

FAMILY MEMBER INFORMATION (Please Print)				PROBAND INFORMATION (Please Print)
First Name	MI	Last Name	Preferred Name	Name of Proband:
DOB (mm/dd/yy)	MRN#	Genetic Sex (required): <input type="checkbox"/> M <input type="checkbox"/> F Gender Identity (optional):		DOB: Sex <input type="checkbox"/> M <input type="checkbox"/> F <input type="checkbox"/> UNK
Address		Phone		Relationship to Proband
City	State	Zip Code	Provider	

SAMPLE INFORMATION	
Sample Instruction based: <input type="checkbox"/> Send saliva kit to address above <input type="checkbox"/> Use stored extracted DNA <input type="checkbox"/> Blood draw planned	Does this individual have a history of: <input type="checkbox"/> Blood Transfusion <input type="checkbox"/> Hematologic Malignancy <input type="checkbox"/> Bone Marrow Transplant <input type="checkbox"/> NONE If the answer is yes to any of these questions, please contact the laboratory to discuss before sending a sample.

PARTICIPANT CONSENT (REQUIRED)		
By signing this form I acknowledge as the related family member/their legal guardian that I have read the attached informed consent document and that I authorize the UCGL to perform genome sequencing as described. Genetic variants that are present in a family member but not in the proband will NOT be detected and therefore not reported. Inheritance of variants present in both a proband and their relative WILL be detected and reported. This includes secondary findings, if the proband has opted to receive them.		
<input type="checkbox"/> OPT-IN: Please check this box if you wish to be recontacted for future research opportunities should they become available.		
Print name of Relative/their Legal guardian	Signature of Relative/their Legal guardian	Date

REQUISITION CONTINUES ON NEXT PAGE



FAMILY MEMBER CLINICAL HISTORY

Please provide the following information regarding the family member to be tested. Phenotypes listed are in HPO terms with the corresponding HPO number (https://hpo.jax.org/app/) This information is needed to facilitate interpretation of whole exome sequencing results.

[-] Negative/None

PRE/PERINATAL HISTORY

[-] Premature birth [0001622]

GROWTH

- [-] Failure to thrive [0001508]
[-] Obesity [0001513]
[-] Short stature [0004322]
[-] Tall stature [0000098]

MOTOR/COGNITIVE DEVELOPMENT

- [-] Aggressive behavior [0006919]
[-] Anxiety [0100852]
[-] Autistic Behavior [0000729]
[-] Delayed speech and language development [0000750]
[-] Hyperactivity [0000752]
[-] Intellectual Disability [0001249]
[-] Learning Disability [0001328]
[-] Sleep disturbance [0002360]

CRANIOFACIAL/DYSMORPHISM

- [-] Abnormal facial shape [0001999]
[-] Oral cleft [0000202]
[-] Macrocephaly [0000256]
[-] Microcephaly [0000252]
[-] Short neck [0000470]

HEARING IMPAIRMENT

- [-] Conductive hearing impairment [0000405]
[-] Mixed hearing impairment [0000410]
[-] Sensorineural hearing impairment [0000407]

GASTROINTESTINAL FINDINGS

- [-] Constipation [0002019]
[-] Diarrhea [0002014]
[-] Gastroesophageal reflux [0002020]
[-] Inflammatory bowel disease [0002037]
[-] Pancreatitis [0001733]
[-] Pyloric Stenosis [0002021]
[-] Vomiting [0002013]

GENITOURINARY

- [-] Abnormality of the genitourinary system [0000119]
Specify: _____ [_____]
Specify: _____ [_____]

HAIR & SKIN FINDINGS

- [-] Abnormal Blistering of the Skin [0008066]
[-] Abnormal nail growth [0030807]
[-] Alopecia [0001596]
[-] Anhidrosis [0000970]

- [-] Eczema [0000964]
[-] Hemangiomas [0001028]
[-] Hypermelanotic macule [0001034]
[-] Hyperextensible skin [0008067]
[-] Hyperpigmentation of the skin [0001000]
[-] Soft skin [0000977]
[-] Telangiectasia [0001009]

STRUCTURAL BRAIN ABNORMALITIES

- [-] Agenesis of corpus Collosum [0001274]
[-] Chiari malformation [0002308]
[-] Ventriculomegaly [0002119]

NEUROLOGICAL FINDINGS

- [-] Abnormality of nervous system [0000707]
[-] Ataxia [0001251]
[-] Dementia [0000726]
[-] Migraine [0002076]
[-] Parkinsonism [0001300]
[-] Peripheral neuropathy [0009830]
[-] Seizure [0001250]
[-] Sensory Neuropathy [0000763]
[-] Syncope [0001279]
[-] Tremor [0001337]
[-] Vertigo [0002321]

