Trio - Whole Exome Sequencing Analysis – Carrier Screening

Patient name	:	**Mr.XXX**	**Mrs.YYY**
Gender/ Age	:	**Male/35 years**	**Female/25 years**
PIN	:	**XX**	**XX**
Sample no	:	**XX**	**XX**
Specimen	:	**Peripheral blood**	**Peripheral blood**
Sample collection date	:	**XX**	**XX**
Sample receipt date	:	**XX**	**XX**
Report date	:	**XX**	**XX**
Referring clinician	:	**XX**	
Hospital/Clinic	:	**XX**	

Clinical history

Mr.XXX and Mrs.YYY are consanguineously married. Their daughter, Baby ZZZ presented with congenital deafness, cerebral palsy, and delayed milestones. No history of fever or infections was reported. Mrs. YYY and Mr. XXX have been evaluated for carrier status of pathogenic variations.

Results

Mr. XXX is found to be carriers of likely pathogenic variants in *PCDH15* gene (p.Tyr579Ter), *CEP250* gene (c.243+2T>C) and *CORIN* gene (c.2540+1dupG).

Mrs. YYY is found to be carriers of uncertain significance variant in the *PCDH15* gene (p.Ile179Lys) and found to be carriers of likely pathogenic variants in the *DNA2* gene (p.Leu626Ter), *FIG4* gene (p.Ser750GlnfsTer10), *GBE1* gene (p.Tyr329Cys), *UCHL1* gene (p.Arg178Ter) and *COL7A1* gene(p.Gln1675_Asp1677dup).

List of variants identified related to the index child phenotype:

Disease	Mr. XXX	Mrs. YYY
Deafness,autosomal recessive 23 **(OMIM#609533)** Usher syndrome, type 1F **(OMIM#602083)** Usher syndrome, type 1D/F digenic **(OMIM#601067)** **Mode of inheritance: AR**	**CARRIER** Gene: *PCDH15* Exon 14, c.1736_1737insAA p.Tyr579Ter Heterozygous **Classification: Likely Pathogenic**	**CARRIER** Gene: *PCDH15* Exon 6, c.536T>A p.Ile179Lys Heterozygous **Classification: Uncertain significance**

The heterozygous variant [*PCDH15*: c.1736_1737insAA; p. Tyr579Ter] identified in the sample of Mr. XXX has been identified in heterozygous state in their daughter - Baby. ZZZ.

The heterozygous variant [*PCDH15*: c.536T>A; p. Ile179Lys] identified in the sample of Mrs. YYY has been identified in heterozygous state in their daughter - Baby.ZZZ.

List of significant carrier variants identified:

Disease	Mr. XXX	Mrs. YYY
Cone-rod dystrophy and hearing loss 2 **(OMIM#618358)** **Mode of inheritance: AR**	**CARRIER** Gene: *CEP250* Intron 5, c.243+2T>C 5' Splice site Heterozygous **Classification: Likely Pathogenic**	**NON - CARRIER**
?Cardiomyopathy, familial hypertrophic, 30, atrial **(OMIM#620734)** **Mode of inheritance: AR**	**CARRIER** Gene: *CORIN* Intron 19, c.2540+1dupG 5' Splice site Heterozygous **Classification: Likely Pathogenic**	**NON - CARRIER**

Progressive external ophthalmoplegia with mitochondrial DNA deletions, autosomal dominant 6 **(OMIM#615156)** **Mode of inheritance: AD** Rothmund-Thomson syndrome, type 4 **(OMIM#620819)** Seckel syndrome 8 **(OMIM#615807)** **Mode of inheritance: AR**	**NON - CARRIER**	**CARRIER** Gene: *DNA2* Exon 13, c.1877T>A p.Leu626Ter Heterozygous **Classification: Likely Pathogenic**
?Polymicrogyria, bilateral temporooccipital **(OMIM#612691)** Charcot-Marie-Tooth disease, type 4J **(OMIM#611228)** Yunis-Varon syndrome **(OMIM#216340)** **Mode of inheritance: AR** Amyotrophic lateral sclerosis 11 **(OMIM#612577)** **Mode of inheritance: AD**	**NON - CARRIER**	**CARRIER** Gene: *FIG4* Exon 20, c.2247dupC p.Ser750GlnfsTer10 Heterozygous **Classification: Likely Pathogenic**
Glycogen storage disease IV **(OMIM#232500)** Polyglucosan body disease, adult form **(OMIM#263570)** **Mode of inheritance: AR**	**NON - CARRIER**	**CARRIER** Gene: *GBE1* Exon 7, c.986A>G p.Tyr329Cys Heterozygous **Classification: Likely Pathogenic**

{?Parkinson disease 5, susceptibility to} **(OMIM#613643)** Spastic paraplegia 79A, autosomal dominant **(OMIM#620221)** **Mode of inheritance: AD** Spastic paraplegia 79B, autosomal recessive **(OMIM#615491)** **Mode of inheritance: AR**	**NON - CARRIER**	**CARRIER** Gene: *UCHL1* Exon 8, c.532C>T p.Arg178Ter Heterozygous **Classification: Likely Pathogenic**
Epidermolysis bullosa dystrophica inversa / Epidermolysis bullosa dystrophica, autosomal recessive / Epidermolysis bullosa dystrophica, localisata variant **(OMIM#226600)** **Mode of inheritance: AR** Epidermolysis bullosa dystrophica, autosomal dominant **(OMIM#131750)** Epidermolysis bullosa dystrophica, Bart type **(OMIM#132000)** Nail disorder, nonsyndromic congenital, 8 **(OMIM#607523)** **Mode of inheritance: AD** Epidermolysis bullosa pruriginosa **(OMIM#604129)** Epidermolysis bullosa, pretibial **(OMIM#131850)**	**NON - CARRIER**	**CARRIER** Gene: *COL7A1* Exon 55, 5022_5030dup p.Gln1675_Asp1677dup Heterozygous **Classification: Likely Pathogenic**

Transient bullous of the newborn **(OMIM#131705)** **Mode of inheritance: AD, AR**		

*Genetic test results are reported based on the recommendation of American College of Medical Genetics [1].
No other variant that warrants to be reported for the given clinical indication was identified.

Variant Interpretation

Interpretation for the significant carrier variant identified in Mr. XXX related to the index child phenotype

***PCDH15*: c.1736_1737insAA**

Variant summary: A heterozygous two base pair insertion in exon 14 of the *PCDH15* gene (chr10:g.54153148insTT, NM_001384140.1, Depth: 138x) that results in the premature truncation of the protein at codon 579 (p.Tyr579Ter) was detected. This variant is a frameshift variant which occurs in an exon of *PCDH15* upstream where nonsense mediated decay is predicted to occur. This variant is predicted to cause loss of normal protein function through protein truncation.

Population frequency: This variant has not been reported in gnomAD database and 1000 genomes database.

