Laboratory of Personalized Genomic Medicine
Department of Pathology and Cell Biology

COLUMBIA UNIVERSITY MEDICAL CENTER

630 West 168th Street
P&S 11th Floor, Room 453
New York, NY 10032
Tel: 212-305-9706
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Informed Consent – Whole Exome Sequencing for Adults

1. The nature of the test and how it will be performed.

What is Whole Exome Sequencing (WES)?

Whole Exome Sequencing (WES) is a new type of genetic test. WES searches through the most important part of a person's entire genetic material, called the "exome", for DNA variation that can cause disease. Instructions in the exome tell our cells how to make the right components to function properly. Abnormalities of this information can lead to disease. Because WES examines a larger portion of the genetic material than traditional tests, it might discover the cause of disease in cases where other tests did not. WES may also reveal information about unexpected diseases. Because WES is more complicated than other genetic tests, the consent and ordering process must be thorough and will be done with the assistance of a genetic counselor and/or your doctor.

How is the test done?

Two tubes (two teaspoons) of blood will be collected from you. Based on your family tree, your genetic counselor or doctor may also recommend that blood be drawn from two or more members of your family, such as your parents or siblings, to help with interpretation of test results. The exome is part of the DNA sequence. DNA from your blood is purified, then the exome sequence is obtained (or "read") using WES. The exome sequence is then searched for changes that might cause disease.

How is this test interpreted?

Once the exome is read, the information obtained is analyzed for differences between your exome sequence and a reference ("normal) sequence. Everyone has places in their exome that differ from the reference. These differences make us unique and usually do not cause medical problems. To determine whether the changes that are found are neutral, or can cause disease, the following steps are taken:

First, the variations in your exome will be compared with a list of mutations that are known to cause medical problems in other people with symptoms similar to yours. Subsequently one will examine whether disruptive mutations not previously described are present in genes that are known to cause the type of disease you have. Changes found will be compared to the changes seen in your selected family members with or without the disease (if available) to confirm that the changes are indeed the cause of your disease.

2. The Primary Purpose of the test (why it is being performed).

The test is being performed to detect one (or more than one) genetic causes for your condition. The condition is _____, which causes _____.

The test results may be complex, so you must obtain genetic counseling before signing this consent.

3. What kinds of results may be obtained, what is their significance for health, and what should you do after receiving the results?

What kind of results may be reported?

There are several different kinds of results that may be reported. All results will go directly to your doctor or your other healthcare provider who ordered the test.

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1. Positive for disease-causing mutation(s): You may have one or more genetic variation(s) that are known to cause a specific genetic condition in other individuals with similar symptoms. The variant or variants would then be called a mutation or mutations and would be interpreted as the cause of your symptoms.

2. No disease causing mutation(s) found: It is possible that the test will not find any genetic change that could explain your symptoms. This type of test result does not mean your condition is not genetic. The result would not take away whatever current diagnoses doctors may have given for your condition.

3. Variant with uncertain significance: Sometimes the test will find a variation that is predicted to be important, but has not been reported or seen before in people with your condition. Such a variant may or may not be the cause of your symptoms. The lab would report it as a "variant with uncertain significance" if there is evidence strongly suggesting that it is related to your condition.

4. "Incidental findings": These are test results that are not related to the symptoms for which the test was ordered. They might indicate that you have another previously undiagnosed, potentially serious condition. Some of these diseases might manifest later during your lifetime and knowing about them might help to prevent development of serious medical conditions. A list of such conditions is provided below. You may decide whether or not you want to be alerted to the presence of these conditions.

