OpenArray Services

Exploring Next Generation Genomic Services

www.openarray.de

powered by AlphaMetrix Biotech

AlphaMetrix provides a comprehensive range of services and can rely on several years of experience with thousands of processed arrays. Each laboratory step is extensively documented, and the quality control system guarantees highest sample integrity and data quality.

We run multiple gene expression and genotyping platforms for the whole range of prokaryotic and eukaryotic samples.

Different types of samples derived from a variety of origins, including clinical samples can be processed. Samples already successfully processed include blood, buccal swabs, saliva, formalin fixed paraffin embedded (FFPE) tissue, fine needle aspirates, PAXgene tubes, and fresh frozen tissue.

Gene-, Exon- and miRNA- Expression	
Platforms	
Affymetrix	GeneTitan and GeneChip 3000 7G
Agilent	Bubble mixing, 2 micron scanner
Illumina	iScan
Protocols for extraction and amplification:	
· Qiagen	
· PreAnalytix	
· NuGEN Ovation	
· Arcturus RiboAmp	
Protocols for array processing:	
· Affymetrix	
· Agilent	
· Illumina	

Genotyping	
Platforms	
Affymetrix	GeneTitan and GeneChip 3000 7G
Agilent	Bubble mixing, 2 micron scanner
Illumina	iScan
NimbleGen	Maui Hybe Station, Agilent Scanner
Protocols for extraction and amplification:	
· Qiagen	
· PreAnalytix	
· Sigma	
Protocols for array processing:	
· Affymetrix	
· Agilent	
· Illumina	
· Roche/NimbleGen	

We care about small and medium sized projects and individualize your experiments.

We work with a highly qualified team of molecular biologists, geneticists, physicians, and specialists in bioinformatics having significant experience in all varieties of microarray applications.

On the basis of our microarray platforms, we optimize the most suitable array technology exclusively for your project by custom designs, statistical advice on replication and sample numbers as well as state-of-the art data-analysis techniques, ensuring the efficient and effective use of your investment.

	Affymetrix	Agilent	Illumina	Nimble-Gen	Roche	Biotrove
GeneExpression						
3’ Orientation	X					
Whole Genome	X	X	X			
qPCR					X	X
FFPE			X			
miRNA	X		X			
Custom Arrays		X				
Genotyping						
SNP Detection	X		X			X
CGH	X	X		X		
Association	X	X	X			
ChIP-chip				X		
Methylation			X	X		
Sequencing						
Resequencing			X		X	
De Novo			X		X	
ChIP- Seq.			X			
Enrichment		X		X		

Questions you may have

What is the best platform for my experiment?

How long does it take?

There is no array available?

Do I have enough sample?

How many biological replicates do I need?

Can you perform the extraction?

Do I get the raw data?

