Whole Exome Sequencing
Gene package Noonan syndrome/RASopathies, prenatal
version 1.3, 30-9-2021

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. 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
A2ML1	610627	100	100	99.79	98.52
BRAF	164757	95.04	94.33	93.05	87.97
CBL	165360	100	100	100	99.36
HRAS	190020	100	100	100	100
KRAS	190070	100	100	100	100
LZTR1	600574	100	100	100	98.72
MAP2K1	176872	100	100	100	98.21
MAP2K2	601263	100	100	98.06	86.80
NRAS	164790	100	100	100	99.85
PPP1CB	600590	100	100	100	98.60
PTPN11	176876	98.37	98.37	98.37	98.37
RAF1	164760	100	100	99.87	97.21
RIT1	609591	100	100	100	100
SHOC2	602775	100	100	100	98.74
SOS1	182530	100	98.47	97.56	94.16
SOS2	601247	99.48	98.09	95.96	88.50
SPRED1	609291	100	100	100	100

- OMIM release used: 18-2-2021
- The statistics above are based on a set of 150 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