Blueprint Genetics

Comprehensive Immune and Cytopenia Panel

Test code: IM0901

Is a 642 gene panel that includes assessment of non-coding variants.

Availability

4 weeks

Gene Set Description

Genes in the Comprehensive Immune and Cytopenia Panel and their clinical significance

Gene	Associated phenotypes	Inheritance	ClinVar	HGMD
ABCB7	Anemia, sideroblastic, and spinocerebellar ataxia	XL	8	9
ABCG5	Sitosterolemia	AR	13	42
ABCG8	Sitosterolemia	AR	18	44
ACD	Dyskeratosis congenita, autosomal dominant 6, Dyskeratosis congenita, autosomal recessive 7	AD/AR	2	8
ACP5	Spondyloenchondrodysplasia with immune dysregulation	AR	12	26
ACTB*	Baraitser-Winter syndrome	AD	55	60
ACTG1*	Deafness, Baraitser-Winter syndrome	AD	27	47
ACTN1	Bleeding disorder, platelet-type 24	AD	7	25
ADA	Severe combined immunodeficiency due to adenosine deaminase deficiency	AR	49	93
ADAM17	Inflammatory skin and bowel disease, neonatal 1	AR	1	7
ADAMTS13	Schulman-Upshaw syndrome, Thrombotic thrombocytopenic purpura, familial	AR	30	183
ADAMTS3	Hennekam lymphangiectasia-lymphedema syndrome	AR	1	3
ADAR	Dyschromatosis symmetrica hereditaria, Aicardi-Goutières syndrome	AD/AR	25	226
ADIPOQ	Complement system	AD/AR	2	8
ADIPOR1*	Complement system	AD/AR		4
ADIPOR2	Complement system	AD/AR	1	1
AICDA	Immunodeficiency with hyper-IgM	AD/AR	14	50
AIRE	Autoimmune polyendocrinopathy syndrome	AD/AR	73	134
AK2	Reticular dysgenesis	AR	14	17
ALAS2	Anemia, sideroblastic, Protoporphyria, erythropoietic	XL	27	103

ALPI	Inflammatory bowel disease	AR		5
ANKRD11*	KBG syndrome	AD	142	132
ANKRD26	Thrombocytopenia	AD	6	21
AP1S3	Psoriasis 15, pustular, susceptibility to	AD		6
AP3B1	Hermansky-Pudlak syndrome	AR	14	34
AP3D1	Hermansky-Pudlak syndrome 10	AR	1	4
APOL1*	Sporadic idiopathic steroid-resistant nephrotic syndrome with focal segmental hyalinosis	AD/AR		1
ARHGEF1	Idiopathic bronchiectasis, Immunodeficiencies with antibody defects	AR		1
ARMC4*	Ciliary dyskinesia	AR	18	17
ARPC1B	Platelet abnormalities with eosinophilia and immune-mediated inflammatory disease	AR	2	4
ATM	Breast cancer, Ataxia-Telangiectasia	AD/AR	1047	1109
ATP6AP1	Immunodeficiency 47	XL	5	5
ATR	Cutaneous telangiectasia and cancer syndrome, Seckel syndrome	AD/AR	10	33
ATRX	Carpenter-Waziri syndrome, Alpha-thalassemia/mental retardation syndrome, Holmes-Gang syndrome, Juberg-Marsidi syndrome, Smith-Fineman-Myers syndrome, Mental retardation-hypotonic facies syndrome	XL	65	165
B2M	Amyloidosis, systemic visceral	AR	8	4
BACH2	BACH2-related immunodeficiency and autoimmunity (BRIDA)	AD		2
BCL10	Immunodeficiency 37	AR	16	1
BCL11B	Immunodeficiency 49	AD	8	12
BCO1	Hypercarotenemia and vitamin A deficiency, autosomal dominant	AD/AR	1	2
BLM	Bloom syndrome	AR	152	119
BLNK	Agammaglobulinemia 4	AR	2	3
BLOC1S3	Hermansky-Pudlak syndrome	AR	2	4
BLOC1S6	Hermansky-Pudlak syndrome	AR	1	2
BRAF*	LEOPARD syndrome, Noonan syndrome, Cardiofaciocutaneous syndrome	AD	134	65
BRCA1*	Pancreatic cancer, Breast-ovarian cancer, familial	AD	2997	2631
BRCA2	Fanconi anemia, Medulloblastoma, Glioma susceptibility, Pancreatic cancer, Wilms tumor, Breast-ovarian cancer, familial	AD/AR	3369	2659
BRIP1	Fanconi anemia, Breast cancer	AD/AR	238	189
BTK	Hypogammaglobulinemia, Agammaglobulinemia and isolated hormone deficiency, Agammaglobulinemia	XL	114	908

C11ORF70	Primary ciliary dyskinesia	AR		5
C15ORF41	Congenital dyserythropoietic anemia	AR	3	3
C17ORF62	Chronic granulomatous disease	AR		1
C1QA	C1q deficiency	AR	2	7
C1QB	C1q deficiency	AR	4	8
C1QBP	Primary immunodeficiency	AD/AR	6	7
C1QC	C1q deficiency	AR	4	10
C1R	Immunodeficiency	AD/AR	15	17
C1S	Complement component C1s deficiency	AD/AR	4	10
C2*	Complement component 2 deficiency	AR	4	9
C21ORF59	Ciliary dyskinesia	AR	5	4
C3	Hemolytic uremic syndrome, atypical, Complement component 3 deficiency, Macular degeneration, age-related	AD/AR	6	87
C3AR1	Complement system	AD/AR	1	4
C4BPA	Complement system	AD/AR		4
C4BPB	Complement system	AD/AR		1
C5	Eculizumab, poor response to, Complement component 5 deficiency	AD/AR	6	18
C5AR1	Complement system	AD/AR		
C5AR2	Complement system	AD/AR		2
C6	Complement component 6 deficiency	AR	8	12
C7	Complement component 7 deficiency	AR	14	31
C8A	Complement component 8 deficiency	AR	2	8
C8B	Complement component 8 deficiency	AR	7	8
C8G	Immunodeficiency	AD/AR		
C9	Complement component 9 deficiency	AR	7	9
CARD11	B-cell expansion with NFKB and T-cell anergy, Immunodeficiency	AD/AR	12	9
CARD14	Psoriasis	AD	9	29
CARD9	Candidiasis, familial, 2	AR	8	25
CASP10	Autoimmune lymphoproliferative syndrome	AD	5	7
CASP8	Caspase 8 defiency	AR	2	7
CBL	Noonan syndrome-like disorder with or without juvenile myelomonocytic leukemia	AD	24	43

CCBE1	Hennekam lymphangiectasia-lymphedema syndrome	AR	6	13
CCDC103	Ciliary dyskinesia	AR	4	5
CCDC114	Ciliary dyskinesia	AR	9	8
CCDC39	Ciliary dyskinesia	AR	39	47
CCDC40	Ciliary dyskinesia	AR	33	43
CCDC65	Ciliary dyskinesia	AR	2	2
CCNK		AD		
CCNO	Ciliary dyskinesia	AR	11	10
CD19	Immunodeficiency, common variable	AR	8	9
CD247	Immunodeficiency	AR	8	4
CD27	Lymphoproliferative syndrome	AR	4	8
CD3D	Immunodeficiency	AR	3	5
CD3E	Immunodeficiency	AR	4	7
CD3G	Immunodeficiency	AR	5	3
CD40	Immunodeficiency with Hyper-IgM	AR	5	10
CD40LG	Immunodeficiency, with hyper-IgM	XL	35	231
CD46*	Hemolytic uremic syndrome, atypical	AD/AR	5	81
CD55	Blood group, Cromer system	BG	7	7
CD59	CD59 deficiency	AR	4	8
CD70	Primary immunodeficiency	AR		4
CD79A	Agammaglobulinemia 3	AR	3	7
CD79B	Agammaglobulinemia 6	AR	2	3
CD81	Immunodeficiency, common variable, 6	AR	1	1
CD8A	CD8 deficiency	AR	1	1
CD93	Complement system	AD/AR		
CDAN1	Anemia, dyserythropoietic congenital	AR	12	61
CDC42	Takenouchi-Kosaki syndrome, Noonan-syndrome like phenotype	AD	11	9
CDCA7	Immunodeficiency-centromeric instability-facial anomalies syndrome 3	AR	4	6
CDK9		AR		1
CDKN2A	Melanoma, familial, Melanoma-pancreatic cancer syndrome	AD	87	232
CEBPA	Acute myeloid leukemia, familial	AD	15	13

CEBPE	Specific granule deficiency 1	AR	3	4
CECR1	Polyarteritis nodosa, ADA2 deficiency	AR	15	50
CENPF	Ciliary dyskinesia -Lethal Ciliopathy	AR	13	8
CFB	Complement factor B deficiency, Hemolytic uremic syndrome, atypical	AD/AR	2	26
CFD	Complement factor D deficiency	AR	2	3
CFH*	Hemolytic uremic syndrome, atypical, Complement factor H deficiency, Basal laminar drusen	AD/AR	18	305
CFHR5	Atypical hemolytic-uremic syndrome with anti-factor H antibodies, C3 glomerulonephritis	AD/AR	4	32
CFI	Hemolytic uremic syndrome, atypical, Complement factor I deficiency	AD/AR	10	143
CFP	Properdin deficiency	XL	5	17
CFTR	Cystic fibrosis, Congenital bilateral absence of the vas deferens	AD/AR	518	1803
CHD7	Isolated gonadotropin-releasing hormone deficiency, CHARGE syndrome	AD	276	860
CHEK2*	Li-Fraumeni syndrome	AD/AR	275	197
CIB1				
CIITA	Bare lymphocyte syndrome	AR	9	15
CLCN7	Osteopetrosis	AD/AR	15	98
CLEC7A	Candidiasis, familial, 4	AR		
CLPB	3-methylglutaconic aciduria with cataracts, neurologic involvement, and neutropenia (MEGCANN)	AR	26	25
CLU	Complement system	AD/AR		17
COG6	Congenital disorder of glycosylation, Shaheen syndrome	AR	10	9
COLEC11	3MC syndrome	AR	6	13
COPA	Autoimmune interstitial lung, joint, and kidney disease	AD	6	6
CORO1A*	Immunodeficiency	AR	41	6
CPT2	Carnitine palmitoyltransferase II deficiency	AR	72	111
CR2	Common variable immunodeficiency	AR	2	16
CREBBP	Rubinstein-Taybi syndrome	AD	175	362
CRP	Complement system	AD/AR		
CSF2RA*	Surfactant metabolism dysfunction, pulmonary	XL	2	17
CSF2RB	Surfactant metabolism dysfunction, pulmonary, 5	AR	2	6
CSF3R	Neutrophilia, hereditary	AD/AR	13	13

