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1 Patient

Informed consent is required for genetic testing. The patient (or parent or guardian in the case of minors under the age of 18 or adults lacking legal capacity) must sign the attached consent form. If the samples are anonymous, we will accept a statement from the physician responsible for the patient indicating that an appropriate informed consent has been obtained (section *"Statement of the existence of informed consent"*).

Patient's full name

2 Genetic study requested

Sequencing Panels

Genetic Muscle Disorders [GMD]

- ☐ S-202008553 Congenital structural GMD [78 genes]
- ☐ S-202008554 Child- and adult-onset structural GMD [64 genes]
- ☐ S-202008552 Limb-girdle muscular dystrophies [43 genes]
- ☐ S-202008620 Distal myopathies [37 genes]
- ☐ S-202008621 Myofibrillar myopathies with protein aggregates [20 genes]
- ☐ S-201602251 Emery-Dreifuss-type muscular dystrophies [7 genes]
- ☐ S-201602252 Dystrophinopathies [DMD gene] NGS sequencing
- ☐ S-202008623 Myopathies related to glycogen metabolism [21 genes]
- ☐ S-201804629 Myopathies related to lipid metabolism [15 genes]
- ☐ S-202008622 Nuclear mitochondrial myopathies [69 genes]
- ☐ S-202008642 Rhabdomyolysis and hyperCKemia [47 genes]
- ☐ S-202008624 Non-dystrophic myotonies [10 genes]
- ☐ S-202008629 Congenital myasthenia extended panel [29 genes]
- ☐ S-202008634 Congenital myasthenia basic panel [6 genes]
- ☐ S-202008626 Arthrogryposis extended panel [86 genes]
- ☐ S-202008665 Multiple pterygium/Escobar and related syndromes [15 genes]
- ☐ S-202008527 Distal arthrogryposis [11 genes]
- ☐ S-202008646 Structural genetic disorders comprehensive panel [133 genes]
- ☐ S-202008656 Metabolic myopathies comprehensive panel [109 genes]
- ☐ S-202008374 GMD comprehensive panel [330 genes]

Hereditary Neuropathies

- ☐ S-202008627 Charcot-Marie-Tooth disease extended panel [77 genes]
- ☐ S-202008637 Demyelinating/intermediate CMT panel [37 genes]
- ☐ S-202008636 Axonal/Intermediate CMT panel [57 genes]
- ☐ S-202008630 CMT basic panel [4 genes]
- ☐ S-202008639 Motor neuropathy/SMN1-negative spinal muscular atrophy panel [38 genes]
- ☐ S-202008641 Hereditary sensory and autonomic neuropathy panel [28 genes]
- ☐ S-202008638 Metabolic neuropathy panel [24 genes]
- ☐ S-202008640 Optic neuropathy panel [13 genes]
- ☐ S-202008657 Neuropathies comprehensive panel [150 genes]

Hereditary Spastic Paraplegia

- ☐ S-202008662 Pure spastic paraplegia [36 genes]
- ☐ S-202008661 Complex spastic paraplegia [90 genes]
- ☐ S-202008635 Spastic paraplegia basic panel [8 genes]
- ☐ S-202008658 Spastic paraplegia comprehensive panel [107 genes]

Ataxia

- ☐ S-202008530 Spinocerebellar ataxia [84 genes]
- ☐ S-202008531 Autosomal dominant spinocerebellar ataxia [24 genes]
- ☐ S-202008532 Autosomal recessive spinocerebellar ataxia [65 genes]
- ☐ S-202008529 Spastic ataxia and ataxia-dystonia syndromes [35 genes]
- ☐ S-202008528 Episodic ataxia [8 genes]
- ☐ S-202008533 Ataxia and atrophy/pontocerebellar hypoplasia [31 genes]
- ☐ S-202008375 Ataxia comprehensive panel [262 genes]

Dementia

- ☐ S-202008557 Alzheimer's disease [5 genes]
- ☐ S-202008631 Frontotemporal dementia basic panel [11 genes]
- ☐ S-202008628 Frontotemporal dementia extended panel [22 genes]
- ☐ S-202008565 Amyotrophic lateral sclerosis - Frontotemporal dementia [15 genes]
- ☐ S-202008644 Dementia comprehensive panel [49 genes]

