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Supplemental Data

Genomic Sequencing for Newborn Screening:

Results of the NC NEXUS Project

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Self-reported race and/or ethnicity	Percentage
White	66%
Black/African American	10%
Asian	5%
Asian and White	3%
White and Black/African American	3%
White and Native American	3%
White and other (unknown, or not reported, or Latino)	3%
Latina/Latino and Hispanic or Latino	2%
Not reported	2%
Adopted from China	1%
Asian and other	1%
Black/African American and Pacific Islander	1%

Self-reported completed education level	Percentage
Graduate degree (both parents)	26%
Graduate degree (one parent) and four years college (one parent)	20%
Four years college (one parent) and partial or two years college (one parent)	14%
Four years college (both parents)	8%
Graduate degree (one parent) and partial or two years college (one parent)	4%
Two or four years college (one parent) and high school/GED (one parent)	4%
High school or GED (both parents)	4%
High school or GED (mother reported only)	4%
Two years college (one parent) and partial college (one parent)	3%
Partial college (one parent) and high school/GED (one parent)	3%
Partial, two or 4 years of college (mother reported only)	3%
Graduate degree (mother reported only)	2%
Graduate degree (one parent) and high school/GED (one parent)	2%

Four years college (one parent) and completed trade school (one parent)	1%
Partial college (both parents)	1%
High school/GED (one parent) and less than high school (one parent)	1%

Table S1. Parents' self-reported demographics in the NC NEXUS study. The demographics were provided by both parents in the study, with the exception of nine individuals in the education level category (indicated by mother reported only). One participant in the NC NEXUS study was adopted from China (as indicated in the table); therefore, their adoptive parents did not report their self-identified race and/or ethnicity information. N=106 NC NEXUS study participants.

NC NEXUS participant	Childhood onset nonactionable category	Adult onset actionable category	Carrier list category	Gene (s)	Disease association with gene (disease inheritance)	Variant and (predicted protein change)	Zygosity in NC NEXUS participant
M001	negative	negative	positive for four variants (*HFE*, *CFTR*, *GUSB*, *AGK*; see gene column)	*HFE, CFTR, GUSB, AGK*	hemochromatosis (AR); cystic fibrosis (AR); mucopolysaccharidosis VII (AR); Sengers syndrome (AR)	*HFE* c.845G>A p.(Cys282Tyr); *CFTR* c.1521_1523del p.(Phe508del); *GUSB* c.1069C>T p.(Arg357*); *AGK* c.523_524del p.(Ile175fs)	heterozygous for all four variants listed in variant column
M002	not requested	negative	not requested	N/A	N/A	N/A	N/A
M003	negative	negative	positive for seven variants (*SIL1*, *CYP21A2*, *SLC26A4*, *SERPINA1*, *ACADM*, *HPS3*, *RNASEH2B*)	*SIL1*, *CYP21A2*, *SLC26A4*, *SERPINA1*, *ACADM*, *HPS3*, *RNASEH2B*	Marinesco-Sjogren syndrome (AR); 21-hydroxylase deficiency (AR); Pendred syndrome (AR); Alpha-1 antitrypsin deficiency (AR); Hermansky-Pudlak syndrome (AR), Aicardi-Goutières syndrome (AR)	*SIL1* c.645+2T>C p.(?); *CYP21A2* c.1360C>T p.(Pro454Ser); *SLC26A4* c.2015G>A p.(Gly672Glu); *SERPINA1* c.1096G>A p.(Glu366Lys); *ACADM* c.985A>G p.(Lys329Glu); *HPS3* c.1682_1683del p.(Cys561fs); *RNASEH2B* c.2T>C p.(Met1Thr)	heterozygous for all seven variants listed in variant column
M005	not requested	negative	positive-*RBM8A* and *HFE* variants	*RBM8A*, *HFE*	thrombocytopenia-absent radius (TAR) syndrome (AR); hemochromatosis (AR)	*RBM8A* n.500C>T c.-21G>A p.(?); *HFE* c.187C>G p.(His63Asp)	heterozygous for both variants listed in variant column
M006	negative	negative	not requested	N/A	N/A	N/A	N/A
M007	negative	positive for *RAD51C* variant	positive for five variants (*RAD51C*, *SMARCAL1*, *TYR*, *SERPINA1*, *AARS2*)	*RAD51C, SMARCAL1, TYR, SERPINA1, AARS2*	ovarian cancer (AD); Fanconi anemia (AR); Schimke immune-osseous dysplasia (AR); Alpha 1 antitrypsin deficiency (AR); combined oxidative phosphorylation deficiency (AR)	*RAD51C* c.905-2_905-1del p.(?); *SMARCAL1* c.2542G>T p.(Glu848*); *TYR* c.1217C>T p.(Pro406Leu); *SERPINA1* c.1096G>A p.(Glu366Lys); *AARS2* c.2599-1G>A p.(?)	heterozygous for all five variants in variant column
M008	negative	negative	positive-*SERPINA1* variant	*SERPINA1*	alpha-1 antitrypsin deficiency (AR)	c.863A>T p.(Glu288Val)	homozygous