CTC1	Cerebroretinal microangiopathy with calcifications and cysts	AR	21	33
CTLA4	Autoimmune lymphoproliferative syndrome, type V	AD	11	34
CTNNBL1				
CTPS1	Immunodeficiency 24	AR	1	1
CTSC	Periodontitis, juvenile, Haim-Munk syndrome, Papillon-Lefevre syndrome	AR	19	92
CXCR2				1
CXCR4	Warts, hypogammaglobulinemia, infections, and myelokathexis (WHIM) syndrome	AD	5	15
CYBA	Chronic granulomatous disease	AR	13	71
CYBB	Chronic granulomatous disease, Immunodeficiency	XL	69	780
CYCS*	Thrombocytopenia	AD	2	3
CYP27A1	Cerebrotendinous xanthomatosis	AR	69	110
DBR1	Immunodeficiency	AR		1
DCLRE1B				1
DCLRE1C*	Omenn syndrome, Severe combined immunodeficiency with sensitivity to ionizing radiation	AR	18	89
DDX11	Warsaw breakage syndrome	AR	7	7
DDX41	Familial myeloproliferative/lymphoproliferative neoplasms, multiple types, susceptibility to	AD	9	21
DDX58	Singleton-Merten syndrome	AD	4	3
DEF6				
DGAT1	Diarrhea	AR	7	11
DGKE	Nephrotic syndrome	AR	17	38
DHFR*	Megaloblastic anemia due to dihydrofolate reductase deficiency	AR	2	5
DKC1	Hoyeraal-Hreidarsson syndrome, Dyskeratosis congenita	XL	48	74
DNAAF1	Ciliary dyskinesia	AR	19	38
DNAAF2	Ciliary dyskinesia	AR	13	6
DNAAF3	Primary ciliary dyskinesia	AD/AR	11	5
DNAAF5	Ciliary dyskinesia	AR	9	5
DNAH1	Spermatogenic failure 18	AR	15	32
DNAH11*	Ciliary dyskinesia	AR	66	130
DNAH5	Ciliary dyskinesia	AR	140	197

DNAH9	Primary ciliary dyskinesia	AR		6
DNAI1	Ciliary dyskinesia	AR	17	35
DNAI2	Ciliary dyskinesia	AR	19	6
DNAJC21	Bone marrow failure syndrome 3	AR	5	11
DNAL1	Ciliary dyskinesia	AR	3	1
DNASE1L3	Systemic lupus erythematosus 16	AR	1	3
DNASE2	Primary immunodeficiency			2
DNMT3B	Immunodeficiency-centromeric instability-facial anomalies syndrome	AR	14	47
DOCK2	Immunodeficiency	AR	7	6
DOCK8	Hyper-IgE recurrent infection syndrome, Mental retardation, autosomal dominant 2	AR	54	168
DRC1	Primary ciliary dyskinesia	AR	5	3
DTNBP1	Hermansky-Pudlak syndrome	AR	2	3
DYX1C1	Ciliary dyskinesia	AR	15	12
EFL1	Shwachman-Diamond syndrome		3	2
EIF2AK3	SED, Wolcott-Rallison type	AR	9	80
ELANE	Neutropenia	AD	43	217
EP300	Rubinstein-Taybi syndrome	AD	63	101
EPCAM	Diarrhea 5, with tufting enteropathy, congenital, Colorectal cancer, hereditary nonpolyposis	AD/AR	38	80
EPG5	Vici syndrome	AR	36	66
EPO			3	4
ERBB2IP			1	5
ERCC2	Xeroderma pigmentosum, Trichothiodystrophy, photosensitive, Cerebrooculofacioskeletal syndrome 2	AR	26	98
ERCC3	Xeroderma pigmentosum, Trichothiodystrophy, photosensitive	AR	10	19
ERCC4	Fanconi anemia, Xeroderma pigmentosum, XFE progeroid syndrome	AR	13	70
ERCC6L2	Bone marrow failure syndrome 2	AR	4	9
ETV6	Thrombocytopenia 5	AD	10	38
EXTL3	Immunoskeletal dysplasia with neurodevelopmental abnormalities (ISDNA)	AR	4	8
FAAP100				
FAAP24				2

FADD	Infections, recurrent, with encephalopathy, hepatic dysfunction, and cardiovascular malformations	AR	2	1
FANCA	Fanconi anemia	AR	191	677
FANCB	Fanconi anemia	XL	11	21
FANCC	Fanconi anemia	AR	94	64
FANCD2*	Fanconi anemia	AR	21	61
FANCE	Fanconi anemia	AR	4	17
FANCF	Fanconia anemia	AR	7	16
FANCG	Fanconi anemia	AR	16	92
FANCI	Fanconi anemia	AR	13	45
FANCL	Fanconi anemia	AR	13	24
FANCM	Fanconi anemia	AR	6	50
FAS	Autoimmune lymphoproliferative syndrome	AD/AR	31	133
FASLG	Autoimmune lymphoproliferative syndrome, type IB	AD	2	10
FAT4	Van Maldergem syndrome 2	AR	13	33
FCGR3A	Immunodeficiency 20	AR		1
FCHO1	Combined immunodeficiency	AR		
FCN1	Complement system	AD/AR		4
FCN2	Complement system	AD/AR		1
FCN3	Immunodeficiency due to Ficolin 3 deficiency	AR	1	
FERMT1	Kindler syndrome	AR	32	83
FERMT3	Leukocyte adhesion deficiency	AR	8	14
FLG*	Icthyosis vulgaris	AD/AR	83	109
FLI1	Thrombocytopenia, Paris-Trousseau type, Bleeding disorder, platelet type 21	AD	7	7
FLNA	Frontometaphyseal dysplasia, Osteodysplasty Melnick-Needles, Otopalatodigital syndrome type 1, Otopalatodigital syndrome type 2, Terminal osseous dysplasia with pigmentary defects, Periventricular nodular heterotopia 1, Melnick-Needles syndrome, Intestinal pseudoobstruction, neuronal, X-linked/Congenital short bowel syndrome, Cardiac valvular dysplasia, X-linked	XL	133	257
FOXN1	T-cell immunodeficiency, congenital alopecia, and nail dystrophy	AD/AR	6	6
FOXP3	Immunodysregulation, polyendocrinopathy, and enteropathy	XL	28	93
FPR1				1

FYB	Thrombocytopenia 3	AR	2	2
G6PC3	Neutropenia, severe congenital, Dursun syndrome	AR	11	37
G6PD	Glucose-6-phosphate dehydrogenase deficiency	XL	45	226
GAS2L2	Primary ciliary dyskinesia	AR		3
GAS8	Ciliary dyskinesia, primary, 33	AR	4	6
GATA1	Anemia, without thrombocytopenia, Thrombocytopenia with beta-thalessemia,, Dyserythropoietic anemia with thrombocytopenia	XL	21	15
GATA2	Myelodysplastic syndrome, Chronic neutropenia associated with monocytopenia, evolving to myelodysplasia and acute myeloid leukemia, Acute myeloid leukemia, Emberger syndrome, Immunodeficiency	AD	30	142
GBA*	Gaucher disease	AR	84	488
GFI1	Neutropenia, severe congenital, 2 autosomal dominant, Neutropenia, nonimmune chronic idiopathic, of adults	AD	2	6
GFI1B	Bleeding disorder, platelet-type, 17	AD	6	9
GINS1	Immunodeficiency	AR	4	4
GLRX5	Spasticity, childhood-onset, with hyperglycinemia	AR	5	6
GNE	Proximal myopathy and ophthalmoplegia, Nonaka myopathy, Sialuria	AD/AR	78	214
GP1BA	Pseudo-von Willebrand disease, Bernard-Soulier syndrome	AD/AR	9	73
GP1BB	Giant platelet disorder, isolated, Bernard-Soulier syndrome	AD/AR	5	53
GP9	Bernard-Soulier syndrome	AR	6	42
GTF2H5	Trichothiodystrophy 3, photosensitive	AR	2	6
GUCY2C	Diarrhea, Meconium ileus	AD/AR	7	10
HAVCR2				
HAX1	Neutropenia, severe congenital	AR	11	21
HELLS	Immunodeficiency-centromeric instability-facial anomalies syndrome 4	AR	6	6
HMOX1	Heme oxygenase 1 deficiency	AR	2	5
HNRNPK	Au-Kline syndrome	AD	14	10
HOXA11	Radioulnar synostosis with amegakaryocytic thrombocytopenia	AD	1	1
HPS1*	Hermansky-Pudlak syndrome	AR	28	55
HPS3*	Hermansky-Pudlak syndrome	AR	10	17
HPS4	Hermansky-Pudlak syndrome	AR	16	22
HPS5	Hermansky-Pudlak syndrome	AR	20	31
HPS6	Hermansky-Pudlak syndrome	AR	13	37

HRAS	Costello syndrome, Congenital myopathy with excess of muscle spindles	AD	43	31
HSPA9	Even-Plus syndrome		5	13
HYDIN*,#	Primary ciliary dyskinesia	AD/AR	5	25
HYOU1	Combined immunodeficiency	AR		2
ICOS	Immunodeficiency, common variable, 1	AR	3	4
ICOSLG			1	
IFIH1	Singleton-Merten syndrome, Aicardi-Goutieres syndrome 7	AD/AR	14	19
IFNAR1				1
IFNAR2	Immunodeficiency 45	AR	1	2
IFNGR1	Immunodeficiency	AD/AR	16	42
IFNGR2	Immunodeficiency	AR	4	18
IGLL1*	Agammaglobulinemia	AR	2	3
IKBKB	Immunodeficiency 15	AR	2	7
IKZF1#	Immunodeficiency, common variable, 13	AD	10	35
IL10	Inflammatory bowel disease	AD/AR	1	5
IL10RA	Inflammatory bowel disease	AR	4	43
IL10RB	Inflammatory bowel disease	AR	2	19
IL12B	Immunodeficiency 28, Immunodeficiency 29	AR	4	13
IL12RB1	Immunodeficiency	AR	13	82
IL12RB2			1	5
IL17F	Candidiasis, familial, 6	AD	1	2
IL17RA	Immunodeficiency 51	AR	8	17
IL17RC	Candiasis, familial, 9	AR	3	4
IL18BP				
IL1RN	Osteomyelitis, sterile multifocal, with periostitis and pustulosis	AR	6	12
IL21	Immunodeficiency, common variable, 11	AR	1	1
IL21R	Immunodeficiency, primary, autosomal recessive, IL21R-related	AD/AR	3	9
IL23R	Primary immunodeficiency	AR	1	
IL2RA	Interleukin 2 receptor, alpha, deficiency	AR	6	6
IL2RB	Primary immunodeficiency	AR		
IL2RG	Combined immunodeficiency	XL	54	243

