Genomic regions harbouring signatures of selection associated with QTLs in pigs from different breeds and production environments

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Introduction

Pigs represents an important livestock species worldwide and are important for livelihoods, food security and economic growth. In developing countries, pigs are reared under harsh environments while providing proteins for resource limited households (Lunney, 2007). Besides providing proteins for humans, pigs are also used as model animals to research on human diseases. Changes in the phenotypic characteristics between domestic and wild pigs are highly noticeable and were driven by natural and artificial selection (Gurgul et al., 2018). Adaptation (natural selection), domestication (artificial selection), as well as breed development creates signatures of selection in genomic regions of populations. Information of signatures of selection is valuable and can be used in management strategies to improve production and adaptability. To date there has not been any study that investigated signatures of selection in South African pig populations.

Methodology

A total of 234 pigs representing 91 non-descript village pigs from Mopani (n = 27), Capricorn (n = 25) in Limpopo and O.R. Tambo (n = 22) and Alfred Nzo (n = 17) in Eastern Cape provinces; 60 commercial pigs from Duroc (n = 20), Large White (n = 20) and South African Landrace (n = 20); 40 indigenous pigs from Kolbroek (n = 20) and Windsnyer (n = 20); 38 wild pigs from Wild Boar (n = 4), Warthog (n = 31) and Bush Pig (n = 3) as well as 5 Asian pigs of the Vietnamese Potbelly were genotyped using the Porcine SNP60K Bead Chip (62 134 SNPs). Quality control removed animals with call rates less than 85%, SNPs with minor allele frequency < 0.02 and Hardy Weinberg Equilibrium of P < 0.0001.
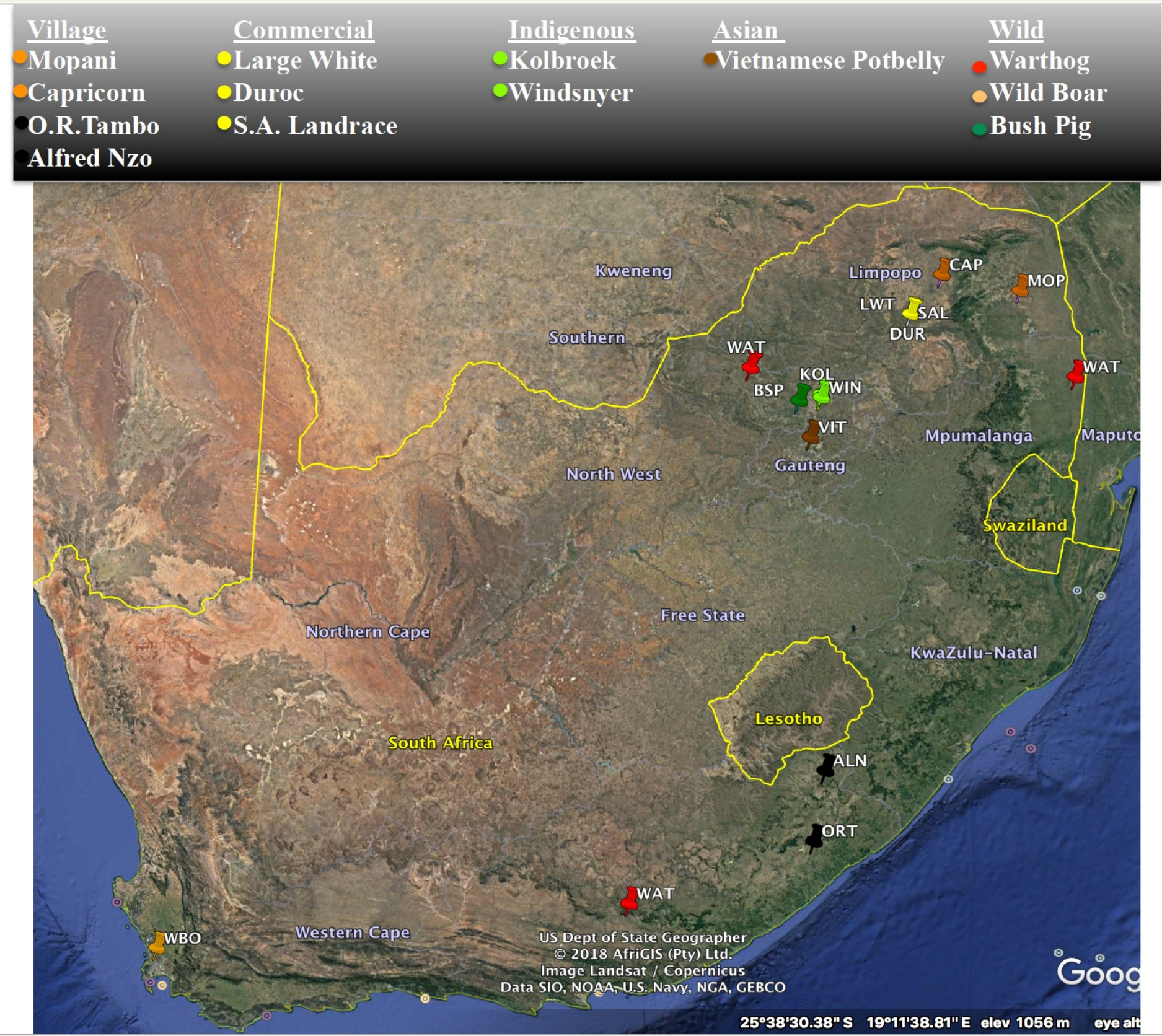
Village	Commercial	Indigenous	Asian	Wild
Mopani	Large White	Kolbroek	Vietnamese Potbelly	Warthog
Capricorn	Duroc	Windsnyer		Wild Boar
O.R.Tambo	S.A. Landrace			Bush Pig
Alfred Nzo				