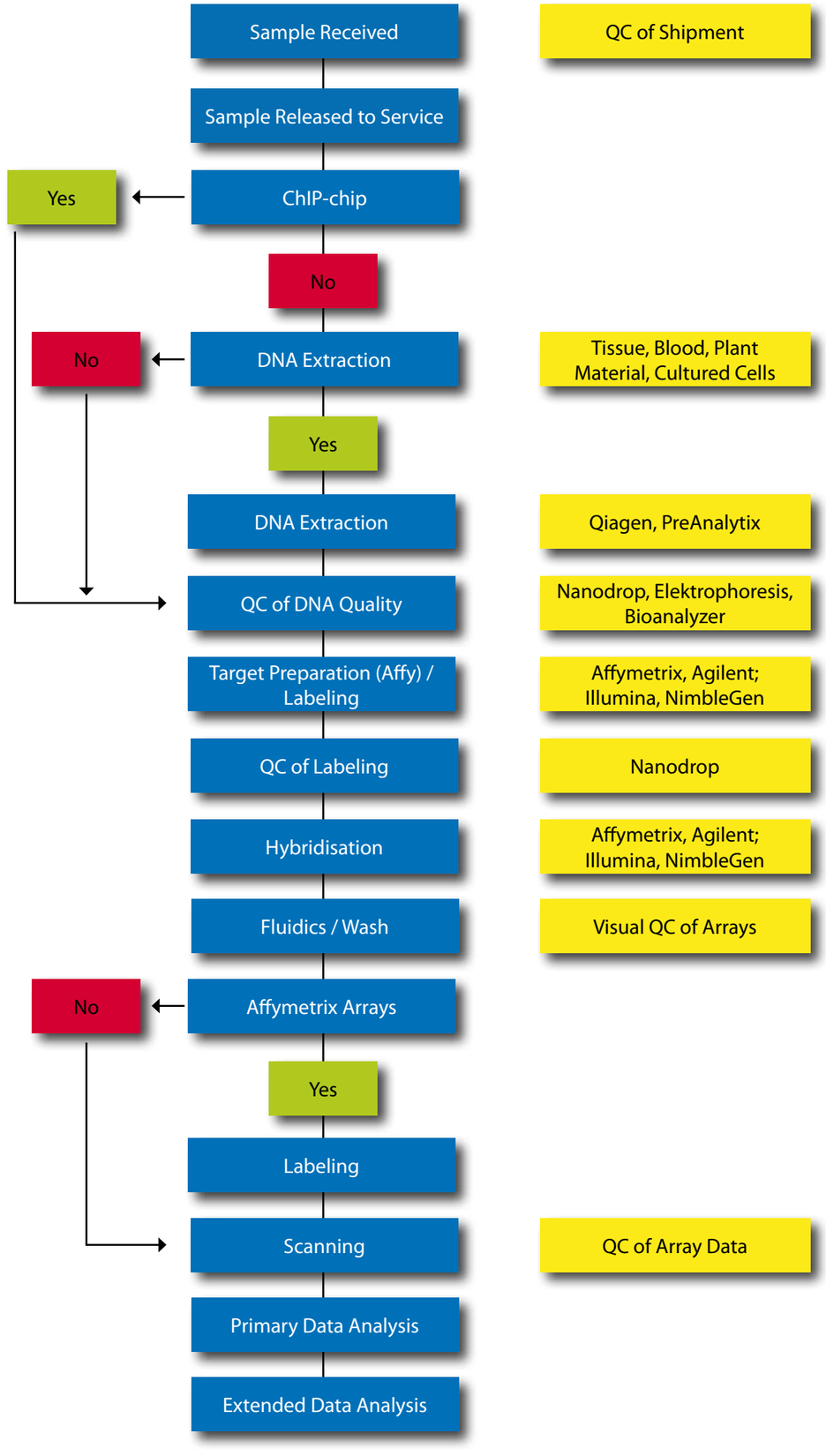
Can you help me with bioinformatics?

I have only few samples, will you process them?

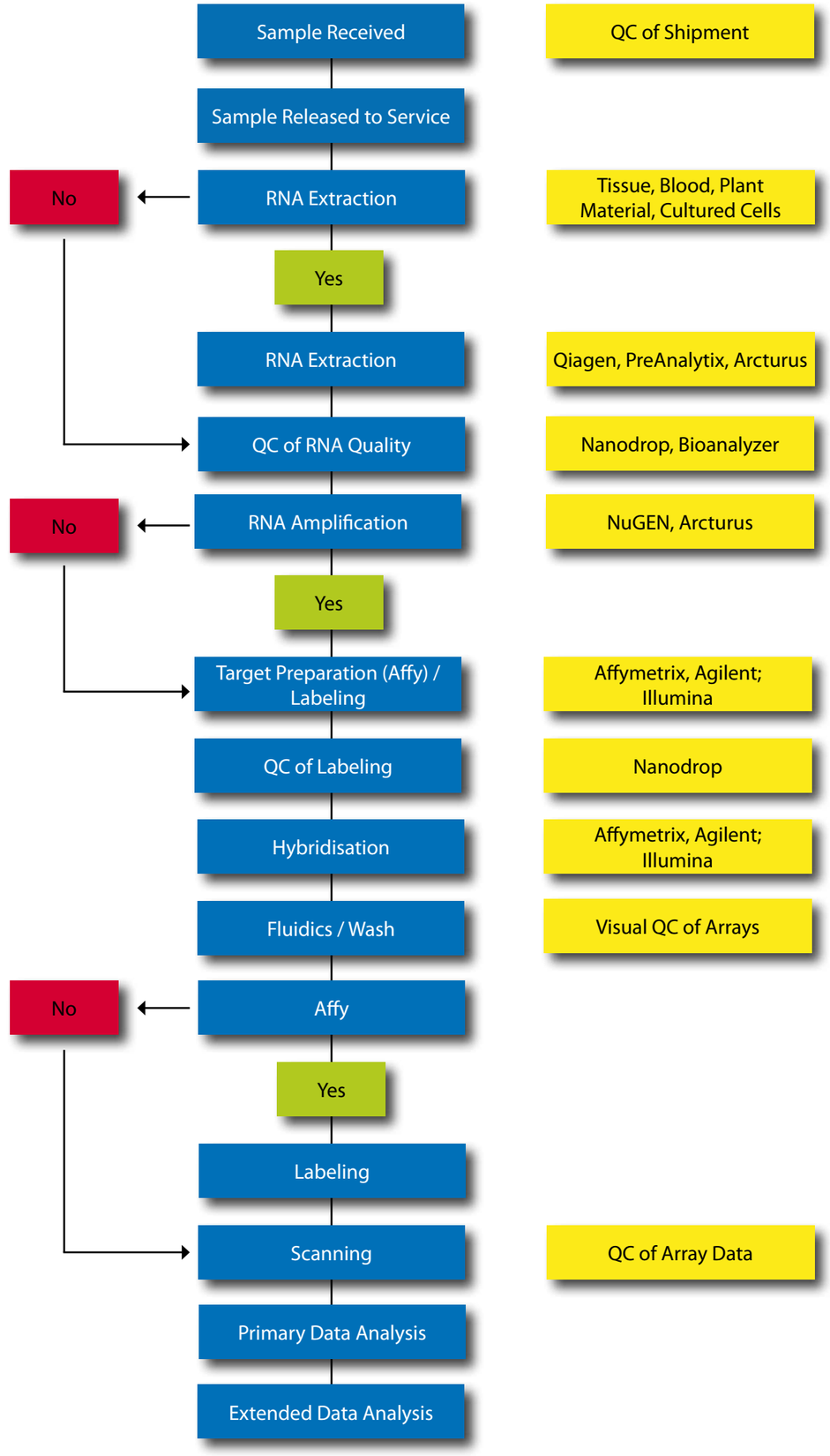
The species I’m interested is just sequenced, can you do an array?