IL36RN	Pustular psoriasis, generalized	AR	6	26
IL6R	Primary immunodeficiency	AR		1
IL6ST	Primary immunodeficiency	AR		
IL7R	Severe combined immunodeficiency, , T-cell negative, B-cell positive, NK cell positive	AR	23	48
INO80			2	6
IRAK1			3	1
IRAK4	IRAK4 deficiency, Invasive pneumococcal disease, recurrent, isolated, 1	AR	12	29
IRF2BP2	Immunodeficiency, common variable, 14	AD	1	2
IRF3	Herpes simplex encephalitis, susceptibility to, 7	AD	1	2
IRF4	Skin/hair/eye pigmentation, variation in, 8	AD		1
IRF7	Immunodeficiency 39	AR	2	2
IRF8	Immunodeficiency 32A (CD11C-positive/CD1C-positive dendritic cell deficiency), Immunodeficiency 32B (monocyte and dendritic cell deficiency)	AD/AR	4	8
IRF9				1
ISG15	Immunodeficiency, with basal ganglia calcification	AR	3	3
ITCH	Autoimmune disease, syndromic multisystem	AR	1	1
ITGA2	Fetal and neonatal alloimmune thrombocytopenia	AD/AR		5
ITGA2B	Glanzmann thrombasthenia	AD/AR	22	234
ITGB2	Leukocyte adhesion deficiency	AR	33	118
ITGB3	Bleeding disorder, platelet-type 24, Thrombocytopenia, neonatal alloimmune, Glanzmann thrombasthenia	AD/AR	18	165
ITK	Lymphoproliferative syndrome	AR	4	11
JAGN1	Neutropenia, severe congenital	AR	8	8
JAK1	Primary immunodeficiency	AR	4	6
JAK2	Thrombocythemia 3	AD	12	22
JAK3	Severe combined immunodeficiency, , T cell-negative, B cell-positive, natural killer cell-negative	AR	30	66
KDM1A	Cleft palate, psychomotor retardation, and distinctive facial features	AD	5	17
KDM6A	Kabuki syndrome	XL	40	69
KIF23	Anemia, dyserythropoietic congenital	AD	1	3
KLF1	Anemia, dyserythropoietic congenital, Blood group, Lutheran inhibitor, Hereditary persistence of fetal hemoglobin	AD/BG	16	45

KMT2A	Wiedemann-Steiner syndrome	AD	117	114
KMT2D	Kabuki syndrome	AD	350	670
KRAS*	Noonan syndrome, Cardiofaciocutaneous syndrome	AD	63	35
LAMTOR2	Immunodeficiency due to defect in MAPBP-interacting protein	AR	1	1
LAT	Immunodeficiency 52	AR	2	18
LCK	Immunodeficiency	AR	2	3
LCT	Lactase deficiency	AR	11	15
LIG1	Primary immunodeficiency	AR		3
LIG4	Severe combined immunodeficiency with sensitivity to ionizing radiation, LIG4 syndrome	AR	18	36
LIPA	Wolman disease, Cholesterol ester storage disease	AR	27	93
LPIN2	Majeed syndrome	AR	12	14
LRBA	Common variable immunodeficiency	AR	23	64
LRRC6	Ciliary dyskinesia	AR	10	19
LRRC8A	Agammaglobulinemia 5	AD	2	2
LYST*	Chediak-Higashi syndrome	AR	50	97
LZTR1	Schwannomatosis, Noonan syndrome	AD/AR	34	71
MAD2L2	Fanconi anemia, complementation group V		1	1
MAGT1	Immunodeficiency, with magnesium defect, Epstein-Barr virus infection and neoplasia, Mental retardation, X-linked 95	XL	8	14
MALT1	Immunodeficiency	AR	3	5
MAN2B1	Mannosidosis, alpha B, lysosomal	AR	63	149
MANBA	Mannosidosis, lysosomal	AR	16	19
MAP2K1	Cardiofaciocutaneous syndrome	AD	45	23
MAP2K2	Cardiofaciocutaneous syndrome	AD	21	35
MAP3K14	Primary immunodeficiency with multifaceted aberrant lymphoid immunity	AR	1	2
MAP3K8	Noonan syndrome	AD		1
MASP1	3MC syndrome	AR	11	22
MASP2	MASP2 deficiency	AR		6
MASTL	Thrombocytopenia	AD		5
MAT2A*	Complement system	AD/AR		2
MBL2	Mannose-binding protein deficiency	AD	2	2

MCIDAS	Primary ciliary dyskinesia	AR	4	3
MCM4	Natural killer cell and glucocorticoid deficiency with DNA repair defect		1	5
MECOM	Radioulnar synostosis with amegakaryocytic thrombocytopenia 2	AD	3	27
MEFV	Familial Mediterranean fever	AD/AR	29	182
MKL1	Primary immunodeficiency	AR		4
MLH1	Muir-Torre syndrome, Endometrial cancer, Mismatch repair cancer syndrome, Colorectal cancer, hereditary nonpolyposis	AD/AR	873	1191
MLPH	Griscelli syndrome, type 3	AR	4	6
MOGS	Congenital disorder of glycosylation	AR	7	8
MPL	Thrombocythemia, Amegakaryocytic thrombocytopenia	AD/AR	23	55
MPO	Myeloperoxidase deficiency	AR	12	14
MRAS	Noonan syndrome	AD	1	2
MRE11A	Ataxia-telangiectasia-like disorder-1	AR	57	56
MS4A1	Immunodeficiency, common variable, 5	AR	1	2
MSH2	Muir-Torre syndrome, Endometrial cancer, Colorectal cancer, hereditary nonpolyposis,, Mismatch repair cancer syndrome	AD/AR	933	1249
MSH6	Endometrial cancer, Mismatch repair cancer syndrome, Colorectal cancer, hereditary nonpolyposis	AD/AR	672	586
MSN*	Immunodeficiency 50	XL	2	2
MTHFD1	Severe combined immunodeficiency	AR	9	11
MVK	Mevalonic aciduria, Hyper-IgD syndrome, Porokeratosis 3, multiple types	AD/AR	35	181
MYD88	MYD88 deficiency	AR	5	5
MYH9	Sebastian syndrome, May-Hegglin anomaly, Epstein syndrome, Fechtner syndrome, Macrothrombocytopenia and progressive sensorineural deafness, Deafness, autosomal dominant 17	AD	25	117
MYO5A	Griscelli syndrome	AR	7	9
MYO5B*	Diarrhea, with microvillus atrophy	AR	14	80
MYSM1			2	3
NAF1		AD		2
NBAS	Infantile liver failure syndrome 2, Short stature, optic nerve atrophy, and Pelger-Huet anomaly (SOPH syndrome)	AR	23	43
NBEAL2	Gray platelet syndrome	AR	10	51
NBN	Breast cancer, Nijmegen breakage syndrome	AD/AR	188	97
NCF1*,#	Chronic granulomatous disease	AR	18	44

NCF2	Chronic granulomatous disease	AR	19	72
NCF4	Granulomatous disease	AR	4	5
NCKAP1L				
NCSTN	Acne inversa, familial 1	AD	7	30
NEUROG3	Diarrhea, malabsorptive, congenital	AR	3	8
NF1*	Watson syndrome, Neurofibromatosis, Neurofibromatosis-Noonan syndrome	AD	1157	2901
NFAT5				3
NFE2L2			11	6
NFIL3				1
NFKB1	Common variable immunodeficiency	AD	8	17
NFKB2	Common variable immunodeficiency	AD	6	11
NFKBIA	Ectodermal dysplasia, anhidrotic, with T-cell immunodeficiency	AD	5	11
NHEJ1	Severe combined immunodeficiency with microcephaly, growth retardation, and sensitivity to ionizing radiation	AR	15	16
NHP2	Dyskeratosis congenita	AR	5	3
NLRC4	Autoinflammation with infantile enterocolitis (AIFEC), Familial cold autoinflammatory syndrome 4	AD	6	8
NLRP1	Palmoplantar carcinoma, multiple self-healing, Autoinflammation with arthritis and dyskeratosis	AD/AR	5	15
NLRP12	Familial cold autoinflammatory syndrome	AD	12	12
NLRP3	Neonatal onset multisystem inflammatory disease (NOMID), Muckle-Wells syndrome, Chronic infantile neurologic cutaneous articular (CINCA) syndrome, Familial cold-induced autoinflammatory syndrome 1	AD	20	136
NME8	Ciliary dyskinesia	AR	1	6
NOD2	Blau syndrome, Sarcoidosis, early-onset	AD	12	70
NOP10	Dyskeratosis congenita	AR	1	1
NRAS	Noonan syndrome	AD	31	14
NSMCE2	Seckel syndrome 10		3	2
NSMCE3	Lung disease, immunodeficiency, and chromosome breakage syndrome (LICS)	AR	2	2
NUP214			1	4
OAS1				
OBFC1			2	2

OFD1	Simpson-Golabi-Behmel syndrome, Retinitis pigmentosa, Orofaciodigital syndrome, Joubert syndrome	XL	153	160
ORAI1	Immunodeficiency, Myopathy, tubular aggregate, 2	AD/AR	9	13
OSTM1	Osteopetrosis, autosomal recessive 5	AR	5	9
OTUD6B	Intellectual developmental disorder with dysmorphic facies, seizures, and distal limb anomalies (IDDFSDA)	AR	6	4
OTULIN	Autoinflammation, panniculitis, and dermatosis syndrome (AIPDS)	AR	8	3
PALB2	Fanconi anemia, Pancreatic cancer, Breast cancer	AD/AR	495	406
PARN*	Pulmonary fibrosis and/or bone marrow failure, Dyskeratosis congenita	AD/AR	15	29
PAX5	Pre-B cell acute lymphoblastic leukemia	AD		7
PEPD	Prolidase deficiency	AR	12	31
PGM3	Immunodeficiency 23	AR	14	15
PIGA*	Multiple congenital anomalies-hypotonia-seizures syndrome	XL	24	27
PIH1D3#	Ciliary dyskinesia, primary, 36	XL	2	12
PIK3CD*	Immunodeficiency	AD	6	12
PIK3R1	Agammaglobulinemia, SHORT syndrome	AD/AR	33	24
PLCG2	Familial cold autoinflammatory syndrome 3 (PLAID), Autoinflammation, antibody deficiency, and immune dysregulation syndrome (APLAID)	AD	7	13
PLEKHM1	Osteopetrosis, autosomal recessive 6	AR	3	4
PLG	Plasminogen deficiency, type I, Angioedema	AD/AR	10	74
PMM2	Congenital disorder of glycosylation	AR	76	128
PMS2*	Mismatch repair cancer syndrome, Colorectal cancer, hereditary nonpolyposis	AD/AR	319	342
PNP	Purine nucleoside phosphorylase deficiency	AR	11	33
POLA1	Pigmentary disorder, reticulate, with systemic manifestations, X-linked, Neurodevelopmental disorder		2	1
POLD1	Colorectal cancer, Mandibular hypoplasia, deafness, progeroid features, and lipodystrophy syndrome, Idiopathic bronchiectasis, Immunodeficiency	AD/AR	3	31
POLD2				
POLE	Colorectal cancer, Facial dysmorphism, immunodeficiency, livedo, and short stature syndrome (FILS syndrome)	AD/AR	8	70
POLE2	Combined immunodeficiency	AR		3
POLR3A	Leukodystrophy, hypomyelinating	AR	29	91
POLR3C			1	