M009	negative	negative	positive-*G6PD* variants	*G6PD*	hemolytic anemia (XL)	c.292G>A p.(Val98Met); c.466A>G p.(Asn156Asp)	heterozygous for both *G6PD* variants
M011	negative	negative	positive-*RPE65* and *IDUA* variants	*RPE65*, *IDUA*	retinitis pigmentosa (AR); Leber congenital amaurosis (AR); mucopolysaccharidosis type I (AR)	*RPE65* c.271C>T p.(Arg91Trp); *IDUA* c.208C>T p.(Gln70*)	heterozygous for both variants in variant column
M013	negative	negative	positive for variants in *HFE*, *GALT*, *VWF*, *KIAA0586*, *ATP13A2*	*HFE*, *GALT*, *VWF*, *KIAA0586*, *ATP13A2*	hemochromatosis (AR); galactosemia (AR); von Willebrand disease type 2N (AR or AD); Joubert syndrome and/or short rib thoracic dysplasia with polydactyly (AR); Kufor-Rakeb syndrome and/or spastic paraplegia (AR)	*HFE* c.845G>A p.(Cys282Tyr); *GALT* c.378-27G>C, c.507+62G>A, c.508-24G>A, c.940A>G p.(Asn314Asp); *VWF* c.2561G>A p.(Arg854Gln); *KIAA0586* c.428del p.(Arg143fs); *ATP13A2* c.2135_2136del p.(Val712fs)	heterozygous for all variants listed in variant column
M014	negative	negative	positive-*WRN* variant	*WRN*	Werner syndrome (AR)	c.561A>G p.(Lys187fs)	heterozygous
M015	not requested	not requested	positive- *HFE* variant	*HFE*	hemochromatosis (AR)	c.187C>G p.(His63Asp)	heterozygous
M017	negative	negative	positive for variants in *HFE*, *PEX1*, *GALT*	*HFE*, *PEX1*, *GALT*	hemochromatosis (AR); Zellweger spectrum disorder (AR); galactosemia (AR)	*HFE* c.187C>G, p.(His63Asp); *PEX1* c.2614C>T p.(Arg872*); *GALT* c.378-27G>C, c.507+62G>A, c.508-24G>A, c.940A>G p.(Asn314Asp)	heterozygous for the *HFE* variant and *PEX1* variant; homozygous for *GALT* variants
HL001	negative	negative	positive- *HFE* and *PHYH* variants	*HFE, PHYH*	hemochromatosis (AR); Refsum disease (AR)	*HFE* c.187C>G p.(His63Asp); *PHYH* c.823C>T p.(Arg275Trp)	heterozygous for both variants in variant column
HL002	negative	negative	positive-*GNE* variant	*GNE*	Nonaka myopathy (AR)	c.1985C>T p.(Ala662Val)	heterozygous
HL004	not requested	negative	positive-*HFE* variant	*HFE*	hemochromatosis (AR)	c.187C>G p.(His63Asp)	heterozygous
HL006	negative	negative	positive-*RBM8A* and *MMAB* variants	*RBM8A*, *MMAB*	thrombocytopenia-absent radius syndrome (AR); methylmalonic acidemia (AR)	*RBM8A* n.500C>T c.-21G>A p.(?); *MMAB* c.556C>T p.(Arg186Trp)	heterozygous for both variants in variant column