Amyotrophic Lateral Sclerosis [ALS]

- ☐ S-202008633 Amyotrophic lateral sclerosis basic panel [3 genes]
- ☐ S-202008565 Amyotrophic lateral sclerosis - Frontotemporal dementia [15 genes]
- ☐ S-202008651 Amyotrophic lateral sclerosis and primary lateral sclerosis comprehensive panel [38 genes]

Movement Disorders

- ☐ S-202008645 Dystonia comprehensive panel [48 genes]
- ☐ S-202008546 Isolated dystonia [8 genes]
- ☐ S-202008547 Myoclonic dystonia [2 genes]
- ☐ S-202008550 Dystonia-parkinsonism [5 genes]
- ☐ S-202008548 Paroxysmal dystonia with other dyskinesias [4 genes]
- ☐ S-202008559 Parkinson's disease and related disorders [25 genes]
- ☐ S-202008632 Parkinson's disease basic panel [8 genes]
- ☐ S-202008663 Young-onset parkinsonism [8 genes]
- ☐ S-201805729 Chorea and Huntington-like disorders [19 genes]
- ☐ S-202008643 Basal ganglia calcification comprehensive panel [13 genes]
- ☐ S-201805369 Aicardi-Goutières syndrome [7 genes]
- ☐ S-202008625 Neurodegeneration with brain iron accumulation syndromes (NBIAS) [14 genes]
- ☐ S-201804729 Paroxysmal movement disorders [18 genes]
- ☐ S-202008276 Neuronal ceroid lipofuscinosis [11 genes]
- ☐ S-202008660 Metabolic movement disorders comprehensive panel [32 genes]

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- ☐ S-202008659 Movement disorders comprehensive panel [152 genes]

Leukodystrophies and Other Hereditary Leukoencephalopathies

- ☐ S-202008607 POLR3-related leukodystrophy [5 genes]
- ☐ S-202008560 Pelizaeus-Merzbacher disease (PMD) and PMD-like diseases (PMLD) [5 genes]
- ☐ S-202008679 Tricotiodystrophy/Tay syndrome [5 genes]
- ☐ S-202008613 Leukodystrophies with intracranial calcifications [24 genes]
- ☐ S-202008615 Leukodystrophies with white matter rarefaction or cystic lesions on MRI [29 genes]
- ☐ S-202008667 Childhood ataxia with central nervous system hypomyelination/vanishing white matter [CACH/VWM] [5 genes]
- ☐ S-202008605 Megalencephalic leukoencephalopathy with subcortical cysts [2 genes]
- ☐ S-202008612 Leukodystrophies with spinal cord involvement on MRI [5 genes]
- ☐ S-202008614 Leukodystrophies with abnormal peaks on magnetic resonance spectroscopy [4 genes]
- ☐ S-202008606 Metachromatic leukodystrophy [3 genes]
- ☐ S-202008610 Leukodystrophies associated with lysosomal disorders [22 genes]
- ☐ S-202008611 Leukodystrophies associated with peroxisomal disorders [19 genes]
- ☐ S-202008608 Leukodystrophies associated with energy and mitochondrial metabolism disorders [16 genes]
- ☐ S-202008609 Leukodystrophies associated with inborn errors of intermediate metabolism [17 genes]
- ☐ S-202008616 Vascular leukoencephalopathies [12 genes]
- ☐ S-202008654 Hypomyelinating leukodystrophies comprehensive panel [40 genes]
- ☐ S-202008653 Leukodystrophies due to inborn errors of metabolism comprehensive panel [73 genes]
- ☐ S-202008655 Leukodystrophies and other hereditary leukoencephalopathies comprehensive panel [142 genes]

