Whole Exome Sequencing
Gene package Craniosynostosis, version 4, 26-2-2021

Technical information
DNA was enriched using Agilent SureSelect DNA + SureSelect OneSeq 300kb CNV Backbone + Human All Exon V7 capture and paired-end sequenced on the Illumina platform (outsourced). The aim is to obtain 10 Giga base pairs per exome with a mapped fraction of 0.99. The average coverage of the exome is ~50x. Duplicate and non-unique reads are excluded. Data are demultiplexed with bcl2fastq Conversion Software from Illumina. Reads are mapped to the genome using the BWA-MEM algorithm (reference: http://bio-bwa.sourceforge.net/). Sequence variant detection is performed by the Genome Analysis Toolkit HaplotypeCaller (reference: http://www.broadinstitute.org/gatk/). The detected sequence variants are filtered and annotated with Alissa Interpret software and classified with Alamut Visual. Copy variant detection is performed using the BAM multiscale reference method using depth of coverage analysis and dynamical bins in NexusClinical. The detected copy number variants are filtered and annotated with the NexusClinical software and classified using UCSC Genome Browser (NCBI37/hg19). It is not excluded that pathogenic variants are being missed using this technology. At this moment, there is not enough information about the sensitivity of this technique with respect to the detection of deletions and duplications of more than 5 nucleotides and of somatic mosaic mutations (all types of sequence changes).

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HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
ABCC9	601439	100	99.86	98.89	95.39
ADAMTSL4	610113	100	99.03	98.03	89.40
ALPL	171760	100	100	100	98.94
ALX3	606014	91.48	78.67	73.22	72.32
ALX4	605420	100	97.49	93.26	75.44
AXIN2	604025	100	100	99.67	95.00
BCL11B	606558	100	98.43	96.33	84.36
BPNT2	614010	No coverage data			
CCBE1	612753	100	100	99.58	94.92
CDC45	603465	100	100	100	96.18
CHST3	603799	100	100	100	97.12
COLEC11	612502	100	100	97.79	89.50
CTSK	601105	100	100	100	98.27
CYP26B1	605207	100	100	99.58	94.02
EFNA4	601380	100	100	100	91.80
EFNB1	300035	100	100	99.82	92.22
ERF	611888	100	100	97.04	79.79
ESCO2	609353	100	100	100	97.93
FGF3	164950	100	97.88	94.47	79.99
FGF9	600921	100	100	99.20	91.23
FGFR1	136350	100	100	99.61	96.92

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
FGFR2	176943	100	100	99.54	97.18
FGFR3	134934	100	99.62	98.10	84.77
FLNA	300017	100	99.43	98.63	95.60
FLNB	603381	100	100	99.61	95.58
FREM1	608944	100	100	99.55	97.23
GLI3	165240	100	100	100	98.10
GNAS	139320	100	100	100	97.95
GNPTAB	607840	100	99.92	99.10	96.36
GPC3	300037	100	99.90	97.06	86.38
GPC4	300168	100	100	99.65	95.02
GUSB	611499	100	100	100	96.42
HRAS	190020	100	100	100	100
HUWE1	300697	99.94	99.04	96.87	87.38
IFT122	606045	100	99.83	98.59	91.64
IFT43	614068	100	100	100	97.33
IGF1R	147370	100	100	99.00	95.39
IHH	600726	100	99.81	97.25	92.85
IL11	147681	96.84	84.79	71.88	42.83
IL11RA	600939	100	99.14	94.02	78.25
IRX5	606195	100	100	95.63	82.01
JAG1	601920	100	98.20	97.58	96.60
KDM6A	300128	100	98.66	94.85	78.84
KMT2D	602113	100	100	99.75	95.33
KPTN	615620	100	100	97.06	83.17
KRAS	190070	100	100	100	100
LRP5	603506	97.91	97.83	96.64	91.64
MASP1	600521	100	100	100	96.96
MCPH1	607117	98.36	95.86	91.18	87.40
MEGF8	604267	99.95	97.91	93.51	79.89
MSX2	123101	100	100	95.78	89.36
NFIX	164005	100	100	97.89	87.43
NOTCH2	600275	99.78	98.49	97.37	93.59
OSTM1	607649	100	91.53	77.50	62.48
P4HB	176790	100	99.43	96.19	83.57
PHEX	300550	100	100	99.55	87.29
POLR1A	616404	100	100	99.47	93.89
POLR1B	602000	95.91	95.91	95.91	94.84
POLR1C	610060	100	100	100	92.16
POLR1D	613715	100	100	100	89.52
POR	124015	100	100	100	98.25
RAB23	606144	100	100	100	98.92

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
RECQL4	603780	100	99.84	98.15	93.37
RUNX2	600211	100	100	100	99.07
SALL1	602218	100	100	100	98.54
SCARF2	613619	96.90	88.73	76.61	60.02
SEC24D	607186	100	99.76	98.32	91.51
SH3PXD2B	613293	100	98.68	96.32	88.84
SIX1	601205	100	100	100	95.07
SKI	164780	97.12	89.76	84.68	71.54
SMAD6	602931	99.23	78.32	62.37	47.07
SOX10	602229	100	98.83	96.64	87.59
SOX6	607257	100	100	99.30	94.81
STAT3	102582	100	100	99.75	94.86
TCF12	600480	100	100	100	98.28
TCOF1	606847	100	99.17	94.44	81.90
TLK2	608439	100	100	99.46	93.54
TWIST1	601622	100	89.70	81.87	67.73
WDR19	608151	100	99.81	98.99	94.93
WDR35	613602	99.99	99.40	97.68	94.88
ZIC1	600470	100	100	99.29	95.43

- OMIM release used: 18-2-2021
- The statistics above are based on a set of 100 samples
- % Covered 10x , 20x, 30x and 50x describes the percentage of a gene's coding sequence (±10bp flanking introns) that is covered at least 10x, 20x, 30x or 50x