Information on Array-CGH diagnostics in our facility

Background information on the method itself:

Array-CGH stands for array based comparative genomic hybridization. It is performed by simultaneous hybridization of differentially labelled sample and reference DNA to probes on a DNA-chip (array). The hybridization pattern to these probes depends on the ratio of respective DNA segment copy numbers in sample and reference. Thus, copy number deviations in the sample are detected. These can either be gains or losses of chromosomal material. The analysis includes a final step, in which it is evaluated, whether or not these distinctive genomic features are of clinical relevance, because among pathogenic abnormalities, the human genome harbors a plethora of benign copy number variations. The number of probes on the array defines the detection limit of imbalances. The more probes it contains, the more exact small imbalances can be mapped in size and location. The smallest detectable imbalance interval is denoted as the respective array resolution.

Overview on diagnostic approaches:

Array-CGH is applied for various clinical questions. With respect to the levels of detection needed for a valid result, we offer analyses on different diagnostic array platforms (BlueGnome, an Illumina company, Cambridge, UK).

	Material	**Array platform**	**Detection limit**
Postnatal analyses	3-5 ml fresh EDTA-blood	CytoChip ISCA 4x180K	Detection of imbalances wider than 90 kb genome-wide, critical genes contain more probes resulting in detection of even smaller intervals (gene dependent)
Prenatal analyses, Aneuploidy detection in losses of pregnancy	Amniocytes, chorionic villi, fresh abortion material, formalin fixed, paraffin embedded abortion material (FFPE)	CytoChip Focus Constitutional	Detection of imbalances of minimal 1 Mb, thus microdeletions, microduplications or imbalances associated with unbalanced translocations are reliably detected

Regarding postnatal analyses:

Array-CGH analyses are performed for patients with clinical suspicion of a microimbalance associated syndrome or a contiguous gene syndrome. These often manifest in a phenotype with developmental or speech delay, as well as signs of dysmorphy. For many syndromes displaying high phenotype variability, a definite diagnosis of a microdeletion or microduplication syndrome is accomplished only after array-CGH.
In cases, in which cytogenetic analysis revealed an unbalanced karyotype, array-CGH can be used for precise mapping of chromosomal breakpoints and further characterization of affected chromosomal segments.
For patients with dysmorphies and balanced structural chromosomal rearrangements, array-CGH might unveal breakpoint associated imbalances and thus, a genetic underlying cause.

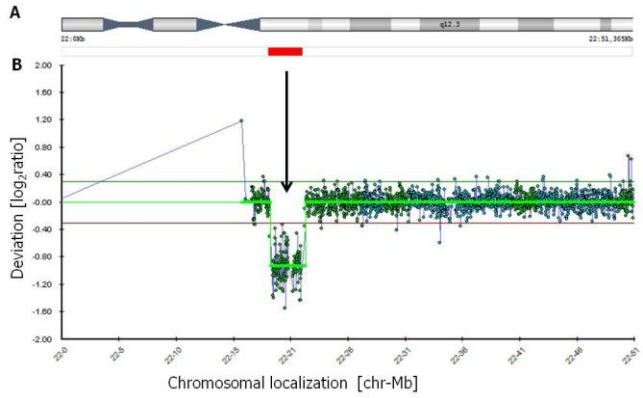
synlab Medizinisches Versorgungszentrum
Humane Genetik München, Zweigniederlassung
der synlab MVZ Augsburg GmbH - synlab.com
CEO: Dr. Bartl Wimmer, Dr. Dr. Mohammad
Naraghi, Andrea Schikora

HypoVereinsbank Stuttgart
Swift-Code HYVEDEMM473
IBAN DE 41 6002 0290 0611 0586 91

Register court
Augsburg HRB 24536
UST-ID DE267015644

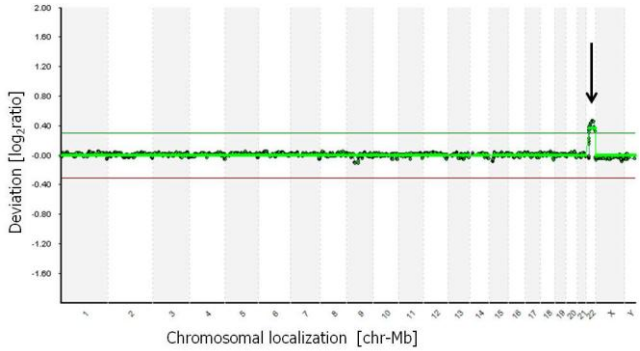
DAkkS Deutsche Akkreditierungsstelle D-PL-13225-01-00
DAkkS Deutsche Akkreditierungsstelle D-ML-13225-01-00

Result of a postnatal analysis displaying a heterozygote deletion 22q11.21 in concordance with the clinical manifestation of 22q11 microdeletion syndrome (DiGeorge syndrome, Shprintzen syndrome):



Panel A: Ideogram of chromosome 22, size and location of the heterozygous loss is indicated by the red bar. The deletion affects the chromosomal band of 22q11.21 and spans an interval of appr. 3.1 million base pairs (Mb).
Panel B: Hybridization profile of chromosome 22-specific probes. The deletion is displayed by probes deviating from normal diploid status (see arrow).

Regarding prenatal analyses and aneuploidy detection in abortion material:



Genome-wide hybridization profile of embryonic DNA from spontaneous abortion. The loss of pregnancy can be explained by trisomy 22, highlighted by the arrow.

Further information:

Please contact us via the Email adress info@humane-genetik.de. We will contact you as soon as possible.

synlab Medizinisches Versorgungszentrum
Humane Genetik München, Zweigniederlassung
der synlab MVZ Augsburg GmbH - synlab.com
CEO: Dr. Bartl Wimmer, Dr. Dr. Mohammad
Naraghi, Andrea Schikora

HypoVereinsbank Stuttgart
Swift-Code HYVEDEMM473
IBAN DE 41 6002 0290 0611 0586 91

Register court
Augsburg HRB 24536
UST-ID DE267015644

DAkkS Deutsche Akkreditierungsstelle D-PL-13225-01-00
DAkkS Deutsche Akkreditierungsstelle D-ML-13225-01-00