Cerebrovascular Diseases

- ☐ S-202008524 Stroke and migraine [5 genes]
- ☐ S-202008536 Cerebral cavernoma [3 genes]
- ☐ S-201906329 CADASIL [the NOTCH3 gene]
- ☐ S-202008556 Cerebral microangiopathy [8 genes]
- ☐ S-202008558 Moyamoya disease [8 genes]
- ☐ S-202008648 Cerebrovascular diseases comprehensive panel [36 genes]

Mitochondrial diseases

- ☐ S-202008538 Specific mitochondrial respiratory chain complexes/OXPHOS deficiency panel [94 genes]
- ☐ S-202008540 mtDNA depletion [18 genes]
- ☐ S-202008674 Leigh syndrome caused by nuclear DNA mutations [70 genes]
- ☐ S-201906357 Pyruvate dehydrogenase (PDH) deficiency [12 genes]
- ☐ S-202008539 Primary coenzyme Q deficiency [13 genes]
- ☐ S-202008652 Mitochondrial nuclear genes comprehensive panel [400 genes]
- ☐ S-201805389 Mitochondrial genome [37 genes]
- ☐ S-201805390 Mitochondrial genome associated with another NGS panel

Epilepsy

- ☐ S-202008555 Neonatal and early-onset epileptic encephalopathy [90 genes]
- ☐ S-202008671 Dravet syndrome and febrile convulsions plus [16 genes]
- ☐ S-202008676 Rett and Rett-like syndrome [41 genes]
- ☐ S-202008666 Angelman-like syndrome panel [12 genes]
- ☐ S-201907249 Tuberous sclerosis [2 genes]
- ☐ S-202008561 Childhood absence epilepsy [5 genes]
- ☐ S-202008562 Focal epilepsy and other forms of familial epilepsy [33 genes]
- ☐ S-202008650 Myoclonic epilepsy comprehensive panel [43 genes]
- ☐ S-202008563 Juvenile myoclonic epilepsy [7 genes]
- ☐ S-202008564 Progressive myoclonic epilepsy [36 genes]
- ☐ S-202008602 Hyperekplexia and paroxysmal disorders related to epilepsy [9 genes]
- ☐ S-202008647 Epileptic encephalopathy comprehensive panel [124 genes]
- ☐ S-202008649 Epilepsy comprehensive panel [271 genes]

CNS Anomalies

- ☐ S-202008537 Neural tube closure defects [5 genes]
- ☐ S-202008526 Brain midline/regionalization alterations [121 genes]
- ☐ S-202008604 Holoprosencephaly [14 genes]
- ☐ S-202008566 Schizencephaly [4 genes]
- ☐ S-202008525 Agenesis of the corpus callosum [106 genes]
- ☐ S-202008681 Neuronal migration disorders/cortical dysplasias [57 genes]
- ☐ S-202008617 Lissencephaly [25 genes]
- ☐ S-202008601 Periventricular nodular heterotopia [9 genes]
- ☐ S-202008567 Band heterotopia [the DCX gene]
- ☐ S-202008664 Polymicrogyria [24 genes]
- ☐ S-202008618 Megalencephaly-polymicrogyria and dysplastic megalencephaly [7 genes]
- ☐ S-202008619 Microcephaly [88 genes]
- ☐ S-202008603 Pontocerebellar hypoplasia [18 genes]

Neurodevelopmental Disorders and Related Genetic Syndromes

- ☐ S-202008543 Intellectual disability and/or autism [865 genes]
- ☐ S-202008542 Intellectual disability [798 genes]
- ☐ S-202008534 Autism [196 genes]
- ☐ S-202008544 Intellectual disability and/or autism and epilepsy [117 genes]
- ☐ S-202008535 BAFopathies (Coffin-Siris syndrome and Nicolaides-Baraitser syndrome) [10 genes]
- ☐ S-201907249 Tuberous sclerosis [2 genes]
- ☐ S-201805369 Aicardi-Goutières syndrome [7 genes]
- ☐ S-202008669 Cockayne syndrome [5 genes]
- ☐ S-202008670 Cornelia de Lange syndrome [10 genes]
- ☐ S-202008672 Joubert syndrome [34 genes]
- ☐ S-202008673 Kabuki syndrome [2 genes]
- ☐ S-202008675 Meckel syndrome [13 genes]
- ☐ S-201906395 RASopathies syndromes [26 genes]
- ☐ S-202008677 Rubinstein-Taybi syndrome [2 genes]
- ☐ S-202008678 Seckel syndrome [9 genes]
- ☐ S-202008680 Sotos syndrome [3 genes]

