Mouse Low Density and Medium Density Linkage Panels

Mouse Low Density (LD) and Medium Density (MD) Linkage Panels from Illumina® enable high-quality SNP genotyping for various mouse genetics studies.

Highlights Of The Mouse LD And MD Linkage Panels

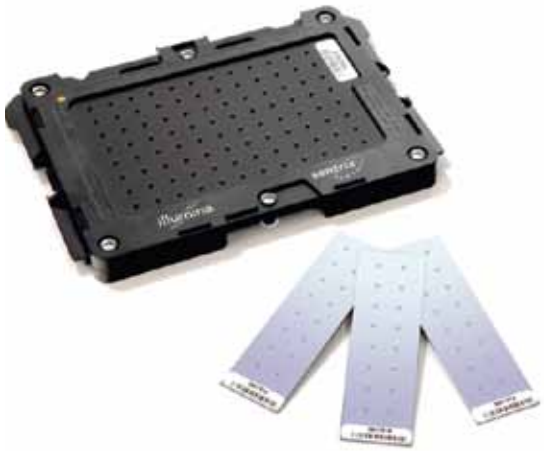
- **High-Quality Data:**
  SNP loci assayed using proven GoldenGate® technology
- **Flexible Approach:**
  optimized panels for various mouse genetics applications
- **High Throughput:**
  access genome-wide coverage quickly and efficiently

Introduction

The mouse has been increasingly recognized as an optimal genetic system for the study of the genetics of complex disease traits. Studies using experimental crosses between inbred animal strains have been successful in mapping quantitative trait loci (QTLs) with effects on a number of different phenotypes. Higher resolution SNP maps may provide opportunity to reduce QTL intervals and thus narrow the search region for candidate genes. With the completion of the mouse genome project, the number of validated mouse single nucleotide polymorphisms (SNPs) has increased dramatically. Greater than 13,000 SNPs have been genotyped across 480 mouse strains using the Illumina GoldenGate® Assay and the Illumina BeadStation. This SNP set is available from the Wellcome-CTC Mouse Strain SNP Genotype Set1. The Mouse LD Linkage Panel consists of 377 loci and has been optimized for application to N2 and F2 mouse genetics crosses, those typically used for mapping QTLs. The Mouse MD Linkage Panel consists of 1,449 loci and is optimal for various mapping applications that include characterization of transgenic, congenic and knockout animals, and genetic mapping in advanced intercross mouse lines.

Illumina's Mouse MD and LD Linkage Panels consist of thoroughly screened and validated SNP loci that have been selected from the Wellcome-CTC Mouse Strain SNP Genotype Set. Both the Mouse LD and MD Linkage Panels offer a low-cost and efficient method for mapping candidate genes, increasing genotyping throughput and obtaining genome-wide genetic data for the identification of QTLs.

Figure 1: Low Or Medium Density Panels Are Deployed In Sentrix® Array Formats



Low Density (LD) or Medium Density (MD) SNP assays for mouse genetic studies can be deployed on the multi-sample Sentrix® Array Matrix or Sentrix BeadChip, up to 96 samples in parallel

Comprehensive Genomic Coverage

Ilumina's Mouse LD Linkage Panel has 377 SNP loci chosen to maximize genetic information across the top ten inbred strains routinely used for mouse crosses (Table 1). More information about these inbred

Table 1: Top Ten Inbred Strains Used To Choose SNP Content In Mouse LD And MD Linkage Panels

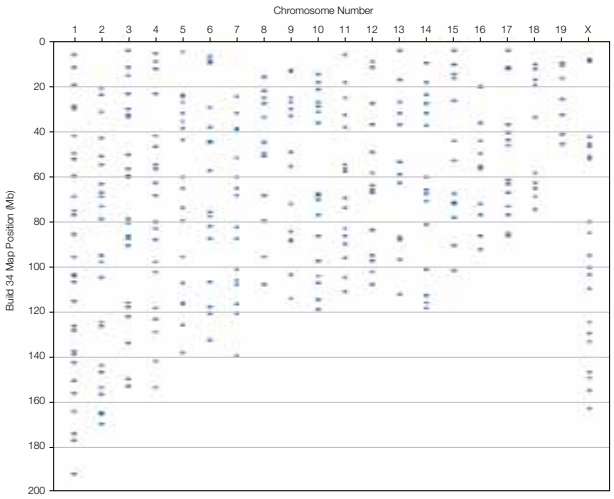
Ten Common Inbred Strains	
129S1/SvImJ	CBA/J
AKR/J	DBA/2J
BALB/cJ	FVB/NJ
C3H/HeJ	NOD/LtJ
C57BL/6J	SJL/J

