Blueprint Genetics

Comprehensive Immune and Cytopenia Panel Plus

REFERRING HEALTHCARE PROFESSIONAL

NAME	HOSPITAL

PATIENT

NAME	DOB	AGE	GENDER	ORDER ID
		1		

PRIMARY SAMPLE TYPE	SAMPLE COLLECTION DATE	CUSTOMER SAMPLE ID
Blood		

SUMMARY OF RESULTS

TEST RESULTS

Negative for explaining the patient's phenotype.

Please see APPENDIX 2: Additional Findings

SEQUENCING PERFORMANCE METRICS

PANEL	GENES	EXONS / REGIONS	BASES	BASES > 20X	MEDIAN COVERAGE	PERCENT > 20X
Comprehensive Immune and Cytopenia Panel	642	8816	1776735	1775461	157	99.93

TARGET REGION AND GENE LIST

The Blueprint Genetics Comprehensive Immune and Cytopenia Panel (version 1, Mar 03, 2020) Plus Analysis includes sequence analysis and copy number variation analysis of the following genes: ABCB7, ABCG5, ABCG8, ACD, ACP5, ACTB*, ACTG1*, ACTN1, ADA, ADAM17, ADAMTS13, ADAMTS3, ADAR, ADIPOQ, ADIPOR1*, ADIPOR2, AICDA, AIRE, AK2, ALAS2, ALPI, ANKRD11*, ANKRD26, AP1S3, AP3B1, AP3D1, APOL1*, ARHGEF1, ARMC4*,#, ARPC1B, ATM, ATP6AP1, ATR, ATRX, B2M, BACH2, BCL10, BCL11B, BCO1, BLM, BLNK, BLOC1S3, BLOC1S6, BRAF*, BRCA1*, BRCA2, BRIP1, BTK, C11ORF70, C15ORF41, C17ORF62, C1QA, C1QB, C1QBP, C1QC, C1R, C1S, C2*, C21ORF59, C3, C3AR1, C4BPA, C4BPB, C5#, C5AR1, C5AR2, C6, C7, C8A, C8B, C8G, C9, CARD11, CARD14, CARD9, CASP10, CASP8, CBL, CCBE1, CCDC103, CCDC114, CCDC39, CCDC40, CCDC65, CCNK, CCNO, CD19, CD247, CD27, CD3D, CD3E, CD3G, CD40, CD40LG, CD46*, CD55#, CD59, CD70, CD79A, CD79B, CD81, CD8A, CD93, CDAN1, CDC42*, CDCA7, CDK9, CDKN2A, CEBPA, CEBPE, CECR1, CENPF, CFB, CFD, CFH*, CFHR5, CFI, CFP, CFTR, CHD7, CHEK2*, CIB1, CIITA, CLCN7, CLEC7A, CLPB, CLU, COG6, COLEC11, COPA, CORO1A*,#, CPT2, CR2, CREBBP, CRP, CSF2RA*,#, CSF2RB, CSF3R, CTC1, CTLA4, CTNNBL1, CTPS1, CTSC, CXCR2, CXCR4, CYBA, CYBB, CYCS*, CYP27A1, DBR1, DCLRE1B, DCLRE1C*, DDX11*, DDX41, DDX58, DEF6, DGAT1, DGKE, DHFR*, DKC1, DNAAF1, DNAAF2, DNAAF3, DNAAF5, DNAH1, DNAH11*, DNAH5, DNAH9, DNAI1, DNAI2, DNAJC21, DNAL1, DNASE1L3, DNASE2, DNMT3B, DOCK2, DOCK8, DRC1, DTNBP1, DYX1C1, EFL1*, EIF2AK3, ELANE, EP300, EPCAM, EPG5, EPO, ERBB2IP, ERCC2, ERCC3, ERCC4, ERCC6L2, ETV6, EXTL3, FAAP100, FAAP24, FADD, FANCA, FANCB, FANCC,

Blueprint Genetics Oy, Keilaranta 16 A-B, 02150 Espoo, Finland
VAT number: FI22307900, CLIA ID Number: 99D2092375, CAP Number: 9257331

