illumina®

CanineHD BeadChip

More than 170,000 evenly spaced and validated SNPs derived from the CanFam2.0 assembly.

CanineDH BeadChip Highlights

- **Unrivaled Call Rates and Accuracy:**
  > 99% average call rates and 99.99% reproducibility
- **Comprehensive and Uniform Coverage:**
  Genome-wide coverage using over 170, 000 evenly spaced markers placed on the CanFam2.0 reference sequence
- **Simple Workflow:**
  PCR-free protocol with the powerful Infinium HD Assay
- **High-Throughput Format:**
  Up to 12 samples can be interrogated in parallel

Introduction

Dogs are arguably man's greatest invention[1], originally domesticated from grey wolves as long as 100,000 years ago. Selective breeding over the last few centuries has led to an incredible amount of biological diversity among modern domestic dog breeds, as they display a wide range of physical traits and behaviors[2]. However, breeding methods and recent bottlenecks experienced in the domestic dog have unintentionally resulted in a high prevalence of specific diseases, including cancers, heart disease, epilepsy, and hip dysplasia.[2] Since humans and canines share a number of common diseases, the domestic dog has been an increasingly important model for understanding the genetic component of human disease.[3] Recent discoveries have also shown that selective breeding has led to large haplotype blocks being carried into the canine genomes. These large genomic regions are ideal for canine genome-wide association studies, where far fewer markers are required to identify genetic disease associations compared human studies. The unique breeding history of the domestic dog offers the research community a powerful opportunity for unraveling the genetic basis of disease, behavioral and morphological traits, and mammalian variation.

In 2005, researchers at the Broad Institute completed the current assembly of the canine genome, CanFam2.0.[3] The Canine Genome Sequencing Project produced a high-quality draft sequence of a female boxer named Tasha. The assembly of Tasha's genome was used to compare sequence data of other key breeds.[2] From these efforts over 2.5 million high quality SNPs have been identified.

The CanineHD Genotyping BeadChip contains more than 170,000 markers placed on the CanFam2.0 reference sequence. Illumina has developed the BeadChip in collaboration with the LUPA Consortium, which includes 22 European universities and other partners such as the Broad Institute. Featuring highly polymorphic SNP content and providing uniform genomic coverage, the CanineHD BeadChip enables the interrogation of genetic variation in any domestic dog breed. Importantly, this BeadChip presents an average of greater than 70 markers per megabase (Mb), providing ample SNP density for robust within-breed association and copy number variation (CNV) studies. In addition, across-breed haplotypes in dogs range between 10-100kb, suggesting that genetic risk factors may be shared across breeds. The dense CanineHD marker set increases the ability to detect across-breed trait and risk factor signals.

The combination of Illumina's proprietary assay technologies, unconstrained locus selection, and high-throughput format presents the most comprehensive solution for whole-genome studies in the domestic dog.

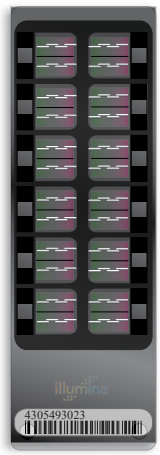
SNP selection strategy

The SNP content featured on the CanineHD BeadChip was selected from the Dog Genome Project 2.5 million SNP set. In addition, 1696 SNPs were identified using a hybridization-based targeted resequencing method of SNP discovery within gaps in the SNP map. SNPs were selected from a diverse set of breeds and picked to represent as many different breeds as possible, while maintaining coverage of ~70 SNPs per Mb. This content selection strategy empowers confident disease mapping in all dog breeds, as can be seen by the successful validation in 26 diverse breeds. (Table 2).

High-Quality Data

The CanineHD BeadChip is powered by the proven Infinium HD Assay, providing the industry's highest call rates, flexible content, and precise CNV detection. The SNPs on the CanineHD BeadChip were subjected to rigorous functional testing across all 26 breeds to ensure strong performance using the Infinium HD Assay. Whole-genome

Figure 1: CanineHD BeadChip



The CanineHD Genotyping BeadChip features more than 170,000 evenly-spaced SNPs across the entire dog genome.

