

Material: Genome-Wide DNA Analysis BeadChips.

Tech data:

- High-throughput multi-sample format for manual processing of 16 samples simultaneously.
- Number of Samples for BeadChip: 4.
- Number of BeadChip for package: 4.
- Number of Markers per sample: around 1,140,000.
- Median space between markers: 1,2 kb (mean intermarker spacing of 2,4 kb).
- Type of marker: within 10 kb of a RefSeq Gene (around 619,000), Non Synonymous SNPs (around 32,100), 100 intervals surrounding genome-wide published peak markers (62,000), rare CNV (5,000) and common CNV.
- Comprehensive and uniform genome-wide coverage (CEU: $r^2 \geq 0.93$ and mean MAF ~ 0.19), high-value regions (MHC, ADME), new content from 1,000 genome project.
- Low quantity of DNA input: 200ng per sample.
- Assay protocol without PCR or ligation steps that enables to target any genomic region with powerful TagSNPs and sensitive CNV detection probes (average stdev of log R ratios < 0.2).
- Automation options available (throughput of up to 576 samples per 5-day week)
- Easy follow-up possible with other complementary GWAS beadchips and custom contents. Exclusive access to the 5 millions markers derived from the ongoing 1000 Genome Projects.
- Suitable to run in the iSCAN / HiSCAN systems (array scanners) from Illumina.
- Data analysis: genotype calls, CNV analysis (including B allele frequency for LOH study) and controls dashboard with GenomeStudio® and additional plug-ins available.
- Genotyping Parameters:
 - Call Frequency: greater than 99%.
 - Reproducibility: around 99.9%.
 - Mendelian Inconsistencies: less than 0.1%.

Cantidad:21

