

11th

**WORLD CONGRESS
ON GENETICS
APPLIED TO
LIVESTOCK PRODUCTION**



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Aotea Centre
Auckland
New Zealand

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**UNIVERSIDADE ESTADUAL PAULISTA
"JÚLIO DE MESQUITA FILHO"**

A photograph of a white Nellore cow standing in a green field under a blue sky. The cow has a large hump and a blue collar with a red and white pattern. The text is overlaid on the image.

Runs of homozygosity and evidence of adaptation in Nellore cattle

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Objective

1. Identify autozygosity islands based on ROH in the genome of the Nellore cattle.
2. Examine their potential biological roles by revealing genomic regions that could be associated with adaptive traits.

Material and Methods

Clarific

GGP-LD B

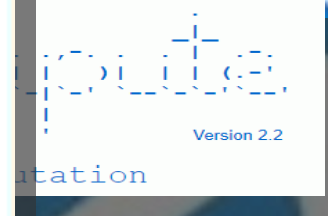
Illumina Bo

GGPi Be
Prof

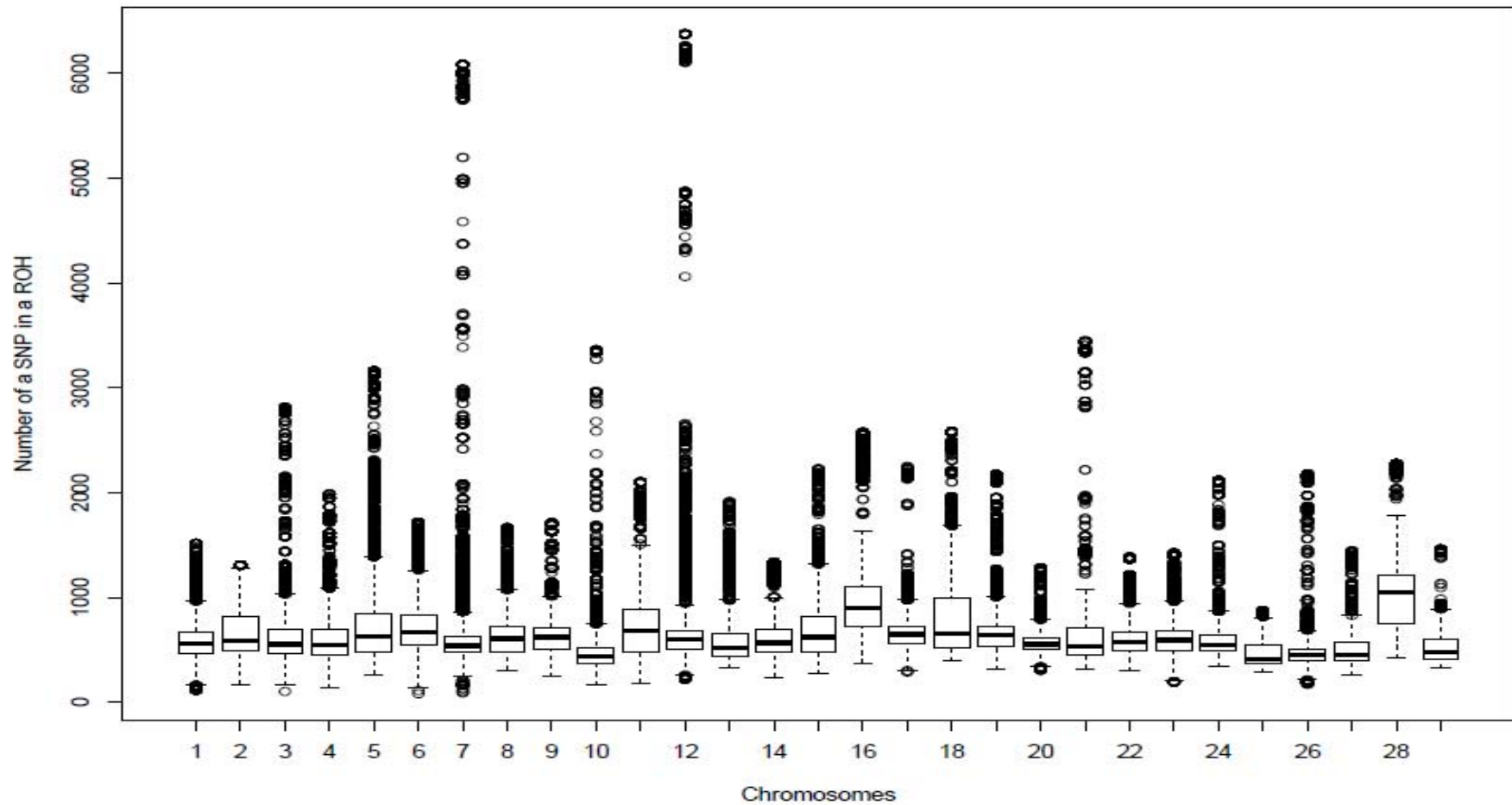
Illumina BovineHD BeadChip 77K
(n=911)