Clinical and Literature evidence: Another stop gained variant in the same amino acid position (p.Tyr579Ter) has been previously classified as pathogenic in ClinVar database for autosomal recessive non syndromic hearing loss 23 [3]. This variant has been previously reported in patients affected with Usher syndrome in compound heterozygous state [4].

***In-silico* prediction:** The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: Deafness, autosomal recessive 23 (OMIM#609533) is caused by homozygous mutation in the *PCDH15* gene (OMIM*605514). Usher syndrome, type 1F (OMIM#602083) and Usher syndrome, type 1D/F digenic (OMIM#601067) are caused by homozygous or compound heterozygous mutation in the *PCDH15* gene (OMIM*605514). Usher syndrome type I is an autosomal recessive condition characterized by profound congenital hearing impairment with unintelligible speech, early retinitis pigmentosa (usually evident within the first decade), and constant vestibular dysfunction. Type I is distinguished from type II (276901) on the basis of severity of hearing loss and the extent of vestibular involvement. Type I patients are profoundly deaf, whereas type II patients are 'hard of hearing.' Vestibular function is defective in type I patients, whereas type II patients have normal vestibular function. Patients with type III (USH3; 276902) have progressive hearing loss. Usher syndrome constitutes a group of autosomal recessive disorders characterized by progressive pigmentary retinopathy and sensorineural hearing loss. Phenotypic distinctions are based on auditory and vestibular differences. Persons with forms of Usher syndrome type

I (USH1) have congenital severe to profound hearing loss and vestibular dysfunction. These diseases follow autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.

This variant has been identified in the sample of their index female child, Baby. ZZZ in heterozygous state.

Interpretation for the uncertain significant carrier variant identified in Mrs. YYY related to the index child phenotype

***PCDH15*: c.536T>A**

Variant summary: A heterozygous missense variation in exon 6 of the *PCDH15* gene (chr10:g.54346423A>T, NM_001384140.1, Depth:74x) that results in the amino acid substitution of Lysine for Isoleucine at codon 179 (p.Ile179Lys) was detected.

Population frequency: This variant has not been reported in gnomAD database and 1000 genomes database.

Clinical evidence: Another missense variant in the same amino acid position (p. Ile179Thr) has been previously classified as variant of uncertain significance in ClinVar database [5].

***In-silico* prediction:** The *in-silico* predictions of the variant are damaging by SIFT and PolyPhen-2 (HumDiv). The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: Deafness, autosomal recessive 23 (OMIM#609533) is caused by homozygous mutation in the *PCDH15* gene (OMIM*605514). Usher syndrome, type 1F (OMIM#602083) and Usher syndrome, type 1D/F digenic (OMIM#601067) are caused by homozygous or compound heterozygous mutation in the *PCDH15* gene (OMIM*605514). Usher syndrome type I is an autosomal recessive condition characterized by profound congenital hearing impairment with unintelligible speech, early retinitis pigmentosa (usually evident within the first decade), and constant vestibular dysfunction. Type I is distinguished from type II (276901) on the basis of severity of hearing loss and the extent of vestibular involvement. Type I patients are profoundly deaf, whereas type II patients are 'hard of hearing.' Vestibular function is defective in type I patients, whereas type II patients have normal vestibular function. Patients with type III (USH3; 276902) have progressive hearing loss. Usher syndrome constitutes a group of autosomal recessive disorders characterized by progressive pigmentary retinopathy and sensorineural hearing loss. Phenotypic distinctions are based on auditory and vestibular differences. Persons with forms of Usher syndrome type I (USH1) have congenital severe to profound hearing loss and vestibular dysfunction. These diseases follow autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as variant of uncertain significance.

This variant has been identified in the sample of their index female child, Baby. ZZZ in heterozygous state.

Interpretation for the significant carrier variants identified in Mr. XXX

***CEP250*: c.243+2T>C**

Variant summary: A heterozygous 5' splice site variation in intron 5 of the *CEP250* gene (chr20:g.35463633T>C, NM_007186.6, Depth: 76x) that affects the in variant GT donor splice site of exon 5 (c.243+2T>C) was detected.

Population frequency: This variant has not been reported in gnomAD database and 1000 genomes databases.

***In-silico* prediction:** The *in-silico* predictions of the variant are disrupted by GeneSplicer, MaxEntScan and PWM. The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: Cone-rod dystrophy and hearing loss 2 (OMIM#618358) is caused by homozygous or compound heterozygous mutation in the *CEP250* gene (OMIM*609689). This disease follows autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.

This variant has not been identified in the sample of their index female child, Baby. ZZZ

***CORIN*: c.2540+1dupG**

Variant summary: A heterozygous 5' splice site variation in intron 19 of the *CORIN* gene (chr4:g.47623570insC, NM_006587.4, Depth: 104x) that affects the in variant GT donor splice site of exon 19 (c.2540+1dupG) was detected

Population frequency: This variant has minor allele frequency of 0.0092% in gnomAD database and has not been reported in 1000 genomes databases.

***In-silico* prediction:** The *in-silico* predictions of the variant are deleterious by CADD and disrupted by GeneSplicer, MaxEntScan, NNSplice and PWM. The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype:?Cardiomyopathy, familial hypertrophic, 30, atrial (OMIM#620734) is caused by homozygous mutation in the *CORIN* gene (OMIM*605236). This disease follows autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.

This variant has not been identified in the sample of their index female child, Baby. ZZZ.

Interpretation for the significant carrier variants identified in Mrs. YYY

***DNA2*: c.1877T>A**

Variant summary: A heterozygous stop gained variation in exon 13 of the *DNA2* gene (chr10:g.68431968A>T, NM_001080449.3, Depth:40x) that results in the premature truncation of the protein at codon 626 (p.Leu626Ter) was detected. This variant is a stop gained variant which occurs in an exon of *DNA2* upstream where nonsense mediated decay is predicted to occur. This variant is predicted to cause loss of normal protein function through protein truncation.

Population frequency: This variant has not been reported in gnomAD database and 1000 genomes database.

***In-silico* prediction:** The *in-silico* predictions of the variant are deleterious by CADD. The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: Progressive external ophthalmoplegia with mitochondrial DNA deletions, autosomal dominant 6 (OMIM#615156) is caused by heterozygous mutation in the *DNA2* gene (OMIM*601810). This disease follows autosomal dominant pattern of inheritance [2]. Rothmund-Thomson syndrome, type 4(OMIM#620819) and Seckel syndrome 8 (OMIM#615807) is caused by homozygous or compound heterozygous mutation in the *DNA2* gene (OMIM*601810). These diseases follow autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.

This variant has been identified in the sample of their index female child, Baby. ZZZ in heterozygous state.

***FIG4*: c.2247dupC**

Variant summary: A heterozygous single base pair insertion in exon 20 of the *FLG* gene (chr6:g.109791437insC, NM_014845.6, Depth:83x) that results in a frameshift and premature truncation of the protein 10 amino acids downstream to codon 750(p.Ser750GlnfsTer10) was detected. This variant is a frameshift variant which occurs in an exon of *FLG* upstream where nonsense mediated decay is predicted to occur. This variant is predicted to cause loss of normal protein function through protein truncation.