Table 2: Mouse Linkage Panels-Data Quality

Panel	No. SNPs	No. Samples	Call Rate	Reproducibility*
Mouse LD Linkage	377	232	99.82%	100%
Mouse MD Linkage	1449	236	99.97%	100%

*Data obtained from 20 replicate DNA samples

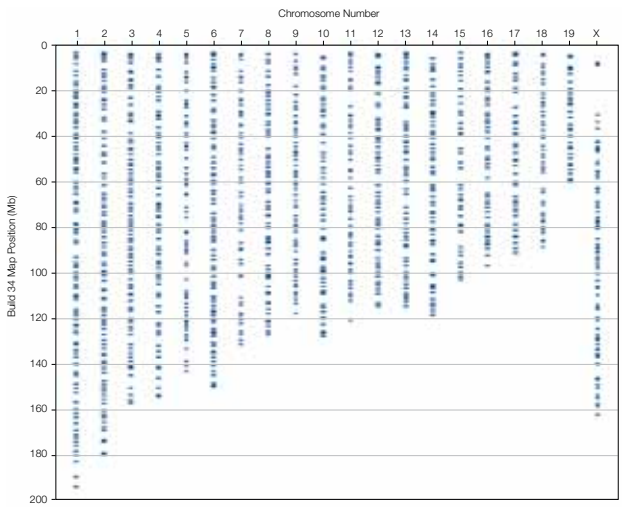
Figure 2: Mouse LD Linkage Panel Genome Coverage



Genome coverage of Mouse LD Linkage Panel by chromosome. Approximately four SNPs per 27 Mb interval across the genome were chosen for the panel.

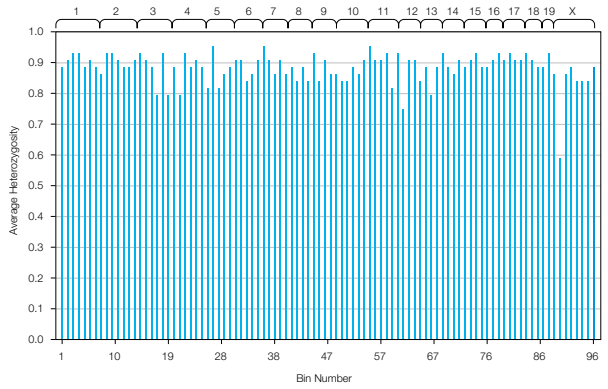
strains is available at the Jackson Laboratory web site2. This panel was designed to include approximately four SNPs per each 27 Mb interval across the entire mouse genome. At least one SNP in each interval was chosen to be informative in crosses involving the C57Bl/6J strain. On average, at least one SNP in each interval is informative for 85% of all possible strain combinations (Figure 2). The theoretical

Figure 3: Mouse MD Linkage Panel Genome Coverage



Genome coverage of Mouse MD Linkage Panel by chromosome. Approximately three SNPs per 5 Mb interval across the genome were chosen for the panel.

Figure 4: Average Heterozygosity In Mouse LD Linkage Panel (4 SNPS/BIN)

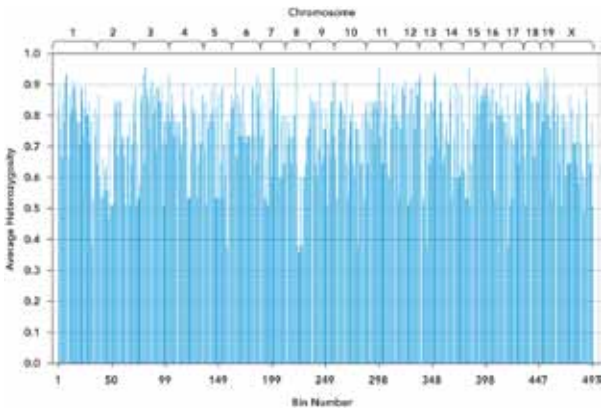


Average heterozygosity content by bin for the Mouse LD Linkage Panel is shown. The genome was divided into 96 bins containing an average 4 SNPs per bin. Average heterozygosity is shown for all pairwise comparisons for 10 common inbred strains within each bin.

number of markers needed to analyze F2 and N2 genetic crosses is 80-100 SNP loci. This panel provides approximately 175-200 informative markers per cross and covers the entire mouse genome.

