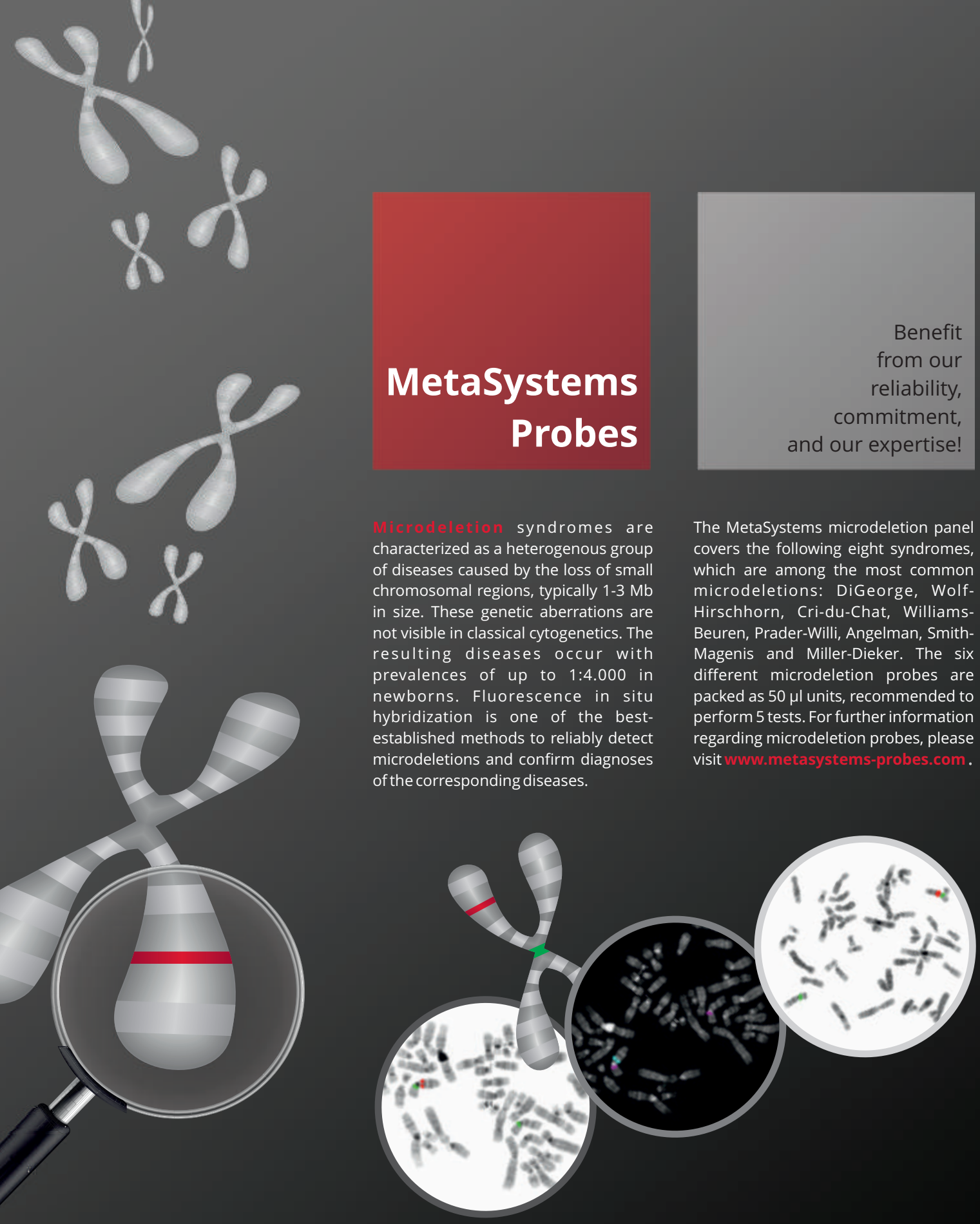
MetaSystems Probes

Benefit from our reliability, commitment, and our expertise!

Microdeletion syndromes are characterized as a heterogenous group of diseases caused by the loss of small chromosomal regions, typically 1-3 Mb in size. These genetic aberrations are not visible in classical cytogenetics. The resulting diseases occur with prevalences of up to 1:4.000 in newborns. Fluorescence in situ hybridization is one of the best-established methods to reliably detect microdeletions and confirm diagnoses of the corresponding diseases.