Population frequency: This variant has a minor allele frequency of 0.0007% in gnomAD database and has not been reported in 1000 genomes databases.

Clinical and Literature evidence: This variant has been previously classified as pathogenic in ClinVar database [6]. This variant has been previously reported in patients affected with Charcot Marie Tooth (CMT) disease type 4J in compound heterozygous state [7].

***In-silico* prediction:** The *in-silico* predictions of the variant are damaging by MutationTaster2. The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: ?Polymicrogyria, bilateral temporooccipital (OMIM#612691) is caused by homozygous mutation in the *FIG4* gene (OMIM*609390). Charcot-Marie-Tooth disease, type 4J (OMIM#611228) is caused by compound heterozygous mutations in the *FIG4* gene (OMIM*609390).Yunis-Varon syndrome

(OMIM#216340) is caused by homozygous or compound heterozygous mutation in the *FIG4* gene (OMIM*609390). These diseases follow autosomal recessive pattern of inheritance [2]. Amyotrophic lateral sclerosis 11(OMIM#612577) is caused by heterozygous mutation in the *FIG4* gene (OMIM*609390). 120240). This disease follows autosomal dominant of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.

This variant has been identified in the sample of their index female child, Baby. ZZZ in heterozygous state.

GBE1: c.986A>G

Variant summary: A heterozygous missense variation in exon 7 of the *GBE1* gene (chr3:g.81642787T>C, NM_000158.4, Depth:69x) that results in the amino acid substitution of Cysteine for Tyrosine at codon 329 (p.Tyr329Cys) was detected.

Population frequency: This variant has minor allele frequency of 0.0526% in gnomAD database and has minor allele frequency of 0.02% in 1000 genomes databases.

Clinical and Literature evidence: This variant has been previously classified as Likely Pathogenic in ClinVar database [8]. This variant has been previously reported in patients affected with Retinoblastoma in homozygous state [9].

***In-silico* prediction:** The *in-silico* predictions of the variant are damaging by SIFT, PolyPhen-2 (HumDiv) and MutationTaster2. The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: Glycogen storage disease IV (OMIM#232500) and Polyglucosan body disease, adult form (OMIM#263570) are caused by homozygous or compound heterozygous mutation in the *GBE1* gene (OMIM*607839). These diseases follow autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.

This variant has been identified in the sample of their index female child, Baby. ZZZ in heterozygous state.

UCHL1: c.532C>T

Variant summary: A heterozygous stop gained variation in exon 8 of the *UCHL1* gene (chr4:g.41264108C>T, NM_004181.5, Depth:88x) that results in the premature truncation of the protein at codon 178 (p.Arg178Ter) was detected. This variant is a stop gained variant which occurs in an exon of *UCHL1* upstream where nonsense mediated decay is predicted to occur. This variant is predicted to cause loss of normal protein function through protein truncation.

Population frequency: This variant has not been reported in gnomAD database and 1000 genomes database.

Clinical and Literature evidence: This variant has been previously classified as pathogenic in ClinVar database [10]. This variant has been previously reported in patients affected with neurodegenerative disorder with spasticity, ataxia, neuropathy, and optic atrophy in heterozygous state [11].

***In-silico* prediction:** The *in-silico* predictions of the variant are deleterious by CADD. The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: {?Parkinson disease 5, susceptibility to} (OMIM#613643) is conferred by heterozygous mutation in the *UCHL1* gene (OMIM*191342). Spastic paraplegia 79A, autosomal dominant (OMIM#620221) is caused by heterozygous mutation in the *UCHL1* gene (OMIM*191342). These diseases follow autosomal dominant pattern of inheritance [2]. Spastic paraplegia 79B, autosomal recessive (OMIM#615491) is caused by homozygous or compound heterozygous mutation in the UCHL1 gene (OMIM*191342). This disease follows autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.
This variant has not been identified in the sample of their index female child, Baby. ZZZ.

***COL7A1*: c.5022_5030dup**

Variant summary: A heterozygous nine base pair insertion in exon 55 of the *COL7A1* gene (chr3:g.48580603ins, NM_000094.4, Depth:84x) that results in an inframe insertion at codon 1675-1677 (p. Gln1675_Asp1677dup) was detected.

Population frequency: This variant has a minor allele frequency of 0.011% in gnomAD database and has not been reported in 1000 genomes databases.

Clinical evidence: This variant has been previously classified as likely pathogenic in ClinVar database [12].

***In-silico* prediction:** The *in-silico* predictions of the variant are deleterious by MutationTaster2. The reference codon is conserved across mammals in PhyloP and GERP++ tools.

OMIM phenotype: Epidermolysis bullosa dystrophica inversa / Epidermolysis bullosa dystrophica, autosomal recessive / Epidermolysis bullosa dystrophica, localisata variant (OMIM#226600) are caused by homozygous or compound heterozygous mutation in the *COL7A1* gene (OMIM*120120). These diseases follow autosomal recessive pattern of inheritance [2]. Epidermolysis bullosa dystrophica, autosomal dominant (OMIM#131750) and Nail disorder, nonsyndromic congenital, 8 (OMIM#607523) are caused by heterozygous mutation in the *COL7A1* gene (OMIM*120120). Epidermolysis bullosa dystrophica, Bart type (OMIM#132000) results from mutation in the *COL7A1* gene (OMIM*120120). These diseases follow autosomal dominant pattern of inheritance [2]. Epidermolysis bullosa pruriginosa (OMIM#604129), Epidermolysis bullosa, pretibial (OMIM#131850) and Transient bullous of the newborn (OMIM#131705) are caused by heterozygous or compound heterozygous mutation in the *COL7A1* gene (OMIM*120120). These diseases follow both autosomal dominant and autosomal recessive pattern of inheritance [2].

Variant classification: Based on the evidence, this variant is classified as a likely pathogenic variant.

This variant has not been identified in the sample of their index female child, Baby. ZZZ.

Recommendations

- Alternative test is strongly recommended to rule out the deletion/duplication.
- Genetic counseling is recommended.

Methodology

DNA extracted from the blood was used to perform whole exome using a whole exome capture kit. The targeted libraries were sequenced to a targeted depth of 80 to 100X using Illumina sequencing platform. This kit has deep exonic coverage of all the coding regions including the difficult to cover regions. The sequences obtained are aligned to human reference genome (GRCh38.p13) using Sentieon aligner and analyzed using Sentieon for removing duplicates, recalibration and re-alignment of indels. Sentieon DNAscope has been used to call the variants. Detected variants were annotated and filtered using the VarSeq software with the workflow implementing the ACMG guidelines for variant classification. The variants were annotated using 1000 genomes(V2), gnomAD (v3.1.2,2.1.1), ClinVar, OMIM, dbSNP, NCBI RefSeq Genes. *In-silico* predictions of the variant was carried out using VS-SIFT, VS-PolyPhen2, PhyloP, GERP++, GeneSplicer, MaxEntScan, NNSplice, PWM Splice Predictor. Only non-synonymous and splice site variants found in the coding regions were used for clinical interpretation. Silent variations that do not result in any change in amino acid in the coding region are not reported.