POLR3F				
POMP	Keratosis linearis with ichthyosis congenita and sclerosing keratoderma	AR	5	4
POT1	Glioma susceptibility 9, Melanoma, cutaneous malignant, susceptibility to 10	AD	2	34
PPP1CB#	Noonan syndrome-like disorder with loose anagen hair 2	AD	8	11
PRF1	Lymphoma, non-Hodgkin, Aplastic anemia, adult-onset, Hemophagocytic lymphohistiocytosis	AR	24	183
PRG4	Camptodactyly-arthropathy-coxa vara-pericarditis syndrome	AR	6	35
PRKACG	Bleeding disorder, platelet-type, 19	AR	1	1
PRKCD	Autoimmune lymphoproliferative syndrome type III	AR	4	6
PRKDC	Immunodeficiency	AR	6	9
PSEN1	Dilated cardiomyopathy (DCM), Acne inversa, familial, 3, Dementia, frontotemporal, Pick disease, Alzheimer disease	AD	57	306
PSENEN	Acne inversa, familial, 2	AD	7	17
PSMB8	Nakajo-Nishimura syndrome, Chronic atypical neutrophilic dermatosis with lipodystrophy and elevated temperature syndrome, Autoinflammation, lipodystrophy, and dermatosis syndrome, Joint contractures, muscular atrophy, microcytic anemia, and panniculitis-induced lipodystrophy syndrome	AR	5	9
PSMG2				
PSTPIP1	Pyogenic sterile arthritis, pyoderma gangrenosum, and acne	AD	5	29
PTEN*	Bannayan-Riley-Ruvalcaba syndrome, Lhermitte-Duclos syndrome, Cowden syndrome	AD	435	638
PTPN11	Noonan syndrome, Metachondromatosis	AD	135	140
PTPRC	Severe combined immunodeficiency, , T-cell negative, B-cell positive, NK cell positive	AR	4	5
PTRF	Lipodystrophy, congenital generalized	AR	9	15
PTX3	Complement system	AD/AR		1
PUS1	Mitochondrial myopathy and sideroblastic anemia	AR	7	9
RAB27A	Griscelli syndrome, Elejalde syndrome	AR	18	54
RAC2	Neutrophil immunodeficiency syndrome	AD	2	3
RAD50	Breast cancer, Nijmegen breakage syndrome-like disorder	AD/AR	183	88
RAD51	Mirror movements 2, Fanconi anemia, complementation group R	AD	7	10
RAD51C	Fanconi anemia, Breast-ovarian cancer, familial	AD/AR	107	125
RAF1	LEOPARD syndrome, Noonan syndrome, Dilated cardiomyopathy (DCM)	AD	45	53

RAG1	Omenn syndrome, Alpha/beta T-cell lymphopenia with gamma/delta T-cell expansion, severe cytomegalovirus infection, and autoimmunity, T cell-negative, B cell-negative, natural killer cell-positive severe combined immunodeficiency, Combined cellular and humoral immune defects with granulomas	AR	47	184
RAG2	Omenn syndrome, Combined cellular and humoral immune defects with granulomas	AR	28	79
RANBP2	Encephalopathy, acute, infection-induced, 3, susceptibility to	AD	41	6
RAP1A			1	
RAP1B				1
RASA2#	Noonan syndrome	AD	1	3
RASGRP1	Primary immunodeficiency	AR	1	3
RBCK1	Polyglucosan body myopathy	AR	11	14
RBM8A*,#	Thrombocytopenia - absent radius	AD/AR	5	12
RECQL4	Baller-Gerold syndrome, RAPADILINO syndrome, Rothmund-Thomson syndrome	AR	82	114
REL		AD/AR		
RELA	Autoimmune lymphoproliferative syndrome	AD	1	3
RELB	Immunodeficiency 53		1	1
RFWD3			2	2
RFX5	Bare lymphocyte syndrome	AR	4	10
RFXANK	MHC class II deficiency	AR	8	16
RFXAP	Bare lymphocyte syndrome	AR	6	9
RHOH	T-cell immunodeficiency with epidermodysplasia verruciformis	AD/AR		1
RIPK1	Primary immunodeficiency	AD/AR	3	1
RIT1	Noonan syndrome	AD	23	26
RLTPR	Combined immunodeficiency	AR	11	8
RMRP	Cartilage-hair hypoplasia, Metaphyseal dysplasia without hypotrichosis, Anauxetic dysplasia	AR	87	123
RNASEH2A	Aicardi-Goutières syndrome	AR	13	21
RNASEH2B	Aicardi-Goutières syndrome	AR	16	41
RNASEH2C	Aicardi-Goutières syndrome	AR	6	14
RNF168	RIDDLE syndrome	AR	4	5
RNF31	HOIP and LUBAC deficiency	AR		1

RNU4ATAC	Roifman syndrome, Microcephalic osteodysplastic primordial dwarfism type 1, Microcephalic osteodysplastic primordial dwarfism type 3	AR	15	24
RORC	Immunodeficiency 42	AR	3	3
RPGR	Retinitis pigmentosa, Cone-rod dystrophy, X-linked, 1, Macular degeneration, X-linked atrophic, Retinitis pigmentosa 3	XL	79	218
RPL10	Autism	XL	4	5
RPL11	Diamond-Blackfan anemia	AD	12	45
RPL15*	Diamond-Blackfan anemia	AD	2	2
RPL18				
RPL19				1
RPL26	Diamond-Blackfan anemia 11	AD	2	1
RPL27	Diamond-Blackfan anemia 16		1	1
RPL35A	Diamond-Blackfan anemia	AD	7	14
RPL36				1
RPL5	Diamond-Blackfan anemia	AD	19	77
RPL9				2
RPS10	Diamond-Blackfan anemia	AD	3	5
RPS14				
RPS15				1
RPS15A				1
RPS19	Diamond-Blackfan anemia	AD	23	172
RPS24	Diamond-Blackfan anemia	AD	6	10
RPS26	Diamond-Blackfan anemia	AD	10	33
RPS27	Diamond-Blackfan anemia 17		1	1
RPS27A				1
RPS28	Diamond-Blackfan anemia 15 with mandibulofacial dysostosis	AD	1	1
RPS29	Diamond-Blackfan anemia	AD	4	4
RPS7	Diamond-Blackfan anemia	AD	2	10
RPSA	Asplenia, isolated congenital	AD	7	8
RRAS	Noonan-syndrome like phenotype	AD/AR		2
RSPH1	Ciliary dyskinesia	AR	14	10
RSPH3	Ciliary dyskinesia, primary, 32	AR	7	5

RSPH4A	Ciliary dyskinesia	AR	18	24
RSPH9	Ciliary dyskinesia	AR	8	12
RTEL1	Pulmonary fibrosis and/or bone marrow failure, Dyskeratosis congenita	AD/AR	58	51
RUNX1	Platelet disorder, familial, with associated myeloid malignancy	AD	47	101
SAMD9	Mirage syndrome, Tumoral calcinosis, normophosphatemic	AD/AR	10	27
SAMD9L	Ataxia-pancytopenia syndrome	AD	4	16
SAMHD1	Aicardi-Goutières syndrome, Chilblain lupus 2	AD/AR	25	56
SAR1B	Chylomicron retention disease (Anderson disease)	AR	8	16
SBDS*	Aplastic anemia, Shwachman-Diamond syndrome, Severe spondylometaphyseal dysplasia	AR	19	90
SBF2	Charcot-Marie-Tooth disease	AR	25	21
SEC23B	Anemia, dyserythropoietic congenital	AR	18	121
SEC61A1	Hyperuricemic nephropathy, familial juvenile 4	AD	4	4
SEMA3E	CHARGE syndrome	AD	1	4
SERPING1	Angioedema, Complement component 4, partial deficiency of	AD/AR	34	563
SH2D1A	Lymphoproliferative syndrome	XL	21	129
SH3BP2	Cherubism	AD	9	16
SH3KBP1			2	1
SHOC2	Noonan-like syndrome with loose anagen hair	AD	2	4
SI	Sucrase-isomaltase deficiency, congenital	AR	12	23
SKIV2L	Trichohepatoenteric syndrome 2	AR	6	33
SLC10A2	Bile acid malabsorption, primary	AD/AR	2	4
SLC19A2	Thiamine-responsive megaloblastic anemia syndrome	AR	14	51
SLC25A38	Anemia, sideroblastic 2, pyridoxine-refractory	AR	7	27
SLC26A3	Diarrhea, secretory chloride, congenital	AR	55	88
SLC29A3	Histiocytosis-lymphadenopathy plus syndrome, Dysosteosclerosis	AR	17	25
SLC35A1	Congenital disorder of glycosylation	AR	4	5
SLC35C1	Congenital disorder of glycosylation, Leukocyte adhesion deficiency	AR	6	7
SLC37A4	Glycogen storage disease	AR	49	113
SLC39A4	Acrodermatitis enteropathica	AR	13	50
SLC39A7	Agammaglobulinemia	AR		

SLC46A1	Folate malabsorption	AR	17	23
SLC5A1	Glucose/galactose malabsorption	AR	3	58
SLC7A7	Lysinuric protein intolerance	AR	55	67
SLC9A3	Diarrhea, secretory sodium, congenital	AR	6	12
SLFN14	Thrombocytopenia	AD/AR	4	4
SLX4	Fanconi anemia	AR	18	72
SMARCAL1	Schimke immunoosseous dysplasia	AR	20	88
SMARCD2	Specific granule defiency 2	AR	3	1
SNX10	Osteopetrosis, autosomal recessive 8	AR	3	13
SOS1	Noonan syndrome	AD	44	71
SOS2	Noonan syndrome 9	AD	4	6
SP110	Hepatic venoocclusive disease with immunodeficiency	AR	8	8
SPAG1	Primary ciliary dyskinesia	AR	18	11
SPINK5	Netherton syndrome	AR	29	85
SPINT2	Diarrhea, secretory sodium, congenital	AR	6	12
SPPL2A	Primary immunodeficiency	AR	1	
SPRED1	Legius syndrome	AD	38	71
SRC	Thrombocytopenia, autosomal dominant, 6	AD	2	1
SRP54	Shwachman-Diamond syndrome	AD	3	
SRP72*	Bone marrow failure syndrome 1	AD	2	5
STAT1	Immunodeficiency	AD/AR	39	122
STAT2	Immunodeficiency	AR	3	6
STAT3	Hyper-IgE recurrent infection syndrome, Autoimmune disease, multisystem, infantile onset	AD	47	152
STAT5B*	Growth hormone insensitivity with immunodeficiency	AD/AR	9	13
STIM1	Stormorken syndrome, Immunodeficiency, Myopathy, tubular aggregate 1	AD/AR	13	24
STK36	Primary ciliary dyskinesia	AR		5
STK4	T-cell immunodeficiency syndrome, recurrent infections, autoimmunity,	AR	3	7
STX11	Hemophagocytic lymphohistiocytosis, familial	AR	8	22
STX3	Microvillus inclusion disease	AR		3
STXBP2	Hemophagocytic lymphohistiocytosis, familial	AR	12	77

