Invitae Chromosomal Microarray Analysis (CMA): Disorders Tested

Invitae Chromosomal Microarray Analysis (CMA) analyzes chromosomal abnormalities associated with developmental disorders, including developmental delay (DD), intellectual disability (ID), multiple congenital anomalies (MCA), dysmorphic features, autism spectrum disorders (ASD), seizures, and epilepsy.

Disorders Tested	Disorder Description	PMID	Genes/ Regions
Developmental delay/intellectual disability (DD/ID)	Disorders that begin in childhood and involve difficulties in intellectual functioning and adaptive behavior, and other lifelong disabilities	20466091	Many
Autism spectrum disorders (ASD)	Developmental disorder that impairs the ability to communicate and interact	20466091	Many
Multiple congenital anomalies (MCA)	Structural defects, present at birth	20466091	Many
The following rows contain examples of some of the most common chromosomal abnormalities that result in DD/ID, ASD, and/or MCA. Please note that not all chromosomal abnormalities are represented here.			
Triploidy	Triploidy occurs when an extra haploid set of chromosomes is present, causing the cells to have 69 chromosomes instead of the usual 46. The majority of triploid pregnancies spontaneously abort during early embryonic development. Although rare, triploid pregnancies can survive to birth. Common phenotypic features include: congenital heart defects, neural tube defects, facial and limb anomalies, microcephaly, and an abnormal, cystic placenta (PMID: 15065101).	15065101	Many
Trisomy 21 (Down syndrome)	Down syndrome is a chromosomal condition that is associated with intellectual disability, a characteristic facial appearance, and weak muscle tone (hypotonia) in infancy (PMID: 15510164).	15510164	Genes on chromosome 21
Trisomy 18 (Edward syndrome)	Trisomy 18, historically called Edwards syndrome, is caused by an extra copy of chromosome 18. Trisomy 18 causes problems with many parts of the body and, like other autosomal trisomies, presents an increased risk of pregnancy loss in the prenatal period and decreased life expectancy after birth. The most common features of trisomy 18 include slow growth before birth (intrauterine growth retardation), low birth weight, feeding and breathing difficulties, profound intellectual disability, malformations of the head, face, and bones, clenched hands with overlapping fingers, kidney problems, rocker-bottom feet, and other congenital anomalies. Not all affected individuals have all of these findings. Trisomy 18 is typically due to a sporadic nondisjunction event (PMID: 17266111, 23703053).	17266111 23703053	Genes on chromosome 18
Trisomy 13 (Patau syndrome) or partial trisomy 13q	Common phenotypic features include craniofacial dysmorphism, hexadactyly, urinary tract/kidney anomalies, umbilical/inguinal hernia, intrauterine growth retardation, oligohydramnios, psychomotor delay, hypochromic anemia, splenomegaly, and ocular anomalies (PMID: 20391329, 15889415).	20391329 15889415	Genes on chromosome 13
1p36 deletion syndrome	The most common features of 1p36 deletion syndrome include brain malformation, a short, wide head (microbrachycephaly), distinctive facial features, low muscle tone (hypotonia), swallowing difficulties (dysphagia), deformities of the fingers and/or toes (brachydactyly, camptodactyly), congenital heart defects, developmental delay, behavior issues, and severe intellectual disability. Some affected individuals also have sensory issues, including vision impairment and hearing loss, as well as seizures, abnormal external genitalia, and skeletal and kidney problems (PMID: 26345236).	26345236	Genes on a portion of chromosome 1
1q21.1 duplication syndrome	Reciprocal microdeletions and microduplications involving this region have been associated with variable features including intellectual disability, autism spectrum disorder, and congenital anomalies including macrocephaly in patients with duplications and microcephaly in patients with the reciprocal deletion. In addition, the 1q21.1 duplication has been found to be significantly enriched in schizophrenia cohorts, as well as in tetralogy of Fallot cohorts (PMID: 1902990, 18784092, 26066539, 23018752).	19029900 18784092 26066539 23018752	Genes on a portion of chromosome 1
