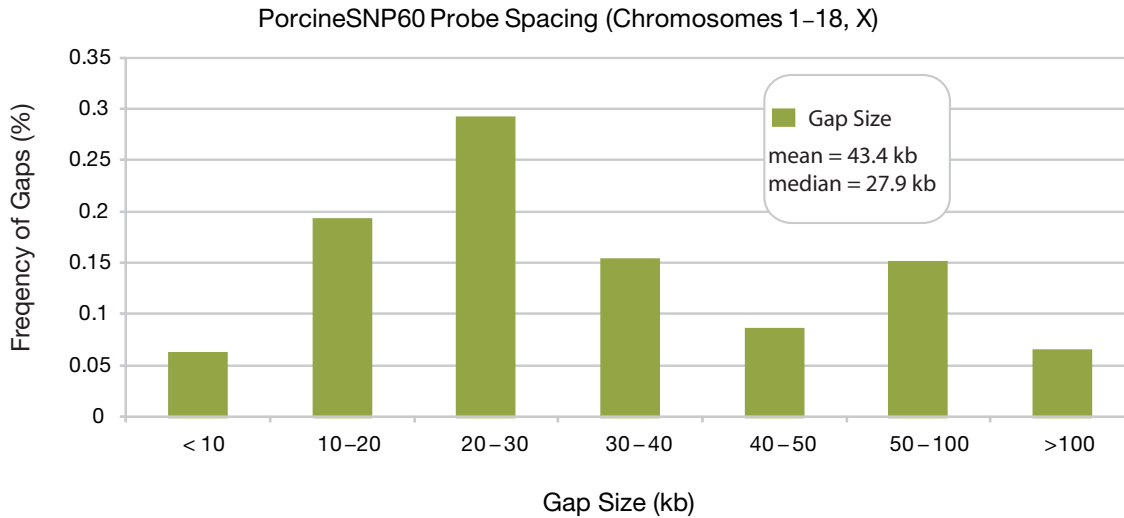


Figure 2: PorcineSNP60 BeadChip Probe Spacing



The PorcineSNP60 BeadChip provides uniform coverage across the porcine genome.

porcine-human comparative map and their position on BAC-based fingerprinted contigs (FPC) map.

High-Quality Data

The 62,163 SNPs on the PorcineSNP60 BeadChip were subjected to rigorous functional testing on multiple breeds to ensure strong performance using the Infinium HD assay. High call rates and accurate genotype calls are required for successful whole-genome association studies. Since complex traits often have relatively small gene effects, potential associations can be missed if the assayed SNP in linkage disequilibrium with the SNP of interest has a low call rate or incorrect genotype call. Illumina ensures that every PorcineSNP60 BeadChip offers > 99% average call rate across common breeds.

Table 1 shows the results from internal validation testing of the PorcineSNP60 BeadChip content using samples provided by collaborators and the Porcine HapMap Consortium. Illumina scientists and collaborators identified and retained 2,596 loci that appear to have an adjacent polymorphism or deletion among the breeds sampled. Although these loci yielded lower call rates when compared to most loci on the panel, they were retained because they may provide biologically relevant information, especially between breed groups. These performance and content validation results clearly demonstrate the robust

Table 1: PorcineSNP60 BeadChip Performance and Specifications

Parameter	Results	Product Specification
Average Call Rate*	99.8%	> 99%
Reproducibility	100%	> 99.9%
Mendelian Inconsistencies	0.08%	< 0.1%

* Based on genotyping 554 reference samples.

data quality delivered by the product. With such high data quality, the PorcineSNP60 BeadChip provides researchers the highest accuracy and reliability for interrogating porcine genotypes in numerous porcine breeds.

Illumina Solutions for Genotyping

The PorcineSNP60 BeadChip is compatible with the BeadArray™ Reader, iScan, and HiScan™SQ systems. These array scanners feature high-performance lasers and powerful optical systems that enable rapid scan times and precise assay detection. The HiScanSQ system can also perform Illumina sequencing by synthesis chemistry, the world's most widely adopted next-generation sequencing platform.

The convenient modular design enables researchers to easily build out the system for evolving research needs. An optional Laboratory Information Management System (LIMS) is available to accurately and efficiently track samples. Robotic automation capabilities can be added to improve throughput for labs processing large numbers of samples. With the Infinium assay workflow, data are processed directly into Illumina's GenomeStudio® software to provide streamlined genotype calling, analysis, and reporting. Researchers can also choose to use Illumina's convenient FastTrack Genotyping service to have samples genotyped and data delivered in a format suitable for GWAS or QTL analysis.

Product Summary

Developed through collaboration between Illumina scientists and leading porcine thought leaders, the PorcineSNP60 BeadChip features more than 62,000 evenly spaced SNPs that provide comprehensive coverage of the porcine genome, enabling a diverse range of genetic research applications. This 12-sample BeadChip, along with the proven Infinium HD Assay, presents a powerful high-throughput solution for whole-genome studies for many porcine breeds.

Table 2: PorcineSNP60 BeadChip Content Validation

Breed	Samples	Polymorphic Loci*	Median MAF	Mean MAF
Birkshire	58	38,573	0.13	0.21
Duroc	76	41,845	0.18	0.20
Hamshire	63	43,496	0.19	0.20
Landrace	76	49,946	0.25	0.24
Large White	132	51,447	0.27	0.26
Meishan	30	30,289	0.07	0.14
Pietrain	87	48,094	0.23	0.23
Synthetic (Large white and Pietrain)	6	39,806	0.17	0.19
Wild boar	20	45,942	0.22	0.22
Other	6	N/A	N/A	N/A
All	554	55,210	0.28	0.29

* MAF > 0.05

Table 3: PorcineSNP60 BeadChip Content Sources

Source	PorcineSNP60 Probes
Wageningen University; Illumina GA sequences ⁴	43,582
Wageningen University; Illumina GA sequences – pilot experiment ⁵	3,422
DIAS	1,202
INRA	2,528
ISU	37
MARC ⁶	12,121
Roslin/Sanger	324
UMB, Norway	35
Other	981
Total	64,232

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