



# GenoBaits<sup>®</sup> 50K Buffalo SNP Panel

**Dual Buffalo Types, Unlimited  
Genomic Possibilities**



The GenoBaits® 50K Buffalo SNP Panel is a comprehensive genotyping solution jointly developed by Dr. Lloyd Low at the Adelaide University and MolBreeding Biotechnology, designed to support advanced genomic research and breeding applications in buffalo. The panel comprises 50,147 genome-wide SNP markers, including 47,310 autosomal SNPs, 2,737 sex chromosome SNPs, and 100 mitochondrial markers, providing balanced and high-resolution genomic coverage. Built using SNP resources derived from both river- and swamp-type buffalo populations, the panel ensures reliable performance across diverse buffalo genetic backgrounds. With its cost-effective design and flexible architecture allowing future probe additions, GenoBaits® offers a scalable and future-ready solution for genomic selection, population analysis, and sustainable buffalo breeding programs worldwide.

## Comprehensive Genetic Representation

Unlike conventional buffalo SNP arrays (mainly from river buffalo resources), this panel is designed with SNPs from both river- and swamp-type buffalo genomes. Integrating representative variants of both subspecies, it enables:

- Accurate genotyping across diverse buffalo populations
- Improved polymorphism detection in both river and swamp buffalo
- Reliable cross-population genomic analysis

## Cost-Effective Genomic Solution

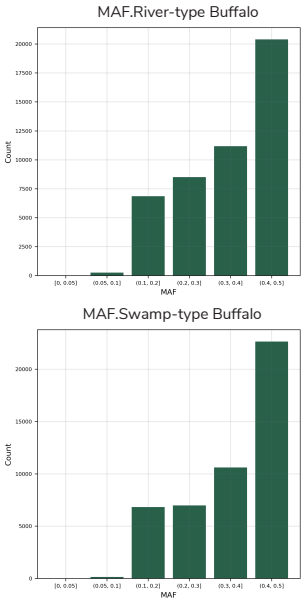
An economical alternative to whole-genome sequencing, with optimized marker density, high information content per SNP, and scalable genotyping for breeding & research. Ideal for large-scale genomic selection, population screening, and routine genetic evaluation.

## Flexible & Future-Ready Design

Built on a modular probe architecture, it supports easy addition of new SNP markers, custom expansion for specific traits/breeds, and continuous updates with emerging genomic discoveries—ensuring long-term usability as buffalo genomic resources advance.

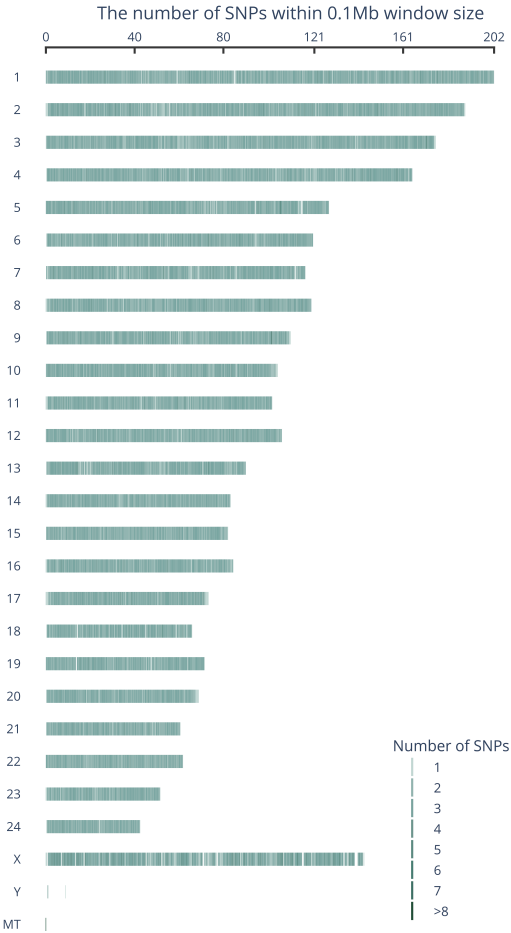
## Powered by Latest Genomic Discoveries

Recent large-scale studies confirm significant genetic differentiation between river and swamp buffaloes, highlighting the need for balanced SNP representation. This panel leverages these advances to deliver a unified genotyping solution for global buffalo breeding systems.



Frequency distribution of 50K SNP MAF

The SNP chip has a high MAF, which provides great potential for successful genomic studies and genomic selection in buffalo.



The distribution of 50K SNP markers on chromosomes

A total of 50,147 SNPs are evenly distributed across 24 autosomes, 2 sex chromosomes, and mitochondrial DNA, with different colors representing the number of SNPs located within 0.1 Mb sliding windows.