STXBP3				1
TAP1	Bare lymphocyte syndrome	AR	1	7
TAP2	Bare lymphocyte syndrome	AR	4	8
TAPBP	Bare lymphocyte syndrome	AR	1	2
TASP1			1	1
TAZ	3-Methylglutaconic aciduria, (Barth syndrome)	XL	45	158
TBK1	Herpes simplex encephalitis, Frontotemporal dementia and/or amyotrophic lateral sclerosis 4	AD	11	133
TBX1	Conotruncal anomaly face syndrome	AD	17	72
TCF3	Agammaglobulinemia 8, autosomal dominant	AD	1	5
TCIRG1	Osteopetrosis, severe neonatal or infantile forms (OPTB1)	AD/AR	48	130
TCN2	Transcobalamin II deficiency	AR	9	35
TERC	Aplastic anemia, Pulmonary fibrosis and/or bone marrow failure, telomere-related, Dyskeratosis congenita	AD	42	73
TERF2				2
TERF2IP				6
TERT	Aplastic anemia, Pulmonary fibrosis and/or bone marrow failure, telomere-related, Dyskeratosis congenita	AD/AR	48	156
TFRC	Immunodeficiency 46	AR	8	2
TGFB1	Diaphyseal dysplasia Camurati-Engelmann	AD	15	23
TGFBR1	Loeys-Dietz syndrome	AD	40	69
TGFBR2	Loeys-Dietz syndrome	AD	58	139
THBD	Thrombophilia due to thrombomodulin defect, Hemolytic uremic syndrome, atypical	AD	5	28
THPO	Thrombocythemia 1	AD	5	10
THRA	Hypothyroidism, congenital, nongoitrous, 6	AD	8	13
THRB	Thyroid hormone resistance	AD/AR	61	165
TICAM1	Herpes simplex encephalitis, susceptibility to, 4	AD/AR		4
TINF2	Revesz syndrome, Dyskeratosis congenita	AD	25	42
TIRAP				1
TLR3	Herpes simplex encephalitis, susceptibility to, 2	AD/AR		14
TMC6	Epidermodysplasia verruciformis	AR	8	7
TMC8	Epidermodysplasia verruciformis	AR	3	9

TMEM173	STING-associated vasculopathy, infantile-onsent (SAVI)	AD	4	10
TNFAIP3	Autoinflammatory syndrome, familial, Behcet-like	AD	8	23
TNFRSF11A	Familial expansile osteolysis, Paget disease of bone, Osteopetrosis, severe neonatal or infantile forms (OPTB1)	AD/AR	8	24
TNFRSF13B	Common variable immunodeficiency, Immunoglobulin A deficiency	AD/AR	7	48
TNFRSF13C	Immunodeficiency, common variable 4	AR	1	3
TNFRSF1A	Periodic fever (TNF receptor-associated periodic syndrome)	AD	19	106
TNFRSF4	Immunodeficiency	AR	1	1
TNFRSF9				
TNFSF11	Osteopetrosis, autosomal recessive 2	AR	3	5
TNFSF12				1
TOP2B			1	1
TP53	Colorectal cancer, Li-Fraumeni syndrome, Ependymoma, intracranial, Choroid plexus papilloma, Breast cancer, familial, Adrenocortical carcinoma, Osteogenic sarcoma, Hepatoblastoma, Non-Hodgkin lymphoma	AD	393	505
TPP2			1	1
TRAC	T-cell receptor-alpha/beta deficiency	AR	1	1
TRADD				3
TRAF3	Herpes simplex encephalitis, susceptibility to, 3	AD	1	1
TRAF3IP2	Candidiasis, familial 8	AR	1	3
TREX1	Vasculopathy, retinal, with cerebral leukodystrophy, Chilblain lupus, Aicardi-Goutières syndrome	AD/AR	30	71
TRIM22				4
TRNT1	Retinitis pigmentosa and erythrocytic microcytosis, Sideroblastic anemia with B-cell immunodeficiency, periodic fevers, and developmental delay	AR	13	26
TSR2	Diamond-Blackfan anemia 14 with mandibulofacial dysostosis	XL	3	2
TTC37	Trichohepatoenteric syndrome, Primary immunodeficiency	AR	12	64
TTC7A	Gastrointestinal defects and immunodeficiency syndrome	AR	21	46
TUBB1	Macrothrombocytopenia	AD	2	7
TYK2	Immunodeficiency	AR	9	9
UBE2T	Fanconi anemia, complementation group T	AR	2	7
UNC119	Immunodeficiency, Cone-rod dystrophy 2	AD	1	5
UNC13D	Hemophagocytic lymphohistiocytosis, familial	AR	22	192

UNC93B1*	Herpes simplex encephalitis, susceptibility to, 1	AR		2
UNG	Immunodeficiency with hyper-IgM, type 5	AR	6	7
USB1	Poikiloderma with neutropenia	AR	24	22
USP18*	Pseudo-TORCH syndrome 2	AR	40	1
VPS13B	Cohen syndrome	AR	351	203
VPS45	Neutropenia, severe congenital, 5, autosomal recessive	AR	3	4
VSIG4	Complement system	XL		2
VTN	Complement system	AD/AR		
WAS	Neutropenia, severe congenital, Thrombocytopenia, Wiskott-Aldrich syndrome	XL	57	439
WDR1		AR		8
WIPF1	Wiskott-Aldrich syndrome 2	AR	2	3
WRAP53	Dyskeratosis congenita	AR	7	6
XIAP*	Lymphoproliferative syndrome	XL	14	96
XRCC2	Hereditary breast cancer	AD/AR	10	21
ZAP70	Selective T-cell defect	AR	15	29
ZBTB24	Immunodeficiency-Centromeric Instability-Facial Anomalies 2	AR	7	17
ZCCHC8				1
ZMYND10	Ciliary dyskinesia	AR	8	16
ZNF341*		AR		5

*

Some, or all, of the gene is duplicated in the genome. Read more.

#

The gene has suboptimal coverage (means <90% of the gene's target nucleotides are covered at >20x with mapping quality score (MQ>20) reads), and/or the gene has exons listed under Test limitations section that are not included in the panel as they are not sufficiently covered with high quality sequence reads.

The sensitivity to detect variants may be limited in genes marked with an asterisk (*) or number sign (#). Due to possible limitations these genes may not be available as single gene tests.

Gene refers to the HGNC approved gene symbol; Inheritance refers to inheritance patterns such as autosomal dominant (AD), autosomal recessive (AR), mitochondrial (mi), X-linked (XL), X-linked dominant (XLD) and X-linked recessive (XLR); ClinVar refers to the number of variants in the gene classified as pathogenic or likely pathogenic in this database (ClinVar); HGMD refers to the number of variants with possible disease association in the gene listed in Human Gene

Mutation Database (HGMD). The list of associated, gene specific phenotypes are generated from CGD or Mitomap databases.

Non-coding disease causing variants covered by the panel

Gene	Genomic location HG19	HGVS	RefSeq	RS-number
ADA	Chr20:43248503	c.1079-15T>A	NM_000022.2	rs387906268
ADA	Chr20:43249076	c.976-34G>A	NM_000022.2	
ALAS2	ChrX:55054634	c.-15-2186C>G	NM_000032.4	
ALAS2	ChrX:55054635	c.-15-2187T>C	NM_000032.4	
ALAS2	ChrX:55054636	c.-15-2188A>G	NM_000032.4	
ALAS2	ChrX:55057617	c.-258C>G	NM_000032.4	rs140772352
ANKRD26	Chr10:27389371	c.-116C>G	NM_014915.2	
ANKRD26	Chr10:27389373	c.-118C>A	NM_014915.2	
ANKRD26	Chr10:27389374	c.-119C>A	NM_014915.2	
ANKRD26	Chr10:27389376	c.-121A>C	NM_014915.2	
ANKRD26	Chr10:27389381	c.-126T>C	NM_014915.2	
ANKRD26	Chr10:27389381	c.-126T>G	NM_014915.2	
ANKRD26	Chr10:27389382	c.-127A>G	NM_014915.2	
ANKRD26	Chr10:27389382	c.-127A>T	NM_014915.2	
ANKRD26	Chr10:27389383	c.-128G>A	NM_014915.2	
ANKRD26	Chr10:27389383	c.-128G>C	NM_014915.2	
ANKRD26	Chr10:27389383	c.-128G>T	NM_014915.2	
ANKRD26	Chr10:27389389	c.-134G>A	NM_014915.2	rs863223318
ATM	Chr11:108093770	c.-174A>G	NM_000051.3	
ATM	Chr11:108094508	c.-31+595G>A	NM_000051.3	
ATM	Chr11:108098321	c.-30-1G>T	NM_000051.3	rs869312754
ATM	Chr11:108138753	c.2639-384A>G	NM_000051.3	
ATM	Chr11:108141209	c.2839-579_2839-576delAAGT	NM_000051.3	
ATM	Chr11:108151710	c.3403-12T>A	NM_000051.3	rs201370733
ATM	Chr11:108158168	c.3994-159A>G	NM_000051.3	rs864622543
ATM	Chr11:108179837	c.5763-1050A>G	NM_000051.3	rs774925473
BRCA1	Chr17:41196424	c.*1271T>C	NM_007294.3	
BRCA1	Chr17:41197588	c.*103_*106delTGTC	NM_007294.3	rs431825382
BRCA1	Chr17:41197637	c.*58C>T	NM_007294.3	rs137892861
BRCA1	Chr17:41197859	c.5468-40T>A	NM_007294.3	rs80358151
BRCA1	Chr17:41199745	c.5407-25T>A	NM_007294.3	rs758780152
BRCA1	Chr17:41206122	c.5277+2916_5277+2946delAAATTCTAGTGCTTTGGATTTTTTCCTCCATinsGG	NM_007294.3	
BRCA1	Chr17:41209164	c.5194-12G>A	NM_007294.3	rs80358079
BRCA1	Chr17:41256984	c.213-11T>G	NM_007294.3	rs80358061

BRCA1	Chr17:41256985	c.213-12A>G	NM_007294.3	rs80358163
BRCA1	Chr17:41256988	c.213-15A>G	NM_007294.3	
BRCA1	Chr17:41276134	c.-19-2A>G	NM_007294.3	
BRCA2	Chr13:32889805	c.-40+1G>A	NM_000059.3	
BRCA2	Chr13:32953872	c.8954-15T>G	NM_000059.3	
BRCA2	Chr13:32971007	c.9502-28A>G	NM_000059.3	rs397508059
BRIP1	Chr17:59858864	c.1629-498A>T	NM_032043.2	
BTK	ChrX:100609705	c.1567-23A>C	NM_000061.2	
BTK	ChrX:100609705	c.1567-23A>G	NM_000061.2	
BTK	ChrX:100613695	c.895-11C>A	NM_000061.2	
BTK	ChrX:100629415	c.240+109C>A	NM_000061.2	
BTK	ChrX:100629416	c.240+108T>G	NM_000061.2	
BTK	ChrX:100629827	c.142-205A>G	NM_000061.2	
BTK	ChrX:100641044	c.-31+6T>G	NM_000061.2	
BTK	ChrX:100641045	c.-31+5G>A	NM_000061.2	
BTK	ChrX:100641045	c.-31+5G>C	NM_000061.2	
BTK	ChrX:100641045	c.-31+5G>T	NM_000061.2	rs1131691354
BTK	ChrX:100641049	c.-31+1G>A	NM_000061.2	
BTK	ChrX:100641049	c.-31+1G>C	NM_000061.2	
BTK	ChrX:100641050	c.-31G>A	NM_000061.2	
BTK	ChrX:100641212	c.-193A>G	NM_000061.2	
C1QB	Chr1:22985931	c.-17-2A>C	NM_000491.3	
C7	Chr5:40931143	c.63-23T>A	NM_000587.2	rs772462732
CCDC39	Chr3:180367941	c.1167+1248A>G	NM_181426.1	
CD40LG	ChrX:135736517	c.289-15T>A	NM_000074.2	
CD40LG	ChrX:135737600	c.347-915A>T	NM_000074.2	
CDKN2A	Chr9:21968346	c.458-105A>G	NM_000077.4	
CDKN2A	Chr9:21972311	c.151-1104C>G	NM_000077.4	
CDKN2A	Chr9:21973573	c.150+1104C>A	NM_000077.4	rs756102261
CFTR	Chr7:117119654	c.-495C>T	NM_000492.3	rs397507565
CFTR	Chr7:117119900	c.-249G>C	NM_000492.3	
CFTR	Chr7:117119984	c.-165G>A	NM_000492.3	rs145483167
CFTR	Chr7:117120064	c.-85C>G	NM_000492.3	
CFTR	Chr7:117120115	c.-34C>T	NM_000492.3	rs756314710
CFTR	Chr7:117120325	c.53+124T>C	NM_000492.3	
CFTR	Chr7:117199500	c.1393-18G>A	NM_000492.3	rs397508199
CFTR	Chr7:117218381	c.1585-9412A>G	NM_000492.3	rs397508229
CFTR	Chr7:117227774	c.1585-19T>C	NM_000492.3	rs778457306
CFTR	Chr7:117229521	c.1680-886A>G	NM_000492.3	rs397508266
CFTR	Chr7:117229524	c.1680-883A>G	NM_000492.3	

CFTR	Chr7:117229530	c.1680-877G>T	NM_000492.3	rs397508261
CFTR	Chr7:117243855	c.2908+19G>C	NM_000492.3	rs370683572
CFTR	Chr7:117246713	c.2909-15T>G	NM_000492.3	rs397508455
CFTR	Chr7:117246840	c.2988+33G>T	NM_000492.3	
CFTR	Chr7:117251609	c.3140-26A>G	NM_000492.3	rs76151804
CFTR	Chr7:117251624	c.3140-11A>G	NM_000492.3	
CFTR	Chr7:117266272	c.3469-1304C>G	NM_000492.3	
CFTR	Chr7:117267864	c.3717+40A>G	NM_000492.3	rs397508595
CFTR	Chr7:117280015	c.3718-2477C>T	NM_000492.3	rs75039782
CFTR	Chr7:117282680	c.3873+33A>G	NM_000492.3	rs397508622
CFTR	Chr7:117288374	c.3874-4522A>G	NM_000492.3	
CHD7	Chr8:61734568	c.2836-15C>G	NM_017780.3	
CHD7	Chr8:61757794	c.5051-15T>A	NM_017780.3	
CHD7	Chr8:61763035	c.5405-17G>A	NM_017780.3	rs794727423
CLCN7	Chr16:1506057	c.916+57A>T	NM_001287.5	
COG6	Chr13:40273614	c.1167-24A>G	NM_020751.2	rs730882236
CTSC	Chr11:88070895	c.-55C>A	NM_001814.4	rs766114323
CYBB	ChrX:37639262	c.-69A>C	NM_000397.3	
CYBB	ChrX:37639264	c.-67T>C	NM_000397.3	
CYBB	ChrX:37639266	c.-65C>T	NM_000397.3	
CYBB	ChrX:37639267	c.-64C>T	NM_000397.3	
CYBB	ChrX:37641330	c.46-11T>G	NM_000397.3	
CYBB	ChrX:37654041	c.483+978G>T	NM_000397.3	
CYBB	ChrX:37656474	c.674+1080A>G	NM_000397.3	
CYBB	ChrX:37656731	c.674+1337T>G	NM_000397.3	
CYBB	ChrX:37657051	c.675-1157A>G	NM_000397.3	
CYBB	ChrX:37664248	c.1152-11T>G	NM_000397.3	
DGKE	Chr17:54925466	c.888+40A>G	NM_003647.2	
DKC1	ChrX:153991099	c.-142C>G	NM_001363.3	rs199422241
DKC1	ChrX:153991100	c.-141C>G	NM_001363.3	
DKC1	ChrX:153993704	c.85-15T>C	NM_001363.3	
DNMT3B	Chr20:31395557	c.2421-11G>A	NM_006892.3	rs547940069
DOCK8	Chr9:317025	c.742-18C>G	NM_203447.3	rs112373444
DOCK8	Chr9:317028	c.742-15T>G	NM_203447.3	rs111627162
DOCK8	Chr9:368196	c.1797+61A>C	NM_203447.3	rs786205596
EP300	Chr22:41537040	c.1879-12A>G	NM_001429.3	
EPCAM	Chr2:47606078	c.556-14A>G	NM_002354.2	rs376155665
FANCA	Chr16:89816056	c.3239+82T>G	NM_000135.2	
FANCA	Chr16:89818822	c.2982-192A>G	NM_000135.2	
FANCA	Chr16:89831215	c.2778+83C>G	NM_000135.2	rs750997715

FANCA	Chr16:89836111	c.2504+134A>G	NM_000135.2	
FANCA	Chr16:89836805	c.2223-138A>G	NM_000135.2	
FANCA	Chr16:89849346	c.1567-20A>G	NM_000135.2	rs775154397
FANCA	Chr16:89864654	c.893+920C>A	NM_000135.2	
FANCC	Chr9:98011653	c.-78-2A>G	NM_000136.2	rs587779898
FANCD2	Chr3:10083186	c.696-121C>G	NM_033084.3	
FANCD2	Chr3:10106024	c.1948-16T>G	NM_033084.3	
FANCI	Chr15:89825208	c.1583+142C>T	NM_001113378.1	
FAS	Chr10:90770494	c.506-16A>G	NM_000043.4	
FASLG	Chr1:172628081	c.-261T>C	NM_000639.1	
FERMT1	Chr20:6074846	c.1139+740G>A	NM_017671.4	rs869312728
FERMT1	Chr20:6103422	c.-20A>G	NM_017671.4	rs869312722
FOXP3	ChrX:49106917	c.*878A>G	NM_014009.3	
FOXP3	ChrX:49106919	c.*876A>G	NM_014009.3	
GATA1	ChrX:48649496	c.-19-2A>G	NM_002049.3	
GATA2	Chr3:128202131	c.1017+572C>T	NM_032638.4	
GATA2	Chr3:128202171	c.1017+532T>A	NM_032638.4	
GBA	Chr1:155208109	c.589-12C>G	NM_000157.3	
GINS1	Chr20:25388397	c.-60A>G	NM_021067.3	
GINS1	Chr20:25388409	c.-48C>G	NM_021067.3	
GP1BB	Chr22:19710933	c.-160C>G	NM_000407.4	rs730882059
HPS3	Chr3:148888270	c.2888-1612G>A	NM_032383.3	rs281865096
IL10RB	Chr21:34668714	c.*52C>T	NM_000628.4	
IL2RG	ChrX:70327278	c.*308A>G	NM_000206.2	
IL2RG	ChrX:70330553	c.270-15A>G	NM_000206.2	
IL2RG	ChrX:70331494	c.-105C>T	NM_000206.2	
IL7R	Chr5:35867853	c.379+288G>A	NM_002185.3	
IRAK4	Chr12:44178047	c.1188+520A>G	NM_016123.3	
ITGA2B	Chr17:42449567	c.*165T>C	NM_000419.3	
ITGA2B	Chr17:42455177	c.2095-19T>A	NM_000419.3	
ITGA2B	Chr17:42458507	c.1211-78A>G	NM_000419.3	
ITGA2B	Chr17:42463181	c.408+11C>A	NM_000419.3	
ITGA2B	Chr17:42470923	c.-4082G>A	NM_000419.3	
ITGB2	Chr21:46320404	c.742-14C>A	NM_000211.3	rs183204825
ITGB2	Chr21:46321660	c.500-12T>G	NM_000211.3	
JAK3	Chr19:17943239	c.2680+89G>A	NM_000215.3	
JAK3	Chr19:17946035	c.1915-11G>A	NM_000215.3	
KLF1	Chr19:12998078	c.-124T>C	NM_006563.3	
KLF1	Chr19:12998108	c.-154C>T	NM_006563.3	rs372651309
LAMTOR2	Chr1:156028185	c.*23C>A	NM_014017.3	