1q21.1 microdeletion syndrome	Small microdeletions involving the 1q21.1-q21.2 region, but not the thrombocytopenia absent radius (TAR) syndrome critical region (see below), have been associated with a range of developmental disorders including: intellectual disability, autism spectrum disorder, abnormal head size, mildly dysmorphic facial features, and other variable features. Other reported findings include cardiac defects, genitourinary anomalies, skeletal abnormalities, and seizures. However, this region has been known to show copy number variation in healthy, unaffected individuals suggesting reduced penetrance and variable expressivity (PMID: 19029900, 18784092, 22199024, 22317977, 21348049, 17236129).	19029900 18784092 22199024 22317977 21348049 17236129	Genes on a portion of chromosome 1
4pter deletion (Wolf-Hirschhorn syndrome)	The most common features of Wolf-Hirschhorn syndrome (WHS) include low birth weight, poor growth (failure to thrive), low muscle tone (hypotonia), a small head (microcephaly), distinctive facial features, seizures, developmental delay, and mild to severe intellectual disability. Other features of WHS may include problems with the bones, teeth, eyes, heart, and other parts of the body. Not all affected individuals have all of these findings and, depending upon the size of the deletion, the severity of the condition is variable (PMID: 34002939).	34002939	CPLX1, CTBP1, FGFRL1, LETM1, NSD2
5pter deletion (cri-du-chat syndrome)	The most common features of cri-du-chat syndrome include low birth weight, poor growth (failure to thrive), low muscle tone (hypotonia), a small head (microcephaly), distinctive facial features, a high-pitched cat-like cry, developmental delays, and moderate to severe intellectual disability. Other features of cri-du-chat syndrome may include behavior issues, congenital heart defects, and problems with other parts of the body. Not all affected individuals have all of these findings and, depending upon the size of the deletion, the severity of the condition is variable (PMID: 26235846).	26235846	Genes on a portion of chromosome 5
7q11.23 deletion (Williams-Beuren syndrome)	Williams-Beuren syndrome (WBS) is a contiguous gene deletion syndrome also known as Williams syndrome or chromosome 7q11.23 deletion syndrome. Typical features associated with WBS include supravalvular aortic stenosis, intellectual disability, over-friendliness and visuo-spatial impairment, connective tissue abnormalities, and distinctive facial features. Congenital heart disease occurs in 80% of patients, with the majority having supravalvular aortic stenosis (SVAS), and a smaller proportion having a discrete supravalvular pulmonary stenosis. Endocrine features, including hypercalcemia, diabetes mellitus, and subclinical hypothyroidism, have also been reported in individuals with WBS. Typical WBS deletions range in size from 1.5-1.8 Mb, with the breakpoints defined between 72,744,454-74,142,513 (hg19); however, patients with larger and smaller WBS deletion have been reported with variable phenotypes (PMID: 20301427). The GTF2I gene has been linked to the specific cognitive profile, while the ELN gene is responsible for the vascular and connective tissue abnormalities.	20301427	GTF2I, MLXIPL, ELN
7q11.23 duplication syndrome	The reciprocal duplication of the Williams-Beuren syndrome critical region is associated with the 7q11.23 duplication syndrome, which is characterized by a variable phenotype that commonly includes intellectual disability, speech and language delay, developmental delay, minor dysmorphic features, and an increased incidence of hypotonia and congenital anomalies such as heart defects, diaphragmatic hernia, and cryptorchidism. Almost half (46%) of individuals with 7q11.23 duplication syndrome have dilation of the ascending aorta (PMID: 26610320). A variety of behavioral issues have also been reported, including autism spectrum disorder, anxiety disorders, and attention deficit hyperactivity disorder (ADHD). In some cases, the duplication has been found to be inherited from a healthy parent.	26610320	Genes on a portion of chromosome 7
11q partial monosomy syndrome (Jacobsen syndrome)	Jacobsen syndrome is a contiguous gene disorder caused by terminal deletions of 11q that can range in size from 7 to 20 Mb, with the proximal breakpoint at 11q23.3. The most common features of Jacobsen syndrome include pre- and post-natal growth retardation, thrombocytopenia or pancytopenia, craniofacial dysmorphism, and intellectual disability. Larger deletions are frequently associated with a greater number and severity of clinical features, while patients with smaller deletions may only present with intellectual disability and craniofacial dysmorphisms (PMID: 26285164).	26285164	Genes on a portion of chromosome 11

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Disorders Tested	Disorder Description	PMID	Genes/ Regions
14q11-q22 deletion syndrome	Chromosome 14q11-q22 deletion syndrome is characterized by multiple phenotypic features including microcephaly, hypotonia, poor growth, mental retardation with poor eye contact, and hypoplasia of the corpus callosum. Dysmorphic features, when reported, were mild and variable, including short nose, long philtrum, and flat nasal bridge (PMID: 21744488).	21744488	Genes on a portion of chromosome 14
14q22 deletion syndrome (Frias syndrome)	Frias syndrome is characterized by short stature, mild exophthalmia, palpebral ptosis, hypertelorism, short square hands with minimal proximal syndactyly, and small broad great toes (PMID: 24311462).	24311462	BMP4
15q13.3 deletion syndrome	Deletions of this region have been reported in association with a highly variable phenotype, which includes a spectrum of neurobehavioral/neuropsychiatric issues, intellectual disability, seizures, variable dysmorphic features, and autism spectrum disorder. However, these deletions have also been found in the phenotypically normal parents of affected children, suggesting that they are associated with both variable expressivity and incomplete penetrance. Recent studies have implicated haploinsufficiency of CHRNA7 as the cause of several key features of the 15q13.3 deletion syndrome including the intellectual disability, seizure, and autism spectrum disorder phenotypes (PMID: 22775350).	22775350	CHRNA7, OTUD7, KLF13
15q24 deletion syndrome	Phenotypic features associated with 15q24 deletion syndrome include mild to moderate developmental delay, hypotonia, growth deficiency, dysmorphic facial features, genital malformation in males, hand and eye anomalies, and joint laxity (PMID: 34922566).	34922566	SIN3A
15q26 duplication (overgrowth syndrome)	Terminal duplications of 15q encompassing the IGF1R gene are associated with overgrowth, distinct facial features, and intellectual disability. Renal anomalies have also been reported, including renal agenesis, horseshoe kidney, and hydronephrosis (PMID: 12404101; 26689622; 22030053; 19133692).	12404101 26689622 22030053 19133692	IGF1R
15q26-qter deletion syndrome	Deletions of 15q26-qter have been associated with variable phenotypes, including intrauterine growth retardation, microcephaly, micrognathia, renal anomalies, lung hypoplasia, congenital heart disease, hearing loss, and delayed growth and development (PMID: 23603061; 18194513). These deletions overlap the CHD2 gene, which is associated with autosomal dominant childhood-onset epileptic encephalopathy. Deletions of CHD2 have been reported in individuals with developmental delay/intellectual disability, epileptic encephalopathy, and autism spectrum disorders (PMID: 27274247). Therefore, neurodevelopmental abnormalities are also expected.	23603061 18194513 27274247	CHD2 and other genes on a portion of chromosome 15
16p11.2 deletion syndrome	Individuals with deletions of this region may present with developmental delay, intellectual disability, psychiatric and behavioral issues, and autism spectrum disorder. In addition, 16p11.2 deletions are associated with a variable spectrum of additional clinical findings including seizures, macrocephaly, structural brain abnormalities, obesity, and vertebral anomalies. 16p11.2 deletions can be de novo or inherited and are subject to incomplete penetrance and variable expressivity (PMID: 33667823).	33667823	SH2B1 and other genes on a portion of chromosome 16
16p11.2 duplication syndrome	Duplications involving the chromosome 16p11.2 region have been reported to confer substantial susceptibility to speech and developmental delay, autism, behavior abnormalities, and seizures. In addition, there may be an increased risk of scoliosis and vertebral anomalies. Incomplete penetrance and variable expressivity of clinical findings in patients with these genomic abnormalities has been noted (PMID: 27207092).	27207092	Genes on a portion of chromosome 16
