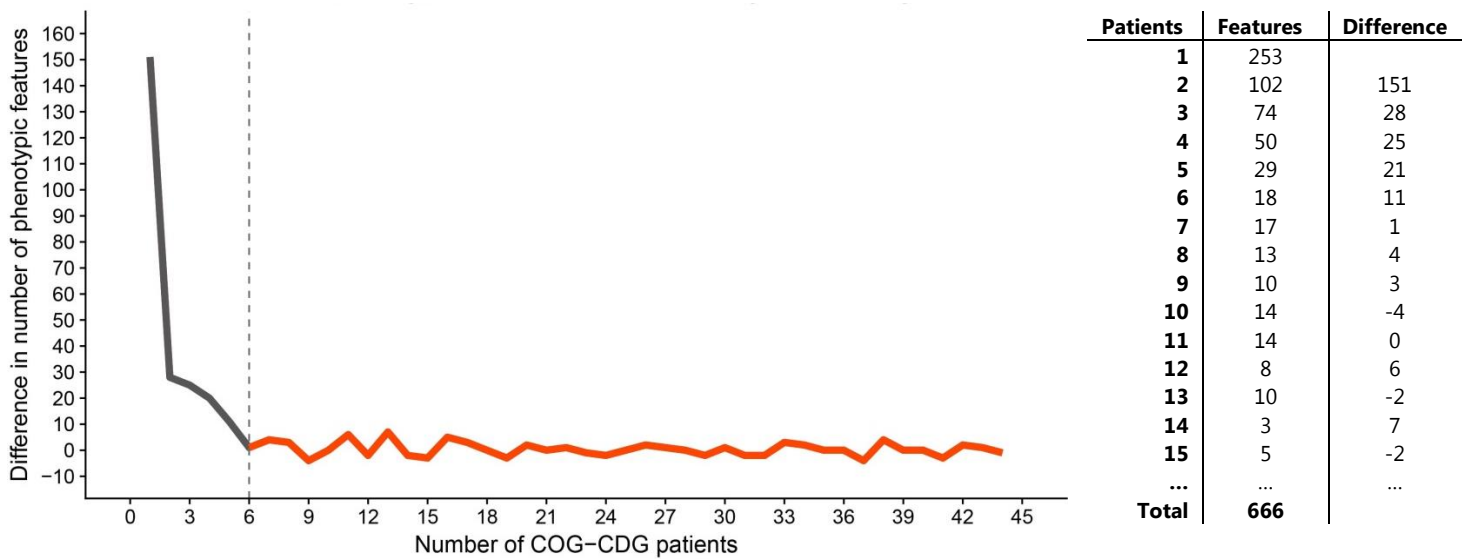
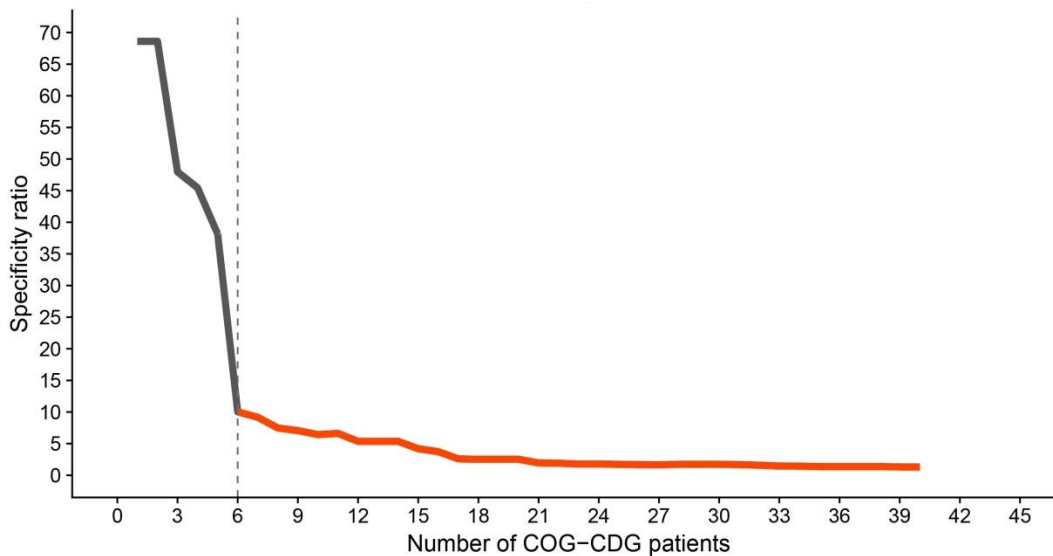


Supplementary Figure 1: Number of phenotypic features versus phenotypic frequency in COG-CDG



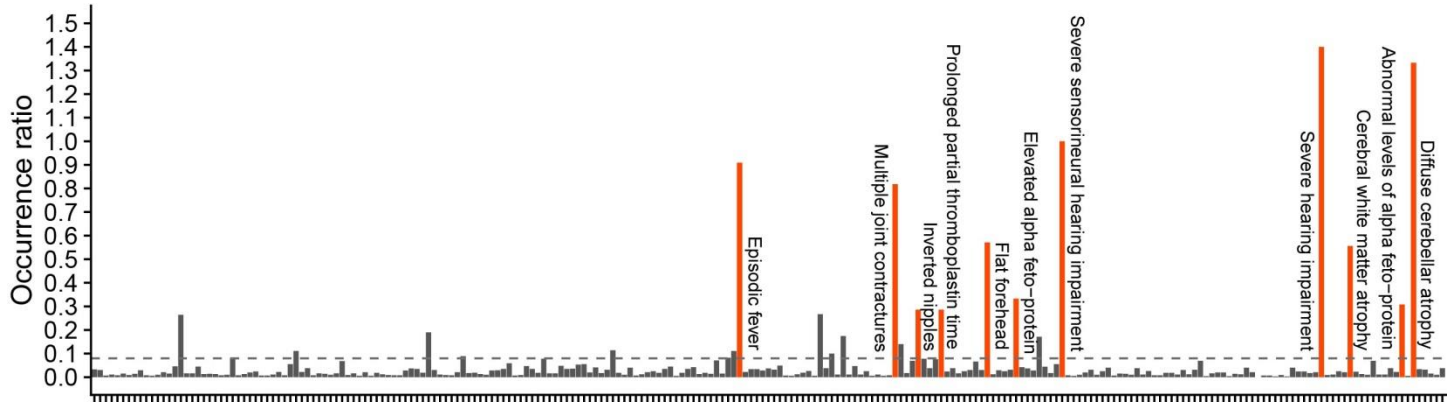
A sliding scale was noted of only one phenotypic feature that is described in all patients, towards many phenotypic features that are described in only one COG-CDG patient (table, column "features"). For features described in at least six COG-CDG patients the number of phenotypic features added to the total list per added patient frequency is very constant (Figure). This suggests that zooming in on features described in at least six COG-CDG patients provides the most relevant focus.

Supplementary Figure 2: Specificity ratio versus phenotypic frequency in COG-CDG



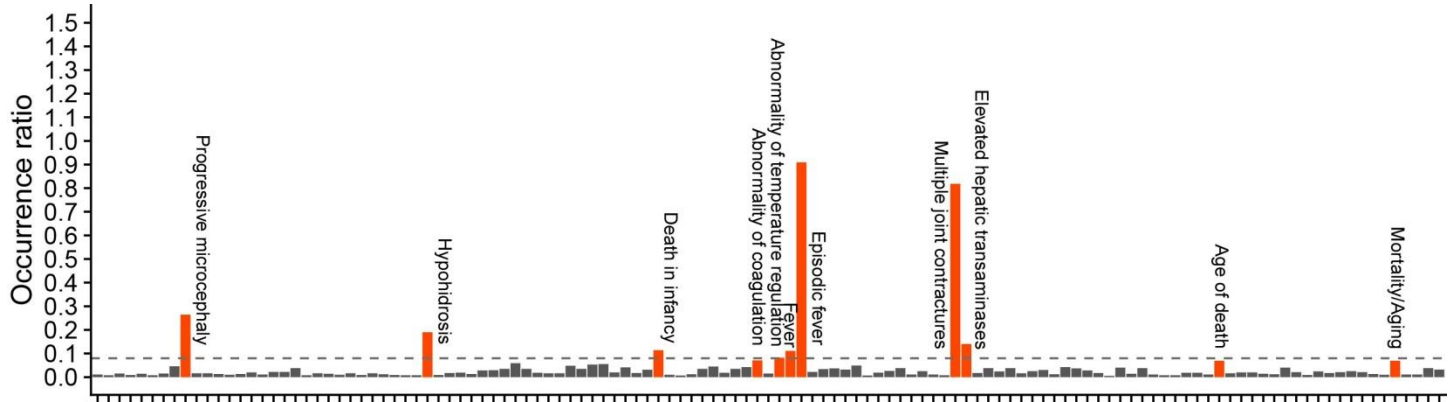
A "specificity ratio" was calculated: the ratio of the median occurrence ratio of the top 10 phenotypic features over the median occurrence ratio of all other phenotypic features. This specificity ratio in relation to the number of COG-CDG patients presenting with a phenotypic feature supported the cut-off value of at least six patients presenting with a certain phenotypic feature.

Supplementary Figure 3: Phenotypic specificity when assessing features present in at least four patients



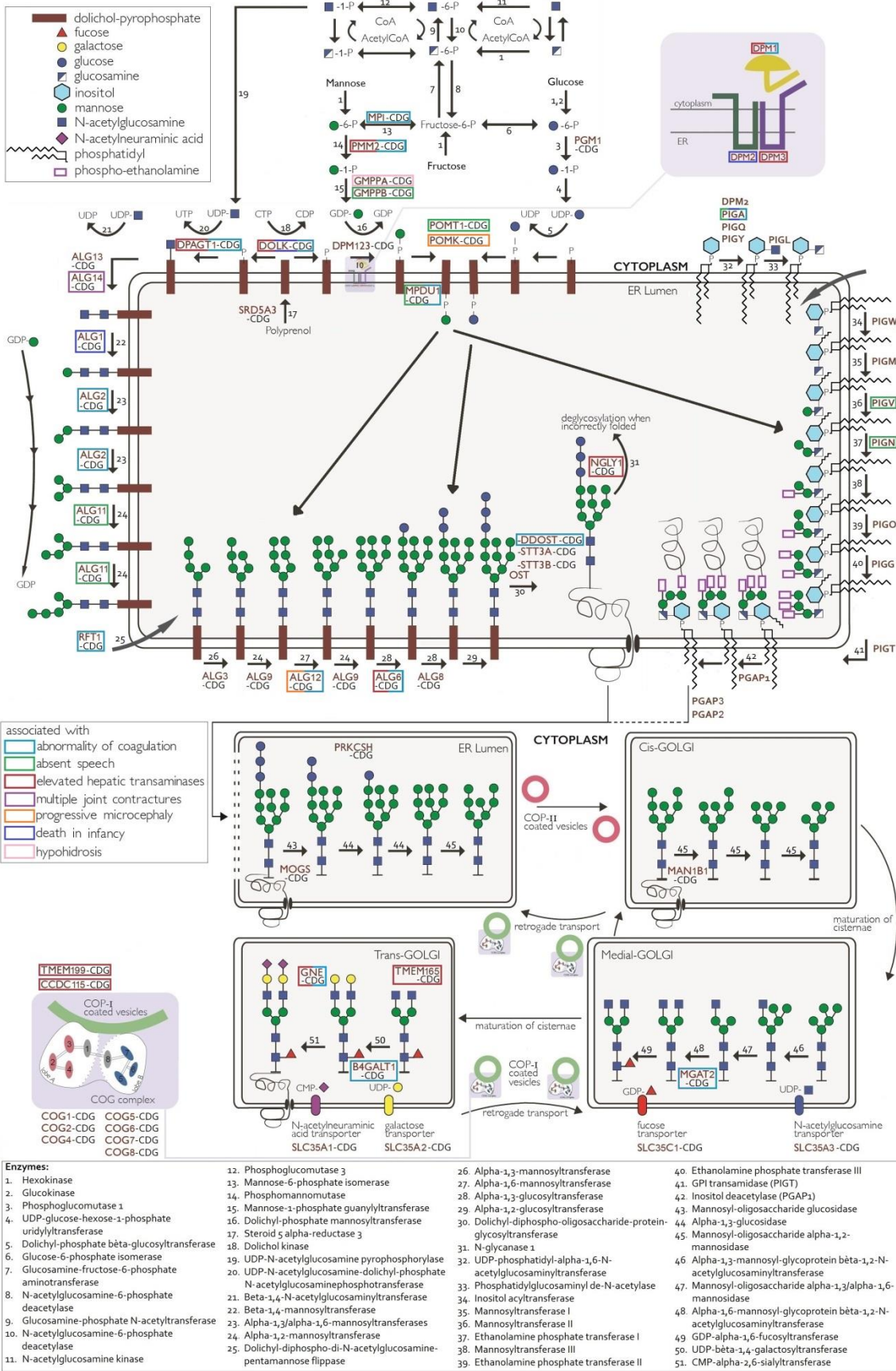
A wider zoom than the cut-off value of a phenotypic feature being present in at least six COG-CDG patients, namely being present in at least four COG-CDG patients, results in a longer list of less relevant features.

Supplementary Figure 4: Phenotypic specificity when assessing features present in at least eight patients



A narrower zoom than the cut-off value of a phenotypic feature being present in at least six COG-CDG patients, namely being present in at least eight COG-CDG patients, results in missing relevant features.

Supplementary Figure 5: Specific phenotypic features in COG-CDG associated with other CDG



The glycosylation process. ER, endoplasmic reticulum; COG, Conserved Oligomeric Golgi; CDG, Congenital Disorder of Glycosylation. Black text: metabolites. Red text: known CDG, caused by a deficiency of the gene encoding the required enzyme. Seven of the ten extracted highly specific phenotypic features are clearly associated with other CDG, depicted in the different colors surrounding the known CDG. For example, abnormality of coagulation and elevated hepatic transaminases are mainly seen in CDG affecting N-glycosylation (process drawn on the left of the ER), while absent speech is seen in CDG affecting O-mannosylation and glycosylphosphatidylinositol anchoring (process drawn on the right of the ER).

Supplementary Notes 1: R code to create figures

```
library('ggplot2')
library('cowplot')

setwd("~/Promotietraject/3) COG-CDG/A) Change of focus")
color<-c('TRUE'='orangered', 'FALSE'='gray34')

# Load files
AllRatios<-read.csv("COG_AllRatios_CSV.csv", sep=";", stringsAsFactors=FALSE)
AllRatios$HPOcode<-factor(AllRatios$HPOcode, levels=unique(AllRatios$HPOcode))
SelRatios<-read.csv("COG_SelRatios_CSV.csv", sep=";", stringsAsFactors=FALSE)
SelRatios$HPOcode<-factor(SelRatios$HPOcode, levels=unique(SelRatios$HPOcode))

# Figure 1A and 1B
p1<-ggplot()+
  geom_bar(data=AllRatios[which(AllRatios[,5]>5),],
  stat='identity', aes(x=HPOcode, y=Ratio, fill=Ratio>=0.08))+
  geom_text(data=AllRatios[which(AllRatios[,6]>=0.08 & AllRatios[,5]>5),],
  aes(x=HPOcode, y=Ratio, label=Feature), size=3, vjust=0)+
  geom_hline(yintercept=0.08, col='gray43', linetype=2)+
  scale_fill_manual(values=color)+
  scale_y_continuous(breaks=seq(0, 1.5, 0.1), limits=c(0, 1.5))+
  labs(x='HPO code', y='Occurrence ratio', title='Phenotypic specificity in
  COG-CDG')+
  theme(axis.text.x=element_text(angle=90, hjust=1, size=7),
  legend.position='none')

p2<-ggplot()+
  geom_bar(data=SelRatios[which(SelRatios[,5]>5),],
  stat='identity', aes(x=HPOcode, y=Ratio, fill=Ratio>=0.07))+
  geom_text(data=SelRatios[which(SelRatios[,6]>=0.07 & SelRatios[,5]>5),],
  aes(x=HPOcode, y=Ratio, label=Feature), size=3, vjust=0)+
  geom_hline(yintercept=0.07, col='gray43', linetype=2)+
  scale_fill_manual(values=color)+
  scale_y_continuous(breaks=seq(0, 1.5, 0.1), limits=c(0, 1.5))+
  labs(x='HPO code', y='Ratio COG-CDG patients over HPO associated genes',
  title='Phenotypic specificity in COG-CDG, excluding super classes of
  episodic fever')+
  theme(axis.text.x=element_text(angle=90, hjust=1, size=7),
  legend.position='none')

plot_grid(p1, p2, ncol=1, axis='rlbt', rel_heights=c(1, 1))
rm(p1, p2)

# Supplementary Figure 1
Diff<-read.csv("COG_difference_CSV.csv", sep=";", stringsAsFactors=FALSE)
ggplot(Diff)+
  geom_line(aes(x=Patients, y=Difference, col=Patients<5), size=2)+
  geom_line(aes(x=Patients, y=Difference, col=Patients>=6), size=2)+
  geom_vline(xintercept=6, col='gray43', linetype=2)+
  scale_color_manual(values=color)+
  scale_y_continuous(breaks=seq(-10, 160, 10), limits=c(-10, 160))+
  scale_x_continuous(breaks=seq(0, 45, 3), limits=c(0, 45))+
  labs(x='Number of COG-CDG patients', y='Difference in number of phenotypic
  features', title='Number of phenotypic features versus phenotypic frequency
  in COG-CDG')+
  theme(legend.position='none')

# Supplementary Figure 2
AllRatios<-AllRatios[order(-AllRatios$Ratio),]
Spec<-setNames(data.frame(matrix(ncol=3, nrow=45)),
c('MedianTop10', 'MedianNoise', 'MedianRatio'))
for(freq in 1:40) {
  Spec[freq, 1]<-median(as.numeric(AllRatios[which(AllRatios[,5]>
(freq-1)), 6][1:10]), na.rm=TRUE)
  Spec[freq, 2]<-median(as.numeric(AllRatios[which(AllRatios[,5]>
(freq-1)), 6][11:length(AllRatios[which(AllRatios[,5]>
(freq-1)), 6])]), na.rm=TRUE)
  Spec[freq, 3]<-(Spec[freq, 1]/Spec[freq, 2])
}
```

```

Spec$Patients<-as.numeric(as.character(rownames(Spec)))
ggplot(Spec)+
  geom_line(aes(x=Patients,y=MedianRatio,col=Patients<5),size=2)+
  geom_line(aes(x=Patients,y=MedianRatio,col=Patients>=6),size=2)+
  geom_vline(xintercept = 6,col='gray43',linetype=2)+
  scale_color_manual(values=color)+
  scale_x_continuous(breaks=seq(0,45,3),limits=c(0,45))+
  scale_y_continuous(breaks=seq(0,70,5),limits=c(0,70))+
  labs(x='Number of COG-CDG patients',y='Specificity ratio',
  title='Specificity ratio versus phenotypic frequency in COG-CDG')+
  theme(legend.position='none')

```

Supplementary Figure 3

```

ggplot()+
  geom_bar(data=AllRatios[which(AllRatios[,5]>3),],
  stat='identity',aes(x=HPOcode,y=Ratio,fill=Ratio>=0.28))+
  geom_text(data=AllRatios[which(AllRatios[,6]>=0.08 & AllRatios[,5]>3),],
  aes(x=HPOcode,y=Ratio,label=Feature),size=3,vjust=0)+
  geom_hline(yintercept=0.08,col='gray43',linetype=2)+
  scale_fill_manual(values=color)+
  scale_y_continuous(breaks=seq(0,1.5,0.1),limits=c(0,1.5))+
  labs(x='HPO code',y='Occurrence ratio', title='Phenotypic specificity in
  COG-CDG')+
  theme(axis.text.x=element_text(angle=90,hjust=1,size=7),
  legend.position='none')

```

Supplementary Figure 4

```

ggplot()+
  geom_bar(data=AllRatios[which(AllRatios[,5]>7),],
  stat='identity',aes(x=HPOcode,y=Ratio,fill=Ratio>=0.06))+
  geom_text(data=AllRatios[which(AllRatios[,6]>=0.08 & AllRatios[,5]>7),],
  aes(x=HPOcode,y=Ratio,label=Feature),size=3,vjust=0)+
  geom_hline(yintercept=0.08,col='gray43',linetype=2)+
  scale_fill_manual(values=color)+
  scale_y_continuous(breaks=seq(0,1.5,0.1),limits=c(0,1.5))+
  labs(x='HPO code',y='Occurrence ratio', title='Phenotypic specificity in
  COG-CDG')+
  theme(axis.text.x=element_text(angle=90,hjust=1,size=7),
  legend.position='none')

```

Supplementary Notes 2: Standard Operating Procedure "Determining phenotypic specificity to facilitate understanding of underlying pathophysiology in rare genetic disorders"

A Standard Operation Procedure for the identification of highly specific phenotypic features in rare genetic disorders, to study shared pathophysiology.

Listing all phenotypic features

1. Perform a literature study. Identify all described cases and collect all data from case-reports and case-series. If you need additional information, do not hesitate to contact the authors.

Example: 45 COG-CDG patients from 32 families, reported in 22 case-reports and case-series.

2. Choose a single case to start with, preferably the one described in most detail

3. For this case, list all described phenotypic features (preferably in an Excel-like program).

Example:

Pregnancy and delivery of the female patient were uncomplicated and at term. The patient suffered from intractable focal seizures, vomiting and loss of consciousness due to intracranial bleedings. Biochemical investigations revealed a normal level for albumin and mildly elevated values for lactate, aspartate aminotransferase and creatine kinase. Metabolic investigations revealed cholestasis and subsequent vitamin K deficiency, explaining in part her intracranial bleedings. The patient died due to brain edema at 5 weeks of age. Since the clinical phenotype of the patient was suspect for a CDG syndrome, initial CDG diagnosis was established by isoelectric focusing (IEF) of the patient's serum transferrin.

Lübbehusen et al. 2010, Human Molecular Genetics

List: intractable focal seizures, vomiting, intracranial bleeding, elevated lactate, elevated aspartate aminotransferase, elevated creatine kinase, cholestasis, vitamin K deficiency

4. For each phenotypic feature, list the most appropriate HPO-term and the associated HPO-code via http://compbio.charite.de/hpoweb/showterm?id=HP:0000118#id=HP_0000118 (Figure 1). In the search bar you can type the phenotypic feature to see the possible HPO-terms. Primary ID on the left renders the HPO-code. In the middle text block, synonyms for the feature are listed and on the right a textual definition is provided. Super classes and subclasses are listed below. Always be as precise as possible, if a subclass is applicable, it is preferred over its superclass.

Figure 1

The screenshot shows the HPO web interface for the term 'Focal seizures'. At the top, there is a search bar with the text 'Enter search terms ...'. Below the search bar, the page title is 'Focal seizures'. The main content area is divided into several sections:

- Primary ID:** HP:0007359
- Alternative IDs:** HP:0002358
- PURL:** http://purl.obolibrary.org/obo/HP_0007359
- Synonyms:** Partial seizures
- Textual definition:** Seizures of which initial semiology indicates, or is consistent with, initial activation of only part of one cerebral hemisphere.
- Logical definition:** 'has part' some Intersection of
 - [increased amount](#)
 - 'inheres in' some [partial seizure](#)
 - 'has modifier' some [abnormal](#)
- Superclasses:** [Seizures](#)
- Subclasses:** [Focal seizures without impairment of consciousness or awareness](#), [Focal motor seizures](#), [Auras](#), [Focal seizures, afebril](#)

Example:

Intractable focal seizures	Focal seizures	HP:0002358
Vomiting	Vomiting	HP:0002013
Intracranial bleeding	Intracranial hemorrhage	HP:0002170
Elevated lactate	Increased serum lactate	HP:0002151

5. Expand the list of phenotypic features by listing the super classes of each of the phenotypic features that you listed. For the patient that you started with, score each phenotypic feature and all super classes. If you do this, you will preserve the tree-like hierarchical structure of HPO.

Example:

		P1	
0. Phenotypic abnormality	HP:0000118	1	
1. Abnormality of the nervous system	HP:0000707	1	
2. Abnormality of nervous system physiology	HP:0012638	1	
3. Seizures	HP:0001250	1	
4. Focal seizures	HP:0002358	1	

When more super classes are applicable, list the most appropriate one. If you cannot choose, list both.

6. When you finished this for the first patient, you can add the second:

Example: add the phenotypic feature "profound intellectual disability" to your list:

		P1	P2
0. Phenotypic abnormality	HP:0000118	1	1
1. Abnormality of the nervous system	HP:0000707	1	1
2. Abnormality of nervous system physiology	HP:0012638	1	1
3. Neurodevelopmental abnormality	HP:0012759	0	1
4. Intellectual disability	HP:0001249	0	1
5. Intellectual disability, profound	HP:0002187	0	1
3. Seizures	HP:0001250	1	0
4. Focal seizures	HP:0002358	1	0

7. Retake step 3-7 until you listed all phenotypic features as detailed as possible for all your patients. Be meticulous in also scoring all appropriate super classes of the phenotypic features.

Example: Supplementary Table 2

Calculating gene occurrence ratios

8. Sum the total number of patients for each listed phenotypic feature.

Example: Supplementary Table 2

9. Calculate the phenotypic frequency by dividing the total number of patients that present with a phenotypic feature over the total number of included patients



Example: Supplementary Table 1

10. Retrieve from HPO for each phenotypic feature the number of associated genes and note this number for each of the phenotypic features and all super classes.



The associated number of genes can be found below the number of associated diseases (Figure 2). HPO is frequently updated, so note the date you last consulted HPO and during your assessment, regularly check if nothing has changed.

Figure 2

66 associated diseases	
Disease id	Disease name
OMIM:607745	SEIZURES, BENIGN FAMILIAL INFANTILE, 3
OMIM:614563	MENTAL RETARDATION, AUTOSOMAL DOMINANT 13
ORPHA:31709	Infantile convulsions and choreoathetosis
ORPHA:369929	Aldosterone-producing adenoma with seizures and neurological abnormalities
ORPHA:1935	Early myoclonic encephalopathy
ORPHA:398189	Focal facial dermal dysplasia type IV

Export to Excel  Export to CSV 

50 associated genes	
Gene	Associated diseases
NHLRC1 (378884)	MYOCLONIC EPILEPSY OF LAFORA (OMIM:254780)
GABRB3 (2562)	Lennox-Gastaut syndrome (ORPHA:2382), EPILEPTIC ENCEPHALOPATHY, EARLY INFANTIL... (OMIM:617113)
GABRG2 (2566)	Dravet syndrome (ORPHA:33069), GENERALIZED EPILEPSY WITH FEBRILE SEIZUR... (OMIM:611277)
SLC25A22 (79751)	Early myoclonic encephalopathy (ORPHA:1935), EPILEPTIC ENCEPHALOPATHY, EARLY INFANTIL... (OMIM:609304)
CLN8 (2055)	CEROID LIPOFUSCINOSIS, NEURONAL, 8, NORT... (OMIM:610003), Progressive epilepsy-intellectual disabi... (ORPHA:1947), CEROID LIPOFUSCINOSIS, NEURONAL, 8 (OMIM:600143)
CACNA1D (776)	Aldosterone-producing adenoma with seizu... (ORPHA:369929), PRIMARY ALDOSTERONISM, SEIZURES, AND NEU... (OMIM:615474), SINUS BRADYCARDIA AND DEAFNESS (OMIM:614896)

Export to Excel  Export to CSV 

Copy Id/Label Graph view

Example: Supplementary Table 1

- Calculate the **gene occurrence ratio** by dividing the frequency in the patient cohort over the number of associated genes.
 Example: episodic fever was noted in 20 patients (Table 1) and the feature is associated with 22 genes. Occurrence ratio is $20/22 = 0.909$. For all occurrence ratios, see Supplementary Table 1.