The MetaSystems microdeletion panel covers the following eight syndromes, which are among the most common microdeletions: DiGeorge, Wolf-Hirschhorn, Cri-du-Chat, Williams-Beuren, Prader-Willi, Angelman, Smith-Magenis and Miller-Dieker. The six different microdeletion probes are packed as 50 µl units, recommended to perform 5 tests. For further information regarding microdeletion probes, please visit **www.metasystems-probes.com** .



MICRODELETIONS

MetaSystems Probes

XL DiGeorge TBX1

(D-5415-050-OG)

The 22q11.2 deletion syndrome (22q11.2DS) includes the DiGeorge- and velo-cardio-facial syndrome and is the most common microdeletion syndrome. Up to 95% of the deletions identified occur de novo and are not inherited. 22q11.2DS related de novo deletions are mediated by non-allelic inter- and intrachromosomal homologous recombination between low copy number repeats on chromosome 22. A deletion of 3 Mb overlapping about 90 genes is detected in the vast majority of 22q11.2DS cases, whereas a smaller fraction is identified with a nested deletion of about 1.5 Mb overlapping with about 55 genes. One of the most thoroughly investigated genes in this region is the T-box transcription factor 1 (TBX1). TBX1 is phylogenetically conserved and has manifold functions during embryonic development. Studies using mouse as a model organism have shown that TBX1 is a key determinant in 22q11.2DS.

XL DiGeorge TBX1 detects deletions in the long arm of chromosome 22. The orange labeled probe hybridizes to the TBX1 gene region at 22q11.21. A green labeled probe hybridizes to the 22cen region and functions as a control probe.

Coming Soon

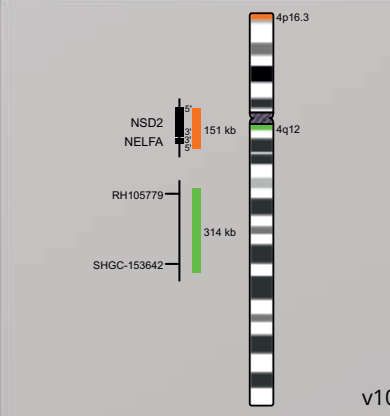
v03.1

XL Wolf-Hirschhorn

(D-5416-050-OG)

The association of partial 4p16 deletions with Wolf-Hirschhorn syndrome (WHS) was first described by Cooper and Hirschhorn in 1961. Most 4p16 deletions in WHS occur de novo, only in the minority of cases the rearranged chromosome is inherited. WHS is a contiguous gene syndrome associated with haploinsufficiency of several closely linked genes. The severity of clinical manifestation depends on the amount of genetic material affected. Two WHS critical regions (WHSCR) have been identified. The classical WHSCR1, spanning 165 kb on chromosomal location 4p16.3, includes the genes NSD2 (nuclear receptor binding SET domain protein 2) and NELFA (negative elongation factor complex member A). WHSCR2 was defined based on the identification of patients with atypical forms of WHS, showing no deletion of WHSCR1. WHSCR2 is located distally to WHSCR1 partially including the gene NSD2, but excluding NELFA.

XL Wolf-Hirschhorn detects deletions in the short arm of chromosome 4. The orange labeled probe hybridizes to the NSD2 (WHSC1) locus at 4p16.3. The green labeled probe hybridizes to a specific locus at 4q12 and functions as a reference probe.



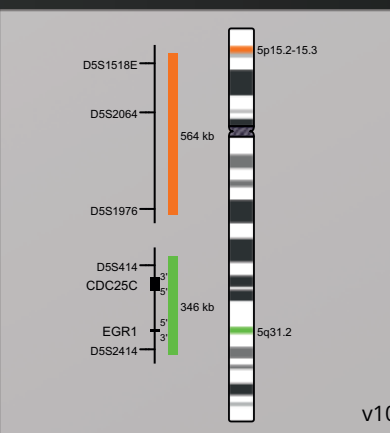
v10.1

XL Cri-Du-Chat

(D-5417-050-OG)

The Cri-du-Chat syndrome (CdCS), or 5p-minus syndrome, was first described by Lejeune et al. in 1963. The name refers to the main clinical feature of the syndrome, a characteristic cat-like cry in early childhood. The majority of patients carry a terminal deletion of the short arm of chromosome 5 with breakpoints ranging from 5p13 to 5p15.2 with a size of up to 40 Mb. Most 5p deletions occur de novo, probably during spermatogenesis. Breakpoints are not well defined and differ between CdCS cases. Only few patients have an interstitial deletion, translocations or other less common aberrations. Patient studies established a link between the size of the deleted region and the CdCS phenotype and identified regions 5p15.2 and 5p15.3 responsible for dysmorphism, mental retardation, and the cat-like cry.