Sequence data attributes

	Mr. XXX	**Mrs. YYY**
Total reads generated	9.59 Gb	7.39 Gb
Data ≥ Q30	96.89%	96.34%

Genetic test results are reported based on the recommendations of American College of Medical Genetics [1], as described below:

Classification	**Interpretation**
Pathogenic	A disease-causing variation in a gene which can explain the patients' symptoms has been detected. This usually means that a suspected disorder for which testing had been requested has been confirmed

Likely Pathogenic	A variant which is very likely to contribute to the development of disease however, the scientific evidence is currently insufficient to prove this conclusively. Additional evidence is expected to confirm this assertion of pathogenicity.
Variant of Uncertain Significance	A variant has been detected, but it is difficult to classify it as either pathogenic (disease causing) or benign (non- disease causing) based on current available scientific evidence. Further testing of the patient or family members as recommended by your clinician may be needed. It is probable that their significance can be assessed only with time, subject to availability of scientific evidence.

Disclaimer

- The classification of variants of unknown significance can change over time. Anderson Diagnostics and Labs cannot be held responsible for it.
- Intronic variants, UTR, Promoter region variants and CNV are not assessed using this assay.
- Certain genes may not be covered completely, and few mutations could be missed. Variants not detected by this assay may impact the phenotype.
- The variations have not been validated by Sanger sequencing.
- The above findings and result interpretation was done based on the clinical indication provided at the time of reporting.
- It is also possible that a pathogenic variant is present in a gene that was not selected for analysis and/or interpretation in cases where insufficient phenotypic information is available.
- Genes with pseudogenes, paralog genes and genes with low complexity may have decreased sensitivity and specificity of variant detection and interpretation due to inability of the data and analysis tools to unambiguously determine the origin of the sequence data in such regions.
- The variants of uncertain significance and variations with high minor allele frequencies which are likely to be benign will be given upon request.
- Incidental or secondary findings that meet the ACMG guidelines can be given upon request [13].

References

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This report has been reviewed and approved by:

			
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APPENDIX: Current gene list used for carrier screening of pathogenic and likely pathogenic variants:

AAAS,AARS2,ABAT,ABCA1,ABCA12,ABCA3,ABCA4,ABCB4,ABCC8,ABCD1,ABCD4,ABCG5,ABCG8,ACAD9,ACADS,ACADSB,ACADVL,ACAT1,ACD,ACKR1,ACO2,ACOX1,ACOX2,ACP2,ACP5,ACTA1,ADAMTS10,ADAMTSL2,ADAMTSL4,ADAR,ADAT3,ADCY6,ADD3,ADGRG6,ADGRV1,ADRB2,ADRB3,ADSL,AEBP1,AGA,AGBL5,AGPAT2,AGRP,AGT,AGTR1,AGXT,AGXT2,AHCY,AHI1,AHSG,AICDA,AIFM1,AIPL1,AIRE,AK1,AKR1C4,AKR1D1,ALAD,ALAS2,ALDH18A1,ALDH6A1,ALDOA,ALDOB,ALG1,ALG12,ALG2,ALG3,ALG9,ALMS1,ALOX12B,ALOXE3,ALPL,ALS2,ALX3,ALX4,AMACR,AMBN,AMHR2,AMMECR1,AMN,AMPD1,AMPD2,AMPD3,AMT,ANGPTL3,ANO10,ANO5,ANTXR1,ANTXR2,AP4B1,AP4E1,AP5Z1,APOC2,APOE,APRT,AQP2,AQP7,ARFGEF2,ARHGDIA,ARHGEF6,ARL2BP,ARL6,ARL6IP1,ASL,ASNS,ASPA,ASPM,ASS1,ATCAY,ATG5,ATIC,ATM,ATP2A1,ATP2B3,ATP6AP2,ATP6V0A2,ATP6V1A,ATP6V1B1,ATP7A,ATP8A2,ATPAF2,ATR,AURKC,AVPR2,B2M,B3GAT3,B4GALNT1,B4GALT1,B4GAT1,B9D1,B9D2,BANF1,BBIP1,BBS1,BBS10,BBS12,BBS2,BBS4,BBS5,BBS7,BCAP31,BCL10,BCS1L,BGN,BIN1,BLNK,BLOC1S3,BLVRA,BMP1,BMP2,BMPR1B,BPGM,BRAT1,BRF1,BSCL2,BSND,BTK,BVES,C12orf57,C12orf65,C19orf12,C1QA,C1QB,C1QC,C3,C8A,C8B,C8orf37,CA12,CA2,CA5A,CA8,CABP2,CABP4,CACNA1D,CACNA1F,CACNA2D4,CAD,CANT1,CAPN1,CARD11,CARD9,CARTPT,CASP14,CASQ2,CASR,CATSPER1,CAV3,CBX2,CCBE1,CCDC103,CCDC114,CCDC115,CCDC22,CCDC28B,CCDC65,CCDC8,CCDC88C,CCNO,CCT5,CD19,CD247,CD27,CD36,CD3D,CD3E,CD3G,CD40,CD40LG,CD46,CD79A,CD79B,CD8A,CDAN1,CDC6,CDH11,CDH3,CDHR1,CDK10,CDK5,CDK5RAP2,CDK6,CDSN,CEBPE,CENPF,CENPJ,CEP104,CEP152,CEP164,CEP19,CEP41,CEP57,CERS3,CFH,CFL2,CFP,CFTR,CHAT,CHIT1,CHKB,CHMP1A,CHRDL1,CHRM3,CHRNA1,CHRND,CHRNE,CHRNG,CHST14,CHST3,CHST6,CHST8,CIB2,CIDEC,CIITA,CIT,CKAP2L,CLCN1,CLCN4,CLCNKA,CLCNKB,CLDN1,CLDN14,CLDN16,CLDN19,CLIC2,CLMP,CLN8,CLP1,CLPB,CLPP,CLRN1,CNGA3,CNGB1,CNGB3,CNNM2,CNPY3,CNTN1,CNTN2,CNTNAP1,CNTNAP2,COASY,COG4,COG6,COL17A1,COL4A3,COL4A4,COL6A1,COL6A2,COL6A3,COL7A1,COL9A2,COLEC11,COLQ,COQ4,COQ6,COQ7,COQ9,COX10,COX14,COX20,COX4I2,COX6A1,COX6B1,COX8A,CPA6,CPLX1,CPN1,CPT1A,CPT2,CRADD,CRAT,CRB1,CRIPT,CRTAP,CRYAB,CRYBB1,CRYBB3,CSF2RB,CSF3R,CSTA,CSTB,CTC1,CTH,CTNNB1,CTNS,CTPS1,CTSA,CTSC,CTSD,CTSF,CTSK,CUBN,CUL7,CWF19L1,CYB5A,CYBA,CYBB,CYP11B1,CYP11B2,CYP17A1,CYP1B1,CYP24A1,CYP26C1,CYP27A1,CYP27B1,CYP2C19,CYP2D6,CYP2R1,CYP2U1,CYP4F22,CYP4V2,CYP7B1,D2HGDH,DAG1,DARS2,DBH,DBT,DCC,DCHS1,DCPS,DCTN1,DCXR,DDB2,DDC,DDHD1,DDHD2,DDOST,DDR2,DDRGK1,DDX11,DDX59,DES,DGKE,DGUOK,DHCR7,DHH,DHODH,DHTKD1,DIS3L2,DKC1,DLAT,DLEC1,DLG3,DLX5,DMD,DNA2,DNAAF1,DNAAF3,DNAH1,DNAH11,DNAI1,DNAJB13,DNAJB2,DNAJC19,DNAJC3,DNAJC6,DNAL4,DNASE1L3,DNM2,DNMT3B,DOCK2,DOK7,DOLK,DPAGT1,DPH1,DPM2,DPYD,DPYS,DRAM2,DRC1,DSC3,DSE,DSG1,DSG4,DSP,DST,DSTYK,DTNBP1,DUOXA2,DYSF,EBP,ECEL1,ECHS1,ECM1,EDAR,EDARADD,EDC3,EDN1,EDN3,EDNRB,EFEMP2,EGFR,EGR2,EIF2B1,EIF2B2,EIF2B3,EIF2B4,EIF2S3,EIF4A3,ELAC2,ELMO2,ELMOD3,ELOVL4,ELP2,EMC1,EMD,EMG1,EMP2,ENAM,ENO3,ENTPD1,EPCAM,EPG5,EPO,EPS8,EPS8L2,EPX,ERBB3,ERCC1,ERCC2,ERCC3,ERCC4,ERCC5,ERCC6,ERLIN1,ERLIN2,ESCO2,ESR1,ESRRB,ETFB,ETFDH,ETHE1,EVC2,EXOSC2,EXOSC3,EXOSC8,EXPH5,EXT1,EXT2,EXTL3,EYS,F12,F13A1,F13B,F2,F5,F7,F9,FA2H,FADD,FAH,FAM126A,FAM20A,FAM20C,FAN1,FANCI,FANCL,FAR1,FARS2,FASLG,FASTKD2,FAT4,FBP1,FBXL4,FBXO7,FCGR2A,FCGR3A,FCN3,FECH,FERMT1,FERMT3,FEZF1,FGA,FGB,FGD4,FGF16,FGF20,FGFR3,FH,FHL1,FIBP,FIG4,FKBP10,FKBP14,FKRP,FKTN,FLAD1,FLI1,FLNB,FLVCR1,FLVCR2,FMO3,FOLR1,FOXI1,FOXN1,FOXP3,FOXRED1,FRAS1,FREM1,FREM2,FRMPD4,FSHB,FSHR,FTL,FTSJ1,FUCA1,FUT1,FUT8,FXN,FYCO1,FZD6,G6PC,G6PC3,GAA,GAB1,GAD1,GALE,GALK1,GALNT3,GALT,GAMT,GAN,GATA1,GATA5,GBA2,GBE1,GCLC,GCNT2,GDAP1,GDF5,GDF6,GDF9,GEMIN4,GFI1B,GFM1,GFPT1,GGCX,GH1,GHRL,GHSR,GJA1,GJB2,GJB3,GJB6,GLB1,GLE1,GLI3,GLIS3,GLRA1,GLRB,GLUL,GLYCTK,GM2A,GMPPA,GMPPB,GNAT1