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)

ADDRESS (15431) 경기도 안산시 단원구 풍전로 37-9 트리플렉스 301동 118호
TEL 0507-1374-9229
FAX 0504-481-6749
E-MAIL bkkim@snapshoot.co.kr

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.

DataSheet

affymetrix

Axiom® Buffalo Genotyping Array

Highest density array for genotyping water buffalo across multiple species and breeds

Axiom® Buffalo Genotyping Array provides the highest genome-wide coverage of polymorphic SNPs across multiple species and breeds of the water buffalo (*Bubalus bubalis bubalis* and *Bubalus bubalis carabanensis*), one of the most important beef and dairy animals in Italy, Brazil, and South Asia.

This array is the only commercially available high-density buffalo genotyping tool.

Highlights

- **Comprehensive content** – 90,000 common and rare markers selected from sequencing initiatives of the water buffalo (*B. bubalis bubalis*)
- **Multiple breeds represented** – Mediterranean, Murrah, Jaffarabadi, and Nili-Ravi
- **Robust assay performance** – SNPs demonstrate a ≥99% call rate and ≥85% conversion rate on Murrah and Mediterranean samples

Applications

Molecular breeding:

- Genomic biomarker discovery
- Marker-assisted selection
- Routine screening
- DNA fingerprinting for animal tracking

Complex trait research:

- High-resolution mapping of genetic loci in complex traits such as milk production, percentage of milk fat, and feed conversion efficiency
- Discovery of genes and pathways underlying simple and complex traits

Conservation and biodiversity:

- Population diversity studies in river and swamp buffalo
- Genomic marker-assisted conservation strategies

Parco Tecnologico Padano

International Buffalo Genome Consortium

Array design

Axiom Buffalo Genotyping Array was designed through the Expert Design Program, facilitated by Affymetrix. The array was developed in collaboration with the International Buffalo Genome Consortium, which included Fondazione Parco Tecnologico Padano in Italy, Iowa State University, and the Agricultural Research Service, United States Department of Agriculture (USDA).

SNP discovery

1. The genome of one Mediterranean female water buffalo (*B. bubalis bubalis*) was assembled at >100x genome sequence coverage.
2. Sequence contigs and paired end reads were aligned from 86 other buffaloes representing 8 breeds and 2 subspecies, including river and swamp types.
3. The sequence reads were aligned to the *Bos taurus* reference genome (UMD3.1).
4. Starting with a list of 16.7 million SNPs and indels, markers that did not have another SNP within 10 bases and had a base pair quality score >10 were included for calculation of minor allele frequency (MAF).
5. A total of 5.8 million SNPs that were polymorphic in at least one breed were selected as candidate SNPs for Axiom Buffalo Genotyping Array.

Marker selection

1. SNPs that met the threshold criteria for predicting reproducibility of SNPs based on Affymetrix' *in silico* design scores were included.
2. Sequences that were highly repetitive in the genome and contained ambiguities were removed.
3. The resulting SNPs were selected for uniform spacing across the genome.

The final array contains 90,000 SNPs, 7,583 probes for sample QC, and 6,853 gender calling probes. The Mediterranean, Murrah, Jaffarabadi, and Nili-Ravi water buffalo breeds are represented in the ratio 30:30:20:20.

Experimental results

A total of 1,056 customer samples representing two different river buffalo breeds (Mediterranea Italiana and Murrah) were genotyped on the array. The samples were prepared with automated target preparation and processed on GeneTitan® MC Instrument.

The genotyping analysis on the data including clustering was automated using Affymetrix Genotyping Console™ Software and Affymetrix SNPolisher™ package. The SNPs were filtered as per the *Best Practice Supplement to Axiom® Genotyping Solution Data Analysis* (P/N 703083).

Array performance was measured in 89,988 SNPs across 1,036 samples that passed the sample QC thresholds. A total of 12 Y SNPs were excluded in this analysis. SNPolisher package refined the clustering based on six genotype cluster classifications, which are listed in Table 1 with summaries of the results for each classification.

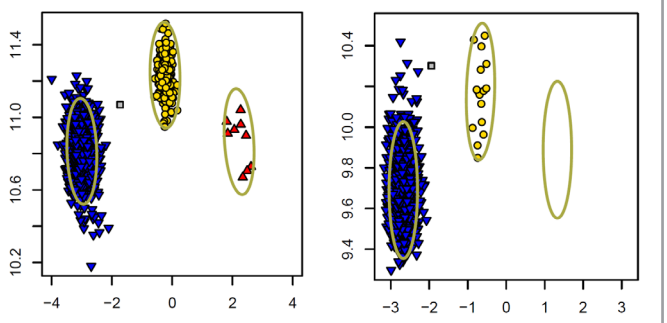
Table 1. Genotyping performance on commercial samples

Genotype cluster category	Percentage of markers	No. of markers
Polymorphic high-resolution	74.8%	67,330
Monomorphic high-resolution	10.3%	9,229
No minor homozygous	1.7%	1,494
Off-target variants	0.1%	83
SNPs with call rate below threshold	4.1%	3,668
Other	9.1%	8,184
Total	**100.0%**	**89,988**

The polymorphic high-resolution marker category has a sample call rate of 99.75% and the average sample reproducibility is 99.96%.

Cluster plots representative of two of the classification categories from the analysis of Axiom® Buffalo Genotyping Array are shown in Figure 1.

Figure 1: The cluster plot on the left is an example of a marker in the "polymorphic high-resolution" category that demonstrates good cluster resolution and at least two examples of the minor allele. The plot on the right shows a marker in the "no minor homozygous" category, which represents markers with two clusters with no representation of the minor allele.



Ordering information

Part number	Description	Details
550431	Axiom® Buffalo Genotyping Array	Contains one plate with 96 arrays. Reagents and GeneTitan® MC consumables must be ordered separately.
901606	Axiom® GeneTitan® Consumables Kit	Contains all GeneTitan® Instrument consumables required to process one array plate
901758	Axiom® 2.0 Reagent Kit	Includes all reagents (except isopropanol) for processing 96 DNA samples

Affymetrix, Inc. Tel: +1-888-362-2447 ■ **Affymetrix UK Ltd.** Tel: +44-(0)-1628-552550 ■ **Affymetrix Japan K.K.** Tel: +81-(0)3-6430-4020
Panomics Solutions Tel: +1-877-726-6642 panomics.affymetrix.com ■ **USB Products** Tel: +1-800-321-9322 usb.affymetrix.com

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P/N DNA01865 Rev. 3

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