1 / 17

FANCD2*, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FAS, FASLG, FAT4, FCGR3A*, FCHO1, FCN1, FCN2, FCN3, FERMT1, FERMT3, FLG*, FLI1, FLNA, FOXN1, FOXP3, FPR1, FYB, G6PC3, G6PD, GAS2L2, GAS8, GATA1, GATA2, GBA*, GFI1, GFI1B, GINS1, GLRX5, GNE, GP1BA, GP1BB, GP9, GTF2H5, GUCY2C, HAVCR2, HAX1, HELLS, HMOX1, HNRNPK*, HOXA11, HPS1*, HPS3, HPS4, HPS5, HPS6, HRAS, HSPA9, HYDIN*,#, HYOU1, ICOS, ICOSLG, IFIH1, IFNAR1, IFNAR2, IFNGR1, IFNGR2, IGLL1*, IKBKB, IKZF1, IL10, IL10RA, IL10RB, IL12B, IL12RB1#, IL12RB2, IL17F, IL17RA, IL17RC, IL18BP, IL1RN, IL21, IL21R, IL23R, IL2RA, IL2RB, IL2RG, IL36RN, IL6R, IL6ST*, IL7R, INO80, IRAK1, IRAK4, IRF2BP2, IRF3, IRF4, IRF7, IRF8, IRF9, ISG15, ITCH, ITGA2, ITGA2B, ITGB2, ITGB3, ITK, JAGN1, JAK1, JAK2, JAK3, KDM1A, KDM6A, KIF23, KLF1, KMT2A, KMT2D, KRAS*, LAMTOR2, LAT, LCK, LCT, LIG1, LIG4, LIPA, LPIN2, LRBA, LRRC6, LRRC8A, LYST, LZTR1, MAD2L2, MAGT1, MALT1, MAN2B1, MANBA, MAP2K1, MAP2K2, MAP3K14, MAP3K8, MASP1, MASP2, MASTL, MAT2A*, MBL2, MCIDAS, MCM4, MECOM, MEFV, MKL1, MLH1, MLPH, MOGS, MPL, MPO, MRAS, MRE11A, MS4A1, MSH2, MSH6, MSN*, MTHFD1, MVK, MYD88, MYH9, MYO5A, MYO5B*, MYSM1, NAF1, NBAS, NBEAL2, NBN, NCF1*,#, NCF2, NCF4, NCKAP1L, NCSTN, NEUROG3, NF1*, NFAT5, NFE2L2, NFIL3, NFKB1, NFKB2, NFKBIA, NHEJ1, NHP2, NLRC4, NLRP1, NLRP12, NLRP3, NME8, NOD2, NOP10, NRAS, NSMCE2, NSMCE3, NUP214, OAS1, OBFC1, OFD1, ORAI1, OSTM1, OTUD6B, OTULIN, PALB2, PARN*, PAX5, PEPD, PGM3, PIGA*, PIH1D3, PIK3CD*, PIK3R1, PLCG2, PLEKHM1*, PLG*, PMM2, PMS2*, PNP, POLA1, POLD1, POLD2, POLE, POLE2, POLR3A, POLR3C, POLR3F, POMP, POT1, PPP1CB, PRF1, PRG4, PRKACG, PRKCD, PRKDC, PSEN1, PSENEN, PSMB8, PSMG2, PSTPIP1, PTEN*, PTPN11, PTPRC, PTRF, PTX3, PUS1, RAB27A, RAC2, RAD50, RAD51, RAD51C, RAF1, RAG1, RAG2, RANBP2*, RAP1A, RAP1B, RASA2, RASGRP1, RBCK1, RBM8A*, RECQL4, REL, RELA*, RELB, RFWD3, RFX5, RFXANK, RFXAP, RHOH, RIPK1, RIT1, RLTPR, RMRP, RNASEH2A, RNASEH2B, RNASEH2C, RNF168, RNF31, RNU4ATAC, RORC, RPGR, RPL10, RPL11, RPL15*, RPL18, RPL19, RPL26, RPL27, RPL35A, RPL36, RPL5, RPL9, RPS10, RPS14, RPS15, RPS15A, RPS19, RPS24, RPS26, RPS27, RPS27A, RPS28, RPS29, RPS7, RPSA, RRAS, RSPH1, RSPH3, RSPH4A, RSPH9, RTEL1, RUNX1, SAMD9, SAMD9L, SAMHD1, SAR1B, SBDS*, SBF2, SEC23B, SEC61A1, SEMA3E, SERPING1, SH2D1A, SH3BP2, SH3KBP1, SHOC2, SI, SKIV2L, SLC10A2, SLC19A2, SLC25A38, SLC26A3, SLC29A3, SLC35A1, SLC35C1, SLC37A4, SLC39A4, SLC39A7, SLC46A1, SLC5A1, SLC7A7, SLC9A3, SLFN14, SLX4, SMARCAL1, SMARCD2, SNX10, SOS1, SOS2, SP110, SPAG1, SPINK5, SPINT2, SPPL2A, SPRED1, SRC, SRP54, SRP72*, STAT1, STAT2, STAT3, STAT5B*, STIM1, STK36, STK4, STX11, STX3, STXBP2, STXBP3, TAP1, TAP2, TAPBP, TASP1, TAZ, TBK1, TBX1, TCF3, TCIRG1, TCN2, TERC, TERF2, TERF2IP, TERT, TFRC, TGFB1, TGFBR1, TGFBR2, THBD, THPO, THRA, THRB, TICAM1, TINF2, TIRAP, TLR3, TMC6, TMC8, TMEM173, TNFAIP3, TNFRSF11A, TNFRSF13B, TNFRSF13C, TNFRSF1A#, TNFRSF4, TNFRSF9, TNFSF11, TNFSF12, TOP2B, TP53, TPP2, TRAC, TRADD, TRAF3, TRAF3IP2, TREX1, TRIM22, TRNT1, TSR2, TTC37, TTC7A, TUBB1, TYK2, UBE2T, UNC119, UNC13D, UNC93B1*, UNG, USB1, USP18*,#, VPS13B, VPS45#, VSIG4, VTN, WAS, WDR1, WIPF1, WRAP53, XIAP*, XRCC2, ZAP70, ZBTB24, ZCCHC8, ZMYND10 and ZNF341*. The following exons are not included in the panel as they are not covered with sufficient high quality sequence reads: ARMC4 (NM_018076:9;NM_001290021:13), C5 (NM_001317164:21), CD55 (NM_001114752:10;NM_001300903:10), CORO1A (NM_007074:11), CSF2RA (NM_001161530:9), HYDIN (NM_001270974:6,8,12,18,20,21,23,26,27,31,35,37,45,47,50,52,57,58,64,70,75,78,82,83), IL12RB1 (NM_153701:10), NCF1 (NM_000265:1,5,8,9,11), TNFRSF1A (NM_001346092:6), USP18 (NM_017414:11) and VPS45 (NM_001279353:13). This panel targets protein coding exons, exon-intron boundaries (± 20 bps) and selected non-coding, deep intronic variants (listed in Appendix 5). This panel should be used to detect single nucleotide variants and small insertions and deletions (INDELs) and copy number variations defined as single exon or larger deletions and duplications. This panel should not be used for the detection of repeat expansion disorders or diseases caused by mitochondrial DNA (mtDNA) mutations. The test does not recognize balanced translocations or complex inversions, and it may not detect low-level mosaicism.