XL Cri-Du-Chat detects deletions in the short arm of chromosome 5. The orange labeled probe hybridizes to a chromosomal locus at 5p15.2-15.3. The green labeled probe hybridizes to a specific locus at 5q31.2 and functions as a reference probe.



v10.1

MICRODELETION

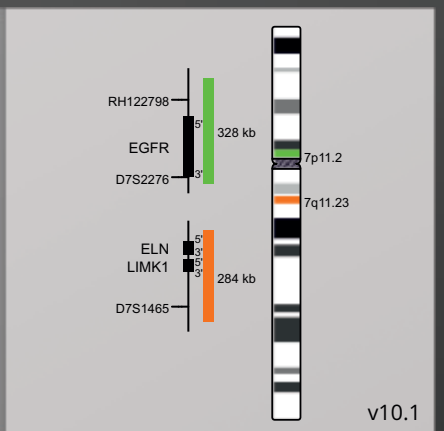
MetaSystems Probes

XL Williams-Beuren

(D-5418-050-OG)

The Williams-Beuren syndrome (WBS) is a contiguous gene deletion syndrome. WBS phenotype is complex, age-dependent and varies between individuals. One of the most fatal and characteristic clinical complications is supravalvular aortic stenosis (SVAS). WBS is associated with a chromosomal microdeletion in region 7q11.23. The common critical region is about 1.6 Mb in size and contains more than 20 genes, including ELN (elastin) and LIMK1 (LIM domain kinase 1). Haploinsufficiency of ELN correlates with cardiovascular problems and is responsible for the SVAS phenotype of WBS patients. Deletions in region 7q11.23 are a consequence of non-allelic homologous recombination between low copy repeat elements flanking the WBS deleted region. Most WBS cases are sporadic, only few cases are transmitted vertically.

XL Williams-Beuren detects deletions in the long arm of chromosome 7. The orange labeled probe hybridizes to the ELN locus at 7q11.23. The green labeled probe hybridizes to a specific locus at 7p11.2 and functions as a reference probe.

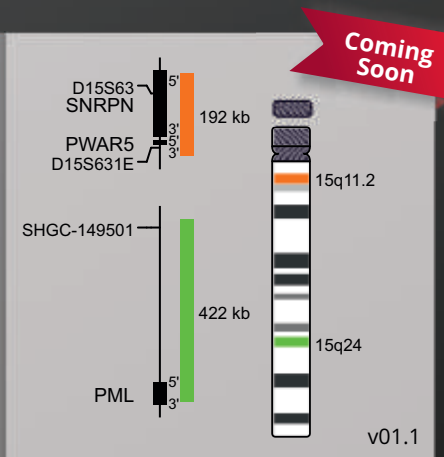


XL Prader-Willi/Angelman

(D-5421-050-OG)

The Prader-Willi syndrome (PWS) and the Angelman syndrome (AS) are complex neurodevelopmental disorders caused by chromosomal deletion of genes in the 15q11-q13 region. In most cases, the corresponding genes are silenced on the sister chromosome via genetic imprinting. The deletion of the paternal segment 15q11-q13 leads to the development of PWS, while patients carrying the maternal deletion of this segment suffer from AS. The most common genetic cause for PWS is the deletion of the paternal 15q11-q13 copy. Maternal uniparental disomy of 15q11-q13 (genes are silenced) or translocations with breaks in the 15q11-q13 region are further mechanisms leading to PWS. Genes located in this region, especially SNRPN (small nuclear ribonucleoprotein polypeptide N) and NDN (necdin) are considered to be crucial for disease development. The absence of the maternal UBE3A (ubiquitin-protein ligase E3A) gene copy located in this segment is critical for the development of AS.

XL Prader-Willi/Angelman detects deletions in the long arm of chromosome 15. The orange labeled probe hybridizes to the SNRPN/PWAR5 locus at 15q11.2. The green labeled probe hybridizes to a specific locus at 15q24 and functions as a control.

