SNAPSHOOT
ENGINEERED FOR A SAFER TOMORROW

현장을 이해하고, 필요한 솔루션을 연결합니다.

산업안전 · 추락방지 시스템
산업용 소재 · 건축자재
제품 제안부터 공급·시공·설치·교육까지



COMPANY INFORMATION

스냅슛 (SNAPSHOOT)

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TECHNICAL DOCUMENTS

인증서 · 데이터시트 · 기술자료

제품의 규격과 성능, 인증 및 적용 조건을 확인하기 위한 자료입니다.

ABOUT SNAPSHOOT

제품 공급을 넘어, 현장에 맞는 해결책으로

스냅슛은 산업현장의 작업 환경과 요구 조건을 바탕으로
적합한 제품과 시스템을 제안합니다. 현장 실사를 통해 설치 조건을 확인하고,
공급부터 시공·설치 및 사용 교육까지 필요한 과정을 함께합니다.

추락방지 시스템

안전대부착설비 · 수평·수직 라이프라인
레일 시스템 · 리지드 포스트

밀폐공간 진입·구조 솔루션

데빗암 · 삼각대 · 구조용 윈치
윈치 안전블록 · 구조장비

산업안전 보호구

전신형 안전대 · 랜야드 · 안전블록
작업 환경에 맞춘 개인보호구

산업용 소재·건축자재

산업용 테이프 · 접착제 · 기능성 소재
구조용 스크류 · 목조건축 자재

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홈페이지 바로가기 →
문서 라이브러리 바로가기 →
시공사례 바로가기 →
문의하기 →

본 페이지는 스냅슛의 자료 제공 안내용 표지입니다. 첨부된 인증서 및 기술자료의 발행 주체, 인증 대상과 적용 범위는 해당 원문을 기준으로 확인해 주세요.

GeneSeek® Genomic Profiler™ Bovine 100K

Leveraging NEOGEN®'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[1], 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:

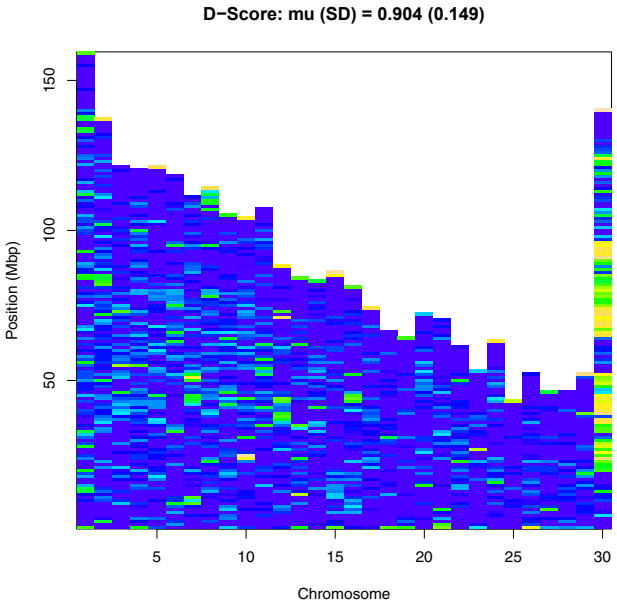
- Better coverage - Average SNP spacing of 29.0 kb
- Even Distribution - Average D score of 0.90 and U score of 0.74
- Appropriate overlap with multiple SNP panels to allow for accurate imputation
- Astounding MAF - weighted average minor allele frequency (MAF) across ten breeds of 0.29
    - High MAF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



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.

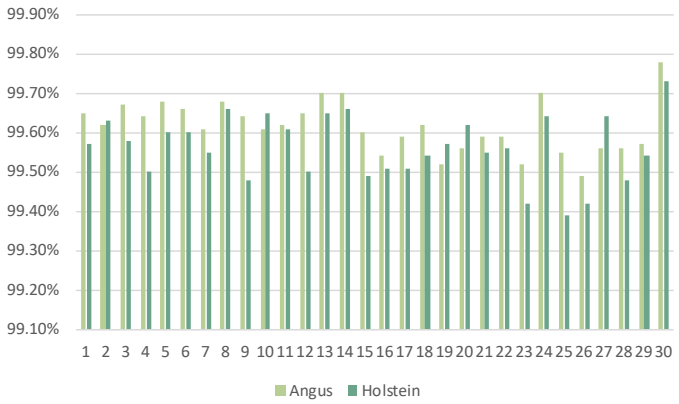
Proportion of SNPs by MAF group					
Breed	0.00–0.04	0.05–0.19	0.20–0.29	0.30–0.50	Average MAF by Breed
Angus	0.07	0.19	0.19	0.55	0.30
Beefmaster	0.05	0.19	0.20	0.56	0.30
Brangus	0.05	0.20	0.21	0.54	0.30
Gelbvieh	0.03	0.15	0.20	0.62	0.33
Hereford	0.08	0.23	0.21	0.49	0.28
Holstein	0.05	0.18	0.19	0.58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

[1] *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*