Determine the cut-off value to meet a minimum sensitivity

- Order all phenotypic features on the total number of patients that present with the phenotypic feature and calculate the number of phenotypic features that were noted in only one patient, the number of phenotypic features that were noted in only two patients, etc. and tabulate this.
 Example: Supplementary Figure 1
- Calculate and plot the differences between these numbers. The cut-off value is the number of patients from whereon the difference in number of phenotypic features is fairly stable.
 Example: Supplementary Figure 1
- This cut-off value can be checked by calculating the specificity ratio. This is the ratio of the median occurrence ratio of the top ten phenotypic features over the median occurrence ratio of all phenotypic features.
 - If no cut-off value is used, calculate the median occurrence ratio of the ten phenotypic features with the highest occurrence ratios. In addition, calculate the median occurrence of all other phenotypic features. The specificity ratio is calculated by dividing the median occurrence ratio of the top ten phenotypic features over the median occurrence ratio of all phenotypic features.
 - Exclude all phenotypic features that are noted in only one patient and calculate the second specificity ratio.
 - Exclude all phenotypic features that are noted in one or two patients and calculate the third specificity ratio.
 - Calculate specificity ratios for all possible phenotypic frequencies and plot this. This should support the cut-off value from step 13.

Example: Supplementary Figure 2

Study highly specific phenotypic features

15. To study the top XX highly specific phenotypic features of a given disease (in the paper top 10 phenotypic features), retrieve the list of associated genes from HPO (Figure 2, Export to Excel).

Example: Table 2

16. Derive the gene encoded protein functions from GeneCards.com or other resources.

Example: for episodic fever one of the genes is ELP1. According to GeneCards this is Elongator Protein Complex 1, a scaffold protein and regulator for three different kinases involved in proinflammatory signaling.

17. Classify the protein functions into – data-driven – categories.

Example: Table 2. ELP1 was categorized in the category "Immune system".

18. Note the number of genes per category to assess differences in distribution over the categories from the different phenotypic features.

Example: Table 1.

19. Based on your research question, decide what might be an interesting phenotypic feature to look into.

Example: for episodic fever even its two super classes (fever (HP:0001945) and abnormality of temperature regulation (HP:0004370)) stood out as highly specific phenotypic features and it was not associated to any other glycosylation disorder, so this phenotypic feature was chosen to (first) look into.

20. Perform literature studies for each of the associated genes and see if you can establish one or multiple pathophysiological pathways where genes are related to. This way you can conceive a hypothesis on the possible function in this pathway of the gene you are studying.

Disclaimer

Please bear in mind that the systematic assessment of phenotypic specificity and shared pathophysiology as described here heavily relies on the extent, specificity and completeness of the initial phenotypic description, and also on the accuracy and completeness of the used open access databases: HPO and GeneCards. For HPO, be aware that it is regularly updated, not always with adjustment of the version (Figure 3).

Figure 3

Ontology version: <http://purl.obolibrary.org/obo/hp/releases/2017-12-12/hp.owl>
Copyright 2018 - Sebastian Köhler & The Phenomics Group Berlin
[Contact: dr.sebastian.koehler@gmail.com](mailto:dr.sebastian.koehler@gmail.com)

Supplementary Table 1: Aligning phenotypic descriptions to assess phenotypic frequency using the Human Phenotype Ontology in COG-CDG – Summarized table

Clinical features	HPO code ^a	COG1	COG2	COG4	COG5	COG6	COG7	COG8	Total	%
		N=3 ^b	N=1	N=2	N=10	N=18	N=8	N=3	N=45	
Abn. of the nervous system	HP:0000707	3	1	2	10	18	8	3	45	100
Microcephaly	HP:0000252	3	1	1	7	15	6	1	34	76
Global developmental delay	HP:0001263	3	1	2	6	16	4	1	33	73
Intellectual disability	HP:0001249	2	1		10	9		2	24	53
Seizures	HP:0001250		1	2	1	4	5	2	15	33
Cerebral atrophy	HP:0002059	2	1	2	1	4	2	1	13	29
Cerebellar atrophy	HP:0001272	2			5	1	2	2	12	27
Reduced tendon reflexes	HP:0001315				4	1	5	2	12	27
Abnormality of the abdomen	HP:0001438	1	1	2	3	12	8	3	30	67
Abnormality of the liver	HP:0001392	1	1	2	2	12	7	2	27	60
Elevated hepatic transam.	HP:0002910			2	1	12	5	2	22	49
Hepatomegaly	HP:0002240	1		1	2	6	5		15	33
Splenomegaly	HP:0001744	1		1	1	8	2		13	29
Growth abnormality	HP:0001507	3		1	6	14	8	2	34	76
Failure to thrive	HP:0001508	1		1	3	12	8	1	26	58
Short stature	HP:0004322	2		1	5	3	3	1	15	33
Muscular hypotonia	HP:0001252	1		2	7	11	8	3	32	71
Abnormality of the face	HP:0000271	3	1	1	4	15	6	2	32	71
Abnormality of the mouth	HP:0000153	2			1	6	4		13	29
Abnormality of the nose	HP:0000366	1			2	5	3	1	12	27
Abn. of the orbital region	HP:0000315	2				6	3	1	12	27
Abnormality of the skull	HP:0000929	1			1	4	5	1	12	27
Abn. of skeletal morphology	HP:0011842	2			6	11	5	1	25	56
Episodic fever	HP:0001954					11	8	1	20	44
Abnormality of blood or blood-forming tissues	HP:0001871	1	1	2	1	9	2	1	17	38
Abnormality of limbs	HP:0040064	3			2	4	4	2	15	33
Abnormality of eye physiology	HP:0012373	1		1	3	5	2	2	14	31
Abnormality of the ear	HP:0000598	2			4	1	6		13	29
Recurrent infections	HP:0002719	1		2	1	7	2		13	29
Abn. of the urinary system	HP:0000079	2			4	3	3	1	13	29
Abn. of circulating protein level	HP:0010876			1	1	5	3	2	12	27
Abn. of the cardiovasc. system	HP:0001626	2				6	4		12	27
Death in infancy	HP:0001522								15	33
Neonatal death	HP:0003811								1	

25-40%	41-55%	56-70%	71-85%	86-100%
--------	--------	--------	--------	---------

a) HPO: Human Phenotype Ontology. b) N: number of patients.

Supplementary Table 2: Aligning phenotypic descriptions using the Human Phenotype Ontology in COG-CDG - Full table

Index	Superclass	Clinical feature	HPO code	COG1	COG2	COG4	COG5	COG6	COG7	COG8	All	Ass. genes	Occ. ratio
1	1	Abnormality of blood or blood-forming tissues	HP:0001871	1	1	2	1	9	2	1	17	944	0.018
2	2	Abnormal bleeding	HP:0001892	0	0	0	0	4	1	1	6	340	0.018
3	3	Gingival bleeding	HP:0000225	0	0	0	0	1	0	0	1	27	0.037
4	3	Epistaxis	HP:0000421	0	0	0	0	1	0	0	1	60	0.017
5	4	Spontaneous, recurrent epistaxis	HP:0004406	0	0	0	0	1	0	0	1	4	0.250
6	3	Internal hemorrhage	HP:0011029	0	0	0	0	4	1	0	5	191	0.026
7	4	Hemorrhage of the eye	HP:0011885	0	0	0	0	1	0	0	1	23	0.043
8	5	Retinal hemorrhage	HP:0000573	0	0	0	0	1	0	0	1	10	0.100
9	4	Intracranial hemorrhage	HP:0002170	0	0	0	0	2	0	0	2	71	0.028
10	5	Subdural hemorrhage	HP:0100309	0	0	0	0	1	0	0	1	1	1.000
11	4	Gastrointestinal bleeding	HP:0002239	0	0	0	0	2	0	0	2	116	0.017
12	3	Subcutaneous hemorrhage	HP:0001933	0	0	0	0	0	0	1	1	174	0.006
13	4	Spontaneous hematomas	HP:0007420	0	0	0	0	0	0	1	1	23	0.043
14	2	Abnormal thrombosis	HP:0001977	0	0	0	0	1	0	0	1	95	0.011
15	3	Disseminated intravascular coagulation	HP:0005521	0	0	0	0	1	0	0	1	3	0.333
16	2	Abnormality of coagulation	HP:0001928	0	1	2	1	3	1	1	9	127	0.071
17	3	Abnormality of the coagulation cascade	HP:0003256	0	0	2	0	1	1	1	5	66	0.076
18	4	Reduced antithrombin III activity	HP:0001976	0	0	1	0	0	0	1	2	8	0.250
19	4	Reduced protein C activity	HP:0005543	0	0	0	0	0	0	1	1	2	0.500
20	4	Reduced protein S activity	HP:0004855	0	0	0	0	0	0	1	1	2	0.500
21	4	Abnormality of the intrinsic pathway	HP:0010989	0	0	0	0	1	0	0	1	23	0.043
22	5	Reduced factor XI activity	HP:0001929	0	0	0	0	1	0	0	1	5	0.200
23	3	Prolonged partial thromboplastin time	HP:0003645	0	0	0	1	3	0	0	4	14	0.286
24	2	Abnormality of thrombocytes	HP:0001872	1	0	1	1	5	1	0	9	260	0.035
25	3	Abnormal platelet count	HP:0011873	1	0	1	1	5	1	0	9	227	0.040
26	4	Thrombocytopenia	HP:0001873	1	0	1	1	5	1	0	9	216	0.042
27	5	Macrothrombocytopenia	HP:0040185	1	0	0	0	0	0	0	1	6	0.167
28	2	Abnormality of bone marrow cell morphology	HP:0005561	1	0	0	0	4	1	0	6	191	0.031
29	3	Abnormality of cells of the erythroid lineage	HP:0012130	1	0	0	0	3	1	0	5	2	2.500
30	4	Abnormality of erythrocytes	HP:0001877	1	0	0	0	3	1	0	5	395	0.013
31	5	Anemia	HP:0001903	1	0	0	0	3	1	0	5	365	0.014
32	3	Abnormality of cells of the monocyte/macrophage lineage	HP:0012144	0	0	0	0	2	0	0	2	33	0.061
33	4	Abnormality of macrophages	HP:0004311	0	0	0	0	1	0	0	1	27	0.037
34	5	Hemophagocytosis	HP:0012156	0	0	0	0	1	0	0	1	8	0.125
35	4	Abnormal monocyte count	HP:0012310	0	0	0	0	1	0	0	1	6	0.167
36	5	Monocytosis	HP:0012311	0	0	0	0	1	0	0	1	4	0.250
37	3	Abnormality of multiple cell lineages in the bone marrow	HP:0012145	0	0	0	0	2	0	0	2	88	0.023
38	4	Pancytopenia	HP:0001876	0	0	0	0	2	0	0	2	56	0.036

39	2	Abnormality of leukocytes	HP:0001881	0	0	0	0	2	0	0	2	418	0.005
40	3	Abnormal leukocyte count	HP:0011893	0	0	0	0	2	0	0	2	218	0.009
41	4	Leukocytosis	HP:0001974	0	0	0	0	2	0	0	2	57	0.035
42	1	Abnormality of connective tissue	HP:0003549	0	0	0	0	1	1	0	2	1019	0.002
43	2	Abnormality of adipose tissue	HP:0009124	0	0	0	0	1	1	0	2	157	0.013
44	3	Lipodystrophy	HP:0009125	0	0	0	0	2	0	0	2	84	0.024
45	3	Abnormality of subcutaneous fat tissue	HP:0001001	0	0	0	0	1	1	0	2	35	0.057
46	4	Abnormal subcutaneous fat tissue distribution	HP:0007552	0	0	0	0	1	1	0	2	7	0.286
47	1	Abnormality of head or neck	HP:0000152	3	1	1	4	15	6	2	32	2186	0.015
48	2	Abnormality of the neck	HP:0000464	2	0	0	1	1	5	0	9	414	0.022
49	3	Short neck	HP:0000470	2	0	0	1	1	5	0	9	238	0.038
50	3	Low posterior hairline	HP:0002162	1	0	0	0	0	0	0	1	69	0.014
51	2	Abnormality of the head	HP:0000234	3	1	1	4	15	6	2	32	2160	0.015
52	3	Abnormality of the face	HP:0000271	3	1	1	4	15	6	2	32	1954	0.016
53	4	Abnormal facial shape	HP:0001999	0	0	0	0	0	1	0	1	625	0.002
54	5	Flat face	HP:0012368	0	0	0	0	0	1	0	1	69	0.014
55	4	Abnormality of the forehead	HP:0000290	1	0	1	1	2	3	0	8	610	0.013
56	5	Narrow forehead	HP:0000341	1	0	0	0	1	3	0	5	61	0.082
57	5	Flat forehead	HP:0004425	0	0	1	0	0	3	0	4	7	0.571
58	5	Abnormality of the metopic suture	HP:0005556	0	0	0	0	1	0	0	1	38	0.026
59	6	Metopic synostosis	HP:0011330	0	0	0	0	1	0	0	1	3	0.333
60	5	Abnormality of the frontal hairline	HP:0000599	0	0	0	1	1	1	0	3	78	0.038
61	6	Low anterior hairline	HP:0000294	0	0	0	1	1	1	0	3	52	0.058
62	4	Abnormality of the nose	HP:0000366	1	0	0	2	5	3	1	12	1109	0.011
63	5	Wide nose	HP:0000445	0	0	0	0	0	3	1	4	73	0.055
64	5	Abnormality of the nares	HP:0005288	1	0	0	0	1	0	0	2	377	0.005
65	6	Anteverted nares	HP:0000463	1	0	0	0	1	0	0	2	363	0.006
66	7	Broad nasal tip	HP:0000455	0	0	0	0	1	0	0	1	57	0.018
67	5	Abnormal nasal morphology	HP:0005105	0	0	0	2	2	3	1	8	642	0.012
68	6	Prominent nose	HP:0000448	0	0	0	2	2	0	1	5	45	0.111
69	6	Short nose	HP:0003196	0	0	0	0	0	3	0	3	204	0.015
70	5	Abnormality of the nasal bridge	HP:0000422	1	0	0	1	2	0	1	5	657	0.008
71	6	Depressed nasal bridge	HP:0005280	0	0	0	0	1	0	1	2	307	0.007
72	6	Wide nasal bridge	HP:0000431	1	0	0	1	1	0	0	3	352	0.009
73	4	Abnormality of the mouth	HP:0000153	2	0	0	1	6	4	0	13	1417	0.009
74	5	Abnormality of mouth size	HP:0011337	1	0	0	0	3	3	0	7	237	0.030
75	6	Narrow mouth	HP:0000160	1	0	0	0	0	3	0	4	136	0.029
76	6	Wide mouth	HP:0000154	0	0	0	0	3	0	0	3	113	0.027
77	5	Abnormality of the oral cavity	HP:0000163	1	0	0	1	5	3	0	10	1213	0.008
78	6	Abnormality of the oral mucosa	HP:0011830	0	0	0	0	1	2	0	3	205	0.015
79	7	Abnormality of the gingiva	HP:0000168	0	0	0	0	1	2	0	3	144	0.021

80	8	Gingival overgrowth	HP:0000212	0	0	0	0	1	2	0	3	75	0.040
81	6	Abnormality of the palate	HP:0000174	1	0	0	1	1	0	0	3	677	0.004
82	7	High palate	HP:0000218	1	0	0	1	1	0	0	3	389	0.008
83	6	Abnormality of the tongue	HP:0000157	0	0	0	0	0	1	0	1	238	0.004
84	7	Protruding tongue	HP:0010808	0	0	0	0	0	1	0	1	19	0.053
85	6	Abnormality of the teeth	HP:0000164	0	0	0	0	4	0	0	4	619	0.006
86	7	Abnormal number of teeth	HP:0006483	0	0	0	0	1	0	0	1	200	0.005
87	8	Reduced number of teeth	HP:0009804	0	0	0	0	1	0	0	1	183	0.005
88	7	Abnormality of dental structure	HP:0011061	0	0	0	0	3	0	0	3	256	0.012
89	8	Carious teeth	HP:0000670	0	0	0	0	2	0	0	2	145	0.014
90	8	Hypoplasia of teeth	HP:0000685	0	0	0	0	2	0	0	2	60	0.033
91	6	Abnormality of the oral frenula	HP:0000190	1	0	0	0	0	0	0	1	29	0.034
92	7	Short lingual frenulum	HP:0000200	1	0	0	0	0	0	0	1	3	0.333
93	5	Abnormality of the lip	HP:0000159	2	0	0	0	4	3	0	9	666	0.014
94	6	Abnormality of upper lip	HP:0000177	2	0	0	0	1	2	0	5	517	0.010
95	7	Abnormality of the philtrum	HP:0000288	2	0	0	0	1	2	0	5	350	0.014
96	8	Smooth philtrum	HP:0000319	1	0	0	0	0	2	0	3	69	0.043
97	8	Long philtrum	HP:0000343	1	0	0	0	1	0	0	2	213	0.009
98	8	Hypoplastic philtrum	HP:0005326	0	0	0	0	1	0	0	1	1	1.000
99	6	Full lips	HP:0012471	0	0	0	0	1	1	0	2	155	0.013
100	6	Thin vermilion border	HP:0000233	2	0	0	0	2	0	0	4	192	0.021
101	7	Thin upper lip vermilion	HP:0000219	2	0	0	0	0	0	0	2	130	0.015
102	5	Pierre-Robin sequence	HP:0000201	1	0	0	0	0	0	0	1	13	0.077
103	4	Abnormality of the midface	HP:0000309	1	0	0	0	0	3	0	4	375	0.008
104	5	Abnormality of malar bones	HP:0012369	0	0	0	0	0	3	0	3	182	0.016
105	6	Malar flattening	HP:0000272	0	0	0	0	0	3	0	3	175	0.017
106	5	Hypoplasia of midface	HP:0011800	1	0	0	0	0	0	0	1	167	0.006
107	4	Abnormality of the orbital region	HP:0000315	2	0	0	0	6	3	1	12	1220	0.010
108	5	Abnormal morphology of the ocular adnexa	HP:0030669	2	0	0	0	6	3	1	12	949	0.013
109	6	Abnormality of the eyelid	HP:0000492	2	0	0	0	5	3	1	11	800	0.014
110	7	Epicanthus	HP:0000286	0	0	0	0	3	0	1	4	316	0.013
111	7	Abnormality of the palpebral fissures	HP:0008050	2	0	0	0	3	3	0	8	481	0.017
112	8	Slanting of the palpebral fissures	HP:0200006	2	0	0	0	0	2	0	4	400	0.010
113	9	Upslanted palpebral fissure	HP:0000582	0	0	0	0	0	2	0	2	162	0.012
114	9	Downslanted palpebral fissures	HP:0000494	2	0	0	0	0	0	0	2	275	0.007
115	8	Abnormal size of the palpebral fissures	HP:0200007	0	0	0	0	3	3	0	6	159	0.038
116	9	Short palpebral fissure	HP:0012745	0	0	0	0	0	3	0	3	70	0.043
117	9	Long palpebral fissure	HP:0000637	0	0	0	0	3	0	0	3	25	0.120
118	6	Abnormality of the eyebrow	HP:0000534	0	0	0	0	1	0	0	1	362	0.003
119	7	Laterally extended eyebrow	HP:0011230	0	0	0	0	1	0	0	1	0	0.000
120	3	Abnormality of the skull	HP:0000929	1	0	0	1	4	5	1	12	1454	0.008

121	4	Abnormality of the calvaria	HP:0002683	0	0	0	0	1	0	0	1	689	0.001
122	5	Abnormality of calvarial morphology	HP:0002658	0	0	0	0	1	0	0	1	31	0.032
123	6	Skull asymmetry	HP:0002678	0	0	0	0	1	0	0	1	5	0.200
124	4	Abnormality of the facial skeleton	HP:0011821	1	0	0	1	3	5	1	11	780	0.014
125	5	Abnormality of the mandible	HP:0000277	1	0	0	1	2	5	1	10	623	0.016
126	6	Retrognathia	HP:0000278	0	0	0	1	3	3	0	7	155	0.045
127	6	Aplasia/hypoplasia of the mandible	HP:0009118	1	0	0	0	0	2	1	4	493	0.008
128	7	Micrognathia	HP:0000347	1	0	0	0	0	2	1	4	489	0.008
129	1	Abnormality of limbs	HP:0040064	3	0	0	2	4	4	2	15	1393	0.011
130	2	Abnormality of the upper limb	HP:0002817	3	0	0	0	0	3	2	8	1007	0.008
131	3	Abnormality of the hand	HP:0001155	3	0	0	0	0	3	2	8	929	0.009
132	4	Split hand	HP:0001171	0	0	0	0	0	0	1	1	54	0.019
133	4	Aplasia/hypoplasia involving bones of the hand	HP:0005927	1	0	0	0	0	0	1	2	329	0.006
134	5	Small hand	HP:0200055	1	0	0	0	0	0	1	2	74	0.027
135	4	Deviation of the hand or of fingers of the hand	HP:0009484	1	0	0	0	0	2	0	3	318	0.009
136	5	Ulnar deviation of the hand or of fingers	HP:0001193	1	0	0	0	0	2	0	3	45	0.067
137	6	Ulnar deviation of the hand	HP:0009487	0	0	0	0	0	2	0	2	13	0.154
138	6	Ulnar deviation of finger	HP:0009465	1	0	0	0	0	0	0	1	33	0.030
139	4	Abnormality of the palm	HP:0100871	1	0	0	0	0	3	0	4	265	0.015
140	5	Abnormality of the skin of the palm	HP:0040211	1	0	0	0	0	3	0	4	183	0.022
141	6	Abnormal palmar dermatoglyphics	HP:0001018	1	0	0	0	0	3	0	4	133	0.030
142	7	Abnormality of the palmar creases	HP:0010490	1	0	0	0	0	3	0	4	128	0.031
143	8	Simian crease	HP:0000954	1	0	0	0	0	3	0	4	107	0.037
144	2	Abnormality of the lower limb	HP:0002814	3	0	0	0	1	0	2	6	1039	0.006
145	3	Abnormality of the lower limb bone	HP:0040069	2	0	0	0	0	0	1	3	474	0.006
146	4	Abnormality of the femur	HP:0002823	1	0	0	0	0	0	1	2	179	0.011
147	5	Abnormality of the femoral neck or head region	HP:0003366	1	0	0	0	0	0	1	2	112	0.018
148	6	Abnormality of the femoral neck	HP:0003367	1	0	0	0	0	0	1	2	96	0.021
149	7	Coxa valga	HP:0003673	1	0	0	0	0	0	1	2	9	0.222
150	7	Broad femoral neck	HP:0006429	1	0	0	0	0	0	0	1	8	0.125
151	3	Abnormality of the foot	HP:0001760	1	0	0	0	1	0	2	4	862	0.005
152	4	Aplasia/hypoplasia involving bones of the feet	HP:0006494	1	0	0	0	0	0	1	2	202	0.010
153	5	Short foot	HP:0001773	1	0	0	0	0	0	1	2	103	0.019
154	4	Positional foot deformity	HP:0005656	1	0	0	0	1	0	1	3	265	0.011
155	5	Talipes	HP:0001883	1	0	0	0	1	0	1	3	264	0.011
156	6	Talipes equinovarus	HP:0001762	1	0	0	0	1	0	1	3	211	0.014
157	7	Bilateral talipes equinovarus	HP:0001776	0	0	0	0	0	0	1	1	3	0.333
158	2	Abnormality of limb bone	HP:0040068	0	0	0	2	4	4	1	11	1025	0.011
159	3	Abnormality of limb bone morphology	HP:0002813	0	0	0	2	4	4	1	11	1003	0.011
160	4	Abnormality of the limb diaphysis	HP:0006504	0	0	0	1	0	0	0	1	182	0.005
161	5	Bowing of the long bones	HP:0006487	0	0	0	1	0	0	0	1	177	0.006

162	6	Bowing of the legs	HP:0002979	0	0	0	1	0	0	0	1	131	0.008
163	7	Genu valgum	HP:0002857	0	0	0	1	0	0	0	1	82	0.012
164	4	Abnormality of digit	HP:0011297	0	0	0	1	4	4	1	10	885	0.011
165	5	Clinodactyly	HP:0030084	0	0	0	1	0	0	1	2	303	0.007
166	6	Finger clinodactyly	HP:0040019	0	0	0	1	0	0	0	1	232	0.004
167	6	Toe clinodactyly	HP:0001863	0	0	0	0	0	0	1	1	13	0.077
168	5	Polydactyly	HP:0010442	0	0	0	0	2	0	0	2	191	0.010
169	5	Abnormality of the finger	HP:0001167	0	0	0	0	2	4	0	6	720	0.008
170	6	Deviation of finger	HP:0004097	0	0	0	0	0	3	0	3	305	0.010
171	7	Overlapping fingers	HP:0010557	0	0	0	0	0	3	0	3	18	0.167
172	6	Long fingers	HP:0100807	0	0	0	0	1	2	0	3	160	0.019
173	6	Abnormality of the thumb	HP:0001172	0	0	0	0	1	4	0	5	242	0.021
174	7	Adducted thumbs	HP:0001181	0	0	0	0	1	4	0	5	56	0.089
175	6	Slender finger	HP:0001238	0	0	0	0	1	1	0	2	95	0.021
176	5	Abnormality of toe	HP:0001780	0	0	0	0	0	2	1	3	427	0.007
177	6	Overlapping toes	HP:0001845	0	0	0	0	0	1	0	1	19	0.053
178	6	Widely spaced toes	HP:0008094	0	0	0	0	0	0	1	1	2	0.500
179	6	Long toes	HP:0010511	0	0	0	0	0	2	0	2	23	0.087
180	7	Long hallux	HP:0001847	0	0	0	0	0	1	0	1	9	0.111
181	1	Abnormality of metabolism/homeostasis	HP:0001939	0	1	2	1	11	8	2	25	1708	0.015
182	2	Abnormality of fluid regulation	HP:0011032	0	0	0	0	0	1	0	1	374	0.003
183	3	Dehydration	HP:0001944	0	0	0	0	0	1	0	1	70	0.014
184	2	Abnormality of temperature regulation	HP:0004370	0	0	0	0	11	8	1	20	244	0.082
185	3	Fever	HP:0001945	0	0	0	0	11	8	1	20	180	0.111
186	4	Episodic fever	HP:0001954	0	0	0	0	11	8	1	20	22	0.909
187	2	Abnormality of cell physiology	HP:0011017	0	0	0	0	1	0	0	1	326	0.003
188	3	Abnormality of B cell physiology	HP:0005372	0	0	0	0	1	0	0	1	142	0.007
189	4	Absent specific antibody respons	HP:0005424	0	0	0	0	1	0	0	1	1	1.000
190	2	Abnormality of ion homeostasis	HP:0003111	0	1	0	0	1	0	0	2	225	0.009
191	3	Abnormality of cation homeostasis	HP:0010929	0	1	0	0	1	0	0	2	203	0.010
192	4	Abnormality of the transition element cation hom.	HP:0011030	0	1	0	0	1	0	0	2	37	0.054
193	5	Abnormality of iron homeostasis	HP:0011031	0	0	0	0	1	0	0	1	28	0.036
194	6	Abnormal serum ferritin	HP:0040133	0	0	0	0	1	0	0	1	22	0.045
195	7	Increased serum ferritin	HP:0003281	0	0	0	0	1	0	0	1	22	0.045
196	5	Abnormality of copper homeostasis	HP:0010836	0	1	0	0	0	0	0	1	9	0.111
197	6	Hypocupremia	HP:0011967	0	1	0	0	0	0	0	1	3	0.333
198	6	Decreased serum ceruloplasmin	HP:0010837	0	1	0	0	0	0	0	1	6	0.167
199	2	Abnormal enzyme/coenzyme activity	HP:0012379	0	0	1	1	2	0	0	4	99	0.040
200	3	Abnormality of alkaline phosphatase activity	HP:0004379	0	0	1	1	2	0	0	4	61	0.066
201	4	Elevated alkaline phosphatase	HP:0003155	0	0	1	1	2	0	0	4	58	0.069
202	2	Abnormality of circulating protein level	HP:0010876	0	0	1	1	5	3	2	12	302	0.040