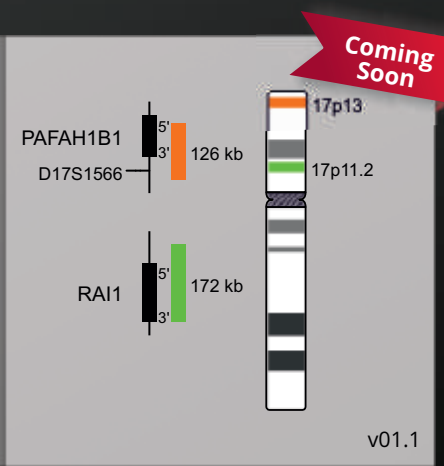


XL Smith-Magenis/Miller-Dieker

(D-5422-050-OG)

While interstitial deletions in the segment 17p11.2 are the genetic basis of the Smith-Magenis syndrome (SMS), deletions of the more distal part 17p13.3 lead to the Miller-Dieker syndrome (MDS). The SMS inducing deletions of 17p11.2 have no preferential breakpoints, but most patients analyzed show deletions smaller than 4 Mb. The key gene responsible for the manifestation of the clinical symptoms of SMS is RAI1 (retinoic acid induced 1), coding for a transcription factor. One of the crucial genes involved in the development of Miller-Dieker lissencephaly and craniofacial dysmorphism is the PAFAH1B1 gene encoding the regulatory subunit of the platelet activating factor acetylhydrolase 1b.

XL Smith-Magenis/Miller-Dieker detects deletions in the short arm of chromosome 17. The orange labeled probe hybridizes to the PAFAH1B1 (Miller-Dieker) locus at 17p13. The green labeled probe hybridizes to the RAI1 (Smith-Magenis) gene region at 17p11.2.



MICRODELETION

MetaSystems
Probes

All Microdeletion Products by MetaSystems Probes

Product	Size	Order No.
XL DiGeorge TBX1	50 µl	D-5415-050-OG
XL Wolf-Hirschhorn	50 µl	D-5416-050-OG
XL Cri-Du-Chat	50 µl	D-5417-050-OG
XL Williams-Beuren	50 µl	D-5418-050-OG
XL Prader-Willi/Angelman	50 µl	D-5421-050-OG
XL Smith-Magenis/Miller-Dieker	50 µl	D-5422-050-OG

For detailed and up-to-date product information please visit
www.metasystems-probes.com/PROBES

If you need customized support please visit
www.metasystems-probes.com/CONTACT

Note

All MetaSystems human FISH probes are classified as IVD products in the EU according to the In-Vitro Diagnostic Medical Device Directive 98/79/EC and are CE labeled, unless otherwise indicated in the product description.

Use all MetaSystems Probes products only within the scope of the intended use.

Some products may not be available in all markets.

Probe map details based on UCSC Genome Browser GRCh37/hg19. Map components not to scale.

Literature

- Edelmann et al (1999) Am J Hum Genet 64:1076-1086
- Jerome and Papaioannou (2001) Nature Genet 27:286-291
- McDonald-McGinn et al (2015) Nat Rev Dis Primers 1:1-19
- Wright et al (1997) Hum Mol Gen 6:317-324
- Zollino (2003) Am J Hum Genet 72:590-597
- Buggenhout (2004) J Med Genet 41:691-698
- Lejeune et al (1963) C R Hebd Seances Acad Sci 257:3098–3102
- Mainarid et al (2001) J Med Genet 38:151-158
- Nguyen et al (2015) Am J Med Genet C Semin Med Genet 169c:224-238
- Wu et al (1998) Am J Med Genet 78:82-89
- Bayés et al (2003) Am J Hum Genet 73:131-151
- Jurado (2003) Horm Res 59 (suppl 1):106-113
- Clayton-Smith and Pembrey (1992) Med Genet 29:412-415
- Butler (2011) Curr Genomics 12(3):204-215
- Kalsner and Chamberlain (2015) Pediatr Clin North Am 62(3):587-606
- Elsea (2008) Eur J Hum Genet 16:412-421
- Blazejewski et al (2018) Front Genet 9:80 (online)
- Falco et al (2017) Appl Clin Genet 10:85-94

MICRODELETIONS

MetaSystems
Probes

MetaSystems Probes

XCyting DNA FISH Probes

EUROPE

Germany, Altlussheim
info@metasystems-probes.com

Italy, Milano
info@metasystems-italy.com

AMERICA

USA, Newton
info@metasystems.org

Argentina, Buenos Aires
info@metasystems-latam.com

ASIA & INDIA

China, Hong Kong
info@metasystems-asia.com

China, Taizhou
info@metasystems-china.com

India, Bangalore
info@metasystems-india.com

Document No. PFS-Microdel-2019-08-01-W
© 2019 by MetaSystems Probes

Magnifier designed by vectorpocket / Freepik.

CONTACT

MetaSystems Probes