*Some, or all, of the gene is duplicated in the genome. Read more: https://blueprintgenetics.com/pseudogene/
#The gene has suboptimal coverage when >90% of the gene's target nucleotides are not covered at >20x with mapping quality score (MQ>20) reads.
The sensitivity to detect variants may be limited in genes marked with an asterisk (*) or number sign (#).

STATEMENT

CLINICAL HISTORY

Patient is a 18-month-old baby with recurrent infections, including Samonella meningitis.

CLINICAL REPORT

Sequence and Del/Dup (CNV) analysis using the Blueprint Genetics (BpG) Comprehensive Immune and Cytopenia Panel did not detect any known disease-causing or rare variants that could explain the patient's phenotype as described to the laboratory at the time of interpretation.

The analysis detected variants that were considered additional findings. Please see APPENDIX 2 for these results.

STEP	DATE
Order date	
Sample received	
Sample in analysis	
Reported	

On Apr 21, 2020 the statement has been prepared by our geneticists and physicians, who have together evaluated the sequencing results:

Hatice Duzkale, MD, MPH, Ph.D., FACMG, CGMB

Senior Geneticist

Juha Koskenvuo, MD, Ph.D.

Lab Director, Chief Medical Officer

APPENDIX 2: ADDITIONAL FINDINGS

This table includes variants that:

1. are not thought to be the likely cause for, or sufficient to cause the patient's phenotype
   a. a single variant (pathogenic, likely pathogenic or variant of uncertain significance) in a gene that causes an autosomal recessive or X-linked recessive disorder
2. are findings potentially relevant to the patient's medical care
   a. risk variants identified in genes included on the panel
   b. potentially disease-causing variants for an autosomal dominant disorder not related to patient's current phenotype
3. indicate carrier status for pathogenic or likely pathogenic variants in a gene that causes an autosomal recessive or X-linked disorder not suspected in the patient

VARIANT TABLE: ADDITIONAL SEQUENCE ALTERATIONS

GENE	TRANSCRIPT	NOMENCLATURE	GENOTYPE	CONSEQUENCE	INHERITANCE	CLASSIFICATION
SLC39A4	NM_130849.3	c.599C>T, p.(Pro200Leu)	HET	missense_variant	AR	**Pathogenic**
	ID	**ASSEMBLY**	**POS**	**REF/ALT**		
	rs121434287	GRCh37/hg19	8:145640679	G/A		
	gnomAD AC/AN	**POLYPHEN**	**SIFT**	**MUTTASTER**	**PHENOTYPE**	
	35/281160	probably damaging	deleterious	disease causing	Acrodermatitis enteropathica	
CR2	**TRANSCRIPT**	**NOMENCLATURE**	**GENOTYPE**	**CONSEQUENCE**	**INHERITANCE**	**CLASSIFICATION**
	NM_001006658.2	c.668A>G, p.(Asn223Ser)	HET	missense_variant	AR	**Variant of uncertain significance**
	ID	**ASSEMBLY**	**POS**	**REF/ALT**		
	rs374710389	GRCh37/hg19	1:207642178	A/G		
	gnomAD AC/AN	**POLYPHEN**	**SIFT**	**MUTTASTER**	**PHENOTYPE**	
	7/282648	probably damaging	deleterious	disease causing	Common variable immunodeficiency	

NOTES REGARDING ADDITIONAL FINDINGS

The patient is heterozygous for a pathogenic variant *SLC39A4* c.599C>T, p.(Pro200Leu). Disease caused by *SLC39A4* variants is inherited in an autosomal recessive manner, and no second rare or potentially disease-causing variant in *SLC39A4* was detected in the patient. Therefore, this heterozygous variant is not expected to be related to the patient's clinical presentation. However, as the patient is a carrier of a pathogenic variant for recessive disease, genetic counseling is recommended.

The *SLC39A4* c.599C>T, p.(Pro200Leu) has been reported at least twice in the literature. Initially, Kury et al. identified the variant in two families with acrodermatitis enteropathica (AE), in both families the variant was identified as homozygous in two affected siblings (PMID: 12068297). Subsequently, Lehnert et el. identified the variant as compound heterozygous together with truncating *SLC39A4* c.1203G>A, p.(Trp401*) variant in a patient with AE (PMID: 16819703). The *SLC39A4* c.599C>T, p.(Pro200Leu) variant has been detected by other laboratories in the context of clinical testing and submitted to ClinVar (variation ID 3537).

The patient is heterozygous for variant of uncertain significance in *CR2*. Diseases caused by variants in this gene

is inherited in an autosomal recessive manner, and no second rare or potentially disease-causing variant in this gene was detected in this patient. Therefore, this heterozygous variant is not expected to be related to the patient's clinical presentation.

The *CR2* variant has been detected by other laboratories in the context of clinical testing and submitted to ClinVar (variation ID 571625).

Readability of the coverage plot may be hindered by faxing. A high quality coverage plot can be found with the full report on nucleus.blueprintgenetics.com.