American College of Medical Genetics and Genomics Secondary Findings List	
Disorder	**Gene**
Hereditary Breast and Ovarian Cancer	BRCA1, BRCA2
Li-Fraumeni Syndrome	TP53
Peutz-Jeghers Syndrome	STK11
Lynch Syndrome	MLH1, MSH2, MSH6, PMS2
Familial adenomatous polyposis	APC
MYH-Associated Polypsosis; Adenomas, multiple colorectal, FAP type 2; Colorectal adenomatous polyposis, autosomal recessive, with pilomatricomas	MUTYH
Juvenile Polyposis	BMPR1A, SMAD4
Von Hippel Lindau Syndrome	VHL
Multiple Endocrine Neoplasia Type 1	MEN1
Multiple Endocrine Neoplasia Type 2	RET
Familial Medullary Thyroid Cancer (FMTC)	RET
PTEN Hamartoma Tumor Syndrome	PTEN
Retinoblastoma	RB1
Hereditary Paraganlioma-Pheochromocytome Syndrome	SDHD, SDHAF2, SDHC, SDHB
Tuberous Sclerosis Complex	TSC1, TSC2
WT1-related Wilms Tumor	WT1
Neurofibromatosis Type 2	NF2
EDS-Vascular type	COL3A1
Marfan Syndrome, Loeys-Dietz Syndromes, and Familial. Thoracic Aortic Aneurysms and Dissections	FBN1, TGFBR1, TGFBR2, SMAD3, ACTA2, MYH11
Hypertrophic Cardiomyopathy, Dilated cardiomyopathy	MYBPC3, MYH7, TNNT2, TNNI3, TPM1, MYL3, ACTC1, PRKAG2, GLA, MYL2, LMNA
Catecholamineric polymorphic ventricular tachycardia	RYR2
Arryhmogenic right ventricular cardiomyopathy	PKP2, DSP, DSC2, TMEM43, DSG2
Romano-Ward Long QT Syndrome Types 1,2 and 3, Brugada Syndrome	KCNQ1, KCNH2, SCN5A
Wilsons Disease	ATP7B
Ornithine Transcarbamylase Deficiency	OTC
Familial Hypercholesterolemia	LDLR, APOB, PCSK9
Malignant Hyperthemia susceptibility	RYR1, CACNA1S

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May I choose whether or not I am provided with the incidental findings?

Yes, this is your choice.

Please state whether you want to be informed about incidental findings causing the conditions listed above.

_____ (Initial) I would like to learn of incidental findings related to the conditions listed.

_____ (Initial) I would NOT like to learn of incidental findings related to the conditions listed.

Are there any types of results that will not be given to me?

Yes, there are a few types of results that will not be included in the report your doctor gets.

1. Some changes in genes might make a person slightly more likely to develop a type of common condition that happens in adults, such as diabetes or heart disease. Because these changes are not well understood, they are not looked at in detail or included in the report.

2. Some changes in genes might make a person much more likely to develop a type of condition that happens in adults, such as Alzheimer's disease. However, these changes do not guarantee that the condition will develop in a given individual, and even though the increased risk is known, no action can be taken to modify it.

3. We might use your relatives' samples to help us diagnose your condition, but we will not report results for these individuals. However, your genetic results might have implications for your relatives. It is important that you discuss these implications with your genetic counselor.

4. You might be carrying a mutation that could have effects on your children, if your partner carries a similar mutation. This is called "carrier" status. We will not report your carrier status for any disease. If you are concerned about carrier status for conditions that might run in your family, you should get tested separately for carrier status. You should discuss these implications with your genetic counselor.

5. A few genes are patented outside of Columbia University, so we may not be able to legally report results from those genes.
6.

What should I do if there is a positive result?

This is a test to identify a genetic cause of your clinical condition. If the test is positive for a genetic cause of your clinical condition or for another mutation that you requested to be informed about, you may wish to consult your physician or have further genetic counseling or undergo further independent testing.

_____ (Initial) I understand that I have the option to seek further independent testing, and that I should obtain genetic counseling to help me understand the results.

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Are there limitations to the testing?
Yes, there are several limitations to WES:

1. At the current time, the test may not reveal 100% of the exome. Therefore, there is a possibility that there could be a mutation or variation that is causing your condition that is not picked up by the WES test.