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
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CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
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GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGACG
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association studies are successful, in part, due to high call rates and accurately called genotypes. Since complex disease traits often have relatively small gene effects, potential associations may be missed if the assayed SNP in linkage disequilibrium with the disease SNP has a low call rate or incorrect genotype call. Illumina ensures that every CanineHD BeadChip offers > 99% call rate on samples meeting the recommended input requirements. This includes samples that were collected from buccal swabs.

Table 1 shows the results from Illumina's internal validation of the CanineHD BeadChip. During development of the BeadChip, loci were identified and retained that appear to have an adjacent or third polymorphism (e.g., deletion or third allele) among the breeds sampled. Although these loci yield lower call rates when compared to the other loci on the panel, they were retained because they may provide biologically relevant information for traits of interest and for future improvements in the genome build.

More than 90% of the SNPs on the CanineHD BeadChip are polymorphic across the samples that were interrogated for product quality testing (Table 2). The average minor allele frequency (MAF) across all 26 breeds is 0.23, while the breed-specific MAFs range from 0.13 to 0.21 (Table 2).

Illumina Solutions for Genotyping

The high-quality data and low per-sample cost of the CanineHD BeadChip are part of the powerful Illumina Whole-Genome Genotyping Solution. In addition, optional automation and the Laboratory Information Management System (LIMS) lower costs by eliminating errors associated with manual processing. Illumina genotyping products can be accessed via Illumina Fast Track Genotyping Services or one's own iScan system. Illumina solutions provide industry-leading levels of accuracy, flexibility, and affordability.

References

1. Coren S (2008) The Modern Dog: A Joyful Exploration of How We Live with Dogs Today. Free Press 288pp.
2. Lindblad-Toh K, Wade CM, Mikkelsen TS, Karlsson EK, Jaffe DB, et al. (2005) Genome Sequence, comparative analysis and haplotype structure of the domestic dog. Nature 438(8): 803-819.
3. Chase K, Carrier DR, Adler FR, Jarvik T, Ostrander EA, et al. (2002) Genetic basis for systems of skeletal quantitative traits: principal component analysis of the canid skeleton. Proc Natl Acad Sci USA 99: 9930-9935.
4. http://www.ncbi.nlm.nih.gov/genome/guide/dog/

Additional Information

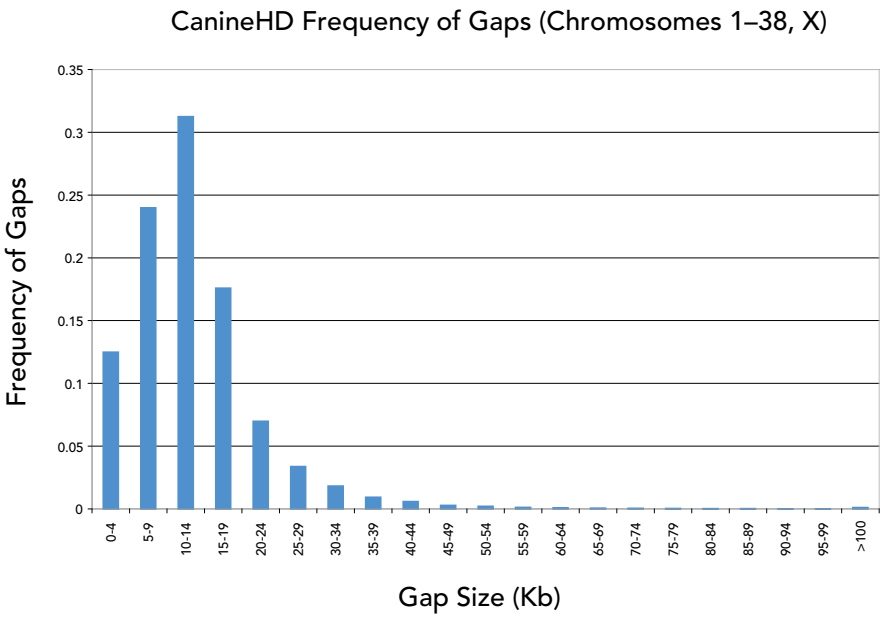
To learn more about Illumina's genotyping solutions, please visit www.illumina.com.