Illumina's Mouse MD Linkage Panel includes 1,449 SNP loci that were again chosen to maximize genetic information across the top ten inbred strains at a higher resolution than our low density panel. SNPs in this panel were chosen to first provide uniform genome distribution at a density of approximately three SNPs per five megabase intervals across the genome. At least one SNP per interval was chosen to be informative for crosses involving the C57Bl/6J strain and the remain-

Figure 5: Average Heterozygosity in Mouse MD Linkage Panel (3 SNPS/BIN)



Average heterozygosity content by bin for the Mouse MD Linkage Panel is shown. The genome was divided into 497 bins containing an average 3 SNPs per bin. Average heterozygosity is shown for all pairwise comparisons for 10 common inbred strains within each bin.

AATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTA
AACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAG
ACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTA
CGTACCATTAAGAGCTACCGTGCAACGAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTA
AATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTA
TTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGACGAA
TATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCA

Ordering Information

Catalog No.	Product	Description
GT-18-121	Mouse LD Linkage Panel (96 Samples, bag)	Mouse LD Linkage Panel is an optimized set of 377 loci for application to N2 and F2 mouse genetics crosses, including mapping quantitative trait loci (QTLs).
GT-18-131	Mouse MD Linkage Panel (96 Samples, bag)	Mouse MD Linkage Panel is an optimized set of 1449 loci for various mapping applications including characterization of transgenic, congenic and knockout animals, and genetic mapping in advanced intercross mouse lines.
GT-95-201	Single-Use Activation Kit (576 Samples)	Used in combination with the GoldenGate Assay Kit. Contains reagents for six, 96-well plates.
GT-95-205	GoldenGate Assay Kit II with UDG (96 Samples)	Sufficient reagent for preparing genotyping reactions for 96 DNA samples. Contains UDG enzyme for contamination control.
FA-12-107	Sentrix Universal-96 Array Matrix	One Sentrix Universal-96 Array Matrix can process 96 samples and up to 384 assays/ sample.
FA-12-109	Sentrix Universal-96 Array Matrix	One Sentrix Universal-96 Array Matrix can process 96 samples and up to 1536 assays/ sample.

ing two SNPs were selected based on allele frequency and optimal spacing. On average, at least one SNP in each interval is informative for 75% of pairwise strain combinations (Figure 3).

SNP map positions of both the Mouse LD and MD Linkage Panels maximize genetic information from crosses involving the top ten inbred mouse strains. Both panels provide even coverage across all twenty mouse chromosomes (Figures 4, 5).

Panel Performance

Both the Mouse LD and MD Linkage Panels were subjected to rigorous functional testing to ensure high-quality, reliable data and suitability for genetic analysis using Illumina's GoldenGate Assay. The testing of both panels was done on a combination of in-house control samples obtained from Jackson Laboratories and samples contributed by scientific collaborators. Samples consisted of pure inbred animals, F1 crosses, F2 crosses and backcrossed animals. A total of 232 samples including 20 replicates were genotyped in the Mouse LD Linkage Panel and 236 samples including 20 replicates in the Mouse MD Linkage Panel. Call rates for both panels were above 99% and reproducibility was 100% for both panels (Table 2).

Illumina Solutions for Mouse Genotyping

The Mouse LD and MD Linkage Panels offer researchers a fast, low-cost, high-throughput, off-the-shelf solution to mouse genetics studies with comprehensive genomic coverage. The high-quality data and low cost-per-genotype of Illumina's Mouse Linkage Panels are made by possible by powerful Illumina technologies that include the GoldenGate Assay with multi-sample Sentrix Array Matrix and BeadChip formats. The highly validated SNP loci and optimal SNP densities are applicable to a variety of mouse genetics applications. Both panels can be accessed via Fast-Track Genotyping Services or with an Illumina Genotyping System.

Reference

1. Wellcome Trust Centre for Human Genetics: http://www.well.ox.ac.uk/mouse/INBREDS
2. The Jackson Laboratory : http://jaxmice.jax.org/info/index.html

Illumina, Inc. • 9885 Towne Centre Drive, San Diego, CA 92121 USA • 1.800.809.4566 toll-free • 1.858.202.4566 tel • techsupport@illumina.com • illumina.com

FOR RESEARCH USE ONLY

© 2010 Illumina, Inc. All rights reserved.
Illumina, illumina*Dx*, Solexa, Making Sense Out of Life, Oligator, Sentrix, GoldenGate, GoldenGate Indexing, DASL, BeadArray, Array of Arrays, Infinium, BeadXpress, VeraCode, IntelliHyb, iSelect, CSPro, GenomeStudio, Genetic Energy, HiSeq, and HiScan are registered trademarks or trademarks of Illumina, Inc. All other brands and names contained herein are the property of their respective owners. Pub. No. 370-2006-006 Current as of 17 Mar 2006

illumina®

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGAGC
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA