Whole Exome Sequencing
Gene package Familial Hemophagocytic Lymphohistiocytosis (fHLH)
Version 2, 26-2-2021

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. Additionally, MPLA analysis was performed for fHLH related genes (probemix P028, version B1; MRC Holland). 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
AP3B1	603401	97.72	95.91	94.30	84.26
AP3D1	607246	97.71	97.16	95.44	86.83
CD27	186711	100	100	100	95.78
CD70	602840	100	100	100	88.78
CORO1A	605000	92.29	91.91	90.49	85.72
CTPS1	123860	100	100	99.01	93.87
FAAP24	610884	100	100	100	94.14
ITK	186973	100	100	99.73	97.05
LYST	606897	100.00	99.81	98.90	94.04
MAGT1	300715	99.69	93.27	90.85	83.63
PRF1	170280	100	100	100	100
RAB27A	603868	100	100	100	99.54
RASGRP1	603962	100	100	100	98.41
RHOG	179505	100	100	100	100
SH2D1A	300490	100	100	100	89.33
STX11	605014	100	100	100	100
STXBP2	601717	100	97.15	92.77	77.46
UNC13D	608897	100	99.85	98.15	88.87
XIAP	300079	100	100	95.53	84.45

- 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

HGNC approved gene symbol	OMIM gene ID (active link to omim.org)	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x