2. The WES report is generated based on current medical knowledge. A mutation that is not known to be the cause of a genetic condition today may be shown to be disease-causing in a year or two. We do not generate updated reports for the test, unless we are requested to do so by the patient. There is a fee associated with providing an updated report.

3. WES is not currently validated to detect large-scale alterations in the DNA content of the patient's cells. These include losses or duplications of many genes. Another genetic test called "microarray" is available for this purpose. A microarray test might be ordered by your physician before the WES testing.

4. WES may not be able to detect genetic disorders that are caused by expansion of repetitive regions of the genome. One example is Fragile X syndrome. If one of these conditions is suspected, your physician should order the appropriate test.

5. WES is not able to detect mutations in the 99% of the DNA that is not part of the exome, including parts of the DNA that help regulate gene function.

6. WES may detect findings of uncertain significance, which cannot be proven with complete certainty to be the cause of your condition (see types of results described above).

7. Finding a disease-causing mutation may not result in a treatment, cure, or a prognosis (knowledge about how a disease is expected to progress).

8. Standard lab limitations caused by human error, such as sample contamination or sample mix-up, may occur but are unlikely.

_____ (Initial) I understand the limitations to WES

4. When DNA testing detects the most common disease-causing changes in a gene, the test result is highly accurate.

5. Implications of positive and negative results for your diagnosis

Predicting the results of the WES in advance is not possible. Predicting in advance what the results will mean for your health is also not possible. This is due to the fact that many genes are tested and many different positive results can be obtained. Each of these different results will have potentially different implications. A negative result (not finding variants) will not change your clinical diagnosis.

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6. Who will have access to the results?

The results of the WES will become a part of your medical record. Test results are stored in the laboratory's computer records, and are normally automatically sent to computerized medical records of New York Presbyterian Hospital and Columbia University. If you do not want these results to be sent to these records, you must inform us about this. Unless you tell us not to transmit them, the results will become part of your electronic medical record. Even if they do not become part of the electronic medical record, the results may be made available to individuals/organizations with legal access to your medical record, on a strict "need-to-know" basis. Those with legal access include, but are not limited to, the physicians and nursing staff directly involved in your care, your current and future insurance carriers, and others specifically authorized by the you or your authorized representative. Columbia University, NewYork-Presbyterian and Weill Cornell Medicine and their related entities participate in an Organized Health Care Arrangement (OHCA). This allows us to share health information to carry out treatment, payment and our joint health care operations, including integrated information system management, health information exchange, financial and billing services, insurance services, insurance, quality improvement, and risk management activities. Organizations that will follow this Notice include Columbia University, NewYork-Presbyterian sites, Weill Cornell Medicine and their related entities.

_____ (Initial) I understand, that the results will be automatically transmitted to my electronic medical records in the NYPH and Columbia University EMRs. I do not object to this.

_____ (Initial) Please do not transmit any of the "incidental" findings to the hospital or university electronic medical records. Only transmit the results related to my present condition. I understand that I must assume responsibility for informing my future physicians about incidental findings that require intervention.

_____ (Initial) Please do not transmit any of the results to the hospital or university electronic medical records. I understand that the results will continue to be part of the laboratory's electronic information system. If test results are not entered into my hospital or university electronic medical records, future physicians may not have access to those results. I understand that I must assume responsibility for informing my future physicians about findings of the WES test that affect my healthcare.

7. How long are the WES results kept in the testing lab?

The laboratory will keep the identified WES raw data in the lab for 5 years. The final report will be kept as long as possible, at least 7 years. After this, the data from which the final report was generated will be de-identified, and will be stored in a database that does not include any names or other information that would link them back to an individual. However, information about the type of disease and the type of symptoms associated with the genetic findings will be preserved. Because this is a new test, it is important to keep track of the types of mutations and variants that are being found in association with particular diseases. This helps us improve our diagnostic capabilities. This might not directly benefit you, but it might benefit future patients with similar conditions. Please indicate your choice below.