Other tests:

- ☐ S-202008723 FXS/FXTAS/FXPOI [FMR1 expansions]
- ☐ S-202009944 Prader-Willi/Angelman syndromes [MS-MLPA of the PWS/AS genomic region]
- ☐ S-202008666 Angelman-like syndrome panel [12 genes]
- ☐ S-202009939 Rett syndrome [Sanger sequencing of the MECP2 gene]

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- ☐ S-202009941 Rett syndrome [gene dosage analysis of the MECP2 gene by MLPA]
- ☐ S-202008676 Rett and Rett-like syndrome [41 genes]
- ☐ S-202009943 Beckwith-Wiedemann/Silver-Russell syndromes [MS-MLPA region 11p15]
- ☐ S-202009942 Silver-Russell syndrome [MS-MLPA chromosome 7]
- ☐ S-202008668 Beckwith-Wiedemann-like syndrome [8 genes]
- ☐ S-202009940 CHARGE syndrome [sequencing of the CHD7 gene]
- ☐ S-202009388 KBG syndrome [Sanger sequencing of the ANKRD11 gene]

Nucleotide expansions

- ☐ S-202008703 Oculopharyngeal muscular dystrophy [*PABPN1* expansions]
- ☐ S-201804669 Myotonic dystrophy type 1 [*DMPK* expansions]
- ☐ S-202008721 Myotonic dystrophy type 2 [*CNBP* expansions]
- ☐ S-201601805 Friedreich ataxia [*FXN* expansions]
- ☐ S-202008193 SCA expansions - Panel 1 [SCA1, SCA2, SCA3, SCA6, SCA7]
- ☐ S-202008722 SCA expansions - Panel 2 [SCA10, SCA12, SCA17]
- ☐ S-202008724 DRPLA [*ATN1* expansions]
- ☐ S-202008723 FXS/FXTAS/FXPOI [*FMR1* expansions]
- ☐ S-201805509 C9orf72-related ALS/FTD [*C9orf72* expansions]
- ☐ S-202008725 Kennedy disease [*AR* expansions]
- ☐ S-202008726 Huntington's disease [*HTT* expansions]
- ☐ S-202008727 Huntington disease-like type 2 [*JPH3* expansions]
- ☐ S-202008728 Unverricht–Lundborg disease [*CSTB* expansions]

MLPA

- ☐ S-201602259 Dystrophinopathy [DMD gene dosage by MLPA]
- ☐ S-201703888 CMT1A/HNPP [PMP22 gene dosage by MLPA]
- ☐ S-201906211 Spinal muscular atrophy [SMN1-SMN2 gene dosage by MLPA]

Other genetic tests

- ☐ S-202109974 Individual sequencing of genes (Sanger)
- ☐ S-202109975 NextGenDx® massive sequencing
- ☐ S-202109976 Massive sequencing with CNVs

Whole exome:

- ☐ S-202110014 Whole-exome - sequencing only (fastq)
- ☐ S-202110013 Whole-exome - annotation of variants
- ☐ S-202110336 Whole-exome - with report tool
- ☐ S-202110015 Whole-exome - with clinical report
- ☐ S-202109977 Targeted exome
  Gene/genes:
- ☐ S-202110133 Trio clinical exome
- ☐ S-202109983 MLPA and methylation-specific MLPA:
  Gene/genes:

SNP array:

- ☐ S-201601485 Index case
- ☐ S-201702726 Family study or confirmation of CNVs

Array CGH:

- ☐ S-202008036 Prenatal array (37K)
- ☐ S-202109987 Postnatal array (60K)
- ☐ S-202109988 Postnatal array (180K)
- ☐ S-202109998 Variant segregation/Family studies
  Variant:
- ☐ Other services:

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3 Patient's authorization

I declare that I have been informed of, that I understand, and that I am in agreement with the type of genetic study indicated above and in which I am voluntarily participating.