Do you have references?

Genotyping Workflow



Gene Expression Workflow



DNA Array Services

Affymetrix

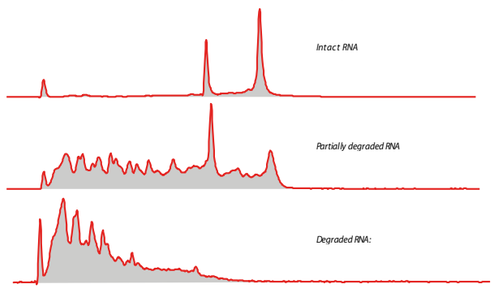
GeneExpression
Affymetrix GeneChips® are the most extensively used microarrays for gene expression profiling. Each transcript is probed with multiple 25-mer oligonucleotides to obtain precise and reliable quantitative data. The GeneChip® family of arrays covers the broadest range of organisms commercially available, including prokaryotes, agriculturally important crops, animals, and all laboratory model organisms. Different array architectures are available that capture specific features of mRNA molecules (3'-arrays, gene arrays and exon arrays).

miRNA
The GeneChip® miRNA Array has the most comprehensive miRNA coverage with 71 organisms on a single array including human, mouse, rat, canine, and rhesus macaque - all important species for research and pharmaceutical drug development. The content of the array is based on the Sanger miRNA database V11 and additional human small nuclear RNAs (snoRNAs and scaRNAs)

Genotyping
Genomic DNA is cut with restriction enzymes and ligated to adapters. A generic primer that recognizes the adapter sequence is used to selectively amplify fragments within a certain size range, thereby reducing the complexity of the genome. The amplified DNA is fragmented, labeled, and hybridized to the array. Advantages of the Mapping Assay technology are the very high number of SNPs which can be interrogated simultaneously (6.0 with >900,000 SNPs), the low amount of genomic DNA needed (250 ng), high call rates (>99%), and high accuracy.

Agilent

GeneExpression
Besides whole genome arrays for human, mouse and rat, Agilent offers a large selection of species specific catalogue arrays (e.g. brassica, rabbit, rice, dog, salmon). These microarrays printed with Agilent's SurePrint technology have all genes and transcripts of the targeted species with one 60-mer oligonucleotide probe representing each sequence. The annotation of the represented genes and transcripts is based on publicly available databases (e.g. RefSeq, Unigene, RIKEN).
Custom array designs can be done on different formats (1x244K, 2x105K, 4x44K, 8x15K).



Genotyping
Agilent's genotyping platform is an integrated solution that gives the resolution and flexibility to perform on a single chip genome-wide as well as customized zoom-in profiling of genomic aberrations, along with simplified experimental design and proven protocols to handle genomic samples with full complexity. Based on 60mer oligonucleotides and a very flexible ink jet printing device, Agilent´s arrays provide a powerful tool for the genome-wide detection of copy number variations (CNVs). The resolution of array-based CGH is up to 150 times better compared to conventional chromosome-based CGH.

