



# GeneSeek<sup>®</sup> Genomic Profiler<sup>™</sup> Bovine 100K

Leveraging NEOGEN<sup>®</sup>'s leading SNP selection processes to precisely choose yet another 50K SNPs spanning the bovine genome.

NEOGEN aspires to remain on the cusp of advanced technology and research. Constantly striving for more, the scientists have designed a new generation high-density, genome-wide genotyping array to assist in quantifying the genetic merit of cattle. Developed using the Multiple Objective Local Optimization (MOLO) algorithm<sup>1</sup>, the GGP Bovine 100K consists of approximately 100,000 SNPs, promising again to provide users with informative, consistent, and accurate data. Together, these attributes will continue to power genetic evaluations, genome-wide association studies, identification of quantitative trait loci, and comparative genetic studies.

## Key Features:

- Better coverage - Average SNP spacing of 29.0 kb
- Even Distribution - Average D score of 0.90 and U score of 0.74
- Appropriate overlap with multiple SNP panels to allow for accurate imputation
- Astounding MAF - weighted average minor allele frequency (MAF) across ten breeds of 0.29
  - High MAF equates to high information content

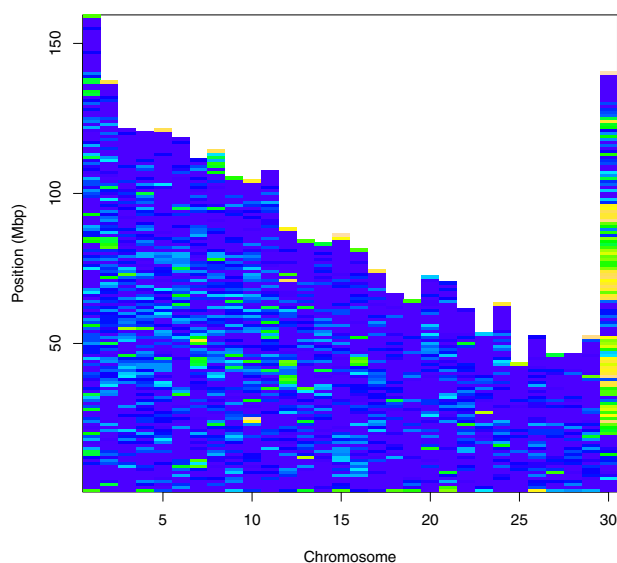
## GGP 100K Bovine Content:

In addition to the original 50,000 SNPs from the GGP Bovine 50K, the new SNP content includes:

- Approximately 50,000 additional SNPs
- Approximately 85% overlap with the Council of Dairy Cattle Breeding (CDCB) virtual evaluation
- Over 35,000 SNP overlap to the Canadian Dairy Network (CDN) Evaluation
- Emphasis placed on MAF in major beef breeds
- Additional defects and conditions

Figure 1: GGP Bovine 100K SNP Density Map

D-Score:  $\mu$  (SD) = 0.904 (0.149)



Coverage and SNP overlap was determined by mapping the existing GGP Bovine 100K SNP panel to the bovine reference genome version ARS 1.2

Calculation of imputation accuracy was conducted using separate populations of Holstein and Angus samples previously characterized on the Illumina Bovine HD.



**Table 1: Distribution of minor allele frequencies (MAF) by breed**

Unfortunately, it is inherent that as the number of SNP in a panel increases, there are less SNP available with high MAF in a breed. Therefore, the average MAF will decrease. This was taken into consideration during the design of the GGP Bovine 100K. It can be seen in Table 1 that the highest proportion of SNPs still have MAF between 0.30 and 0.50.

Breed	Proportion of SNPs by MAF group				Average MAF by Breed
	0.00–0.04	0.05–0.19	0.20–0.29	0.30–0.50	
Angus	0.07	0.19	0.19	0.55	0.30
Beefmaster	0.05	0.19	0.20	0.56	0.30
Brangus	0.05	0.20	0.21	0.54	0.30
Gelbvieh	0.03	0.15	0.20	0.62	0.33
Hereford	0.08	0.23	0.21	0.49	0.28
Holstein	0.05	0.18	0.19	0.58	0.31
Jersey	0.05	0.18	0.19	0.58	0.31
Limousin	0.04	0.17	0.21	0.59	0.31
Red Angus	0.05	0.19	0.20	0.55	0.30
Simmental	0.03	0.15	0.20	0.62	0.33

**Table 2: SNP overlap to other common panels**

SNP Panel	Panel SNP Count	Overlap to GGP Bovine 100K
Illumina LD v2	7,931	7,866
Illumina Bovine 50K v2	54,609	32,442
Illumina Bovine 50K v3	53,218	32,865
GGP Indicus 50K	54,791	18,844
GGP Bovine HD 150K	139,376	70,552
GGP F250	221,115	23,254
Illumina Bovine HD 770K	777,962	87,670

**Figure 2: Imputation accuracy to Illumina Bovine HD, by chromosome**

Average imputation accuracy to the Illumina Bovine HD is >99.5% in both Angus and Holstein animals. Consistently provides increased genomic prediction accuracy across 11 traits in a population of 5,400 Holstein animals compared to competing products.

**References;**

<sup>1</sup> Wu XL, Xu J, Feng G, Wiggans GR, Taylor JF, et al. (2016) Optimal Design of Low-Density SNP Arrays for Genomic Prediction: Algorithm and Applications. PLOS ONE 11(9): e0161719. <https://doi.org/10.1371/journal.pone.0161719>