Blueprint Genetics Oy, Keilaranta 16 A-B, 02150 Espoo, Finland
VAT number: FI22307900, CLIA ID Number: 99D2092375, CAP Number: 9257331

6 / 17

Blueprint Genetics Oy, Keilaranta 16 A-B, 02150 Espoo, Finland
VAT number: FI22307900, CLIA ID Number: 99D2092375, CAP Number: 9257331

9 / 17
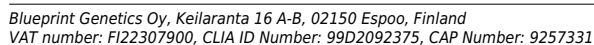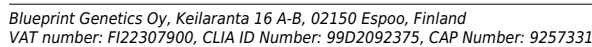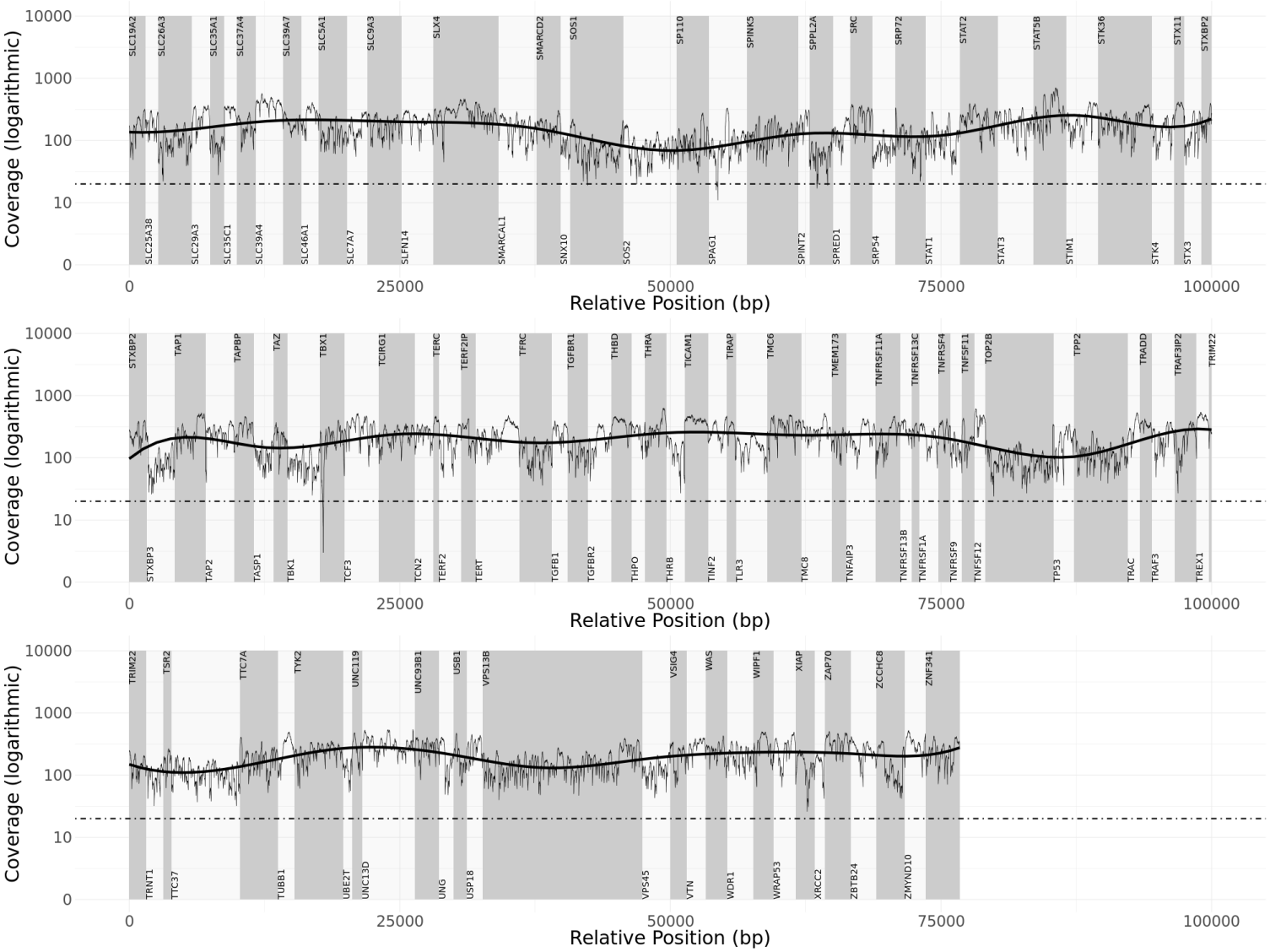
APPENDIX 5: SUMMARY OF THE TEST

PLUS ANALYSIS

Laboratory process: When required, the total genomic DNA was extracted from the biological sample using bead-based method. DNA quality and quantity were assessed using electrophoretic methods. After assessment of DNA quality, qualified genomic DNA sample was randomly fragmented using non-contact, isothermal sonochemistry processing. Sequencing library was prepared by ligating sequencing adapters to both ends of DNA fragments. Sequencing libraries were size-selected with bead-based method to ensure optimal template size and amplified by polymerase chain reaction (PCR). Regions of interest (exons and intronic targets) were targeted using hybridization-based target capture method. The quality of the completed sequencing library was controlled by ensuring the correct template size and quantity and to eliminate the presence of leftover primers and adapter-adapter dimers. Ready sequencing libraries that passed the quality control were sequenced using the Illumina's sequencing-by-synthesis method using paired-end sequencing (150 by 150 bases). Primary data analysis converting images into base calls and associated quality scores was carried out by the sequencing instrument using Illumina's proprietary software, generating CBCL files as the final output.