Illumina

GeneExpression
Illumina BeadArray technology employs 50-mer oligonucleotides for high selectivity and sensitivity with 100% hybridization-based array QC. High feature redundancy (average 30 beads per transcript) results in high-confidence gene expression measurements.
Two different array types exist for human and mouse samples. Ref-8 arrays probe more than 24,000 well-annotated RefSeq transcripts with 8 samples per slide (12 samples/slide for RatRef-12). The WG-6 arrays contain the entire Ref-8 content plus additional 20,000 confirmed UniGene transcripts with 6 samples per slide (not available for rat). For high throughput projects, the Human-HT-12 array exists with the same content as the Human WG-6 array but lower feature redundancy and 12 samples per slide.

miRNA
We offer genome-wide miRNA profiling for human and mouse samples probing 1146 and 656 miRNAs, respectively, using Illumina's miRNA expression profiling assay. Based on miRBase and recently discovered, novel content, miRNA detection is performed with the sensitive DASL assay. This highly specific assay achieves single nucleotide discrimination between closely related miRNA species and is suitable for FFPE tissue samples. Only 100-200 ng total RNA input is required. Employing universal BeadChips, 12, 16 or 96 samples can be analyzed with a single hybridization.

Genotyping
Illumina´s whole-genome SNP genotyping chips are suited for whole-genome association studies and CNV analyses. The SNP genotyping chips are characterized by excellent call rates (>99%) as well as a high feature redundancy (>20fold). Various multiplex formats (2, 4, 12plex) are available.

Methylation
Genome-wide methylation patterns can be determined with the Illumina Infinium Methylation27 BeadArray, probing ~27.000 CpG Sites in approx. 13,000 loci, including cancer-related genes and miRNA promoters. With 12 samples per slide and minimal DNA input, the system is optimally suited for medium to high throughput methylation projects.

NimbleGen

Genotyping
Roche NimbleGen offers ultra-high resolution CGH/CNV arrays with up to 2.1 million probes for comprehensive analysis of DNA copy number variation. In addition to the 2.1M array format, multiplex arrays are available for higher throughput and cost-effective analysis of either 3 or 12 samples on a single slide. Roche NimbleGen offers several types of CGH/CNV arrays for a variety of organisms to meet your specific research needs:

ChIP-chip
The combination of chromatin immunoprecipitation (ChIP) and high resolution tiling arrays is a powerful approach to identify transcription factor binding sites or chromatin modifications. Successful ChIP depends on numerous factors, such as antibody binding and crosslinking, or chromatin shearing, which often requires thorough optimization. Thus, we offer ChIP-on-Chip as a core service, starting from enriched and amplified DNA after immunoprecipitation. Roche NimbleGen provides the most sensitive ChIP-chip (chromatin immunoprecipitation on chip) microarrays and services on the market. These arrays enable rapid identification of precise binding sites of specific DNA-binding proteins—such as transcription factors, histones, and polymerases—within a target genome, as well as uncover chromatin remodeling in any region of a genome. NimbleGen ChIP-chip microarrays have become the platform of choice supported by an ever-growing list of peer-reviewed publications.

Sequencing Services

Roche 454

The Genome Sequencer FLX System, with long-read GS FLX Titanium chemistry, is the flagship 454 Sequencing platform. Offering more than 1 million high-quality reads per run and read lengths of 400 bases, the system is ideally suited for de novo sequencing of whole genomes and transcriptomes of any size, metagenomic characterization of complex samples, resequencing studies and more. The GS FLX System is at the heart of breakthrough scientific discoveries and hundreds of peer-reviewed publications to date

Illumina

Illumina's Genome AnalyzerIIe offers a powerful combination of accuracy, read lengths, and paired-end insert sizes at a price that is accessible to labs of any size. Illumina's proven sequencing by synthesis technology is based on the streamlined workflow and unmatched performance that has made it the most widely adopted platform worldwide

Whole-Genome Chromatin IP Sequencing (ChIP-Seq)
Illumina ChIP-Seq combines chromatin immunoprecipitation (ChIP) with massively parallel DNA sequencing to identify binding sites of DNA-associated proteins. Illumina ChIP-Seq technology precisely and cost-effectively maps global binding sites for a protein of interest.

qPCR Applications

We offer qPCR service based on latest technology with the Roche Lightcycler© LC480 for 384 well plates and a Qiagen BioRobot for automated plate setup, permitting high throughput qPCR studies for array validation, or as stand-alone experiments. We offer the entire range of qPCR applications to meet your demands. You will benefit from our long-standing experience in qPCR.