16p13.11 deletion and duplication syndromes	Recurrent deletions and duplications of this region are considered risk factors for neurodevelopmental disease including autism, intellectual disability, epilepsy, and learning difficulties. In addition, 16p13.11 duplications have been associated with developmental delay, behavioral problems, schizophrenia, dysmorphic features, short stature, congenital heart defects, and skeletal manifestations (PMID: 21150890). However, 16p13.11 deletions and duplications can be de novo or inherited and are subject to incomplete penetrance and variable expressivity. There appears to be a male bias in the penetrance of the neurodevelopmental features associated with 16p13.11 copy number variations, resulting in an increased likelihood of neurodevelopmental abnormalities in males with CNVs of 16p13.11 compared to females with CNVs of 16p13.11 (PMID: 23637818). In addition, 16p13.11 duplications may be a risk factor for adult-onset thoracic aortic aneurysms and dissections (TAAD), as this region includes the MYH11 gene, which itself is associated with familial TAAD (PMID: 21698135).	21150890 23637818 21698135	MYH11
16p13.3 duplication syndrome	Individuals with 16p13.3 duplication syndrome present with variable intellectual disability, speech problems, behavioral issues, dysmorphic features, mild arthrogryposis, hand abnormalities, and occasionally, other congenital anomalies involving the heart, genitalia, palate, or eyes (PMID: 23063576).	23063576	CREBBP
17p12 deletion (hereditary neuropathy with liability to pressure palsies (HNPP))	Heterozygous deletions of PMP22 are associated with hereditary neuropathy with liability to pressure palsies (HNPP). HNPP is characterized by repeated focal pressure neuropathies such as carpal tunnel syndrome and peroneal palsy with foot drop, although there is large clinical variability (PMID: 20301566; 24646194). Other possible features include muscle weakness and atrophy, reduced tendon reflexes, and pes cavus foot deformity (PMID: 20301566). The initial episode often occurs in the second or third decade, though symptoms can present anytime from childhood to late adulthood and can range in severity.	20301566 24646194	PMP22
17p12 duplication (Charcot-Marie-Tooth disease type 1A (CMT1A))	Duplications of PMP22 are associated with autosomal dominant Charcot-Marie-Tooth disease type 1A (CMT1A). CMT1A is a demyelinating peripheral neuropathy characterized by distal muscle weakness and atrophy, sensory loss, and slow nerve conduction velocity (PMID: 10869062; 15765265; 15703022). Symptoms are usually slowly progressive and often associated with additional features including pes cavus foot deformity, and bilateral foot drop (PMID: 21944474). Onset of symptoms typically occurs between approximately 5 and 25 years of age, although the onset can range from infancy to the fourth decade.	10869062; 15765265; 15703022	PMP22
17q11.2 deletion syndrome	Patients with 17q11.2 deletions involving NF1 and adjacent genes often show variable facial dysmorphism, intellectual disability, developmental delay, an excessive number of early-onset neurofibromas, and an increased risk for malignant peripheral nerve sheath tumors. Additionally, deletions and truncating variants involving the RNF135 gene are associated with autosomal dominant overgrowth, macrocephaly, and facial dysmorphism syndrome; haploinsufficiency of RNF135 likely contributes to the overall phenotype seen in patients with 17q11.2 deletions (PMID: 34168676).	34168676	NF1, RNF135
17q12 deletion syndrome (renal cysts and diabetes syndrome (RCAD))	17q12 deletion syndrome is characterized by structural or functional abnormalities of the kidney and urinary tract, maturity-onset diabetes of the young type 5 (MODY5), and neurodevelopmental or neuropsychiatric disorders including global developmental delay, intellectual disability, autism spectrum disorder, schizophrenia, and bipolar disorder. However, this syndrome shows variable expressivity and incomplete penetrance. The HNF1B gene encompassed in this deletion is associated with autosomal dominant renal cysts and diabetes syndrome and has been established as the cause of the renal, urogenital, and endocrine abnormalities that occur as part of the recurrent 17q12 deletion syndrome (PMID: 27409573).	27409573	HNF1B and other genes on a portion of chromosome 17

