

# Genes and Molecular Mechanisms Associated with Mastitis in Dairy Cattle

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## Introduction

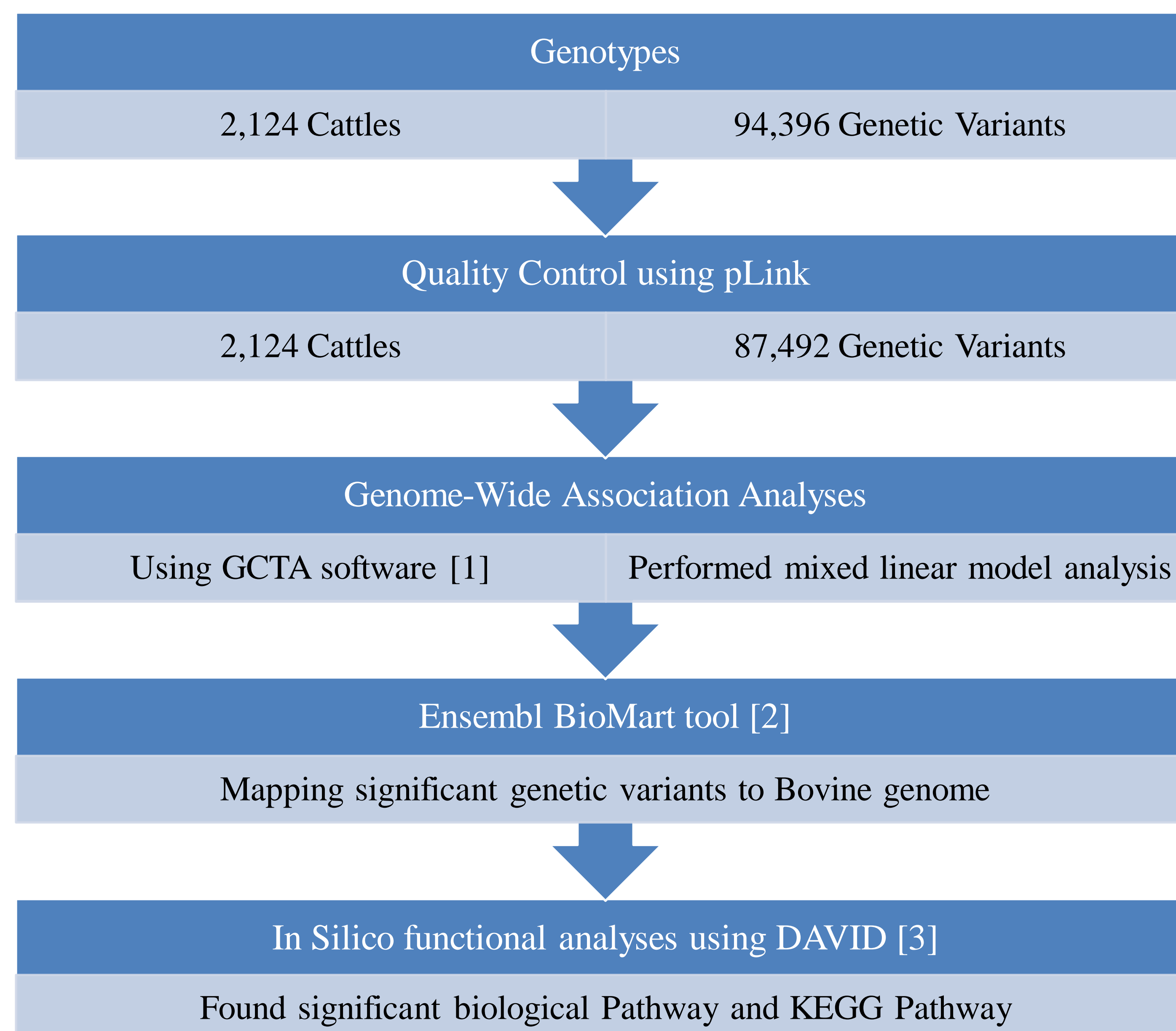
- The dairy industry accounts for 7.57 billion dollars of California's economy. There is a significant financial loss due to reduction in milk from the costliest disease called mastitis ranging from \$155 to \$224 for each case.
- Mastitis can be caused by a multitude of reasons from physical trauma to genetic factors.
- Detecting mutations in heifer will allow us to accurately predict the genomic values for Mastitis.