,GNB3,GNB5,GNE,GNMT,GNPAT,GNPTAB,GNRH1,GNRHR,GNS,GORAB,GP9,GPC3,GPC6,GPD1,GPI,GPIHBP1,GPR179,GPR68,GPSM2,GPT2,GPX1,GRHL2,GRHPR,GRIA3,GRID2,GRIN1,GRIP1,GRM1,GRN,GRXCR1,GRXCR2,GSS,GSTZ1,GTPBP2,GTPBP3,GUCY2C,GUCY2D,GUF1,GULOP,GUSB,GYG1,GYS1,GYS2,H6PD,HADH,HADHA,HADHB,HAL,HAMP,HARS2,HAX1,HBB,HCFC1,HEPACAM,HERC1,HESX1,HEXB,HFE,HGD,HGF,HINT1,HK1,HMGCL,HMGCS2,HNF1A,HNMT,HOXA2,HOXB1,HPCA,HPD,HPGD,HPS1,HPS3,HPS4,HPS5,HPS6,HPSE2,HR,HSD17B3,HSD3B2,HSD3B7,HSPA9,HTRA2,HYAL1,HYLS1,IARS2,ICOS,IDS,IER3IP1,IFNAR2,IFNGR1,IFT140,IFT27,IFT43,IFT52,IGBP1,IGF1,IGF1R,IGHM,IGHMBP2,IGKC,IGLL1,IGSF1,IGSF3,IHH,IKBKB,IL10RA,IL10RB,IL11RA,IL12B,IL17RC,IL1RN,IL21R,IL2RA,IL2RG,IL36RN,IL7R,ILDR1,IMPG2,ING1,INPP5K,INS,INTU,INVS,IQCB1,IRF1,IRF7,IRF8,IRX5,ISCA2,ISCU,ISG15,ITGA2B,ITGA3,ITGA6,ITGA7,ITGB2,ITGB3,ITGB6,ITK,ITPA,ITPR3,IVD,IYD,JAGN1,JAK3,JAM3,JPH1,JUP,KANK2,KATNB1,KCNJ1,KCNJ10,KCNJ11,KCNJ13,KCNMA1,KCNV2,KCTD7,KERA,KHDC3L,KHK,KIAA0556,KIAA0753,KIF1A,KIF1C,KISS1,KISS1R,KIZ,KLC2,KLHDC8B,KLHL15,KLHL3,KLHL41,KLHL7,KLK4,KNG1,KPTN,KRAS,KRT1,KRT10,KRT14,KRT25,KRT5,KRT74,KRT83,KRT85,KY,KYNU,L1CAM,L2HGDH,LAMA1,LAMA2,LAMB1,LAMB2,LAMB3,LAMC2,LAMTOR2,LBR,LCK,LCT,LEMD2,LEP,LGI4,LHB,LHCGR,LHFPL5,LIG4,LIM2,LINS1,LIPC,LIPE,LIPH,LIPN,LIPT1,LMAN1,LMAN2L,LMF1,LMNA,LMOD3,LONP1,LPAR6,LPIN1,LPL,LRAT,LRBA,LRIG2,LRIT3,LRP2,LRPAP1,LRPPRC,LRRC6,LRSAM1,LRTOMT,LSS,LTBP2,LZTFL1,MAB21L2,MAD2L2,MAG,MAMLD1,MAN1B1,MAN2B1,MAOA,MAP3K8,MAPKBP1,MAPT,MARS2,MASP1,MAT1A,MBOAT7,MBTPS2,MC1R,MC2R,MC4R,MCCC1,MCEE,MCM5,MCM9,MECR,MED12,MED25,MEGF10,MEGF8,MEOX1,MET,METTL23,MFF,MFN2,MFRP,MFSD2A,MGAT2,MGME1,MGP,MID1,MID2,MITF,MKKS,MKS1,MLC1,MLPH,MMAA,MMACHC,MMADHC,MMP1,MMP2,MMP20,MOCOS,MOCS1,MOCS2,MOGS,MPDU1,MPDZ,MPI,MPL,MPLKIP,MPO,MPV17,MPZ,MRAP,MRPL3,MRPL44,MRPS16,MRPS2,MRPS22,MRPS34,MRPS7,MS4A1,MSH2,MSH3,MSH5,MSH6,MSMO1,MSN,MTFMT,MTHFD1,MTHFR,MTM1,MTMR2,MTPAP,MTR,MTRR,MTTP,MYH2,MYH7,MYL3,MYO18B,MYO1E,MYO7A,NAGA,NAGS,NANS,NARS2,NAT2,NBN,NCAPD2,NCAPH,NCF2,NCF4,NDE1,NDP,NDRG1,NDST1,NDUFA1,NDUFA10,NDUFA11,NDUFA12,NDUFA13,NDUFA2,NDUFA9,NDUFAF1,NDUFAF2,NDUFAF3,NDUFAF4,NDUFAF5,NDUFAF6,NDUFB11,NDUFB3,NDUFB9,NDUFS1,NDUFS2,NDUFS6,NDUFS8,NDUFV1,NDUFV2,NECAP1,NEFL,NEK8,NEK9,NEU1,NEUROG3,NGF,NGLY1,NHLRC1,NHP2,NIPAL4,NLRP1,NLRP7,NMNAT1,NOP10,NPC1,NPC2,NPHP1,NPHP4,NPHS1,NPHS2,NPPA,NPR2,NR0B2,NR1H4,NR2E3,NSDHL,NSUN2,NT5C3A,NT5E,NTHL1,NTRK1,NUP62,NUP93,NYX,OAT,OCA2,OGDH,OGT,OPA3,OPHN1,OPLAH,ORC1,ORC6,OSTM1,OTC,OTOF,OTOG,P2RY12,PADI3,PADI6,PAH,PAM16,PANK2,PAPSS2,PARK7,PAX3,PAX4,PAX7,PC,PCDH12,PCDH15,PCK1,PCK2,PCLO,PCNA,PCNT,PCSK1,PCYT1A,PDE6B,PDE6C,PDE6D,PDE6G,PDE6H,PDP1,PDSS2,PDX1,PEPD,PET100,PEX11B,PEX12,PEX13,PEX14,PEX16,PEX19,PEX2,PEX26,PEX3,PEX5,PEX6,PGAM2,PGAP1,PGAP2,PGAP3,PGK1,PGR,PHF6,PHGDH,PHKA1,PHKA2,PHKB,PHKG2,PHOX2A,PHYH,PIGC,PIGG,PIGL,PIGM,PIGO,PIGT,PIGV,PIGW,PIGY,PIH1D3,PIK3R1,PIK3R5,PKHD1,PKLR,PLA2G5,PLA2G6,PLA2G7,PLAA,PLCB1,PLCD1,PLCE1,PLCZ1,PLEKHG2,PLG,PLK4,PLOD1,PLOD3,PLP1,PMM2,PMP22,PMPCA,PNKP,PNLIP,PNP,PNPLA1,PNPLA2,PNPLA6,PNPLA8,PNPO,POC1B,POGLUT1,POLG,POLH,POLR1D,POLR3A,POLR3B,POMC,POMGNT1,POMGNT2,POMK,POMT1,POMT2,POP1,POR,POU3F4,PPARG,PPARGC1B,PPIB,PPP1R15B,PPP2R1B,PQBP1,PRDM5,PRDX1,PREPL,PRF1,PRG4,PRICKLE1,PRKACG,PRKRA,PRMT7,PROC,PROP1,PRPH,PRPH2,PRPS1,PRRX1,PRSS1,PRSS12,PRSS56,PRX,PSAP,PSAT1,PSMB4,PSMB8,PSMB9,PSMC3IP,PSPH,PTCH2,PTCHD1,PTGER2,PTH1R,PTPN14,PTPRF,PTRH2,PTS,PUS3,PYCR1,PYCR2,PYGL,PYGM,QDPR,RAB18,RAB23,RAB27A,RAB28,RAB33B,RAB39B,RAG1,RAG2,RAPSN,RARB,RASGRP2,RBBP8,RBCK1,RBM10,RBM8A,RBMX,RBP3,RBP4,RCBTB1,RD3,RDH11,RDH12,RDH5,RDX,REEP6,RELN,REN,RFT1,RFX5,RFX6,RFXAP,RHO,RIN2,RIPK4,