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17q12 duplication syndrome	17q12 duplication syndrome is associated with a broad range of phenotypic features that include an increased risk of intellectual disability, developmental delays, behavioral abnormalities, and seizures. Approximately one third of individuals have eye or vision problems; cardiac and renal anomalies occur in rare cases. Notably, 17q12 duplications have also been found in unaffected family members of affected patients, suggesting incomplete penetrance and/or expressivity (PMID: 27409573, 23307502).	27409573 23307502	HNF1B and other genes on a portion of chromosome 17
17q21.31 deletion syndrome (Koolen-De Vries syndrome)	17q21.31 deletion syndrome is associated with variable phenotypes including low birth weight, neonatal hypotonia, oromotor dyspraxia, developmental delay and learning disability, behavioral problems, epilepsy, heart defects (ASD, VSD), and kidney/urological anomalies (PMID: 26306646).	26306646	KANSL1 and other genes on a portion of chromosome 17
18p deletion syndrome	Overlapping 18p deletions of various sizes are associated with chromosome 18p deletion syndrome,which is characterized by intellectual disability, growth delay, short stature, varying abnormalities of the limbs, genitalia, eyes, heart and brain, and specific craniofacial dysmorphisms including microcephaly (PMID: 18284672). Holoprosencephaly has been reported in cases with 18p deletions encompassing the TGIF1 gene (PMID: 23850725; 24091065).	18284672 23850725 24091065	TGIF1 and other genes on a portion of chromosome 18
19p13.13 deletion syndrome, Malan syndrome and Sotos syndrome 2	Chromosome 19p13.13 deletion syndrome is characterized by psychomotor and language delay, intellectual disability, overgrowth, macrocephaly, and ophthalmologic and gastrointestinal findings including strabismus, optic nerve atrophy or hypoplasia, and abdominal pain and vomiting (PMID: 20613546). Of note, deletions and nonsense variants in the NFIX gene, which is located in this region, have been associated with a Sotos-like overgrowth syndrome known as Malan syndrome or Sotos syndrome 2, which is characterized by tall stature, intellectual disability and/or macrocephaly (PMID: 27688808).	20613546 27688808	NFIX and other genes on a portion of chromosome 19
19p13.13 duplication syndrome	Patients with partial trisomy of 19p spanning 19p13.3 have been reported with clinical features including intrauterine growth restriction, profound psychomotor delay, microcephaly, epilepsy, sensorineural hearing loss, dysmorphic facial features, and urogenital malformations. Primary immunodeficiency and skeletal malformations have also been reported (PMID: 24431329, 25858326, 23897601).	24431329 25858326 23897601	Genes on a portion of chromosome 19
22q11 tetrasomy (Cat eye syndrome)	Cat eye syndrome is characterized by the combination of coloboma of the iris and anal atresia with fistula, downslanting palpebral fissures, preauricular tags and/or pits, and frequent occurrence of heart and renal malformations. Cat eye syndrome is often due to tetrasomy of proximal 22q [inv dup(22)(q11)], most often in the form of a supernumerary dicentric bisatellited chromosome (PMID: 7912885; 6785205; 11693792).	7912885 6785205 11693792	Genes on a portion of chromosome 22
22q11.21 deletion syndrome (DiGeorge)	The most common features of 22q11.2 deletion syndrome include an opening beneath the tissue in the roof of the mouth (submucosal cleft palate), feeding difficulties, distinctive facial features, congenital heart defects, a reduced amount of calcium in the blood (hypocalcemia), and immune deficiency that leads to recurrent infections. Other features of 22q11.2 deletion syndrome may include low muscle tone (hypotonia), kidney problems, mild short stature, developmental delays, mild to severe intellectual disability, speech impairment, behavior issues, attention deficit hyperactivity disorder (ADHD), and social difficulties. Not all individuals with 22q11.21 deletion syndrome have all of these findings, and the severity of the condition is variable. Some individuals are so mildly affected that they are never clinically diagnosed. 22q11.2 deletion syndrome may occur sporadically (de novo) or may be inherited from a parent (PMID: 27189754).	27189754	TBX1