ANCP
ASSOCIAÇÃO NACIONAL DE
CRIADORES E PESQUISADORES



control
samples
14 SNPs



Material and Methods

Functional annotation

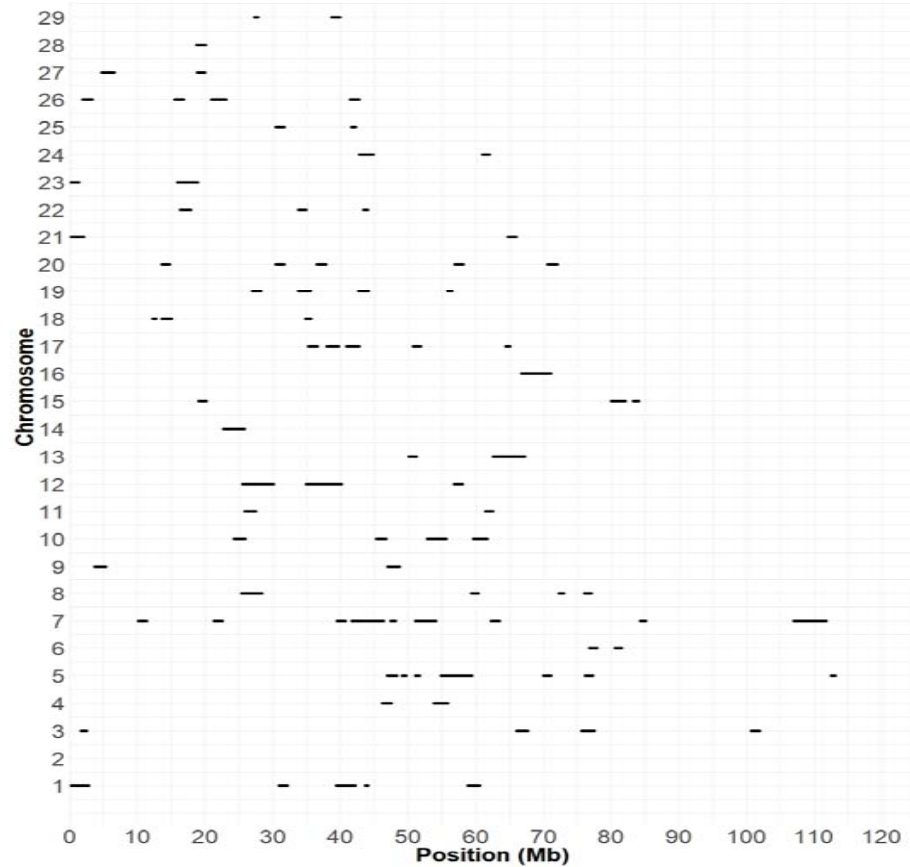
Map Viewer (UMD3.1.1)

1,533 genes identified

DAVID v6.8 tool
($p < 0.01$)

- Gene Ontology (GO) terms
- KEGG pathways
(Kyoto Encyclopedia of Genes and Genomes)

Results and Discussion



Results and Discussion

- Overlapped with previous studies on several cattle breeds

[SÖLKNER et al., 2014 (Brahman, Gyr, and Nellore)
GASPA et al., 2014 (Italian Holstein)
SZMATOŁA et al., 2016 (Holstein, Red Polish, Simmental, and Limousin)
PERIPOLLI et al. 2017 (Gyr)

Harbor targets of positive selection in cattle

Results and Discussion

Table 1. Gene Ontology terms and KEGG pathways annotation analysis enriched ($P < 0.01$) based on autozygosity islands set of genes.

Gene Ontology Terms	Genes	P-value
Biological Process		
(GO:0007186) G-protein coupled receptor signaling pathway	72	1.89E-04
(GO:0019373) Epoxygenase P450 pathway	6	3.04E-04
(GO:0030163) Protein catabolic process	10	1.07E-03
(GO:0006508) Proteolysis	22	2.72E-03
Molecular Function		
(GO:0005549) Odorant binding	32	2.01E-08
(GO:0004984) Olfactory receptor activity	82	1.91E-06
(GO:0004930) G-protein coupled receptor activity	87	8.58E-05
(GO:0004190) Aspartic-type endopeptidase activity	10	7.13E-04
(GO:0008392) Arachidonic acid epoxygenase activity	6	1.09E-03
(GO:0008395) Steroid hydroxylase activity	6	6.23E-03
Cellular Component		
(GO:0005886) Plasma membrane	200	1.78E-08
KEGG pathway		
(bta04740) Olfactory transduction	114	6.55E-08

Results and Discussion

Epoxygenase P450 pathway (GO:0019373) - BP

Displays potent **vasodilatory**, fibrinolytic, **angiogenic**, and **anti-inflammatory** properties.

Key role in explaining important biological mechanisms underlying **heat tolerance** and **parasite resistance** in indicine cattle.

Results and Discussion

Protein catabolic (GO:0030163) - BP

Found to play an important role in the **immune** and **inflammatory response**.

Significantly enriched in a GWS on TIAR in mouse macrophages
(RNA-binding protein) (Kharraz et al., 2016)



Regulates translation and stability of mRNA-encoding proteins
important for the **inflammatory response**

Results and Discussion

Olfactory receptor activity (GO:0004984) - MF

Combines with an odorant and transmits a signal to initiate a cell activity in response to detection of smell.

Drosophila larvae foraging for food under conditions of limited resources (Asahina et al., 2008)



Sense of smell is necessary for effective foraging and survival to adulthood - survival advantage



Results and Discussion

Olfactory transduction (bta04740) - KEGG pathway

Abo-Ismael et al. (2014): Significant SNPs for feed efficiency in crossbred beef cattle.

Do et al. (2014): Residual feed intake in pigs.

Snelling et al. (2012): Reproductive traits in crossbred heifers (puberty, follicle count, and pregnancy).

Final Considerations

- Cattle have undergone separate evolution - Favored in tropical regions (evolutionary traits).
- The survivability and adaptive benefits - Increased dosage of genes related to the IR and OS.
- Feed efficiency – Ability to feed in harsh environments
- ❖ Explain the indicine acquired traits – Develop wide range of environments.
- ❖ Indicine: Source of genomic information – Discovery/Validation of genomic regions controlling important adaptive traits.
- ❖ ROH may contribute to future fine mapping studies seeking for regions that explain these traits.



Thank you!

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