RIPPLY2,RLBP1,RLIM,RMRP,RNASEH1,RNASEH2A,RNASEH2C,RNASET2,RNF168,RNU4ATAC,ROBO3,ROM1,ROR2,RORC,RPE65,RPIA,RPL10,RS1,RSPH1,RSPH3,RSPO1,RSPO4,RSPRY1,RTEL1,RTN4IP1,RTTN,RUSC2,S1PR2,SACS,SAG,SALL2,SAMD9,SAMHD1,SAR1B,SARS2,SBDS,SBF2,SC5D,SCARB2,SCN4A,SCN5A,SCN9A,SCNN1A,SCNN1B,SCNN1G,SCO1,SCO2,SCYL1,SDHAF1,SDR9C7,SEC23B,SEC24D,SEMA4A,SEPSECS,SERAC1,SERPINA1,SERPINA6,SERPINB7,SERPINB8,SERPINC1,SERPINE1,SERPINF2,SERPING1,SERPINH1,SETX,SFRP4,SFTPB,SFXN4,SGCA,SGCD,SGCG,SGSH,SHPK,SIGMAR1,SIL1,SIM1,SIX6,SKIV2L,SLC10A2,SLC12A3,SLC12A5,SLC13A5,SLC16A1,SLC17A5,SLC18A3,SLC19A2,SLC1A1,SLC1A4,SLC22A12,SLC22A18,SLC22A5,SLC24A4,SLC24A5,SLC25A12,SLC25A13,SLC25A15,SLC25A19,SLC25A20,SLC25A22,SLC25A26,SLC25A32,SLC25A4,SLC25A46,SLC26A1,SLC26A2,SLC26A3,SLC26A4,SLC26A5,SLC29A3,SLC2A1,SLC2A10,SLC2A2,SLC2A9,SLC30A10,SLC33A1,SLC34A1,SLC34A2,SLC34A3,SLC35A1,SLC35C1,SLC36A2,SLC37A4,SLC38A8,SLC39A13,SLC39A4,SLC45A2,SLC46A1,SLC4A11,SLC4A4,SLC52A2,SLC52A3,SLC5A1,SLC5A2,SLC5A5,SLC5A7,SLC6A17,SLC6A19,SLC6A20,SLC6A3,SLC6A5,SLC6A9,SLC7A14,SLC7A7,SLC7A9,SLC9A1,SLITRK6,SLURP1,SLX4,SMARCAL1,SMG9,SMIM1,SMOC1,SMOC2,SMPD1,SNAI2,SNAP29,SNIP1,SNORD118,SNX10,SNX14,SOD1,SOHLH1,SOST,SP110,SPARC,SPATA16,SPATA5,SPG11,SPG21,SPINK1,SPINK5,SPINT2,SPR,SPRTN,SPTA1,SQSTM1,SRD5A2,SRD5A3,SSR4,STAC3,STAMBP,STAR,STAT2,STIL,STIM1,STRA6,STRADA,STT3A,STT3B,STUB1,STX11,SUFU,SULT2B1,SUMF1,SUN5,SUOX,SYCE1,SYNE4,SZT2,TAC3,TACO1,TACR3,TACSTD2,TAF13,TAF4B,TAF6,TANGO2,TAP1,TARS2,TAT,TAZ,TBC1D24,TBC1D7,TBCD,TBX15,TBX19,TBX21,TBX6,TCAP,TCHH,TCIRG1,TCN2,TCTN2,TCTN3,TDO2,TDP2,TDRD7,TEC,TECR,TECTA,TELO2,TEX14,TEX15,TF,TFAM,TFG,TFRC,TG,TGDS,TGFB1,TGM1,TGM3,TGM5,THOC6,THRB,TIA1,TICAM1,TIMM50,TIMM8A,TJP2,TK2,TLE6,TLR3,TMC1,TMC6,TMC8,TMEM107,TMEM126A,TMEM126B,TMEM138,TMEM216,TMEM237,TMPRSS3,TMPRSS6,TNFRSF10B,TNFRSF11B,TNFRSF13B,TNFSF11,TNIK,TNNI3,TOE1,TPI1,TPK1,TPMT,TPO,TPP1,TRAC,TRAF3IP1,TRAF3IP2,TRAIP,TRAPPC11,TRAPPC9,TREH,TREM2,TREX1,TRH,TRIM32,TRIM37,TRIP13,TRIP4,TRMT10A,TRMT10C,TRMT5,TSHB,TSHR,TSPAN7,TSPEAR,TSPYL1,TSR2,TTC25,TTC37,TTI2,TTLL5,TTPA,TUB,TUBA8,TUBB8,TUBGCP4,TUBGCP6,TUFM,TULP1,TWIST2,TXN2,TXNL4A,TXNRD2,TYK2,TYR,TYROBP,TYRP1,UBE3B,UCHL1,UCP1,UCP3,UGT1A1,UMPS,UNC80,UPB1,UQCC2,UQCC3,UQCRB,UQCRQ,UROC1,UROD,UROS,USB1,USH1C,USH1G,USH2A,USP27X,USP8,UVSSA,VAC14,VARS,VARS2,VDR,VHL,VIPAS39,VLDLR,VPS11,VPS33B,VPS37A,VPS53,VRK1,VWA3B,WARS2,WAS,WBP2,WDR19,WDR35,WDR45B,WDR62,WDR81,WFS1,WNK1,WNT10B,WNT3,WNT7A,WRAP53,WRN,WWOX,XDH,XPA,XPC,XPNPEP3,XRCC1,XRCC2,XRCC4,YARS2,YME1L1,YY1AP1,ZAP70,ZBTB16,ZBTB24,ZBTB42,ZC4H2,ZFYVE26,ZIC3,ZMPSTE24,ZMYND10,ZMYND15,ZNF335,ZNF408,ZNF423,ZNF469,ZNF513,ZP1,ABCB7,ACACA,AFP,ALG6,ANK3,ATP2B2,CC2D1A,CEP120,CEP83,COL4A6,DENND5A,DLD,DMXL2,DNM1L,FANCB,FANCC,GAS8,ITPR1,KDM5C,LAMA3,LOXHD1,LRP1,MED23,MYO3A,NBAS,NDUFS7,NKX32,PHF8,PIBF1,PLEC,SLC25A38,SYNJ1,TECPR2,TOR1AIP1,UBE2T,ADAMTS18,AK2,ARL13B,BRWD3,DOCK8,DYNC2H1,EIF2AK4,GLDN,GP1BA,GTF2E2,IFT172,IFT80,IL1RAPL1,JAK2,KIF4A,LRP4,LYST,MATN3,MMP21,MYPN,ORC4,PLCB4,POC1A,PTPRQ,SLC4A1,SLCO1B3,SPTBN2,TUSC3,UNG,USP9X,WDR34,ANO6,AP1S1,ARSB,ASAH1,BCKDHB,COG2,CP,CYP21A2,KIAA1109,KRT18,LAS1L,LHX3,LIFR,MAK,MARVELD2,MASP2,MUSK,MYO5A,NALCN,NEK1,NUP107,PAK3,PLOD2,PRKCD,SUCLG1,TBXAS1,TMEM231,TRIP11,VPS13A,WNT10A,AASS,ADA,CEP290,ERCC6L2,GSC,HSPD1,IL17RD,LAMC3,MLH1,SLCO2A1,SPEG,TMTC3,TRPM6,TTC21B,ABCB11,ATP6AP1,CENPE,CEP78,COL11A2,DCLRE1C,HES7,ITPR2,LIPA,MCM8,MUTYH,NADK2,NBEAL2,P3