203	3	Abnormality of circulating enzyme level	HP:0011021	0	0	0	0	3	3	2	8	212	0.038
204	4	Abnormal levels of creatine kinase in blood	HP:0040081	0	0	0	0	3	3	2	8	211	0.038
205	5	Elevated serum creatine phosphokinase	HP:0003236	0	0	0	0	3	3	2	8	209	0.038
206	3	Abnormal levels of alpha feto-protein	HP:0045056	0	0	1	1	2	0	0	4	13	0.308
207	4	Elevated alpha feto-protein	HP:0006254	0	0	1	1	2	0	0	4	12	0.333
208	2	Abnormality of carbohydrate metabolism/homeostasis	HP:0011013	0	0	0	0	0	1	0	1	528	0.002
209	3	Abnormal glucose homeostasis	HP:0011014	0	0	0	0	0	1	0	1	468	0.002
210	4	Abnormality of blood glucose concentration	HP:0011015	0	0	0	0	0	1	0	1	178	0.006
211	5	Hypoglycaemia	HP:0001943	0	0	0	0	0	1	0	1	157	0.006
212	6	Recurrent hypoglycaemia	HP:0001988	0	0	0	0	0	1	0	1	8	0.125
213	2	Abnormality of lipid metabolism	HP:0003119	0	0	1	0	0	0	0	1	180	0.006
214	3	Abnormality of cholesterol metabolism	HP:0003107	0	0	1	0	0	0	0	1	64	0.016
215	4	Hypercholesterolemia	HP:0003124	0	0	1	0	0	0	0	1	33	0.030
216	2	Hyperbilirubinemia	HP:0002904	0	0	0	1	1	0	0	2	52	0.038
217	3	Unconjugated hyperbilirubinemia	HP:0008282	0	0	0	1	0	0	0	1	5	0.200
218	3	Conjugated hyperbilirubinemia	HP:0002908	0	0	0	0	1	0	0	1	17	0.059
219	2	Abnormality of vitamin metabolism	HP:0100508	0	0	0	0	1	0	0	1	58	0.017
220	3	Abnormality of vitamin K metabolism	HP:0100831	0	0	0	0	1	0	0	1	6	0.167
221	4	Vitamin K deficiency	HP:0011892	0	0	0	0	1	0	0	1	6	0.167
222	1	Abnormality of prenatal development or birth	HP:0001197	0	0	0	1	6	1	0	8	465	0.017
223	2	Abnormality of the amniotic fluid	HP:0001560	0	0	0	1	2	1	0	4	227	0.018
224	3	Oligohydramnios	HP:0001562	0	0	0	1	1	1	0	3	88	0.034
225	3	Polyhydramnios	HP:0001561	0	0	0	0	1	0	0	1	143	0.007
226	2	Hydrops fetalis	HP:0001789	0	0	0	0	1	0	0	1	44	0.023
227	2	Premature birth	HP:0001622	0	0	0	0	4	0	0	4	100	0.040
228	2	Prenatal movement abnormality	HP:0001557	0	0	0	0	1	0	0	1	112	0.009
229	3	Decreased fetal movement	HP:0001558	0	0	0	0	1	0	0	1	101	0.010
230	1	Abnormality of the abdomen	HP:0001438	1	1	2	3	12	8	3	30	544	0.055
231	2	Abnormality of the abdominal organs	HP:0002012	1	1	2	3	12	8	3	30	895	0.034
232	3	Abnormality of the liver	HP:0001392	1	1	2	2	12	7	2	27	769	0.035
233	4	Decreased liver function	HP:0001410	0	1	0	0	2	0	0	3	171	0.018
234	5	Hepatic failure	HP:0001399	0	0	0	0	2	0	0	2	137	0.015
235	4	Hepatomegaly	HP:0002240	1	0	1	2	6	5	0	15	392	0.038
236	4	Elevated hepatic transaminases	HP:0002910	0	0	2	1	12	5	2	22	157	0.140
237	4	Cirrhosis	HP:0001394	0	0	1	1	2	0	0	4	112	0.036
238	4	Hepatic necrosis	HP:0002605	0	0	0	0	1	0	0	1	25	0.040
239	4	Abnormality of the biliary system	HP:0004297	0	0	1	1	5	3	0	10	262	0.038
240	5	Cholestasis	HP:0001396	0	0	1	1	5	3	0	10	187	0.053
241	6	Jaundice	HP:0000952	0	0	0	1	1	2	0	4	145	0.028
242	4	Abnormality of the hepatic vasculature	HP:0006707	0	0	0	1	0	0	0	1	48	0.021
243	5	Portal hypertension	HP:0001409	0	0	0	1	0	0	0	1	46	0.022

244	4	Hepatitis	HP:0012115	0	0	1	0	0	0	1	2	64	0.031
245	3	Abnormality of the spleen	HP:0001743	1	0	1	1	8	2	0	13	373	0.035
246	4	Splenomegaly	HP:0001744	1	0	1	1	8	2	0	13	290	0.045
247	3	Abnormality of the gastrointestinal tract	HP:0011024	0	0	0	2	3	5	1	11	980	0.011
248	4	Morphological abnormality of the GI tract	HP:0012718	0	0	0	2	3	1	1	7	752	0.009
249	5	Abnormality of the esophagus	HP:0002031	0	0	0	1	2	1	0	4	141	0.028
250	6	Gastroesophageal reflux	HP:0002020	0	0	0	1	0	1	0	2	170	0.012
251	6	Esophageal varix	HP:0002040	0	0	0	0	1	0	0	1	18	0.056
252	6	Dysphagia	HP:0002015	0	0	0	0	1	0	0	1	207	0.005
253	5	Abnormality of the large intestine	HP:0002250	0	0	0	0	0	0	1	1	144	0.007
254	6	Abnormal large intestine physiology	HP:0012700	0	0	0	0	0	0	1	1	35	0.029
255	7	Bowel incontinence	HP:0002607	0	0	0	0	0	0	1	1	29	0.034
256	5	Anorectal anomaly	HP:0012732	0	0	0	1	1	0	0	2	208	0.010
257	6	Abnormality of the anus	HP:0004378	0	0	0	1	1	0	0	2	147	0.014
258	7	Ectopic anus	HP:0004397	0	0	0	0	1	0	0	1	35	0.029
259	8	Anus anteposition	HP:0001545	0	0	0	0	1	0	0	1	16	0.063
260	7	Anal stenosis	HP:0002025	0	0	0	1	0	0	0	1	27	0.037
261	4	Functional abnormality of the GI tract	HP:0012719	0	0	0	0	2	4	0	6	547	0.011
262	5	Gastrointestinal obstruction	HP:0004796	0	0	0	0	0	3	0	3	68	0.044
263	5	Gastrointestinal inflammation	HP:0004386	0	0	0	0	2	1	0	3	51	0.059
264	6	Inflammation of the large intestine	HP:0002037	0	0	0	0	2	1	0	3	28	0.107
265	7	Colitis	HP:0002583	0	0	0	0	1	0	0	1	22	0.045
266	8	Acute colitis	HP:0100282	0	0	0	0	1	0	0	1	5	0.200
267	9	Enterocolitis	HP:0004387	0	0	0	0	1	0	0	1	5	0.200
268	2	Abdominal symptom	HP:0011458	1	0	1	2	6	6	0	16	995	0.016
269	3	Anorexia	HP:0002039	0	0	0	0	1	0	0	1	64	0.016
270	3	Nausea and vomiting	HP:0002017	0	0	0	0	2	0	0	2	307	0.007
271	4	Vomiting	HP:0002013	0	0	0	0	2	0	0	2	161	0.012
272	3	Diarrhea	HP:0002014	0	0	1	0	4	2	0	7	205	0.034
273	3	Feeding difficulties	HP:0011968	1	0	1	2	1	6	0	11	529	0.021
274	1	Abnormality of the breast	HP:0000769	1	0	0	0	3	1	0	5	273	0.018
275	2	Abnormality of the nipple	HP:0004404	0	0	0	0	3	1	0	4	135	0.030
276	3	Inverted nipples	HP:0003186	0	0	0	0	3	1	0	4	14	0.286
277	2	Abnormal intermamillary distance	HP:0040157	1	0	0	0	0	0	0	1	72	0.014
278	3	Wide intermamillary distance	HP:0006610	1	0	0	0	0	0	0	1	72	0.014
279	1	Abnormality of the cardiovascular system	HP:0001626	2	0	0	0	6	4	0	12	1667	0.007
280	2	Abnormality of cardiovascular system morphology	HP:0030680	2	0	0	0	6	3	0	11	1149	0.010
281	3	Abnormal heart morphology	HP:0001627	2	0	0	0	6	3	0	11	910	0.012
282	4	Abnormality of the heart valves	HP:0001654	1	0	0	0	1	1	0	3	305	0.010
283	5	Abnormality of the aortic valve	HP:0001646	1	0	0	0	1	0	0	2	167	0.012
284	6	Aortic regurgitation	HP:0001659	1	0	0	0	1	0	0	2	59	0.034

285	6	Dysplastic aortic valve	HP:0005176	0	0	0	0	1	0	0	1	0	0.000
286	5	Abnormality of the atrioventricular valves	HP:0006705	1	0	0	0	0	1	0	2	148	0.014
287	6	Abnormality of the mitral valve	HP:0001633	1	0	0	0	0	0	0	1	126	0.008
288	7	Mitral stenosis	HP:0001718	1	0	0	0	0	0	0	1	12	0.083
289	8	Parachute mitral valve	HP:0011571	1	0	0	0	0	0	0	1	0	0.000
290	6	Abnormality of the tricuspid valve	HP:0001702	0	0	0	0	0	1	0	1	36	0.028
291	7	Tricuspid insufficiency	HP:0005180	0	0	0	0	0	1	0	1	17	0.059
292	4	Abnormality of cardiac atrium	HP:0005120	1	0	0	0	4	2	0	7	244	0.029
293	5	Atrial septal defect	HP:0001631	0	0	0	0	4	2	0	6	241	0.025
294	6	Secundum atrial septal defect	HP:0001684	0	0	0	0	1	2	0	3	7	0.429
295	6	Patent foramen ovale	HP:0001655	0	0	0	0	1	0	0	1	26	0.038
296	4	Abnormality of cardiac ventricle	HP:0001713	1	0	0	0	2	3	0	6	342	0.018
297	5	Abnormality of the ventricular septum	HP:0010438	0	0	0	0	2	3	0	5	245	0.020
298	6	Ventricular septal defect	HP:0001629	0	0	0	0	2	3	0	5	240	0.021
299	5	Ventricular hypertrophy	HP:0001714	1	0	0	0	0	0	0	1	74	0.014
300	6	Left ventricular hypertrophy	HP:0001712	1	0	0	0	0	0	0	1	54	0.019
301	4	Hypoplastic heart	HP:0001961	0	0	0	0	1	0	0	1	22	0.045
302	3	Congenital malformation of the great arteries	HP:0011603	0	0	0	0	3	0	0	3	240	0.013
303	4	Persistent ductus arteriosus	HP:0001643	0	0	0	0	3	0	0	3	192	0.016
304	2	Abnormality of cardiovascular system physiology	HP:0011025	0	0	0	0	0	2	0	2	775	0.003
305	3	Arrhythmia	HP:0011675	0	0	0	0	0	1	0	1	311	0.003
306	4	Tachycardia	HP:0001649	0	0	0	0	0	1	0	1	99	0.010
307	3	Congestive heart failure	HP:0001635	0	0	0	0	0	1	0	1	160	0.006
308	1	Abnormality of the ear	HP:0000598	2	0	0	4	1	6	0	13	1466	0.009
309	2	Hearing abnormality	HP:0000364	2	0	0	2	1	2	0	7	986	0.007
310	3	Hearing impairment	HP:0000365	2	0	0	2	1	2	0	7	969	0.007
311	4	Severe hearing impairment	HP:0012714	2	0	0	2	1	2	0	7	5	1.400
312	5	Severe sensorineural hearing impairment	HP:0008625	0	0	0	2	1	2	0	5	5	1.000
313	5	Severe conductive hearing impairment	HP:0012717	1	0	0	0	0	0	0	1	0	0.000
314	5	Mixed hearing impairment	HP:0000410	1	0	0	0	0	0	0	1	18	0.056
315	2	Abnormality of the outer ear	HP:0000356	2	0	0	3	0	5	0	10	760	0.013
316	3	Abnormal location of ears	HP:0000357	2	0	0	3	0	5	0	10	490	0.020
317	4	Low set ears	HP:0000369	2	0	0	3	0	5	0	10	463	0.022
318	4	Posteriorly rotated ears	HP:0000358	2	0	0	3	0	2	0	7	289	0.024
319	3	Abnormality of the pinna	HP:0000377	0	0	0	0	0	2	0	2	493	0.004
320	4	Abnormality of the helix	HP:0011039	1	0	0	0	0	0	0	1	93	0.011
321	5	Cleft helix	HP:0009902	1	0	0	0	0	0	0	1	2	0.500
322	4	Abnormality of the antihelix	HP:0009738	1	0	0	0	0	0	0	1	23	0.043
323	4	Microtia	HP:0008551	1	0	0	0	0	0	0	1	86	0.012
324	3	Abnormality of the auditory canal	HP:0000372	1	0	0	0	0	0	0	1	61	0.016
325	4	Stenosis of the external auditory canal	HP:0000402	1	0	0	0	0	0	0	1	24	0.042

326	2	Abnormality of the middle ear	HP:0000370	1	0	0	0	0	0	0	1	334	0.003
327	3	Morphological abnormality of the middle ear	HP:0008609	1	0	0	0	0	0	0	1	16	0.063
328	4	Cholesteatoma	HP:0009797	1	0	0	0	0	0	0	1	2	0.500
329	2	Abnormality of the inner ear	HP:0000359	1	0	0	0	0	0	0	1	674	0.001
330	3	Morphological abnormality of the inner ear	HP:0011390	1	0	0	0	0	0	0	1	55	0.018
331	4	Morphological abnormality of the vestibule of the inner ear	HP:0011376	1	0	0	0	0	0	0	1	20	0.050
332	5	Morphological abnormality of the semicircular channel	HP:0011380	1	0	0	0	0	0	0	1	17	0.059
333	6	Morphological abnormality of the lateral semicircular channel	HP:0040106	1	0	0	0	0	0	0	1	0	0.000
334	1	Abnormality of the endocrine system	HP:0000818	0	0	0	0	2	0	0	2	942	0.002
335	2	Abnormality of the thymus	HP:0000777	0	0	0	0	1	0	0	1	44	0.023
336	3	Thymus hyperplasia	HP:0010516	0	0	0	0	1	0	0	1	2	0.500
337	2	Abnormality of circulating hormone level	HP:0003117	0	0	0	0	1	0	0	1	293	0.003
338	3	Abnormal serum insulin-like growth factor 1 level	HP:0030352	0	0	0	0	1	0	0	1	9	0.111
339	4	Decreased serum insulin-like growth factor 1	HP:0030353	0	0	0	0	1	0	0	1	6	0.167
340	2	Abnormality of the adrenal glands	HP:0000834	0	0	0	0	1	0	0	1	172	0.006
341	3	Abnormality of adrenal morphology	HP:0011732	0	0	0	0	1	0	0	1	71	0.014
342	4	Adrenal hypoplasia	HP:0000835	0	0	0	0	1	0	0	1	23	0.043
343	1	Abnormality of the eye	HP:0000478	2	0	1	3	6	3	2	17	2050	0.008
344	2	Abnormal eye morphology	HP:0012372	2	0	0	0	2	1	0	5	1646	0.003
345	3	Abnormality of the globe	HP:0012374	2	0	0	0	2	1	0	5	1644	0.003
346	4	Abnormality of globe location	HP:0100886	2	0	0	0	0	1	0	3	643	0.005
347	5	Hypertelorism	HP:0000316	1	0	0	0	0	1	0	2	475	0.004
348	5	Proptosis	HP:0000520	1	0	0	0	0	0	0	1	177	0.006
349	4	Abnormality of the uvea	HP:0000553	0	0	0	0	1	0	0	1	402	0.002
350	5	Abnormality of the iris	HP:0000525	0	0	0	0	1	0	0	1	323	0.003
351	6	Abnormality of the pupil	HP:0000615	0	0	0	0	1	0	0	1	41	0.024
352	7	Abnormal pupillary function	HP:0007686	0	0	0	0	1	0	0	1	19	0.053
353	8	Miosis	HP:0000616	0	0	0	0	1	0	0	1	9	0.111
354	4	Abnormality of the anterior segment of the globe	HP:0004328	0	0	0	0	1	0	0	1	896	0.001
355	5	Abnormality of the cornea	HP:0000481	0	0	0	0	1	0	0	1	503	0.002
356	6	Decreased corneal reflex	HP:0008000	0	0	0	0	1	0	0	1	2	0.500
357	4	Abnormality of the posterior segment of the globe	HP:0004329	1	0	0	0	1	0	0	2	888	0.002
358	5	Abnormality of the fundus	HP:0001098	1	0	0	0	1	0	0	2	885	0.002
359	6	Abnormality of the optic nerve	HP:0000587	0	0	0	0	1	0	0	1	560	0.002
360	7	Abnormality of optic disc	HP:0012795	0	0	0	0	1	0	0	1	464	0.002
361	8	Optic atrophy	HP:0000648	0	0	0	0	1	0	0	1	415	0.002
362	6	Abnormality of the retina	HP:0000479	1	0	0	0	0	0	0	1	646	0.002
363	7	Macular abnormality	HP:0001103	1	0	0	0	0	0	0	1	145	0.007
364	2	Abnormal eye physiology	HP:0012373	1	0	1	3	5	2	2	14	1624	0.009
365	3	Abnormality of vision	HP:0000504	0	0	0	2	0	1	0	3	797	0.004
366	4	Visual impairment	HP:0000505	0	0	0	2	0	1	0	3	557	0.005

367	5	Cortical visual impairment	HP:0100704	0	0	0	2	0	0	0	2	57	0.035
368	3	Abnormality of refraction	HP:0000539	0	0	0	1	0	0	0	1	369	0.003
369	4	Hypermetropia	HP:0000540	0	0	0	1	0	0	0	1	123	0.008
370	3	Abnormality of eye movement	HP:0000496	1	0	1	2	4	1	2	11	1086	0.010
371	4	Abnormal conjugate eye movement	HP:0000549	1	0	0	2	4	1	2	10	627	0.016
372	5	Strabismus	HP:0000486	1	0	0	2	4	1	2	10	612	0.016
373	6	Esotropia	HP:0000565	1	0	0	0	0	1	2	4	59	0.068
374	4	Abnormal involuntary eye movements	HP:0012547	0	0	1	0	0	0	0	1	694	0.001
375	5	Nystagmus	HP:0000639	0	0	1	0	0	0	0	1	692	0.001
376	3	Ptosis	HP:0000508	0	0	0	0	1	0	0	1	441	0.002
377	4	Bilateral ptosis	HP:0001488	0	0	0	0	1	0	0	1	13	0.077
378	3	Abnormal visual electrophysiology	HP:0030453	0	0	0	0	1	0	0	1	200	0.005
379	4	Abnormal electroretinogram	HP:0000512	0	0	0	0	1	0	0	1	160	0.006
380	5	Undetectable electroretinogram	HP:0000550	0	0	0	0	1	0	0	1	20	0.050
381	1	Abnormality of the genitourinary system	HP:0000119	2	0	0	4	3	3	1	13	1672	0.008
382	2	Abnormality of the genital system	HP:0000078	2	0	0	1	0	0	0	3	1059	0.003
383	3	Abnormal genital system morphology	HP:0012243	2	0	0	1	0	0	0	3	962	0.003
384	4	Abnormal external genitalia	HP:0000811	2	0	0	1	0	0	0	3	792	0.004
385	5	Abnormality of male external genitalia	HP:0000032	2	0	0	1	0	0	0	3	769	0.004
386	6	Abnormality of the testis	HP:0000035	2	0	0	1	0	0	0	3	677	0.004
387	7	Cryptorchidism	HP:0000028	2	0	0	1	0	0	0	3	515	0.006
388	8	Unilateral cryptorchidism	HP:0012741	1	0	0	0	0	0	0	1	5	0.200
389	6	Abnormality of the penis	HP:0000036	1	0	0	1	0	0	0	2	507	0.004
390	7	Displacement of the external urethral meatus	HP:0100627	1	0	0	0	0	0	0	1	243	0.004
391	8	Hypospadias	HP:0000047	1	0	0	0	0	0	0	1	229	0.004
392	7	Hypoplasia of penis	HP:0008736	0	0	0	1	0	0	0	1	327	0.003
393	8	Micropenis	HP:0000054	0	0	0	1	0	0	0	1	160	0.006
394	2	Abnormality of the urinary system	HP:0000079	2	0	0	4	3	3	1	13	1229	0.011
395	3	Abnormality of the urinary system physiology	HP:0011277	0	0	0	0	0	1	0	1	700	0.001
396	4	Abnormality of urine homeostasis	HP:0003110	0	0	0	0	0	1	0	1	438	0.002
397	5	Proteinuria	HP:0000093	0	0	0	0	0	1	0	1	141	0.007
398	6	Mild proteinuria	HP:0012595	0	0	0	0	0	1	0	1	0	0.000
399	3	Abnormality of the upper urinary tract	HP:0010935	2	0	0	0	3	1	0	6	886	0.007
400	4	Abnormality of the kidney	HP:0000077	2	0	0	0	3	1	0	6	863	0.007
401	5	Abnormal renal morphology	HP:0012210	1	0	0	0	3	1	0	5	670	0.007
402	6	Hyperechogenic kidneys	HP:0004719	0	0	0	0	1	0	0	1	5	0.200
403	6	Abnormality of the nephron	HP:0012575	0	0	0	0	1	0	0	1	166	0.006
404	7	Abnormality of the renal tubule	HP:0000091	0	0	0	0	1	0	0	1	76	0.013
405	6	Abnormality of the renal pelvis	HP:0010944	1	0	0	0	0	1	0	2	142	0.014
406	7	Dilatation of the renal pelvis	HP:0010946	1	0	0	0	0	1	0	2	141	0.014
407	8	Hydronephrosis	HP:0000126	1	0	0	0	0	1	0	2	141	0.014

408	6	Renal hypoplasia/aplasia	HP:0008678	0	0	0	0	1	0	0	1	201	0.005
409	7	Renal agenesis	HP:0000104	0	0	0	0	1	0	0	1	96	0.010
410	8	Unilateral kidney agenesis	HP:0000122	0	0	0	0	1	0	0	1	32	0.031
411	5	Abnormal renal physiology	HP:0012211	1	0	0	0	0	0	0	1	454	0.002
412	6	Hemolytic uremic syndrome	HP:0005575	1	0	0	0	0	0	0	1	3	0.333
413	6	Renal insufficiency	HP:0000083	1	0	0	0	0	0	0	1	282	0.004
414	3	Abnormality of the lower urinary tract	HP:0010936	0	0	0	4	1	1	1	7	456	0.015
415	4	Abnormality of the bladder	HP:0000014	0	0	0	4	1	1	1	7	234	0.030
416	5	Funcitonal abnormality of the bladder	HP:0000009	0	0	0	4	1	1	1	7	210	0.033
417	6	Neurogenic bladder	HP:0000011	0	0	0	2	0	1	0	3	9	0.333
418	6	Urinary incontinence	HP:0000020	0	0	0	2	0	0	1	3	57	0.053
419	1	Abnormality of the immune system	HP:0002715	1	0	2	1	8	2	0	14	1251	0.011
420	2	Abnormality of the lymphatic system	HP:0100763	0	0	0	0	1	0	0	1	459	0.002
421	3	Abnormality of the lymph nodes	HP:0002733	0	0	0	0	1	0	0	1	145	0.007
422	4	Lymphadenopathy	HP:0002716	0	0	0	0	1	0	0	1	137	0.007
423	5	Generalized lymphadenopathy	HP:0008940	0	0	0	0	1	0	0	1	1	1.000
424	2	Abnormality of immune system physiology	HP:0010978	1	0	2	1	7	2	0	13	950	0.014
425	3	Recurrent infections	HP:0002719	1	0	2	1	7	2	0	13	528	0.025
426	4	Recurrent respiratory infections	HP:0002205	0	0	1	0	1	0	0	2	339	0.006
427	4	Recurrent urinary tract infections	HP:0000010	0	0	0	1	0	0	0	1	83	0.012
428	3	Abnormality of humoral immunity	HP:0005368	1	0	0	0	3	0	0	4	163	0.025
429	4	Abnormality of complement system	HP:0005339	1	0	0	0	0	0	0	1	23	0.043
430	4	Abnormal immunoglobulin level	HP:0010701	0	0	0	0	3	0	0	3	140	0.021
431	5	Hypogammaglobulinemia	HP:0004313	0	0	0	0	2	0	0	2	97	0.021
432	5	Hypergammaglobulinemia	HP:0010702	0	0	0	0	1	0	0	1	49	0.020
433	3	Immunodeficiency	HP:0002721	0	0	0	0	2	0	0	2	180	0.011
434	4	Combined immunodeficiency	HP:0005387	0	0	0	0	2	0	0	2	18	0.111
435	1	Abnormality of the integument	HP:0001574	0	0	1	1	9	5	1	17	1777	0.010
436	2	Abnormality of the skin	HP:0000951	0	0	0	1	4	5	1	11	1454	0.008
437	3	Abnormality of skin morphology	HP:0007517	0	0	0	1	4	5	1	11	1356	0.008
439	4	Abnormal elasticity of skin	HP:0010647	0	0	0	1	0	5	0	6	144	0.042
440	5	Abnormally lax or hyperextensible skin	HP:0008067	0	0	0	1	0	5	0	6	109	0.055
441	6	Cutis laxa	HP:0000973	0	0	0	1	0	2	0	3	73	0.041
438	6	Excessive wrinkled skin	HP:0100678	0	0	0	1	0	5	0	6	35	0.171
442	4	Thickened skin	HP:0001072	0	0	0	0	3	0	1	4	359	0.011
443	5	Epidermal thickening	HP:0011368	0	0	0	0	3	0	1	4	326	0.012
444	6	Hyperkeratosis	HP:0000962	0	0	0	0	3	0	1	4	215	0.019
445	6	Hyperkeratosis pilaris	HP:0040180	0	0	0	0	0	0	1	1	3	0.333
446	4	Dry skin	HP:0000958	0	0	0	1	2	0	1	4	114	0.035
447	4	Abnormality of epidermal morphology	HP:0011124	0	0	0	1	0	0	0	1	50	0.020
448	5	Scaling skin	HP:0040189	0	0	0	1	0	0	0	1	14	0.071

