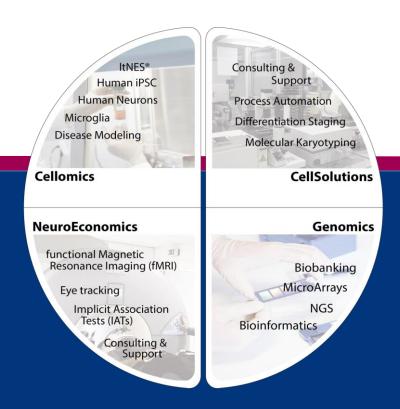
Microarray-Products for SNP-, Methylation-, and Expression-Analysis



Our expertise - your benefit!





LIFE & BRAIN is a biomedical enterprise and commercial hub of the University of Bonn Medical center. LIFE & BRAIN was founded in 2002 and is located at the University Hospital Campus in Bonn, Germany. As a center of innovation, LIFE & BRAIN acts as a revolving door between academic research and industry. Innovative research results are recognized early and developed further into marketable biomedical products and services. Scientific excellence, market-oriented translational research and plans for spinoffs grow together in a network structure supported by creative external collaborations.

Integrating a unique set of expertise in Cellomics, Genomics and NeuroCognition research LIFE & BRAIN aims at delivering the next generation of products for disease modeling and prediction, compound development and tissue regeneration. The combination of technological know-how and scientific excellence makes LIFE & BRAIN the perfect partner for academic and commercial research.





LIFE & BRAIN Genomics is one of the leading service providers for all types of microarray experiments using Illumina and Affymetrix technology in Europe and has long-standing experience in high-throughput generation of "omics" data from biomaterial of humans as well as model organisms. Having a close collaboration with the excellent and internationally renowned Institute of Human Genetics in Bonn, LIFE & BRAIN Genomics is continuously developing new applications and pipelines for state of the art generation and interpretation of these "omics" data.

Thus the combination of technological know-how and scientific excellence make **LIFE & BRAIN Genomics** the perfect partner for academic and commercial research.

Our key fields of expertise are:

- Nucleic acid extraction from blood and tissues
- Genome-wide and targeted SNP genotyping
- Molecular Karyotyping
- Expression profiling
- Methylation analysis
- Bioinformatics













Array-based solution for genotyping, methylation-, mRNA- and miRNA-profiling

Genotyping

➤ Human Infinium family



- 200-500ng gDNA
- 250,000 to 5 million SNPs
- GWAS
- Sample Stratification
- CNV analysis
- Molecular Karyotyping
- NGS Validation

Methylation

➤ Meth EPIC



- > 850,000 sites
- 500ng bisulfit converted gDNA
- FFPE ready
- Compatible to the Meth 450k

mRNA



- > Clariom-S
- ➤ Gene ST
- > Clariom-D
- FFPE ready
- From 10pg RNA

miRNA

➤ miRNA 4.0









Genotyping – the Illumina Human SNP Array family

- high throughput genotyping of up-to-date genomic content
- flexibility to profile 500,000 up to 5 million SNPs genome-wide
- only 200-500ng genomic DNA input
- suitable for Copy Number Variant analysis and Molecular Karyotyping
- can be customized

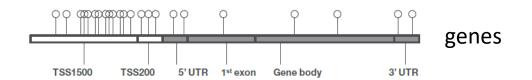


Infinium MicroArray	Samples	Markers	MAF (CEU) covered	% CEU covered		Mean interSNP
millium wicroarray	per Chip	per sample	IVIAF (CEO) COVETEU	1KGP (MAF >5%)	1KGP (MAF >1%)	spacing
Human Omni5Exome	4	>5 million	>1% + rare variants	0.87	0.84	0.63kb
Human Omni2.5Exome	8	>2.5 million	>2.5% + rare variants	0.83	0.73	1.13kb
Human OmniExpressExome	8	> 950.000	>5% + rare variants	0.73	0.58	3.0kb
Human OmniExpress-HTS	24	> 700.000	>5%	0.73	0.58	4.1kb
HumanCoreExome	24	> 480.000	>5% + rare variants	0.59	0.46	5.3kb
Global Screening Array	24	> 640.000	> 0.1%	0.95	0.93	5.0 kb



Methylation analysis –

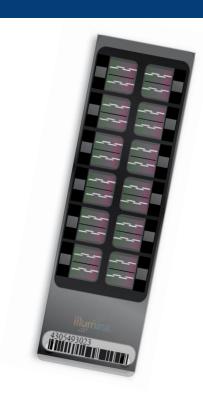
the Illumina Infinium Methylation EPIC Bead Chip