_____ (Initial) I agree to my WES data being stored indefinitely in a de-identified way.

_____ (Initial) I do not want my WES data being stored indefinitely, even if it is de-identified.

8. Statement that no additional tests will be performed on this sample, without specific, signed authorization by the patient/legal representative, and that after 60 days, unless consent is given, the sample will be destroyed.

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How long are the samples kept in the lab?

Blood and DNA samples are normally discarded after 60 days following test completion, unless you provide us consent to store the DNA after testing is performed. Storing your sample may allow you to request testing in the future without having to obtain a new sample, or to participate in future research, should you wish to do so.

_____ (Initial) Please keep DNA used in WES testing indefinitely for future testing should I desire such testing, or if I want to participate in research in the future. I understand that no additional genetic tests will be performed without my specific consent/instructions. The DNA may be used only for quality control purposes. There is no guarantee of availability past 60 days. If I decide to participate in research in the future, I will instruct the laboratory, and there will be a requirement of a separate IRB-approved consent).

_____ (Initial) Do not keep my DNA used in my WES testing linked to information that could identify who I am. I consent to the use of my de-identified DNA for quality control purposes or for research in which my identity cannot be determined. I understand that any research using the de-identified DNA will require a specific IRB approval and oversight.

_____ (Initial) Please discard DNA and other biologic materials used in my WES testing, 60 days after all testing is completed.

9. What are the risks of testing?

1. Identification of familial relationships: WES may identify familial relationships other than those originally reported. For example, non-paternity (when the reported father of the child is not the biological father) or half sibling-ships (when siblings do not share the same father AND mother) would be detected. You may choose whether or not to be informed of this information, in case it is revealed during the testing.

2. Discrimination. The genetic non-discrimination law prevents insurance companies from using your genetic information to deny health insurance coverage. However, the law does not cover life insurance, disability insurance or long term care insurance. The detection of an incidental condition may affect your future ability to buy these forms of insurance or get the best insurance rates. By New York State Law, your consent is required for the release of these results to insurance companies. However, you may be required to release this information to the insurance companies for your contract with them to be valid.

3. Requirement for further testing: WES may identify genetic changes that may require additional testing to evaluate. This could result in anxiety, uncertainty, and additional expenses that may or may not be covered by your insurance.

4. Detection of untreatable conditions. WES may identify serious, untreatable genetic conditions. It can result in unexpected psychological trauma, both for you and your family. The detection of such a condition could also affect the health or health care needs of your siblings, children, or other close relatives.

10. Statement of Financial Responsibility

_____ (Initial) I understand that I, having requested testing to be performed, am responsible for the cost of this testing and will be required to pay for any/all of the test cost if health insurance does not reimburse the laboratory. In addition, if health insurance pays for the test, I understand that the laboratory is required to bill me for the co-pay or coinsurance that is required by my health plan.

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11. CONSENT FOR WES TESTING

All of the above has been explained to me, to my satisfaction, and my signature below attests to the same.

Whole Exome Sequencing Participant (person being tested):

Print Name: _____ **Signature:** _____ **Date:** _____

Health care provider obtaining consent:

Print Name: _____ **Signature:** _____ **Date:** _____

11a. Consent of family members submitting a sample for evaluation of patient's results.

Blood samples obtained from family members can help evaluate the results obtained on the person being tested. The results obtained from these samples will be used solely for this purpose. When providing the sample, you have a choice as to whether you wish to be informed of test results for your sample. Each family member being tested should elect an option below, sign, and date in the appropriate areas.

Family Member #1:

_____ (Initial) Please do NOT independently evaluate my sample. If questioned by an insurance carrier, I can state that I have not been tested for these conditions.

_____ (Initial) Please include my status in the patient's report if I share mutation(s) identified in the patient only in genes related to the *primary reason* for testing. I understand that if questioned by an insurance carrier, I should state that I have been tested for this condition. I do not wish to be informed of test results related to incidental findings in the secondary genes listed above (Section 3.4).