22q11.21 duplication syndrome (reciprocal to DiGeorge)	The chromosome 22q11.21 duplication syndrome manifests a highly variable phenotype that may include intellectual and/or learning disability, delayed psychomotor development, growth delay, and/or hypotonia. Additional clinical features overlapping those of DGS/VCFS have also been reported in some individuals with 22q11.21 duplications, including congenital heart defects, urogenital abnormalities, and velopharyngeal insufficiency (PMID: 18707033; 18076674; 19254783; 20301749). However, a significant fraction of cases have been reported to be familial, suggesting reduced penetrance and variable expressivity (PMID: 18414210).	18707033 18076674 19254783 20301749 18414210	TBX1
22q13 duplication syndrome (SHANK3)	A hyperkinetic neuropsychiatric disorder has been attributed to interstitial duplication of chromosome 22q13 including SHANK3 (PMID: 24153177). Mild to moderate intellectual disability, autism spectrum disorder, microcephaly, and mild dysmorphic facial features have also been reported in patients with duplications encompassing the terminal 22q region (PMID: 19239079).	24153177 19239079	SHANK3
Xp11.22 duplication	Males with Xp11.22 duplications encompassing HUWE1 typically present with varying levels of intellectual disabilities, developmental and speech delays, dysmorphic features, early puberty, constipation, infantile epilepsy, and/or hand and foot abnormalities (PMID: 26692240; 25652354; 18252223). There are reports of heterozygous females demonstrating mild clinical features.	26692240 25652354 18252223	HUWE1
Xq28 MECP2 duplication syndrome	In males, duplications including MECP2 are associated with X-linked syndromic intellectual disability, Lubs type, also known as MECP2 duplication syndrome, which is characterized by severe developmental delay and intellectual disability, autism, hypotonia, macrocephaly, and/or seizures (PMID: 22877836; 20082459; 20425814; 20301461; 24721901).	22877836 20082459 20425814 20301461 24721901	MECP2
Alpha-thalassemia intellectual disability syndrome, also known as ATR-16 syndrome	Individuals with ATR-16 present with alpha-thalassemia trait or mild hemoglobin H disease and mild to severe intellectual disability. In some cases, individuals can also have mild, nonspecific dysmorphic features, club foot, microcephaly, and short stature (PMID: 34524523).	34524523	HBA1, HBA2, and SOX8
Miller-Dieker lissencephaly syndrome (MDLS)	MDLS is characterized by lissencephaly, dysmorphic features, severe mental handicap, epilepsy, and reduced life expectancy. Congenital heart disease, omphalocele and joint contractures are also reported (PMID: 29628935).	29628935	YWHAE, PAFAFH1B1
Neurofibromatosis type I (NF1)	Heterozygous loss-of-function variants including deletions in NF1 are associated with neurofibromatosis type 1, which is characterized by non cancerous patches of coffee-colored skin (café-au-lait spots), freckles in the underarms and groin areas, harmless bumps in the eyes (Lisch nodules) and noncancerous growths such as fleshy tumors located on or just under the skin (neurofibromas) (PMID: 20301288, 20027112).	20301288 20027112	NF1
Potocki-Lupski syndrome	Potocki-Lupski syndrome is characterized by infantile hypotonia, failure to thrive, cardiovascular malformations, developmental delay, intellectual disability, and behavioral abnormalities (PMID: 28837307).	28837307	RAI1

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Disorders Tested	Disorder Description	PMID	Genes/ Regions