## Objective

- To detect genomic value that is resistant to mastitis
- To test the association between these specific genomic value and mastitis disease
- To understand the molecular mechanisms behind these associations

## Methods and Materials

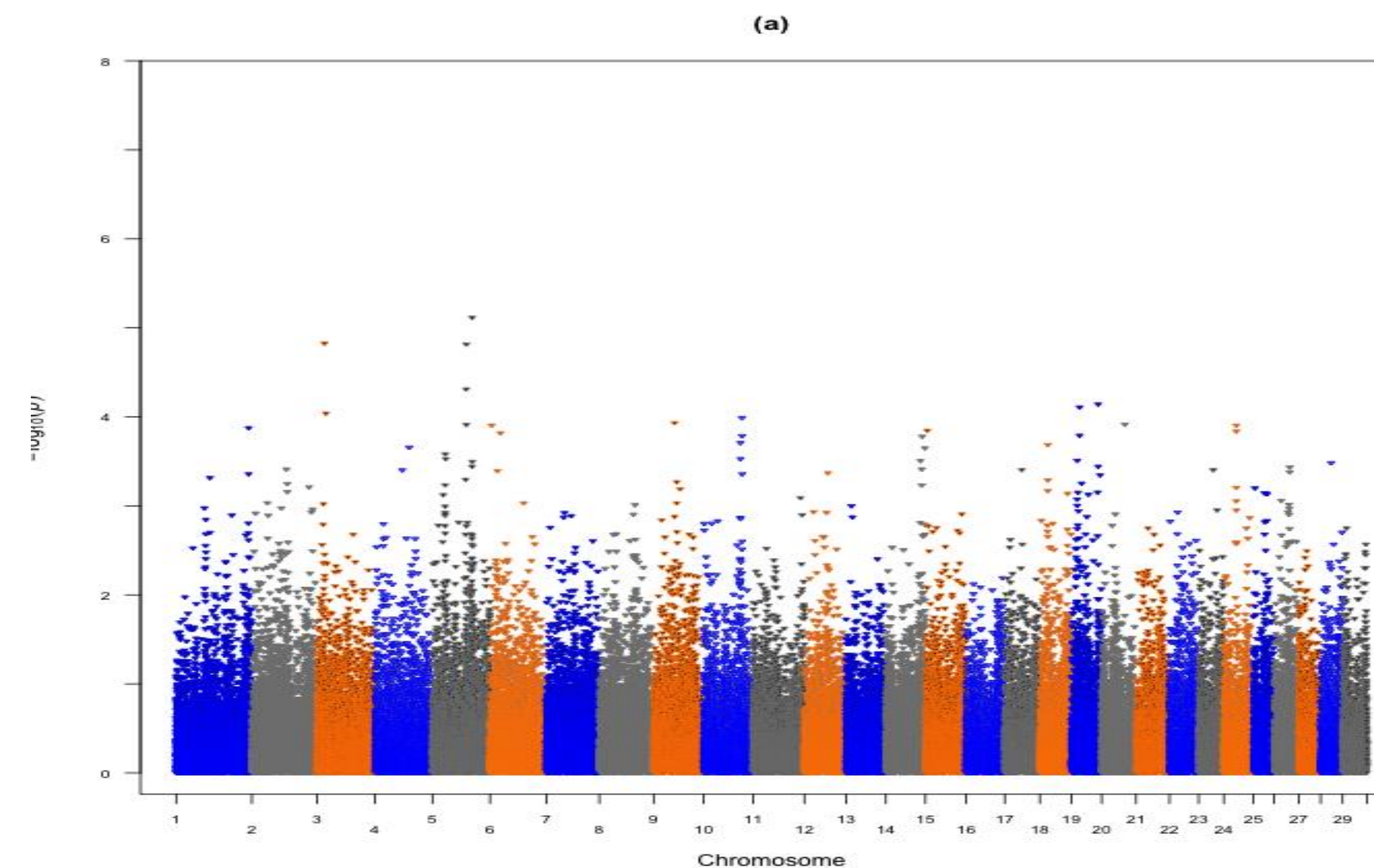
- The quality control for genotypes and subsequent analyses are illustrated in **Figure 1**.