MUSCULOSKELETAL FINDINGS

- [-] Arachnodactyly [0001166]
[-] Exercise intolerance [0003546]
[-] Hemihypertrophy [0001528]
[-] Hypertonia [0001276]
[-] Hypotonia [0001252]
[-] Joint Hypermobility [0001382]
[-] Muscle weakness [0001324]
[-] Myalgia [0003326]
[-] Osteoarthritis [0002758]
[-] Osteopenia [0000938]
[-] Pectus carinatum [0000768]
[-] Scoliosis [0002650]

EYE DEFECTS & VISION

- [-] Abnormality of vision [0000504]
Specify: _____ [_____]
[-] Ptosis [0000508]
[-] Retinal detachment [0000541]
[-] Strabismus [0000486]

ENDOCRINE

- [-] Delayed puberty [0000823]
[-] Diabetes Insipidus [0000873]
[-] Diabetes Mellitus [0000819]
[-] Hyperthyroidism [0000836]
[-] Hypothyroidism [0000821]
[-] Hypoparathyroidism [0000829]
[-] Maturity-onset diabetes of the young [0004904]

METABOLIC/RESPIRATORY FINDINGS

- [-] Abnormal circulating metabolite concentration [0032180]
[-] Asthma [0002099]
[-] Increased CPK [0003236]
[-] Pneumothorax [0002107]
[-] Pulmonary fibrosis [0002206]

CARDIAC FINDINGS

- [-] Abnormal heart morphology [0001627]
[-] Amyloidosis [0011034]
[-] Arrhythmia [0011675]
[-] Bradycardia [0001662]
[-] Dilated cardiomyopathy [0001644]
[-] Hypertension [0000822]
[-] Mitral valve prolapse [0001634]
[-] Prolonged QTc interval [0005184]
[-] Supraventricular tachycardia [0004755]

VASCULAR SYSTEM

- [-] Arteriovenous malformation [0100026]
[-] Epistaxis [0000421]
[-] Stroke [0001297]
[-] Vascular dilatation [0002617]

HEMATOLOGIC/IMMUNOLOGIC FINDINGS

- [-] Anemia [0001903]
[-] Immunodeficiency [0002721]
[-] Neutropenia [0001875]
[-] Pancytopenia [0001876]
[-] Recurrent infections [0002719]
[-] Thrombocytopenia [0001873]

CANCER

- [-] Type of cancer _____
[-] Age at Diagnosis _____
[-] Family History of Cancer (attach pedigree)

OTHER FEATURES

Phenotype [HPO# https://hpo.jax.org/app/]

- _____ [_____]
_____ [_____]
_____ [_____]
_____ [_____]
_____ [_____]

ADDITIONAL HISTORY (or attach records)

[Empty space for additional history or records]



INFORMED CONSENT

ABOUT THE GENOME ANALYSIS TEST

Genome sequence analysis simultaneously evaluates both the protein-coding and non-coding regions of the nuclear genome. The non-coding regions include promoter, intronic and untranslated regions. An individual's nuclear genome represents approximately 20,000 genes. This test also includes screening for a select group of repeat expansion disorders. In addition, this test analyzes the mitochondrial DNA (mtDNA) genome which encodes 37 genes and is exclusively maternally inherited. Disorders of mitochondrial energy metabolism, or oxidative phosphorylation (OXPHOS) disorders, are characterized by reduced activity of one or more mitochondrial respiratory chain complexes. While much of the data generated from sequencing the genome is not well understood at this time, genome sequencing may potentially detect pathogenic variants that are not assessed by exome sequencing.

The purpose of this test is to determine if there is a possible genetic reason for your family member's health condition. Finding a genetic cause may improve future medical care and treatment options and inform family planning.

Detailed medical and family history are needed for accurate interpretation of results. Clinical photographs can also be helpful.

Genetic counseling and/or clinical genetics consultation are recommended before and after the test is performed. Clinical reports are released only to the certified healthcare professional(s) listed on the order form. You may choose to request a copy of the clinical report from the healthcare professional who ordered the test.

FAMILY MEMBER TESTING

Any samples submitted to assist in the analysis of the patient's genome (such as the parents, sibling, or other relative) will have sequencing performed but will not be analyzed separately. They will only be utilized if submitted before the patient's data is analyzed, or within 30 days of receipt of proband, whichever is first.

Family member data are ONLY used for interpretation of the patient's genome sequencing findings. Genetic variants that may be in a family member, but are NOT present in the proband, are not reported.

