



SNP 6.0 Genotyping Service



Asuragen now offers genotyping services based on Affymetrix Genome-Wide SNP 6.0 array. This array provides high-performance, high-powered and low-cost genotyping with highly accurate and sensitive detection of copy number state across the human genome. In combination with Asuragen's service expertise you have the tools to carry out a whole-genome study and bring power to your research.

Key Benefits Include

- Over 1.8 million features
 - More than 906,600 single nucleotide polymorphisms
 - More than 946,000 copy number probes
- Average HapMap concordance exceeds 99.7%
- Approach increases the overall statistical genetic power to detect associations

As a part of SNP 6.0 genotyping service the following analyses are performed:

1. Genotype calls produced using the Birdseed v2 algorithm, developed by the Broad Institute
2. Copy number variation analysis based on the Canary algorithm listing NC state calls. Annotations listed from the Toronto Database of Genomic Variants.

Deliverables

- **Raw data files**
- **Analysis Report includes:**
 - Project Description
 - Intensity QC
 - Genotype Summary
 - Filtered SNP List and SNP Summary Statistics
 - Copy Number QC and Copy Number Segment Summary
 - CHP, CNCHP, CNVCHP files
- **Figures:**
 - Karyoview of each sample representing cytobands depicting gains and losses for each chromosome (.PDF Format)

CA0068	QC, Nanodrop and Gel Electrophoresis, DNA, for aCGH and SNP 6.0
CA0092	Target Preparation, Affymetrix SNP 6.0
CC0380	Affymetrix Genome-Wide SNP 6.0 Array
CA0093	Array Processing and Scanning, Affymetrix SNP 6.0

Contact Asuragen to learn more.