**Figure 1.** Workflow for data analyses

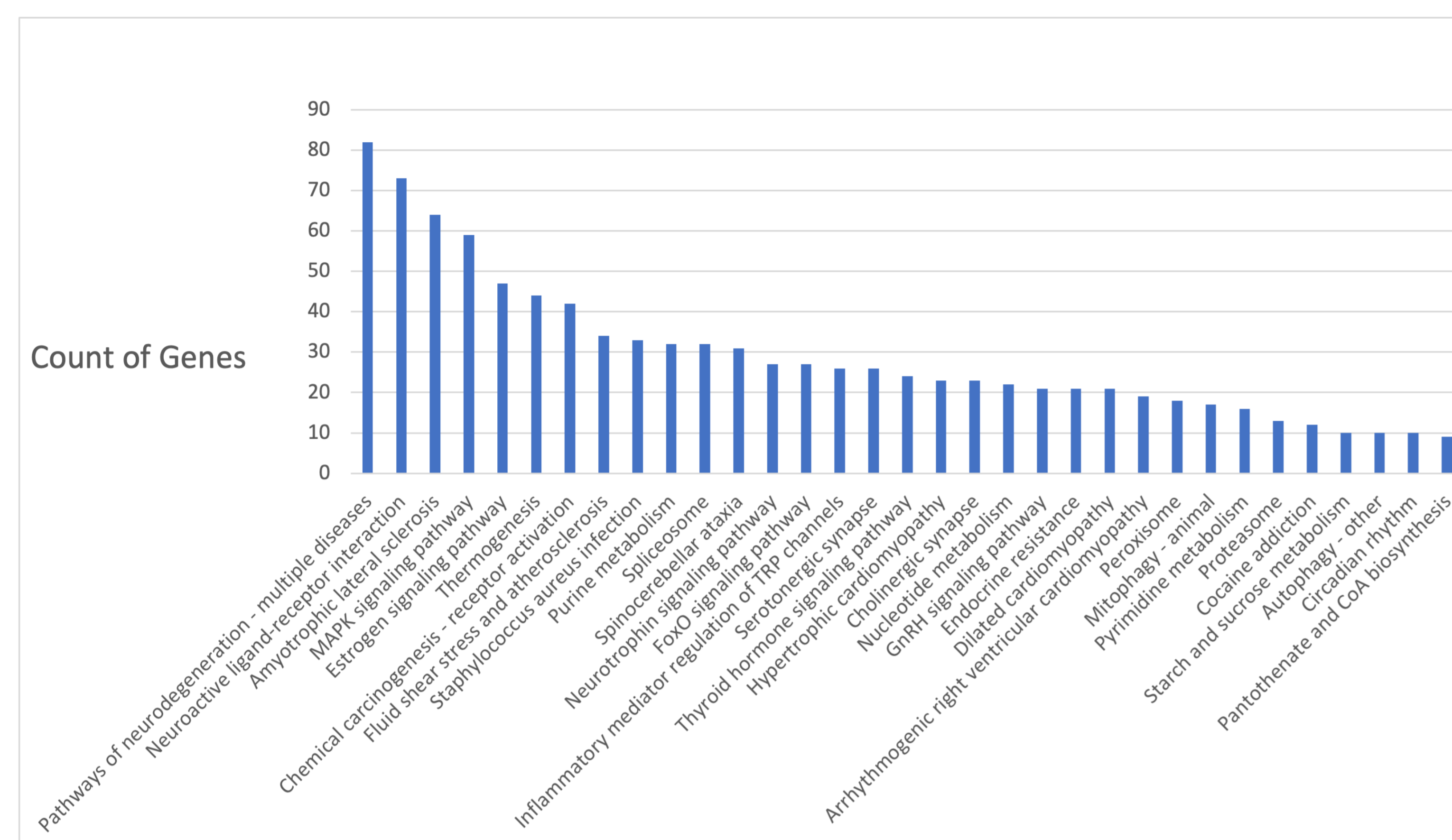
## Results and Discussion

- The identified top 10 SNPs from GWAS with the lowest p-value in the mixed linear model were mapped to 25 genes.
  - The top significant genetic variants were located on Bos taurus autosomes 5, 3, 19, 10, 9, and 20



