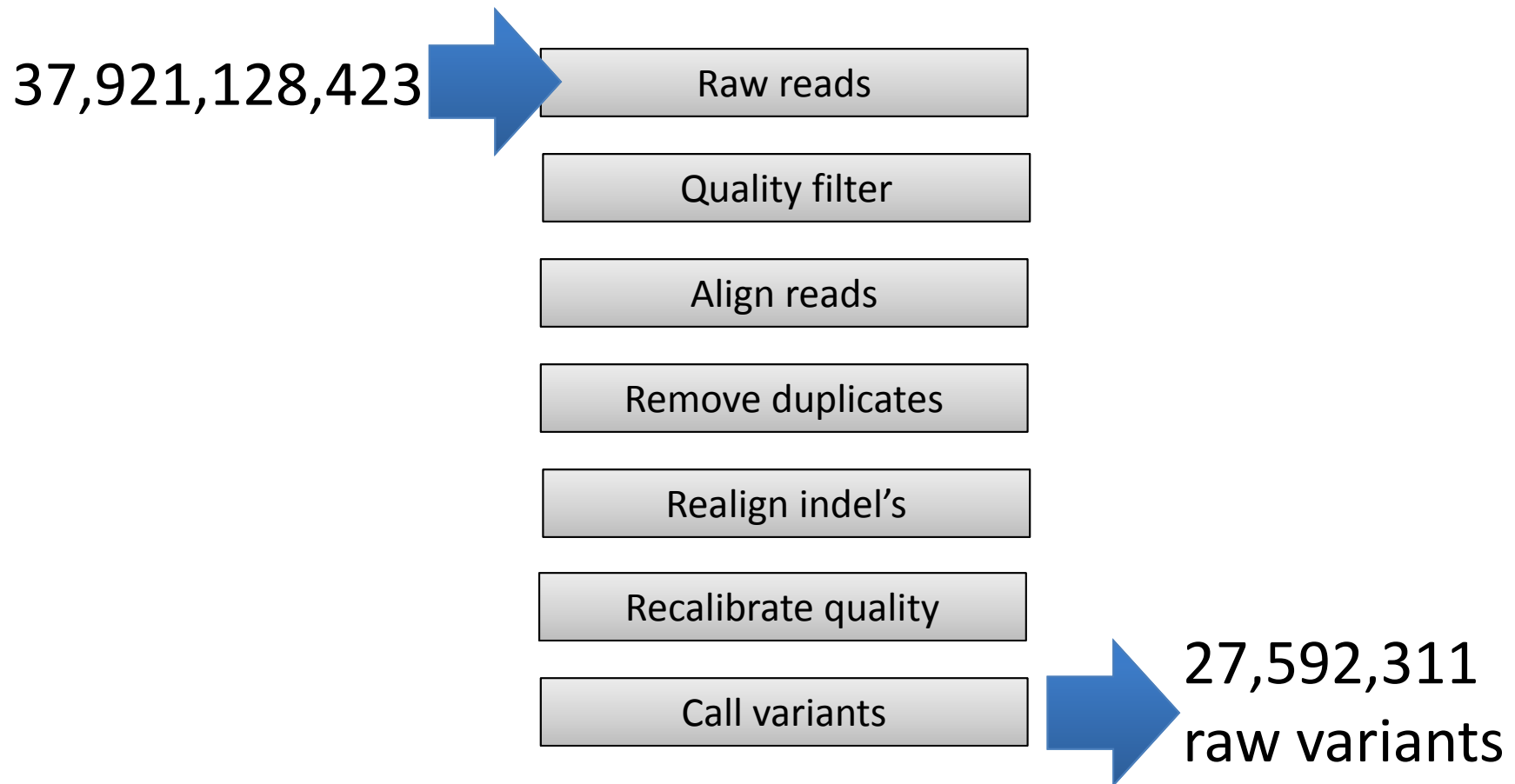
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27 Landrace and 88 Duroc pigs were sequenced
to at least 10X per animal

