

Genotyping	
Service Title	Genome-Wide Human SNP 6.0 assay
Workflow Code	AFFY_SNP
Short Service Description	This array contains more than 1.8 million markers of genetic variation of which more than 906,600 are single nucleotide polymorphisms (SNPs) and more than 946,00 probes for the detection of copy number variation (CNV). This single array enables the researcher to detect de novo copy number changes and perform association studies by genotyping both SNP and known copy number polymorphisms.
Base Price (Price per unit)	Price on enquiry
Turn Around Time	5 days per batch of 24
Detailed Description and background	
The following applications are enabled when the SNP 6.0 array is used in conjunction with the Affymetrix Genotyping Console™ - SNP genotyping for association studies, CNP genotyping for association studies and de novo CNV and LOH detection for association studies and cytogenetics research. Positive and negative controls are included to monitor assay performance and possible contamination.	
Service Details	
The recommended sample size for any study is 48. For smaller studies please discuss the details with CPGR. DNA must be of good quality (good 260/280 ratios 1.8 - 2.1; 260/230 ratios >1.8), non-degraded and not contaminated with PCR products. For each sample to be analysed a total of 500ng of DNA is required for the parallel Nsp and Sty assays. Following restriction digests with Sty 1 and Nsp 1, the DNA is ligated to adaptors that recognise the cohesive 4bp overhangs. PCR is carried out using a generic primer to amplify the adaptor-ligated DNA - this assay has been optimized to preferentially amplify fragments in the 200- 1,100 bp size range. The Sty 1 and Nsp1 products are combined and purified and subsequently fragmented, labelled and hybridised to the SNP 6.0 array. Following hybridization, the arrays are washed and stained using the GeneChip Fluidics Station 450 and scanned using the GeneChip® Scanner 3000 7G. The initial analyses is carried out to determine the quality of the data using Genotyping Console. Bioinformatics support is available if required.	
Service Deliverable	
Following initial analyses using Affymetrix Genotyping Console, the raw data files are sent to the client with a data QC report. If required, bioinformatics support can be provided.	
Sample/Info Submission Info	
One sample per array. At least 700 ng of good quality DNA (in RNase free water) is required at a minimum concentration of 70ng/ul, 260/280 ratios 1.8-2.1 and 260/230 ratios >1.80. Samples should be submitted on dry ice with a sample submission form (this will be sent to the client in advance) providing all the sample details required.	
Pricing Details	Price on request
Key Words	Association studies, CNV, LOH, Loss of heterozygosity, copy number variation, DNA
Sample Shipping Address	Institute of Infectious Disease and Molecular Medicine, UCT, Faculty of Health Sciences, Wernher and Beit Building, Level 2, Lab S2.09, Anzio Road, Observatory, Cape Town 7925, South Africa
Related services	Bioinformatics, custom genotyping, GWAS