Bioinformatics and quality control: Base called raw sequencing data was transformed into FASTQ format using Illumina's software (bcl2fastq). Sequence reads of each sample were mapped to the human reference genome (GRCh37/hg19). Burrows-Wheeler Aligner (BWA-MEM) software was used for read alignment. Duplicate read marking, local realignment around indels, base quality score recalibration and variant calling were performed using GATK algorithms (Sentieon) for nDNA. Variant data for was annotated using a collection of tools (VcfAnno and VEP) with a variety of public variant databases including but not limited to gnomAD, ClinVar and HGMD. The median sequencing depth and coverage across the target regions for the tested sample were calculated based on MQ0 aligned reads. The sequencing run included in-process reference sample(s) for quality control, which passed our thresholds for sensitivity and specificity. The patient's sample was subjected to thorough quality control measures including assessments for contamination and sample mix-up. Copy number variations (CNVs), defined as single exon or larger deletions or duplications (Del/Dups), were detected from the sequence analysis data using a proprietary bioinformatics pipeline. The difference between observed and expected sequencing depth at the targeted genomic regions was calculated and regions were divided into segments with variable DNA copy number. The expected sequencing depth was obtained by using other samples processed in the same sequence analysis as a guiding reference. The sequence data were adjusted to account for the effects of varying guanine and cytosine content.

Interpretation: The clinical interpretation team assessed the pathogenicity of the identified variants by evaluating the information in the patient requisition, reviewing the relevant scientific literature and manually inspecting the sequencing data if needed. All available evidence of the identified variants was compared to classification criteria. Reporting was carried out using HGNC-approved gene nomenclature and mutation nomenclature following the HGVS guidelines. Likely benign and benign variants were not reported.

Variant classification: Our variant classification follows the Blueprint Genetics Blueprint Genetics Variant Classification Schemes modified from the ACMG guideline 2015. Minor modifications were made to increase reproducibility of the variant classification and improve the clinical validity of the report.

Databases: The pathogenicity potential of the identified variants were assessed by considering the predicted consequence of the change, the degree of evolutionary conservation as well as the number of reference population databases and mutation databases such as, but not limited to, the gnomAD, ClinVar, HGMD Professional and Alamut Visual. In addition, the clinical relevance of any identified CNVs was evaluated by reviewing the relevant literature and databases such as Database of Genomic Variants and DECIPHER. For interpretation of mtDNA variants specific databases including e.g. Mitomap, HmtVar and 1000G were used.

Confirmation of sequence alterations: Sequence variants classified as pathogenic, likely pathogenic and variants of uncertain significance (VUS) were confirmed using bi-directional Sanger sequencing when they did not meet our stringent NGS quality metrics for a true positive call. In addition, prenatal case with diagnostic findings were confirmed.

Confirmation of copy number variants: CNVs (Deletions/Duplications) were confirmed using a digital PCR assay if they covered less than 10 exons (heterozygous), less than 3 exons (homo/hemizygous) or were not confirmed at least three times previously at our laboratory. Furthermore, CNVs of any size were not confirmed when the breakpoints of the call could be

determined.

Analytic validation: This laboratory-developed test has been independently validated by Blueprint Genetics. The sensitivity of this panel is expected to be in the same range as the validated whole exome sequencing laboratory assay used to generate the panel data (sensitivity for SNVs 99.65%, indels 1-50 bps 99.07%, one-exon deletion 92.3% and two exons CNV 100%, and specificity >99.9% for most variant types). It does not detect very low level mosaicism as a variant with minor allele fraction of 14.6% can be detected in 90% of the cases.

Test restrictions: A normal result does not rule out the diagnosis of a genetic disorder since some DNA abnormalities may be undetectable by the applied technology. Test results should always be interpreted in the context of clinical findings, family history, and other relevant data. Inaccurate, or incomplete information may lead to misinterpretation of the results.

Technical limitations: This test does not detect the following: complex inversions, gene conversions, balanced translocations, repeat expansion disorders unless specifically mentioned, non-coding variants deeper than ±20 base pairs from exon-intron boundary unless otherwise indicated (please see the list of non-coding variants covered by the test). Additionally, this test may not reliably detect the following: low level mosaicism, stretches of mononucleotide repeats, indels larger than 50bp, single exon deletions or duplications, and variants within pseudogene regions/duplicated segments. The sensitivity of this test may be reduced if DNA is extracted by a laboratory other than Blueprint Genetics. Laboratory error is also possible. Please see the Analytic validation above.

Regulation and accreditations: This test was developed and its performance characteristics determined by Blueprint Genetics (see Analytic validation). It has not been cleared or approved by the US Food and Drug Administration. This analysis has been performed in a CLIA-certified laboratory (#99D2092375), accredited by the College of American Pathologists (CAP #9257331) and by FINAS Finnish Accreditation Service, (laboratory no. T292), accreditation requirement SFS-EN ISO 15189:2013. All the tests are under the scope of the ISO 15189 accreditation (excluding mtDNA testing and digital PCR confirmation).