HL007	negative	negative	positive-*GALT* and *F5* variants	*GALT*, *F5*	galactosemia (AR); Factor V deficiency (AR)	*GALT* c.563A>G p.(Gln188Arg); *F5* c.1601G>A p.(Arg534Gln)	heterozygous for both variants in variant column
HL008	negative	negative	positive-*SERPINA1* variant	*SERPINA1*	alpha-1 antitrypsin deficiency (AR)	c.863A>T p.(Glu288Val)	heterozygous
HL015	positive-*OCRL* variant	negative	negative	*OCRL*	Lowe syndrome (XL)	c.741G>A p.(Trp247*)	Hemizygous
HL016	negative	negative	positive-*MMACHC* variant	*MMACHC*	methylmalonic acidemia w/homocystinuria type cbIC (AR)	c.331C>T p.(Arg111*)	heterozygous
HL017	negative	negative	negative	N/A	N/A	N/A	N/A
HL019	negative	negative	negative	N/A	N/A	N/A	N/A
HL022	negative	negative	positive-*CYP21A2* and *APTX* variants	*CYP21A2*, *APTX*	21-hydroxylase deficiency (AR); ataxia w/oculomotor apraxia (AR)	*CYP21A2* c.1360C>T p.(Pro454Ser); *APTX* c.837G>A p.(Trp279*)	heterozygous for both variants in variant column
HL023	negative	negative	positive for variants in *IGHMBP2*, *G6PC*, *SERPINA1*, *NR2E3*, *HFE*, *GALT*	*IGHMBP2*, *G6PC*, *SERPINA1*, *NR2E3*, *HFE*, *GALT*	Charcot-Marie-Tooth disease axonal type 2S (AR); spinal muscular atrophy with respiratory distress (AR); glycogen storage disease type I (AR); alpha-1 antitrypsin deficiency (AR); retinitis pigmentosa (AR); enhanced S-cone syndrome (AR); hemochromatosis (AR); galactosemia (AR)	*IGHMBP2* c.1488C>A p.(Cys496*); *G6PC* c.562G>A p.(Gly188Ser); *SERPINA1* c.1096G>A p.(Glu366Lys); *NR2E3* c.932G>A p.(Arg311Gln); *HFE* c.845G>A p.(Cys282Tyr); *GALT* c.378-27G>C, c.507+62G>A, c.508-24G>A, c.940A>G p.(Asn314Asp)	heterozygous for all variants listed in variant column
HL025	negative	negative	positive-*IDUA* and *F5* variants	*IDUA*, *F5*	MPS I (AR); Factor V deficiency (AR)	*IDUA* c.979G>C p.(Ala327Pro); *F5* c.1601G>A p.(Arg534Gln)	heterozygous for both variants in variant column
HL027	negative	negative	positive for three variants (*GNRHR*, *ATP13A2*, *RBM8A*)	*GNRHR*, *ATP13A2*, *RBM8A*	Hypogonadotropic hypogonadism 7 w/or w/o anosmia (AR); Kufor-Rakeb syndrome and spastic paraplegia (both AR); thrombocytopenia absent radius (TAR) syndrome (AR)	*GNRHR* c.785G>A p.(Arg262Gln); *ATP13A2* c.558-1G>T p.(?); *RBM8A* n.500C>T c.-21G>A p.(?)	heterozygous for all three variants in variant column