Table 1: CanineHD BeadChip Performance Data and Specifications

Parameter	Percent	Product Specification
Average Call Rate	99.80%	> 99%
Reproducibility	> 99.9%	> 99.9%
Mendelian Inconsistencies	0.002%	< 0.1%

Results based on 435 DNA samples including 18 replicates and 27 trios across 172,115 loci.

Figure 2: CanineHD BeadChip Probe Spacing



The CanineHD BeadChip provides uniform coverage across the entire genome.

Table 2: Diversity of Breeds Used to Evaluate CanineHD BeadChip

Breed	# of DNA samples	Call Rate*†	Polymorphic Loci (MAF ≥ 0.05)	Average MAF
Beagle	10	99.80	115,254	0.17
Belgian Tervuren	16	99.83	104,987	0.17
Bernese Mountain Dog	12	99.82	90,276	0.15
Border Collie	9	99.79	122,895	0.18
Brittany Spaniel	12	99.83	115,629	0.19
Cocker Spaniel	14	99.79	113,082	0.18
Dachshund	12	99.78	118,943	0.20
Dalmatian	7	99.82	113,425	0.17
Elkhound	12	99.80	115,411	0.19
English Bulldog	12	99.84	86,573	0.14
English Setter	12	99.82	106,909	0.17
Eurasian	12	99.76	106,752	0.17
Finnish Spitz	12	99.78	96,674	0.16
German Shepherd	12	99.74	93,864	0.15
Golden Retriever	15	99.77	114,278	0.18
Greenland Sled Dog	12	99.77	85,193	0.13
Greyhound	11	99.84	97,562	0.16
Jack Russell Terrier	12	99.81	126,387	0.21
Labrador Retriever	14	99.81	119,140	0.19
Nova Scotia Duck Tolling Retriever	40	99.81	108,811	0.17
Poodles	11	99.80	122,433	0.21
Rottweiler	12	99.83	95,217	0.15
Shar Pei	11	99.75	109,599	0.18
Standard Poodle	12	99.81	120,422	0.20
Weimeraner	26	99.79	94,108	0.15
Yorkshire Terrier	12	99.82	116,526	0.19
Total among all breeds	**352**	**99.80**	**143,889**	**0.23**

* Call rates across sample set include loci that appear to have deletion or third polymorphism.

† The CanineHD BeadChip was also validated with 12 samples of Alopex (Fox), indicating approximately 1400 markers that appeared to segregate. This resulted in a call rate of 98.81.

AAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCA
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Ordering Information

Catalog No.	Product	DESCRIPTION
WG-440-1001	CanineHD Whole Genome Genotyping Kit (for 48 Samples)	Each package contains four BeadChips and reagents for processing 48 samples.
WG-440-1002	CanineHD Whole Genome Genotyping Kit (for 288 Samples)	Each package contains 24 BeadChips and reagents for processing 288 samples.
WG-440-1003	CanineHD Whole Genome Genotyping Kit (for 1152 Samples)	Each package contains 96 BeadChips and reagents for processing 1152 samples.
FT-310-1236	CanineHD FastTrack Service Project	Illumina's FastTrack Services requires a minimum of 94 samples and 1.5 µg of DNA for each sample.

Each CanineHD Genotyping BeadChip can process twelve samples in parallel and assay 172,155 markers per sample

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