

Craniofacial microsomia

Gene panel

Gene panel information

Gene panel	Craniofacial microsomia
Version	1
Total genes	27
Activation date	Monday 23 september 2024
Publisher	Center for Medical Genetics, Ghent

Genes

Gene	% at least 20 x covered*	OMIM gene id	OMIM Phenotypes
AMIGO2	99.96 %	615690	No OMIM phenotypes
CDT1	99.68 %	605525	Meier-Gorlin syndrome 4, 613804 (3), Autosomal recessive
CLTCL1	99.44 %	601273	No OMIM phenotypes
CRKL	99.64 %	602007	No OMIM phenotypes
DACH1	99.92 %	603803	No OMIM phenotypes
DACH2	99.73 %	300608	No OMIM phenotypes
EYA3	97.53 %	601655	No OMIM phenotypes
FANCB	99.51 %	300515	Fanconi anemia, complementation group B, 300514 (3), X-linked recessive
FGF3	99.74 %	164950	Deafness, congenital with inner ear agenesis, microtia, and microdontia, 610706 (3), Autosomal recessive
GSC2	98.81 %	601845	No OMIM phenotypes
HIRA	99.48 %	600237	No OMIM phenotypes
HMX1	99.9 %	142992	Oculoauricular syndrome, 612109 (3), Autosomal recessive
HOXA2	100 %	604685	Microtia with or without hearing impairment (AD), 612290 (3), Autosomal recessive, Autosomal dominant; ?Microtia, hearing impairment, and cleft palate (AR), 612290 (3), Autosomal recessive, Autosomal dominant
HSPA9	99.8 %	600548	Even-plus syndrome, 616854 (3), Autosomal recessive; Anemia, sideroblastic, 4, 182170 (3), Autosomal dominant
MAPK1	99.73 %	176948	No OMIM phenotypes
MARS1	99.43 %	156560	Spastic paraplegia 70, autosomal recessive, 620323 (3), Autosomal recessive; Interstitial lung and liver disease, 615486 (3), Autosomal recessive; ?Trichothiodystrophy 9, nonphotosensitive, 619692 (3), Autosomal recessive; Charcot-Marie-Tooth disease, axonal, type 2U, 616280 (3), Autosomal dominant
MYT1	99.94 %	600379	No OMIM phenotypes
OTX2	99.98 %	600037	Retinal dystrophy, early-onset, with or without pituitary dysfunction, 610125 (3), Autosomal dominant; Pituitary hormone deficiency, combined, 6, 613986 (3), Autosomal dominant; Microphthalmia, syndromic 5, 610125 (3), Autosomal dominant
SF3B2	99.75 %	605591	Craniofacial microsomia, 164210 (3), Autosomal dominant
SIX1	99.98 %	601205	Deafness, autosomal dominant 23, 605192 (3), Autosomal dominant; Branchioototic syndrome 3, 608389 (3), Autosomal dominant
SIX5	99.24 %	600963	Branchiootorenal syndrome 2, 610896 (3)
TBX1	98.71 %	602054	Tetralogy of Fallot, 187500 (3), Autosomal dominant; DiGeorge syndrome, 188400 (3), Autosomal dominant; Conotruncal anomaly face syndrome, 217095 (3); Velocardiofacial syndrome, 192430 (3), Autosomal dominant
TCOF1	99.76 %	606847	Treacher Collins syndrome 1, 154500 (3), Autosomal dominant

Craniofacial microsomia

Gene panel

Gene	% at least 20 x covered*	OMIM gene id	OMIM Phenotypes
VWA1	99.7 %	611901	Neuronopathy, distal hereditary motor, autosomal recessive 7, 619216 (3), Autosomal recessive
YPEL1	99.98 %	608082	<i>No OMIM phenotypes</i>
ZIC3	99.87 %	300265	Congenital heart defects, nonsyndromic, multiple types, 1, X-linked, 306955 (3), X-linked recessive; Heterotaxy, visceral, 1, X-linked, 306955 (3), X-linked recessive; VACTERL association, X-linked, 314390 (3), X-linked recessive
ZYG11B	97.89 %	618673	<i>No OMIM phenotypes</i>

Craniofacial microsomia

Gene panel

Explanation

OMIM release used for OMIM disease identifiers and descriptions: **2025-11-12**

Gene symbols used are according to the HGNC guidelines (corresponding to Ensembl database release 105).

Each Phenotype is followed by its MIM number, phenotype mapping key and inheritance pattern.

Possible phenotype mapping keys

- (1) the disorder is placed on the map based on its association with a gene, but the underlying defect is not known
- (2) the disorder has been placed on the map by linkage; no mutation has been found
- (3) the molecular basis for the disorder is known; a mutation has been found in the gene
- (4) a contiguous gene deletion or duplication syndrome, multiple genes are deleted or duplicated causing the phenotype

Brackets, "[]", indicate "nondiseases," mainly genetic variations that lead to apparently abnormal laboratory test values (e.g., dysalbuminemic euthyroidal hyperthyroxinemia).

Braces, "{ }", indicate mutations that contribute to susceptibility to multifactorial disorders (e.g., diabetes, asthma) or to susceptibility to infection (e.g., malaria).

A question mark, "?", before the phenotype name indicates that the relationship between the phenotype and gene is provisional. More details about this relationship are provided in the comment field of the map and in the gene and phenotype OMIM entries.

* The column '% at least 20 x covered' shows the percentage of the coding sequence (+/-20 nucleotides of the flanking introns) of that gene that is on average at least 20 x covered. This according to the experience with exome sequencing in our laboratory and based on the current method.