CpG sites

Feature	Covered on array
Total # sites	> 850,000
RefSeq genes	99%
CpG islands	> 95%
Island shores	> 90%
Island shelves	> 80%
HMM islands	> 60K
FANTOM 5 enhancers	> 23K
Predicted enhancers	> 80K
DNase hypersensitivity sites	> 47K





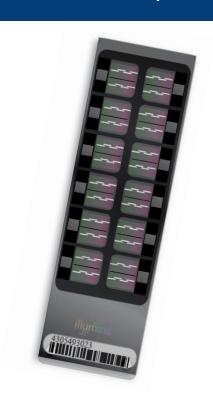
Methylation analysis –

the Illumina Infinium Methylation EPIC Bead Chip

- only 500ng bisulfite converted genomic DNA input
- bioinformatic service available
- special protocol for FFPE samples available

HumanMethylation450 BeadChip	Standard Protocol	FFPE Protocol
Reproducibility (Technical replicates)	r²≥ 98%	r²≥ 98%
Number of sites detected*	≥99%	≥ 95%

^{*}Based on non-cancer samples, recommended sample input amounts of high-quality DNA as confirmed by PicoGreen and following all other Illumina recommendations as per respective User Guides.





Expression analysis –

the Affymetrix Gene ST 2.0 Arrays

- Comprehensive expression analysis incl. Isoforms
- available for mouse, rat and human
- 200 ng RNA input
- Suitable for FFPE samples

Specifications				
	Human	Mouse	Rat	
Oligonucleotide probe length	25-mer probes	25-mer probes	25-mer probes	
Total number of distinct probes	764,885	770,317	722,254	
Interrogated strand	Sense	Sense	Sense	
Resolution (number of probes per gene)	26 (median)	27 (median)	26 (median)	
Estimated number of genes	28,869	28,853	27,342	
Gene-level probe sets with Ensembl support	28,132	27,543	26,008	
Gene-level probe sets with putative full-length transcript support (GenBank and RefSeq)	19,734	19,434	9,916	

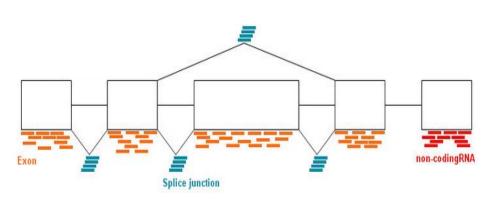


Genomic locus	Classical 3' Assay	WT Assay
Presumed standard transcript	 •	•
Transcripts with undefined 3' end		•
Non-polyadenylated messages		•
Truncated transcripts		•
Alternative polyadenylation sites		•
Degraded samples		•
Genomic deletions		•
Alternative splicing		•
Alternative 5' start sites		•



Expression analysis –

the Affymetrix Transcriptome Array



- Exon skipping
- Mutually exclusive exons
- Alternative 5' donor sites
- Alternative 3' acceptor sites
- Intron retention

Available for human, mouse and rat



Array content summary

Array protein coding content	No.
Genes (transcript clusters)	44,699
Transcripts	245,349
Exons	560,472
Exon clusters	296,058

Array non-protein coding content	No.
Genes (transcript clusters)	22,829
Transcripts	40,914
Exons	109,930
Exon clusters	82,444



miRNA expression analysis –

the Affymetrix miRNA 4.0

- 100% miRBase v20 coverage
- 30,424 mature miRNA (all organisms)
- 5,214 human, mouse, and rat miRNA
- 1,996 human snoRNA, scaRNA
- 3,770 probe sets unique to human, mouse, and rat pre-miRNA hairpin sequences

Array content description	
miRBase	Release 20
Ensembl (BioMart Export)	Release 73
snoRNAbase	Version 3
mirTarbase	Release 4.5
MicroCosm Targets	11/2013
Organisms (including viruses)	203
Total mature miRNA probe sets	30,434
Probes/probe set for mature miRNA	9
Human mature miRNA probe sets	2,578
Mouse mature miRNA probe sets	1,908
Rat mature miRNA probe sets	728
Human snoRNA and scaRNA probe sets	1,996
Human pre-miRNA probe sets	2,025
Mouse pre-miRNA probe sets	1,255
Rat pre-miRNA probe sets	490



Specifications

Performance	
Reproducibility (inter- and intra-lot)	>0.95
Transcripts detected at 1.3 amol in 130 ng	85%
Dynamic range	4 logs
Total RNA input	130-1,000 ng
Probe feature size	11 µm
Probe length	Up to 25-mer



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