



Next Generation Sequencing Service at SDGS

Table of Contents

Table of Contents	1
Testing Workflow	3
Library Preparation.....	3
Data Analysis	3
Post analysis.....	5
Confirmation of variants detected by NGS	5
Next Generation Sequencing Panels.....	6
Inborn Errors of Metabolism	6
Glycogen Storage Diseases (GSDs)	6
Fatty Acid Metabolism Disorders.....	7
Peroxisomal Disorders.....	8
Hyperammonaemia / Urea Cycle Disorders.....	9
Rhabdomyolysis / Metabolic Myopathies	10
Cystic fibrosis (newborn screening pilot study).....	11
Familial Hypercholesterolemia panel	11
IEM-mini panel	11
Connective Tissue Disorders	12
Ehlers Danlos Syndrome (EDS).....	12
Familial Thoracic Aortic Aneurysm (FTAA) panel	12
Osteogenesis Imperfecta (OI) panels	13
Familial Porencephaly (FP) panel.....	13
Alport Syndrome (AP) panel.....	14
Bethlem Myopathy panel	14
Cutis Laxa (CL) panel	14
Stickler Syndrome panel.....	14
Hereditary Cancer Panels	15
Breast and Ovarian cancer genes	15
Colorectal Cancer gene panels (wet work in Leeds Central YNE GLH lab)	16
Renal Cancer gene Panel.....	16
Polycystic Disease Panels	18
Polycystic Kidney and Liver Disease	18
Autosomal Dominant Polycystic Kidney Disease – primary panel	18
Autosomal Recessive Polycystic Kidney Disease	18
Autosomal Dominant Polycystic Liver Disease.....	18
Autosomal Dominant Tubulointerstitial Kidney Disease (aka Medullary cystic & Glomerulocystic kidney disease)	18
Polycystic Kidney and Liver Disease full panel.....	18
Neurogenetic Disorders.....	20
Hereditary Spastic Paraparesis 88 gene panel	20
Spinal Muscular Atrophy 29 gene panel.....	22
Familial Amyotrophic Lateral Sclerosis with or without Frontotemporal Dementia 42 gene panel	24
Dementia 27 gene panel.....	25
Hereditary Dystonia 73 gene panel.....	27
Hereditary Parkinsonism 53 gene panel	29
Hereditary Chorea 30 gene panel.....	31
Abnormal Metal Transport 9 gene panel.....	32
Hemiplegic Migraine 10 gene panel.....	33

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 1 of 44	

Episodic Ataxia 11 gene panel	33
Hereditary Ataxia (Stage 1) 107 gene panel	34
Hereditary Ataxia (Stage 2) 54 gene panel	38
Haematology disorders	41
Bleeding & Thrombotic disorders.....	41
Bone Marrow Failure Disorders.....	41
Haems mini-panel.....	43
Oncology	44

Testing Workflow

Library Preparation

SureSelect/Illumina

- Shearing of genomic DNA using the Covaris E220 sonicator.
- End repair, A tailing and ligation of adaptors using SureSelectXT library system (Agilent Technologies).
- Enrichment by SureSelect target enrichment (Agilent Technologies) using custom in house designed probes. Samples have barcode tags added following target enrichment.
- Sequencing on the Illumina HiSeq using the HiSeq Rapid SBS Kit v2 performing 2 x 108 bp paired end reads.

SureSelect/Illumina lab work performed in Leeds (Central YNE GLH lab)

- Shearing of genomic DNA using the Covaris E220 sonicator.
- End repair, A tailing and ligation of adaptors using SureSelectXT library system (Agilent Technologies).
- Enrichment by SureSelect target enrichment (Agilent Technologies) using custom in house designed probes. Samples have barcode tags added following target enrichment.
- Sequencing on the Illumina NextSeq using the NextSeq 500/550 High Output Kit v2.5 (300 Cycles), performing paired 150bp reads.

AmpliSeq/Ion Torrent

- Generate amplicon libraries using Ion AmpliSeq (Thermo Fisher Scientific) primer pools, and add patient specific barcodes.
- Ion Chef System provides automated, high-throughput preparation of template-positive Ion Sphere Particles (ISPs) and Ion 520, 530 or 540 chip loading.
- Sequencing on the Ion S5 or S5 Prime system.

Data Analysis

- Based on the open source 'Best Practices' workflow by the Broad Institute (for additional information, see <http://www.broadinstitute.org/gatk/guide/best-practices>).
- BWA alignment of reads to human genome build hg19.
- Generation of depth of coverage reports. Checked using Alamut Visual (Interactive Biosoftware).
- For SureSelect/Illumina: a minimum threshold of 30-fold read depth is set for exonic sequences and intronic sequences up to and including 5 bp from exon. A minimum

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 3 of 44	

threshold of 18-fold read depth is set for intronic sequences from 6 bp to 25 bp from exon. For AmpliSeq/Ion Torrent minimum 50x for exonic regions and ± 5 bp into introns and minimum 30x for intronic regions between 6 and 25bp from exons.

- Identification of variants using HaplotypeCaller. Annotation from dbSNP and COSMIC (currently dbSNP150 and COSMIC v67 but updated with new releases)
- Variants filtered against in-house polymorphism lists and Best Practice Guidelines for the evaluation of pathogenicity and the reporting of sequence variants in clinical molecular genetics (Association for Clinical Genetic Science).
- Assessment of copy number variants using DeCON software

SureSelect/Illumina lab work performed in Leeds (Central YNE GLH lab)

- Samples are analysed using varDB, a tool for filtering variants designed, built, and maintained by Leeds Genetics Laboratory as part of the YNE GLH.
- Genes and transcripts of interest are applied to each Sample. Variants are filtered using the following criteria against annotations derived from Alamut Batch v1.9 (database version 2018-01-18):
 - In a Gene associated with the Sample.
 - In a Transcript associated with the Sample.
 - Does not have an artefact signature (relative to locally sequenced population).
 - Has a HGMD classification of DM or DM? (irrespective of population frequency)
 - Has an ExAC All or gnomAD All frequency less than 0.06.
 - For synonymous variants:
 - distNearestSS between -3 and 3
 - nearestSSChange less than -0.1
 - localSS_varMaxEntScore greater than 4.0
 - For intronic variants:
 - nearestSSChange less than -0.1
 - localSS_varMaxEntScore greater than 4.0
- Individual variant calls which pass filtering are then investigated further to check whether they are genuine variant calls.
- Genuine variant calls are then classified by Clinical Scientists according to the ACMG Variant Classification guidelines.

Post analysis

- Confirmation of clinically significant sequence variants by Sanger sequencing and/or MLPA as necessary (see below).
- Filling of gaps with low depth of coverage by Sanger sequencing as necessary. Gaps that fall within genes that have an individual whole gene sequencing service listed on the UKGTN service website as filled. The locations of all gaps that are not filled by Sanger sequencing are clearly indicated on the report.
- Creation of a diagnostic report combining clonal and Sanger sequence data that includes clinical interpretation of all the variants identified that are clearly pathogenic, likely to be pathogenic or have uncertain clinical significance.

Confirmation of variants detected by NGS

A risk assessment was carried out in June 2016 regarding the necessity for confirming variants identified by NGS using orthogonal technology (typically Sanger sequencing). The risk assessment was based on best practice guidelines, analysis of the quality of NGS data produced and the robustness of the tube transfer checking process within the laboratory.

The conclusion was: -

SDGS will no longer performs confirmation of single nucleotide substitution variants rated as class 3, 4 and 5, with a QUAL score of ≥ 3000 (and depth of coverage of $\geq 30x$ [$\geq 18x$ for -25_-6 and +6_+25]), when detected by SureSelect NGS workflows run on the MiSeq and HiSeq2500 platforms.

Exclusions to this include: -

- Indel variants - these are confirmed by Sanger sequencing, regardless of their QUAL score.
- Ampliseq/S5/S5Prime – all variants are confirmed by Sanger sequencing.
- Rare genes with highly homologous pseudogenes
- Somatic cancer panels

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 5 of 44	

Next Generation Sequencing Panels

Inborn Errors of Metabolism

(SureSelect Design ID: 0660881)

Glycogen Storage Diseases (GSDs)			
Condition	Gene	Subpanel(s)	Primary transcript
Glycogen storage disease III	<i>AGL</i>	Liver/Muscle/Heart	NM_000642.2
Glycogen storage disease XII	<i>ALDOA</i>	Muscle	NM_000034.3
Glycogen storage disease XIII	<i>ENO3</i>	Muscle	NM_001976.4
Epilepsy, progressive myoclonic 2A (Lafora)	<i>EPM2A</i>	Generalised	NM_005670.3
Fructose-1,6-bisphosphatase deficiency	<i>FBP1</i>	Liver	NM_000507.3
N/A - no mutations reported in gene to date	<i>FBP2</i>	Muscle	NM_003837.2
Glycogen storage disease Ia	<i>G6PC</i>	Liver	NM_000151.2
Glycogen storage disease II	<i>GAA</i>	Generalised/Muscle	NM_000152.3
Glycogen storage disease IV / Adult polyglucosan body disease	<i>GBE1</i>	Liver/Muscle/Heart	NM_000158.3
Glycogen storage disease XV	<i>GYG1</i>	Muscle/Heart	NM_004130.3
N/A - no mutations reported in gene to date	<i>GYG2</i>	Liver	NM_003918.2
Glycogen storage disease 0, muscle	<i>GYS1</i>	Muscle/Heart	NM_002103.4
Glycogen storage disease, type 0	<i>GYS2</i>	Liver	NM_021957.3
Danon disease	<i>LAMP2</i>	Generalised	NM_002294.2
Glycogen storage disease XI	<i>LDHA</i>	Muscle	NM_005566.3
Epilepsy, progressive myoclonic 2B (Lafora)	<i>NHLRC1</i>	Generalised	NM_198586.2
Hemolytic anaemia due to phosphofructokinase deficiency	<i>PFKL</i>	Liver	NM_002626.4
Glycogen storage disease VII	<i>PFKM</i>	Muscle	NM_00116686.1
Glycogen storage disease X	<i>PGAM2</i>	Muscle	NM_000290.3
Phosphoglycerate kinase 1 deficiency	<i>PGK1</i>	Muscle	NM_000291.3
GSD XIV, Phosphoglucomutase 1 deficiency	<i>PGM1</i>	Muscle	NM_002633.2
GSD Ixd; muscle phosphorylase kinase deficiency	<i>PHKA1</i>	Muscle	NM_002637.3
Glycogen storage disease IXa1; GSD9A1	<i>PHKA2</i>	Liver	NM_000292.2
Glycogen storage disease IXb; GSD9B	<i>PHKB</i>	Liver	NM_000293.2
N/A - no mutations reported in gene to date	<i>PHKG1</i>	Muscle	NM_006213.3
Glycogen storage disease IXc	<i>PHKG2</i>	Liver	NM_000294.2
Glycogen storage disease of heart, lethal congenital	<i>PRKAG2</i>	Heart	NM_016203.3
Glycogen storage disease VI	<i>PYGL</i>	Liver	NM_002863.4
Glycogen storage disease, type V; McArdle disease	<i>PYGM</i>	Muscle	NM_005609.2
RBCK1 deficiency	<i>RBCK1</i>	Muscle/Heart	NM_031229.2
Fanconi-Bickel syndrome	<i>SLC2A2</i>	Liver	NM_000340.1
Glycogen storage disease Ib / Ic	<i>SLC37A4</i>	Liver	NM_001164277.1

32 genes

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 6 of 44	

Fatty Acid Metabolism Disorders			
Condition	Gene	Subpanel(s)	Primary transcript
ACAD9 deficiency (complex I deficiency)	<i>ACAD9</i>	FAO	NM_014049.4
MCAD deficiency	<i>ACADM</i>	FAO	NM_000016.4
SCAD deficiency	<i>ACADS</i>	SCAD	NM_000017.2
VLCAD deficiency	<i>ACADVL</i>	FAO	NM_000018.2
Beta-ketothiolase deficiency	<i>ACAT1</i>	Ketolysis	NM_000019.3
CPTI deficiency	<i>CPT1A</i>	FAO	NM_001876.3
CPTI deficiency (muscle)	<i>CPT1B</i>	FAO	NM_004377.3
CPTII deficiency	<i>CPT2</i>	FAO	NM_000098.2
MADD	<i>ETFA</i>	FAO	NM_000126.3
MADD	<i>ETFB</i>	FAO	NM_001985.2
MADD (riboflavin-responsive)	<i>ETFDH</i>	FAO	NM_004453.2
HADH (SCHAD) deficiency	<i>HADH</i>	FAO	NM_001184705.2
Mitochondrial TFP deficiency	<i>HADHA</i>	FAO	NM_000182.4
Mitochondrial TFP deficiency	<i>HADHB</i>	FAO	NM_000183.2
Mitochondrial HMG-CoA lyase deficiency	<i>HMGCL</i>	FAO	NM_000191.2
Mitochondrial HMG-CoA synthase deficiency	<i>HMGCS2</i>	FAO	NM_005518.3
SCOT deficiency	<i>OXCT1</i>	Ketolysis	NM_000436.3
Systemic primary carnitine deficiency (carnitine transporter)	<i>SLC22A5</i>	FAO	NM_003060.3
CACT deficiency	<i>SLC25A20</i>	FAO	NM_000387.5
Riboflavin deficiency (RFVT1)	<i>SLC52A1</i>	FAO	NM_001104577.1
Brown-Vialetto-van Laere syndrome (RFVT2)	<i>SLC52A2</i>	FAO	NM_024531.4
Brown-Vialetto-van Laere syndrome (RFVT3)	<i>SLC52A3</i>	FAO	NM_033409.3

22 genes

FAO - Fatty acid oxidaton/ketogenesis

Ketolysis - Ketolysis

SCAD - Suspected SCAD (by specific request secondary to/combined with FAO panel)

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 7 of 44	

Peroxisomal Disorders		
Condition	Gene	Primary transcript
X-linked adrenoleukodystrophy	<i>ABCD1</i>	NM_000033.3
Peroxisomal Acyl-CoA oxidase deficiency	<i>ACOX1</i>	NM_004035.6
Rhizomelic chondrodysplasia punctata type 3 (RCDP3)	<i>AGPS</i>	NM_003659.3
Type I primary hyperoxaluria (HP1)	<i>AGXT</i>	NM_000030.2
Alpha-methylacyl-CoA racemase (AMACR) deficiency	<i>AMACR</i>	NM_014324.5
Encephalopathy, lethal, due to defective mitochondrial peroxisomal fission	<i>DNM1L</i>	NM_012062.4
Rhizomelic chondrodysplasia punctata type 2 (RCDP2) (DHAPAT deficiency)	<i>GNPAT</i>	NM_014236.3
D-Bifunctional protein deficiency	<i>HSD17B4</i>	NM_001199291.1
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX1</i>	NM_000466.2
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX2</i>	NM_000318.2
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX3</i>	NM_003630.2
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX5</i>	NM_001131023.1
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX6</i>	NM_000287.3
Rhizomelic chondrodysplasia punctata type 1 (RCDP1)	<i>PEX7</i>	NM_000288.3
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX10</i>	NM_002617.3
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX11B</i>	NM_003846.2
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX12</i>	NM_000286.2
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX13</i>	NM_002618.3
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX14</i>	NM_004565.2
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX16</i>	NM_004813.2
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX19</i>	NM_002857.3
Peroxisome Biogenesis Disorders, Zellweger Syndrome Spectrum	<i>PEX26</i>	NM_017929.5
Adult Refsum disease	<i>PHYH</i>	NM_006214.3
Leukoencephalopathy with dystonia and motor neuropathy	<i>SCP2</i>	NM_002979.4