H2,PIK3CA,RAB3GAP2,SUCLA2,AFF2,ALDH1A3,AP3D1,ATP8B1,BRAF,COL11A1,COL18A1,FGG,IDUA,ITGB4,NPHP3,NRXN1,PNPT1,PRKDC,PTEN,RECQL4,SDHA,SEC23A,SI,SLC12A1,SLC25A1,TBC1D23,ADAM22,AGRN,ALDH7A1,ATRX,CASP8,FGF5,HEXA,IBA57,ITGA8,NR0B1,POF1B,SH3PXD2B,SH3TC2,SP7,ABCD3,ALDH4A1,AUH,CD81,INPP5E,MED17,MYO15A,PLEKHG5,SLC12A6,VPS13C,WNT1,ACADM,AR,DMP1,FGD1,GOSR2,IQCE,MDH2,MIPEP,PCCB,PROM1,PTPRO,SBF1,ACE,ATP13A2,COL27A1,DCDC2,DNAJC21,FANCD2,GHR,PXDN,SH2D1A,SLC24A1,SLC6A8,CNNM4,GCH1,GP6,KRT8,MMAB,NAA10,RBM28,STAG3,TNFRSF4,ATF6,COL25A1,DOCK6,HACE1,KIF14,LAT,MCM4,OTOGL,PUS1,SLC11A2,ST14,BRCA1,CC2D2A,CFI,DNAL1,GIPC3,HIBCH,KLKB1,MCCC2,OPA1,SCP2,SPAG1,TAPBP,TBCK,UBA1,UBA5,VPS13B,CLCF1,HFM1,MAGED2,OFD1,PTPN22,SIPA1L3,SLCO1B1,TALDO1,THOC2,UBE2A,AP3B1,COA6,HTT,PPT1,RP1,TRIT1,CEP135,DSC2,IL17RA,PIEZO1,RB1,SLC3A1,CFAP53,CFD,NEK2,SLC19A3,AP3B2,DHFR,DNAJC12,GPX4,ICK,LTBP4,SASS6,CRB2,GALC,PEX1,PFKM,POLA1,RMND1,TP53RK,VPS45,ARHGEF18,COL1A2,LDHA,UPF3B,ANOS1,ASPH,HOXC13,NIN,FMN2,GATM,GCDH,GLRX5,MANBA,RUBCN,SPG7,CARS2,CR2,FLNA,NSMCE2,TMEM199,WDR73,ERBB2,OCRL,RASSF1,CDH23,MERTK,ARNT2,PGM1,TAP2,UBR1,EPM2A,GK,SLC35D1,TERT,TMEM165,TMEM70,TSEN15,XIAP,F10,GATAD1,LCAT,PPA2,TMIE,TMPRSS15,FBXO31,INPPL1,TAF1,UQCRC2,ORAI1,EML1,HMX1,PIEZO2,XYLT2,DHCR24,HPRT1,RAX,CLCN2,DOCK7,KIF7,NAGLU,NDUFS3,PIGN,NUP155,PI4KA,SURF1,TTC7A,CYP2A6,RNF216,CHRNB1,NT5C2,PYROXD1,RAD51C,TRNT1,TENM3,CTDP1,ADAMTS13,NUS1,POU1F1,TBC1D20,AGL,NDUFS4,PAX1,SLC39A14,APOB,CPS1,HSPG2,REEP2,NME8,MYO5B,DDX3X,SERPINB6,MCPH1,TCTN1,CCDC174,LMBR1,DLL3,CAST,MEFV,BFSP1,LTBP3,SMARCD2,AMH,P3H1,SARDH,TRAPPC2,BRCA2,GPHN,PINK1,RAB3GAP1,RYR1,MSRB3,PIP5K1C,TMCO1,POLE,WDR60,CDCA7,FGF3,PTF1A,SYNE1,SDCCAG8,CLEC7A,FOXE1,PCBD1,TYMP,MECP2,C2,CEP63,LARP7,HELLS,TH,POLR1C,APC2,NNT,AFG3L2,ABCC2,POMP,TMEM67,CLCN5,SGCB,PGM3,ROGDI,TRMU,CCDC151,TTN,GALNS,EIF2AK3,PMS2,TTC19,PDHX,TRDN,ACER3,AIMP2,MYBPC1,ALDH5A1,VMA21,NFU1,CLIC5,TAF2,MCOLN1,FTCD,MPC1,INSR,LTC4S,DEAF1,ARHGEF9,SLC39A8,HLADQB1,TKT,BLM,PROS1,TSEN54,PKD1L1,CYC1,MME,TRIOBP,CPAMD8,CLN6,FANCE,IMPAD1,SOBP,BCAM,NEFH,PRDM8,GPR88,HLADQA1,NCAPD3,ABCC6,F8,TCTEX1D2,DHDDS,DMGDH,CUL4B,BCKDHA,ESPN,ENPP1,TECRL,FOXO1,EIF2B5,TRIM2,BUB1B,IFT122,VWF,CAPN3,LRP5,SYN1,AK7,SCARF2,CCDC88A,EDA,ARSA,PEX10,HSD17B4,MTO1,B4GALT7,LMNB2,CRBN,COA5,DGAT1,FANCA,TBCE,AGPS,CYB5R3,TSEN2,CHEK2,GJC2,SYT14,ANKLE2,BMPER,DYM,GCSH,LDLRAP1,AP1S2,CLN5,MYO6,DPY19L2,PTPRC,MALT1,TAPT1,DIAPH1,KIAA0586,WNT4,IL12RB1,AP4M1,ADAM17,CISD2,GP1BB,ADCY1,EPB41,STS,GRM6,CSPP1,TSFM,KCNQ1,COQ2,GNPTG,DCAF17,CDC45,EARS2,TFR2,TNNT1,CHSY1,FRMD4A,IGFBP7,PCCA,CD59,ERCC8,LMBRD1,GLDC,ADGRG1,SUGCT,GSR,WDR72,AGK,BOLA3,DUOX2,RPGRIP1L,CDT1,ACY1,ADAMTS2,SLC35A3,VAX1,XYLT1,TEX11,SCN1B,COL13A1,ST3GAL5,ST3GAL3,CDC14A,ADAMTS17,LARS2,B3GLCT,ALG8,PARN,GRIK2,ANKS6,MAGI2,ATAD3A,APTX,C2CD3,PEX7,RRM2B,GCK,GPNMB,ATP7B,ITCH,LYRM7,VPS33A,ZC3H14,EVC,AIMP1,MFSD8,RNASEH2B,MMP13,DPM1,NUBPL,ARMC4,IFNGR2,TPM3,TP53,TNFRSF13C,STAT1,TTC8,BBS9,KREMEN1,C15orf41,ARV1,PIGA,SLC9A3,GBA,EOGT,PDE10A,ALDH3A2,IFT81,RARS2,CD55,LIMS2,FTO,PHC1,ABHD5,B3GALNT2,CORO1A,GDF1,HLCS,PDZD7,ARX,ARG1,ATOH7,FBLN5,WDPCP,CRLF1,USP18,IMPA1,IFT74,MVK,RFXANK,SMS,ZNF141,CLN3,PRDM12,FRRS1L,SOX18,ETFA,MICU1,SDC3,COX15,PDSS1,KCNE1,DYNC2LI1,CERS1,NAT8L,HERC2,TNXB,AKR1C2,OTULIN,BLOC1S6,NEB,ATP6V1E1,RPGR,DNAAF5,FOXE3,AP4S1,ACAN,LIAS,BHLHA9,ASCC1,HGSNAT,CFHR3,HTRA1,MLYCD,ABHD12,OCLN,SDHD,TPRN,BTD,ADK,OTOA,HSD11B2,B3GALT6,TMLHE,HYDIN,CFHR1,OPN1LW