449	2	Abnormality of the skin adnexa	HP:0011138	0	0	1	0	6	1	0	8	945	0.008
450	3	Abnormality of the hair	HP:0001595	0	0	1	0	1	1	0	3	827	0.004
451	4	Abnormality of hair density	HP:0011357	0	0	1	0	0	0	0	1	244	0.004
452	5	Thick hair	HP:0100874	0	0	1	0	0	0	0	1	10	0.100
453	4	Abnormal hair quantity	HP:0011362	0	0	0	0	0	1	0	1	431	0.002
454	5	Hypertrichosis	HP:0000998	0	0	0	0	0	1	0	1	122	0.008
455	4	Abnormality of hair pigmentation	HP:0009887	0	0	0	0	1	0	0	1	95	0.011
456	5	Hypopigmentation of hair	HP:0005599	0	0	0	0	1	0	0	1	84	0.012
457	3	Abnormality of the sweat gland	HP:0000971	0	0	0	0	7	0	0	7	8	0.875
458	4	Hypohidrosis or hyperhidrosis	HP:0007550	0	0	0	0	7	0	0	7	159	0.044
459	5	Hypohidrosis	HP:0000966	0	0	0	0	11	0	0	11	58	0.190
460	1	Abnormality of the musculature	HP:0003011	1	1	2	7	11	8	3	33	1928	0.017
461	2	Abnormality of muscle morphology	HP:0011805	0	0	0	1	0	2	1	4	1024	0.004
462	3	Decreased muscle mass	HP:0003199	0	0	0	1	0	2	1	4	51	0.078
463	2	Abnormality of muscle physiology	HP:0011804	1	1	2	7	11	8	3	33	1633	0.020
464	3	Abnormal muscle tone	HP:0003808	1	1	2	7	11	8	3	33	1368	0.024
465	4	Muscular hypotonia	HP:0001252	1	0	2	7	11	7	3	31	1123	0.028
466	5	Generalized hypotonia	HP:0001290	1	0	1	1	1	2	0	6	660	0.009
467	5	Axial hypotonia	HP:0008936	0	0	1	0	2	0	0	3	91	0.033
468	4	Hypertonia	HP:0001276	0	1	1	1	0	1	0	4	607	0.007
469	5	Limb hypertonia	HP:0002509	0	0	1	1	0	0	0	2	19	0.105
470	5	Spasticity	HP:0001257	0	1	0	1	0	1	0	3	490	0.006
471	6	Spastic tetraplegia	HP:0002510	0	1	0	1	0	0	0	2	55	0.036
472	6	Opisthotonus	HP:0002179	0	0	0	0	0	1	0	1	25	0.040
473	1	Abnormality of the nervous system	HP:0000707	3	1	2	10	18	8	3	45	2863	0.016
474	2	Abnormality of the nervous system morphology	HP:0012639	3	1	2	10	16	7	3	42	2033	0.021
475	3	Morphological abnormality of the CNS	HP:0002011	3	1	2	10	16	7	3	42	1872	0.022
476	4	Abnormality of brain morphology	HP:0012443	3	1	2	10	16	7	3	42	1724	0.024
477	5	Abnormality of the forebrain morphology	HP:0100547	3	1	2	7	16	7	2	38	1198	0.032
478	6	Abnormality of the cerebrum	HP:0002060	3	1	2	7	16	7	2	38	1177	0.032
479	7	Aplasia/hypoplasia of the cerebrum	HP:0007364	3	1	2	7	16	7	2	38	897	0.042
480	8	Microcephaly	HP:0000252	3	1	1	7	15	6	1	34	736	0.046
481	9	Progressive microcephaly	HP:0000253	1	0	0	2	6	5	0	14	53	0.264
482	9	Postnatal microcephaly	HP:0005484	0	1	0	0	0	0	0	1	51	0.020
483	8	Atrophy/degeneration affecting cerebrum	HP:0007369	2	1	2	1	4	2	1	13	355	0.037
484	9	Cerebral atrophy	HP:0002059	2	1	2	1	4	2	1	13	348	0.037
485	8	Aplasia/hypoplasia of the corpus callosum	HP:0007370	0	1	1	0	6	3	0	11	400	0.028
486	9	Hypoplasia of the corpus callosum	HP:0002079	0	1	1	0	5	3	0	10	206	0.049
487	9	Agenesis of the corpus callosum	HP:0001274	0	0	0	0	1	0	0	1	187	0.005
488	7	Abnormality of the cerebral subcortex	HP:0010993	0	0	0	1	2	2	0	5	510	0.010
489	8	Abnormality of the cerebral white matter	HP:0002500	0	0	0	1	2	2	0	5	474	0.011

490	9	Cerebral white matter atrophy	HP:0012762	0	0	0	1	2	2	0	5	9	0.556
491	10	Abnormality of the periventricular white matter	HP:0002518	0	0	0	0	2	0	0	2	37	0.054
492	11	Periventricular leukomalacia	HP:0006970	0	0	0	0	2	0	0	2	8	0.250
493	5	Abnormality of the hindbrain morphology	HP:0011282	3	0	1	5	3	2	2	16	886	0.018
494	6	Abnormality of the metencephalon	HP:0011283	3	0	1	5	3	2	2	16	886	0.018
495	7	Abnormality of the cerebellum	HP:0001317	3	0	1	5	3	2	2	16	884	0.018
496	8	Cerebellar atrophy	HP:0001272	2	0	0	5	1	2	2	12	202	0.059
497	9	Diffuse cerebellar atrophy	HP:0100275	0	0	0	3	0	0	1	4	3	1.333
498	8	Ataxia	HP:0001251	0	0	1	4	0	0	1	6	602	0.010
499	9	Dysmetria	HP:0001310	0	0	0	3	0	0	1	4	85	0.047
500	9	Dysdiadochokinesis	HP:0002075	0	0	0	3	0	0	0	3	30	0.100
501	9	Truncal ataxia	HP:0002078	0	0	0	1	0	0	0	1	30	0.033
502	9	Gait ataxia	HP:0002066	0	0	0	3	0	0	0	3	78	0.038
503	10	Progressive gait ataxia	HP:0007240	0	0	0	3	0	0	0	3	5	0.600
504	8	Aplasia/hypoplasia of the cerebellum	HP:0007360	0	0	0	0	2	0	0	2	235	0.009
505	9	Cerebellar hypoplasia	HP:0001321	0	0	0	0	2	0	0	2	146	0.014
506	8	Cerebellar malformation	HP:0002438	1	0	0	0	0	0	0	1	219	0.005
507	9	Abnormality of the cerebellar vermis	HP:0002334	1	0	0	0	0	0	0	1	178	0.006
508	10	Aplasia/hypoplasia of the cereb. vermis	HP:0006817	1	0	0	0	0	0	0	1	163	0.006
509	11	Hypoplastic cerebellar vermis	HP:0001320	1	0	0	0	0	0	0	1	141	0.007
510	5	Abnormality of brain stem morphology	HP:0002363	0	0	0	1	0	0	1	2	82	0.024
511	6	Atrophy/degeneration affecting the brain stem	HP:0007366	0	0	0	1	0	0	1	2	11	0.182
512	5	Abnormality of the cerebral ventricles	HP:0002118	2	0	0	1	2	4	1	10	516	0.019
513	6	Ventriculomegaly	HP:0002119	2	0	0	1	2	4	1	10	381	0.026
514	5	Abnormality of the pituitary gland	HP:0012503	0	1	0	0	1	0	0	2	212	0.009
515	6	Abnormal size of pituitary gland	HP:0012504	0	1	0	0	0	0	0	1	6	0.167
516	7	Small pituitary gland	HP:0012506	0	1	0	0	0	0	0	1	2	0.500
517	6	Abnormality of the anterior pituitary	HP:0011747	0	0	0	0	1	0	0	1	194	0.005
518	7	Hyperpituitarism	HP:0010514	0	0	0	0	1	0	0	1	68	0.015
519	8	Thyroid-stimulating hormone excess	HP:0002925	0	0	0	0	1	0	0	1	11	0.091
520	4	Abnormal CNS myelination	HP:0011400	0	0	0	1	2	1	0	4	131	0.031
521	5	Delayed CNS myelination	HP:0002188	0	0	0	1	2	1	0	4	15	0.267
522	3	Abnormal peripheral nervous system morphology	HP:0000759	0	0	0	1	0	1	2	4	635	0.006
523	4	Peripheral neuropathy	HP:0009830	0	0	0	1	0	1	2	4	420	0.010
524	2	Abnormality of nervous system physiology	HP:0012638	3	1	2	10	17	7	3	43	2474	0.017
525	3	Abnormality of higher mental function	HP:0011446	0	0	0	3	1	0	0	4	1024	0.004
526	4	Reduced consciousness	HP:0004372	0	0	0	0	1	0	0	1	234	0.004
527	5	Lethargy	HP:0001254	0	0	0	0	1	0	0	1	103	0.010
528	4	Neurological speech impairment	HP:0002167	0	0	0	3	1	0	0	4	635	0.006
529	5	Dysarthria	HP:0001260	0	0	0	3	0	0	0	3	359	0.008
530	3	Neurodevelopmental abnormality	HP:0012759	3	1	2	10	16	4	2	38	1801	0.021

531	4	Intellectual disability	HP:0001249	2	1	0	10	9	0	2	24	1290	0.019
532	5	Mild intellectual disability	HP:0001256	0	0	0	3	0	0	0	3	137	0.022
533	5	Moderate intellectual disability	HP:0002342	2	0	0	3	0	0	0	5	50	0.100
534	5	Severe intellectual disability	HP:0010864	0	0	0	4	0	0	0	4	159	0.025
535	4	Neurodevelopmental delay	HP:0012758	3	1	2	6	16	4	1	33	1310	0.025
536	5	Global developmental delay	HP:0001263	3	1	2	6	16	4	1	33	1123	0.029
537	6	Mild global developmental delay	HP:0011342	2	0	0	2	2	0	0	6	22	0.273
538	6	Moderate global developmental delay	HP:0011343	1	0	1	0	0	0	0	2	7	0.286
539	6	Severe global developmental delay	HP:0011344	0	0	0	1	1	0	0	2	66	0.030
540	6	Profound global developmental delay	HP:0012736	0	0	0	1	0	2	0	3	24	0.125
541	5	Delayed speech and language development	HP:0000750	0	0	1	4	0	0	1	6	291	0.021
542	6	Absent speech	HP:0001344	0	0	1	4	0	0	1	6	77	0.078
543	4	Developmental regression	HP:0002376	0	0	1	0	0	0	1	2	197	0.010
544	3	Seizures	HP:0001250	0	1	2	1	4	5	2	15	1174	0.013
545	4	Generalized seizures	HP:0002197	0	1	0	1	0	0	0	2	136	0.015
546	5	Generalized tonic seizures	HP:0010818	0	1	0	0	0	0	0	1	10	0.100
547	4	Focal seizures	HP:0007359	0	0	0	0	1	0	0	1	50	0.020
548	3	Abnormal nervous system electrophysiology	HP:0001311	0	0	0	0	0	3	0	3	334	0.009
549	4	Abnormality of central nervous system electrophysiology	HP:0030178	0	0	0	0	0	3	0	3	257	0.012
550	5	EEG abnormality	HP:0002353	0	0	0	0	0	3	0	3	246	0.012
551	3	Reduced tendon reflexes	HP:0001315	0	0	0	4	1	5	2	12	347	0.035
552	4	Areflexia	HP:0001284	0	0	0	0	1	2	0	3	160	0.019
553	4	Hyporeflexia	HP:0001265	0	0	0	4	0	2	2	8	226	0.035
554	5	Hyporeflexia of lower limbs	HP:0002600	0	0	0	1	0	0	0	1	16	0.063
555	3	Abnormality of central motor function	HP:0011442	0	0	1	2	0	0	0	3	1294	0.002
556	4	Upper motor neuron dysfunction	HP:0002493	0	0	1	1	0	0	0	2	944	0.002
557	5	Hyperreflexia	HP:0001347	0	0	1	1	0	0	0	2	502	0.004
558	4	Abnormality of coordination	HP:0011443	0	0	0	1	0	0	0	1	657	0.002
559	5	Slurred speech	HP:0001350	0	0	0	1	0	0	0	1	25	0.040
560	6	Slow slurred speech	HP:0007164	0	0	0	1	0	0	0	1	2	0.500
561	3	Abnormality of movement	HP:0100022	0	0	1	2	1	0	1	5	1069	0.005
562	4	Involuntary movements	HP:0004305	0	0	1	0	0	0	1	2	558	0.004
563	5	Myoclonus	HP:0001336	0	0	0	0	0	0	1	1	143	0.007
564	4	Gait disturbance	HP:0001288	0	0	0	2	1	0	0	3	536	0.006
565	5	Broad-based gait	HP:0002136	0	0	0	1	0	0	0	1	33	0.030
566	5	Inability to walk	HP:0002540	0	0	0	1	1	0	0	2	53	0.038
567	3	Behavioral abnormality	HP:0000708	0	0	0	3	2	1	0	6	965	0.006
568	4	Short attention span	HP:0000736	0	0	0	1	0	0	0	1	144	0.007
569	5	Attention deficit hyperactive disorder	HP:0007018	0	0	0	1	0	0	0	1	146	0.007
570	4	Abnormal emotion/affect behavior	HP:0100851	0	0	0	0	1	1	0	2	246	0.008
571	5	Irritability	HP:0000737	0	0	0	0	0	1	0	1	104	0.010

572	5	Abnormal aggressive, impulsive or violent behav.	HP:0006919	0	0	0	0	1	1	0	2	146	0.014
573	6	Aggressive behaviour	HP:0000718	0	0	0	0	1	1	0	2	121	0.017
574	4	Autistic behaviour	HP:0000729	0	0	0	2	1	0	0	3	205	0.015
575	4	Stereotypic behaviours	HP:0000733	0	0	0	0	1	0	0	1	66	0.015
576	3	Encephalopathy	HP:0001298	0	0	0	0	0	0	1	1	170	0.006
577	4	Acute encephalopathy	HP:0006846	0	0	0	0	0	0	1	1	25	0.040
578	1	Abnormality of the respiratory system	HP:0002086	1	0	0	0	3	5	0	9	1215	0.007
579	2	Abnormal respiratory system morphology	HP:0012252	1	0	0	0	2	3	0	6	818	0.007
580	3	Abnormality of the upper respiratory tract	HP:0002087	0	0	0	0	1	1	0	2	340	0.006
581	4	Abnormality of the larynx	HP:0001600	0	0	0	0	0	1	0	1	146	0.007
582	5	Laryngomalacia	HP:0001601	0	0	0	0	0	1	0	1	46	0.022
583	4	Abnormality of the tracheobronchial system	HP:0005607	0	0	0	0	1	0	0	1	226	0.004
584	5	Abnormality of the bronchi	HP:0002109	0	0	0	0	1	0	0	1	108	0.009
585	6	Bronchiectasis	HP:0002110	0	0	0	0	1	0	0	1	84	0.012
586	3	Abnormality of the lung	HP:0002088	1	0	0	0	1	2	0	4	676	0.006
587	4	Pneumothorax	HP:0002107	0	0	0	0	1	0	0	1	24	0.042
588	4	Abnormality of the pulmonary vasculature	HP:0004930	1	0	0	0	0	2	0	3	99	0.030
589	5	Abnormality of the pulmonary artery	HP:0004414	1	0	0	0	0	2	0	3	81	0.037
590	6	Elevated pulmonary artery pressure	HP:0004890	1	0	0	0	0	2	0	3	94	0.032
591	7	Pulmonary hypertension	HP:0002092	1	0	0	0	0	2	0	3	94	0.032
592	2	Functional respiratory abnormality	HP:0002795	0	0	0	0	2	3	0	5	816	0.006
593	3	Respiratory insufficiency	HP:0002093	0	0	0	0	2	3	0	5	408	0.012
594	4	Neonatal respiratory distress	HP:0002643	0	0	0	0	2	2	0	4	23	0.174
595	5	Neonatal asphyxia	HP:0012768	0	0	0	0	0	2	0	2	1	2.000
596	1	Abnormality of the skeletal system	HP:0000924	2	0	0	6	11	5	1	25	2129	0.012
597	2	Abnormality of skeletal morphology	HP:0011842	2	0	0	6	11	5	1	25	2049	0.012
598	3	Skeletal dysplasia	HP:0002652	0	0	0	0	7	0	0	7	149	0.047
599	3	Abnormal axial skeleton morphology	HP:0009121	2	0	0	4	2	0	1	9	1706	0.005
600	4	Abnormality of the vertebral column	HP:0000925	2	0	0	4	1	0	1	8	922	0.009
601	5	Abnormality of the vertebrae	HP:0003468	2	0	0	0	0	0	0	2	316	0.006
602	6	Abnormal form of the vertebral bodies	HP:0003312	1	0	0	0	0	0	0	1	235	0.004
603	7	Vertebral clefting	HP:0008428	1	0	0	0	0	0	0	1	22	0.045
604	8	Butterfly vertebrae	HP:0003316	1	0	0	0	0	0	0	1	10	0.100
605	6	Vertebral segmentation defect	HP:0003422	1	0	0	0	0	0	0	1	103	0.010
606	5	Abnormality of the curvature of the vert. column	HP:0010674	1	0	0	4	1	0	1	7	705	0.010
607	6	Scoliosis	HP:0002650	1	0	0	4	1	0	1	7	649	0.011
608	7	Thoracic scoliosis	HP:0002943	1	0	0	0	0	0	0	1	14	0.071
609	7	Kyphoscoliosis	HP:0002751	1	0	0	0	0	0	0	1	94	0.011
610	4	Abnormality of the thorax	HP:0000765	2	0	0	0	1	0	0	3	541	0.006
611	5	Abnormality of the rib cage	HP:0001547	2	0	0	0	1	0	0	3	254	0.012
612	6	Asymmetry of the thorax	HP:0001555	0	0	0	0	1	0	0	1	8	0.125

613	6	Abnormality of the ribs	HP:0000772	2	0	0	0	0	0	0	2	199	0.010
614	7	Rib fusion	HP:0000902	2	0	0	0	0	0	0	2	27	0.074
615	7	Rib gap	HP:0030280	1	0	0	0	0	0	0	1	1	1.000
616	8	Posterior rib gap	HP:0030282	1	0	0	0	0	0	0	1	1	1.000
617	3	Abnormal appendicular skeleton morphology	HP:0011844	1	0	0	0	1	2	0	4	1084	0.004
618	4	Abnormality of long bone morphology	HP:0011314	1	0	0	0	0	2	0	3	470	0.006
619	5	Short long bones	HP:0003026	1	0	0	0	0	1	0	2	153	0.013
620	5	Abnormality of epiphysis morphology	HP:0005930	0	0	0	0	0	1	0	1	205	0.005
621	6	Absent epiphyses	HP:0010577	0	0	0	0	0	1	0	1	13	0.077
622	7	Absent knee epiphyses	HP:0006400	0	0	0	0	0	1	0	1	1	1.000
623	4	Abnormality of pelvic girdle bone morphology	HP:0002644	1	0	0	0	1	0	0	2	388	0.005
624	5	Abnormality of the hip bone	HP:0003272	1	0	0	0	1	0	0	2	329	0.006
625	6	Hip dysplasia	HP:0001385	0	0	0	0	1	0	0	1	91	0.011
626	6	Abnormality of the ilium	HP:0002867	1	0	0	0	0	0	0	1	72	0.014
627	7	Squared iliac bones	HP:0003177	1	0	0	0	0	0	0	1	4	0.250
628	6	Abnormality of the hip joint	HP:0001384	1	0	0	0	0	0	0	1	200	0.005
629	7	Abnormality of the acetabulum	HP:0003170	1	0	0	0	0	0	0	1	49	0.020
630	8	Flat acetabular roof	HP:0003180	1	0	0	0	0	0	0	1	16	0.063
631	3	Abnormal joint morphology	HP:0001367	1	0	0	2	9	3	1	16	999	0.016
632	4	Abnormality of joint mobility	HP:0011729	1	0	0	2	9	3	1	16	795	0.020
633	5	Joint hypermobility	HP:0001382	0	0	0	2	9	0	0	11	229	0.048
634	5	Flexion contracture	HP:0001371	1	0	0	2	1	3	1	8	492	0.016
635	6	Congenital contracture	HP:0002803	0	0	0	0	1	1	0	2	120	0.017
636	7	Arthrogryposis multiplex congenita	HP:0002804	0	0	0	0	1	0	0	1	102	0.010
637	7	Distal arthrogryposis	HP:0005684	0	0	0	0	0	1	0	1	12	0.083
638	6	Multiple joint contractures	HP:0002828	0	0	0	0	7	2	0	9	11	0.818
639	6	Flexion contracture of digit	HP:0030044	1	0	0	2	0	2	0	5	216	0.023
640	7	Camptodactyly	HP:0012385	1	0	0	2	0	2	0	5	212	0.024
641	8	Camptodactyly of finger	HP:0100490	1	0	0	2	0	2	0	5	146	0.034
642	9	Camptodactyly of 2nd - 5th fingers	HP:0001215	1	0	0	1	0	0	0	2	1	2.000
643	6	Limb joint contracture	HP:0003121	0	0	0	1	0	0	1	2	256	0.008
644	7	Contractures of the joints of upper limbs	HP:0100360	0	0	0	1	0	0	1	2	208	0.010
645	8	Elbow flexion contracture	HP:0002987	0	0	0	1	0	0	0	1	46	0.022
646	7	Contractures of the joints of lower limbs	HP:0005750	0	0	0	1	0	0	1	2	94	0.021
647	8	Knee flexion contracture	HP:0006380	0	0	0	1	0	0	0	1	39	0.026
648	3	Abnormal bone structure	HP:0003330	1	0	0	0	1	1	0	3	565	0.005
649	4	Abnormal bone ossification	HP:0011849	0	0	0	0	0	1	0	1	497	0.002
650	5	Abnormal enchondral ossification	HP:0003336	0	0	0	0	0	1	0	1	100	0.010
651	6	Abnormal humeral ossification	HP:0012791	0	0	0	0	0	1	0	1	1	1.000
652	7	Absent humeral epiphyseal ossification	HP:0003892	0	0	0	0	0	1	0	1	0	0.000
653	4	Abnormality of bone mineral density	HP:0004348	1	0	0	0	1	0	0	2	419	0.005

654	5	Reduced bone mineral density	HP:0004349	1	0	0	0	1	0	0	2	360	0.006
655	6	Osteopenia	HP:0000938	1	0	0	0	1	0	0	2	176	0.011
656	1	Growth abnormality	HP:0001507	3	0	1	6	14	8	2	34	1708	0.020
657	2	Growth delay	HP:0001510	3	0	1	6	3	7	1	21	1206	0.017
658	3	Short stature	HP:0004322	2	0	1	5	3	3	1	15	919	0.016
659	3	Intrauterine growth retardation	HP:0001511	2	0	0	2	1	5	0	10	319	0.031
660	2	Abnormality of body weight	HP:0004323	1	0	1	3	12	8	1	26	1060	0.025
661	3	Decreased body weight	HP:0004325	1	0	1	3	12	8	1	26	870	0.030
662	4	Failure to thrive	HP:0001508	1	0	1	3	12	8	1	26	637	0.041
663	1	Mortality/Aging	HP:0040006	0	0	1	0	8	7	0	16	231	0.069
664	2	Age of death	HP:0011420	0	0	1	0	8	7	0	16	231	0.069
665	3	Death in infancy	HP:0001522	0	0	1	0	7	7	0	15	132	0.114
666	3	Neonatal death	HP:0003811	0	0	0	0	1	0	0	1	17	0.059

Supplementary Table 3: Genes associated to phenotypic features discussed throughout the manuscript