24 genes

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 8 of 44	

Hyperammonaemia / Urea Cycle Disorders			
Condition	Gene	Subpanel(s)	Primary transcript
Arginase deficiency (hyperargininemia)	<i>ARG1</i>	UCD/Hyperamm	NM_000045.2
Argininosuccinic aciduria	<i>ASL</i>	UCD/Hyperamm	NM_000048.3
Citrullinemia type I	<i>ASS1</i>	UCD/Hyperamm	NM_000050.4
Carbamoylphosphate synthetase I (CPS1) deficiency	<i>CPS1</i>	CPS_NAGS/UCD/Hyperamm	NM_001875.3
Hyperinsulinism-hyperammonemia syndrome	<i>GLUD1</i>	Hyperamm	NM_005271.3
MMA (mutase)	<i>MUT</i>	Hyperamm	NM_000255.3
N-acetyl glutamate synthetase (NAGS) deficiency	<i>NAGS</i>	CPS_NAGS/UCD/Hyperamm	NM_153006.2
Ornithine aminotransferase (OAT) deficiency	<i>OAT</i>	Hyperamm	NM_000274.3
Ornithine transcarbamylase (OTC) deficiency	<i>OTC</i>	UCD/Hyperamm	NM_000531.5
PA	<i>PCCA</i>	Hyperamm	NM_000282.3
PA	<i>PCCB</i>	Hyperamm	NM_001178014.1
Citrullinaemia type 2 (citrin deficiency)	<i>SLC25A13</i>	UCD/Hyperamm	NM_014251.2
HHH syndrome	<i>SLC25A15</i>	UCD/Hyperamm	NM_014252.3
Lysinuric protein intolerance	<i>SLC7A7</i>	Hyperamm	NM_001126105.2

14 genes

CPS_NAGS - CPS1 and NAGS only

UCD - Urea cycle disorders

Hyperamm - Hyperammonaemia

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 9 of 44	

Rhabdomyolysis / Metabolic Myopathies			
Condition	Gene	Original panel	Primary transcript
very long-chain acyl-CoA dehydrogenase (VLCAD) deficiency	<i>ACADVL</i>	FAO	NM_000018.2
Glycogen storage disease III	<i>AGL</i>	GSD	NM_000642.2
Glycogen storage disease XII	<i>ALDOA</i>	GSD	NM_000034.2
Muscular dystrophy, limb-girdle, type IC; Myopathy, distal, Tateyama type; Rippling muscle disease	<i>CAV3</i>	Rhabdo	NM_001234.3
CARNITINE PALMITOYLTRANSFERASE I, MUSCLE	<i>CPT1B</i>	FAO	NM_004377.3
Carnitine palmitoyltransferase II (CPT II) deficiency	<i>CPT2</i>	FAO	NM_000098.2
Glycogen storage disease XIII	<i>ENO3</i>	GSD	NM_001976.4
MADD	<i>ETFAO</i>	FAO	NM_000126.3
MADD	<i>ETFB</i>	FAO	NM_001985.2
MADD (riboflavin-responsive)	<i>ETFDH</i>	FAO	NM_004453.2
N/A - no mutations reported to date	<i>FBP2</i>	GSD	NM_003837.2
Glycogen storage disease II	<i>GAA</i>	GSD	NM_000152.3
Glycogen storage disease IV / Polyglucosan body disease, adult form	<i>GBE1</i>	GSD	NM_000158.3
Glycogen storage disease XV	<i>GYG1</i>	GSD	NM_004130.3
Glycogen storage disease 0, muscle	<i>GYS1</i>	GSD	NM_002103.4
Mitochondrial TFP deficiency	<i>HADHA</i>	FAO	NM_000182.4
Mitochondrial TFP deficiency	<i>HADHB</i>	FAO	NM_000183.2
Hereditary myopathy with lactic acidosis	<i>ISCU</i>	Rhabdo	NM_213595.2
Glycogen storage disease XI	<i>LDHA</i>	GSD	NM_005566.3
Autosomal recessive recurrent acute myoglobinuria	<i>LPIN1</i>	Rhabdo	NM_145693.2
Glycogen storage disease VII	<i>PFKM</i>	GSD	NM_00116686.1
Glycogen storage disease X	<i>PGAM2</i>	GSD	NM_000290.3
Phosphoglycerate kinase 1 deficiency	<i>PGK1</i>	GSD	NM_000291.3
Glycogen storage disease XIV	<i>PGM1</i>	GSD	NM_002633.2
GSD Ixd; muscle phosphorylase kinase deficiency	<i>PHKA1</i>	GSD	NM_002637.3
	<i>PHKG1</i>	GSD	NM_006213.3
Glycogen storage disease, type V; McArdle disease	<i>PYGM</i>	GSD	NM_005609.2
RBCK1 deficiency	<i>RBCK1</i>	GSD	NM_031229.2
Central Core Disease	<i>RYR1</i>	Rhabdo	NM_000540.2
Systemic primary carnitine deficiency (carnitine transporter)	<i>SLC22A5</i>	FAO	NM_003060.3

30 genes

GSD - Glycogen Storage Diseases

FAO - Fatty Acid oxidaton/metbaolism disorders

Rhabdo - genes unique to rhabdomyolysis/metaboilc myopathies panel

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 10 of 44	

Cystic fibrosis (newborn screening pilot study)

(Ampliseq Design ID: CFTRexon!00Yp)

Condition	Gene	Subpanel(s)	Primary transcript
Cystic Fibrosis	<i>CFTR</i>	332 pathogenic variants from CFTR2 database	NM_000492.3

Familial Hypercholesterolemia panel

(wet work in Leeds Central YNE GLH lab – FH panel)

Condition	Gene	Primary transcript
Familial hypercholesterolaemia	LDLR	NM_000527.4
Autosomal dominant type B hypercholesterolaemia	APOB	NM_000384.2
Familial hypercholesterolaemia 3	PCSK9	NM_174936.3
Autosomal recessive hypercholesterolaemia	LDLRAP1	NM_015627.2

IEM-mini panel

(Ampliseq Design ID: WG_IAD162775_197)

Condition	Gene	Primary transcript
Wilson disease	ATP7B	NM_000053.3
Primary trimethylaminuria; fish odour syndrome	FMO3	NM_006894.5
GLUT1 deficiency syndrome	SLC2A1	NM_006516.2
Glycogen storage disease, type V; McArdle disease	PYGM	NM_005609.3
MCAD deficiency	ACADM	NM_000016.5
Glutaric acidaemia type I	GCDH	NM_000159.3
Hypophosphatasia	ALPL	NM_000478.5
CPTII deficiency	CPT2	NM_000098.2
VLCAD deficiency	ACADVL	NM_000018.2
Glycogen storage disease, type 0	GYS2	NM_021957.3
Glycogen storage disease II	GAA	NM_000152.4
Glycogen storage disease VII	PFKM	NM_00116686.1
Fructose-1,6-bisphosphatase deficiency	FBP1	NM_000507.3
Carbamoylphosphate synthetase I (CPS1) deficiency	CPS1	NM_001875.4
N-acetyl glutamate synthetase (NAGS) deficiency	NAGS	NM_153006.2
Argininosuccinic aciduria	ASL	NM_000048.3
Citrullinemia type I	ASS1	NM_000050.4
Androgen insensitivity syndrome	AR	NM_000044.3
X-linked adrenoleukodystrophy	ABCD1	NM_000033.3
Crigler-Najjar syndrome	UGT1A1	NM_000463.2

Connective Tissue Disorders

(SureSelect Design ID: 0782441).

Ehlers Danlos Syndrome (EDS)		
Subpanel	Gene	Primary transcript
Vascular	<i>COL3A1</i>	NM_000090.3
	<i>COL1A1</i>	NM_000088.3
Classical	<i>COL5A1</i>	NM_000093.3
	<i>COL5A2</i>	NM_000393.3
	<i>COL1A1</i>	NM_000088.3
Kyphoscoliotic	<i>B4GALNT7</i>	NM_007255.2
	<i>CHST14</i>	NM_130468.3
	<i>DSE</i>	NM_001080976
	<i>FKBP14</i>	NM_017946.2
	<i>PLOD2</i>	NM_000302.3
	<i>PRDM5</i>	NM_018699.2
	<i>RIN2</i>	NM_001242581.1
	<i>SLC39A13</i>	NM_001128225.2
	<i>ZNF469</i>	NM_00127464.1
	<i>TGFBR1</i>	NM_004612.2
	<i>TGFBR2</i>	NM_001024847.2
Dermatosparaxis	<i>ADAMTS2</i>	NM_014244.4
EDS-Arthrochalasic	<i>COL1A1</i> (Exons 6-10)	NM_000088.3
	<i>COL1A2</i> (Exons 6-10)	NM_000089.3
Classical-like EDS	<i>TNXB</i>	NM_019105.6

Familial Thoracic Aortic Aneurysm (FTAA) panel		
Condition	Gene	Primary transcript
FTAA	<i>ACTA2</i>	NM_001613.2
FTAA	<i>CBS</i>	NM_000071.2
FTAA	<i>COL1A1</i>	NM_000088.3
EDS-Vascular	<i>COL3A1</i>	NM_000090.3
Marfan's Syndrome	<i>FBN1</i>	NM_000138.4
Beal's Syndrome	<i>FBN2</i>	NM_001999.3
FTAA	<i>FLNA</i>	NM_001110556.1
FTAA	<i>GATA5</i>	NM_080473.4
FTAA	<i>MFAP5</i>	NM_003480.3
FTAA	<i>MYH11</i>	NM_002474.2
FTAA	<i>MYLK</i>	NM_053025.3
FTAA	<i>NOTCH1</i>	NM_017617.3

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 12 of 44	

FTAA	<i>PRKG1</i>	NM_006258.2
FTAA	<i>SKI</i>	NM_003036.3
FTAA	<i>SLC2A10</i>	NM_030777.3
FTAA	<i>SMAD3</i>	NM_005902.3
FTAA	<i>SMAD4</i>	NM_005359.3
FTAA	<i>TGFB2</i>	NM_001135599.2
FTAA	<i>TGFB3</i>	NM_003239.2
Loeys-Dietz Syndrome	<i>TGFBR1</i>	NM_004612.2
Loey's Dietz Syndrome/Marfan's syndrome	<i>TGFBR2</i>	NM_001024847.2
FTAA	<i>SLC2A10</i>	NM_000071.2

Osteogenesis Imperfecta (OI) panels		
Subpanels	Gene	Primary transcript
Dominant, Extended	<i>COL1A1</i>	NM_001025295.2
Dominant, Extended	<i>COL1A2</i>	NM_006129.4
Dominant	<i>IFITM5</i> (c.-14 only)	NM_001199.3
Recessive, Extended	<i>BMP1</i>	NM_052854.3
Recessive, Extended	<i>BMP1</i>	NM_006371.4
Recessive, Extended	<i>CREB3L1</i>	NM_021939.3
Recessive, Extended	<i>CRTAP</i>	NM_001025295.2
Recessive, Extended	<i>FKBP10</i>	NM_22356.3
Recessive, Extended	<i>IFITM5</i> full	NM_152860.1
Recessive, Extended	<i>LEPRE1</i> (P3H1)	NM_000918.2
Recessive, Extended	<i>OSX</i> (SP7)	NM_182943.2
Recessive, Extended	<i>P4HB</i>	NM_005032.6
Recessive, Extended	<i>PLOD2</i>	NM_000942.4
Recessive, Extended	<i>PLS3</i>	NM_014822.2
Recessive, Extended	<i>PPIB</i>	NM_000942.4
Recessive, Extended	<i>SEC24D</i>	NM_014822.2
Recessive, Extended	<i>SERPINF1</i>	NM_002615.5
Recessive, Extended	<i>SERPINH1</i>	NM_001235.2
Recessive, Extended	<i>SPARC</i>	NM_003118.3
Recessive, Extended	<i>TAPT1</i>	NM_153365.2
Recessive, Extended	<i>TMEM38B</i>	NM_018112.1
Recessive, Extended	<i>WNT1</i>	NM_005430.3
Recessive, Extended	<i>XYLT2</i>	NM_022167.3

Familial Porencephaly (FP) panel		
Condition	Gene	Primary transcript
Familial Porencephaly	<i>COL4A1</i>	NM_001845.4

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 13 of 44	

Familial Porencephaly	COL4A2	NM_001846.2
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Alport Syndrome (AP) panel		
Condition	Gene	Primary transcript
Alport Syndrome	COL4A3	NM_000091.4
Alport Syndrome	COL4A4	NM_000092.4
Alport Syndrome	COL4A5	NM_000495.3

Bethlem Myopathy panel		
Condition	Gene	Primary transcript
Bethlem Myopathy	COL6A1	NM_001848.2
Bethlem Myopathy	COL6A2	NM_001849.3
Bethlem Myopathy	COL6A3	NM_004369.3

Cutis Laxa (CL) panel		
Condition	Gene	Primary transcript
Cutis Laxa	ATP6V0A2	NM_012463.3
Cutis Laxa	ATP7A	NM_000052.4
Cutis Laxa	EFEMP2(FBLN4)	NM_016938.4
Cutis Laxa	ELN	NM_000501.2
Cutis Laxa	FBLN5	NM_006329.3
Cutis Laxa	LTBP4	NM_003573.2 (NG_021201.1)
Cutis Laxa	PYCR1	NM_006907.2

Stickler Syndrome panel		
Condition	Gene	Primary transcript
Stickler syndrome	COL11A1	NM_001854.3
Stickler syndrome	COL11A1	NM_080629.2
Stickler syndrome	COL11A2	NM_080680.2
Stickler syndrome	COL2A1	NM_001844.4
Stickler syndrome	COL9A1	NM_001851.4
Stickler syndrome	COL9A2	NM_001852.3
Stickler syndrome	COL9A3	NM_001853.3