Genetic testing may reveal that the true biological relationships in a family are not as they were reported. This includes non-paternity (the stated father of an individual is not the biological father) and consanguinity (the parents of an individual are related by blood). Incorrect information about the biological relationships in your family may result in incorrect interpretation of results, incorrect diagnoses, and/or inconclusive test results. If you have any concerns about any such issues, please discuss them confidentially with your genetic counselor or ordering provider.

GENOME ANALYSIS RESULT REPORTING

In general, the laboratory will only report results that may explain the patient's clinical features.

You will also receive secondary findings *if* the primary patient has chosen to receive secondary findings. The American College of Medical Genetics and Genomics (ACMG) identified a subset of genes and disorders for which treatment is available that may reduce morbidity and/or mortality. These findings may be unrelated to the reason for referral but may impact medical decision-making if identified. Only DNA changes known to cause disease will be reported.

Due to limited knowledge on their genetic causes, variants related to complex multifactorial diseases such as asthma, lupus, and type 2 diabetes, will not be reported.

Genetic variants not known to be clinically relevant will not be reported.

One report is generated for the patient. If samples from parents, siblings or other relatives were utilized as part of the interpretation of the patient's genome test, the results will indicate if the variant(s) were de novo (new event), or inherited from the mother, the father or present in a sibling or other relative.

CONSENT CONTINUES ON NEXT PAGE



INFORMED CONSENT continued

POSSIBLE TEST RESULTS

The genetic variants found by genome sequencing will be classified according to the guidelines from the American College of Medical Genetics and Genomics (ACMG). Three possible test results include:

- Positive (pathogenic or likely pathogenic variant): a variant was found that likely caused the patient’s condition or carries an increased risk for developing the disorder in the future. This result may be important for other family members.
- Negative: no disease-causing variants were found. This result does not eliminate the possibility of a genetic condition not discovered by this test.
- Variant of uncertain clinical significance (VUS): a variant was found, but it is currently unknown whether that change could have caused the patient’s condition. A VUS may be benign or disease-causing, but more research is needed.

Because medical and scientific knowledge are constantly changing, new information that becomes available in the future may replace or add to the information UPMC Clinical Genomics laboratory (UCGL) used to interpret the results.

RISKS & LIMITATIONS

As with all laboratory testing, there is a small risk of getting an erroneous result.

Because many different genes and conditions are being analyzed, there is a risk that genetic information will be revealed that is not directly related to the reason genome sequencing was ordered. This information might relate to diseases or symptoms that may develop in conditions that have no current treatment. The severity and clinical course of the genetic condition may not be known.

Additional variants may exist and may contribute to or cause disease but not be identified by this analysis. Some parts of our DNA are naturally difficult to analyze because of features like repetitive sequences, very similar gene copies, or high GC content. These areas may produce lower-quality data and increase the chance that some variants are missed. Genome sequence analysis also has technical limits. It generally cannot detect certain types of changes, such as balanced structural rearrangements, low-level mosaicism, methylation abnormalities, or changes in highly repetitive regions. Mitochondrial DNA sequencing has its own limitations as well; variants present at very low levels (below about 5–10%) may not be detected, and the accuracy of finding deletions or duplications is not fully established. The repeat expansion disorder screening included in this test can only suggest that certain genes are unlikely to explain the patient’s symptoms. It is not intended to provide a diagnosis.

Interpretation of findings is limited by what is currently known about the genes and diseases being tested.

DATA & UPDATED INFORMATION

Information about genetic disease is continually changing. Additionally, a patient’s clinical presentation or family history may also change over time. It is the responsibility of the patient and ordering provider to be aware of any changes in the patient’s symptoms and to communicate them to the laboratory. The laboratory will also re-contact the referring physician if the lab learns that new information about the genes tested has been identified.

The physician can initiate a request for variant interpretation review, reanalysis of sequencing data and release of raw data. There may be a charge associated with such requests.

Sharing health history and genetic information can ultimately help health care providers deliver better care for their patients and provide researchers opportunities to make discoveries. UPMC submits de-identified information to public databases to contribute to the advancement of medical knowledge.

PRIVACY/PATIENT CONFIDENTIALITY

The United States Federal Government has enacted the Genetic Information and Non-discrimination Act (GINA) that prohibit discrimination, based on genetic test results, by health insurance companies and employers. These laws also prohibit unauthorized disclosure of this information. For more information you can visit <https://www.eeoc.gov/laws/statutes/gina.cfm> However, this law does not consider the possible impact these results may have on obtaining disability or life insurance.

Data and personal information will be stored and protected in strict confidence complying with regulatory requirements (e.g., HIPAA and equivalent protections), and I acknowledge that I have read and understand UPMC’s privacy policy.

CONSENT CONTINUES ON NEXT PAGE



