Why Should I Choose The Affymetrix Platform For SNP Analysis?

GeneChip® Mapping Arrays enable linkage, association, and copy number studies at a high throughput level. A platform that supports genomic research on a single Array. It also provides the highest resolution across the genome to detect and define chromosomal aberrations.

The combination of the SNP + CNV Array and Genotyping Console 2.1 provides a great set of tools for researchers who would like to study copy number changes in cancer as well as copy number variation in association studies. The average median SNP + CNV inter-marker distance is 680 base pairs. It also has the highest coverage of known copy number variants (90.5% of 3400 known regions). This gives researchers more power and confidence to detect chromosomal aberrations and makes it easier to define boundaries and breakpoints.
To perform LOH and allele-specific analyses allele-specific copy number is provided. Advantage of including this information is in the ability to differentiate between mechanisms which cause the underlying biological effect. For example, a copy-neutral event is only detectable with this additional information. A copy neutral event is detected as no change in copy number but LOH is present.

Key Features For SNP 6.0 Array

SNP 6.0 Gene Array

- 49 format array
- 5 µm feature size
- PM only
- CN/SNP combined intermarker genome coverage of 680 bp
- 500 ng of total genomic DNA is required per sample
- 3-4 replicated probe pairs per SNP to compensate for the short oligo (25mer)
- contains over 906,600 SNPs. All screened in 500 distinct samples (270 HapMap plus diversity panels)
- The unbiased selection of 494,000 SNPs from 5.0 and 500k tiled on the 6.0
- 482,000 SNPs (historical SNPs from 500k and 5.0) out of the 494,000 SNPs can be analyzed with the default library file and the SNP 6.0 genotyping algorithm (Birdseed)

Selection of additional 424,000 SNPs :

- Tag SNPs
- SNPs from chromosomes X
- Y Chromosome SNPs (257 in default, 900 in full)
- Y Chromosome CN Probes (8,583)
- Mitochondrial SNPs (119 in default, 465 in full)

- 100K New SNPs added to the HapMap database
- SNPs in recombination hotspots

Contains 946,000 Non-Polymorphic Probes

- 202,000 probes targeting 5,677 known CNV regions from the Toronto Database of Genomic Variants
- Regions resolve into 3,182 distinct, non-overlapping segments; on average 61 probes per region
- 744,000 probes, evenly spaced along the genome

Average Minor Allele Frequency (MAF)	19.6% in HapMap Caucasians 18.2% in HapMap Asians 20.6% in HapMap Africans
Average Heterozygosity	26.7% in HapMap Caucasians 24.6% in HapMap Asians 28.5% in HapMap Africans