Prader-Willi/Angelman syndrome	This test can detect if a piece of chromosome 15 is missing, but it cannot tell whether PWS or AS may result. Paternal deletions of this region are associated with Prader-Willi syndrome (PWS) and maternal deletions are associated with Angelman syndrome (AS). The most common features of PWS include low muscle tone (hypotonia), feeding difficulties during early infancy, poor growth (failure to thrive), sleep disorders, behavior issues, developmental delays, mild to moderate intellectual disability, social difficulties, and, during childhood and adulthood, an increased appetite (hyperphagia) that leads to morbid obesity. Other features of PWS may include distinctive facial features, short stature, underdeveloped sex organs (hypogonadotropic hypogonadism), delayed puberty, and infertility. Not all affected individuals have all of these findings and, depending upon the size of the deletion, the severity of the condition is variable. The most common features of AS include a small head (microcephaly), seizures, developmental delays, severe intellectual disability, severe speech impairment, difficulty with balance and coordination (ataxia), and a happy disposition. Other features of AS may include distinctive facial features, sleep disorders, light skin and hair, and unusual behaviors, such as hand flapping. Not all affected individuals have all of these findings and, depending upon the size of the deletion, the severity of the condition is variable (PMID: 32269945).	32269945	HERC2, IPW, MAGEL2, MKRN3, MKRN3-AS1, NPAP1, PWAR1, PWRN1, SNORD115-1, SNORD116-1, SNRPN, UBE3A
Smith-Magenis syndrome	Smith-Magenis syndrome is characterized by mild to severe intellectual disabilities, delayed speech and language, sleep disturbances, behavioral issues including self-injurious behavior, and characteristic facial features (PMID: 20301487).	20301487	RAI1
Thrombocytopenia absent radius (TAR) syndrome	TAR syndrome is a rare autosomal recessive disorder that is characterized by bilateral absence of the radii (thumbs remain present) and transient thrombocytopenia. Thrombocytopenia is usually congenital or develops in the first few weeks of life, and often decreases with age. There is a risk of gastrointestinal and intra-cerebral bleeding in the first few years of life. Intolerance to cow's milk is common and may exacerbate thrombocytopenia. Intellect is usually normal. Other abnormalities include additional skeletal anomalies of the upper and lower limbs, dysmorphic features, cardiac anomalies and genitourinary anomalies (PMID: 12471199). TAR syndrome is caused by compound heterozygosity for 1) a microdeletion or other loss of function variant in RBM8A and 2) one of two common single nucleotide variants that are located in non-coding regions of the RBM8A gene (PMID: 22366785, 17236129).	12471199 22366785 17236129	RBM8A
Wilms tumor, aniridia, genitourinary anomalies, and mental retardation syndrome (WAGR)	Overlapping 11p13 deletions including WT1 and PAX6 are associated with Wilms tumor, aniridia, genitourinary anomalies, and mental retardation syndrome (WAGR), also known as chromosome 11p13 deletion syndrome. WAGR syndrome is an autosomal dominant condition characterized by Wilms tumor, aniridia, genitourinary anomalies, and intellectual disability with or without obesity. This condition exhibits significant variability, even within the same family (PMID: 36158055, 34970513).	36158055 34970513	WT1, PAX6

Invitae Chromosomal Microarray Analysis (CMA): Clinical Summary

Indications for Invitae Chromosomal Microarray Analysis (CMA)	
Signs and Symptoms	This test may be appropriate for individuals with unexplained developmental delays/intellectual disability, autism spectrum disorder, and multiple congenital anomalies including dysmorphic facial features. This test may also be appropriate for individuals who have complex, syndromic symptoms that have a suspected genetic etiology that do not correspond well with a single genetic condition.
Clinical Sensitivity	The clinical sensitivity of this test is dependent on the individual's underlying genetic condition. For each condition, the table below shows the percentage of clinical cases in which a pathogenic variant is expected through chromosomal microarray analysis. Chromosomal disorders are genetically heterogeneous. For conditions not listed in the table, the clinical sensitivity is unknown or not well-established. The percentage of patients with developmental disorders, autism spectrum disorders, and/or multiple congenital anomalies and a pathogenic variant detectable on chromosomal microarray has not been determined. A negative genetic test result does not rule out the possibility that an individual may have a developmental disorder.