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 14 of 44	

Hereditary Cancer Panels

Breast and Ovarian cancer genes (wet work in Leeds Central YNE GLH lab – Breast Ovarian Bowel BOB panel)			
Breast & Ovarian cancer – primary			
Condition	OMIM	Gene	Primary transcript
Breast-ovarian cancer, familial, 1	604370	<i>BRCA1</i>	NM_007294.3
Breast-ovarian cancer, familial, 2	612555	<i>BRCA2</i>	NM_000059.3
Breast cancer, susceptibility to	114480	<i>PALB2</i>	NM_024675.3
Li-Fraumeni Syndrome (optional)	151623	<i>TP53</i>	NM_000546.5
Ovarian cancer			
Breast-ovarian cancer, familial, 1	604370	<i>BRCA1</i>	NM_007294.3
Breast-ovarian cancer, familial, 2	612555	<i>BRCA2</i>	NM_000059.3
Breast cancer, susceptibility to	114480	<i>PALB2</i>	NM_024675.3
Breast cancer, early-onset	114480	<i>BRIP1</i>	NM_032043.2
Breast-ovarian cancer, familial, susceptibility to, 3	613399	<i>RAD51C</i>	NM_058216.2
Breast-ovarian cancer, familial, susceptibility to, 4	614291	<i>RAD51D</i>	NM_002878.3
Colorectal cancer, hereditary nonpolyposis, type 2	609310	<i>MLH1</i>	NM_000249.3
Colorectal cancer, hereditary nonpolyposis, type 1	120435	<i>MSH2</i>	NM_000251.2
Colorectal cancer, hereditary nonpolyposis, type 5	614350	<i>MSH6</i>	NM_000179.2
Colorectal cancer, hereditary nonpolyposis, type 4	614337	<i>PMS2</i>	NM_000535.5
Colorectal cancer, hereditary nonpolyposis, type 8	613244	<i>EPCAM</i>	NM_002354.2
Extended Breast & Ovarian cancer			
Breast-ovarian cancer, familial, 1	604370	<i>BRCA1</i>	NM_007294.3
Breast-ovarian cancer, familial, 2	612555	<i>BRCA2</i>	NM_000059.3
Breast cancer, susceptibility to	114480	<i>PALB2</i>	NM_024675.3
Li-Fraumeni Syndrome	151623	<i>TP53</i>	NM_000546.5
Breast cancer susceptibility	114480	<i>ATM</i>	NM_000051.3
Breast cancer, early-onset	114480	<i>BRIP1</i>	NM_032043.2
Breast-ovarian cancer, familial, susceptibility to, 3	613399	<i>RAD51C</i>	NM_058216.2
Breast-ovarian cancer, familial, susceptibility to, 4	614291	<i>RAD51D</i>	NM_002878.3
Breast cancer, lobular	114480	<i>CDH1</i>	NM_004360.4
Breast cancer, susceptibility to	114480	<i>CHEK2</i>	NM_007194.3
Cowden Syndrome	158350	<i>PTEN</i>	NM_000314.4
Peutz-Jeghers Syndrome	175200	<i>STK11</i>	NM_000455.4
Colorectal cancer, hereditary nonpolyposis, type 2	609310	<i>MLH1</i>	NM_000249.3
Colorectal cancer, hereditary nonpolyposis, type 1	120435	<i>MSH2</i>	NM_000251.2
Colorectal cancer, hereditary nonpolyposis, type 5	614350	<i>MSH6</i>	NM_000179.2
Colorectal cancer, hereditary nonpolyposis, type 4	614337	<i>PMS2</i>	NM_000535.5

Breast and Ovarian cancer genes (wet work in Leeds Central YNE GLH lab – Breast Ovarian Bowel BOB panel)**Breast & Ovarian cancer – primary**

Condition	OMIM	Gene	Primary transcript
Colorectal cancer, hereditary nonpolyposis, type 8	613244	<i>EPCAM</i>	NM_002354.2

Colorectal Cancer gene panels (wet work in Leeds Central YNE GLH lab – Breast Ovarian Bowel BOB panel)**Primary – HNPCC/Lynch syndrome**

Condition	OMIM	Gene	Primary transcript
Colorectal cancer, hereditary nonpolyposis, type 2	609310	<i>MLH1</i>	NM_000249.3
Colorectal cancer, hereditary nonpolyposis, type 1	120435	<i>MSH2</i>	NM_000251.2
Colorectal cancer, hereditary nonpolyposis, type 5	614350	<i>MSH6</i>	NM_000179.2
Colorectal cancer, hereditary nonpolyposis, type 4	614337	<i>PMS2</i>	NM_000535.5
Colorectal cancer, hereditary nonpolyposis, type 8	613244	<i>EPCAM</i>	NM_002354.2

Primary – FAP/MUTYH polyposis

Condition	OMIM	Gene	Primary transcript
Familial Adenomatous Polyposis	175100	<i>APC</i>	NM_000038.5
Colorectal cancer, hereditary nonpolyposis, type 1	120435	<i>MUTYH</i>	NM_001128425.1

Extended colorectal cancer panel

Condition	OMIM	Gene	Primary transcript
Familial Adenomatous Polyposis	175100	<i>APC</i>	NM_000038.5
Polyposis, juvenile intestinal	174900	<i>BMPR1A</i>	NM_004329.2
Colorectal cancer, hereditary nonpolyposis, type 2	609310	<i>MLH1</i>	NM_000249.3
Colorectal cancer, hereditary nonpolyposis, type 1	120435	<i>MSH2</i>	NM_000251.2
Colorectal cancer, hereditary nonpolyposis, type 5	614350	<i>MSH6</i>	NM_000179.2
Colorectal cancer, hereditary nonpolyposis, type 1	120435	<i>MUTYH</i>	NM_001128425.1
Colorectal cancer, hereditary nonpolyposis, type 4	614337	<i>PMS2</i>	NM_000535.5
Cowden Syndrome	158350	<i>PTEN</i>	NM_000314.4
Polyposis, juvenile intestinal	174900	<i>SMAD4</i>	NM_005359.5
Peutz-Jeghers Syndrome	175200	<i>STK11</i>	NM_000455.4
Colorectal cancer, susceptibility to, 10	612591	<i>POLD1</i>	NM_001308632.1
Colorectal cancer, susceptibility to, 12	615083	<i>POLE</i>	NM_006231.3
Colorectal cancer, hereditary nonpolyposis, type 8	613244	<i>EPCAM</i>	NM_002354.2

Renal Cancer gene Panel

Condition	OMIM	Gene	Primary transcript
Paragangliomas 4	115310	<i>SDHB</i>	NM_003000.2

Renal Cancer gene Panel			
Condition	OMIM	Gene	Primary transcript
Leiomyomatosis and renal cell cancer	150800	<i>FH</i>	NM_000143.3
von Hippel-Lindau syndrome	193300	<i>VHL</i>	NM_000551.2
Tumor predisposition syndrome	614327	<i>BAP1</i>	NM_004656.3
Melanoma, and renal cell carcinoma, susceptibility to, 8	614456	<i>MITF</i>	NM_000248.3
Renal cell carcinoma, papillary, 1, familial and somatic	605074	<i>MET</i>	NM_001127500.2
Tuberous sclerosis-1	191100	<i>TSC1</i>	NM_000368.4
Tuberous sclerosis-2	191092	<i>TSC2</i>	NM_000548.4
Cowden syndrome 1	158350	<i>PTEN</i>	NM_000314.4
Wilms tumor, type 1	194070	<i>WT1</i>	NM_024426.4
Birt-Hogg-Dube syndrome	135150	<i>FLCN</i>	NM_144997.6
Renal cell carcinoma	144700	<i>HNF1A</i>	NM_001306179.1

Polycystic Disease Panels

(SureSelect Design ID: 3144591).

Polycystic Kidney and Liver Disease			
Autosomal Dominant Polycystic Kidney Disease – primary panel			
Condition	OMIM	Gene	Primary transcript
Polycystic kidney disease 1	173900	<i>PKD1</i>	NM_001009944.2
Polycystic kidney disease 2	613095	<i>PKD2</i>	NM_000297.3
Autosomal Recessive Polycystic Kidney Disease			
Condition	OMIM	Gene	Primary transcript
Polycystic kidney disease 4	263200	<i>PKHD1</i>	NM_138694.3
Polycystic kidney disease 5	617610	<i>DZIP1L</i>	NM_173543.2
Autosomal Dominant Polycystic Liver Disease			
Condition	OMIM	Gene	Primary transcript
Polycystic liver disease 1	174050	<i>PRKCSH</i>	NM_002743.3
Polycystic liver disease 2	617004	<i>SEC63</i>	NM_007214.4
Polycystic liver disease 4 with or without kidney cysts	617875	<i>LRP5</i>	NM_002335.2
Polycystic kidney disease 3	600666	<i>GANAB</i>	NM_198335.3
Polycystic kidney disease 4, with hepatic disease	263200	<i>PKHD1</i>	NM_138694.3
Polycystic liver disease 3 with or without kidney cysts	617874	<i>ALG8</i>	NM_024079.4
Polycystic liver disease	609214	<i>SEC61B</i>	NM_006808.2
Polycystic kidney disease 6 with or without polycystic liver disease	618061	<i>DNAJB11</i>	NM_016306.5
Polycystic kidney disease 1	173900	<i>PKD1</i>	NM_001009944.2
Polycystic kidney disease 2	613095	<i>PKD2</i>	NM_000297.3
Autosomal Dominant Tubulointerstitial Kidney Disease (aka Medullary cystic & Glomerulocystic kidney disease)			
Condition	OMIM	Gene	Primary transcript
Hyperuricemic nephropathy, familial juvenile 2	613092	<i>REN</i>	NM_000537.3
Medullary cystic kidney disease 2	603860	<i>UMOD</i>	NM_003361.3
Renal cysts and diabetes syndrome	137920	<i>HNF1B</i>	NM_000458.3
Hyperuricemic nephropathy, familial juvenile, 4	617056	<i>SEC61A1</i>	NM_006808.2
Tuberous sclerosis-1	191100	<i>TSC1</i>	NM_000368.4
Tuberous sclerosis-2	191092	<i>TSC2</i>	NM_000548.4
Polycystic Kidney and Liver Disease full panel			
Condition	OMIM	Gene	Primary transcript
Polycystic kidney disease 1	173900	<i>PKD1</i>	NM_001009944.2
Polycystic kidney disease 2	613095	<i>PKD2</i>	NM_000297.3
Polycystic kidney disease 4, with hepatic disease	263200	<i>PKHD1</i>	NM_138694.3
Polycystic kidney disease 5	617610	<i>DZIP1L</i>	NM_173543.2

Polycystic Kidney and Liver Disease**Autosomal Dominant Polycystic Kidney Disease – primary panel**

Condition	OMIM	Gene	Primary transcript
Polycystic liver disease 1	174050	<i>PRKCSH</i>	NM_002743.3
Polycystic liver disease 2	617004	<i>SEC63</i>	NM_007214.4
Polycystic liver disease 4 with or without kidney cysts	617875	<i>LRP5</i>	NM_002335.2
Polycystic kidney disease 3	600666	<i>GANAB</i>	NM_198335.3
Polycystic liver disease 3 with or without kidney cysts	617874	<i>ALG8</i>	NM_024079.4
Polycystic liver disease	609214	<i>SEC61B</i>	NM_006808.2
Polycystic kidney disease 6 with or without polycystic liver disease	618061	<i>DNAJB11</i>	NM_016306.5
Hyperuricemic nephropathy, familial juvenile 2	613092	<i>REN</i>	NM_000537.3
Medullary cystic kidney disease 2	603860	<i>UMOD</i>	NM_003361.3
Renal cysts and diabetes syndrome	137920	<i>HNF1B</i>	NM_000458.3
Hyperuricemic nephropathy, familial juvenile, 4	617056	<i>SEC61A1</i>	NM_006808.2
Tuberous sclerosis-1	191100	<i>TSC1</i>	NM_000368.4
Tuberous sclerosis-2	191092	<i>TSC2</i>	NM_000548.4

Neurogenetic Disorders

Neurogenetic Motor Disorders

(SureSelect Design ID: 0836801).

Hereditary Spastic Paraparesis 88 gene panel			
Condition	OMIM	Gene	Primary transcript
Adrenoleukodystrophy, ALD	300100	<i>ABCD1</i>	NM_000033.3
Ataxia, spastic, 5, autosomal recessive, SPAX5	614487	<i>AFG3L2</i>	NM_006796.2
Spastic paraplegia 9A, autosomal dominant, SPG9A	601162	<i>ALDH18A1</i>	NM_002860.3
Spastic paralysis, infantile onset ascending, IAHS	607225	<i>ALS2</i>	NM_020919.3
Spastic paraplegia 63, SPG63	615686	<i>AMPD2</i>	NM_001257360.1
Pettigrew syndrome, PGS	304340	<i>AP1S2</i>	NM_001272071.1
Spastic paraplegia 47, autosomal recessive, SPG47	614066	<i>AP4B1</i>	NM_006594.4
Spastic paraplegia 51, autosomal recessive, SPG51	613744	<i>AP4E1</i>	NM_007347.4
Spastic paraplegia 50, autosomal recessive, SPG50	612936	<i>AP4M1</i>	NM_004722.3
Spastic paraplegia 52, autosomal recessive, SPG52	614067	<i>AP4S1</i>	NM_007077.4
Spastic paraplegia 48, autosomal recessive, SPG48	613647	<i>AP5Z1</i>	NM_014855.2
Argininemia	207800	<i>ARG1</i>	NM_001244438.1
Spastic paraplegia 61, autosomal recessive, SPG61	615685	<i>ARL6IP1</i>	NM_015161.2
Spastic paraplegia 66, SPG66		<i>ARSI</i>	NM_001012301.2
Spastic paraplegia 3A, autosomal dominant, SPG3A	182600	<i>ATL1</i>	NM_015915.4
Spastic paraplegia		<i>ATP2B4</i>	NM_001001396.2
Spastic paraplegia 26, autosomal recessive, SPG26	609195	<i>B4GALNT1</i>	NM_001478.4
Spastic paraplegia 17, autosomal dominant, SPG17	270685	<i>BSCL2</i>	NM_032667.6
Spastic paraplegia 55, autosomal recessive, SPG55	615035	<i>C12orf65</i>	NM_152269.4
Spastic paraplegia 43, autosomal recessive, SPG43	615043	<i>C19orf12</i>	NM_001031726.2
Neuropathy, hereditary sensory, with spastic paraplegia,	256840	<i>CCT5</i>	NM_012073.4
Spastic paraplegia 73, autosomal dominant, SPG73	616282	<i>CPT1C</i>	NM_001199752.2
Cerebrotendinous xanthomatosis, CTX	213700	<i>CYP27A1</i>	NM_000784.3
Spastic paraplegia 56, autosomal recessive, SPG56	615030	<i>CYP2U1</i>	NM_183075.2
Spastic paraplegia 5A, autosomal recessive, SPG5A	270800	<i>CYP7B1</i>	NM_004820.3
Spastic paraplegia 28, autosomal recessive, SPG28	609340	<i>DDHD1</i>	NM_001160148.1
Spastic paraplegia 54, autosomal recessive, SPG54	615033	<i>DDHD2</i>	NM_015214.2
Spastic paraplegia		<i>DNM2</i>	NM_001005360.2
Leukoencephalopathy with vanishing white matter, VWM	603896	<i>EIF2B5</i>	NM_003907.2
Spastic paraplegia 64, autosomal recessive, SPG64	615683	<i>ENTPD1</i>	NM_001164178.1
Spastic paraplegia 62, autosomal recessive, SPG62		<i>ERLIN1</i>	NM_001100626.1
Spastic paraplegia 18, autosomal recessive, SPG18	611225	<i>ERLIN2</i>	NM_007175.6
Spastic paraplegia 35, autosomal recessive, SPG35	612319	<i>FA2H</i>	NM_024306.4
Spastic paraplegia		<i>FARS2</i>	NM_006567.3