Gene	Gene name (GeneCards)	Gene	Gene name (GeneCards)
Abnormality of temperature regulation (HP:0004370), 244 genes		Abnormally lax or hyperextensible skin (HP:0008067), 109 genes	
ABCA1	ATP Binding Cassette Subfamily A Member 1	ABCC6	ATP Binding Cassette Subfamily C Member 6
ABCA12	ATP Binding Cassette Subfamily A Member 12	ACD	ACD Shelterin Complex Subunit And Telomerase Recruitment Factor
ABCC2	ATP Binding Cassette Subfamily C Member 2	ADAMTS2	ADAM Metallopeptidase With Thrombospondin Type 1 Motif 2
ABL1	ABL Proto-Oncogene 1, Non-Receptor Tyrosine Kinase	AKT3	AKT Serine/Threonine Kinase 3
ACADSB	Acyl-CoA Dehydrogenase Short/Branched Chain	ALDH18A1	Aldehyde Dehydrogenase 18 Family Member A1
ADA	Adenosine Deaminase	ANTXR1	ANTXR Cell Adhesion Molecule 1
ADA2	Adenosine Deaminase 2	ARID1B	AT-Rich Interaction Domain 1B
ADAMTS13	ADAM Metallopeptidase With Thrombospondin Type 1 Motif 13	ATP6V0A2	ATPase H+ Transporting V0 Subunit A2
AK2	Adenylate Kinase 2	ATP6V1A	ATPase H+ Transporting V1 Subunit A
ALG11	ALG11 Alpha-1,2-Mannosyltransferase	ATP6V1E1	ATPase H+ Transporting V1 Subunit E1
ALPL	Alkaline Phosphatase, Biom mineralization Associated	ATP7A	ATPase Copper Transporting Alpha
AQP2	Aquaporin 2	B3GALT6	Beta-1,3-Galactosyltransferase 6
ASCL1	Achaete-Scute Family BHLH Transcription Factor 1	B3GAT3	Beta-1,3-Glucuronyltransferase 3
ATM	ATM Serine/Threonine Kinase	B4GALT7	Beta-1,4-Galactosyltransferase 7
ATP1A2	ATPase Na+/K+ Transporting Subunit Alpha 2	BAZ1B	Bromodomain Adjacent To Zinc Finger Domain 1B
ATP7A	ATPase Copper Transporting Alpha	BRAF	B-Raf Proto-Oncogene, Serine/Threonine Kinase
AVP	Arginine Vasopressin	C1R	Complement C1r
AVPR2	Arginine Vasopressin Receptor 2	C1S	Complement C1s
BCL10	BCL10 Immune Signaling Adaptor	CD96	CD96 Molecule
BCL2	BCL2 Apoptosis Regulator	CHST14	Carbohydrate Sulfotransferase 14
BCL6	BCL6 Transcription Repressor	CHST3	Carbohydrate Sulfotransferase 3
BCR	BCR Activator Of RhoGEF And GTPase	CLIP2	CAP-Gly Domain Containing Linker Protein 2
BDNF	Brain Derived Neurotrophic Factor	COL1A1	Collagen Type I Alpha 1 Chain
BIRC3	Baculoviral IAP Repeat Containing 3	COL1A2	Collagen Type I Alpha 2 Chain
BLNK	B Cell Linker	COL3A1	Collagen Type III Alpha 1 Chain
BRCA2	BRCA2, DNA Repair Associated	COL5A1	Collagen Type V Alpha 1 Chain
BTK	Bruton Tyrosine Kinase	COL5A2	Collagen Type V Alpha 2 Chain
BTNL2	Butyrophilin Like 2	CSTA	Cystatin A
C4A	Complement C4A (Rodgers Blood Group)	DKC1	Dyskerin Pseudouridine Synthase 1
CACNA1A	Calcium Voltage-Gated Channel Subunit Alpha1 A	EED	Embryonic Ectoderm Development
CCND1	Cyclin D1	EFEMP2	EGF Containing Fibulin Like Extracellular Matrix Protein 2
CCR1	C-C Motif Chemokine Receptor 1	ELN	Elastin
CD27	CD27 Molecule	ENPP1	Ectonucleotide Pyrophosphatase/Phosphodiesterase 1
CD79A	CD79a Molecule	EXT1	Exostosin Glycosyltransferase 1
CD79B	CD79b Molecule	EZH2	Enhancer Of Zeste 2 Polycomb Repressive Complex 2 Subunit
CHD7	Chromodomain Helicase DNA Binding Protein 7	FBLN5	Fibulin 5
CHEK2	Checkpoint Kinase 2	FBN1	Fibrillin 1
CHRNA1	Cholinergic Receptor Nicotinic Alpha 1 Subunit	FGD1	FYVE, RhoGEF And PH Domain Containing 1
CHRND	Cholinergic Receptor Nicotinic Delta Subunit	FGF10	Fibroblast Growth Factor 10
CHRNA3	Cholinergic Receptor Nicotinic Gamma Subunit	FGF20	Fibroblast Growth Factor 20
CLCF1	Cardiotrophin Like Cytokine Factor 1	FGFR2	Fibroblast Growth Factor Receptor 2
CLCN7	Chloride Voltage-Gated Channel 7	FGFR3	Fibroblast Growth Factor Receptor 3
CLEC7A	C-Type Lectin Domain Containing 7A	FIG4	FIG4 Phosphoinositide 5-Phosphatase
COL1A1	Collagen Type I Alpha 1 Chain	FKBP14	FKBP Prolyl Isomerase 14
COX1	Mitochondrially Encoded Cytochrome C Oxidase I	FOXC1	Forkhead Box C1
COX2	Mitochondrially Encoded Cytochrome C Oxidase II	GGCX	Gamma-Glutamyl Carboxylase
COX3	Mitochondrially Encoded Cytochrome C Oxidase III	GORAB	Golgin, RAB6 Interacting
CRLF1	Cytokine Receptor Like Factor 1	GPX4	Glutathione Peroxidase 4
CTLA4	Cytotoxic T-Lymphocyte Associated Protein 4	GSN	Gelsolin
CYBA	Cytochrome B-245 Alpha Chain	GTF2I	General Transcription Factor III
CYBB	Cytochrome B-245 Beta Chain	GTF2IRD1	GTF2I Repeat Domain Containing 1

<i>CYP11B2</i>	Cytochrome P450 Family 11 Subfamily B Member 2	<i>HPGD</i>	15-Hydroxyprostaglandin Dehydrogenase
<i>CYP21A2</i>	Cytochrome P450 Family 21 Subfamily A Member 2	<i>HRAS</i>	HRas Proto-Oncogene, GTPase
<i>DBH</i>	Dopamine Beta-Hydroxylase	<i>IFT43</i>	Intraflagellar Transport 43
<i>DCLRE1C</i>	DNA Cross-Link Repair 1C	<i>KRAS</i>	KRAS Proto-Oncogene, GTPase
<i>DDB2</i>	Damage Specific DNA Binding Protein 2	<i>LIMK1</i>	LIM Domain Kinase 1
<i>DDC</i>	Dopa Decarboxylase	<i>LTBP4</i>	Latent Transforming Growth Factor Beta Binding Protein 4
<i>DGUOK</i>	Deoxyguanosine Kinase	<i>MAP2K1</i>	Mitogen-Activated Protein Kinase Kinase 1
<i>DIS3L2</i>	DIS3 Like 3'-5' Exoribonuclease 2	<i>MAP2K2</i>	Mitogen-Activated Protein Kinase Kinase 1
<i>DST</i>	Dystonin	<i>MAPRE2</i>	Microtubule Associated Protein RP/EB Family Member 2
<i>EDA</i>	Ectodysplasin A	<i>MEGF8</i>	Multiple EGF Like Domains 8
<i>EDAR</i>	Ectodysplasin A Receptor	<i>MLXIPL</i>	MLX Interacting Protein Like
<i>EDARADD</i>	EDAR Associated Death Domain	<i>MRPS16</i>	Mitochondrial Ribosomal Protein S16
<i>EDN3</i>	Endothelin 3	<i>MRPS22</i>	Mitochondrial Ribosomal Protein S22
<i>ELANE</i>	Elastase, Neutrophil Expressed	<i>NAA10</i>	N(Alpha)-Acetyltransferase 10, NatA Catalytic Subunit
<i>ELP1</i>	Elongator Complex Protein 1	<i>NBAS</i>	Neuroblastoma Amplified Sequence
<i>ERAP1</i>	Endoplasmic Reticulum Aminopeptidase 1	<i>NPR2</i>	Natriuretic Peptide Receptor 2
<i>ERCC2</i>	ERCC Excision Repair 2, TFIIH Core Complex Helicase Subunit	<i>NSD1</i>	Nuclear Receptor Binding SET Domain Protein 1
<i>ERCC3</i>	ERCC Excision Repair 3, TFIIH Core Complex Helicase Subunit	<i>OSMR</i>	Oncostatin M Receptor
<i>ERCC4</i>	ERCC Excision Repair 4, Endonuclease Catalytic Subunit	<i>PARN</i>	Poly(A)-Specific Ribonuclease
<i>ERCC5</i>	ERCC Excision Repair 5, Endonuclease	<i>PAX2</i>	Paired Box 2
<i>F5</i>	Coagulation Factor V	<i>PDGFRB</i>	Platelet Derived Growth Factor Receptor Beta
<i>FAS</i>	Fas Cell Surface Death Receptor	<i>PEX1</i>	Peroxisomal Biogenesis Factor 1
<i>FBP1</i>	Fibrillin 1	<i>PIK3R1</i>	Phosphoinositide-3-Kinase Regulatory Subunit 1
<i>FOXP1</i>	Forkhead Box P1	<i>PITX2</i>	Paired Like Homeodomain 2
<i>GAA</i>	Glucosidase Alpha, Acid	<i>PLOD1</i>	Procollagen-Lysine,2-Oxoglutarate 5-Dioxygenase 1
<i>GALC</i>	Galactosylceramidase	<i>PRDM5</i>	PR/SET Domain 5
<i>GATA2</i>	GATA Binding Protein 2	<i>PTDSS1</i>	Phosphatidylserine Synthase 1
<i>GCDH</i>	Glutaryl-CoA Dehydrogenase	<i>PTEN</i>	Phosphatase And Tensin Homolog
<i>GCH1</i>	GTP Cyclohydrolase 1	<i>PTPN11</i>	Protein Tyrosine Phosphatase, Non-Receptor Type 11
<i>GDNF</i>	Glial Cell Derived Neurotrophic Factor	<i>PYCR1</i>	Pyrroline-5-Carboxylate Reductase 1
<i>GLA</i>	Galactosidase Alpha	<i>RAF1</i>	Raf-1 Proto-Oncogene, Serine/Threonine Kinase
<i>GPC3</i>	Glypican 3	<i>RFC2</i>	Replication Factor C Subunit 2
<i>GPR35</i>	G Protein-Coupled Receptor 35	<i>RIN2</i>	Ras And Rab Interactor 2
<i>H19</i>	H19 Imprinted Maternally Expressed Transcript	<i>RIT1</i>	Ras Like Without CAAX 1
<i>HBB</i>	Hemoglobin Subunit Beta	<i>RPS6KA3</i>	Ribosomal Protein S6 Kinase A3
<i>HERC2</i>	HECT And RLD Domain Containing E3 Ubiquitin Protein Ligase 2	<i>RTEL1</i>	Regulator Of Telomere Elongation Helicase 1
<i>HEXB</i>	Hexosaminidase Subunit Beta	<i>SKI</i>	SKI Proto-Oncogene
<i>HLA-B</i>	Major Histocompatibility Complex, Class I, B	<i>SLC26A2</i>	Solute Carrier Family 26 Member 2
<i>HLA-DPB1</i>	Major Histocompatibility Complex, Class II, DP Beta 1	<i>SLC2A10</i>	Solute Carrier Family 2 Member 10
<i>HLA-DRB1</i>	Major Histocompatibility Complex, Class II, DR Beta 1	<i>SLC39A13</i>	Solute Carrier Family 39 Member 13
<i>HMGCL</i>	3-Hydroxy-3-Methylglutaryl-CoA Lyase	<i>SLC6A8</i>	Solute Carrier Family 6 Member 8
<i>HSPG2</i>	Heparan Sulfate Proteoglycan 2	<i>SLC7A7</i>	Solute Carrier Family 7 Member 7
<i>HTR1A</i>	5-Hydroxytryptamine Receptor 1A	<i>SMARCA2</i>	SWI/SNF Related, Matrix Associated, Actin Dependent Regulator Of Chromatin, Subfamily A, Member 2
<i>IGH</i>	Immunoglobulin Heavy Locus	<i>SPINT2</i>	Serine Peptidase Inhibitor, Kunitz Type 2
<i>IGHM</i>	Immunoglobulin Heavy Constant Mu	<i>SRD5A3</i>	Steroid 5 Alpha-Reductase 3
<i>IGLL1</i>	Immunoglobulin Lambda Like Polypeptide 1	<i>SUZ12</i>	SUZ12 Polycomb Repressive Complex 2 Subunit
<i>IKZF1</i>	IKAROS Family Zinc Finger 1	<i>TBL2</i>	Transducin Beta Like 2
<i>IL10</i>	Interleukin 10	<i>TBX15</i>	T-Box 15
<i>IL12A</i>	Interleukin 12A	<i>TERT</i>	Telomerase Reverse Transcriptase
<i>IL12A-AS1</i>	IL12A Antisense RNA 1	<i>TGM5</i>	Transglutaminase 5
<i>IL12B</i>	Interleukin 12B	<i>TINF2</i>	TERF1 Interacting Nuclear Factor 2
<i>IL17F</i>	Interleukin 17F	<i>TNXB</i>	Tenascin XB

<i>NLRP3</i>	NLR Family Pyrin Domain Containing 3	<i>AGL</i>	Amylo-Alpha-1, 6-Glucosidase, 4-Alpha-Glucanotransferase
<i>NME1</i>	NME/NM23 Nucleoside Diphosphate Kinase 1	<i>AGPAT2</i>	1-Acylglycerol-3-Phosphate O-Acyltransferase 2
<i>NOD2</i>	Nucleotide Binding Oligomerization Domain Containing 2	<i>AKR1D1</i>	Aldo-Keto Reductase Family 1 Member D1
<i>NOTCH3</i>	Notch Receptor 3	<i>ALAS2</i>	5'-Aminolevulinate Synthase 2
<i>NPAP1</i>	Nuclear Pore Associated Protein 1	<i>ALDOB</i>	Aldolase, Fructose-Bisphosphate B
<i>NTRK1</i>	Neurotrophic Receptor Tyrosine Kinase 1	<i>ALG6</i>	ALG6 Alpha-1,3-Glucosyltransferase
<i>ORAI1</i>	ORAI Calcium Release-Activated Calcium Modulator 1	<i>ALMS1</i>	ALMS1 Centrosome And Basal Body Associated Protein
<i>PAX8</i>	Paired Box 8	<i>AMACR</i>	Alpha-Methylacyl-CoA Racemase
<i>PHOX2B</i>	Paired Like Homeobox 2b	<i>ATM</i>	ATM Serine/Threonine Kinase
<i>PIK3R1</i>	Phosphoinositide-3-Kinase Regulatory Subunit 1	<i>ATP6AP1</i>	ATPase H+ Transporting Accessory Protein 1
<i>POU6F2</i>	POU Class 6 Homeobox 2	<i>ATP7B</i>	ATPase Copper Transporting Beta
<i>PRKAR1A</i>	Protein Kinase CAMP-Dependent Type I Regulatory Subunit Alpha	<i>ATP8B1</i>	ATPase Phospholipid Transporting 8B1
<i>PRNP</i>	Prion Protein	<i>ATRX</i>	ATRX, Chromatin Remodeler
<i>PRSS1</i>	Serine Protease 1	<i>BCS1L</i>	BCS1 Homolog, Ubiquinol-Cytochrome C Reductase Complex Chaperone
<i>PRTN3</i>	Proteinase 3	<i>BRCA1</i>	BRCA1, DNA Repair Associated
<i>PSMB8</i>	Proteasome Subunit Beta 8	<i>BRCA2</i>	BRCA2, DNA Repair Associated
<i>PSTPIP1</i>	Proline-Serine-Threonine Phosphatase Interacting Protein 1	<i>BSCL2</i>	BSCL2, Seipin Lipid Droplet Biogenesis Associated
<i>PTPN22</i>	Protein Tyrosine Phosphatase Non-Receptor Type 22	<i>CAVIN1</i>	Caveolae Associated Protein 1
<i>PTPN3</i>	Protein Tyrosine Phosphatase Non-Receptor Type 3	<i>CBS</i>	Cystathionine-Beta-Synthase
<i>PTS</i>	6-Pyruvoyltetrahydropterin Synthase	<i>CC2D2A</i>	Coiled-Coil And C2 Domain Containing 2A
<i>PWARI</i>	Prader Willi/Angelman Region RNA 1	<i>CCDC115</i>	Coiled-Coil Domain Containing 115
<i>PWRN1</i>	Prader-Willi Region Non-Protein Coding RNA 1	<i>CD19</i>	CD19 Molecule
<i>QDPR</i>	Quinoid Dihydropteridine Reductase	<i>CD81</i>	CD81 Molecule
<i>RAB27A</i>	RAB27A, Member RAS Oncogene Family	<i>CDKN2A</i>	Cyclin Dependent Kinase Inhibitor 2A
<i>RAG1</i>	Recombination Activating 1	<i>COG2</i>	COG complex subunit 2
<i>RAG2</i>	Recombination Activating 2	<i>COG4</i>	COG complex subunit 4
<i>RB1</i>	RB Transcriptional Corepressor 1	<i>COG6</i>	COG complex subunit 6
<i>REST</i>	RE1 Silencing Transcription Factor	<i>COG8</i>	COG complex subunit 8
<i>RET</i>	Ret Proto-Oncogene	<i>CPT1A</i>	Carnitine Palmitoyltransferase 1A
<i>RMRP</i>	RNA Component Of Mitochondrial RNA Processing Endoribonuclease	<i>CPT2</i>	Carnitine Palmitoyltransferase 2
<i>RUNX1</i>	RUNX Family Transcription Factor 1	<i>CR2</i>	Complement C3d Receptor 2
<i>RYR1</i>	Ryanodine Receptor 1	<i>CYC1</i>	Cytochrome C1
<i>SCN4A</i>	Sodium Voltage-Gated Channel Alpha Subunit 4	<i>CYP7B1</i>	Cytochrome P450 Family 7 Subfamily B Member 1
<i>SCN9A</i>	Sodium Voltage-Gated Channel Alpha Subunit 9	<i>DAXX</i>	Death Domain Associated Protein
<i>SHANK3</i>	SH3 And Multiple Ankyrin Repeat Domains 3	<i>DCDC2</i>	Doublecortin Domain Containing 2
<i>SLC11A1</i>	Solute Carrier Family 11 Member 1	<i>DDOST</i>	Dolichyl-Diphosphooligosaccharide--Protein Glycosyltransferase Non-Catalytic Subunit
<i>SLC12A1</i>	Solute Carrier Family 12 Member 1	<i>DGUOK</i>	Deoxyguanosine Kinase
<i>SLC19A3</i>	Solute Carrier Family 19 Member 3	<i>DLD</i>	Dihydrolipoamide Dehydrogenase
<i>SLC25A19</i>	Solute Carrier Family 25 Member 19	<i>DMD</i>	Dystrophin
<i>SLC25A20</i>	Solute Carrier Family 25 Member 20	<i>DOLK</i>	Dolichol Kinase
<i>SLC29A3</i>	Solute Carrier Family 29 Member 3	<i>DPAGT1</i>	Dolichyl-Phosphate N-Acetylglucosaminophosphotransferase 2
<i>SLCO1B1</i>	Solute Carrier Organic Anion Transporter Family Member 1B1	<i>DPM1</i>	Dolichyl-Phosphate Mannosyltransferase Subunit 1, Catalytic
<i>SLCO1B3</i>	Solute Carrier Organic Anion Transporter Family Member 1B3	<i>DPM3</i>	Dolichyl-Phosphate Mannosyltransferase Subunit 3
<i>SNORD115-1</i>	Small Nucleolar RNA, C/D Box 115-1	<i>EIF2AK3</i>	Eukaryotic Translation Initiation Factor 2 Alpha Kinase 3
<i>SNORD116-1</i>	Small Nucleolar RNA, C/D Box 116-1	<i>ERCC4</i>	ERCC Excision Repair 4, Endonuclease Catalytic Subunit
<i>SNRPN</i>	Small Nuclear Ribonucleoprotein Polypeptide N	<i>F5</i>	Coagulation Factor V
<i>SNX10</i>	Sorting Nexin 10	<i>FAH</i>	Fumarylacetoacetate Hydrolase
<i>SPINK1</i>	Serine Peptidase Inhibitor, Kazal Type 1	<i>FAN1</i>	FANCD2 And FANCI Associated Nuclease 1
<i>SPR</i>	Sepiapterin Reductase	<i>FBXL4</i>	F-Box And Leucine Rich Repeat Protein 4
<i>STAC3</i>	SH3 And Cysteine Rich Domain 3	<i>G6PC</i>	Glucose-6-Phosphatase Catalytic Subunit

<i>STAT3</i>	Signal Transducer And Activator Of Transcription 3	<i>GDF2</i>	Growth Differentiation Factor 2	
<i>STAT4</i>	Signal Transducer And Activator Of Transcription 4	<i>GLRX5</i>	Glutaredoxin 5	
<i>STIM1</i>	Stromal Interaction Molecule 1	<i>GNAS</i>	GNAS Complex Locus	
<i>STX11</i>	Syntaxin 11	<i>GNE</i>	Glucosamine (UDP-N-Acetyl)-2-Epimerase/N-Acetylmannosamine Kinase	
<i>STXBP2</i>	Syntaxin Binding Protein 2	<i>GNMT</i>	Glycine N-Methyltransferase	
<i>TBX3</i>	T-Box 3	<i>GPD1</i>	Glycerol-3-Phosphate Dehydrogenase 1	
<i>TCF3</i>	Transcription Factor 3	<i>GPR35</i>	G Protein-Coupled Receptor 35	
<i>TCF4</i>	Transcription Factor 4	<i>GYS2</i>	Glycogen Synthase 2	
<i>TCIRG1</i>	T Cell Immune Regulator 1, ATPase H ⁺ Transporting V0 Subunit A3	<i>HADH</i>	Hydroxyacyl-CoA Dehydrogenase	
<i>TLR4</i>	Toll Like Receptor 4	<i>HADHA</i>	Hydroxyacyl-CoA Dehydrogenase/3-Ketoacyl-CoA Thiolase/Enoyl-CoA Hydratase (Trifunctional Protein), Alpha Subunit	
<i>TMEM165</i>	Transmembrane Protein 165	<i>HADHB</i>	Hydroxyacyl-CoA Dehydrogenase/3-Ketoacyl-CoA Thiolase/Enoyl-CoA Hydratase (Trifunctional Protein), Beta Subunit	
<i>TMEM173</i>	Transmembrane Protein 173	<i>HAMP</i>	Hepcidin Antimicrobial Peptide	
<i>TNFAIP3</i>	TNF Alpha Induced Protein 3	<i>HBB</i>	Hemoglobin Subunit Beta	
<i>TNFRSF1A</i>	TNF Receptor Superfamily Member 1A	<i>HFE</i>	Hemochromatosis	
<i>TNFSF11</i>	TNF Superfamily Member 11	<i>HFE2</i>	Hemochromatosis Type 2 (Juvenile)	
<i>TP53</i>	Tumor Protein P53	<i>HLA-B</i>	Major Histocompatibility Complex, Class I, B	
<i>TRAF3IP2</i>	TRAF3 Interacting Protein 2	<i>HNF1A</i>	HNF1 Homeobox A	
<i>TRAPPC9</i>	Trafficking Protein Particle Complex 9	<i>HNF1B</i>	HNF1 Homeobox B	
<i>TREX1</i>	Three Prime Repair Exonuclease 1	<i>HNF4A</i>	Hepatocyte Nuclear Factor 4 Alpha	
<i>TRIP13</i>	Thyroid Hormone Receptor Interactor 13	<i>HSD17B4</i>	Hydroxysteroid 17-Beta Dehydrogenase 4	
<i>TRNF</i>	Mitochondrially Encoded TRNA-Phe (UUU/C)	<i>HSD3B7</i>	Hydroxy-Delta-5-Steroid Dehydrogenase, 3 Beta-And Steroid Delta-Isomerase 7	
<i>TRNH</i>	Mitochondrially Encoded TRNA-His (CAU/C)	<i>IARS</i>	Isoleucyl-TRNA Synthetase	
<i>TRNL1</i>	Mitochondrially Encoded TRNA-Leu (UUA/G) 1	<i>ICOS</i>	Inducible T-Cell Costimulator	
<i>TRNQ</i>	Mitochondrially Encoded TRNA-Gln (CAA/G)	<i>IER3IP1</i>	Immediate Early Response 3 Interacting Protein 1	
<i>TRNS1</i>	Mitochondrially Encoded TRNA-Ser (UCN) 1	<i>IFT172</i>	Intraflagellar Transport 172	
<i>TRNS2</i>	Mitochondrially Encoded TRNA-Ser (AGU/C) 2	<i>IKZF1</i>	IKAROS Family Zinc Finger 1	
<i>TRNW</i>	Mitochondrially Encoded TRNA-Trp (UGA/G)	<i>INPP5E</i>	Inositol Polyphosphate-5-Phosphatase E	
<i>TSC1</i>	TSC Complex Subunit 1	<i>JAG1</i>	Jagged 1	
<i>TSC2</i>	TSC Complex Subunit 2	<i>JAK2</i>	Janus Kinase 2	
<i>TSPYL1</i>	TSPY Like 1	<i>KIF23</i>	Kinesin Family Member 23	
<i>UBAC2</i>	UBA Domain Containing 2	<i>KRAS</i>	KRAS Proto-Oncogene, GTPase	
<i>UNC13D</i>	Unc-13 Homolog D	<i>LARS</i>	Leucyl-TRNA Synthetase	
<i>VPS11</i>	VPS11, CORVET/HOPS Core Subunit	<i>LBR</i>	Lamin B Receptor	
<i>WAS</i>	WASP Actin Nucleation Promoting Factor	<i>LHX1</i>	LIM Homeobox 1	
<i>WIPF1</i>	WAS/WASL Interacting Protein Family Member 1	<i>LIPT1</i>	Lipoyltransferase 1	
<i>WT1</i>	WT1 Transcription Factor	<i>MARS</i>	Methionyl-TRNA Synthetase	
<i>XIAP</i>	X-Linked Inhibitor Of Apoptosis	<i>MPV17</i>	MPV17, Mitochondrial Inner Membrane Protein	
<i>XPA</i>	XPA, DNA Damage Recognition And Repair Factor	<i>MRPL3</i>	Mitochondrial Ribosomal Protein L3	
<i>XPC</i>	XPC Complex Subunit, DNA Damage Recognition And Repair Factor	<i>MRPL44</i>	Mitochondrial Ribosomal Protein L44	
Fever (HP:0001945), 180 genes		<i>MRPS16</i>	Mitochondrial Ribosomal Protein S16	Mitochondrial Membrane
<i>ABCC2</i>	ATP Binding Cassette Subfamily C Member 2	<i>MS4A1</i>	Membrane Spanning 4-Domains A1	
<i>ABL1</i>	ABL Proto-Oncogene 1, Non-Receptor Tyrosine Kinase	<i>MST1</i>	Macrophage Stimulating 1	
<i>ADA</i>	Adenosine Deaminase	<i>MVK</i>	Mevalonate Kinase	
<i>ADA2</i>	Adenosine Deaminase 2	<i>NFKB1</i>	Nuclear Factor Kappa B Subunit 1	
<i>ADAMTS13</i>	ADAM Metallopeptidase With Thrombospondin Type 1 Motif 13	<i>NFKB2</i>	Nuclear Factor Kappa B Subunit 2	
<i>AK2</i>	Adenylate Kinase 2	<i>NGLY1</i>	N-Glycanase 1	
<i>ALPL</i>	Alkaline Phosphatase, Biom mineralization Associated	<i>NR1H4</i>	Nuclear Receptor Subfamily 1 Group H Member 4	
<i>AQP2</i>	Aquaporin 2	<i>OCLN</i>	Occludin	
<i>ATM</i>	ATM Serine/Threonine Kinase	<i>OFD1</i>	OFD1, Centriole And Centriolar Satellite Protein	
<i>ATP1A2</i>	ATPase Na ⁺ /K ⁺ Transporting Subunit Alpha 2	<i>PALB2</i>	Partner And Localizer Of BRCA2	
<i>AVP</i>	Arginine Vasopressin	<i>PALLD</i>	Palladin, Cytoskeletal Associated Protein	
		<i>PEX13</i>	Peroxisomal Biogenesis Factor 13	