_____ (Initial) Please include my status in the patient's report if I share any mutation(s) identified in the patient, including test results related to *incidental findings in the secondary genes* listed above (Section 3.4). I understand that if questioned by an insurance carrier, I CANNOT state that I have not been tested for these conditions. Further, I understand that my sample will not be independently tested for incidental findings in the secondary genes and that mutations in these genes will only be reported to me if they were first seen in the patient.

Name of Family Member: _____Relationship to Patient: _____

Signature: _____**Date:** _____

Blood samples obtained from family members can help evaluate the results obtained on the person being tested. The results obtained from these samples will be used solely for this purpose. When providing the sample, you have a choice as to whether you wish to be informed of test results for your sample. Each family member being tested should elect an option below, sign, and date in the appropriate areas.

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Family Member #2:

_____ (Initial) Please do NOT independently evaluate my sample. If questioned by an insurance carrier, I can state that I have not been tested for these conditions.

_____ (Initial) Please include my status in the patient's report if I share mutation(s) identified in the patient only in genes related to the *primary reason* for testing. I understand that if questioned by an insurance carrier, I should state that I have been tested for this condition. I do not wish to be informed of test results related to incidental findings in the secondary genes listed above (Section 3.4).

_____ (Initial) Please include my status in the patient's report if I share any mutation(s) identified in the patient, including test results related to *incidental findings in the secondary genes* listed above (Section 3.4). I understand that if questioned by an insurance carrier, I CANNOT state that I have not been tested for these conditions. Further, I understand that my sample will not be independently tested for incidental findings in the secondary genes and that mutations in these genes will only be reported to me if they were first seen in the patient.

Name of Family Member: _____Relationship to Patient: _____

Signature: _____Date: _____

Notice to Health Care Practitioner:

The above document is a consent form for clinical whole exome sequencing. Currently, the laboratory will only accept whole exome test requests after the patient/parent or legal guardian/next of kin has received genetic counseling from a genetic counselor, clinical geneticist, or neurogeneticist with experience in counseling patients for such a test. By NY State law, he patient/parent needs to be counseled about issues related to the current condition, the possibilities of detecting unsuspected conditions as well as other issue related to health insurance, and possible effects on life insurance. Please explain the above consent to the patient, or authorized representative/guardian, and obtain an informed consent. Please explain the list of potential incidental findings that may be reported to the patient.

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Whole Exome Sequencing Patient Medical Questionnaire

To support the laboratory analysis, please provide a detailed clinical picture of the patient's clinical syndrome, the clinical differential diagnosis, *and* a pedigree. All of these will help in the interpretation of the pathogenicity of the variants that will be found.

Patient Information:			
Last Name:	First Name:	Date of Birth:	Today's Date:
Gender: ☐ Male ☐ Female	Ethnic Background: ☐ African American ☐ Ashkenazi Jewish ☐ Asian ☐ Caucasian ☐ Hispanic ☐ Native American ☐ Other Jewish ☐ Other _____		

Reason for Testing / Clinical Information	
Clinical Diagnosis:	Age of Onset:
Positive Family History: ☐ Yes ☐ No ☐ N/A If yes, explain:	Deceased? ☐ Yes ☐ No Autopsy: ☐ Yes ☐ No