NON-CODING VARIANTS COVERED BY THE PANEL:

NM_000022.2(ADA):c.1079-15T>A
NM_000022.2(ADA):c.976-34G>A
NM_000032.4(ALAS2):c.-15-2186C>G
NM_000032.4(ALAS2):c.-15-2187T>C
NM_000032.4(ALAS2):c.-15-2188A>G
NM_000032.4(ALAS2):c.-258C>G
NM_014915.2(ANKRD26):c.-116C>G
NM_014915.2(ANKRD26):c.-118C>A
NM_014915.2(ANKRD26):c.-119C>A
NM_014915.2(ANKRD26):c.-121A>C
NM_014915.2(ANKRD26):c.-126T>C
NM_014915.2(ANKRD26):c.-126T>G
NM_014915.2(ANKRD26):c.-127A>G
NM_014915.2(ANKRD26):c.-127A>T
NM_014915.2(ANKRD26):c.-128G>A
NM_014915.2(ANKRD26):c.-128G>C
NM_014915.2(ANKRD26):c.-128G>T
NM_014915.2(ANKRD26):c.-134G>A
NM_000051.3(ATM):c.-174A>G
NM_000051.3(ATM):c.-31+595G>A
NM_000051.3(ATM):c.-30-1G>T
NM_000051.3(ATM):c.2639-384A>G
NM_000051.3(ATM):c.2839-579_2839-576delAAGT
NM_000051.3(ATM):c.3403-12T>A
NM_000051.3(ATM):c.3994-159A>G
NM_000051.3(ATM):c.5763-1050A>G
NM_007294.3(BRCA1):c.*1271T>C

NM_007294.3(BRCA1):c.*103_*106delTGTC
NM_007294.3(BRCA1):c.*58C>T
NM_007294.3(BRCA1):c.5468-40T>A
NM_007294.3(BRCA1):c.5407-25T>A
NM_007294.3(BRCA1):c.5277+2916_5277+2946delAAATTCTAGTGCTTTGGATTTTTTCCTCCATinsGG
NM_007294.3(BRCA1):c.5194-12G>A
NM_007294.3(BRCA1):c.213-11T>G
NM_007294.3(BRCA1):c.213-12A>G
NM_007294.3(BRCA1):c.213-15A>G
NM_007294.3(BRCA1):c.-19-2A>G
NM_000059.3(BRCA2):c.-40+1G>A
NM_000059.3(BRCA2):c.8954-15T>G
NM_000059.3(BRCA2):c.9502-28A>G
NM_032043.2(BRIP1):c.1629-498A>T
NM_000061.2(BTK):c.1567-23A>C
NM_000061.2(BTK):c.1567-23A>G
NM_000061.2(BTK):c.895-11C>A
NM_000061.2(BTK):c.240+109C>A
NM_000061.2(BTK):c.240+108T>G
NM_000061.2(BTK):c.142-205A>G
NM_000061.2(BTK):c.-31+6T>G
NM_000061.2(BTK):c.-31+5G>A
NM_000061.2(BTK):c.-31+5G>C
NM_000061.2(BTK):c.-31+5G>T
NM_000061.2(BTK):c.-31+1G>A
NM_000061.2(BTK):c.-31+1G>C
NM_000061.2(BTK):c.-31G>A
NM_000061.2(BTK):c.-193A>G
NM_000491.3(C1QB):c.-17-2A>C
NM_000587.2(C7):c.63-23T>A
NM_181426.1(CCDC39):c.1167+1248A>G
NM_000074.2(CD40LG):c.289-15T>A
NM_000074.2(CD40LG):c.347-915A>T
NM_000077.4(CDKN2A):c.458-105A>G
NM_000077.4(CDKN2A):c.151-1104C>G
NM_000077.4(CDKN2A):c.150+1104C>A
NM_000492.3(CFTR):c.-495C>T
NM_000492.3(CFTR):c.-249G>C
NM_000492.3(CFTR):c.-165G>A
NM_000492.3(CFTR):c.-85C>G
NM_000492.3(CFTR):c.-34C>T
NM_000492.3(CFTR):c.53+124T>C
NM_000492.3(CFTR):c.1393-18G>A
NM_000492.3(CFTR):c.1585-9412A>G
NM_000492.3(CFTR):c.1585-19T>C
NM_000492.3(CFTR):c.1680-886A>G
NM_000492.3(CFTR):c.1680-883A>G
NM_000492.3(CFTR):c.1680-877G>T
NM_000492.3(CFTR):c.2908+19G>C
NM_000492.3(CFTR):c.2909-15T>G
NM_000492.3(CFTR):c.2988+33G>T