<i>HLA-B</i>	Major Histocompatibility Complex, Class I, B	<i>AKR1D1</i>	1 Aldo-Keto Reductase Family 1 Member D1
<i>HLA-DPB1</i>	Major Histocompatibility Complex, Class II, DP Beta 1	<i>ALG12</i>	ALG12 Alpha-1,6-Mannosyltransferase
<i>HLA-DRB1</i>	Major Histocompatibility Complex, Class II, DR Beta 1	<i>ALG2</i>	ALG2 Alpha-1,3/1,6-Mannosyltransferase
<i>HMGCL</i>	3-Hydroxy-3-Methylglutaryl-CoA Lyase	<i>ALG6</i>	ALG6 Alpha-1,3-Glucosyltransferase
<i>HTR1A</i>	5-Hydroxytryptamine Receptor 1A	<i>AMACR</i>	Alpha-Methylacetyl-CoA Racemase
<i>IGH</i>	Immunoglobulin Heavy Locus	<i>ANO6</i>	Anoctamin 6
<i>IGHM</i>	Immunoglobulin Heavy Constant Mu	<i>ATP6V0A2</i>	ATPase H+ Transporting V0 Subunit A2
<i>IGLL1</i>	Immunoglobulin Lambda Like Polypeptide 1	<i>ATP6V1A</i>	ATPase H+ Transporting V1 Subunit A
<i>IKZF1</i>	IKAROS Family Zinc Finger 1	<i>ATP6V1E1</i>	ATPase H+ Transporting V1 Subunit E1
<i>IL10</i>	Interleukin 10	<i>B4GALT1</i>	Beta-1,4-Galactosyltransferase 1
<i>IL12A</i>	Interleukin 12A	<i>BCS1L</i>	BCS1 Homolog, Ubiquinol-Cytochrome C Reductase Complex Chaperone
<i>IL12A-AS1</i>	IL12A Antisense RNA 1	<i>BRAF</i>	B-Raf Proto-Oncogene, Serine/Threonine Kinase
<i>IL12B</i>	Interleukin 12 B	<i>COG4</i>	COG complex subunit 4
<i>IL23R</i>	Interleukin 23 Receptor	<i>CTC1</i>	CST Telomere Replication Complex Component 1
<i>IL2RG</i>	Interleukin 2 Receptor Subunit Gamma	<i>CYP7B1</i>	Cytochrome P450 Family 7 Subfamily B Member 1
<i>IL36RN</i>	Interleukin 36 Receptor Antagonist	<i>DDOST</i>	Dolichyl-Diphosphooligosaccharide--Protein Glycosyltransferase Non-Catalytic Subunit
<i>IL6</i>	Interleukin 6	<i>DKC1</i>	Dyskerin Pseudouridine Synthase 1
<i>IL7R</i>	Interleukin 7 Receptor	<i>DLD</i>	Dihydrolipoamide Dehydrogenase
<i>IRF8</i>	Interferon Regulatory Factor 8	<i>DOLK</i>	Dolichol Kinase
<i>JAK2</i>	Janus Kinase 2	<i>DPAGT1</i>	Dolichyl-Phosphate N-Acetylglucosaminephosphotransferase 2
<i>KCNJ1</i>	Potassium Voltage-Gated Channel Subfamily J Member 1	<i>DPM1</i>	Dolichyl-Phosphate Mannosyltransferase Subunit 1, Catalytic
<i>KLRC4</i>	Killer Cell Lectin Like Receptor C4	<i>F10</i>	Coagulation Factor X
<i>LACC1</i>	Laccase Domain Containing 1	<i>F11</i>	Coagulation Factor XI
<i>LBR</i>	Lamin B Receptor	<i>F12</i>	Coagulation Factor XII
<i>LIFR</i>	LIF Receptor Alpha	<i>F13A1</i>	Coagulation Factor XIII A Chain
<i>LIG4</i>	DNA Ligase 4	<i>F13B</i>	Coagulation Factor XIII B Chain
<i>LIPA</i>	Lipase A, Lysosomal Acid Type	<i>F2</i>	Coagulation Factor II, Thrombin
<i>LPIN1</i>	Lipin 1	<i>F5</i>	Coagulation Factor V
<i>LPIN2</i>	Lipin 2	<i>F7</i>	Coagulation Factor VII
<i>LRRC8A</i>	Leucine Rich Repeat Containing 8 VRAC Subunit A	<i>F8</i>	Coagulation Factor VIII
<i>LYST</i>	Lysosomal Trafficking Regulator	<i>F9</i>	Coagulation Factor IX
<i>MALT1</i>	MALT1 Paracaspase	<i>FAH</i>	Fumarylacetoacetate Hydrolase
<i>MEFV</i>	MEFV, Pyrin Innate Immunity Regulator	<i>FGA</i>	Fibrinogen Alpha Chain
<i>MIF</i>	Macrophage Migration Inhibitory Factor	<i>FGB</i>	Fibrinogen Beta Chain
<i>MLX</i>	MAX Dimerization Protein MLX	<i>FGG</i>	Fibrinogen Gamma Chain
<i>MST1</i>	Macrophage Stimulating 1	<i>FLNA</i>	Filamin A
<i>MVK</i>	Mevalonate Kinase	<i>GATA2</i>	GATA Binding Protein 2
<i>MYD88</i>	Myeloid Differentiation Primary Response 88	<i>GATA6</i>	GATA Binding Protein 6
<i>MYH3</i>	Myosin Heavy Chain 3	<i>GFI1B</i>	Growth Factor Independent 1B Transcriptional Repressor
<i>NCF1</i>	Neutrophil Cytosolic Factor 1	<i>GGCX</i>	Gamma-Glutamyl Carboxylase
<i>NCF2</i>	Neutrophil Cytosolic Factor 2	<i>GNE</i>	Glucosamine (UDP-N-Acetyl)-2-Epimerase/N-Acetylmannosamine Kinase
<i>NCF4</i>	Neutrophil Cytosolic Factor 4	<i>GPR35</i>	G Protein-Coupled Receptor 35
<i>ND1</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 1	<i>HADH</i>	Hydroxyacyl-CoA Dehydrogenase
<i>ND4</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 4	<i>HRG</i>	Histidine Rich Glycoprotein
<i>ND5</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 5	<i>HSD3B7</i>	Hydroxy-Delta-5-Steroid Dehydrogenase, 3 Beta-And Steroid Delta-Isomerase 7
<i>ND6</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 6	<i>IDH1</i>	Isocitrate Dehydrogenase (NADP(+)) 1, Cytosolic
<i>NGF</i>	Nerve Growth Factor	<i>IDH2</i>	Isocitrate Dehydrogenase (NADP(+)) 2, Mitochondrial
<i>NGLY1</i>	N-Glycanase 1	<i>KAT6B</i>	Lysine Acetyltransferase 6B
<i>NLRC4</i>	NLR Family CARD Domain Containing 4	<i>KLKB1</i>	Kallikrein B1
<i>NLRP12</i>	NLR Family Pyrin Domain Containing 12	<i>KRAS</i>	KRAS Proto-Oncogene, GTPase

<i>NLRP3</i>	NLR Family Pyrin Domain Containing 3	<i>LARS</i>	Leucyl-TRNA Synthetase
<i>NME1</i>	NME/NM23 Nucleoside Diphosphate Kinase 1	<i>LMAN1</i>	Lectin, Mannose Binding 1
<i>NOD2</i>	Nucleotide Binding Oligomerization Domain Containing 2	<i>LMNA</i>	Lamin A/C
<i>NOTCH3</i>	Notch Receptor 3	<i>LYST</i>	Lysosomal Trafficking Regulator
<i>NTRK1</i>	Neurotrophic Receptor Tyrosine Kinase 1	<i>LZTR1</i>	Leucine Zipper Like Transcription Regulator 1
<i>ORAI1</i>	ORAI Calcium Release-Activated Calcium Modulator 1	<i>MAP2K1</i>	Mitogen-Activated Protein Kinase Kinase 1
<i>PIK3R1</i>	Phosphoinositide-3-Kinase Regulatory Subunit 1	<i>MCFD2</i>	Multiple Coagulation Factor Deficiency 2
<i>POU6F2</i>	POU Class 6 Homeobox 2	<i>MGAT2</i>	Mannosyl (Alpha-1,6-)-Glycoprotein Beta-1,2-N-Acetylglucosaminyltransferase
<i>PRKAR1A</i>	Protein Kinase CAMP-Dependent Type I Regulatory Subunit Alpha	<i>MPDU1</i>	Mannose-P-Dolichol Utilization Defect 1
<i>PRNP</i>	Prion Protein	<i>MPI</i>	Mannose Phosphate Isomerase
<i>PRSS1</i>	Serine Protease 1	<i>MST1</i>	Macrophage Stimulating 1
<i>PRTN3</i>	Proteinase 3	<i>MYD88</i>	Myeloid Differentiation Primary Response 88
<i>PSMB8</i>	Proteasome Subunit Beta 8	<i>NBEAL2</i>	Neurobeachin Like 2
<i>PSTPIP1</i>	Proline-Serine-Threonine Phosphatase Interacting Protein 1	<i>NHP2</i>	NHP2 Ribonucleoprotein
<i>PTPN22</i>	Protein Tyrosine Phosphatase Non-Receptor Type 22	<i>NOP10</i>	NOP10 Ribonucleoprotein
<i>PTPN3</i>	Protein Tyrosine Phosphatase Non-Receptor Type 3	<i>NR1H4</i>	Nuclear Receptor Subfamily 1 Group H Member 4
<i>PTS</i>	6-Pyruvoyltetrahydropterin Synthase	<i>NRAS</i>	NRAS Proto-Oncogene, GTPase
<i>QDPR</i>	Quinoid Dihydropteridine Reductase	<i>ORAI1</i>	ORAI Calcium Release-Activated Calcium Modulator 1
<i>RAB27A</i>	RAB27A, Member RAS Oncogene Family	<i>PARN</i>	Poly(A)-Specific Ribonuclease
<i>RAG1</i>	Recombination Activating 1	<i>PEX1</i>	Peroxisomal Biogenesis Factor 1
<i>RAG2</i>	Recombination Activating 2	<i>PEX10</i>	Peroxisomal Biogenesis Factor 10
<i>RB1</i>	RB Transcriptional Corepressor 1	<i>PEX11B</i>	Peroxisomal Biogenesis Factor 11B
<i>REST</i>	RE1 Silencing Transcription Factor	<i>PEX12</i>	Peroxisomal Biogenesis Factor 12
<i>RMRP</i>	RNA Component Of Mitochondrial RNA Processing Endoribonuclease	<i>PEX13</i>	Peroxisomal Biogenesis Factor 13
<i>RUNX1</i>	RUNX Family Transcription Factor 1	<i>PEX14</i>	Peroxisomal Biogenesis Factor 14
<i>RYR1</i>	Ryanodine Receptor 1	<i>PEX16</i>	Peroxisomal Biogenesis Factor 16
<i>SLC11A1</i>	Solute Carrier Family 11 Member 1	<i>PEX19</i>	Peroxisomal Biogenesis Factor 19
<i>SLC12A1</i>	Solute Carrier Family 12 Member 1	<i>PEX2</i>	Peroxisomal Biogenesis Factor 2
<i>SLC19A3</i>	Solute Carrier Family 19 Member 3	<i>PEX26</i>	Peroxisomal Biogenesis Factor 26
<i>SLC29A3</i>	Solute Carrier Family 29 Member 3	<i>PEX3</i>	Peroxisomal Biogenesis Factor 3
<i>SLCO1B1</i>	Solute Carrier Organic Anion Transporter Family Member 1B1	<i>PEX5</i>	Peroxisomal Biogenesis Factor 5
<i>SLCO1B3</i>	Solute Carrier Organic Anion Transporter Family Member 1B3	<i>PEX6</i>	Peroxisomal Biogenesis Factor 6
<i>SPINK1</i>	Serine Peptidase Inhibitor, Kazal Type 1	<i>PIGA</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class A
<i>STAT3</i>	Signal Transducer And Activator Of Transcription 3	<i>PLAT</i>	Plasminogen Activator, Tissue Type
<i>STAT4</i>	Signal Transducer And Activator Of Transcription 4	<i>PLG</i>	Plasminogen
<i>STIM1</i>	Stromal Interaction Molecule 1	<i>PMM2</i>	Phosphomannomutase 2
<i>STX11</i>	Syntaxin 11	<i>PRF1</i>	Perforin 1
<i>STXBP2</i>	Syntaxin Binding Protein 2	<i>PROC</i>	Protein C, Inactivator Of Coagulation Factors Va And VIIIa
<i>TCF3</i>	Transcription Factor 3	<i>PROS1</i>	Protein S
<i>TCF4</i>	Transcription Factor 4	<i>PTH1R</i>	Parathyroid Hormone 1 Receptor
<i>TLR4</i>	Toll Like Receptor 4	<i>PTPN11</i>	Protein Tyrosine Phosphatase, Non-Receptor Type 11
<i>TMEM165</i>	Transmembrane Protein 165	<i>RAF1</i>	Raf-1 Proto-Oncogene, Serine/Threonine Kinase
<i>TMEM173</i>	Transmembrane Protein 173	<i>RASA2</i>	RAS P21 Protein Activator 2
<i>TNFAIP3</i>	TNF Alpha Induced Protein 3	<i>RBM8A</i>	RNA Binding Motif Protein 8A
<i>TNFRSF1A</i>	TNF Receptor Superfamily Member 1A	<i>RFT1</i>	RFT1 Homolog
<i>TP53</i>	Tumor Protein P53	<i>RIT1</i>	Ras Like Without CAAX 1
<i>TREX1</i>	Three Prime Repair Exonuclease 1	<i>RRAS</i>	RAS Related
<i>TRIP13</i>	Thyroid Hormone Receptor Interactor 13	<i>RTKL1</i>	Regulator Of Telomere Elongation Helicase 1
<i>TRNF</i>	Mitochondrially Encoded TRNA-Phe (UUU/C)	<i>RYR1</i>	Ryanodine Receptor 1
<i>TRNH</i>	Mitochondrially Encoded TRNA-His (CAU/C)	<i>SERAC1</i>	Serine Active Site Containing 1
<i>TRNL1</i>	Mitochondrially Encoded TRNA-Leu (UUA/G) 1	<i>SERPINC1</i>	Serpin Family C Member 1
<i>TRNQ</i>	Mitochondrially Encoded TRNA-Gln (CAA/G)	<i>SERPINF2</i>	Serpin Family H Member 1

<i>ACTB</i>	Actin Beta	<i>KIF5C</i>	Kinesin Family Member 5C
<i>ACTC1</i>	Actin Alpha Cardiac Muscle 1	<i>KLHL15</i>	Kelch Like Family Member 15
<i>ACTG1</i>	Actin Gamma 1	<i>MCOLN1</i>	Mucolipin 1
<i>ACTN2</i>	Actinin Alpha 2	<i>MDH2</i>	Malate Dehydrogenase 2
<i>ACVR1</i>	Activin A Receptor Type 1	<i>MECP2</i>	Methyl-CpG Binding Protein 2
<i>ACY1</i>	Aminoacylase 1	<i>MFF</i>	Mitochondrial Fission Factor
<i>ADCY1</i>	Adenylate Cyclase 1	<i>MFSD2A</i>	Major Facilitator Superfamily Domain Containing 2A
<i>ADGRV1</i>	Adhesion G Protein-Coupled Receptor V1	<i>MID2</i>	Midline 2
<i>ADK</i>	Adenosine Kinase	<i>MPDU1</i>	Mannose-P-Dolichol Utilization Defect 1
<i>AFF4</i>	AF4/FMR2 Family Member 4	<i>NACCC1</i>	Nucleus Accumbens Associated 1
<i>AGBL5</i>	ATP/GTP Binding Protein Like 5	<i>NEXMIF</i>	Neurite Extension And Migration Factor
<i>AHSG</i>	Alpha 2-HS Glycoprotein	<i>PIGA</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class A
<i>AIFM1</i>	Apoptosis Inducing Factor Mitochondria Associated 1	<i>PIGN</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class N
<i>AIPL1</i>	Aryl Hydrocarbon Receptor Interacting Protein Like 1	<i>PIGV</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class V
<i>AK2</i>	Adenylate Kinase 2	<i>PNPT1</i>	Polyribonucleotide Nucleotidyltransferase 1
<i>AKT1</i>	AKT Serine/Threonine Kinase 1	<i>POMT1</i>	Protein O-Mannosyltransferase 1
<i>ALG11</i>	ALG11 Alpha-1,2-Mannosyltransferase	<i>PRDM16</i>	PR/SET Domain 16
<i>ALMS1</i>	ALMS1 Centrosome And Basal Body Associated Protein	<i>PRPS1</i>	Phosphoribosyl Pyrophosphate Synthetase 1
<i>ALOX12B</i>	Arachidonate 12-Lipoxygenase, 12R Type	<i>PURA</i>	Purine Rich Element Binding Protein A
<i>ALOXE3</i>	Arachidonate Lipoxygenase 3	<i>PYCR2</i>	Pyrroline-5-Carboxylate Reductase 2
<i>ALX3</i>	ALX Homeobox 3	<i>RARS2</i>	Arginyl-TRNA Synthetase 2, Mitochondrial
<i>AMER1</i>	APC Membrane Recruitment Protein 1	<i>RERE</i>	Arginine-Glutamic Acid Dipeptide Repeats
<i>AMMECR1</i>	Alport Syndrome, Mental Retardation, Midface Hypoplasia And Elliptocytosis Chromosomal Region Gene 1	<i>SETBP1</i>	SET Binding Protein 1
<i>ANKH</i>	ANKH Inorganic Pyrophosphate Transport Regulator	<i>SIK1</i>	Salt Inducible Kinase 1
<i>ANKRD1</i>	Ankyrin Repeat Domain 1	<i>SKI</i>	SKI Proto-Oncogene
<i>ANKRD11</i>	Ankyrin Repeat Domain 11	<i>SLC16A2</i>	Solute Carrier Family 16 Member 2
<i>ANOS1</i>	Anosmin 1	<i>SLC25A12</i>	Solute Carrier Family 25 Member 12
<i>ANTXR1</i>	ANTXR Cell Adhesion Molecule 1	<i>SLC2A1</i>	Solute Carrier Family 2 Member 1
<i>AP1S1</i>	Adaptor Related Protein Complex 1 Subunit Sigma 1	<i>SLC33A1</i>	Solute Carrier Family 33 Member 1
<i>AP1S2</i>	Adaptor Related Protein Complex 1 Subunit Sigma 2	<i>SLC9A6</i>	Solute Carrier Family 9 Member 6
<i>APC</i>	APC Regulator Of WNT Signaling Pathway	<i>SMARCA2</i>	SWI/SNF Related, Matrix Associated, Actin Dependent Regulator Of Chromatin, Subfamily A, Member 2
<i>APC2</i>	APC Regulator Of WNT Signaling Pathway 2	<i>SMARCE1</i>	SWI/SNF Related, Matrix Associated, Actin Dependent Regulator Of Chromatin, Subfamily E, Member 1
<i>APOPT1</i>	Cytochrome C Oxidase Assembly Factor 8	<i>SPATA5</i>	Spermatogenesis Associated 5
<i>ARHGDI1A</i>	Rho GDP Dissociation Inhibitor Alpha	<i>ST3GAL5</i>	ST3 Beta-Galactoside Alpha-2,3-Sialyltransferase 5
<i>ARHGEF18</i>	Rho/Rac Guanine Nucleotide Exchange Factor 18	<i>STXBP1</i>	Syntaxin Binding Protein 1
<i>ARHGEF6</i>	Rac/Cdc42 Guanine Nucleotide Exchange Factor 6	<i>TCF4</i>	Transcription Factor 4
<i>ARID1A</i>	AT-Rich Interaction Domain 1A	<i>TCTN2</i>	Tectonic Family Member 2
<i>ARID1B</i>	AT-Rich Interaction Domain 1B	<i>TELO2</i>	Telomere Maintenance 2
<i>ARID2</i>	AT-Rich Interaction Domain 2	<i>TMEM231</i>	Transmembrane Protein 231
<i>ARL2BP</i>	ADP Ribosylation Factor Like GTPase 2 Binding Protein	<i>UBA5</i>	Ubiquitin Like Modifier Activating Enzyme 5
<i>ARL6</i>	ADP Ribosylation Factor Like GTPase 6	<i>UBE3A</i>	Ubiquitin Protein Ligase E3A
<i>ARNT2</i>	Aryl Hydrocarbon Receptor Nuclear Translocator 2	<i>UNC80</i>	Unc-80 Homolog, NALCN Channel Complex Subunit
<i>ARSB</i>	Arylsulfatase B	<i>UQCRCQ</i>	Ubiquinol-Cytochrome C Reductase Complex III Subunit VII
<i>ARSE</i>	Arylsulfatase E	<i>VPS11</i>	VPS11, CORVET/HOPS Core Subunit
<i>ARVCF</i>	ARVCF Delta Catenin Family Member	<i>WDR45</i>	WD Repeat Domain 45
<i>ASCL1</i>	Achaete-Scute Family BHLH Transcription Factor 1	<i>ZDHHHC15</i>	Zinc Finger DHHC-Type Containing 15
<i>ASPA</i>	Aspartoacylase	<i>ZEB2</i>	Zinc Finger E-Box Binding Homeobox 2
<i>ASPM</i>	Abnormal Spindle Microtubule Assembly		
<i>ASXL1</i>	Additional Sex Combs Like 1, Transcriptional Regulator		
<i>ATP1A2</i>	ATPase Na ⁺ /K ⁺ Transporting Subunit Alpha 2		
			Multiple joint contractures (HP:0002828), 11 genes
		<i>ALG14</i>	ALG14 UDP-N-Acetylglucosaminyltransferase Subunit

<i>DNAI1</i>	Dynein Axonemal Intermediate Chain 1	<i>ERCC2</i>	ERCC Excision Repair 2, TFIIH Core Complex Helicase Subunit
<i>DNAJC3</i>	DnaJ Heat Shock Protein Family (Hsp40) Member C3	<i>ERCC5</i>	ERCC Excision Repair 5, Endonuclease
<i>DNASE1L3</i>	Deoxyribonuclease 1 Like 3	<i>ERCC6</i>	ERCC Excision Repair 6, Chromatin Remodeling Factor
<i>DNMT1</i>	DNA Methyltransferase 1	<i>FAN1</i>	FANCD2 And FANCI Associated Nuclease 1
<i>DOLK</i>	Dolichol Kinase	<i>FARS2</i>	Phenylalanyl-TRNA Synthetase 2, Mitochondrial
<i>DSG2</i>	Desmoglein 2	<i>FGFR3</i>	Fibroblast Growth Factor Receptor 3
<i>DSPP</i>	Dentin Sialophosphoprotein	<i>FLI1</i>	Fli-1 Proto-Oncogene, ETS Transcription Factor
<i>DUSP6</i>	Dual Specificity Phosphatase 6	<i>FRAS1</i>	Fraser Extracellular Matrix Complex Subunit 1
<i>DUX4</i>	Double Homeobox 4	<i>FREM2</i>	FRAS1 Related Extracellular Matrix Protein 2
<i>DVL1</i>	Dishevelled Segment Polarity Protein 1	<i>GBA</i>	Glucosylceramidase Beta
<i>DVL3</i>	Dishevelled Segment Polarity Protein 3	<i>GCSH</i>	Glycine Cleavage System Protein H
<i>EBP</i>	EBP Cholesterol Delta-Isomerase	<i>GDF5</i>	Growth Differentiation Factor 5
<i>ECE1</i>	Endothelin Converting Enzyme 1	<i>GLB1</i>	Galactosidase Beta 1
<i>ECHS1</i>	Enoyl-CoA Hydratase, Short Chain 1	<i>GLDC</i>	Glycine Decarboxylase
<i>EDC3</i>	Enhancer Of MRNA Decapping 3	<i>GLUL</i>	Glutamine synthetase family
<i>EDN1</i>	Endothelin 1	<i>GPC3</i>	Glypican 3
<i>EDN3</i>	Endothelin 3	<i>GPC4</i>	Glypican 4
<i>EDNRA</i>	Endothelin Receptor Type A	<i>GPR161</i>	G Protein-Coupled Receptor 161
<i>EDNRB</i>	Endothelin Receptor Type B	<i>GRIP1</i>	Glutamate Receptor Interacting Protein 1
<i>EFNB1</i>	Ephrin B1	<i>HDAC6</i>	Histone Deacetylase 6
<i>EFTUD2</i>	Elongation Factor Tu GTP Binding Domain Containing 2	<i>HESX1</i>	HESX Homeobox 1
<i>EHMT1</i>	Euchromatic Histone Lysine Methyltransferase 1	<i>HSPG2</i>	Heparan Sulfate Proteoglycan 2
<i>ELAC2</i>	ElaC Ribonuclease Z 2	<i>HTRA2</i>	HtrA Serine Peptidase 2
<i>ELMOD3</i>	ELMO Domain Containing 3	<i>IDUA</i>	Iduronidase, Alpha-L-
<i>ELN</i>	Elastin	<i>ITGA6</i>	Integrin Subunit Alpha 6
<i>ENPP1</i>	Ectonucleotide Pyrophosphatase/Phosphodiesterase 1	<i>ITGB4</i>	Integrin Subunit Beta 4
<i>EP300</i>	E1A Binding Protein P300	<i>ITPA</i>	Inosine Triphosphatase
<i>EPG5</i>	Ectopic P-Granules Autophagy Protein 5 Homolog	<i>KRAS</i>	KRAS Proto-Oncogene, GTPase
<i>EPS8</i>	Epidermal Growth Factor Receptor Pathway Substrate 8	<i>LAMA3</i>	Laminin Subunit Alpha 3
<i>ERCC1</i>	ERCC Excision Repair 1, Endonuclease Non-Catalytic Subunit	<i>LAMB3</i>	Laminin Subunit Beta 3
<i>ERCC2</i>	ERCC Excision Repair 2, TFIIH Core Complex Helicase Subunit	<i>LAMC2</i>	Laminin Subunit Gamma 2
<i>ERCC3</i>	ERCC Excision Repair 3, TFIIH Core Complex Helicase Subunit	<i>LHX4</i>	LIM Homeobox 4
<i>ERCC4</i>	ERCC Excision Repair 4, Endonuclease Catalytic Subunit	<i>LIPA</i>	Lipase A, Lysosomal Acid Type
<i>ERCC5</i>	ERCC Excision Repair 5, Endonuclease	<i>LIPT1</i>	Lipoyltransferase 1
<i>ERCC6</i>	ERCC Excision Repair 6, Chromatin Remodeling Factor	<i>LMNA</i>	Lamin A/C
<i>ERCC8</i>	ERCC Excision Repair 8, CSA Ubiquitin Ligase Complex Subunit	<i>LMOD1</i>	Leiomodin 1
<i>ERF</i>	ETS2 Repressor Factor	<i>LTC4S</i>	Leukotriene C4 Synthase
<i>ESPN</i>	Espin	<i>MESP2</i>	Mesoderm Posterior BHLH Transcription Factor 2
<i>ESRRB</i>	Estrogen Related Receptor Beta	<i>MLH1</i>	MutL Homolog 1
<i>EXOSC8</i>	Exosome Component 8	<i>MLH3</i>	MutL Homolog 3
<i>EXT1</i>	Exostosin Glycosyltransferase 1	<i>MRPS22</i>	Mitochondrial Ribosomal Protein S22
<i>EYA1</i>	EYA Transcriptional Coactivator And Phosphatase 1	<i>MSH2</i>	MutS Homolog 2
<i>EYA4</i>	EYA Transcriptional Coactivator And Phosphatase 4	<i>MSH6</i>	MutS Homolog 6
<i>EYS</i>	Eyes Shut Homolog	<i>MYH11</i>	Myosin Heavy Chain 11
<i>FAM161A</i>	FAM161 Centrosomal Protein A	<i>MYLK</i>	Myosin Light Chain Kinase
<i>FAM20C</i>	FAM20C Golgi Associated Secretory Pathway Kinase	<i>MYO5B</i>	Myosin VB
<i>FANCA</i>	FA Complementation Group A	<i>NADK2</i>	NAD Kinase 2, Mitochondrial
<i>FANCB</i>	FA Complementation Group B	<i>NAXE</i>	NAD(P)HX Epimerase
<i>FANCC</i>	FA Complementation Group C	<i>NRAS</i>	NRAS Proto-Oncogene, GTPase
<i>FANCD2</i>	FA Complementation Group D2	<i>OCRL</i>	OCRL, Inositol Polyphosphate-5-Phosphatase
<i>FANCE</i>	FA Complementation Group E	<i>PEX1</i>	Peroxisomal Biogenesis Factor 1
<i>FANCF</i>	FA Complementation Group F	<i>PEX10</i>	Peroxisomal Biogenesis Factor 10
<i>FANCG</i>	FA Complementation Group G	<i>PEX11B</i>	Peroxisomal Biogenesis Factor 11B
<i>FANCI</i>	FA Complementation Group I	<i>PEX12</i>	Peroxisomal Biogenesis Factor 12
<i>FANCL</i>	FA Complementation Group L	<i>PEX13</i>	Peroxisomal Biogenesis Factor 13