Hereditary Spastic Paraparesis 88 gene panel			
Condition	OMIM	Gene	Primary transcript
Amyotrophic lateral sclerosis 11, ALS11	612577	<i>FIG4</i>	NM_014845.5
Spastic paraplegia 68, SPG68		<i>FLRT1</i>	NM_013280.4
Cerebral palsy, spastic quadriplegic, 1, CPSQ1	603513	<i>GAD1</i>	NM_000817.2
Giant axonal neuropathy-1, GAN1	256850	<i>GAN</i>	NM_022041.3
Spastic paraplegia 46, autosomal recessive, SPG46	614409	<i>GBA2</i>	NM_020944.2
Spastic paraplegia		<i>GCH1</i>	NM_000161.2
Oculodentodigital dysplasia, ODDD	164200	<i>GJA1</i>	NM_000165.3
Spastic paraplegia 44, autosomal recessive, SPG44	613206	<i>GJC2</i>	NM_020435.3
Tay-Sachs disease, TSD	272800	<i>HEXA</i>	NM_000520.4
Spastic paraplegia 13, autosomal dominant, SPG13	605280	<i>HSPD1</i>	NM_002156.4
Spastic paraplegia 74, autosomal recessive, SPG74	616451	<i>IBA57</i>	NM_001010867.3
Mental retardation, X-linked, syndromic, Claes-Jensen type, MRXSCJ	300534	<i>KDM5C</i>	NM_004187.3
Spastic paraplegia 8, autosomal dominant, SPG8	603563	<i>KIAA0196</i>	NM_014846.3
Spastic paraplegia 30, autosomal recessive, SPG30	610357	<i>KIF1A</i>	NM_001244008.1
Spastic ataxia 2, autosomal recessive, SPAX2	611302	<i>KIF1C</i>	NM_006612.5
Spastic paraplegia 10, autosomal dominant, SPG10	604187	<i>KIF5A</i>	NM_004984.2
Spastic paraplegia		<i>KLC4</i>	NM_201523.2
MASA syndrome, MASA	303350	<i>L1CAM</i>	NM_000425.3
Spastic paraplegia		<i>LYST</i>	NM_000081.3
Spastic paraplegia		<i>MAG</i>	NM_002361.3
Spastic paraplegia 70, SPG70		<i>MARS</i>	NM_004990.3
Spastic ataxia 3, autosomal recessive, SPAX3	611390	<i>MARS2</i>	NM_138395.3
Spastic paraplegia		<i>MT-ATP6</i>	NC_012920.1
Ataxia, spastic, 4, SPAX4	613672	<i>MTPAP</i>	NM_018109.3
Spastic paraplegia 6, autosomal dominant, SPG6	600363	<i>NIPA1</i>	NM_144599.4
Spastic paraplegia 45, autosomal recessive, SPG45	613162	<i>NT5C2</i>	NM_012229.4
Spastic paraplegia 67, SPG67		<i>PGAP1</i>	NM_024989.3
Spastic paraplegia 2, X-linked, SPG2	312920	<i>PLP1</i>	NM_001128834.2
Spastic paraplegia 39, autosomal recessive, SPG39	612020	<i>PNPLA6</i>	NM_001166111.1
Alzheimer disease, type 3, with spastic paraparesis and apraxia, AD3	607822	<i>PSEN1</i>	NM_000021.3
Spastic paraplegia 69, SPG69		<i>RAB3GAP2</i>	NM_012414.3
Spastic paraplegia 31, autosomal dominant, SPG31	610250	<i>REEP1</i>	NM_001164730.1
Spastic paraplegia 72, autosomal recessive, SPG72	615625	<i>REEP2</i>	NM_001271803.1
Spastic paraplegia 12, autosomal dominant, SPG12	604805	<i>RTN2</i>	NM_005619.4
Spastic ataxia, Charlevoix-Saguenay type, SACS	270550	<i>SACS</i>	NM_014363.5
Amyotrophic lateral sclerosis 16, juvenile, ALS16	614373	<i>SIGMAR1</i>	NM_005866.3
Allan-Herndon-Dudley syndrome, AHDS	300523	<i>SLC16A2</i>	NM_006517.4
Dystonia 9, DYT9	601042	<i>SLC2A1</i>	NM_006516.2

Hereditary Spastic Paraparesis 88 gene panel			
Condition	OMIM	Gene	Primary transcript
Spastic paraplegia 42, autosomal dominant, SPG42	612539	<i>SLC33A1</i>	NM_001190992.1
Spastic paraplegia 4, autosomal dominant, SPG4	182601	<i>SPAST</i>	NM_014946.3
Spastic paraplegia 11, autosomal recessive, SPG11	604360	<i>SPG11</i>	NM_025137.3
Spastic paraplegia 20, autosomal recessive, SPG20	275900	<i>SPG20</i>	NM_015087.4
Mast syndrome	248900	<i>SPG21</i>	NM_016630.6
Spastic paraplegia 7, autosomal recessive, SPG7	607259	<i>SPG7</i>	NM_003119.3
Spastic paraplegia 49, autosomal recessive, SPG49	615031	<i>TECPR2</i>	NM_014844.3
Spastic paraplegia 57, autosomal recessive, SPG57	615658	<i>TFG</i>	NM_006070.5
Spastic paraplegia 59, autosomal recessive, SPG59		<i>USP8</i>	NM_005154.4
Spastic ataxia 1, autosomal dominant, SPAX1	108600	<i>VAMP1</i>	NM_014231.4
Spastic paraplegia 53, autosomal recessive, SPG53	614898	<i>VPS37A</i>	NM_152415.2
Neurodegeneration with brain iron accululation 5, NBIA5	300894	<i>WDR45</i>	NM_007075.3
Spastic paraplegia 60, autosomal recessive, SPG60		<i>WDR48</i>	NM_020839.3
Spastic paraplegia 71, SPG71		<i>ZFR</i>	NM_016107.3
Spastic paraplegia 15, autosomal recessive, SPG15	270700	<i>ZFYVE26</i>	NM_015346.3
Spastic paraplegia 33, autosomal dominant, SPG33	610244	<i>ZFYVE27</i>	NM_001002261.3

Spinal Muscular Atrophy 29 gene panel			
Condition	OMIM	Gene	Primary transcript
Charcot-Marie-Tooth disease, axonal, type 2N, CMT2N	613287	<i>AARS</i>	NM_001605.2
Spinal muscular atrophy with progressive myoclonic epilepsy, SMAPME	159950	<i>ASAH1</i>	NM_004315.4
Spinal muscular atrophy, distal, X-linked 3, SMAX3	300489	<i>ATP7A</i>	NM_000052.4
Spinal muscular atrophy, lower extremity-predominant, 2, AD, SMALED2	609797	<i>BICD2</i>	NM_001003800.1
Spastic paraplegia 17, autosomal dominant, SPG17	270685	<i>BSCL2</i>	NM_032667.6
Spinal muscular atrophy, Jokela type, SMAJ	615048	<i>CHCHD10</i>	NM_001301339.1
Neuropathy, distal hereditary motor, type VIIB, HMN7B	607641	<i>DCTN1</i>	NM_004082.4
Spinal muscular atrophy, distal, autosomal recessive, 5, DSMA5	614881	<i>DNAJB2</i>	NM_001039550.1
Spinal muscular atrophy, lower extremity-predominant 1, AD, SMALED1	158600	<i>DYNC1H1</i>	NM_001376.4
Pontocerebellar hypoplasia, type 1B, PCH1B	614678	<i>EXOSC3</i>	NM_016042.3
Pontocerebellar hypoplasia, type 1C, PCH1C	616081	<i>EXOSC8</i>	NM_181503.2
Neuronopathy, distal hereditary motor, type IID, HMN2D	615575	<i>FBXO38</i>	NM_030793.4
Neuropathy, distal hereditary motor, type VA, HMN5A	600794	<i>GARS</i>	NM_002047.2
Tay-Sachs disease, TSD	272800	<i>HEXA</i>	NM_000520.4
Neuropathy, distal hereditary motor, type IIB, HMN2B	608634	<i>HSPB1</i>	NM_001540.3
Neuronopathy, distal hereditary motor, type IIC, HMN2C	613376	<i>HSPB3</i>	NM_006308.2
Neuropathy, distal hereditary motor, type IIA, HMN2A	158590	<i>HSPB8</i>	NM_014365.2

Spinal Muscular Atrophy 29 gene panel			
Condition	OMIM	Gene	Primary transcript
Spinal muscular atrophy, distal, autosomal recessive, 1, DSMA1	604320	<i>IGHMBP2</i>	NM_002180.2
Spinal muscular atrophy		<i>LAS1L</i>	NM_031206.4
Spinal muscular atrophy, distal, autosomal recessive, 4, DSMA4	611067	<i>PLEKHG5</i>	NM_198681.3
Neuronopathy, distal hereditary motor, type VB, HMN5B	614751	<i>REEP1</i>	NM_001164730.1
Cardioencephalomyopathy, fatal infantile, due to cytochrome c oxidase deficiency 1, CEMCOX1	604377	<i>SCO2</i>	NM_005138.2
Spinal muscular atrophy, distal, autosomal recessive, 2, DSMA2	605726	<i>SIGMAR1</i>	NM_005866.3
Neuronopathy, distal hereditary motor, type VIIA, HMN7A	158580	<i>SLC5A7</i>	NM_021815.4
Spinal muscular atrophy-1, SMA1	253300	<i>SMN1</i>	NM_000344.3
Scapuloperoneal spinal muscular atrophy, SPSMA	181405	<i>TRPV4</i>	NM_021625.4
Spinal muscular atrophy, X-linked 2, infantile, SMAX2	301830	<i>UBA1</i>	NM_003334.3
Spinal muscular atrophy, late-onset, Finkel type, SMAFK	182980	<i>VAPB</i>	NM_004738.4
Pontocerebellar hypoplasia type 1A, PCH1A	607596	<i>VRK1</i>	NM_003384.2

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 23 of 44	

Neurodegenerative Disorders

(SureSelect Design ID: 0836801).

Familial Amyotrophic Lateral Sclerosis with or without Frontotemporal Dementia 42 gene panel			
Condition	OMIM	Gene	Primary transcript
Primary lateral sclerosis, juvenile, PLSJ	606353	<i>ALS2</i>	NM_020919.3
Amyotrophic lateral sclerosis 9, ALS9	611895	<i>ANG</i>	NM_001145.4
Familial Amyotrophic Lateral Sclerosis		<i>ANXA11</i>	NM_145869.1
Familial Amyotrophic Lateral Sclerosis		<i>ARHGEF28</i>	NM_001080479.2
Spinocerebellar ataxia 2, SCA2	183090	<i>ATXN2</i>	NM_002973.3
Frontotemporal dementia and/or amyotrophic lateral sclerosis 2, FTDALS2	615911	<i>CHCHD10</i>	NM_001301339.1
Amyotrophic lateral sclerosis 17, ALS17	614696	<i>CHMP2B</i>	NM_014043.3
Cerebrotendinous xanthomatosis, CTX	213700	<i>CYP27A1</i>	NM_000784.3
Familial Amyotrophic Lateral Sclerosis		<i>DAO</i>	NM_001917.4
Neuropathy, distal hereditary motor, type VIIB, HMN7B	607641	<i>DCTN1</i>	NM_004082.4
Amyotrophic lateral sclerosis 19, ALS19	615515	<i>ERBB4</i>	NM_005235.2
Familial Amyotrophic Lateral Sclerosis		<i>EWSR1</i>	NM_013986.3
Amyotrophic lateral sclerosis 11, ALS11	612577	<i>FIG4</i>	NM_014845.5
Amyotrophic lateral sclerosis 6, with or without frontotemporal dementia, ALS6	608030	<i>FUS</i>	NM_004960.3
Spastic paraplegia 46, autosomal recessive, SPG46	614409	<i>GBA2</i>	NM_020944.2
Frontotemporal lobar degeneration with TDP43 inclusions, GRN related,	607485	<i>GRN</i>	NM_002087.3
Amyotrophic lateral sclerosis 20, ALS20	615426	<i>HNRNPA1</i>	NM_031157.2
Inclusion body myopathy with early-onset Paget disease with or without frontotemporal dementia 2, IBMPFD2	615422	<i>HNRNPA2B1</i>	NM_031243.2
Frontotemporal Dementia, FTD	600274	<i>MAPT</i>	NM_005910.5
Amyotrophic lateral sclerosis 21, ALS21	606070	<i>MATR3</i>	NM_199189.2
Amyotrophic lateral sclerosis, susceptibility to, ALS1	105400	<i>NEFH</i>	NM_021076.3
Familial Amyotrophic Lateral Sclerosis		<i>NEK1</i>	NM_001199397.1
Amyotrophic lateral sclerosis 12, ALS12	613435	<i>OPTN</i>	NM_001008211.1
Amyotrophic lateral sclerosis 18, ALS18	614808	<i>PFN1</i>	NM_005022.3
Amyotrophic lateral sclerosis, susceptibility to, ALS1	105400	<i>PRPH</i>	NM_006262.3
Amyotrophic lateral sclerosis 4, juvenile, ALS4	602433	<i>SETX</i>	NM_015046.5
Amyotrophic lateral sclerosis 16, juvenile, ALS16	614373	<i>SIGMAR1</i>	NM_005866.3
Amyotrophic lateral sclerosis 1, ALS1	105400	<i>SOD1</i>	NM_000454.4
Spastic paraplegia 4, autosomal dominant, SPG4	182601	<i>SPAST</i>	NM_014946.3
Amyotrophic lateral sclerosis 5, juvenile, ALS5	602099	<i>SPG11</i>	NM_025137.3
Spastic paraplegia 20, autosomal recessive, SPG20	275900	<i>SPG20</i>	NM_015087.4
Frontotemporal dementia and/or amyotrophic lateral sclerosis 3, FTDALS3	616437	<i>SQSTM1</i>	NM_003900.4