NM_000492.3(CFTR):c.3140-26A>G
NM_000492.3(CFTR):c.3140-11A>G
NM_000492.3(CFTR):c.3469-1304C>G
NM_000492.3(CFTR):c.3717+40A>G
NM_000492.3(CFTR):c.3718-2477C>T
NM_000492.3(CFTR):c.3873+33A>G
NM_000492.3(CFTR):c.3874-4522A>G
NM_017780.3(CHD7):c.2836-15C>G
NM_017780.3(CHD7):c.5051-15T>A
NM_017780.3(CHD7):c.5405-17G>A
NM_001287.5(CLCN7):c.916+57A>T
NM_020751.2(COG6):c.1167-24A>G
NM_001814.4(CTSC):c.-55C>A
NM_000397.3(CYBB):c.-69A>C
NM_000397.3(CYBB):c.-67T>C
NM_000397.3(CYBB):c.-65C>T
NM_000397.3(CYBB):c.-64C>T
NM_000397.3(CYBB):c.46-11T>G
NM_000397.3(CYBB):c.483+978G>T
NM_000397.3(CYBB):c.674+1080A>G
NM_000397.3(CYBB):c.674+1337T>G
NM_000397.3(CYBB):c.675-1157A>G
NM_000397.3(CYBB):c.1152-11T>G
NM_003647.2(DGKE):c.888+40A>G
NM_001363.3(DKC1):c.-142C>G
NM_001363.3(DKC1):c.-141C>G
NM_001363.3(DKC1):c.85-15T>C
NM_006892.3(DNMT3B):c.2421-11G>A
NM_203447.3(DOCK8):c.742-18C>G
NM_203447.3(DOCK8):c.742-15T>G
NM_203447.3(DOCK8):c.1797+61A>C
NM_001429.3(EP300):c.1879-12A>G
NM_002354.2(EPCAM):c.556-14A>G
NM_000135.2(FANCA):c.3239+82T>G
NM_000135.2(FANCA):c.2982-192A>G
NM_000135.2(FANCA):c.2778+83C>G
NM_000135.2(FANCA):c.2504+134A>G
NM_000135.2(FANCA):c.2223-138A>G
NM_000135.2(FANCA):c.1567-20A>G
NM_000135.2(FANCA):c.893+920C>A
NM_000136.2(FANCC):c.-78-2A>G
NM_033084.3(FANCD2):c.696-121C>G
NM_033084.3(FANCD2):c.1948-16T>G
NM_001113378.1(FANCI):c.1583+142C>T
NM_000043.4(FAS):c.506-16A>G
NM_000639.1(FASLG):c.-261T>C
NM_017671.4(FERMT1):c.1139+740G>A
NM_017671.4(FERMT1):c.-20A>G
NM_014009.3(FOXP3):c.*878A>G
NM_014009.3(FOXP3):c.*876A>G
NM_002049.3(GATA1):c.-19-2A>G

NM_032638.4(GATA2):c.1017+572C>T
NM_032638.4(GATA2):c.1017+532T>A
NM_000157.3(GBA):c.589-12C>G
NM_021067.3(GINS1):c.-60A>G
NM_021067.3(GINS1):c.-48C>G
NM_000407.4(GP1BB):c.-160C>G
NM_032383.3(HPS3):c.2888-1612G>A
NM_000628.4(IL10RB):c.*52C>T
NM_000206.2(IL2RG):c.*308A>G
NM_000206.2(IL2RG):c.270-15A>G
NM_000206.2(IL2RG):c.-105C>T
NM_002185.3(IL7R):c.379+288G>A
NM_016123.3(IRAK4):c.1188+520A>G
NM_000419.3(ITGA2B):c.*165T>C
NM_000419.3(ITGA2B):c.2095-19T>A
NM_000419.3(ITGA2B):c.1211-78A>G
NM_000419.3(ITGA2B):c.408+11C>A
NM_000419.3(ITGA2B):c.-4082G>A
NM_000211.3(ITGB2):c.742-14C>A
NM_000211.3(ITGB2):c.500-12T>G
NM_000215.3(JAK3):c.2680+89G>A
NM_000215.3(JAK3):c.1915-11G>A
NM_006563.3(KLF1):c.-124T>C
NM_006563.3(KLF1):c.-154C>T
NM_014017.3(LAMTOR2):c.*23C>A
NM_000243.2(MEFV):c.-382C>G
NM_000249.3(MLH1):c.-42C>T
NM_000249.3(MLH1):c.-27C>A
NM_000249.3(MLH1):c.117-11T>A
NM_000249.3(MLH1):c.454-13A>G
NM_000249.3(MLH1):c.885-9_887dupTCCTGACAGTTT
NM_000249.3(MLH1):c.1558+13T>A
NM_000251.2(MSH2):c.-225G>C
NM_000251.2(MSH2):c.-181G>A
NM_000251.2(MSH2):c.-78_-77delTG
NM_000179.2(MSH6):c.*15A>C
NM_001080467.2(MYO5B):c.4852+11A>G
NM_001042492.2(NF1):c.-273A>C
NM_001042492.2(NF1):c.-272G>A
NM_001042492.2(NF1):c.61-7486G>T
NM_001042492.2(NF1):c.288+2025T>G
NM_001042492.2(NF1):c.587-14T>A
NM_001042492.2(NF1):c.587-12T>A
NM_001042492.2(NF1):c.888+651T>A
NM_001042492.2(NF1):c.888+744A>G
NM_001042492.2(NF1):c.888+789A>G
NM_001042492.2(NF1):c.889-12T>A
NM_001042492.2(NF1):c.1260+1604A>G
NM_001042492.2(NF1):c.1261-19G>A
NM_001042492.2(NF1):c.1392+754T>G
NM_001042492.2(NF1):c.1393-592A>G