HL028	negative	negative	positive-*SERPINA1* variant	*SERPINA1*	alpha-1 antitrypsin deficiency (AR)	*SERPINA1* c.1096G>A p.(Glu366Lys)	heterozygous
NB002	negative	negative	negative	N/A	N/A	N/A	N/A
NB003	negative	negative	positive-*HFE* variant	*HFE*	hemochromatosis (AR)	c.187C>G p.(His63Asp)	heterozygous
NB004	negative	negative	positive for 4 variants (*CFTR*, *POLG*, *SERPINA1*, *SLC7A9*)	*CFTR*, *POLG*, *SERPINA1*, *SLC7A9*	cystic fibrosis (AR); *POLG*-related spectrum disorders (AD or AR); alpha-1 antitrypsin deficiency (AR); cystinuria (AR)	*CFTR* c.1521_1523del p.(Phe508del); *POLG* c.1399G>A p.(Ala467Thr); *SERPINA1* c.863A>T p.(Glu288Val); *SLC7A9* c.544G>A p.(Ala182Thr)	heterozygous for all four variants in variant column
NB005	negative	negative	negative	N/A	N/A	N/A	N/A
NB007	not requested	negative	positive-*HFE* variant	*HFE*	hemochromatosis (AR)	c.187C>G p.(His63Asp)	heterozygous
NB008	negative	negative	positive-*ERCC6* and *G6PD* variants	*ERCC6, G6PD*	Cockayne syndrome (AR); hemolytic anemia (XL)	*ERCC6* c.3952_3953del p.(Arg1318fs); *G6PD* c.292G>A p.(Val98Met); c.466A>G p.(Asn156Asp)	heterozygous for all variants in variant column
NB011	negative	negative	negative	N/A	N/A	N/A	N/A
NB012	negative	negative	negative	N/A	N/A	N/A	N/A
NB013	negative	negative	positive for four variants (*ARMC4*, *PFKM*, *PMM2*, *CEP290*)	*ARMC4*, *PFKM*, *PMM2*, *CEP290*	Primary ciliary dyskinesia (AR); glycogen storage disease type VII (AR); congenital disorder of glycosylation, type Ia (AR); range of disorders, including Senior-Loken or Joubert syndrome (AR)	*ARMC4* c.2219G>A p.(Trp740*); *PFKM* c.496C>T p.(Arg166*); *PMM2* c.422G>A p.(Arg141His); *CEP290* c.4437+1G>A p.(?)	heterozygous for all four variants in variant column
NB015	negative	negative	positive for 4 variants in *GALT*	*GALT*	galactosemia (AR)	c.378-27G>C, c.507+62G>A, c.508-24G>A, c.940A>G p.(Asn314Asp). (These variants are associated with the Duarte 2 allele).	heterozygous for all variants in variant column
NB017	negative	negative	positive-*DYNC2H1* variant	*DYNC2H1*	short-rib thoracic dysplasia (AR)	c.8283del p.(Phe2761fs)	heterozygous
NB018	negative	negative	positive- *HFE* variant	*HFE*	hemochromatosis (AR)	c.845G>A p.(Cys282Tyr)	heterozygous

NB020	negative	negative	positive-*GAA* and *CDK5RAP2* variants	*GAA*, *CDK5RAP2*	glycogen storage disease type II (AR); primary microcephaly (AR)	*GAA* c.-32-13T>G p.(?); *CDKRAP2* c.4114C>T p.(Arg1372*)	heterozygous for both variants in variant column
NB025	negative	negative	positive-*HFE* variant	*HFE*	hemochromatosis (AR)	c.187C>G p.(His63Asp)	heterozygous
NB028	not requested	negative	not requested	N/A	N/A	N/A	N/A
NB031	negative	negative	positive-*MCCC1* variant	*MCCC1*	3-methylcrotonyl-coA carboxylase (3-MCC) deficiency (AR)	c.1483C>T p.(Gln495*)	heterozygous
NB033	negative	negative	positive for four variants (*SERPINA1*, *DARS2*, *MCPH1*, *HFE*)	*SERPINA1*, *DARS2*, *MCPH1*, *HFE*	alpha-1 antitrypsin deficiency (AR); leukoencephalopathy with brain stem and spinal cord involvement and lactate elevation (AR); primary microcephaly (AR); hemochromatosis (AR)	*SERPINA1* c.863A>T p.(Glu288Val); *DARS2* c.493-1G>C p.(?); *MCPH1* c.2214+2T>C p.(?); *HFE* c.187C>G p.(His63Asp)	heterozygous for all four variants in variant column
NB037	negative	negative	positive-*USH2A* and *DOCK8* variants	*USH2A*, *DOCK8*	Usher syndrome (AR); hyper-IgE recurrent infection syndrome (AR)	*USH2A* c.6937G>T p.(Gly2313Cys); *DOCK8* c.54-1G>T p.(?)	heterozygous for both variants in variant column
NB040	negative	positive, *BRCA2* variant	positive- *ASL* and *DNAH11* variants	*BRCA2* (adult onset category), *ASL* (carrier), *DNAH11* (carrier)	hereditary breast and ovarian cancer (AD); argininosuccinic aciduria (AR); primary ciliary dyskinesia (AR)	*BRCA2* c.7480C>T p.(Arg2494*); *ASL* c.544C>T p.(Arg182*); *DNAH11* c.6983+1G>A p.(?)	heterozygous for all variants in variant column
NB041	not requested	negative	positive-*GALT* variant	*GALT*	classical galactosemia (AR)	c.563A>G p.(Gln188Arg)	heterozygous
NB042	negative	not requested	not requested	N/A	N/A	N/A	N/A
NB043	negative	negative	positive for three variants (*BBS1*, *VWF*, *CD36*)	*BBS1*, *VWF*, *CD36*	Bardet-Biedl syndrome (AR); von Willebrand disease (AD or AR); platelet glycoprotein IV deficiency (AR)	*BBS1* c.1169T>G p.(Met390Arg); *VWF* c.2561G>A p.(Arg854Gln); *CD36* c.787_808del p.(Val263fs)	heterozygous for all three variants in variant column
NB044	negative	negative	negative	N/A	N/A	N/A	N/A
NB047	negative	negative	positive for three variants (*RBM8A*, *HFE*, *SERPINA1*)	*RBM8A*, *HFE*, *SERPINA1*	TAR syndrome (AR); hemochromatosis (AR); alpha-1 antitrypsin deficiency (AR)	*RBM8A* n.500C>T c.-21G>A p.(?); *HFE* c.187C>G p.(His63Asp); *SERPINA1* c.187C>T p.(Arg63Cys)	heterozygous for *RBM8A* variant and *SERPINA1* variant; homozygous for *HFE*