<i>FANCM</i>	FA Complementation Group M	<i>PEX14</i>	Peroxisomal Biogenesis Factor 14
<i>FARS2</i>	Phenylalanyl-TRNA Synthetase 2, Mitochondrial	<i>PEX16</i>	Peroxisomal Biogenesis Factor 16
<i>FAS</i>	Fas Cell Surface Death Receptor	<i>PEX19</i>	Peroxisomal Biogenesis Factor 19
<i>FASTKD2</i>	FAST Kinase Domains 2	<i>PEX2</i>	Peroxisomal Biogenesis Factor 2
<i>FAT4</i>	FAT Atypical Cadherin 4	<i>PEX26</i>	Peroxisomal Biogenesis Factor 26
<i>FBN1</i>	Fibrillin 1	<i>PEX3</i>	Peroxisomal Biogenesis Factor 3
<i>FERMT1</i>	Fermitin Family Member 1	<i>PEX5</i>	Peroxisomal Biogenesis Factor 5
<i>FEZF1</i>	FEZ Family Zinc Finger 1	<i>PEX6</i>	Peroxisomal Biogenesis Factor 6
<i>FGF10</i>	Fibroblast Growth Factor 10	<i>PHOX2B</i>	Paired Like Homeobox 2b
<i>FGF17</i>	Fibroblast Growth Factor 17	<i>PIGA</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class A
<i>FGF3</i>	Fibroblast Growth Factor 3	<i>PIK3CA</i>	Phosphatidylinositol-4,5-Bisphosphate 3-Kinase Catalytic Subunit Alpha
<i>FGF8</i>	Fibroblast Growth Factor 8	<i>PLEC</i>	Plectin
<i>FGF9</i>	Fibroblast Growth Factor 9	<i>PLXND1</i>	Plexin D1
<i>FGFR1</i>	Fibroblast Growth Factor Receptor 1	<i>PMS1</i>	PMS1 Homolog 1, Mismatch Repair System Component
<i>FGFR2</i>	Fibroblast Growth Factor Receptor 2	<i>PMS2</i>	PMS1 Homolog 2, Mismatch Repair System Component
<i>FGFR3</i>	Fibroblast Growth Factor Receptor 3	<i>PQBP1</i>	Polyglutamine Binding Protein 1
<i>FGFRL1</i>	Fibroblast Growth Factor Receptor Like 1	<i>PROKR2</i>	Prokineticin Receptor 2
<i>FHL2</i>	Four And A Half LIM Domains 2	<i>PRPS1</i>	Phosphoribosyl Pyrophosphate Synthetase 1
<i>FIBP</i>	FGF1 Intracellular Binding Protein	<i>PSAP</i>	Prosaposin
<i>FIG4</i>	FIG4 Phosphoinositide 5-Phosphatase	<i>PTF1A</i>	Pancreas Specific Transcription Factor, 1a
<i>FKBP14</i>	FKBP Prolyl Isomerase 14	<i>RBM8A</i>	RNA Binding Motif Protein 8A
<i>FKTN</i>	Fukutin	<i>RET</i>	Ret Proto-Oncogene
<i>FLCN</i>	Folliculin	<i>REV3L</i>	REV3 Like, DNA Directed Polymerase Zeta Catalytic Subunit
<i>FLII</i>	FLII Actin Remodeling Protein	<i>RMND1</i>	Required For Meiotic Nuclear Division 1 Homolog
<i>FLNA</i>	Filamin A	<i>ROBO1</i>	Roundabout Guidance Receptor 1
<i>FLNB</i>	Filamin B	<i>ROR2</i>	Receptor Tyrosine Kinase Like Orphan Receptor 2
<i>FLRT3</i>	Fibronectin Leucine Rich Transmembrane Protein 3	<i>SCN4A</i>	Sodium Voltage-Gated Channel Alpha Subunit 4
<i>FMR1</i>	Fragile X Mental Retardation 1	<i>SCO2</i>	SCO2, Cytochrome C Oxidase Assembly Protein
<i>FOXC1</i>	Forkhead Box C1	<i>SLC25A19</i>	Solute Carrier Family 25 Member 19
<i>FOXG1</i>	Forkhead Box G1	<i>SMOC1</i>	SPARC Related Modular Calcium Binding 1
<i>FOXI1</i>	Forkhead Box I1	<i>SNRPB</i>	Small Nuclear Ribonucleoprotein Polypeptides B And B1
<i>FOXRED1</i>	FAD Dependent Oxidoreductase Domain Containing 1	<i>SUOX</i>	Sulfite Oxidase
<i>FRAS1</i>	Fraser Extracellular Matrix Complex Subunit 1	<i>TFAM</i>	Transcription Factor A, Mitochondrial
<i>FREM2</i>	FRAS1 Related Extracellular Matrix Protein 2	<i>TGFBR2</i>	Transforming Growth Factor Beta Receptor 2
<i>FRG1</i>	FSHD Region Gene 1	<i>TMEM70</i>	Transmembrane Protein 70
<i>FSCN2</i>	Fascin Actin-Bundling Protein 2, Retinal	<i>TSEN54</i>	TRNA Splicing Endonuclease Subunit 54
<i>FSHR</i>	Follicle Stimulating Hormone Receptor	<i>TSPYL1</i>	TSPY Like 1
<i>FTO</i>	FTO Alpha-Ketoglutarate Dependent Dioxygenase	<i>TUFM</i>	Tu Translation Elongation Factor, Mitochondrial
<i>FUCA1</i>	Alpha-L-Fucosidase 1	<i>UBR1</i>	Ubiquitin Protein Ligase E3 Component N-Recognin 1
<i>FXN</i>	Frataxin	<i>VPS33B</i>	VPS33B, Late Endosome And Lysosome Associated
<i>G6PC3</i>	Glucose-6-Phosphatase Catalytic Subunit 3	<i>WASHC5</i>	WASH Complex Subunit 5
<i>GAA</i>	Glucosidase Alpha, Acid	<i>WDR11</i>	WD Repeat Domain 11
<i>GABBR2</i>	Gamma-Aminobutyric Acid Type B Receptor Subunit 2		
<i>GABRD</i>	Gamma-Aminobutyric Acid Type A Receptor Delta Subunit		
<i>GALC</i>	Galactosylceramidase		
<i>GALE</i>	UDP-Galactose-4-Epimerase		
<i>GALNS</i>	Galactosamine (N-Acetyl)-6-Sulfatase		
<i>GAS8</i>	Growth Arrest Specific 8		
<i>GATA1</i>	GATA Binding Protein 1		
<i>GATA2</i>	GATA Binding Protein 2		
<i>GATA3</i>	GATA Binding Protein 3		
<i>GATAD1</i>	GATA Zinc Finger Domain Containing 1		
<i>GBA</i>	Glucosylceramidase Beta		

<i>GBA2</i>	Glucosylceramidase Beta 2
<i>GCK</i>	Glucokinase
<i>GDF3</i>	Growth Differentiation Factor 3
<i>GDF5</i>	Growth Differentiation Factor 5
<i>GDF6</i>	Growth Differentiation Factor 6
<i>GDNF</i>	Glial Cell Derived Neurotrophic Factor
<i>GFER</i>	Growth Factor, Augmenter Of Liver Regeneration
<i>GIPC3</i>	GIPC PDZ Domain Containing Family Member 3
<i>GJA1</i>	Gap Junction Protein Alpha 1
<i>GJB1</i>	Gap Junction Protein Beta 1
<i>GJB2</i>	Gap Junction Protein Beta 2
<i>GJB3</i>	Gap Junction Protein Beta 3
<i>GJB4</i>	Gap Junction Protein Beta 4
<i>GJB6</i>	Gap Junction Protein Beta 6
<i>GJC2</i>	Gap Junction Protein Gamma 2
<i>GLA</i>	Galactosidase Alpha
<i>GLB1</i>	Galactosidase Beta 1
<i>GLI3</i>	GLI Family Zinc Finger 3
<i>GLIS3</i>	GLIS Family Zinc Finger 3
<i>GLYCTK</i>	Glycerate Kinase
<i>GMNN</i>	Geminin DNA Replication Inhibitor
<i>GMPPA</i>	GDP-Mannose Pyrophosphorylase A
<i>GMPPB</i>	GDP-Mannose Pyrophosphorylase B
<i>GNAS</i>	GNAS Complex Locus
<i>GNRH1</i>	Gonadotropin Releasing Hormone 1
<i>GNRHR</i>	Gonadotropin Releasing Hormone 1
<i>GNS</i>	Glucosamine (N-Acetyl)-6-Sulfatase
<i>GP1BB</i>	Glycoprotein Ib Platelet Subunit Beta
<i>GPC3</i>	Glypican 3
<i>GPC4</i>	Glypican 4
<i>GPSM2</i>	G Protein Signaling Modulator 2
<i>GRHL2</i>	Grainyhead Like Transcription Factor 2
<i>GRIP1</i>	Glutamate Receptor Interacting Protein 1
<i>GRXCR1</i>	Glutaredoxin And Cysteine Rich Domain Containing 1
<i>GRXCR2</i>	Glutaredoxin And Cysteine Rich Domain Containing 2
<i>GSC</i>	Goosecoid Homeobox
<i>GSDME</i>	Gasdermin E
<i>GTF2E2</i>	General Transcription Factor IIE Subunit 2
<i>GTF2I</i>	General Transcription Factor Iii
<i>GTF2IRD1</i>	GTF2I Repeat Domain Containing 1
<i>GUCA1B</i>	Guanylate Cyclase Activator 1B
<i>GUCY2D</i>	Guanylate Cyclase 2D, Retinal
<i>GUSB</i>	Glucuronidase Beta
<i>HACE1</i>	HECT Domain And Ankyrin Repeat Containing E3 Ubiquitin Protein Ligase 1
<i>HARS</i>	Histidyl-TRNA Synthetase
<i>HARS2</i>	Histidyl-TRNA Synthetase 2, Mitochondrial
<i>HBB</i>	Hemoglobin Subunit Beta
<i>HCCS</i>	Holocytochrome C Synthase
<i>HDAC4</i>	Histone Deacetylase 4
<i>HDAC8</i>	Histone Deacetylase 8
<i>HESX1</i>	HESX Homeobox 1
<i>HGF</i>	Hepatocyte Growth Factor
<i>HGSNAT</i>	Heparan-Alpha-Glucosaminide N-Acetyltransferase
<i>HIRA</i>	Histone Cell Cycle Regulator
<i>HLA-DPB1</i>	Major Histocompatibility Complex, Class II, DP Beta 1
<i>HNF1B</i>	HNF1 Homeobox B
<i>HNF4A</i>	Hepatocyte Nuclear Factor 4 Alpha
<i>HOXA1</i>	Homeobox A1
<i>HOXA11</i>	Homeobox A11

<i>HOXA2</i>	Homeobox A2
<i>HOXB1</i>	Homeobox B1
<i>HS6ST1</i>	Heparan Sulfate 6-O-Sulfotransferase 1
<i>HSD17B10</i>	Hydroxysteroid 17-Beta Dehydrogenase 10
<i>HSD17B4</i>	Hydroxysteroid 17-Beta Dehydrogenase 4
<i>HTRA2</i>	HtrA Serine Peptidase 2
<i>HYMAI</i>	Hydatidiform Mole Associated And Imprinted
<i>IARS</i>	Isoleucyl-TRNA Synthetase
<i>IARS2</i>	Isoleucyl-TRNA Synthetase 2, Mitochondrial
<i>IDH3B</i>	Isocitrate Dehydrogenase (NAD(+)) 3 Beta
<i>IDS</i>	Iduronate 2-Sulfatase
<i>IDUA</i>	Iduronidase, Alpha-L-
<i>IFT140</i>	Intraflagellar Transport 140
<i>IFT172</i>	Intraflagellar Transport 172
<i>IFT27</i>	Intraflagellar Transport 27
<i>IGBP1</i>	Immunoglobulin Binding Protein 1
<i>IGF1</i>	Insulin Like Growth Factor 1
<i>IL17RD</i>	Interleukin 17 Receptor D
<i>ILDR1</i>	Immunoglobulin Like Domain Containing Receptor 1
<i>IMPAD1</i>	Inositol Monophosphatase Domain Containing 1
<i>IMPDH1</i>	Inosine Monophosphate Dehydrogenase 1
<i>IMPG2</i>	Interphotoreceptor Matrix Proteoglycan 2
<i>INS</i>	Insulin
<i>IQCB1</i>	IQ Motif Containing B1
<i>IQSEC2</i>	IQ Motif And Sec7 Domain 2
<i>IRX5</i>	Iroquois Homeobox 5
<i>ITGB6</i>	Integrin Subunit Beta 6
<i>ITM2B</i>	Integral Membrane Protein 2B
<i>JMJD1C</i>	Jumonji Domain Containing 1C
<i>KARS</i>	Lysyl-TRNA Synthetase
<i>KAT6B</i>	Lysine Acetyltransferase 6B
<i>KCNAB2</i>	Potassium Voltage-Gated Channel Subfamily A Regulatory Beta Subunit 2
<i>KCNC3</i>	Potassium Voltage-Gated Channel Subfamily C Member 3
<i>KCNE1</i>	Potassium Voltage-Gated Channel Subfamily E Regulatory Subunit 1
<i>KCNE5</i>	Potassium Voltage-Gated Channel Subfamily E Regulatory Subunit 5
<i>KCNH1</i>	Potassium Voltage-Gated Channel Subfamily H Regulatory Subunit 1
<i>KCNJ10</i>	Potassium Voltage-Gated Channel Subfamily J Member 10
<i>KCNJ11</i>	Potassium Voltage-Gated Channel Subfamily J Member 11
<i>KCNJ13</i>	Potassium Voltage-Gated Channel Subfamily J Member 13
<i>KCNQ1</i>	Potassium Voltage-Gated Channel Subfamily Q Member 1
<i>KCNQ4</i>	Potassium Voltage-Gated Channel Subfamily Q Member 4
<i>KDM6A</i>	Lysine Demethylase 6A
<i>KDSR</i>	3-Ketodihydrosphingosine Reductase
<i>KIF7</i>	Kinesin Family Member 7
<i>KISS1</i>	KiSS-1 Metastasis Suppressor
<i>KISS1R</i>	KISS1 Receptor
<i>KIT</i>	KIT Proto-Oncogene, Receptor Tyrosine Kinase
<i>KITLG</i>	KIT Ligand
<i>KIZ</i>	Kizuna Centrosomal Protein
<i>KLHL7</i>	Kelch Like Family Member 7
<i>KLLN</i>	Killin, P53 Regulated DNA Replication Inhibitor
<i>KMT2A</i>	Lysine Methyltransferase 2A
<i>KMT2D</i>	Lysine Methyltransferase 2D
<i>KRAS</i>	KRAS Proto-Oncogene, GTPase

<i>KYNU</i>	Kynureninase
<i>L2HGDH</i>	L-2-Hydroxyglutarate Dehydrogenase
<i>LAMA4</i>	Laminin Subunit Alpha 4
<i>LAMB1</i>	Laminin Subunit Beta 1
<i>LARS</i>	Leucyl-TRNA Synthetase
<i>LARS2</i>	Leucyl-TRNA Synthetase 2, Mitochondrial
<i>LCA5</i>	Lebercilin LCA5
<i>LDB3</i>	LIM Domain Binding 3
<i>LEMD3</i>	LEM Domain Containing 3
<i>LETM1</i>	Leucine Zipper And EF-Hand Containing Transmembrane Protein 1
<i>LHFPL5</i>	LHFPL Tetraspan Subfamily Member 5
<i>LHX1</i>	LIM Homeobox 1
<i>LHX3</i>	LIM Homeobox 3
<i>LIG4</i>	DNA Ligase 4
<i>LIMK1</i>	LIM Domain Kinase 1
<i>LMNA</i>	Lamin A/C
<i>LMNB1</i>	Lamin B1
<i>LMNB2</i>	Lamin B2
<i>LMX1B</i>	LIM Homeobox Transcription Factor 1 Beta
<i>LONP1</i>	Lon Peptidase 1, Mitochondrial
<i>LOR</i>	Loricrin
<i>LOXHD1</i>	Lipoxygenase Homology Domains 1
<i>LRAT</i>	Lecithin Retinol Acyltransferase
<i>LRP2</i>	LDL Receptor Related Protein 2
<i>LRP4</i>	LDL Receptor Related Protein 4
<i>LRP5</i>	LDL Receptor Related Protein 5
<i>LRTOMT</i>	Leucine Rich Transmembrane And O-Methyltransferase Domain Containing
<i>LZTFL1</i>	Leucine Zipper Transcription Factor Like 1
<i>LZTR1</i>	Leucine Zipper Like Transcription Regulator 1
<i>MAD2L2</i>	Mitotic Arrest Deficient 2 Like 2
<i>MAF</i>	MAF BZIP Transcription Factor
<i>MAFB</i>	MAF BZIP Transcription Factor B
<i>MAK</i>	Male Germ Cell Associated Kinase
<i>MAN2B1</i>	Mannosidase Alpha Class 2B Member 1
<i>MANBA</i>	Mannosidase Beta
<i>MAP2K1</i>	Mitogen-Activated Protein Kinase Kinase 1
<i>MAP3K20</i>	Mitogen-Activated Protein Kinase Kinase Kinase 20
<i>MAP3K7</i>	Mitogen-Activated Protein Kinase Kinase Kinase 7
<i>MAPK1</i>	Mitogen-Activated Protein Kinase 1
<i>MARS2</i>	Methionyl-TRNA Synthetase 2, Mitochondrial
<i>MARVELD2</i>	MARVEL Domain Containing 2
<i>MASP1</i>	Mannan Binding Lectin Serine Peptidase 1
<i>MBTPS2</i>	Membrane Bound Transcription Factor Peptidase, Site 2
<i>MCM2</i>	Minichromosome Maintenance Complex Component 2
<i>MCTP2</i>	Multiple C2 And Transmembrane Domain Containing 2
<i>MECOM</i>	MDS1 And EVI1 Complex Locus
<i>MECP2</i>	Methyl-CpG Binding Protein 2
<i>MED12</i>	Mediator Complex Subunit 12
<i>MEGF8</i>	Multiple EGF Like Domains 8
<i>MEOX1</i>	Mesenchyme Homeobox 1
<i>MERTK</i>	MER Proto-Oncogene, Tyrosine Kinase
<i>MFN2</i>	Mitofusin 2
<i>MGAT2</i>	Mannosyl (Alpha-1,6-)-Glycoprotein Beta-1,2-N-Acetylglucosaminyltransferase
<i>MGP</i>	Matrix Gla Protein
<i>MIR96</i>	MicroRNA 96
<i>MITF</i>	Melanocyte Inducing Transcription Factor
<i>MKKS</i>	McKusick-Kaufman Syndrome

<i>MKS1</i>	MKS Transition Zone Complex Subunit 1
<i>MLXIPL</i>	MLX Interacting Protein Like
<i>MOGS</i>	Mannosyl-Oligosaccharide Glucosidase
<i>MORC2</i>	MORC Family CW-Type Zinc Finger 2
<i>MPZ</i>	Myelin Protein Zero
<i>MSRB3</i>	Methionine Sulfoxide Reductase B3
<i>MYBPC3</i>	Myosin Binding Protein C, Cardiac
<i>MYCN</i>	MYCN Proto-Oncogene, BHLH Transcription Factor
<i>MYD88</i>	Myeloid Differentiation Primary Response 88
<i>MYH14</i>	Myosin Heavy Chain 14
<i>MYH3</i>	Myosin Heavy Chain 3
<i>MYH6</i>	Myosin Heavy Chain 6
<i>MYH7</i>	Myosin Heavy Chain 7
<i>MYH9</i>	Myosin Heavy Chain 9
<i>MYO15A</i>	Myosin XVA
<i>MYO1A</i>	Myosin IA
<i>MYO3A</i>	Myosin IIIA
<i>MYO6</i>	Myosin VI
<i>MYO7A</i>	Myosin VIIA
<i>MYPN</i>	Myopalladin
<i>NAA10</i>	N(Alpha)-Acetyltransferase 10, NatA Catalytic Subunit
<i>NAGA</i>	Alpha-N-Acetylgalactosaminidase
<i>NAGLU</i>	N-Acetyl-Alpha-Glucosaminidase
<i>NALCN</i>	Sodium Leak Channel, Non-Selective
<i>ND1</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 1
<i>ND4</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 4
<i>ND5</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 5
<i>ND6</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 6
<i>NDP</i>	Norrin Cystine Knot Growth Factor NDP
<i>NDRG1</i>	N-Myc Downstream Regulated 1
<i>NDUFA1</i>	NADH:Ubiquinone Oxidoreductase Subunit A1
<i>NDUFA10</i>	NADH:Ubiquinone Oxidoreductase Subunit A10
<i>NDUFA11</i>	NADH:Ubiquinone Oxidoreductase Subunit A11
<i>NDUFA12</i>	NADH:Ubiquinone Oxidoreductase Subunit A12
<i>NDUFA2</i>	NADH:Ubiquinone Oxidoreductase Subunit A2
<i>NDUFA9</i>	NADH:Ubiquinone Oxidoreductase Subunit A9
<i>NDUFAF1</i>	NADH:Ubiquinone Oxidoreductase Complex Assembly Factor 1
<i>NDUFAF2</i>	NADH:Ubiquinone Oxidoreductase Complex Assembly Factor 2
<i>NDUFAF3</i>	NADH:Ubiquinone Oxidoreductase Complex Assembly Factor 3
<i>NDUFAF4</i>	NADH:Ubiquinone Oxidoreductase Complex Assembly Factor 4
<i>NDUFAF5</i>	NADH:Ubiquinone Oxidoreductase Complex Assembly Factor 5
<i>NDUFAF6</i>	NADH:Ubiquinone Oxidoreductase Complex Assembly Factor 6
<i>NDUFB11</i>	NADH:Ubiquinone Oxidoreductase Subunit B11
<i>NDUFB3</i>	NADH:Ubiquinone Oxidoreductase Subunit B3
<i>NDUFB9</i>	NADH:Ubiquinone Oxidoreductase Subunit B9
<i>NDUFS1</i>	NADH:Ubiquinone Oxidoreductase Core Subunit S1
<i>NDUFS2</i>	NADH:Ubiquinone Oxidoreductase Core Subunit S2
<i>NDUFS3</i>	NADH:Ubiquinone Oxidoreductase Core Subunit S3
<i>NDUFS4</i>	NADH:Ubiquinone Oxidoreductase Core Subunit S4
<i>NDUFS6</i>	NADH:Ubiquinone Oxidoreductase Core Subunit S6
<i>NDUFS7</i>	NADH:Ubiquinone Oxidoreductase Core Subunit S7
<i>NDUFS8</i>	NADH:Ubiquinone Oxidoreductase Core Subunit S8

<i>NDUFV1</i>	NADH:Ubiquinone Oxidoreductase Core Subunit V1
<i>NDUFV2</i>	NADH:Ubiquinone Oxidoreductase Core Subunit V2
<i>NEBL</i>	Nebulette
<i>NEDD4L</i>	NEDD4 Like E3 Ubiquitin Protein Ligase
<i>NEK2</i>	NIMA Related Kinase 2
<i>NELFA</i>	Negative Elongation Factor Complex Member A
<i>NEU1</i>	Neuraminidase 1
<i>NEXN</i>	Nexilin F-Actin Binding Protein
<i>NF2</i>	Neurofibromin 2
<i>NFIX</i>	Nuclear Factor I X
<i>NHP2</i>	NHP2 Ribonucleoprotein
<i>NIPAL4</i>	NIPA Like Domain Containing 4
<i>NIPBL</i>	NIPBL Cohesin Loading Factor
<i>NLRC4</i>	NLR Family CARD Domain Containing 4
<i>NLRP12</i>	NLR Family Pyrin Domain Containing 12
<i>NLRP3</i>	NLR Family Pyrin Domain Containing 3
<i>NMNAT1</i>	Nicotinamide Nucleotide Adenylyltransferase 1
<i>NOG</i>	Noggin
<i>NOP10</i>	NOP10 Ribonucleoprotein
<i>NOTCH2</i>	Notch Receptor 2
<i>NOTCH3</i>	Notch Receptor 3
<i>NPHP1</i>	Nephrocystin 1
<i>NR2E3</i>	Nuclear Receptor Subfamily 2 Group E Member 3
<i>NR5A1</i>	Nuclear Receptor Subfamily 5 Group A Member 1
<i>NRAS</i>	NRAS Proto-Oncogene, GTPase
<i>NRL</i>	Neural Retina Leucine Zipper
<i>NRTN</i>	Neurturin
<i>NSD1</i>	Nuclear Receptor Binding SET Domain Protein 1
<i>NSD2</i>	Nuclear Receptor Binding SET Domain Protein 2
<i>NSDHL</i>	NAD(P) Dependent Steroid Dehydrogenase-Like
<i>NSMF</i>	NMDA Receptor Synaptonuclear Signaling And Neuronal Migration Factor
<i>NSUN2</i>	NOP2/Sun RNA Methyltransferase 2
<i>NTNG1</i>	Netrin G1
<i>NUBPL</i>	Nucleotide Binding Protein Like
<i>NUP107</i>	Nucleoporin 107
<i>NUS1</i>	NUS1 Dehydrodolichyl Diphosphate Synthase Subunit
<i>OFD1</i>	OFD1, Centriole And Centriolar Satellite Protein
<i>OPA1</i>	OPA1 Mitochondrial Dynamin Like GTPase
<i>ORC1</i>	Origin Recognition Complex Subunit 1
<i>ORC4</i>	Origin Recognition Complex Subunit 4
<i>ORC6</i>	Origin Recognition Complex Subunit 6
<i>OSBPL2</i>	Oxysterol Binding Protein Like 2
<i>OTOA</i>	Otoancorin
<i>OTOF</i>	Otoferlin
<i>OTOG</i>	Otogelin
<i>OTOGL</i>	Otogelin Like
<i>OTUD6B</i>	OTU Domain Containing 6B
<i>OTX2</i>	Orthodenticle Homeobox 2
<i>P2RX2</i>	Purinergic Receptor P2X 2
<i>PALB2</i>	Partner And Localizer Of BRCA2
<i>PARN</i>	Poly(A)-Specific Ribonuclease
<i>PAX1</i>	Paired Box 1
<i>PAX2</i>	Paired Box 2
<i>PAX3</i>	Paired Box 3
<i>PCDH15</i>	Protocadherin Related 15
<i>PCLO</i>	Piccolo Presynaptic Cytomatrix Protein
<i>PCNT</i>	Pericentrin
<i>PCYT1A</i>	Phosphate Cytidyltransferase 1, Choline, Alpha
<i>PDE4D</i>	Phosphodiesterase 4D