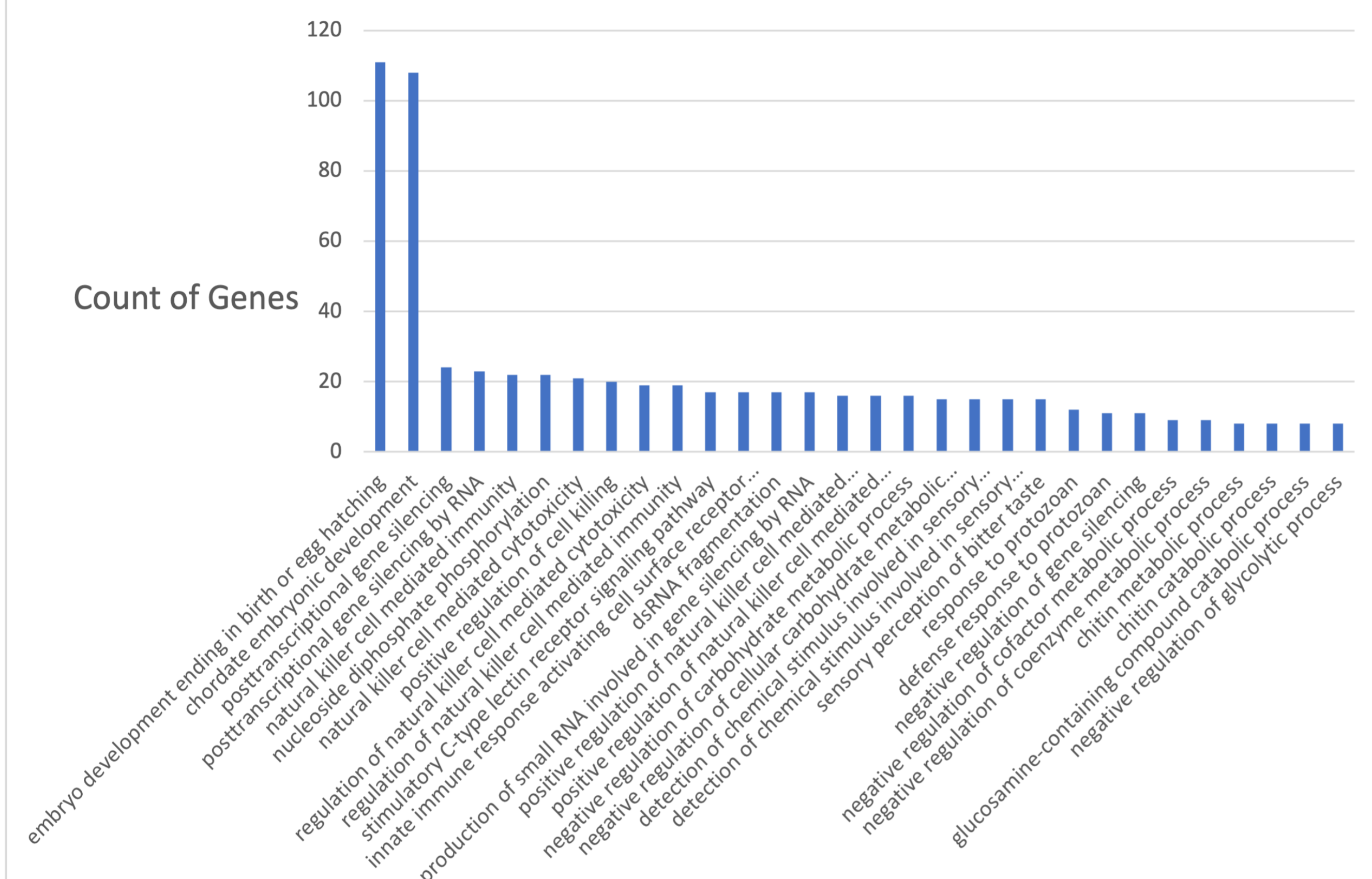
**Figure 2 .** The most significant chromosomes associated with mastitis produced from Genome-Wide Association Analyses are presented on the Manhattan plot.

- With these significant genes inputted into DAVID Enrichment analyses identify the most significant KEGG Pathway and biological Pathway.



**Figure 3.** The most significant KEGG Pathway resulted from enrichment.

## Results and Discussion Cont.



- The most significant KEGG Pathways were neurodegeneration, neuroactive ligand-receptor interaction, and amyotrophic lateral sclerosis.
- The most significant biological Pathways were positive regulation of metabolic process, regulation of signaling, and positive regulation of cellular metabolic process.

## Conclusions

- The study identified candidate genes that is associated with heifers being born with mastitis disease. These genes are involved in potential pathways including metabolic pathway.
- Further validation of the identified genomic regions will be performed to test the correlation of these genes and its association with mastitis.
- This may include looking at SNPs with higher density

## References

- [1] Yang et al. 2011. Am J Hum Genet, 88: 76-82
- [2] <http://useast.ensembl.org/biomart/martview>
- [3] Huang et al. 2009. Nature Protoc., 4: 44-57.
- [4] Ariel O et al. (2021). BMC genomics vol.22.:

## Acknowledgements