NB050	negative	negative	positive- *F7* and *HFE* variants	*F7*, *HFE*	Factor VII deficiency (AR); hemochromatosis (AR)	*F7* c.1151C>T p.(Thr384Met); *HFE* c.187C>G p.(His63Asp)	heterozygous for both variants in variant column
NB052	negative	negative	positive- *MPL* variant	*MPL*	congenital amegakaryocytic thrombocytopenia (AR)	c.1192del p.(Trp398fs)	heterozygous
NB053	not requested	negative	negative	N/A	N/A	N/A	N/A
NB055	negative	negative	positive for variants in *GALT*, *ATP7B* and *CFTR*	*GALT*, *ATP7B*, *CFTR*	galactosemia (AR); Wilson disease (AR); cystic fibrosis (AR)	*GALT* c.378-27G>C, c.507+62G>A, c.508-24G>A, c.940A>G p.(Asn314Asp); *ATP7B* c.1934T>G p.(Met645Arg); *CFTR* c.1519_1521del p.(Ile507del)	heterozygous for all variants in variant column
NB058	not requested	negative	positive- *GJB2* variant	*GJB2*	nonsyndromic hearing loss and deafness (AR)	c.101T>C p.(Met34Thr)	heterozygous
NB060	negative	negative	positive- *MYO3A* and *RBM8A* variants	*MYO3A*, *RBM8A*	sensorineural hearing loss/deafness (AR); TAR syndrome (AR)	*MYO3A* c.4681C>T p.(Arg1561*); *RBM8A* n.500C>T c.-21G>A p.(?)	heterozygous for both variants in variant column

Table S2: Additional findings in the NC NEXUS cohort.

The NC NEXUS participant column includes “M” (indicating inborn errors of metabolism cohort), “HL” (indicating hearing loss cohort) or “NB” (indicating healthy/well-child cohort) followed by the participant number. Each row in the table represents one NC NEXUS participant. “Positive” indicates the presence of likely pathogenic or pathogenic variants in genes in an additional findings category (childhood-onset nonactionable, adult-onset actionable, and carrier status). “Negative” indicates the absence of likely pathogenic or pathogenic variants found in genes in the additional findings categories. The “Gene” column indicates the gene(s) in which the additional finding variants were found (if requested). The “Variant and (predicted protein change)” column indicates the coding change in the DNA reference sequence and predicted change of the protein in parentheses. The “Zygosity in NC NEXUS participant” column indicates the zygosity for each variant found in additional findings for each participant (if requested). AR= autosomal recessive pattern of inheritance; N/A= not applicable; XL= X-linked pattern of inheritance; MPS I= mucopolysaccharidosis type I.

Gene	Refseq chromosome reference, Refseq transcript, variant	Chromosome coordinates of variant (hg38)	Canonical allele identifier from ClinGen Allele Registry	Accession number of variants in ClinVar
AARS2	NC_000006.12(NM_020745.3):c.2559-1G>A	chr6:44301465	CA364336148	VCV000873458
ACADM	NC_000001.11(NM_000016.5):c.199T>C	chr1:75732724	CA252836	VCV000003597
ACADM	NC_000001.11(NM_000016.5):c.799G>A	chr1:75749509	CA252824	VCV000003588
ACADM	NC_000001.11(NM_000016.5):c.985A>G	chr1:75761161	CA252821	VCV000003586
AGK	NC_000007.14(NM_018238.3):c.523_524del	chr7:141621734-141621735	CA834306559	VCV000873475
APTX	NC_000009.12(NM_001195248.1):c.837G>A	chr9:32974495	CA253152	VCV000004431
ARMC4	NC_000010.11(NM_018076.4):c.2219G>A	chr10:27936759	CA5453275	VCV000242859
ASL	NC_000007.14(NM_000048.3):c.544C>T	chr7:66086763	CA220291	VCV000092362
ATP13A2	NC_000001.11(NM_022089.3):c.558-1G>T	chr1:17002374	CA338260662	VCV000873473
ATP13A2	NC_000001.11(NM_022089.3):c.2135_2136del	chr1:16991849-16991850	CA915940655	VCV000873463
ATP7B	NC_000013.11(NM_000053.3):c.1934T>G	chr13:51961849	CA252899	VCV000003862
BBS1	NC_000011.10(NM_024649.4):c.1169T>G	chr11:66526181	CA223760	VCV000012143
BCKDHA	NC_000019.10(NM_000709.4):c.1312T>A	chr19:41424582	CA115507	VCV000100009
BRCA2	NC_000013.11(NM_000059.3):c.7480C>T	chr13:32356472	CA025108	VCV000038099
CD36	NC_000007.14(NM_001001547.2):c.787_808del	chr7:80669991-80670012	CA4315410	VCV000873470
CDK5RAP2	NC_000009.12(NM_001011649.2):c.4114C>T	chr9:120419851	CA5213660	VCV000873462
CEP290	NC_000012.12(NM_025114.3):c.4437+1G>A	chr12:88086038	CA6711940	VCV000285948
CEMIP/KIAA1199	NC_000015.10(NM_018689.2):c.58C>T	chr15:80873937	CA7692526	N/A
CFTR	NC_000007.14(NM_000492.3):c.1519_1521del	chr7:117559590-117559592	CA340628	VCV000007106
CFTR	NC_000007.14(NM_000492.3):c.1521_1523del	chr7:117559592-117559594	CA118639	VCV000007105
CYP21A2	NC_000006.12(NM_000500.7):c.1360C>T	chr6:32041006	CA341186	VCV000012159
DARS2	NC_000001.11(NM_018122.4):c.493-1G>C	chr1:173833375	CA1250153	VCV000873471
DNAH11	NC_000007.14(NM_001277115.1):c.6983+1G>A	chr7:21711861	CA4181054	VCV000873476
DOCK8	NC_000009.12(NM_203447.3):c.54-1G>T	chr9:271626	CA4957100	VCV000265359
DSC2	NC_000018.10(NM_024422.6):c.631-2A>G	chr18:31087815	CA022880	VCV000016850
DYNC2H1	NC_000011.10(NM_001080463.1):c.8283del	chr11:103203748	CA601231441	VCV000873461
ERCC6	NC_000010.11(NM_000124.3):c.3952_3953del	chr10:49461382-49461383	CA274713	VCV000190171
F5	NC_000001.11(NM_000130.4):c.1601G>A	chr1:169549811	CA114378	VCV000000642
F7	NC_000013.11(NM_000131.4):c.1151C>T	chr13:113118758	CA7060229	VCV000420160
F11	NC_000004.12(NM_000128.3):c.1489C>T	chr4:186286423	CA3164011	VCV000280137
F11	NC_000004.12(NM_000128.3):c.1608G>C	chr4:186287715	CA3164056	VCV000873465
G6PC	NC_000017.11(NM_000151.3):c.562G>A	chr17:42909418	CA321440	VCV000214465
G6PD	NC_000023.11(NM_000402.4):c.292G>A	chrX:154536002	CA090913	VCV000037123
G6PD	NC_000023.11(NM_000402.4):c.466A>G	chrX:154535277	CA120939	VCV000100055
GAA	NC_000017.11(NM_000152.4):c.-32-13T>G	chr17:80104542	CA116606	VCV000004027
GALT	NC_000009.12(NM_000155.3):c.940A>G	chr9:34649445	CA116380	VCV000003613
GALT	NC_000009.12(NM_000155.3):c.563A>G	chr9:34648170	CA312566	VCV000003614
GJB2	NC_000013.11(NM_004004.5):c.35del	chr13:20189552	CA127023	VCV000017004
GJB2	NC_000013.11(NM_004004.5):c.101T>C	chr13:20189481	CA172206	VCV000017000
GNE	NC_000009.12(NM_001128227.2):c.1985C>T	chr9:36218224	CA253717	VCV000006035
GNRHR	NC_000004.12(NM_000406.2):c.785G>A	chr4:67740682	CA130198	VCV000016024
GUSB	NC_000007.14(NM_000181.3):c.1069C>T	chr7:65974701	CA199717	VCV000000908
HFE	NC_000006.12(NM_000410.3):c.187C>G	chr6:26090951	CA113797	VCV000000010
HFE	NC_000006.12(NM_000410.3):c.845G>A	chr6:26092913	CA113795	VCV000000009

HPS3	NC_000003.12(NM_032383.4):c.1682_1683del	chr3:149157522-149157523	CA2660145	VCV000662551
IDUA	NC_000004.12(NM_000203.4):c.208C>T	chr4:987858	CA204563	VCV000011909
IDUA	NC_000004.12(NM_000203.4):c.979G>C	chr4:1002275	CA234128	VCV000167190
IGHMBP2	NC_000011.10(NM_002180.2):c.1488C>A	chr11:68933864	CA6153662	VCV000234316
KIAA0586	NC_000014.9(NM_001244189.1):c.428del	chr14:58432439	CA204046	VCV000204593
LDLR	NC_000019.10(NM_000527.4):c.502G>A	chr19:11105408	CA023709	VCV000183136
LOXHD1	NC_000018.10(NM_144612.6):c.2914G>A	chr18:46560230	CA8952596	VCV000228822
LOXHD1	NC_000018.10(NM_144612.6):c.3161C>T	chr18:46559503	CA8952552	VCV000873467
MARVELD2	NC_000005.10(NM_001038603.3):c.1183-1G>A	chr5:69432526	CA3294206	VCV000001195
MCCC1	NC_000003.12(NM_020166.4):c.1483C>T	chr3:183037329	CA355320552	VCV000873469
MCPH1	NC_000008.11(NM_024596.4):c.2214+2T>C	chr8:6499931	CA4610864	VCV000873472
MLYCD	NC_000016.10(NM_012213.3):c.1013T>C	chr16:83915020	CA8197484	VCV000432061
MMAB	NC_000012.12(NM_052845.3):c.556C>T	chr12:109561068	CA312714	VCV000003095
MMACHC	NC_000001.11(NM_015506.2):c.331C>T	chr1:45508266	CA251789	VCV000001424
MPL	NC_000001.11(NM_005373.2):c.1192del	chr1:43346818	CA915940656	VCV000873477
MYH14	NC_000019.10(NM_024729.3):c.5942G>C	chr19:50309744	CA406966312	VCV000873466
MYO3A	NC_000010.11(NM_017433.4):c.4681C>T	chr10:26203058	CA5445544	VCV000631635
MYO7A	NC_000011.10(NM_000260.4):c.5824G>A	chr11:77207370	CA132400	VCV000043299
NR2E3	NC_000015.10(NM_014249.3):c.932G>A	chr15:71813573	CA117575	VCV000005532
OCRL	NC_000023.11(NM_000276.3):c.741G>A	chrX:129560568	CA414551955	VCV000873459
OTC	NC_000023.11(NM_000531.6):c.1061T>G	chrX:38421078	CA224450	VCV000097104
PAH	NC_000012.12(NM_000277.2):c.117C>G	chr12:102912842	CA251537	VCV000000605
PAH	NC_000012.12(NM_000277.2):c.194T>C	chr12:102894893	CA251544	VCV000000636
PAH	NC_000012.12(NM_000277.2):c.284_286del	chr12:102894801-102894803	CA251535	VCV000000604
PAH	NC_000012.12(NM_000277.2):c.782G>A	chr12:102852875	CA251528	VCV000000582
PAH	NC_000012.12(NM_000277.2):c:814G>T	chr12:102852843	CA251532	VCV000000596
PAH	NC_000012.12(NM_000277.2):c.842C>T	chr12:102852815	CA220589	VCV000000589
PAH	NC_000012.12(NM_000277.2):c.896T>G	chr12:102851703	CA251541	VCV000000613
PAH	NC_000012.12(NM_000277.2):c.1222C>T	chr12:102840493	CA251523	VCV000000577
PAH	NC_000012.12(NM_000277.2):c.1315+1G>A	chr12:102840399	CA251522	VCV000000576
PEX1	NC_000007.14(NM_000466.2):c.2614C>T	chr7:92499808	CA4341072	VCV000265395
PFKM	NC_000012.12(NM_001166686.1):c.496C>T	chr12:48132913	CA114806	VCV000001158
PHYH	NC_000010.11(NM_006214.3):c.823C>T	chr10:13283695	CA118904	VCV000007580
PMM2	NC_000016.10(NM_000303.2):c.422G>A	chr16:8811153	CA220621	VCV000007706
POLG	NC_000015.10(NM_002693.2):c.1399G>A	chr15:89327201	CA123140	VCV000013496
RAD51C	NC_000017.11(NM_058216.2):c.905-2_905-1del	chr17:58724038-58724039	CA166374	VCV000141768
RBM8A	NC_000001.11(NM_005105.5):c.-21G>A	chr1:145927447	CA249745	VCV000030464
RNASEH2B	NC_000013.11(NM_024570.3):c.2T>C	chr13:50910078	CA388258350	VCV000661979
RPE65	NC_000001.11(NM_000329.2):c.271C>T	chr1:68444858	CA226531	VCV000013115
SERPINA1	NC_000014.9(NM_000295.4):c.187C>T	chr14:94383051	CA325650	VCV000017974
SERPINA1	NC_000014.9(NM_000295.4):c.863A>T	chr14:94380925	CA127679	VCV000017969
SERPINA1	NC_000014.9(NM_000295.4):c.1096G>A	chr14:94378610	CA127676	VCV000017967
SIL1	NC_000005.10(NM_022464.4):c.645+2T>C	chr5:139026799	CA252368	VCV000002624
SLC22A5	NC_000005.10(NM_003060.4):c.506G>A	chr5:132384155	CA312938	VCV000006421
SLC26A4	NC_000007.14(NM_000441.1):c.2015G>A	chr7:107702038	CA261423	VCV000043532
SLC26A4	NC_000007.14(NM_000441.1):c.626G>T	chr7:107674970	CA253304	VCV000004821
SLC26A4	NC_000007.14(NM_000441.1):c.1151A>G	chr7:107690125	CA261398	VCV000004820
SLC7A9	NC_000019.10(NM_014270.4):c.544G>A	chr19:32862521	CA211245	VCV000005782
SMARCAL1	NC_000002.12(NM_014140.3):c.2542G>T	chr2:216478216	CA253017	VCV000004171
SOX10	NC_000022.11(NM_006941.3):c.482G>A	chr22:37978082	CA10228669	VCV000873468
TECTA	NC_000011.10(NM_005422.2):c.5597C>T	chr11:121168064	CA6327783	VCV000236058
TMPRSS3	NC_000021.9(NM_024022.2):c.208del	chr21:42389043	CA273243	VCV000165492
TMPRSS3	NC_000021.9(NM_024022.2):c.1151T>A	chr21:42376584	CA10042329	VCV000873474
TYR	NC_000011.10(NM_000372.4):c.1217C>T	chr11:89284805	CA227519	VCV000003777
USH2A	NC_000001.11(NM_206933.2):c.1256G>T	chr1:216324240	CA252239	VCV000002359
USH2A	NC_000001.11(NM_206933.2):c.2299del	chr1:216247095	CA252226	VCV000002351

USH2A	NC_000001.11(NM_206933.2):c.3686T>G	chr1:216199752	CA344867902	VCV000873464
USH2A	NC_000001.11(NM_206933.2):c.4338_4339del	chr1:216190280-216190281	CA252228	VCV000002353
USH2A	NC_000001.11(NM_206933.2):c.6937G>T	chr1:215970645	CA1394996	VCV000384319
VWF	NC_000012.12(NM_000552.4):c.2561G>A	chr12:6034812	CA114139	VCV000000296
WRN	NC_000008.11(NM_000553.5):c.561A>G	chr8:31067089	CA275342	VCV000198099

Table S3. Summary table of all variants reported in the NC NEXUS study.
Table contains columns describing: the gene in which each variant was found (represented by gene symbol); Refseq chromosome reference number, Refseq transcript number and variant; chromosome coordinates of each variant (hg38); the canonical allele identifier of each variant in the ClinGen Allele Registry; the variants' accession numbers in the ClinVar database.