Familial Amyotrophic Lateral Sclerosis with or without Frontotemporal Dementia 42 gene panel

Condition	OMIM	Gene	Primary transcript
Familial Amyotrophic Lateral Sclerosis		<i>SS18L1</i>	NM_198935.2
Familial Amyotrophic Lateral Sclerosis		<i>TAF15</i>	NM_139215.2
Amyotrophic lateral sclerosis 10, with or without FTD, ALS10	612069	<i>TARDBP</i>	NM_007375.3
Frontotemporal dementia and/or amyotrophic lateral sclerosis 4, FTDALS4	616439	<i>TBK1</i>	NM_013254.3
Amyotrophic lateral sclerosis 22 with or without frontotemporal dementia, ALS22	616208	<i>TUBA4A</i>	NM_006000.2
Amyotrophic lateral sclerosis 15, with or without frontotemporal dementia, ALS15	300857	<i>UBQLN2</i>	NM_013444.3
Amyotrophic lateral sclerosis 8, ALS8	608627	<i>VAPB</i>	NM_004738.4
Amyotrophic lateral sclerosis 14, with or without frontotemporal dementia, ALS14	613954	<i>VCP</i>	NM_007126.3
Familial Amyotrophic Lateral Sclerosis		<i>VPS54</i>	NM_016516.2
Pontocerebellar hypoplasia type 1A, PCH1A	607596	<i>VRK1</i>	NM_003384.2

Dementia 27 gene panel

Condition	OMIM	Gene	Primary transcript
Cerebral amyloid angiopathy, APP Related	605714	<i>APP</i>	NM_000484.3
Alzheimer disease 1, familial, AD	104300	<i>APP</i>	NM_000484.3
Frontotemporal dementia and/or amyotrophic lateral sclerosis 2, FTDALS2	615911	<i>CHCHD10</i>	NM_001301339.1
Frontotemporal Dementia, Chromosome 3-Linked, FTD3	600795	<i>CHMP2B</i>	NM_014043.3
Leukoencephalopathy, diffuse hereditary, with spheroids, HDLS	221820	<i>CSF1R</i>	NM_005211.3
Cerebrotendinous xanthomatosis, CTX	213700	<i>CYP27A1</i>	NM_000784.3
Perry syndrome	168605	<i>DCTN1</i>	NM_004082.4
Neuropathy, hereditary sensory, type IE, HSN1E	614116	<i>DNMT1</i>	NM_001130823.2
Amyotrophic lateral sclerosis 6, with or without frontotemporal dementia, ALS6	608030	<i>FUS</i>	NM_004960.3
Frontotemporal lobar degeneration with TDP43 inclusions, GRN related	607485	<i>GRN</i>	NM_002087.3
Inclusion body myopathy with early-onset Paget disease with or without frontotemporal dementia 2, IBMPFD2	615422	<i>HNRNPA2B1</i>	NM_031243.2
Cerebral arteriopathy, autosomal recessive, with subcortical infarcts and leukoencephalopathy, CARASIL	600142	<i>HTRA1</i>	NM_002775.4
Cerebral amyloid angiopathy, ITM2B-related, 1	176500	<i>ITM2B</i>	NM_021999.4
Frontotemporal Dementia, FTD	600274	<i>MAPT</i>	NM_005910.5
Amyotrophic lateral sclerosis 21, ALS21	606070	<i>MATR3</i>	NM_199189.2
Cerebral arteriopathy with subcortical infarcts and leukoencephalopathy, CADASIL	125310	<i>NOTCH3</i>	NM_000435.2
Gerstmann-Straussler disease, GSD	137440	<i>PRNP</i>	NM_000311.3
Alzheimer disease, type 3, AD3	607822	<i>PSEN1</i>	NM_000021.3
Alzheimer disease-4, AD4	606889	<i>PSEN2</i>	NM_000447.2

Dementia 27 gene panel			
Condition	OMIM	Gene	Primary transcript
Mast syndrome	248900	<i>SPG21</i>	NM_016630.6
Frontotemporal dementia and/or amyotrophic lateral sclerosis 3, FTDALS3	616437	<i>SQSTM1</i>	NM_003900.4
Amyotrophic lateral sclerosis 10, with or without FTD, ALS10	612069	<i>TARDBP</i>	NM_007375.3
Frontotemporal dementia and/or amyotrophic lateral sclerosis 4, FTDALS4	616439	<i>TBK1</i>	NM_013254.3
Polycystic lipomembranous osteodysplasia with sclerosing leukoencephalopathy, PLOSL	221770	<i>TREM2</i>	NM_018965.3
Amyotrophic lateral sclerosis 22 with or without frontotemoral dementia, ALS22	616208	<i>TUBA4A</i>	NM_006000.2
Polycystic lipomembranous osteodysplasia with sclerosing leukoencephalopathy, PLOSL	221770	<i>TYROBP</i>	NM_006000.2
Amyotrophic lateral sclerosis 15, with or without frontotemporal dementia, ALS15	300857	<i>UBQLN2</i>	NM_013444.3
Amyotrophic lateral sclerosis 14, with or without frontotemporal dementia, ALS14	613954	<i>VCP</i>	NM_007126.3

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 26 of 44	

Neurogenetic Movement Disorders

(SureSelect Design ID: 3156571)

Hereditary Dystonia 73 gene panel			
Condition	OMIM	Gene	Primary Transcript
Aicardi-Goutieres, AGS6	615010	<i>ADAR</i>	NM_001111.4
Dyschromatosis Symmetrica Hereditaria, DSH	127400	<i>ADAR</i>	NM_001111.4
Dyskinesia, Familial, With Facial Myokymia, FDFM	606703	<i>ADCY5</i>	NM_183357.2
Ataxia, Spastic, 5, Autosomal Recessive, SPAX5;	604581	<i>AFG3L2</i>	NM_006796.2
Spinocerebellar Ataxia 28, SCA28	610246	<i>AFG3L2</i>	NM_006796.2
Dystonia 24, DYT24	615034	<i>ANO3</i>	NM_031418.2
Ataxia, Early Onset, With Oculomotor Apraxia And Hypoalbuminemia, EAOH	606350	<i>APTX</i>	NM_175073.4
Spinocerebellar Ataxia, Autosomal Recessive 25, SCAR25	617584	<i>ATG5</i>	NM_004849.1
Ataxia-Telangiectasia, AT	208900	<i>ATM</i>	NM_000051.3
Cerebellar Ataxia, Areflexia, Pes Cavus, Optic Atrophy, And Sensorineural Hearing Loss, CAPOS	601338	<i>ATP1A3</i>	NM_152296.4
Dystonia 12, DYT12	128235	<i>ATP1A3</i>	NM_152296.4
Alternating Hemiplegia Of Childhood 2, AHC2	614820	<i>ATP1A3</i>	NM_152296.4
Kufor-Rakeb Syndrome, KRS	606693	<i>ATP13A2</i>	NM_022089.3
Wilson Disease, WD	606882	<i>ATP7B</i>	NM_000053.3
Neurodegeneration With Brain Iron Accumulation 4, SPG43 / NBIA4	614298	<i>C19orf12</i>	NM_001031726.3
Dystonia 23, DYT23	614860	<i>CACNA1B</i>	NM_000718.3
Mitochondrial Dna Depletion Syndrome 7 (Hepatocerebral Type), MTDPS7	271245	<i>CCNY</i>	NM_145012.5
Dystonia 23, DYT23	614860	<i>CIZ1</i>	NM_001257975.1
Frontotemporal Dementia, Chromosome 3-Linked; , FTD3	600795	<i>CHMP2B</i>	NM_014043.3
Coenzyme Q10 Deficiency, Primary, 5, COQ10D5	614654	<i>COQ9</i>	NM_020312.3
Neurodegeneration With Brain Iron Accumulation 6, NBIA6	615643	<i>COASY</i>	NM_025233.6
Aceruloplasminemia,	604290	<i>CP</i>	NM_000096.3
Myoclonic Epilepsy Of Unverricht And Lundborg	254800	<i>CSTB</i>	NM_000100.3
Spastic Paraplegia 56, Autosomal Recessive, SPG56	615030	<i>CYP2U1</i>	NM_183075.2
Cerebrotendinous Xanthomatosis; , CTX	606530	<i>CYP27A1</i>	NM_000784.3
Perry Syndrome,	168605	<i>DCTN1</i>	NM_004082.4
Woodhouse-Sakati Syndrome,	241080	<i>DCAF17</i>	NM_025000.3
Spastic Paraplegia 35, Autosomal Recessive, SPG35	612319	<i>FA2H</i>	NM_024306.4
Parkinson Disease 15, Autosomal Recessive Early-Onset, PARK15	260300	<i>FBX07</i>	NM_012179.3
Rett Syndrome, Congenital Variant,	613454	<i>FOXP1</i>	NM_005249.4
Neurodegeneration With Brain Iron Accumulation 3, NBIA3	606159	<i>FTL</i>	NM_000146.3

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 27 of 44	

Hereditary Dystonia 73 gene panel			
Condition	OMIM	Gene	Primary Transcript
Parkinson Disease, Late-Onset, PD	168600	<i>GBA</i>	NM_001005741.2
Dystonia, Dopa-Responsive, DRD	128230	<i>GCH1</i>	NM_000161.2
Dystonia 25, DYT25	615073	<i>GNAL</i>	NM_001142339.2
Neurodevelopmental Disorder With Involuntary Movements, NEDIM	617493	<i>GNAO1</i>	NM_020988.2
3-Methylglutaconic Aciduria, Type VIII, MGCA8	617248	<i>HTRA2</i>	NM_013247.4
Dystonia 28, Childhood-Onset, DYT28	617284	<i>KMT2B</i>	NM_014727.2
Dystonia, Childhood-Onset, With Optic Atrophy And Basal Ganglia Abnormalities, DYTOABG	617282	<i>MECR</i>	NM_016011.4
Niemann-Pick Disease, Type C1 Niemann-Pick Disease, Type D, Included, NPC1	257220	<i>NPC1</i>	NM_000271.4
Niemann-Pick Disease, Type C2, NPC2	607625	<i>NPC2</i>	NM_006432.3
Neurodegeneration With Brain Iron Accumulation 1, NBIA1	234200	<i>PANK2</i>	NM_153638.3
Hypoprebetalipoproteinemia, Acanthocytosis, Retinitis Pigmentosa, And Pallidal Degeneration	607236	<i>PANK2</i>	NM_153638.3
Parkinson Disease 2, Autosomal Recessive Juvenile, PARK2	600116	<i>PRKN</i>	NM_004562.2
Parkinson Disease 7, Autosomal Recessive Early-Onset, PARK7	606324	<i>PARK7</i>	NM_007262.4
Parkinson Disease 6, Autosomal Recessive Early-Onset, PARK6	605909	<i>PINK1</i>	NM_032409.2
Neurodegeneration With Brain Iron Accumulation 2b, NBIA2A/2B	610217	<i>PLA2G6</i>	NM_003560.3
Paroxysmal Nonkinesigenic Dyskinesia 1, PNKD1	118800	<i>PNKD</i>	NM_015488.4
Ataxia-Oculomotor Apraxia 4, AOA4	616267	<i>PNKP</i>	NM_007254.3
Spinocerebellar Ataxia 14, SCA14	605361	<i>PRKCG</i>	NM_002739.3
Dystonia 16, DYT16	612067	<i>PRKRA</i>	NM_003690.4
Episodic Kinesigenic Dyskinesia 1; EKD1 (Dystonia 10; DYT10)	614386	<i>PRRT2</i>	NM_145239.2
Microphthalmia, Syndromic 12, MCOPS12	615524	<i>RARB</i>	NM_000965.4
Lissencephaly 2; LIS2 And Myoclonus Dystonia, LIS2	257320	<i>RELN</i>	NM_005045.3
Epileptic Encephalopathy, Early Infantile, 6, EIEE6	607208	<i>SCN1A</i>	NM_001165963.1
Neonatal Epilepsy With Late-Onset Episodic Ataxia.,		<i>SCN2A</i>	NM_021007.2
Dystonia 11, Myoclonic, DYT11	159900	<i>SGCE</i>	NM_003919.2
Mental Retardation, X-Linked, Syndromic, Christianson Type, MRXSCH	300243	<i>SLC9A6</i>	NM_006359.2
Allan-Herndon-Dudley Syndrome, AHDS	300095	<i>SLC16A2</i>	NM_006517.4
Dystonia 9, DYT9	138140	<i>SLC2A1</i>	NM_006516.2
Hypermanesemia With Dystonia, Polycythemia, And Cirrhosis, HMDPC	613280	<i>SLC30A10</i>	NM_018713.2
Hypermanesemia With Dystonia 2, HMNDYT2	608736	<i>SLC39A14</i>	NM_015359.5
Parkinsonism-Dystonia, Infantile, PKDYS	613135	<i>SLC6A3</i>	NM_001044.4
Parkinson Disease 1, Autosomal Dominant, PARK1	168601	<i>SNCA</i>	NM_000345.3

Hereditary Dystonia 73 gene panel			
Condition	OMIM	Gene	Primary Transcript
Parkinson Disease 4, Autosomal Dominant, PARK4	605543	SNCA	NM_000345.3
Spastic Paraplegia 11, Autosomal Recessive, SPG11	604360	SPG11	NM_025137.1
Dystonia, Dopa-Responsive, Due To Sepiapterin Reductase Deficiency	612716	SPR	NM_003124.4
Mitochondrial Depletion Disorder		SUCLA2	NM_003850.2
Epileptic Encephalopathy, Early Infantile, 53, EIEE53	617389	SYNJ1	NM_003895.3
Dystonia 3, Torsion, X-Linked, DYT3	314250	TAF1	NM_004606.3
Segawa Syndrome, Autosomal Recessive	605407	TH	NM_199292.2
Dystonia 6, Torsion, DYT6	602629	THAP1	NM_018105.2
Dystonia 1, Torsion, Autosomal Dominant, DYT1	128100	TOR1A	NM_000113.2
Dystonia 4, Torsion, Autosomal Dominant, DYT4	128101	TUBB4A	NM_006087.3
Striatonigral Degeneration, Childhood-Onset, SNDC	617054	VAC14	NM_018052.4
Choreoacanthocytosis, CHAC	200150	VPS13A	NM_033305.2
Neurodegeneration With Brain Iron Accumulation 5, NBIA5	300894	WDR45	NM_007075.3
Galloway-Mowat Syndrome 1, GAMOS1	251300	WDR73	NM_032856.3
Basal Ganglia Calcification, Idiopathic, 6, IBGC6	616413	XPR1	NM_004736.3
Gabriele-De Vries Syndrome, GADEV5	617557	YY1	NM_003403.4