Clinical Sensitivity of Invitae Chromosomal Microarray Analysis (CMA)

Disorder	Gene	% of Disorder Attributed to Gene	References
Developmental delay/intellectual disability (DD/ID)	chromosomal anomaly detectable by CMA	19%	19362174
Autism spectrum disorders (ASD)	chromosomal anomaly detectable by CMA	18%	20231187
Trisomy 21 (Down syndrome)	chr21	>99%	26062604
Trisomy 18 (Edward syndrome)	chr18	>99%	23088440
Trisomy 13 (Patau syndrome) or partial trisomy 13q	chr13	>99%	30855930
1p36 deletion syndrome	deletion of 1p36.22-p36.33	>99%	26345236
1q21.1 duplication syndrome	duplication of 1q21.1-q21.2	>99%	33429818
1q21.1 microdeletion syndrome	deletion of 1q21.1-q21.2	>99%	21348049
4pter deletion (Wolf-Hirschhorn syndrome)	deletion of 4pter	High	34002939 35550183
5pter deletion (cri-du-chat syndrome)	deletion of 5pter	>90%	29494067
7q11.23 deletion (Williams-Beuren syndrome)	deletion of 7q11.23	>99%	31334998
7q11.23 duplication syndrome	duplication of 7q11.23	>99%	26610320
11q partial monosomy syndrome (Jacobsen syndrome)	deletion of 11qter	High	31895838
14q11-q22 deletion syndrome	deletion of 114q11-q22	High	32415730
14q22 deletion syndrome (Frias syndrome)	deletion of 14q22.1-q22.3 including BMP4	High	24311462
15q13.3 deletion syndrome	deletion of 15q13.3	>99%	21290787
15q24 deletion syndrome	deletion of 15q24	>99%	22359776
15q26 duplication (overgrowth syndrome)	duplication of 15q26	High	17056309
15q26-qter deletion syndrome	deletion of 15q26-qter	Unknown	
16p11.2 deletion syndrome	deletion of 16p11.2	>99%	20301775
16p11.2 duplication syndrome	duplication of 16p11.2	High	33321999
16p13.11 deletion and duplication syndromes	deletion or duplication of 16p13.11	Unknown	35470466 29191162
16p13.3 duplication syndrome	duplication of 16p13.3	Unknown	24035902
17p12 deletion (hereditary neuropathy with liability to pressure palsies (HNPP))	deletions encompassing PMP22	~80%	20301566
17p12 duplication (Charcot-Marie-Tooth disease type 1A (CMT1A))	duplications encompassing PMP22	High	32693030
17q11.2 deletion syndrome	deletions encompassing NF1 and RNF135	Unknown	34168676
17q12 deletion syndrome (renal cysts and diabetes syndrome (RCAD))	deletion of 17q12	>99%	27929632
17q12 duplication syndrome	duplication of 17q12	>99%	26925472
17q21.31 deletion syndrome (Koolen-De Vries syndrome)	deletions encompassing KANSL1	~95%	20301783
18p deletion syndrome	deletion of 18p	High	28137337
19p13.13 deletion syndrome, Malan syndrome and Sotos syndrome 2	deletions encompassing NFIX	High	25118028 31574590
19p13.13 duplication syndrome		Unknown	
22q11 tetrasomy (Cat eye syndrome)		Unknown	
22q11.21 deletion syndrome (DiGeorge)	deletion of 22q11.2 (TXB1, DGCR8, CRKL, SNAP29, PRODH)	>99%	20301696
22q11.21 duplication syndrome (reciprocal to DiGeorge)		Unknown	
22q13 duplication syndrome (SHANK3)		Unknown	
Xp11.22 duplication	duplications encompassing HUWE1	High	26587761
Xq28 MECP2 duplication syndrome	duplications encompassing MECP2	>99%	20301461
Alpha-thalassemia intellectual disability syndrome, also known as ATR-16 syndrome	deletions encompassing ATRX	<5%	20301622
Miller-Dieker lissencephaly syndrome (MDLS)	deletion of chromosome 17p13.3	90%	29628935
Neurofibromatosis type I (NF1)	deletions encompassing NF1	~5-11%	20301288
Potocki-Lupski syndrome	duplication of 17p11.2	>99%	28837307
Prader-Willi syndrome	deletion of 15q11.2-q13	65-75%	20301505
Angleman syndrome	deletion of 15q11-q13	70-80%	26040994
Smith-Magenis syndrome	deletion of 17p11.2 including RAI1	90-95%	20301487
Thrombocytopenia absent radius (TAR) syndrome	deletions encompassing RBM8A, when in combination with one of the common non-coding SNVs	~48%	20301781
Wilms tumor, aniridia, genitourinary anomalies, and mental retardation syndrome (WAGR)	deletion of 11p13	High	16199712