MEFV	Chr16:3306969	c.-382C>G	NM_000243.2	
MLH1	Chr3:37034997	c.-42C>T	NM_000249.3	rs41285097
MLH1	Chr3:37035012	c.-27C>A	NM_000249.3	rs587779001
MLH1	Chr3:37038099	c.117-11T>A	NM_000249.3	rs267607711
MLH1	Chr3:37050292	c.454-13A>G	NM_000249.3	rs267607749
MLH1	Chr3:37061788	c.885-9_887dupTCCTGACAGTTT	NM_000249.3	rs63751620
MLH1	Chr3:37070436	c.1558+13T>A	NM_000249.3	rs267607834
MSH2	Chr2:47630106	c.-225G>C	NM_000251.2	rs138068023
MSH2	Chr2:47630150	c.-181G>A	NM_000251.2	rs786201698
MSH2	Chr2:47630251	c.-78_-77delTG	NM_000251.2	rs587779182
MSH6	Chr2:48034014	c.*15A>C	NM_000179.2	
MYO5B	Chr18:47365503	c.4852+11A>G	NM_001080467.2	
NF1	Chr17:29422055	c.-273A>C	NM_001042492.2	
NF1	Chr17:29422056	c.-272G>A	NM_001042492.2	
NF1	Chr17:29475515	c.61-7486G>T	NM_001042492.2	
NF1	Chr17:29488136	c.288+2025T>G	NM_001042492.2	
NF1	Chr17:29508426	c.587-14T>A	NM_001042492.2	
NF1	Chr17:29508428	c.587-12T>A	NM_001042492.2	
NF1	Chr17:29510334	c.888+651T>A	NM_001042492.2	
NF1	Chr17:29510427	c.888+744A>G	NM_001042492.2	
NF1	Chr17:29510472	c.888+789A>G	NM_001042492.2	
NF1	Chr17:29527428	c.889-12T>A	NM_001042492.2	
NF1	Chr17:29530107	c.1260+1604A>G	NM_001042492.2	
NF1	Chr17:29533239	c.1261-19G>A	NM_001042492.2	
NF1	Chr17:29534143	c.1392+754T>G	NM_001042492.2	
NF1	Chr17:29540877	c.1393-592A>G	NM_001042492.2	
NF1	Chr17:29542762	c.1527+1159C>T	NM_001042492.2	
NF1	Chr17:29548419	c.1642-449A>G	NM_001042492.2	rs863224655
NF1	Chr17:29553439	c.2002-14C>G	NM_001042492.2	
NF1	Chr17:29554225	c.2252-11T>G	NM_001042492.2	
NF1	Chr17:29556025	c.2410-18C>G	NM_001042492.2	
NF1	Chr17:29556027	c.2410-16A>G	NM_001042492.2	
NF1	Chr17:29556028	c.2410-15A>G	NM_001042492.2	
NF1	Chr17:29556031	c.2410-12T>G	NM_001042492.2	
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NF1	Chr17:29563299	c.3974+260T>G	NM_001042492.2	
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NF1	Chr17:29588715	c.4578-14T>G	NM_001042492.2	

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NF1	Chr17:29657848	c.5812+332A>G	NM_001042492.2	rs863224491
NF1	Chr17:29661577	c.5813-279A>G	NM_001042492.2	
NF1	Chr17:29664375	c.6428-11T>G	NM_001042492.2	
NF1	Chr17:29664618	c.6642+18A>G	NM_001042492.2	
NF1	Chr17:29676126	c.7190-12T>A	NM_001042492.2	
NF1	Chr17:29685177	c.7971-321C>G	NM_001042492.2	
NF1	Chr17:29685481	c.7971-17C>G	NM_001042492.2	
NF1	Chr17:29685665	c.8113+25A>T	NM_001042492.2	
OFD1	ChrX:13768358	c.935+706A>G	NM_003611.2	rs730880283
OFD1	ChrX:13773245	c.1130-22_1130-19delAATT	NM_003611.2	rs312262865
PALB2	Chr16:23649285	c.109-12T>A	NM_024675.3	rs774949203
PARN	Chr16:14724045	c.-165+2C>T	NM_001134477.2	
PMM2	Chr16:8898599	c.179-25A>G	NM_000303.2	rs760689221
PMM2	Chr16:8941558	c.640-23A>G	NM_000303.2	
PNP	Chr14:20942914	c.286-18G>A	NM_000270.3	
POLR3A	Chr10:79769273	c.1909+22G>A	NM_007055.3	rs191875469
POLR3A	Chr10:79769277	c.1909+18G>A	NM_007055.3	rs267608677
PTEN	Chr10:89622883–89623482			
PTEN	Chr10:89622988	c.-1239A>G	NM_000314.6	
PTEN	Chr10:89623049	c.-1178C>T	NM_000314.6	
PTEN	Chr10:89623056	c.-1171C>T	NM_000314.6	rs587779981
PTEN	Chr10:89623116	c.-1111A>G	NM_000314.6	
PTEN	Chr10:89623226	c.-1001T>C	NM_000314.4	
PTEN	Chr10:89623296	c.-931G>A	NM_000314.4	rs587781959
PTEN	Chr10:89623306	c.-921G>T	NM_000314.4	
PTEN	Chr10:89623331	c.-896T>C	NM_000314.4	
PTEN	Chr10:89623365	c.-862G>T	NM_000314.4	rs587776675
PTEN	Chr10:89623373	c.-854C>G	NM_000314.4	
PTEN	Chr10:89623462	c.-765G>A	NM_000314.4	
PTEN	Chr10:89692749	c.254-21G>C	NM_000314.4	
PTEN	Chr10:89725294	c.*65T>A	NM_000314.4	
PTPN11	Chr12:112915602	c.934-59T>A	NM_002834.3	
RAG2	Chr11:36619652	c.-28G>C	NM_000536.3	
RNASEH2B	Chr13:51501530	c.65-13G>A	NM_024570.3	
RPGR	ChrX:38160137	c.1059+363G>A	NM_001034853.1	
RPS7	Chr2:3622941	c.-19+1G>T	NM_001011.3	
RPS7	Chr2:3622942	c.-19+2T>C	NM_001011.3	
RPSA	Chr3:39448260	c.-34+5G>C	NM_002295.4	

SEC23B	Chr20:18488060	c.-571A>G	NM_006363.4	rs559854357
SEC23B	Chr20:18488615	c.-16A>G	NM_006363.4	
SEC23B	Chr20:18491731	c.221+31A>G	NM_006363.4	
SEC23B	Chr20:18491863	c.221+163A>G	NM_006363.4	rs573898514
SEC23B	Chr20:18492791	c.222-78C>T	NM_006363.4	rs150393520
SEC23B	Chr20:18526845	c.1743+168A>G	NM_006363.4	rs111951711
SERPING1	Chr11:57365055	c.-163C>T	NM_000062.2	
SERPING1	Chr11:57365057	c.-161A>G	NM_000062.2	
SERPING1	Chr11:57365720	c.-22-2A>C	NM_000062.2	
SERPING1	Chr11:57365720	c.-22-2A>G	NM_000062.2	
SERPING1	Chr11:57365721	c.-22-1G>A	NM_000062.2	
SERPING1	Chr11:57373471	c.686-12A>G	NM_000062.2	
SERPING1	Chr11:57373867	c.890-14C>G	NM_000062.2	
SERPING1	Chr11:57381788	c.1250-13G>A	NM_000062.2	
SLC39A4	Chr8:145641963	c.192+19G>A	NM_130849.3	rs368996660
SPINK5	Chr5:147465956	c.283-12T>A	NM_006846.3	
SPINK5	Chr5:147484503	c.1431-12G>A	NM_006846.3	rs368134354
SPINK5	Chr5:147491511	c.1820+53G>A	NM_006846.3	rs754599628
TBX1	Chr22:19743578	c.-777C>T	NM_080647.1	
TBX1	Chr22:19743735	c.-620A>C	NM_080647.1	rs536892777
TCIRG1	Chr11:67806587	c.-5+1G>C	NM_006019.3	
TCIRG1	Chr11:67806587	c.-5+1G>T	NM_006019.3	
TCIRG1	Chr11:67816893	c.1887+132T>C	NM_006019.3	
TCIRG1	Chr11:67816903	c.1887+142T>A	NM_006019.3	
TCIRG1	Chr11:67816907	c.1887+146G>A	NM_006019.3	
TCIRG1	Chr11:67816910	c.1887+149C>T	NM_006019.3	
TCN2	Chr22:31011112	c.581-176A>G	NM_000355.3	rs372866837
TCN2	Chr22:31011112	c.581-176A>T	NM_000355.3	
TERC	Chr3:169482870	n.-22C>T	NR_001566.1	
TERC	Chr3:169482906		NR_001566.1	
TERT	Chr5:1295161	c.-57A>C	NM_198253.2	
TGFBR2	Chr3:30648317	c.-59C>T	NM_001024847.2	
THBD	Chr20:23030443	c.-302C>A	NM_000361.2	
TP53	Chr17:7577647	c.673-39G>A	NM_000546.5	
TP53	Chr17:7579601	c.97-11C>G	NM_000546.5	
TP53	Chr17:7590694	c.-29+1G>T	NM_000546.5	
TRNT1	Chr3:3188088	c.609-26T>C	NM_182916.2	
TTC7A	Chr2:47249223	c.1510+105T>A	NM_020458.2	
UNC13D	Chr17:73826245	c.2831-13G>A	NM_199242.2	
UNC13D	Chr17:73827442	c.2448-13G>A	NM_199242.2	rs753762300

UNC13D	Chr17:73839907	c.118-307G>A	NM_199242.2	
UNC13D	Chr17:73839908	c.118-308C>T	NM_199242.2	
ZAP70	Chr2:98349927	c.838-80G>A	NM_001079.3	rs113994173
ZAP70	Chr2:98354447	c.1624-11G>A	NM_001079.3	rs730880318

Test strengths

The strengths of this test include:

- CAP accredited laboratory
- CLIA-certified personnel performing clinical testing in a CLIA-certified laboratory
- Powerful sequencing technologies, advanced target enrichment methods and precision bioinformatics pipelines ensure superior analytical performance
- Careful construction of clinically effective and scientifically justified gene panels
- Some of the panels include the whole mitochondrial genome (please see the Panel Content section)
- Our Nucleus online portal providing transparent and easy access to quality and performance data at the patient level
- Our publicly available analytic validation demonstrating complete details of test performance
- ~2,000 non-coding disease causing variants in our clinical grade NGS assay for panels (please see 'Non-coding disease causing variants covered by this panel' in the Panel Content section)
- Our rigorous variant classification scheme
- Our systematic clinical interpretation workflow using proprietary software enabling accurate and traceable processing of NGS data
- Our comprehensive clinical statements

Test limitations

This test does not detect the following:

- Complex inversions
- Gene conversions
- Balanced translocations
- Some of the panels include the whole mitochondrial genome but not all (please see the Panel Content section)
- Repeat expansion disorders unless specifically mentioned
- Non-coding variants deeper than ±20 base pairs from exon-intron boundary unless otherwise indicated (please see above Panel Content / non-coding variants covered by the panel).