<i>PDE6A</i>	Phosphodiesterase 6A
<i>PDE6B</i>	Phosphodiesterase 6B
<i>PDE6G</i>	Phosphodiesterase 6G
<i>PDGFRB</i>	Platelet Derived Growth Factor Receptor Beta
<i>PDX1</i>	Pancreatic And Duodenal Homeobox 1
<i>PDZD7</i>	PDZ Domain Containing 7
<i>PEPD</i>	Peptidase D
<i>PET100</i>	PET100 Cytochrome C Oxidase Chaperone
<i>PEX1</i>	Peroxisomal Biogenesis Factor 1
<i>PEX10</i>	Peroxisomal Biogenesis Factor 10
<i>PEX11B</i>	Peroxisomal Biogenesis Factor 11B
<i>PEX12</i>	Peroxisomal Biogenesis Factor 12
<i>PEX13</i>	Peroxisomal Biogenesis Factor 13
<i>PEX14</i>	Peroxisomal Biogenesis Factor 14
<i>PEX16</i>	Peroxisomal Biogenesis Factor 16
<i>PEX19</i>	Peroxisomal Biogenesis Factor 19
<i>PEX2</i>	Peroxisomal Biogenesis Factor 2
<i>PEX26</i>	Peroxisomal Biogenesis Factor 26
<i>PEX3</i>	Peroxisomal Biogenesis Factor 3
<i>PEX5</i>	Peroxisomal Biogenesis Factor 5
<i>PEX6</i>	Peroxisomal Biogenesis Factor 6
<i>PEX7</i>	Peroxisomal Biogenesis Factor 7
<i>PGM3</i>	Phosphoglucomutase 3
<i>PHEX</i>	Phosphate Regulating Endopeptidase Homolog X-Linked
<i>PHF6</i>	PHD Finger Protein 6
<i>PHOX2B</i>	Paired Like Homeobox 2b
<i>PHYH</i>	Phytanoyl-CoA 2-Hydroxylase
<i>PIEZO1</i>	Piezo Type Mechanosensitive Ion Channel Component 1
<i>PIEZO2</i>	Piezo Type Mechanosensitive Ion Channel Component 2
<i>PIGA</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class A
<i>PIGL</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class L
<i>PIGV</i>	Phosphatidylinositol Glycan Anchor Biosynthesis Class V
<i>PIK3CA</i>	Phosphatidylinositol-4,5-Bisphosphate 3-Kinase Catalytic Subunit Alpha
<i>PIK3R1</i>	Phosphoinositide-3-Kinase Regulatory Subunit 1
<i>PITX2</i>	Paired Like Homeodomain 2
<i>PJVK</i>	Pejvakin
<i>PLA2G6</i>	Phospholipase A2 Group VI
<i>PLAGL1</i>	PLAG1 Like Zinc Finger 1
<i>PLN</i>	Phospholamban
<i>PLOD3</i>	Procollagen-Lysine,2-Oxoglutarate 5-Dioxygenase 3
<i>PLP1</i>	Proteolipid Protein 1
<i>PLXND1</i>	Plexin D1
<i>PMP22</i>	Peripheral Myelin Protein 22
<i>PNPLA1</i>	Patatin Like Phospholipase Domain Containing 1
<i>PNPLA2</i>	Patatin Like Phospholipase Domain Containing 2
<i>PNPLA6</i>	Patatin Like Phospholipase Domain Containing 6
<i>PNPLA8</i>	Patatin Like Phospholipase Domain Containing 8
<i>PNPT1</i>	Polyribonucleotide Nucleotidyltransferase 1
<i>POGZ</i>	Pogo Transposable Element Derived With ZNF Domain
<i>POLA1</i>	DNA Polymerase Alpha 1, Catalytic Subunit
<i>POLD1</i>	DNA Polymerase Delta 1, Catalytic Subunit
<i>POLG</i>	DNA Polymerase Gamma, Catalytic Subunit
<i>POLR1C</i>	RNA Polymerase I And III Subunit C
<i>POLR1D</i>	RNA Polymerase I And III Subunit D
<i>POMGNT1</i>	Protein O-Linked Mannose N-Acetylglucosaminyltransferase 1 (Beta 1,2-)
<i>POMK</i>	Protein-O-Mannose Kinase
<i>POR</i>	Cytochrome P450 Oxidoreductase
<i>PORCN</i>	Porcupine O-Acyltransferase

<i>POU3F4</i>	POU Class 3 Homeobox 4
<i>POU4F3</i>	POU Class 4 Homeobox 3
<i>PPP1R15B</i>	Protein Phosphatase 1 Regulatory Subunit 15B
<i>PQBP1</i>	Polyglutamine Binding Protein 1
<i>PRCD</i>	Photoreceptor Disc Component
<i>PRDM16</i>	PR/SET Domain 16
<i>PRDM5</i>	PR/SET Domain 5
<i>PRKAR1A</i>	Protein Kinase CAMP-Dependent Type I Regulatory Subunit Alpha
<i>PRKDC</i>	Protein Kinase, DNA-Activated, Catalytic Subunit
<i>PROK2</i>	Prokineticin 2
<i>PROKR2</i>	Prokineticin Receptor 2
<i>PROM1</i>	Prominin 1
<i>PRPF3</i>	Pre-mRNA Processing Factor 3
<i>PRPF31</i>	Pre-mRNA Processing Factor 31
<i>PRPF4</i>	Pre-mRNA Processing Factor 4
<i>PRPF6</i>	Pre-mRNA Processing Factor 6
<i>PRPF8</i>	Pre-mRNA Processing Factor 8
<i>PRPH2</i>	Peripherin 2
<i>PRPS1</i>	Phosphoribosyl Pyrophosphate Synthetase 1
<i>PRRT2</i>	Proline Rich Transmembrane Protein 2
<i>PRRX1</i>	Paired Related Homeobox 1
<i>PRTN3</i>	Proteinase 3
<i>PSEN1</i>	Presenilin 1
<i>PSEN2</i>	Presenilin 2
<i>PSMC3IP</i>	PSMC3 Interacting Protein
<i>PTDSS1</i>	Phosphatidylserine Synthase 1
<i>PTEN</i>	Phosphatase And Tensin Homolog
<i>PTH1R</i>	Parathyroid Hormone 1 Receptor
<i>PTPN11</i>	Protein Tyrosine Phosphatase, Non-Receptor Type 11
<i>PTPN22</i>	Protein Tyrosine Phosphatase Non-Receptor Type 22
<i>PTPRQ</i>	Protein Tyrosine Phosphatase Receptor Type Q
<i>PTRH2</i>	Peptidyl-TRNA Hydrolase 2
<i>PYCR2</i>	Pyrroline-5-Carboxylate Reductase 2
<i>RAB23</i>	RAB23, Member RAS Oncogene Family
<i>RAD21</i>	RAD21 Cohesin Complex Component
<i>RAD51</i>	RAD51 Recombinase
<i>RAD51C</i>	RAD51 Paralog C
<i>RAF1</i>	Raf-1 Proto-Oncogene, Serine/Threonine Kinase
<i>RAI1</i>	Retinoic Acid Induced 1
<i>RAP1A</i>	RAP1A, Member Of RAS Oncogene Family
<i>RAP1B</i>	RAP1B, Member Of RAS Oncogene Family
<i>RASA2</i>	RAS P21 Protein Activator 2
<i>RBM20</i>	RNA Binding Motif Protein 20
<i>RBM8A</i>	RNA Binding Motif Protein 8A
<i>RBP3</i>	Retinol Binding Protein 3
<i>RD3</i>	Retinal Degeneration 3, GUCY2D Regulator
<i>RDH12</i>	Retinol Dehydrogenase 12
<i>RDX</i>	Radixin
<i>RECQL4</i>	RecQ Like Helicase 4
<i>REEP6</i>	Receptor Accessory Protein 6
<i>RERE</i>	Arginine-Glutamic Acid Dipeptide Repeats
<i>RET</i>	Ret Proto-Oncogene
<i>REV3L</i>	REV3 Like, DNA Directed Polymerase Zeta Catalytic Subunit
<i>RFC2</i>	Replication Factor C Subunit 2
<i>RFT1</i>	RFT1 Homolog
<i>RGR</i>	Retinal G Protein Coupled Receptor
<i>RHO</i>	Rhodopsin
<i>RIPOR2</i>	RHO Family Interacting Cell Polarization Regulator 2

<i>RIT1</i>	Ras Like Without CAAX 1
<i>RLBP1</i>	Retinaldehyde Binding Protein 1
<i>RMND1</i>	Required For Meiotic Nuclear Division 1 Homolog
<i>RNASET2</i>	Ribonuclease T2
<i>RNF135</i>	Ring Finger Protein 135
<i>RNR1</i>	RNA, Ribosomal 45S Cluster 1
<i>ROBO3</i>	Roundabout Guidance Receptor 3
<i>ROM1</i>	Retinal Outer Segment Membrane Protein 1
<i>ROR2</i>	Receptor Tyrosine Kinase Like Orphan Receptor 2
<i>RP1</i>	RP1 Axonemal Microtubule Associated
<i>RP2</i>	RP2 Activator Of ARL3 GTPase
<i>RP9</i>	RP9 Pre-mRNA Splicing Factor
<i>RPE65</i>	Retinoid Isomerohydrolase RPE65
<i>RPGR</i>	Retinitis Pigmentosa GTPase Regulator
<i>RPGRIP1</i>	RPGR Interacting Protein 1
<i>RPL10</i>	Ribosomal Protein L10
<i>RPL11</i>	Ribosomal Protein L11
<i>RPS23</i>	Ribosomal Protein S23
<i>RPS26</i>	Ribosomal Protein S26
<i>RPS28</i>	Ribosomal Protein S28
<i>RPS6KA3</i>	Ribosomal Protein S6 Kinase A3
<i>RRAS</i>	RAS Related
<i>RREB1</i>	Ras Responsive Element Binding Protein 1
<i>RRM2B</i>	Ribonucleotide Reductase Regulatory TP53 Inducible Subunit M2B
<i>RTEL1</i>	Regulator Of Telomere Elongation Helicase 1
<i>RUNX2</i>	RUNX Family Transcription Factor 2
<i>S1PR2</i>	Sphingosine-1-Phosphate Receptor 2
<i>SAG</i>	S-Antigen Visual Arrestin
<i>SALL1</i>	Spalt Like Transcription Factor 1
<i>SALL4</i>	Spalt Like Transcription Factor 4
<i>SBF2</i>	SET Binding Factor 2
<i>SC5D</i>	Sterol-C5-Desaturase
<i>SCN1A</i>	Sodium Voltage-Gated Channel Alpha Subunit 1
<i>SCN5A</i>	Sodium Voltage-Gated Channel Alpha Subunit 5
<i>SCO1</i>	SCO Cytochrome C Oxidase Assembly Protein 1
<i>SDCCAG8</i>	Serologically Defined Colon Cancer Antigen 8
<i>SDHA</i>	Succinate Dehydrogenase Complex Flavoprotein Subunit A
<i>SDHB</i>	Succinate Dehydrogenase Complex Iron Sulfur Subunit B
<i>SDHC</i>	Succinate Dehydrogenase Complex Subunit C
<i>SDHD</i>	Succinate Dehydrogenase Complex Subunit D
<i>SEC23B</i>	SEC23 Homolog B, Coat Complex II Component
<i>SEC24C</i>	SEC24 Homolog C, COPII Coat Complex Component
<i>SEM1</i>	SEM1 26S Proteasome Complex Subunit
<i>SEMA3A</i>	Semaphorin 3A
<i>SEMA3C</i>	Semaphorin 3C
<i>SEMA3D</i>	Semaphorin 3D
<i>SEMA3E</i>	Semaphorin 3E
<i>SEMA4A</i>	Semaphorin 4A
<i>SERAC1</i>	Serine Active Site Containing 1
<i>SERPINB6</i>	Serpin Family B Member 6
<i>SETD2</i>	SET Domain Containing 2
<i>SETD5</i>	SET Domain Containing 5
<i>SF3B4</i>	Splicing Factor 3b Subunit 4
<i>SGCD</i>	Sarcoglycan Delta
<i>SGSH</i>	N-Sulfoglucosamine Sulfohydrolase
<i>SH3TC2</i>	SH3 Domain And Tetratricopeptide Repeats 2
<i>SHANK3</i>	SH3 And Multiple Ankyrin Repeat Domains 3
<i>SHOC2</i>	SHOC2 Leucine Rich Repeat Scaffold Protein

<i>SIN3A</i>	SIN3 Transcription Regulator Family Member A
<i>SIX1</i>	SIX Homeobox 1
<i>SIX5</i>	SIX Homeobox 5
<i>SIX6</i>	SIX Homeobox 6
<i>SKI</i>	SKI Proto-Oncogene
<i>SLC17A8</i>	Solute Carrier Family 17 Member 8
<i>SLC19A2</i>	Solute Carrier Family 19 Member 2
<i>SLC25A4</i>	Solute Carrier Family 25 Member 4
<i>SLC26A2</i>	Solute Carrier Family 26 Member 2
<i>SLC26A4</i>	Solute Carrier Family 26 Member 4
<i>SLC26A5</i>	Solute Carrier Family 26 Member 5
<i>SLC29A3</i>	Solute Carrier Family 29 Member 3
<i>SLC33A1</i>	Solute Carrier Family 33 Member 1
<i>SLC39A8</i>	Solute Carrier Family 39 Member 8
<i>SLC4A11</i>	Solute Carrier Family 4 Member 11
<i>SLC52A2</i>	Solute Carrier Family 52 Member 2
<i>SLC52A3</i>	Solute Carrier Family 52 Member 3
<i>SLC7A14</i>	Solute Carrier Family 7 Member 14
<i>SLITRK6</i>	SLIT And NTRK Like Family Member 6
<i>SLX4</i>	SLX4 Structure-Specific Endonuclease Subunit
<i>SMAD4</i>	SMAD Family Member 4
<i>SMARCA4</i>	SWI/SNF Related, Matrix Associated, Actin Dependent Regulator Of Chromatin, Subfamily A, Member 4
<i>SMARCB1</i>	SWI/SNF Related, Matrix Associated, Actin Dependent Regulator Of Chromatin, Subfamily B, Member 1
<i>SMARCE1</i>	SWI/SNF Related, Matrix Associated, Actin Dependent Regulator Of Chromatin, Subfamily E, Member 1
<i>SMC1A</i>	Structural Maintenance Of Chromosomes 1A
<i>SMC3</i>	Structural Maintenance Of Chromosomes 3
<i>SMCHD1</i>	Structural Maintenance Of Chromosomes Flexible Hinge Domain Containing 1
<i>SNAI2</i>	Snail Family Transcriptional Repressor 2
<i>SNAP29</i>	Synaptosome Associated Protein 29
<i>SNRNP200</i>	Small Nuclear Ribonucleoprotein U5 Subunit 200
<i>SNRNPB</i>	Small Nuclear Ribonucleoprotein Polypeptides B And B1
<i>SNX10</i>	Sorting Nexin 10
<i>SNX14</i>	Sorting Nexin 14
<i>SOS1</i>	SOS Ras/Rac Guanine Nucleotide Exchange Factor 1
<i>SOS2</i>	SOS Ras/Rac Guanine Nucleotide Exchange Factor 2
<i>SOST</i>	Sclerostin
<i>SOX10</i>	SRY-Box 10
<i>SOX11</i>	SRY-Box 11
<i>SOX2</i>	SRY-Box 2
<i>SOX3</i>	SRY-Box 3
<i>SOX9</i>	SRY-Box 9
<i>SPATA5</i>	Spermatogenesis Associated 5
<i>SPATA7</i>	Spermatogenesis Associated 7
<i>SPECC1L</i>	Sperm Antigen With Calponin Homology And Coiled-Coil Domains 1 Like
<i>SPIDR</i>	Scaffold Protein Involved In DNA Repair
<i>SPRY4</i>	Sprouty RTK Signaling Antagonist 4
<i>SPTLC1</i>	Serine Palmitoyltransferase Long Chain Base Subunit 1
<i>SQSTM1</i>	Sequestosome 1
<i>SRCAP</i>	Snf2 Related CREBBP Activator Protein
<i>SRP72</i>	Signal Recognition Particle 72
<i>SRY</i>	Sex Determining Region Y
<i>ST3GAL5</i>	ST3 Beta-Galactoside Alpha-2,3-Sialyltransferase 5
<i>STAMBP</i>	STAM Binding Protein
<i>STAT3</i>	Signal Transducer And Activator Of Transcription 3
<i>STRC</i>	Stereocilin
<i>SUCLA2</i>	Succinate-CoA Ligase ADP-Forming Beta Subunit

<i>SUCLG1</i>	Succinate-CoA Ligase Alpha Subunit
<i>SUMF1</i>	Sulfatase Modifying Factor 1
<i>SURF1</i>	SURF1 Cytochrome C Oxidase Assembly Factor
<i>SYNE4</i>	Spectrin Repeat Containing Nuclear Envelope Family Member 4
<i>SYT2</i>	Synaptotagmin 2
<i>TAC3</i>	Tachykinin 3
<i>TACO1</i>	Translational Activator Of Cytochrome C Oxidase I
<i>TACR3</i>	Tachykinin Receptor 3
<i>TAF1</i>	TATA-Box Binding Protein Associated Factor 1
<i>TANGO2</i>	Transport And Golgi Organization 2 Homolog
<i>TAZ</i>	Tafazzin
<i>TBC1D24</i>	TBC1 Domain Family Member 24
<i>TBL2</i>	Transducin Beta Like 2
<i>TBX1</i>	T-Box 1
<i>TBX15</i>	T-Box 15
<i>TBX22</i>	T-Box 22
<i>TBX4</i>	T-Box 4
<i>TCAP</i>	Titin-Cap
<i>TCF12</i>	Transcription Factor 12
<i>TCIRG1</i>	T Cell Immune Regulator 1, ATPase H+ Transporting V0 Subunit A3
<i>TCOF1</i>	Treacle Ribosome Biogenesis Factor 1
<i>TCTN3</i>	Tectonic Family Member 3
<i>TECTA</i>	Tectorin Alpha
<i>TELO2</i>	Telomere Maintenance 2
<i>TERC</i>	Telomerase RNA Component
<i>TERT</i>	Telomerase Reverse Transcriptase
<i>TFAP2A</i>	Transcription Factor AP-2 Alpha
<i>TFAP2B</i>	Transcription Factor AP-2 Beta
<i>TGFB1</i>	Transforming Growth Factor Beta 1
<i>TGM1</i>	Transglutaminase 1
<i>THRB</i>	Thyroid Hormone Receptor Beta
<i>TIMM8A</i>	Translocase Of Inner Mitochondrial Membrane 8A
<i>TIMMDC1</i>	Translocase Of Inner Mitochondrial Membrane Domain Containing 1
<i>TINF2</i>	TERF1 Interacting Nuclear Factor 2
<i>TK2</i>	Thymidine Kinase 2
<i>TMC1</i>	Transmembrane Channel Like 1
<i>TMEM126A</i>	Transmembrane Protein 126A
<i>TMEM126B</i>	Transmembrane Protein 126B
<i>TMIE</i>	Transmembrane Inner Ear
<i>TMPO</i>	Thymopoietin
<i>TNC</i>	Tenascin C
<i>TNFRSF11A</i>	TNF Receptor Superfamily Member 11a
<i>TNFRSF11B</i>	TNF Receptor Superfamily Member 11b
<i>TNFSF11</i>	TNF Superfamily Member 11
<i>TNNC1</i>	Troponin C1, Slow Skeletal And Cardiac Type
<i>TNNI3</i>	Troponin I3, Cardiac Type
<i>TNNT2</i>	Troponin T2, Cardiac Type
<i>TOPORS</i>	TOP1 Binding Arginine/Serine Rich Protein
<i>TP63</i>	Tumor Protein P63
<i>TPM1</i>	Tropomyosin 1
<i>TPRN</i>	Taperin
<i>TRAPPC11</i>	Trafficking Protein Particle Complex 11
<i>TRIM32</i>	Tripartite Motif Containing 32
<i>TRIOBP</i>	TRIO And F-Actin Binding Protein
<i>TRIP13</i>	Thyroid Hormone Receptor Interactor 13
<i>TRMU</i>	TRNA 5-Methylaminomethyl-2-Thiouridylate Methyltransferase

<i>TRNC</i>	Mitochondrially Encoded TRNA-Cys (UGU/C)
<i>TRNE</i>	Mitochondrially Encoded TRNA-Glu (GAA/G)
<i>TRNF</i>	Mitochondrially Encoded TRNA-Phe (UUU/C)
<i>TRNH</i>	Mitochondrially Encoded TRNA-His (CAU/C)
<i>TRNI</i>	Mitochondrially Encoded TRNA-Ile (AUU/C)
<i>TRNK</i>	Mitochondrially Encoded TRNA-Lys (AAA/G)
<i>TRNL1</i>	Mitochondrially Encoded TRNA-Leu (UUA/G) 1
<i>TRNN</i>	Mitochondrially Encoded TRNA-Asn (AAU/C)
<i>TRNP</i>	Mitochondrially Encoded TRNA-Pro (CCN)
<i>TRNQ</i>	Mitochondrially Encoded TRNA-Gln (CAA/G)
<i>TRNS1</i>	Mitochondrially Encoded TRNA-Ser (UCN) 1
<i>TRNS2</i>	Mitochondrially Encoded TRNA-Ser (AGU/C) 2
<i>TRNT1</i>	TRNA Nucleotidyl Transferase 1
<i>TRNV</i>	Mitochondrially Encoded TRNA-Val (GUN)
<i>TRNW</i>	Mitochondrially Encoded TRNA-Trp (UGA/G)
<i>TRPS1</i>	Transcriptional Repressor GATA Binding 1
<i>TRPV4</i>	Transient Receptor Potential Cation Channel Subfamily V Member 4
<i>TSHZ1</i>	Teashirt Zinc Finger Homeobox 1
<i>TSPEAR</i>	Thrombospondin Type Laminin G Domain And EAR Repeats
<i>TSR2</i>	TSR2 Ribosome Maturation Factor
<i>TTC19</i>	Tetratricopeptide Repeat Domain 19
<i>TTC8</i>	Tetratricopeptide Repeat Domain 8
<i>TTN</i>	Titin
<i>TTR</i>	Transthyretin
<i>TUB</i>	TUB Bipartite Transcription Factor
<i>TULP1</i>	TUB Like Protein 1
<i>TWIST1</i>	Twist Family BHLH Transcription Factor 1
<i>TWIST2</i>	Twist Family BHLH Transcription Factor 2
<i>TWNK</i>	Twinkle MtDNA Helicase
<i>TXNL4A</i>	Thioredoxin Like 4A
<i>TXNRD2</i>	Thioredoxin Reductase 2
<i>TYMP</i>	Thymidine Phosphorylase
<i>TYR</i>	Tyrosinase
<i>UBE2T</i>	Ubiquitin Conjugating Enzyme E2 T
<i>UBR1</i>	Ubiquitin Protein Ligase E3 Component N-Recognin 1
<i>UFD1</i>	Ubiquitin Recognition Factor In ER Associated Degradation 1
<i>UGT1A1</i>	UDP Glucuronosyltransferase Family 1 Member A1
<i>USB1</i>	U6 SnRNA Biogenesis Phosphodiesterase 1
<i>USH1C</i>	USH1 Protein Network Component Harmonin
<i>USH1G</i>	USH1 Protein Network Component Sans
<i>USH2A</i>	Usherin
<i>USP9X</i>	Ubiquitin Specific Peptidase 9 X-Linked
<i>VCL</i>	Vinculin
<i>VHL</i>	Von Hippel-Lindau Tumor Suppressor
<i>VPS11</i>	VPS11, CORVET/HOPS Core Subunit
<i>VPS13B</i>	Vacuolar Protein Sorting 13 Homolog B
<i>WAC</i>	WW Domain Containing Adaptor With Coiled-Coil
<i>WDPCP</i>	WD Repeat Containing Planar Cell Polarity Effector
<i>WDR11</i>	WD Repeat Domain 11
<i>WFS1</i>	Wolframin ER Transmembrane Glycoprotein
<i>WHRN</i>	Whirlin
<i>WNT10B</i>	Wnt Family Member 10B
<i>WNT5A</i>	Wnt Family Member 5A
<i>WRAP53</i>	WD Repeat Containing Antisense To TP53
<i>XPA</i>	XPA, DNA Damage Recognition And Repair Factor
<i>XPC</i>	XPC Complex Subunit, DNA Damage Recognition And Repair Factor

<i>XPNPEP3</i>	X-Prolyl Aminopeptidase 3
<i>XRCC2</i>	X-Ray Repair Cross Complementing 2
<i>XRCC4</i>	X-Ray Repair Cross Complementing 4
<i>XYLT2</i>	Xylosyltransferase 2
<i>YAP1</i>	Yes Associated Protein 1
<i>ZBTB20</i>	Zinc Finger And BTB Domain Containing 20
<i>ZFP57</i>	ZFP57 Zinc Finger Protein
<i>ZIC1</i>	Zic Family Member 1
<i>ZMPSTE24</i>	Zinc Metallopeptidase STE24
<i>ZNF408</i>	Zinc Finger Protein 408
<i>ZNF469</i>	Zinc Finger Protein 469
<i>ZNF513</i>	Zinc Finger Protein 513

Severe hearing impairment (HP:0012714), 5 genes

<i>BRAF</i>	B-Raf Proto-Oncogene, Serine/Threonine Kinase
<i>GPSM2</i>	G Protein Signaling Modulator 2
<i>PTPN11</i>	Protein Tyrosine Phosphatase, Non-Receptor Type 11
<i>RAF1</i>	Raf-1 Proto-Oncogene, Serine/Threonine Kinase
<i>TRIOBP</i>	TRIO And F-Actin Binding Protein