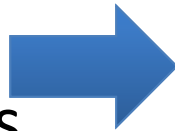
Reads of 100 bp insert size 300

From reads to variants



Filtering variants

27,592,311
raw variants



maf 0.05

Max 2 alleles per site

Depth 5-30 per sample

Min mapping qual. 30

No SNP's within 5 bp of
indel

No indel within 10 bp of
indel

F = -1 removed



17,264,200
variants

Functional annotation

Annotation	All variants
intergenic	67%
intron	24%
downstream gene	4.7%
synonymous	0.36%
missense	0.25%

Duroc vs Landrace

Segregating sites in Landrace

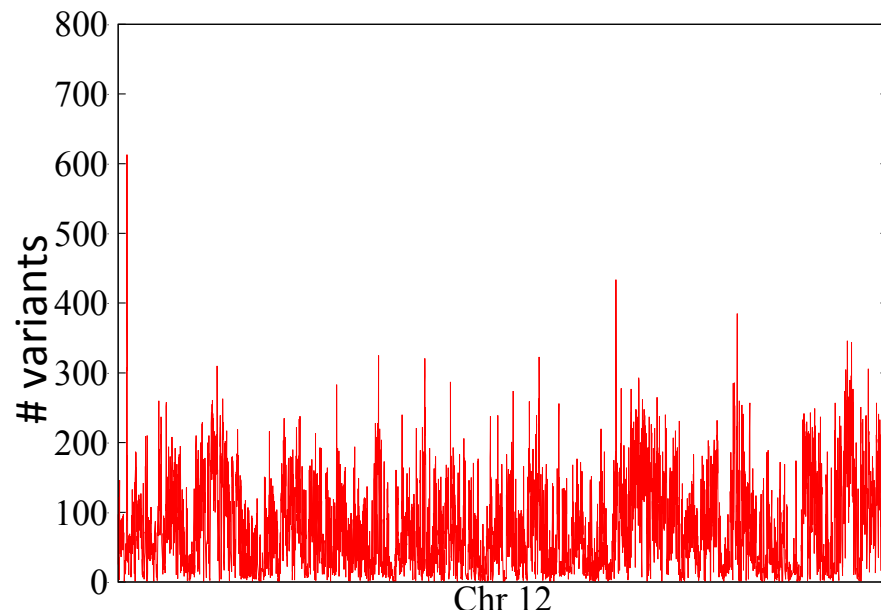
13,918,083

Segregating sites in Duroc

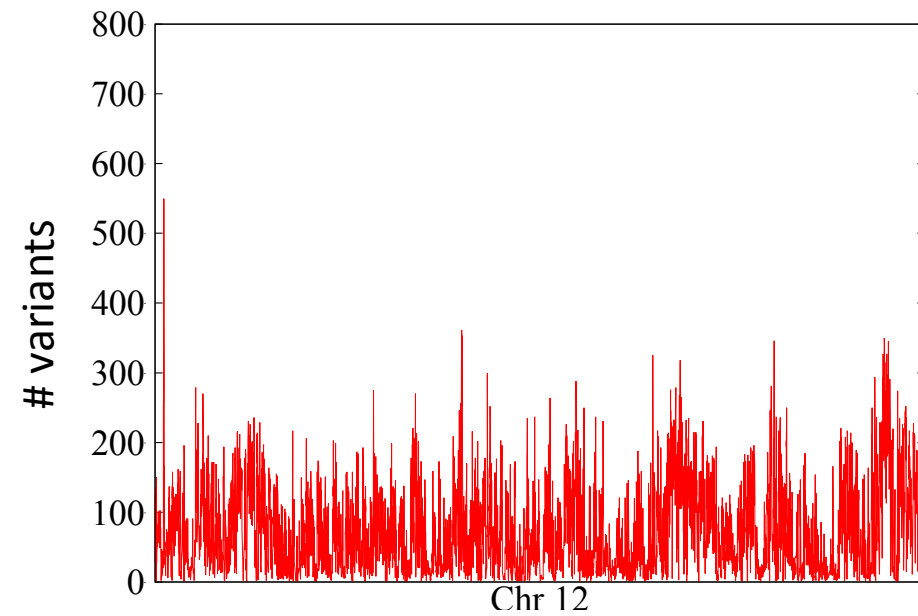
15,494,483

Chr 12

Duroc



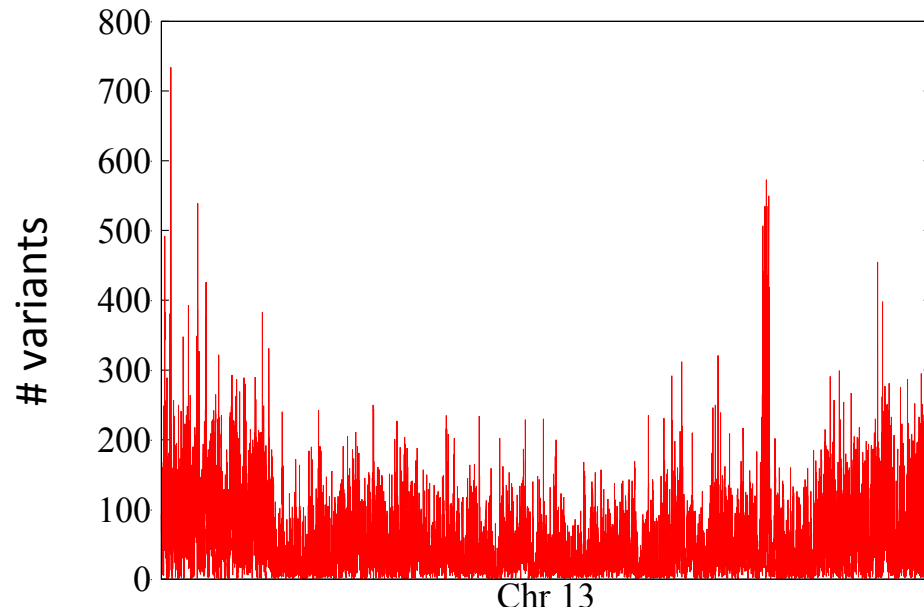
Landrace



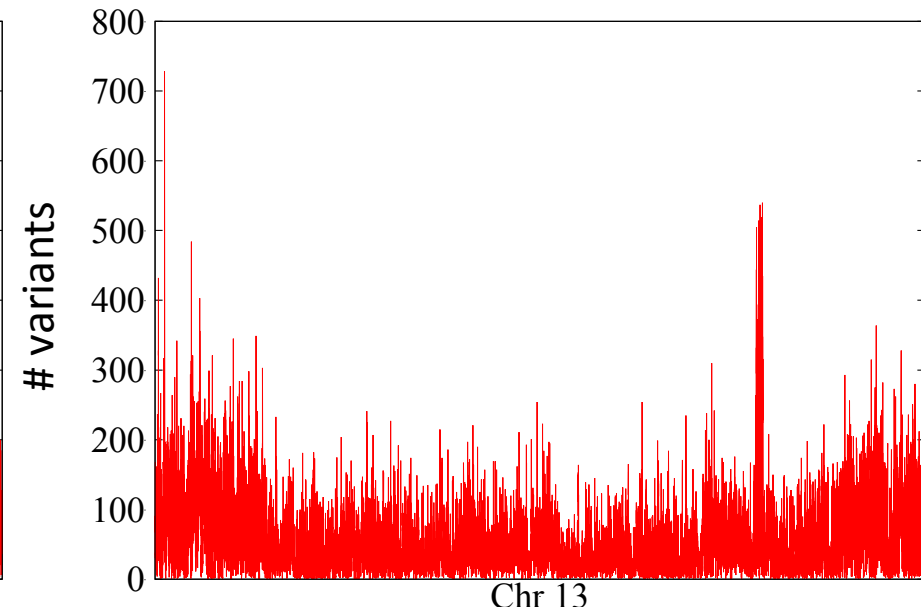
Per 10 kb

Chr 13

Duroc



Landrace

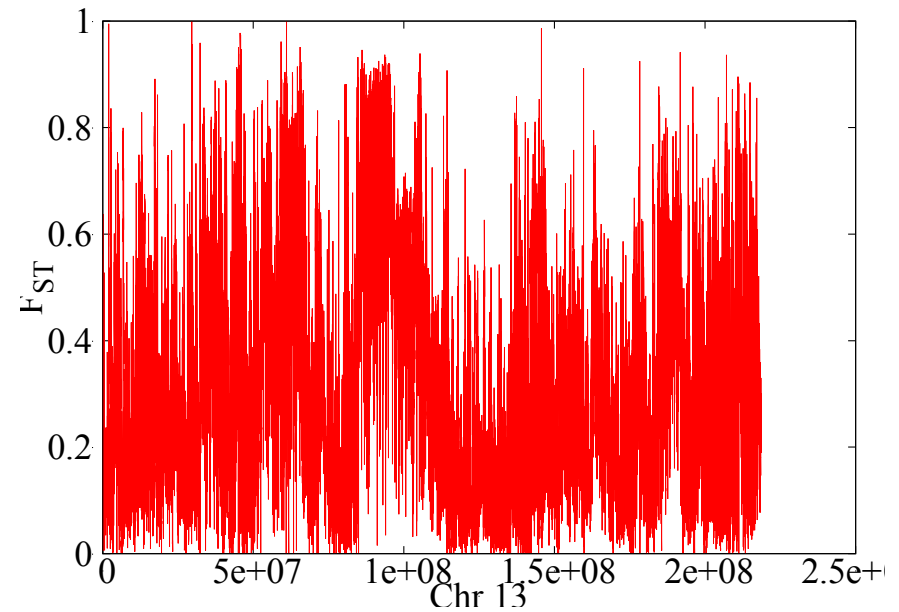
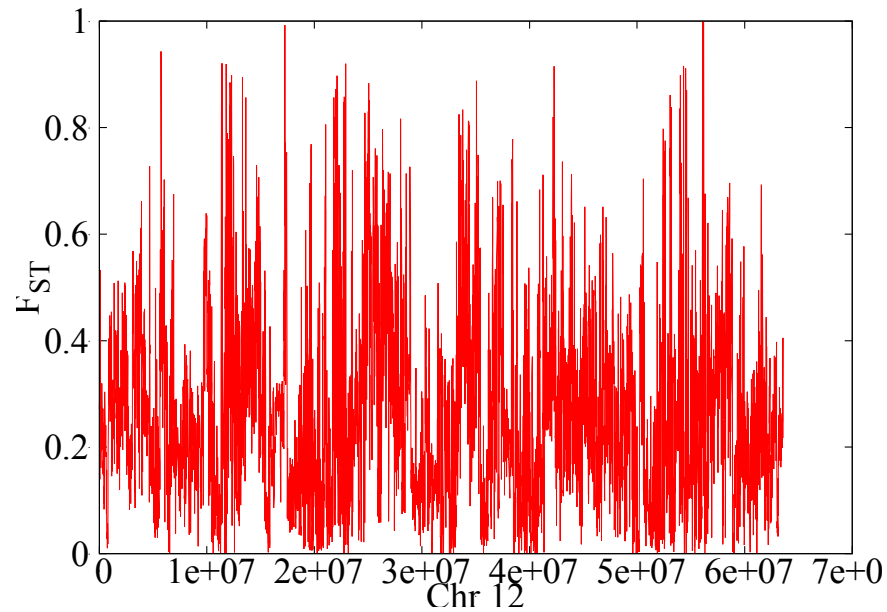


Per 10 kb

Duroc vs Landrace

Weir's weighted F_{ST} : 0.33

F_{ST} bins of 10 Kb



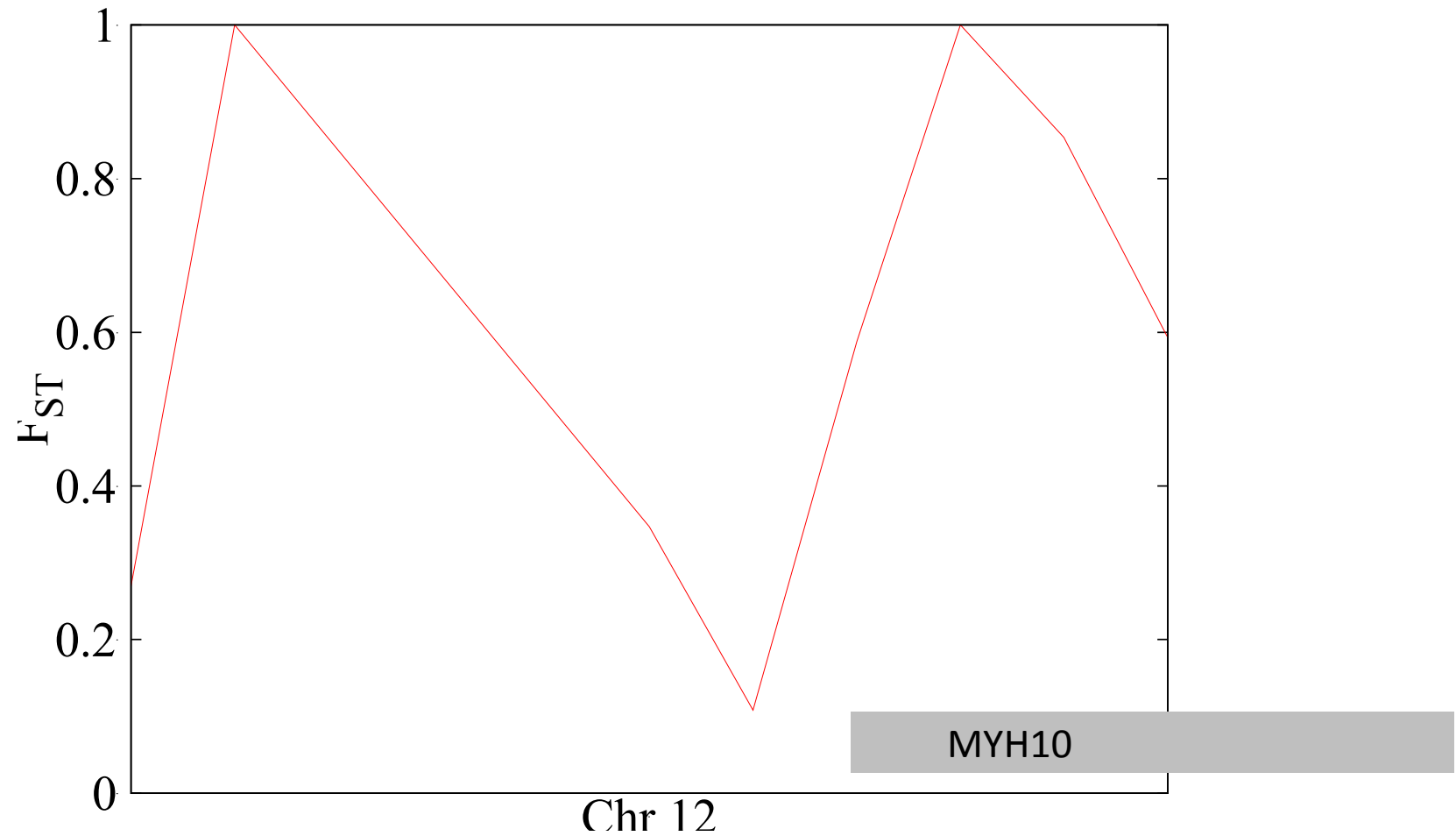
31 bins $F_{st}=1$

All with very low
variation

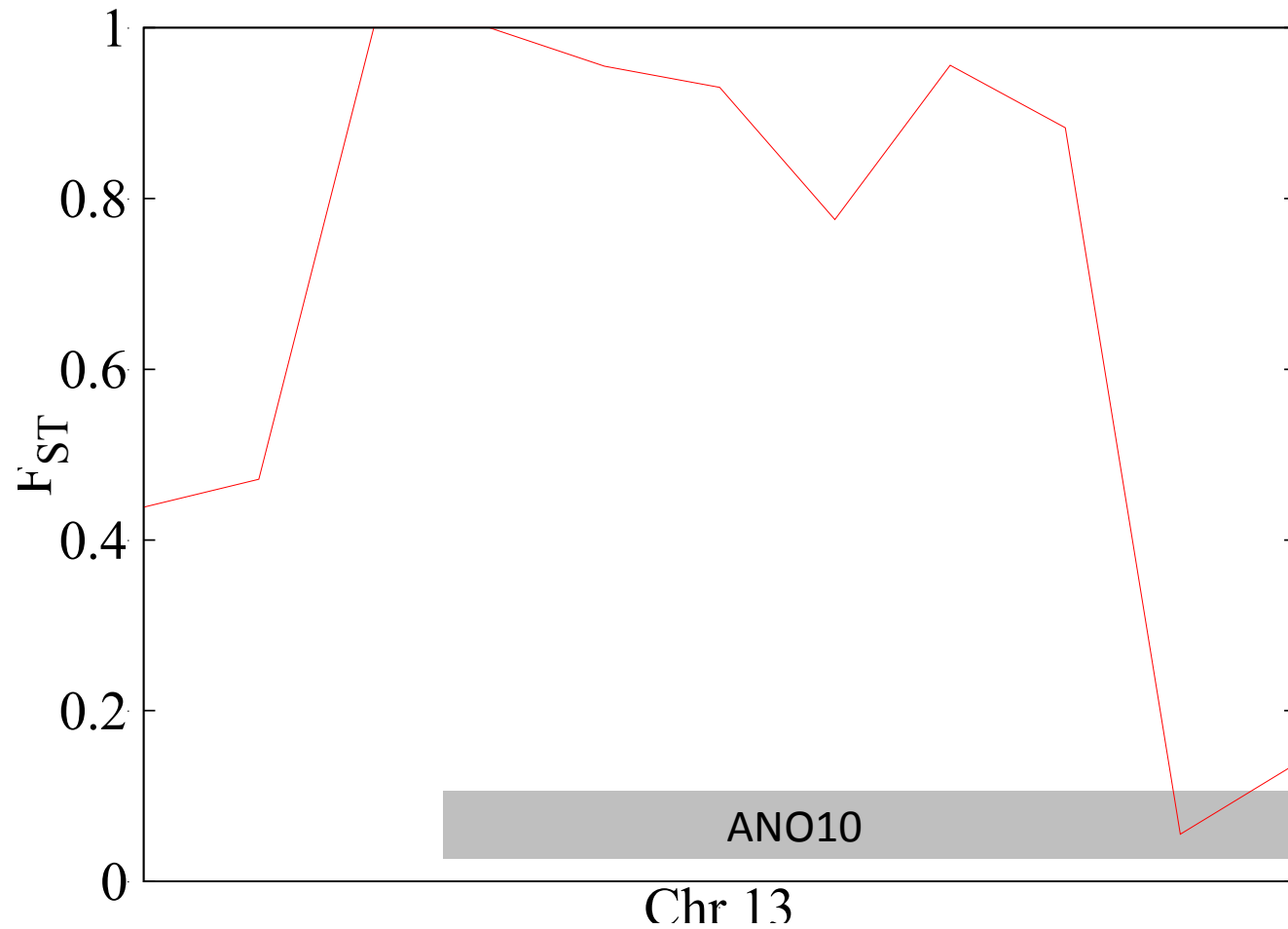
Chr	bin/chr	#variant/bin
1	2	1
3	1	6
5	1	2
6	1	1
7	2	1.5
8	3	1.3
9	3	1
11	2	1
12	2	2.5
13	3	1
14	6	1.16
15	4	2.25
18	1	2

Annotation	All variants	binned $F_{st} = 1$
intergenic	67%	63%
intron	24%	27%
downstream gene	4.7%	10%
missense	0.25%	0
synonymous	0.36%	0

Window size 100 Kb



Window size 100 Kb



Conclusions

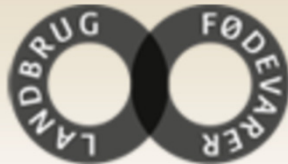
Levels of variation similar in Duroc and Landrace

High F_{ST} between the two breeds

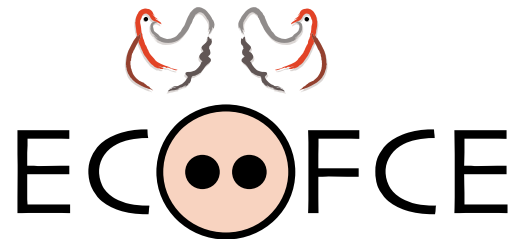
Bins with $F_{ST} = 1$ contained interesting genes

Thank you for your attention

Danish Pig
Research Centre



For providing samples



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