This test may not reliably detect the following:

- Low level mosaicism in nuclear genes (variant with a minor allele fraction of 14.6% is detected with 90% probability)
- Stretches of mononucleotide repeats
- Low level heteroplasmy in mtDNA (>90% are detected at 5% level)
- Indels larger than 50bp
- Single exon deletions or duplications
- Variants within pseudogene regions/duplicated segments
- Some disease causing variants present in mtDNA are not detectable from blood, thus post-mitotic tissue such as skeletal muscle may be required for establishing molecular diagnosis.

The sensitivity of this test may be reduced if DNA is extracted by a laboratory other than Blueprint Genetics.

Customization (removing or adding genes) is not currently available for this panel.

For additional information, please refer to the Test performance section and see our Analytic Validation.

Test Performance

The genes on the panel have been carefully selected based on scientific literature, mutation databases and our experience.

Our panels are sectioned from our high-quality, clinical grade NGS assay. Please see our sequencing and detection performance table for details regarding our ability to detect different types of alterations (Table).

Assays have been validated for various sample types including EDTA-blood, isolated DNA (excluding from formalin fixed paraffin embedded tissue), saliva and dry blood spots (filter cards). These sample types were selected in order to maximize the likelihood for high-quality DNA yield. The diagnostic yield varies depending on the assay used, referring healthcare professional, hospital and country. Plus analysis increases the likelihood of finding a genetic diagnosis for your patient, as large deletions and duplications cannot be detected using sequence analysis alone. Blueprint Genetics' Plus Analysis is a combination of both sequencing and deletion/duplication (copy number variant (CNV)) analysis.

The performance metrics listed below are from an initial validation performed at our main laboratory in Finland. The performance metrics of our laboratory in Seattle, WA, are equivalent.

Performance of Blueprint Genetics high-quality, clinical grade NGS sequencing assay for panels.

	Sensitivity % (TP/(TP+FN)	Specificity %
Single nucleotide variants	99.89% (99,153/99,266)	>99.9999%
Insertions, deletions and indels by sequence analysis		
1-10 bps	99.2% (7,745/7,806)	>99.9999%
11-50 bps	99.13% (2,524/2,546)	>99.9999%
Copy number variants (exon level dels/dups)		
1 exon level deletion (heterozygous)	100% (20/20)	NA
1 exon level deletion (homozygous)	100% (5/5)	NA
1 exon level deletion (het or homo)	100% (25/25)	NA
2-7 exon level deletion (het or homo)	100% (44/44)	NA
1-9 exon level duplication (het or homo)	75% (6/8)	NA
Simulated CNV detection		
5 exons level deletion/duplication	98.7%	100.00%
Microdeletion/-duplication sdrs (large CNVs, n=37))		
Size range (0.1-47 Mb)	100% (25/25)	

The performance presented above reached by Blueprint Genetics high-quality, clinical grade NGS sequencing assay with the following coverage metrics

Mean sequencing depth	143X
Nucleotides with >20x sequencing coverage (%)	99.86%

Performance of Blueprint Genetics Mitochondrial Sequencing Assay.

	Sensitivity %	Specificity %
ANALYTIC VALIDATION (NA samples; n=4)		
Single nucleotide variants		
Heteroplasmic (45-100%)	100.0% (50/50)	100.0%
Heteroplasmic (35-45%)	100.0% (87/87)	100.0%
Heteroplasmic (25-35%)	100.0% (73/73)	100.0%
Heteroplasmic (15-25%)	100.0% (77/77)	100.0%
Heteroplasmic (10-15%)	100.0% (74/74)	100.0%
Heteroplasmic (5-10%)	100.0% (3/3)	100.0%
Heteroplasmic (<5%)	50.0% (2/4)	100.0%
CLINICAL VALIDATION (n=76 samples)		
All types		
Single nucleotide variants n=2026 SNVs		
Heteroplasmic (45-100%)	100.0% (1940/1940)	100.0%
Heteroplasmic (35-45%)	100.0% (4/4)	100.0%
Heteroplasmic (25-35%)	100.0% (3/3)	100.0%
Heteroplasmic (15-25%)	100.0% (3/3)	100.0%
Heteroplasmic (10-15%)	100.0% (9/9)	100.0%
Heteroplasmic (5-10%)	92.3% (12/13)	99.98%
Heteroplasmic (<5%)	88.9% (48/54)	99.93%
Insertions and deletions by sequence analysis n=40 indels		
Heteroplasmic (45-100%) 1-10bp	100.0% (32/32)	100.0%
Heteroplasmic (5-45%) 1-10bp	100.0% (3/3)	100.0%
Heteroplasmic (<5%) 1-10bp	100.0% (5/5)	99,997%
SIMULATION DATA /(mitomap mutations)		
Insertions, and deletions 1-24 bps by sequence analysis; n=17		
Homoplasmic (100%) 1-24bp	100.0% (17/17)	99.98%

Heteroplasmic (50%)	100.0% (17/17)	99.99%
Heteroplasmic (25%)	100.0% (17/17)	100.0%
Heteroplasmic (20%)	100.0% (17/17)	100.0%
Heteroplasmic (15%)	100.0% (17/17)	100.0%
Heteroplasmic (10%)	94.1% (16/17)	100.0%
Heteroplasmic (5%)	94.1% (16/17)	100.0%
Copy number variants (separate artifical mutations; n=1500)		
Homoplasmic (100%) 500 bp, 1kb, 5 kb	100.0%	100.0%
Heteroplasmic (50%) 500 bp, 1kb, 5 kb	100.0%	100.0%
Heteroplasmic (30%) 500 bp, 1kb, 5 kb	100.0%	100.0%
Heteroplasmic (20%) 500 bp, 1kb, 5 kb	99.7%	100.0%
Heteroplasmic (10%) 500 bp, 1kb, 5 kb	99.0%	100.0%
The performance presented above reached by following coverage metrics at assay level (n=66)		
	Mean of medians	Median of medians
Mean sequencing depth MQ0 (clinical)	18224X	17366X
Nucleotides with >1000x MQ0 sequencing coverage (%) (clinical)	100%	
rho zero cell line (=no mtDNA), mean sequencing depth	12X	

Bioinformatics

The target region for each gene includes coding exons and ±20 base pairs from the exon-intron boundary. In addition, the panel includes non-coding and regulatory variants if listed above (Non-coding variants covered by the panel). Some regions of the gene(s) may be removed from the panel if specifically mentioned in the 'Test limitations" section above. If the test includes the mitochondrial genome the target region gene list contains the mitochondrial genes. The sequencing data generated in our laboratory is analyzed with our proprietary data analysis and annotation pipeline, integrating state-of-the art algorithms and industry-standard software solutions. Incorporation of rigorous quality control steps throughout the workflow of the pipeline ensures the consistency, validity and accuracy of results. Our pipeline is streamlined to maximize sensitivity without sacrificing specificity. We have incorporated a number of reference population databases and mutation databases including, but not limited, to 1000 Genomes Project, gnomAD, ClinVar and HGMD into our clinical interpretation software to make the process effective and efficient. For missense variants, *in silico* variant prediction tools such as SIFT, PolyPhen,MutationTaster are used to assist with variant classification. Through our online ordering and statement reporting system, Nucleus, ordering providers have access to the details of the analysis, including patient specific sequencing metrics, a gene level coverage plot and a list of regions with suboptimal coverage (<20X for nuclear genes and <1000X for mtDNA) if applicable. This reflects our mission to build fully transparent diagnostics where ordering providers can easily visualize the crucial details of the analysis process.

Clinical Interpretation

We provide customers with the most comprehensive clinical report available on the market. Clinical interpretation requires a fundamental understanding of clinical genetics and genetic principles. At Blueprint Genetics, our PhD molecular geneticists,

medical geneticists and clinical consultants prepare the clinical statement together by evaluating the identified variants in the context of the phenotypic information provided in the requisition form. Our goal is to provide clinically meaningful statements that are understandable for all medical professionals regardless of whether they have formal training in genetics.

Variant classification is the corner stone of clinical interpretation and resulting patient management decisions. Our classifications follow the ACMG guideline 2015.

The final step in the analysis is orthogonal confirmation. Sequence and copy number variants classified as pathogenic, likely pathogenic and variants of uncertain significance (VUS) are confirmed using bi-directional Sanger sequencing or by orthogonal methods such as qPCR/ddPCR when they do not meet our stringent NGS quality metrics for a true positive call.

Our clinical statement includes tables for sequencing and copy number variants that include basic variant information (genomic coordinates, HGVS nomenclature, zygosity, allele frequencies, in silico predictions, OMIM phenotypes and classification of the variant). In addition, the statement includes detailed descriptions of the variant, gene and phenotype(s) including the role of the specific gene in human disease, the mutation profile, information about the gene's variation in population cohorts and detailed information about related phenotypes. We also provide links to the references, abstracts and variant databases used to help ordering providers further evaluate the reported findings if desired. The conclusion summarizes all of the existing information and provides our rationale for the classification of the variant.

Identification of pathogenic or likely pathogenic variants in dominant disorders or their combinations in different alleles in recessive disorders are considered molecular confirmation of the clinical diagnosis. In these cases, family member testing can be used for risk stratification. We do not recommend using variants of uncertain significance (VUS) for family member risk stratification or patient management. Genetic counseling is recommended.

Our interpretation team analyzes millions of variants from thousands of individuals with rare diseases. Our internal database and our understanding of variants and related phenotypes increases with every case analyzed. Our laboratory is therefore well-positioned to re-classify previously reported variants as new information becomes available. If a variant previously reported by Blueprint Genetics is re-classified, our laboratory will issue a follow-up statement to the original ordering health care provider at no additional cost.

CPT code(s) *

81162, 81218, 81249, 81222, 81223, 81292, 81294, 81295, 81297, 81298, 81300, 81317, 81319, 81321, 81323, 81307, 81351, 81403 X2, 81404 X7, 81405 X10, 81406 X13, 81407 X2, 81408 X2, 81479

* The CPT codes provided are based on AMA guidelines and are for informational purposes only. CPT coding is the sole responsibility of the billing party. Please direct any questions regarding coding to the payer being billed.

Sample Requirements

- Blood (min. 1ml) in an EDTA tube
- Extracted DNA, min. 2 µg in TE buffer or equivalent
- Saliva (Please see Sample Requirements for accepted saliva kits)

Label the sample tube with your patient's name, date of birth and the date of sample collection.

We do not accept DNA samples isolated from formalin-fixed paraffin-embedded (FFPE) tissue. In addition, if the patient is affected with a hematological malignancy, DNA extracted from a non-hematological source (e.g. skin fibroblasts) is strongly recommended.

Please note that, in rare cases, mitochondrial genome (mtDNA) variants may not be detectable in blood or saliva in which case DNA extracted from post-mitotic tissue such as skeletal muscle may be a better option.

Read more about our sample requirements here.