Hereditary Parkinsonism 53 gene panel			
Condition	OMIM	Gene	Primary Transcript
Dystonia 24, DYT24	615034	ANO3	NM_031418.2
Kufor-Rakeb Syndrome, KRS	606693	ATP13A2	NM_022089.3
Cerebellar Ataxia, Areflexia, Pes Cavus, Optic Atrophy, And Sensorineural Hearing Loss;, CAPOS	601338	ATP1A3	NM_152296.4
Neurodegeneration With Brain Iron Accumulation 4, SPG43 / NBIA4	614298	C19orf12	NM_001031726.3
Parkinson Disease 22, PARK22	616710	CHCHD2	NM_016139.3
Msa1, Susceptibility To, MSA1	146500	COQ2	NM_015697.7
Aceruloplasminemia	604290	CP	NM_000096.3
Leukoencephalopathy, Hereditary Diffuse, With Spheroids, HDLS	221820	CSF1R	NM_005211.3
Perry Syndrome	168605	DCTN1	NM_004082.4
Parkinson Disease 19, Juvenile-Onset, PARK19	615528	DNAJC6	NM_001256864.1
Parkinson Disease 21, PARK21	616361	DNAJC13	NM_015268.3
Parkinson Disease 15, Autosomal Recessive Early-Onset, PARK15	260300	FBX07	NM_012179.3
Neurodegeneration With Brain Iron Accumulation 3, NBIA3	606159	FTL	NM_000146.3

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 29 of 44	

Hereditary Parkinsonism 53 gene panel			
Condition	OMIM	Gene	Primary Transcript
Parkinson Disease, Late-Onset, PD	168600	<i>GBA</i>	NM_001005741.2
Dystonia, Dopa-Responsive, DRD	128230	<i>GCH1</i>	NM_000161.2
Frontotemporal Lobar Degeneration With TDP43 Inclusions, GRN-Related	607485	<i>GRN</i>	NM_002087.3
Tay-Sachs Disease, GM2-Gangliosidosis, Several Forms, TSD	272800	<i>HEXA</i>	NM_000520.5
Sandhoff Disease	268800	<i>HEXB</i>	NM_000521.3
Parkinson Disease 13, Autosomal Dominant, Susceptibility To, PARK13	610297	<i>HTRA2</i>	NM_013247.4
Parkinson Disease 8, Autosomal Dominant, PARK8	607060	<i>LRRK2</i>	NM_198578.3
Parkinson-Dementia Syndrome	260540	<i>MAPT</i>	NM_005910.5
Cerebral arteriopathy with subcortical infarcts and leukoencephalopathy 1		<i>NOTCH3</i>	NM_000435.2
3-Methylglutaconic Aciduria, Type III, MGCA3	258501	<i>OPA3</i>	NM_025136.3
Neurodegeneration With Brain Iron Accumulation 1, NBIA1	234200	<i>PANK2</i>	NM_153638.3
Hypoprebetalipoproteinemia, Acanthocytosis, Retinitis Pigmentosa, And Pallidal Degeneration,	607236	<i>PANK2</i>	NM_153638.3
Parkinson Disease 7, Autosomal Recessive Early-Onset, PARK7	606324	<i>PARK7</i>	NM_007262.4
Parkinson Disease 6, Autosomal Recessive Early-Onset, PARK6	605909	<i>PINK1</i>	NM_032409.2
Neurodegeneration With Brain Iron Accumulation 2b, NBIA2A/2B	610217	<i>PLA2G6</i>	NM_003560.3
Parkinson Disease 2, Autosomal Recessive Juvenile, PARK2	600116	<i>PRKN</i>	NM_004562.2
Dystonia 16	612067	<i>PRKRA</i>	NM_003690.4
Alzheimer Disease 3	607822	<i>PSEN1</i>	NM_000021.3
Alzheimer Disease 4	606889	<i>PSEN2</i>	NM_000447.2
Waisman Syndrome, WSMN	311510	<i>RAB39B</i>	NM_171998.3
Parkinsonism-Dystonia, Infantile, PKDYS	613135	<i>SLC6A3</i>	NM_001044.4
Basal Ganglia Calcification, Idiopathic, 1, IBGC1	213600	<i>SLC20A2</i>	NM_006749.4
Hypermanganesemia With Dystonia 1, HMNDYT1	613280	<i>SLC30A10</i>	NM_018713.2
Hypermanganesemia With Dystonia 2, HMNDYT2	608736	<i>SLC39A14</i>	NM_015359.5
Niemann-Pick Disease, Type B	607616	<i>SMPD1</i>	NM_000543.4
Niemann-Pick Disease, Type A	257200	<i>SMPD1</i>	NM_000543.4
Parkinson Disease 1, Autosomal Dominant, PARK1	168601	<i>SNCA</i>	NM_000345.3
Parkinson Disease 4, Autosomal Dominant, PARK4	605543	<i>SNCA</i>	NM_000345.3
Dementia, Lewy Body, DLB	127750	<i>SNCB</i>	NM_001001502.2
Juvenile Parkinsonism		<i>SPG11</i>	NM_025137.1
Dystonia, Dopa-Responsive, Due To Sepiapterin Reductase Deficiency	612716	<i>SPR</i>	NM_003124.4
Parkinson Disease 20, Early-Onset, PARK20	615530	<i>SYNJ1</i>	NM_003895.3

Hereditary Parkinsonism 53 gene panel			
Condition	OMIM	Gene	Primary Transcript
Dystonia 3, Torsion, X-Linked, DYT3	314250	<i>TAF1</i>	NM_004606.3
Segawa Syndrome, Autosomal Recessive	605407	<i>TH</i>	NM_199292.2
Dystonia 6, Torsion, DYT6	602629	<i>THAP1</i>	NM_018105.2
Dystonia 1, Torsion, Autosomal Dominant, DYT1	128100	<i>TOR1A</i>	NM_000113.2
Dystonia 4, Torsion, Autosomal Dominant, DYT4	128101	<i>TUBB4A</i>	NM_006087.3
Parkinson Disease Type 5, PARK5	613643	<i>UCHL1</i>	NM_004181.4
Parkinson Disease 23, Autosomal Recessive Early-Onset; PARK23, PARK23	616840	<i>VPS13C</i>	NM_020821.2
Chorea-Acanthocytosis, CHAC	200150	<i>VPS13A</i>	NM_033305.2
Parkinson Disease 17, PARK17	614203	<i>VPS35</i>	NM_018206.5
Neurodegeneration With Brain Iron Accumulation 5, NBIA5	300894	<i>WDR45</i>	NM_007075.3
Basal Ganglia Calcification, Idiopathic, 6, IBGC6	616413	<i>XPR1</i>	NM_004736.3

Hereditary Chorea 30 gene panel			
Condition	OMIM	Gene	Primary Transcript
Dyskinesia, Familial, With Facial Myokymia, FDFM	606703	<i>ADCY5</i>	NM_183357.2
Ataxia Telangiectasia, ATM	208900	<i>ATM</i>	NM_000051.3
Wilson Disease, WD	277900	<i>ATP7B</i>	NM_000053.3
Cerebellar Ataxia, Mental Retardation, And Dysequilibrium Syndrome 4, CAMRQ4	615268	<i>ATP8A2</i>	NM_016529.5
Aceruloplasminemia	604290	<i>CP</i>	NM_000096.3
Rett Syndrome, Congenital Variant	613454	<i>FOXP1</i>	NM_005249.4
Friedreich Ataxia 1, FRDA	229300	<i>FXN</i>	NM_000144.4
Gm2-Gangliosidosis, Ab Variant,	272750	<i>GM2A</i>	NM_000405.4
Neurodevelopmental Disorder With Involuntary Movements, NEDIM	617493	<i>GNAO1</i>	NM_020988.2
Chorea, Benign Hereditary, BHC	118700	<i>NKX2-1</i>	NM_001079668.2
3-Methylglutaconic Aciduria, Type III, MGCA3	258501	<i>OPA3</i>	NM_025136.3
Dyskinesia, Limb And Orofacial, Infantile-Onset, IOLOD	616921	<i>PDE10A</i>	NM_001130690.2
Basal Ganglia Calcification, Idiopathic, 4, IBGC4	615007	<i>PDGFRB</i>	NM_002609.3
Paroxysmal Nonkinesigenic Dyskinesia 1, PNKD1, DYT8	118800	<i>PNKD</i>	NM_015488.4
Huntington Disease-Like 1, HDL1	603218	<i>PRNP</i>	NM_000311.4
Microphthalmia, Syndromic 12, MCOPS12	615524	<i>RARB</i>	NM_000965.4
Gordon Holmes Syndrome, GDHS	212840	<i>RNF216</i>	NM_207111.3
Epileptic Encephalopathy, Early Infantile, 6, EIEE6	607208	<i>SCN1A</i>	NM_001165963.1
Epileptic Encephalopathy, Early Infantile, 13, EIEE13	614558	<i>SCN8A</i>	NM_014191.3
Pontocerebellar Hypoplasia, Type 2d, PCH2D	613811	<i>SEPSECS</i>	NM_016955.3

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 31 of 44	

Hereditary Chorea 30 gene panel			
Condition	OMIM	Gene	Primary Transcript
Parkinsonism-Dystonia, Infantile, PKDYS	613135	<i>SLC6A3</i>	NM_001044.4
Basal Ganglia Calcification, Idiopathic, 1, IBGC1	213600	<i>SLC20A2</i>	NM_006749.4
Severe Motor Delay And Intellectual Disability		<i>SYT1</i>	NM_005639.2
Pontocerebellar Hypoplasia, Type 2b, PCH2B	612389	<i>TSEN2</i>	NM_025265.3
Pontocerebellar Hypoplasia, Type 2a, PCH2A	277470	<i>TSEN34</i>	NM_024075.4
Pontocerebellar Hypoplasia, Type 2a, PCH2A	277470	<i>TSEN54</i>	NM_207346.2
Pontocerebellar Hypoplasia, Type 2e, Parkinson Disease Type 17, PCH2E	615851	<i>VPS53</i>	NM_001128159.2
Chorea-Acanthocytosis, CHAC	200150	<i>VPS13A</i>	NM_033305.2
Mcleod Syndrome, MCLDS	300842	<i>XK</i>	NM_021083.3
Basal Ganglia Calcification, Idiopathic, 6, IBGC6	616413	<i>XPR1</i>	NM_004736.3

Abnormal Metal Transport 9 gene panel			
Condition	OMIM	Gene	Primary Transcript
Wilson Disease, WD	277900	<i>ATP7B</i>	NM_000053.3
Neurodegeneration With Brain Iron Accumulation 4, SPG43 / NBIA4	614298	<i>C19orf12</i>	NM_001031726.3
Aceruloplasminemia	604290	<i>CP</i>	NM_000096.3
Neurodegeneration With Brain Iron Accumulation 3, NBIA3	606159	<i>FTL</i>	NM_000146.3
Neurodegeneration With Brain Iron Accumulation 1, NBIA1	234200	<i>PANK2</i>	NM_153638.3
Neurodegeneration With Brain Iron Accumulation 2b, NBIA2A/2B	610217	<i>PLA2G6</i>	NM_003560.3
Hypermanganesemia With Dystonia 1, HMNDYT1	613280	<i>SLC30A10</i>	NM_018713.2
Hypermanganesemia With Dystonia 2, HMNDYT2	608736	<i>SLC39A14</i>	NM_015359.5
Neurodegeneration With Brain Iron Accumulation 5, NBIA5	300894	<i>WDR45</i>	NM_007075.3

Paroxysmal neurological disorders
(SureSelect Design ID: 3097261)

Hemiplegic Migraine 10 gene panel			
Condition	OMIM Gene Ref	Gene	Primary transcript
Familial hemiplegic migraine type 2; Alternating hemiplegia of childhood type 1	182340	<i>ATP1A2</i>	NM_000702.3
Alternating hemiplegia of childhood type 2	182350	<i>ATP1A3</i>	NM_152296.4
Familial hemiplegic migraine, type 1 (with progressive cerebellar ataxia)	601011	<i>CACNA1A</i>	NM_001127221.1
Susceptibility to migraine type 6, with or without aura	601013	<i>CACNA1E</i>	NM_001205293.1
Susceptibility to migraine type 13, with or without aura	613655	<i>KCNK18</i>	NM_181840.1
Seizures, benign familial infantile, 2	614386	<i>PRRT2</i>	NM_145239.2
Familial hemiplegic migraine, type 3	182389	<i>SCN1A</i>	NM_001165963.1
Episodic ataxia, type 6	600111	<i>SLC1A3</i>	NM_004172.4
Dystonia 9 GLUT1 deficiency syndrome	138140	<i>SLC2A1</i>	NM_006516.2
Retinal vasculopathy with cerebral leukodystrophy	606609	<i>TREX1</i>	NM_033629.4

Episodic Ataxia 11 gene panel			
Condition	OMIM Gene Ref	Gene	Primary transcript
Episodic ataxia type 2 Spinocerebellar ataxia type 6 Early infantile epileptic encephalopathy type 42	601011	<i>CACNA1A</i>	NM_001127221.1
Episodic ataxia type 5	601949	<i>CACNB4</i>	NM_000726.3
Episodic ataxia type 1 (including episodic ataxia / myokymia syndrome)	176260	<i>KCNA1</i>	NM_000217.2
Episodic kinesigenic dyskinesia 1	614386	<i>PRRT2</i>	NM_145239.2
Episodic ataxia type 6	600111	<i>SLC1A3</i>	NM_004172.4
Dystonia 9 GLUT1 deficiency syndrome	138140	<i>SLC2A1</i>	NM_006516.2
Spinocerebellar ataxia type 27	601515	<i>FGF14</i>	NM_175929.2
Intellectual disability, ataxia and arthrogryposis	611549	<i>NALCN</i>	NM_052867.2
Early infantile epileptic encephalopathy type 11	182390	<i>SCN2A</i>	NM_021007.2
Early infantile epileptic encephalopathy type 4	602926	<i>STXBP1</i>	NM_003165.3
Episodic ataxia type 8	609890	<i>UBR4</i>	NM_020765.2

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 33 of 44	

Hereditary Ataxia Stages 1 and 2

(SureSelect Design ID: 3097261)

