Cancer SNP Panel

The Cancer Single Nucleotide Polymorphism (SNP) Panel from Illumina® delivers high-quality data and provides a cost-effective, efficient tool for conducting candidate gene-based association studies in cancer.

INTRODUCTION

The candidate gene approach can be a powerful tool for the identification of genetic associations to complex disease traits. Candidate gene studies using targeted SNPs are faster and more cost-effective than alternative approaches that may require complete re-sequencing of candidate genes or larger studies that require whole-genome genotyping panels. The Illumina Cancer SNP Panel contains > 1,400 SNPs derived from > 400 genes thought to be involved in cancer. The Illumina Cancer SNP Panel provides cancer genetics researchers an efficient, cost-effective tool to conduct candidate gene-based association studies.

Cancer SNP Panel content was selected from the National Cancer Institute's Cancer Genome Anatomy Project SNP500 Cancer Database[1]. The goal of the project is to provide a central resource of newly discovered variants or to validate existing variants by re-sequencing 102 ethnically diverse reference samples.

HIGHLIGHTS OF THE CANCER SNP PANEL

- High-Quality Data: SNP loci assayed using proven GoldenGate® technology
- Relevant Content: coverage of over 400 genes useful for molecular epidemiology studies in cancer
- Efficient Process: simplified sample management and multi-sample processing

TABLE 1: CANCER PANEL DATA QUALITY

Population	Total Samples	Replicates	Trios	Call Rate	Reproducibility	Mendelian Inconsistencies
CEU	95	5	30	99.63%	100%	0.05%
CHB/JPT	94	5	N/A*	99.90%	100%	N/A*
YRI	95	5	30	99.82%	100%	0.01%
Total	**269**	**15**	**60**	**99.78%**	**100%**	**0.08%**

CEU = Utah residents with ancestry from Northern and Western Europe
CHB/JPT = Han Chinese in Beijing, China/Japanese in Tokyo, Japan
YRI = Yoruba in Ibadan, Nigeria
*No parental DNA samples available

TABLE 2: GENOTYPE CONCORDANCE

Dataset	No. Samples	No. Loci	% Concordance
HapMap	269	1030	99.66%
SNP500	102	809	99.90%

PROVEN PERFORMANCE

The SNP assays included on the Cancer SNP Panel were subjected to rigorous functional testing to ensure strong performance and suitability for association studies using Illumina's GoldenGate® Assay. To determine call rate, reproducibility and Mendelian inconsistencies, three populations were studied: Utah residents with ancestry from Northern and Western Europe (CEU), Han Chinese in Beijing, China /Japanese in Tokyo, Japan (CHB/JPT) and Yoruba in Ibadan, Nigeria (YRI; *Table 1*). Genotype concordance was assessed by comparing loci in the Illumina Cancer SNP Panel to genotype data from the SNP500 Cancer Database. Eight-hundred nine loci on the Cancer SNP Panel were tested via sequencing and validated with at least one additional genotyping platform. As shown in *Table 2*, 81,764 out of 81,844 genotypes (99.90%) were concordant between genotypes called using the GoldenGate® Assay-based Cancer SNP Panel and genotypes validated by both sequencing and at least one alternative genotyping platform in a common set of 102 DNA samples. In addition, concordance with the International HapMap Project[2] was extremely high *(99.66%, Table 2)*.

Minor allele frequencies (MAFs) for loci in the same three ethnic groups were determined using the Cancer SNP Panel. The mean MAFs were 0.25, 0.22 and 0.21 for the CEU, CHB/JPT and YRI populations, respectively. The Cancer SNP Panel loci have MAFs within the appropriate range to accurately assess disease associations.

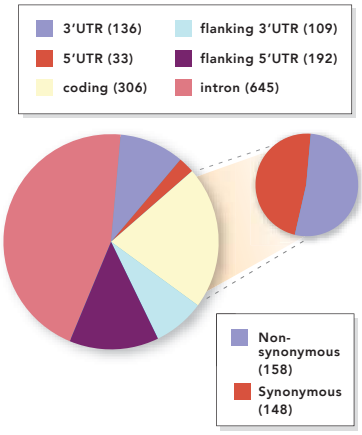
DIVERSE GENE COVERAGE

SNPs in over 400 genes in the SNP500 Database are represented in the Illumina Cancer SNP Panel. SNPs in the panel were chosen to be within 10kb of each gene and to represent several pathways thought to be involved in the etiology of various types of cancers including apoptosis, oncogenesis, tumor suppression and G-protein coupled receptor protein signaling. The distribution of SNPs by gene region includes > 300 coding SNPs of which 158 cause amino acid changes in the resulting protein (*Figure 2*). In the Cancer SNP Panel, > 3 SNP assays were selected, on average, for each gene represented (*Table 3*).

ILLUMINA SOLUTIONS FOR GENOTYPING

The high-quality data and low cost per genotype of the Illumina Cancer SNP Panel are made possible by powerful Illumina technologies that include the GoldenGate Assay with multi-sample Sentrix® Array Matrix and BeadChip formats. Illumina's genotyping solutions enable linkage and association mapping, as well as high-resolution, genome-wide scans. Whether utilizing standard or custom content, Illumina genotyping panels can be accessed via FastTrack Genotyping Services or with an Illumina System. Illumina solutions lead the industry in accuracy, flexibility and affordability.

FIGURE 2: DISTRIBUTION OF SNPS BY GENE REGION



Distribution of SNPs within the Cancer SNP Panel are shown by gene region. The number of SNP assays per region are listed within parentheses.

ORDERING INFORMATION

CATALOG NO.	PRODUCT	DESCRIPTION
GT-17-211	Cancer SNP Panel	One oligo pool (OPA) for 1,421 SNP loci residing in cancer candidate genes sufficient for 96 samples.
GT-95-201	Single-Use Activation Kit (576 Samples)	Used in combination with the GoldenGate Assay Kit. Contains reagents for six, 96-well plates of samples.
GT-95-206	GoldenGate Assay Kit II with UDG (96 Samples)	Prepares genotyping reactions for 96 DNA samples. Contains UDG enzyme for contamination control.
FA-12-109	Sentrix Universal-96 Array Matrix	One Sentrix Universal-96 Array Matrix can process 96 samples and up to 1536 assays/sample.

TABLE 3: SNP COVERAGE PER GENE

Mean SNPs/gene	3.5
Median SNPs/gene	3.0
Minimum SNPs/gene	1
Maximum SNPs/gene	23
Total genes	**408**
Total SNPs	**1421**

On average, > 3 SNPs per gene are included on the Cancer SNP Panel for a total 1,421 SNPs.

REFERENCES

(1) Packer, B.R., Yeager, M., Staats, B., Welch, R., Crenshaw, A., Kiley, M., Eckert, A., Beerman, M., Miller, E., Bergen, A., Rothman, N., Strausberg, R., Chanock, S.J. (2004). SNP500Cancer: a public resource for sequence validation and assay development for genetic variation in candidate genes. *Nucleic Acids Res.* Jan 1; 32 Database issue: D528-32. http://snp500cancer.nci.nih.gov/

(2) The International HapMap Consortium. (2003). The International HapMap Project. *Nature* 426, 789-796. http:/www.hapmap.org

ADDITIONAL INFORMATION

To learn more about the Cancer SNP Panel or other Illumina products and services, visit our website or contact us.

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