Figure 1: Map showing geographic locations of the 13 pig populations in the study

Results and Discussion

After quality check, a total of 27 422 SNPs were retained for further analysis. The iHS method used to detect positive selection within a population, identified potential genomic regions in all 13 populations included in this study. However, the number of regions differed greatly between the different populations, ranging from 87 for CAP to 4 for BSP (Table 1).

Table 1: Summaries of the number of potential regions detected in iHS

Pop	Chromosomes	No. of Regions	No. of SNPs
ALN	1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 13, 14, 15, 16, 17	40	49
ORT	1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17	71	94
CAP	1, 3, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18	87	115
MOP	1, 2, 3, 4, 5, 6, 8, 9, 13, 15, 16	68	81
LWT	1, 2, 4, 5, 7, 8, 9, 12, 13, 14	34	51
SAL	1, 2, 7, 8, 9, 11, 14, 15, 17	31	43
DUR	1, 2, 6, 7, 14	12	17
KOL	1, 2, 3, 4, 5, 14, 16	17	20
WIN	2, 3, 4, 5, 8, 9, 10, 13, 14	22	30
VIT	15	1	1
WAT	3, 6, 9, 10, 11, 18	10	10
WBO	1, 2, 5, 13, 14	32	46
BSP	7, 8, 15	4	4

Results and Discussion

The regions displaying significant selection were distributed on different chromosomes, harbouring genes associated with important traits. The strongest selection signal (-log10 [2φ -| iHS |]) = 24.09) was observed on chromosome 13 in WBO (Figure 1).
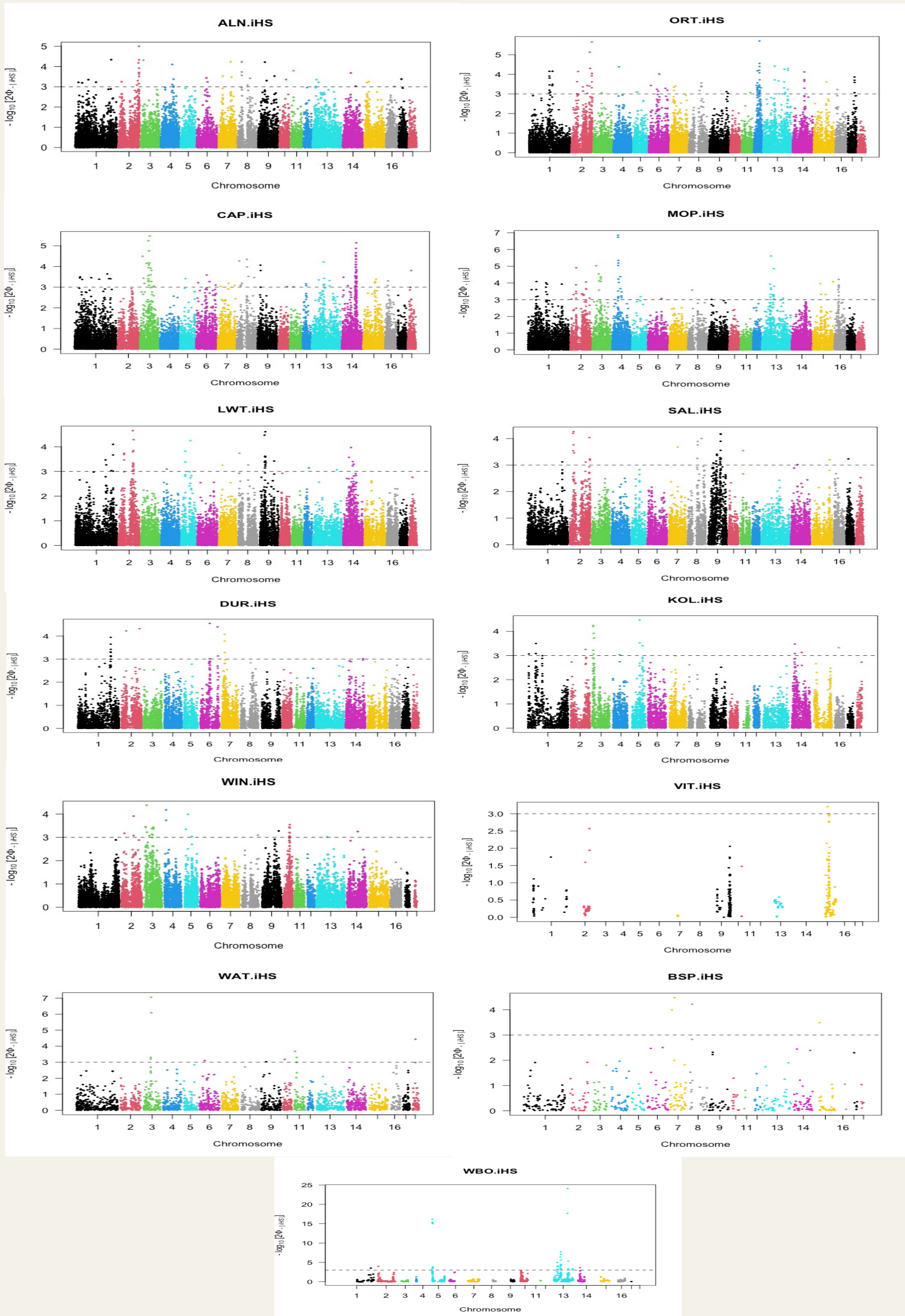

Figure 1:Manhattan plot of the genome-wide distribution of selection of signatures detected by iHS across the 18 chromosomes

Several regions displayed significant evidence of positive selection and included genes and QTLs associated with meat and carcass quality. Chromosome 4 showed the most signatures linked to mostly meat and carcass quality traits. Among the indigenous Kolbroek and Windsnyer breeds also included the JPH1 gene observed on chromosome 4 that has previously been linked to meat and carcass quality in pigs (Qin et al. 2020).