Hereditary Ataxia (Stage 1) 107 gene panel				
Condition	OMIM	Inheritance	Gene	Primary Transcript
Achalasia-Addisonianism-Alacrima syndrome; AAAS; AAAS	231550	AR	AAAS	NM_015665.5
Anemia, sideroblastic and spinocerebellar ataxia; ASAT	301310	XL	ABCB7	NM_004299.4
Polyneuropathy, hearing loss, ataxia, retinitis pigmentosa, and cataract; PHARC	612674	AR	ABHD12	NM_001042472.2
Coenzyme Q10 deficiency, primary, 4; CoQ10D4	612016	AR	ADCK3	NM_020247.4
Spinocerebellar ataxia 28 ; SCA28	610246	AD	AFG3L2	NM_006796.2
Spastic ataxia 5, autosomal recessive; SPAX5	614487	AR	AFG3L2	NM_006796.2
Spastic paraplegia 63; SPG63	615686	AR	AMPD2	NM_001257360.1
Spinocerebellar ataxia, autosomal recessive 10; SCAR10	613728	AR	ANO10	NM_018075.3
Pettigrew syndrome; PGS	304340	XL	AP1S2	NM_001272071.1
Ataxia, early onset, with oculomotor apraxia and hypoalbuminemia; EAOH	606350	AR	APTX	NM_175073.4
Metachromatic leukodystrophy; MLD	250100	AR	ARSA	NM_000487.5
Cerebellar ataxia, cayman type; ATCAY; ATCAY	601238	AR	ATCAY	NM_033064.4
Ataxia-telangiectasia; AT	208900	AR	ATM	NM_000051.3
Cerebellar ataxia, areflexia, pes cavus, optic atrophy, and sensorineural hearing loss; CAPOS	601338	AD	ATP1A3	NM_152296.4
Dystonia 12; DYT12	128235	AD	ATP1A3	NM_152296.4
Alternating hemiplegia of childhood 2; AHC2	614820	AD	ATP1A3	NM_152296.4
Cerebellar ataxia, mental retardation, and dysequilibrium syndrome 3; CAMRQ3	613227	AR	CA8	NM_004056.4
Episodic ataxia, type 2; EA2	601011	AD	CACNA1A	NM_001127221.1
Spinocerebellar ataxia type 42; SCA42	604065	AD	CACNA1G	NM_018896.4
Cerebellar ataxia, nonprogressive, with mental retardation; CANPMR	614756	AD	CAMTA1	NM_015215.3
Mental retardation and microcephaly with pontine and cerebellar hypoplasia; micpch; MICPCH	300749	XL	CASK	NM_003688.3
Pontocerebellar hypoplasia, type 8; PCH8	614961	AR	CHMP1A	NM_002768.4
Cerebellar ataxia		AR	CLN6	NM_017882.2
Mitochondrial complex iv deficiency	220110	AR	COX20	NM_198076.4
Aceruloplasminemia	604290	AR	CP	NM_000096.3

Hereditary Ataxia (Stage 1) 107 gene panel				
Condition	OMIM	Inheritance	Gene	Primary Transcript
Pinocerebellar ataxia, autosomal recessive 17; SCAR17	616127	AR	<i>CWF19L1</i>	NM_018294.5
Spastic paraplegia 56, autosomal recessive; SPG56	615030	AR	<i>CYP2U1</i>	NM_183075.2
Cerebrotendinous xanthomatosis; CTX	606530	AR	<i>CYP27A1</i>	NM_000784.3
Leukoencephalopathy with brainstem and spinal cord involvement and lactate elevation; lbsl; LBSL	611105	AR	<i>DARS2</i>	NM_018122.4
Spastic paraplegia 54, autosomal recessive; SPG54	615033	AR	<i>DDHD2</i>	NM_015214.2
Ceroid lipofuscinosis, neuronal, 4B, Parry type	162350	AD	<i>DNAJC5</i>	NM_025219.2
Cerebellar ataxia, deafness, and narcolepsy; ADCADN	604121	AD	<i>DNMT1</i>	NM_001005360.2
Leukoencephalopathy with vanishing white matter; VWN	603896	AR	<i>EIF2B1</i>	NM_001414.3
Leukoencephalopathy with vanishing white matter; VWN	603896	AR	<i>EIF2B2</i>	NM_014239.3
Leukoencephalopathy with vanishing white matter; VWN	603896	AR	<i>EIF2B3</i>	NM_020365.4
Leukoencephalopathy with vanishing white matter; VWN	603896	AR	<i>EIF2B4</i>	NM_015636.3
Leukoencephalopathy with vanishing white matter; VWN	603896	AR	<i>EIF2B5</i>	NM_003907.2
Spinocerebellar ataxia 34; SCA34	133190	AD	<i>ELOVL4</i>	NM_022726.3
Epilepsy, progressive myoclonic 2A (Lafora)	254780	AR	<i>EPM2A</i>	NM_005670.3
Pontocerebellar hypoplasia, type 1b; PCH1B	614678	AR	<i>EXOSC3</i>	NM_016042.3
Spinocerebellar ataxia 27; SCA27	609307	AD	<i>FGF14</i>	NM_175929.2
Posterior column ataxia with retinitis pigmentosa; AXPC1; AXPC1	609033	AR	<i>FLVCR1</i>	NM_014053.3
Neurodegeneration due to cerebral folate transport deficiency	613068	AR	<i>FOLR1</i>	NM_016725.2
Friedreich ataxia (including Friedreich ataxia with retained reflexes); FRDA (FARR)	606829	AR	<i>FXN</i>	NM_000144.4
Spastic paraplegia 46, autosomal recessive; SPG46	609471	AR	<i>GBA2</i>	NM_020944.2
Spastic paraplegia 44, autosomal recessive; SPG44	613206	AR	<i>GJC2</i>	NM_020435.3
Epilepsy, progressive myoclonic, 6; EPM6; EPM6	614018	AR	<i>GOSR2</i>	NM_004287.3
Spinocerebellar ataxia, autosomal recessive 18; SCAR18	616204	AR	<i>GRID2</i>	NM_001510.3
Spinocerebellar ataxia, autosomal recessive 13; SCAR13	614831	AR	<i>GRM1</i>	NM_001278064.1

Hereditary Ataxia (Stage 1) 107 gene panel				
Condition	OMIM	Inheritance	Gene	Primary Transcript
Tay-Sachs disease, GM2-gangliosidosis, several forms; TSD	272800	AR	<i>HEXA</i>	NM_000520.5
Sandhoff disease;	268800	AR	<i>HEXB</i>	NM_000521.3
Spinocerebellar ataxia 15; SCA15	147265	AD	<i>ITPR1</i>	NM_001168272.1
Spinocerebellar ataxia 29, congenital nonprogressive; SCA29		?	<i>ITPR1</i>	NM_001168272.1
Episodic ataxia, type1 (including episodic ataxia/myokymia syndrome); EA1	176260	AD	<i>KCNA1</i>	NM_000217.2
Spinocerebellar ataxia 13; SCA13	176264	AD	<i>KCNC3</i>	NM_004977.2
Spinocerebellar ataxia 19; SCA19	605411	AD	<i>KCND3</i>	NM_004980.4
Spinocerebellar ataxia 22; SCA22		AD	<i>KCND3</i>	NM_004980.4
Seizures, sensorineural deafness, ataxia, mental retardation, and electrolyte imbalance; sesames; SESAMES	612780	AR	<i>KCNJ10</i>	NM_002241.4
Spastic ataxia 2, autosomal recessive; SPAX2	611302	AR	<i>KIF1C</i>	NM_006612.5
Spastic ataxia 3, autosomal recessive; SPAX3	611390	AR	<i>MARS2</i>	NM_138395.3
Methylmalonic aciduria and homocystinuria, CBLC type;	277400	AR	<i>MMACHC</i>	NM_015506.2
Ataxia-telangiectasia-like disorder 1; ATLD1	604391	AR	<i>MRE11A</i>	NM_005591.3
Abetalipoproteinemia; ABL	200100	AR	<i>MTTP</i>	NM_000253.3
Myoclonic Epilepsy Of Lafora;	254780	AR	<i>NHLRC1</i>	NM_198586.2
Niemann-pick disease, type C1; NPC1	257220	AR	<i>NPC1</i>	NM_000271.4
Niemann-pick disease, type C2; NPC2	607625	AR	<i>NPC2</i>	NM_006432.3
Mental retardation, x-linked, with cerebellar hypoplasia and distinctive facial appearance; MRX60	300486	XL	<i>OPHN1</i>	NM_002547.2
Gillespie syndrome; GLSP	206700	AD	<i>PAX6</i>	NM_000280.4
Spinocerebellar ataxia 23; SCA23	131340	AD	<i>PDYN</i>	NM_024411.4
Peroxisome biogenesis disorder 8a (Zellweger); PBD8A	614876	AR	<i>PEX16</i>	NM_004813.2
Peroxisome biogenesis disorder 8b; PBD8B	614877	AR	<i>PEX16</i>	NM_004813.2
Neurodegeneration with brain iron accumulation 2b; NBIA2A/2B	610217	AR	<i>PLA2G6</i>	NM_003560.3
Spinocerebellar ataxia, autosomal recessive 2; SCAR2	213200	AR	<i>PMPCA</i>	NM_015160.2
Ataxia-oculomotor apraxia 4; AOA4	616267	AR	<i>PNKP</i>	NM_007254.3
Spastic paraplegia 39; SPG39	612020	AR	<i>PNPLA6</i>	NM_006702.4
Sensory ataxic neuropathy, dysarthria, and ophthalmoparesis; SANDO	607459	AR	<i>POLG</i>	NM_002693.2
Leukodystrophy, hypomyelinating, 7, with or without oligodontia and/or hypogonadotropic hypogonadism; HLD7	607694	AR	<i>POLR3A</i>	NM_007055.3

Hereditary Ataxia (Stage 1) 107 gene panel				
Condition	OMIM	Inheritance	Gene	Primary Transcript
Spinocerebellar ataxia 14; SCA14	176980	AD	<i>PRKCG</i>	NM_002739.3
Huntington disease-like 1; HDL1	603218	AD	<i>PRNP</i>	NM_000311.4
Episodic kinesigenic dyskinesia 1 (Dystonia 10); EKD1 /DYT10	614386	AD	<i>PRRT2</i>	NM_145239.2
Gordon Holmes syndrome; GDHS	212840	AR	<i>RNF216</i>	NM_207111.3
Autosomal dominant sensory ataxia-1 (SNAX1); SNAX1	608984	AD	<i>RNF170</i>	NM_001160223.1
Spastic ataxia, Charlevoix-Saguenay type; SACS; SACS	604490	AR	<i>SACS</i>	NM_014363.5
Chylomicron retention disease; CMRD	246700	AR	<i>SAR1B</i>	NM_001033503.2
Pontocerebellar hypoplasia, type 2D; PCH2D	613811	AR	<i>SEPSECS</i>	NM_016955.3
Spinocerebellar ataxia, autosomal recessive 1; SCAR1	608465	AR	<i>SETX</i>	NM_015046.5
(Ataxia-oculomotor apraxia-2; AOA2); AOA2		AR	<i>SETX</i>	NM_015046.5
Marinesco-Sjogren syndrome; MSS; MSS	608005	AR	<i>SIL1</i>	NM_001037633.1
Episodic ataxia, type 6; EA6	600111	AD	<i>SLC1A3</i>	NM_004172.4
Dystonia 9; DYT9	138140	AD	<i>SLC2A1</i>	NM_006516.2
Mental retardation, x-linked, syndromic, christianson type; MRXSCH; MRXSCH	300243	XLD	<i>SLC9A6</i>	NM_006359.2
Spinocerebellar ataxia, autosomal recessive 20; SCAR20	616354	AR	<i>SNX14</i>	NM_153816.5
Spastic paraplegia 7, autosomal recessive; SPG7	602783	AR	<i>SPG7</i>	NM_003119.3
Spinocerebellar ataxia 5; SCA5	604985	AR	<i>SPTBN2</i>	NM_006946.2
Spinocerebellar ataxia, autosomal recessive 14; SCAR14		AD	<i>SPTBN2</i>	NM_006946.2
Congenital disorder of glycosylation, type 1Q; CDG1Q	611715	AR	<i>SRD5A3</i>	NM_024592.4
Spinocerebellar ataxia, autosomal recessive 16; SCAR16	615768	AR	<i>STUB1</i>	NM_005861.3
Spinocerebellar ataxia, autosomal recessive 8; SCAR8	610743	AR	<i>SYNE1</i>	NM_033071.3
Spinocerebellar ataxia 35; SCA35	613900	AD	<i>TGM6</i>	NM_198994.2
Spinocerebellar ataxia 21; SCA21	607454	AD	<i>TMEM240</i>	NM_001114748.1
Spinocerebellar ataxia, autosomal recessive 7; SCAR7	609270	AR	<i>TPP1</i>	NM_000391.3
Pontocerebellar hypoplasia, type 2b; PCH2B	612389	AR	<i>TSEN2</i>	NM_025265.3
Pontocerebellar hypoplasia, type 2a; PCH2A	277470	AR	<i>TSEN54</i>	NM_207346.2
Spinocerebellar ataxia 11; SCA11	611695	AD	<i>TTBK2</i>	NM_173500.3
Mitochondrial complex III deficiency, nuclear type 2; MC3DN2	615157	AR	<i>TTC19</i>	NM_017775.3
Vitamin E, familial isolated deficiency of; VED	600415	AR	<i>TTPA</i>	NM_000370.3

Hereditary Ataxia (Stage 1) 107 gene panel				
Condition	OMIM	Inheritance	Gene	Primary Transcript
Dystonia 4, torsion, autosomal dominant; DYT4	128101	AD	<i>TUBB4A</i>	NM_006087.3
Spinocerebellar ataxia, infantile-onset; IOSCA	606075	AR	<i>TWINK</i>	NM_006087.3
Spastic ataxia 1, autosomal dominant; SPAX1	185880	AD	<i>VAMP1</i>	NM_014231.4
Cerebellar ataxia, mental retardation, and dysequilibrium syndrome 1; CAMRQ1	224050	AR	<i>VLDLR</i>	NM_003383.3
Pontocerebellar hypoplasia, type 1a; PCH1A	607596	AR	<i>VRK1</i>	NM_003384.2
Galloway-mowat syndrome; GAMOS	251300	AR	<i>WDR73</i>	NM_032856.3
Cerebellar ataxia, mental retardation, and dysequilibrium syndrome 2; CAMRQ2	610185	AR	<i>WDR81</i>	NM_001163809.1
Wolfram syndrome 1; WFS1	222300	AR	<i>WFS1</i>	NM_006005.3
Spinocerebellar ataxia, autosomal recessive 12; SCAR12	605131	AR	<i>WWOX</i>	NM_016373.3