NM_001042492.2(NF1):c.1527+1159C>T
NM_001042492.2(NF1):c.1642-449A>G
NM_001042492.2(NF1):c.2002-14C>G
NM_001042492.2(NF1):c.2252-11T>G
NM_001042492.2(NF1):c.2410-18C>G
NM_001042492.2(NF1):c.2410-16A>G
NM_001042492.2(NF1):c.2410-15A>G
NM_001042492.2(NF1):c.2410-12T>G
NM_001042492.2(NF1):c.2991-11T>G
NM_001042492.2(NF1):c.3198-314G>A
NM_001042492.2(NF1):c.3974+260T>G
NM_001042492.2(NF1):c.4110+945A>G
NM_001042492.2(NF1):c.4173+278A>G
NM_001042492.2(NF1):c.4578-14T>G
NM_001042492.2(NF1):c.5269-38A>G
NM_001042492.2(NF1):c.5610-456G>T
NM_001042492.2(NF1):c.5812+332A>G
NM_001042492.2(NF1):c.5813-279A>G
NM_001042492.2(NF1):c.6428-11T>G
NM_001042492.2(NF1):c.6642+18A>G
NM_001042492.2(NF1):c.7190-12T>A
NM_001042492.2(NF1):c.7971-321C>G
NM_001042492.2(NF1):c.7971-17C>G
NM_001042492.2(NF1):c.8113+25A>T
NM_003611.2(OFD1):c.935+706A>G
NM_003611.2(OFD1):c.1130-22_1130-19delAATT
NM_024675.3(PALB2):c.109-12T>A
NM_001134477.2(PARN):c.-165+2C>T
NM_000303.2(PMM2):c.179-25A>G
NM_000303.2(PMM2):c.640-23A>G
NM_000270.3(PNP):c.286-18G>A
NM_007055.3(POLR3A):c.1909+22G>A
NM_007055.3(POLR3A):c.1909+18G>A
chr10:g.89622883-89623482
NM_000314.6(PTEN):c.-1239A>G
NM_000314.6(PTEN):c.-1178C>T
NM_000314.6(PTEN):c.-1171C>T
NM_000314.6(PTEN):c.-1111A>G
NM_000314.4(PTEN):c.-1001T>C
NM_000314.4(PTEN):c.-931G>A
NM_000314.4(PTEN):c.-921G>T
NM_000314.4(PTEN):c.-896T>C
NM_000314.4(PTEN):c.-862G>T
NM_000314.4(PTEN):c.-854C>G
NM_000314.4(PTEN):c.-765G>A
NM_000314.4(PTEN):c.254-21G>C
NM_000314.4(PTEN):c.*65T>A
NM_002834.3(PTPN11):c.934-59T>A
NM_000536.3(RAG2):c.-28G>C
NM_024570.3(RNASEH2B):c.65-13G>A
NM_001034853.1(RPGR):c.1059+363G>A

NM_001011.3(RPS7):c.-19+1G>T
NM_001011.3(RPS7):c.-19+2T>C
NM_002295.4(RPSA):c.-34+5G>C
NM_006363.4(SEC23B):c.-571A>G
NM_006363.4(SEC23B):c.-16A>G
NM_006363.4(SEC23B):c.221+31A>G
NM_006363.4(SEC23B):c.221+163A>G
NM_006363.4(SEC23B):c.222-78C>T
NM_006363.4(SEC23B):c.1743+168A>G
NM_000062.2(SERPING1):c.-163C>T
NM_000062.2(SERPING1):c.-161A>G
NM_000062.2(SERPING1):c.-22-2A>C
NM_000062.2(SERPING1):c.-22-2A>G
NM_000062.2(SERPING1):c.-22-1G>A
NM_000062.2(SERPING1):c.686-12A>G
NM_000062.2(SERPING1):c.890-14C>G
NM_000062.2(SERPING1):c.1250-13G>A
NM_130849.3(SLC39A4):c.192+19G>A
NM_006846.3(SPINK5):c.283-12T>A
NM_006846.3(SPINK5):c.1431-12G>A
NM_006846.3(SPINK5):c.1820+53G>A
NM_080647.1(TBX1):c.-777C>T
NM_080647.1(TBX1):c.-620A>C
NM_006019.3(TCIRG1):c.-5+1G>C
NM_006019.3(TCIRG1):c.-5+1G>T
NM_006019.3(TCIRG1):c.1887+132T>C
NM_006019.3(TCIRG1):c.1887+142T>A
NM_006019.3(TCIRG1):c.1887+146G>A
NM_006019.3(TCIRG1):c.1887+149C>T
NM_000355.3(TCN2):c.581-176A>G
NM_000355.3(TCN2):c.581-176A>T
NR_001566.1(TERC):n.-22C>T
chr3:g.169482906-169482906
NM_198253.2(TERT):c.-57A>C
NM_001024847.2(TGFBR2):c.-59C>T
NM_000361.2(THBD):c.-302C>A
NM_000546.5(TP53):c.673-39G>A
NM_000546.5(TP53):c.97-11C>G
NM_000546.5(TP53):c.-29+1G>T
NM_182916.2(TRNT1):c.609-26T>C
NM_020458.2(TTC7A):c.1510+105T>A
NM_199242.2(UNC13D):c.2831-13G>A
NM_199242.2(UNC13D):c.2448-13G>A
NM_199242.2(UNC13D):c.118-307G>A
NM_199242.2(UNC13D):c.118-308C>T
NM_001079.3(ZAP70):c.838-80G>A
NM_001079.3(ZAP70):c.1624-11G>A

GLOSSARY OF USED ABBREVIATIONS:

AD = autosomal dominant

AF = allele fraction (proportion of reads with mutated DNA / all reads)

AR = autosomal recessive

CNV = Copy Number Variation e.g. one exon or multiexon deletion or duplication

gnomAD = genome Aggregation Database (reference population database; >138,600 individuals)

gnomAD AC/AN = allele count/allele number in the genome Aggregation Database (gnomAD)

HEM = hemizygous

HET = heterozygous

HOM = homozygous

ID = rsID in dbSNP

MT = Mitochondria

MutationTaster = *in silico* prediction tools used to evaluate the significance of identified amino acid changes.

Nomenclature = HGVS nomenclature for a variant in the nucleotide and the predicted effect of a variant in the protein level

OMIM = Online Mendelian Inheritance in Man®

PolyPhen = *in silico* prediction tool used to evaluate the significance of amino acid changes.

POS = genomic position of the variant in the format of chromosome:position

SIFT = *in silico* prediction tool used to evaluate the significance of amino acid changes.