There were a number of regions displaying significant evidence of selection were identified using XP-EHH to identify genomic regions under selection between pairs of populations. The number of regions differed between the different populations paired, with VIT_WBO having the least number of regions (1 region) and WAT_EC had the most (61 regions). VIT_LIM on chromosome 9 though it was not associated with any QTL (Figure 6.2) Another region on chromosome 2 (113.82 Mbp) that was identified in the DUR_EC and DUR_LWT populations harbour the FER gene associated with important production traits including meat and carcass quality traits.
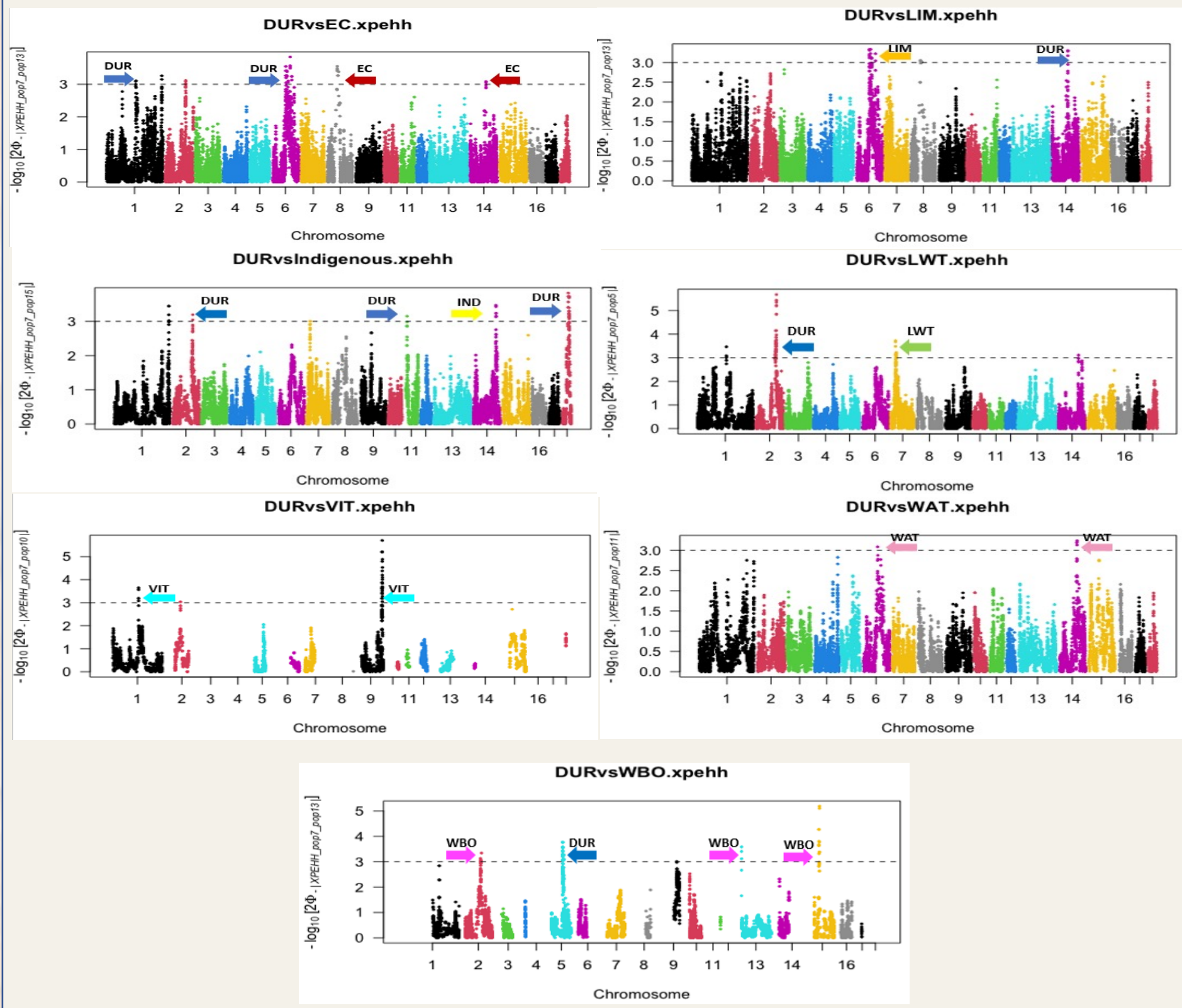

Figure 2:Manhattan plot of the genome-wide distribution of selection of signatures detected by XP-EHH across the 18 chromosomes (Duroc Group)

Results and Discussion

Conclusion

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