I understand that I may be affected by or be a carrier of a hereditary genetic disorder, the diagnosis of which may be confirmed by a laboratory study analyzing DNA obtained from my biological samples. I hereby give my consent to have my sample sent to Health in Code S.L., a company with a level of data protection in accordance with European legislation, to carry out the indicated genetic study, as well as to the center or centers designated by it, complying with ethical considerations and current legal regulations:

☐ Si ☐ No

I understand that:

- Genetic disorders may be inherited by family members and that the results of my test may have implications for my own family.

- In the case of a genetic study of a mutation, the determination of the mutation is diagnostic, while non-determination does not exclude the pathology. A negative test does not exclude the possibility of having the disease (some diseases have multiple causes and it is not possible to test for all of them).

- Occasionally, there may be unusual alterations in the DNA structure of certain individuals that may yield results that are difficult to interpret, making the diagnosis difficult and even making it impossible to obtain conclusive results.

- Although the methods used to perform this diagnostic testing are extremely sensitive and specific, there is always a small chance of failure of the technique or of an interpretation error. For this reason, repeating the test or performing additional ones may be necessary in some cases, which may or may not require obtaining new samples, particularly in those cases where quality of the biological sample is suboptimal.

- Given the complexity of genetic studies based on DNA and the important implications of the results of a genetic study, I will be informed of said results by a physician or genetic expert, always with the highest confidentiality level from both medical and laboratory personnel.

- I may change my mind at any time and withdraw the authorization for the genetic study given by me in this document, thereby revoking my decision to continue with the analysis.

- The only people who will have access to the test results will be members of the Health in Code, S.L. team and health service professionals involved in patient care.

- It is possible to obtain unexpected information during the sample analysis process, and I hereby declare that I want to be informed about it:

☐ Si ☐ No

- It is possible that information concerning the relatives of the sample donor will be obtained. We recommend that the latter (or his/her legal representative) should be the person who shares said information. In any event, the approval of each family member will be required.

Current legislation requires Health in Code, S.L. to keep clinical documentation under conditions that ensure its proper maintenance and security for purposes of due patient care for at least five years after the assistance process has ended. I am aware and accept that a DNA aliquot will be kept in the laboratory for subsequent studies and/or confirmation tests:

☐ Si ☐ No

In addition, I consent to the biological sample being used by the entity Health in Code, S.L. for research purposes approved by the relevant ethics committee after the termination of the study, always maintaining the patient's anonymity.

☐ Si ☐ No

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In which case, you are informed of:

- The purpose of the research related to the pathology whose diagnosis is intended and to other related lines of research.
- The expected benefits of the research, which will consist of a greater understanding of the pathologies studied, their development, and related population studies.
- The possibility that you will be contacted later for the purpose of collecting new data or obtaining new samples.
- The right to revoke this consent at any time and without any justification whatsoever and to decide to have the sample destroyed or anonymized.
- The obligation of Health in Code, S.L. to destroy or anonymize the sample once the research has finished and after the statutory storage period, unless authorization for longer storage has been given.
- Your right to know the genetic data obtained from the analysis of your biological samples.
- The confidentiality of the information obtained, with solely members of the Health in Code, S.L. research team having access to personal data.
- The possibility that information concerning the relatives of the sample donor may be obtained. We recommend that the latter (or his/her legal representative) be the person who shares said information. In any event, the approval of each family member will be required.
- If applicable, I hereby authorize the extraction of biological samples and the genetic study of dependent minor/s in my care to be used under the terms and conditions previously described for the genetic test for the aforementioned disease.

Name of the patient or legal representative*
*If the patient is a minor or lacks legal capacity

National Identification Number of the patient or legal representative

Signature of patient or legal representative

Date

4 Statement of the existence of informed consent

☐ I hereby declare that the patient identified on this request is aware of the information on said request and has signed the Informed Consent form to permit this genetic study to be carried out and that this has been included in his/her clinical record.

Physician's signature

Date