Hereditary Ataxia (Stage 2) 54 gene panel				
Condition	OMIM	Inheritance	Gene	Primary Transcript
Joubert syndrome 3; JBTS3	608629	AR	<i>AHI1</i>	NM_017651.4
Wilson disease; WD	606882	AR	<i>ATP7B</i>	NM_000053.3
Joubert syndrome 17; JBTS17	614615	AR	<i>C5orf42</i>	NM_023073.3
Coach syndrome;	216360	AR	<i>CC2D2A</i>	NM_001080522.2
Joubert syndrome 15; JBTS15	614464	AR	<i>CEP41</i>	NM_018718.2
Joubert syndrome 5; JBTS5	610188	AR	<i>CEP290</i>	NM_025114.3
Cerebellar ataxia;		AR	<i>CLN6</i>	NM_017882.2
Spinocerebellar ataxia, autosomal recessive 7; SCAR7	609270	AR	<i>COPRS</i>	NM_018405.3
Mitochondrial complex iv deficiency;	220110	AR	<i>COX14</i>	NM_032901.3
Mitochondrial complex iv deficiency or Leigh syndrome;	220110	AR	<i>COX10</i>	NM_001303.3
Mitochondrial complex iv deficiency;	220110	AR	<i>COX6B1</i>	NM_001863.4
Msa1, susceptibility to; MSA1	146500	AR/AD	<i>COQ2</i>	NM_015697.7
Coenzyme Q10 deficiency, primary, 5; COQ10D5	614654	AR	<i>COQ9</i>	NM_020312.3
Mental retardation, autosomal dominant 19; MRD19	615075	AD	<i>CTNNB1</i>	NM_001904.3
Joubert syndrome 21; JBTS21	615636	AR	<i>CSPP1</i>	NM_024790.6
Pyruvate dehydrogenase e2 deficiency; PDHDD	245348	AR	<i>DLAT</i>	NM_001931.4
Spinocerebellar ataxia 26; SCA26	130610	AD	<i>EEF2</i>	NM_001961.3
Mitochondrial complex iv deficiency;	220110	AR	<i>FASTKD2</i>	NM_014929.3
Neurodegeneration with brain iron accumulation 3; NBIA3;	134790	AD	<i>FTL</i>	NM_000146.3

Hereditary Ataxia (Stage 2) 54 gene panel				
Condition	OMIM	Inheritance	Gene	Primary Transcript
Krabbe disease	245200	AR	<i>GALC</i>	NM_000153.3
Gaucher disease, type I	230800	AR	<i>GBA</i>	NM_001005741.2
Frontotemporal lobar degeneration with TDP43 inclusions	607485	AR	<i>GRN</i>	NM_002087.3
Spinocerebellar ataxia 18; SCA18	603502	AD	<i>IFRD1</i>	NM_001550.3
Sensorimotor neuropathy with ataxia; SMNA	603502	AD	<i>IFRD1</i>	NM_001550.3
Joubert syndrome 1; JBTS1	213300	AR	<i>INPP5E</i>	NM_019892.4
Early-onset epileptic encephalopathy		AD	<i>KCNA2</i>	NM_004974.3
Poretti-Boltshauser syndrome; PTBHS	615960	AR	<i>LAMA1</i>	NM_005559.3
No known		?	<i>LIG3</i>	NM_013975.3
Epilepsy, progressive myoclonic, 9; EPM9	616540	AR	<i>LMNB2</i>	NM_032737.3
Congenital contractures of the limbs and face, hypotonia, and developmental delay; CLIFAHDD	616266	AD	<i>NALCN</i>	NM_052867.2
Joubert syndrome 4; JBTS4	609583	AR	<i>NPHP1</i>	NM_000272.3
Coenzyme q10 deficiency, primary, 2; COQ10D2	614651	AR	<i>PDSS1</i>	NM_014317.3
Coenzyme q10 deficiency, primary, 3; COQ10D3	614652	AR	<i>PDSS2</i>	NM_020381.3
Mitochondrial complex iv deficiency	220110	AR	<i>PET100</i>	NM_001171155.1
Peroxisome biogenesis disorder 5b; PBD5B	614867	AR	<i>PEX2</i>	NM_000318.2
Peroxisome biogenesis disorder 4a (Zellweger); PBD4A	614862	AR	<i>PEX6</i>	NM_000287.3
Not known		AR	<i>PITRM1</i>	NM_001242309.1
Coach syndrome	216360	AR	<i>RPGRIP1L</i>	NM_015272.2
Occult macular dystrophy; OCMD	613587	AR	<i>RP1L1</i>	NM_178857.5
Epileptic encephalopathy, early infantile, 11; EIEE11	613721	AD	<i>SCN2A</i>	NM_021007.2
Mitochondrial complex iv deficiency	220110	AR	<i>SCO1</i>	NM_004589.3
Spinocerebellar ataxia, autosomal recessive 21; SCAR21; SCAR21	616719	AR	<i>SCYL1</i>	NM_020680.3
Allan-Herndon-Dudley syndrome; AHDS; AHDS	300095	XL	<i>SLC16A2</i>	NM_006517.4
Basal ganglia calcification, idiopathic, 1; IBGC1	213600	AD	<i>SLC20A2</i>	NM_006749.4
Spinocerebellar ataxia with blindness and deafness		AR	<i>SLC52A2</i>	NM_024531.4
Niemann-pick disease, type b	607616	AR	<i>SMPD1</i>	NM_000543.4
Niemann-pick disease, type a	257200	AR	<i>SMPD1</i>	NM_000543.4
Epileptic encephalopathy, early infantile, 4; EIEE4	612164	AD	<i>STXBP1</i>	NM_003165.3

Hereditary Ataxia (Stage 2) 54 gene panel

Condition	OMIM	Inheritance	Gene	Primary Transcript
Mitochondrial complex iv deficiency	220110	AR	<i>TACO1</i>	NM_016360.3
Spinocerebellar ataxia, autosomal recessive 23; SCAR23	616949	AR	<i>TDP2</i>	NM_016614.2
Spastic paraplegia 49, autosomal recessive; SPG49	615031	AR	<i>TECPR2</i>	NM_014844.3
Joubert syndrome 6; JBTS6	610688	AR	<i>TMEM67</i>	NM_153704.5
Coach syndrome	216360	AR	<i>TMEM67</i>	NM_153704.5
Joubert syndrome 16; JBTS16	614465	AR	<i>TMEM138</i>	NM_016464.4
Joubert syndrome 2; JBTS2	608091	AR	<i>TMEM216</i>	NM_001173990.2
Joubert syndrome 20; JBTS20	614970	AR	<i>TMEM231</i>	NM_001077416.2
Wieacker-Wolff syndrome; WRWF	341580	XLR	<i>ZC4H2</i>	NM_018684.3

Haematology disorders

Bleeding & Thrombotic disorders

(SureSelect Design ID: 0657461)

Sub-panels			
Disease Names	Gene(s)	OMIM	Primary Transcript
ADAMTS13 deficiency	<i>ADAMTS13</i>	274150	NM_139025.4
Factor V deficiency	<i>F5</i>	227400	NM_000130.4
Haemophilia A	<i>F8</i>	306700	NM_000132.3
Haemophilia A and B (where the type of haemophilia is unknown)	<i>F8</i> <i>F9</i>	306700 306900	NM_000132.3 NM_000133.3
Haemophilia A and 2N VWD (where the cause of reduced FVIII:C is unknown)	<i>F8</i> <i>VWF</i>	306700 277480	NM_000132.3 NM_000552.3
Factor XIII deficiency	<i>F13A1</i> <i>F13B</i>	613225 613235	NM_000129.3 NM_001994.2
Fibrinogen disorders	<i>FGA</i> <i>FGB</i> <i>FGG</i>	134820 134830 134850	NM_000508.3 NM_005141.4 NM_021870.2
Glanzmann thrombasthenia	<i>ITGAT2B</i> <i>ITGB3</i>	273800 273800	NM_000419.3 NM_000212.2
MYH9 related disorders	<i>MYH9</i>	160775	NM_002473.5
von Willebrand disease	<i>VWF</i>	277480	NM_000552.3

Bone Marrow Failure Disorders

(SureSelect Design ID: 0724921)

Sub-panels			
Condition	OMIM	Gene	Primary transcript
Fanconi anaemia, complementation group A	227650	<i>FANCA</i>	NM_000135.2
Fanconi anaemia, complementation group B	300514	<i>FANCB</i>	NM_001018113.1
Fanconi anaemia, complementation group C	227645	<i>FANCC</i>	NM_000136.2
Fanconi anaemia, complementation group D1	605724	<i>BRCA2</i>	NM_000059.3
Fanconi anaemia, complementation group D2	227646	<i>FANCD2</i>	NM_033084.3
Fanconi anaemia, complementation group E	600901	<i>FANCE</i>	NM_021922.2

Date of issue: 14 Sep 2020	Version number: 9
Author: Miranda Durkie	Authorised by: Richard Kirk
Page 41 of 44	

Fanconi anaemia, complementation group F	603467	<i>FANCF</i>	NM_022725.3
Fanconi anaemia, complementation group G	614082	<i>FANCG</i>	NM_004629.1
Fanconi anaemia, complementation group I	609053	<i>FANCI</i>	NM_032043.2
Fanconi anaemia, complementation group J	609054	<i>BRIP1</i>	NM_001113378.1
Fanconi anaemia, complementation group L	614083	<i>FANCL</i>	NM_001114636.1
Fanconi anaemia, complementation group M	614087	<i>FANCM</i>	NM_020937.3
Fanconi anaemia, complementation group N	610832	<i>PALB2</i>	NM_024675.3
Fanconi anaemia, complementation group O	613390	<i>RAD51C</i>	NM_058216.2
Fanconi anaemia, complementation group P	613951	<i>SLX4</i>	NM_032444.2
Fanconi anaemia, complementation group Q	615272	<i>ERCC4</i>	NM_005236.2
Diamond-Blackfan Anaemia	305371	<i>GATA1</i>	NM_002049.3
	603634	<i>RPL5</i>	NM_000969.3
	604175	<i>RPL11</i>	NM_000975.3
	180468	<i>RPL35A</i>	NM_000996.2
	603658	<i>RPS7</i>	NM_001011.3
	603632	<i>RPS10</i>	NM_001014.4
	130620	<i>RPS14</i>	NM_00102507.1
	180472	<i>RPS17</i>	NM_001021.5
	603474	<i>RPS19</i>	NM_001022.3
	602412	<i>RPS24</i>	NM_001142285.1
Myelodysplastic syndrome	603701	<i>RPS26</i>	NM_001029.3
	137295	<i>GATA2</i>	NM_001145661.1
	159530	<i>MPL</i>	NM_005373.2
	607444	<i>SBDS</i>	NM_016038.2
	151385	<i>RUNX1</i>	NM_001754.4
Severe Congenital Neutropenia	602122	<i>SRP72</i>	NM_006947.3
	130130	<i>ELANE</i>	NM_001972.3
	611045	<i>G6PC3</i>	NM_138387.3
	600871	<i>GFI1</i>	NM_005263.4
	605998	<i>HAX1</i>	NM_006118.3
Thrombocytopenia with absent radii	300392	<i>WAS</i>	NM_000377.2
	605313	<i>RBM8A</i> (& microarray)	NM_005105.4

Haems mini-panel

(Ampliseq Design ID: IAD162775_197)

Condition	Gene	Primary transcript
Thrombophilia due to thrombin deficiency	<i>F2</i>	NM_000506.4
Haemophilia A	<i>F8</i>	NM_000132.3
Haemophilia B	<i>F9</i>	NM_000133.3
Factor XI deficiency	<i>F11</i>	NM_000128.3
Bernard-Soulier syndrome	<i>GP1BA</i>	NM_000173.6
Bernard-Soulier syndrome	<i>GP1BB</i>	NM_000407.4
Bernard-Soulier syndrome	<i>GP9</i>	NM_000174.4
Congenital amegakaryocytic thrombocytopenia	<i>MPL</i>	NM_005373.2
Protein C deficiency	<i>PROC</i>	NM_000312.3
Protein S deficiency	<i>PROS1</i>	NM_000313.3
Antithrombin deficiency	<i>SERPINC1</i>	NM_000488.3
Vit K- dependent clotting factor type 2	<i>VKORC1</i>	NM_024006.5
Factor VII deficiency	<i>F7</i>	NM_000131.4
Factor X deficiency	<i>F10</i>	NM_000504.3
Vit K- dependent clotting factor type 1	<i>GGCX</i>	NM_000821.6
Thrombophilia (due to APC resistance)	<i>F5</i>	NM_000130.4
Thrombotic thrombocytopenic purpura, familial	<i>ADAMTS13</i>	NM_139025.4
von Willebrand disease	<i>VWF</i>	NM_000552.4
Factor XIII A deficiency	<i>F13A1</i>	NM_000129.3
Factor XIII B deficiency	<i>F13B</i>	NM_001994.2
Nijmegen breakage syndrome	<i>NBN</i>	NM_002485.4
Neutropenia, severe congenital 1, autosomal dominant	<i>ELANE</i>	NM_001972.3
Leukemia, acute lymphoblastic, susceptibility to, 3	<i>PAX5</i>	NM_016734.2
Thrombocytopenia 5	<i>ETV6</i>	NM_001987.4
Neutropenia, severe congenital, 7, autosomal recessive****	<i>CSF3R</i>	NM_156039.3
Leukemia, acute myeloid	<i>GATA2</i>	NM_001145661.1
Leukemia, acute myeloid	<i>RUNX1</i>	NM_001754.4
Leukemia, acute myeloid	<i>CEBPA</i>	NM_001287424.1
autosomal dominant nonsyndromic thrombocytopenia-2 (THC2)	<i>ANKRD26</i>	NM_014915.2
Myeloproliferative/lymphoproliferative neoplasms, familial (multiple types), susceptibility to	<i>DDX41</i>	NM_016222.3
Bone marrow failure syndrome 1	<i>SRP72</i>	NM_006947.3
Hemochromatosis	<i>HFE</i>	NM_000410.3
Hemochromatosis, type 2A	<i>HFE2 (HJV)</i>	NM_213653.3
Hemochromatosis, type 2B	<i>HAMP</i>	NM_021175.3
Hemochromatosis, type 3	<i>TFR2</i>	NM_003227.3
Hemochromatosis, type 4	<i>SLC40A1</i>	NM_014585.5
Combined factor V and VIII deficiency	<i>LMAN1</i>	NM_005570.3
Combined factor V and VIII deficiency	<i>MCFD2</i>	NM_139279.5
Glanzmann's thrombasthenia	<i>ITGA2B</i>	NM_000419.4
Glanzmann's thrombasthenia	<i>ITGB3</i>	NM_000212.2
Fibrinogen deficiency	<i>FGA</i>	NM_000508.4
Fibrinogen deficiency	<i>FGB</i>	NM_005141.4
Fibrinogen deficiency	<i>FGG</i>	NM_021870.2

Oncology

Pharmacogenetics solid tumour panel

(Ampliseq Design ID: IAD113764.231)

Pharmacogenetics			
Condition	OMIM	Gene	Primary transcript
Pharmacogenetics Solid Cancer NGS Panel	131550	<i>EGFR</i>	NM_005228.3
	114500	<i>KRAS</i>	NM_033360.2
	164790	<i>NRAS</i>	NM_002524.3
	171834	<i>PIK3CA</i>	NM_006218.2
	164757	<i>BRAF</i>	NM_004333.4
	116806	<i>CTNNB1</i>	NM_001904.3
	164920	<i>KIT</i>	NM_000222.2
	173490	<i>PDGFRA</i>	NM_006206.4
	147700	<i>IDH1</i>	NM_001282386.1
	147650	<i>IDH2</i>	NM_002168.3