• Assay Design and Evaluation
Depending on your needs, experimental questions and study size, we will advise you on the choice of the detection formats. We will also design primers and probes for you. Each assay is optimized and evaluated to obtain optimal specificity and sensitivity.

• Expression Profiling (Relative Quantification of mRNA)
RT-qPCR is considered the gold standard for gene expression studies. After assay development, we will measure raw Cp values for your target genes and a choice of appropriate reference genes. After evaluation of the reference genes, we will calculate normalized expression values.

• Absolute Quantification
Using known standards, a calibration curve is generated to determine absolute copy numbers of your target gene in your sample.

• DNA Copy Number Calculation
Following the same principles as for calculation of relative expression, we apply qPCR to determine gains and losses in genomic DNA compared to a blend of standard genomic DNAs (human) or any reference DNA suitable for your samples.

• Gene Scanning/High-Resolution Melting Analysis
High resolution melting (HRM) analysis is a fast and inexpensive method for genotyping known SNPs or identifying new polymorphisms. DNA methylation status of CpG sites can be determined in bisulphate-treated DNA.

• SNP Genotyping
With the widely used TaqMan® probes, the genotypes of any known SNP can easily be identified.

Data Analysis

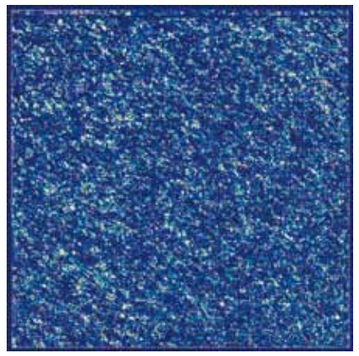
The final step in microarray experiments is the data analysis step, which should answer the biological question asked at the beginning.
This is absolutely vital for a successful study. A standard array analysis is included with each microarray processing. Advanced array analysis is optional on a per study basis.

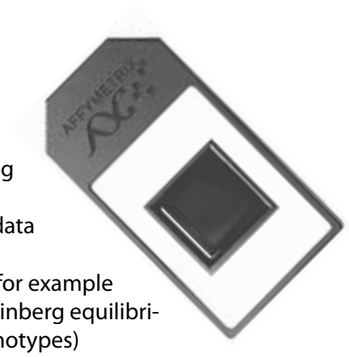
Said this, the analysis strategy should be carefully considered during the planning phase of the experiment. Depending on your specific type of experiment and biological question, our scientific staff offers advice in experimental design and statistical issues. We offer a steadily growing palette of tools to extract meaningful results from your experiment, regardless of whether your data were generated in our laboratory or on another array platform.

Gene Expression/Methylation

Preprocessing and statistical methods:
• Quality control, normalization, summarization
• Parametric tests (t-Test, ANOVA, limma, …)
• Non-parametric tests(Mann-Whitney, Wilcoxon, Rank Products, …)
• Supervised (class prediction) and unsupervised machine learning (clustering)
• Principal Component Analysis

Data mining :
• Gene set enrichment analysis
• Gene ontology and pathway analysis
• Building interaction networks
• Literature mining





Genotyping

Basic genotyping analysis:
• Experimental data processing
• Data filtering (for example using Hardy-Weinberg equilibrium, missing genotypes)
• Genotype calling

Additional and customized services:
• Statistical tests for association (using various models, e.g. dominant / recessive) and sample clustering.
• Visualization and determination of the Linkage Disequilibrium (LD) structure within the genotype data.
• Identify genes and gather all forms of annotation in the genomic regions of interest.
• Integrate genotype data with expression data to identify genomic regions regulating expression.
• Haplotype estimation and haplotype association analysis.
• Genomic structural variation identification, CNV and LOH analysis of SNP microarray data.

More Information on our webpage

Have a look at our web page and be inspired by our integrated solutions. Use our implemented search tool to find the right answer for your questions.

There you will find the latest news about AlphaMetrix and their services. You will be informed about upcoming exhibitions, events and web conferences, where you can contact AlphaMetrix and it's specialists.

For constant information you can apply for our newsletter. Naturally you also find our range of products on the web with detailed information, especially concerning the technical data.

In addition you can download further information as PDF.

www.openarray.de

LIMS for Life Science

DNA

Microarrays

PCR

Cycler

Laser Microdissection

LCM

Array Processing

Array Hybridisation

powered by

AlphaMetrix Biotech

AlphaMetrix
Carl-Zeiss-Straße 41
63322 Rödermark
www.alphametrix.de
Tel. 06074/211 62 40
Fax 06074/211 62 41