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Infinium® ShrimpLD-24 v1.0 BeadChip

A high-powered genotyping tool to advance aquaculture breeding programs of Pacific white shrimp.

Highlights

- **Excellent Call Rates and Accuracy**
  >99% mean call rate and >99.9% reproducibility
- **High-Value Content with Comprehensive Coverage**
  Evenly distributed polymorphic SNPs with 1 cM mean spacing
- **High-Throughput and Flexible Format**
  Up to 24 samples can be genotyped in parallel

Introduction

The Infinium ShrimpLD-24 v1.0 BeadChip (Figure 1) enables genomic selection and evaluation for family identification within Pacific white shrimp (*Litopenaeus vannamei*) to advance aquaculture breeding programs. The array contains over 6400 genome-wide single nucleotide polymorphisms (SNPs), validated using family brood stock from multiple existing breeding programs (Table 1). The SNP panel has been built for a production environment, tested for association with economically important traits (Quantitative Trait Loci or QTL), and evaluated for predictive performance to facilitate economical, family-based breeding decisions. The 24-sample BeadChip and the proven Infinium HD assay enable automated, high-throughput genotype calling for production-scale genomic selection and family structure testing for Pacific white shrimp.

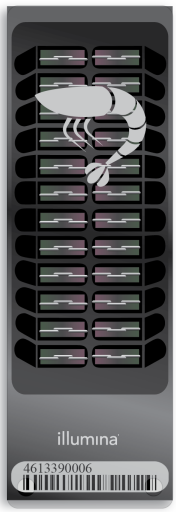

Figure 1: Infinium ShrimpLD-24 v1.0 BeadChip—The Infinium Shrimp LD-24 v1.0 BeadChip enables family structure testing for Pacific white shrimp.

Table 1: Product Information

Feature	Description
Species	*Litopenaeus vannamei*
Total Number of Markers	6465
Capacity for Custom Bead Types	80,000
Number of Samples per BeadChip	24
DNA Input Requirement	200 ng
Assay	Infinium HD
Instrument Support	iScan® or HiScan® System
Sample Throughput[a]	5760 samples / week
Scan Time per Sample	iScan System: 2.5 min HiScan System: 3.5 min

L. vannamei Unrelated Individuals	Content		
	MAF > 5%	MAF > 2.5%	MAF > 1%
	6200	6267	6286

Data Performance	Value	Product Specification
Call Rate[b]	99.4%	> 99%
Reproducibility[c]	100%	> 99.9%
Mendelian Inconsistencies[d]	<0.0001	< 0.1%

Interlocus Distance[e]			
Distance (cM)	Mean	Median	90th%
	2.76	1.5	6.6

a. Estimate assumes 2 iScan Systems, 1 Autoloader 2.x, 3 Tecan robots, and a 5-day work week.
b. Value based on 484 unrelated indiviuals.
c. Value based on 22 replicates.
d. Value based on 629 parent-child pairs and 43 parent-parent-child trios.
e. Values based on 4390 mapped markers (excluding 0 cM instances).

Abbreviations: cM, centimorgan; MAF, minor allele frequency.

Content Design Strategy

The Infinium ShrimpLD-24 v1.0 BeadChip was built in collaboration with researchers from James Cook University, Australia. Developers strategically selected informative markers within the *L. vannamei* genome from a dataset of over 350,000 putative variants. SNPs were stringently filtered using the following criteria: 1) prioritize common variants over rare variants, 2) minimum read depth (to ensure accurate MAF estimates), 3) maximum read depth (to avoid duplicated regions), 4) map position, and 5) SNP flanking sequence quality. Publicly available and validated content from published sources is also included (Table 2).

Content Sources

- A privately funded SNP discovery project involving sequencing of 30 representative individuals from multiple commercial and industry domesticated shrimp breeding lines
- A validated SNP and EST dataset from the *L. vannamei* genetic linkage map project[1]
- A combination of putative and validated SNP content identified through bioinformatic and resequencing studies[2]

Add-On Research Content

Content on the Infinium ShrimpLD-24 v1.0 BeadChip was validated using samples representing industry broodstock. Illumina scientists retained additional content that can be made available to researchers looking to interrogate biologically relevant content that will inform improvements in the genome build, but that are not suitable for a production environment (Table 2). These performance and content validation results clearly demonstrate robust data quality and an attention to research as well as industry needs.

Table 2: Infinium ShrimpLD-24 v1.0 BeadChip Content

Content Category	Number of SNPs
Validated Content	
Ciobanu et al, 2010	145
Du et al, 2009	137
NGS Discovery Novel SNPs	
Mapped Content	4390
Unmapped Content	1793
Total Production Content	6465
Non-Production Research Content	373
Total in Manifest	6838

Scanning and Automation Options

The iScan System offers the flexibility to meet a variety of throughput needs. Automating assay processing with a liquid-handling robot and Autoloader 2.x reduces hands-on time and enables scanning to occur 24 hours per day. Scanners and components are modular, creating a tunable system that can be configured to match any scale of project.

High Quality Data

The SNP content on the Infinium ShrimpLD-24 v1.0 BeadChip were subjected to rigorous functional testing against over 2000 samples representing industry broodstock to ensure strong performance using the Infinium HD assay. Every Infinium ShrimpLD-24 v1.0 BeadChip offers >99% call rate across the *L. vannamei* genome, ensuring high-quality and accurate data for genomic prediction.

Summary

Developed in collaboration with experts in aquaculture, the Infinium ShrimpLD-24 v1.0 Beadchip contains over 6400 evenly spaced markers. These strategically selected and stringently filtered markers provide an overview of the *L. vannamei* genome enabling production applications. The 24-sample Beadchip combined with the proven Infinium HD assay present a powerful, high-throughput solution for genomic selection and family structure testing in the Pacific white shrimp.

Learn More

To learn more about the Infinium ShrimpLD-24 v1.0 BeadChip and other Illumina genotyping products and services, visit www.illumina.com/techniques/popular-applications/genotyping.html

Ordering Information

Product Name	Catalog No.
Infinium ShrimpLD-24 v1.0 Kit (48 samples)	20013012
Infinium ShrimpLD-24 v1.0 Kit (288 samples)	20013013
Infinium ShrimpLD-24 v1.0 Kit (1152 samples)	20013014
Infinium ShrimpLD-24 v1.0 FTS	20013015

References

1. Du ZQ, Ciobanu DC, Onteru SK, et al. A gene-based SNP linkage map for pacific white shrimp, *Litopenaeus vannamei*. *Anim Genet*. 2009;41(3):286-294.
2. Ciobanu DC, Bastiaansen JW, Magrin J, et al. A major SNP resource for dissection of phenotypic and genetic variation in Pacific white shrimp (*Litopenaeus vannamei*). *Anim Genet*. 2010;41(1):39-47.

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