Symptoms		***Signs***	
Cramps after exercise	☐ Yes ☐ No ☐ N/A	Asthenia	☐ Yes ☐ No ☐ N/A
Dementia	☐ Yes ☐ No ☐ N/A	Cerebellar Signs	☐ Yes ☐ No ☐ N/A
Developmental Delay	☐ Yes ☐ No ☐ N/A	Cerebral Blindness	☐ Yes ☐ No ☐ N/A
Episodic Coma	☐ Yes ☐ No ☐ N/A	Congestive Heart Failure	☐ Yes ☐ No ☐ N/A
Exercise Intolerance	☐ Yes ☐ No ☐ N/A	Diabetes Mellitus	☐ Yes ☐ No ☐ N/A
Gastrointestinal Pseudo-Obstruction	☐ Yes ☐ No ☐ N/A	Floppy Baby	☐ Yes ☐ No ☐ N/A
Headache	☐ Yes ☐ No ☐ N/A	Hearing Loss	☐ Yes ☐ No ☐ N/A
Migraine Headache	☐ Yes ☐ No ☐ N/A	Hirsute	☐ Yes ☐ No ☐ N/A
Myoclonus	☐ Yes ☐ No ☐ N/A	Hypoparathyroidism	☐ Yes ☐ No ☐ N/A
Myoglobinuria	☐ Yes ☐ No ☐ N/A	Hypothyroidism	☐ Yes ☐ No ☐ N/A
Nausea / Vomiting	☐ Yes ☐ No ☐ N/A	Opthalmoplegia	☐ Yes ☐ No ☐ N/A
Neuropathy	☐ Yes ☐ No ☐ N/A	Optic Atrophy	☐ Yes ☐ No ☐ N/A
Perinatal Insult	☐ Yes ☐ No ☐ N/A	Ptosis	☐ Yes ☐ No ☐ N/A
Proximal Limb Weakness	☐ Yes ☐ No ☐ N/A	Respiratory Insufficiency	☐ Yes ☐ No ☐ N/A
Seizures	☐ Yes ☐ No ☐ N/A	Retinopathy	☐ Yes ☐ No ☐ N/A
Stroke	☐ Yes ☐ No ☐ N/A	Short Stature	☐ Yes ☐ No ☐ N/A
Other:		Other:	

Laboratory Studies					
Elevated Lactate	☐ Yes	☐ No	☐ N/A	ECG – Pre-excitation	☐ Yes ☐ No ☐ N/A
Elevated Pyruvate	☐ Yes	☐ No	☐ N/A	EMG/NCS – Myopathic	☐ Yes ☐ No ☐ N/A
Elevated CSF Protein	☐ Yes	☐ No	☐ N/A	EMG/NCS - Neurogenic	☐ Yes ☐ No ☐ N/A
ECG – Heart Block	☐ Yes	☐ No	☐ N/A	Circle: Axonal Heart Block Demyelinating Pre-excitation Mixed	
Resting Serum Lactate: ☐ NORMAL ☐ ABNORMAL ☐ N/A If elevated, state level:_____				Resting Serum Creatine Kinase: ☐ NORMAL ☐ ABNORMAL ☐ N/A If elevated, state CK level outside episodes of myoglobinuria: _____	
Ischemic Exercise Test: ☐ NORMAL ☐ ABNORMAL ☐ N/A				Other:	

Imaging Studies						
Angiogram	☐ NORMAL	☐ ABNORMAL	☐ N/A	CT	☐ NORMAL	☐ ABNORMAL ☐ N/A
MRI	☐ NORMAL	☐ ABNORMAL	☐ N/A	BG Calcification	☐ Yes ☐ No	☐ N/A
SPECT	☐ NORMAL	☐ ABNORMAL	☐ N/A	Other:		
CBF	☐ NORMAL	☐ ABNORMAL	☐ N/A			

Additional Relevant Clinical Information:

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Description of high-throughput sequencing tests for genetic disorders offered by the Personalized Genomic Medicine Laboratory of Columbia University Medical Center

Overview

The human genome contains in excess of 20000 protein coding genes. In a constantly updated encyclopedia of Mendelian human disorders, OMIM, as of October 16, 2012, there are about 3600 phenotypes described in which the molecular basis of the disease is known. There is also an additional 3600 phenotypes listed that have no known molecular basis to date. The number of genes described on the site is past 14,000, and all these genes are thought to be relevant to human disease, although maybe only half of them have a confirmed role in one or more genetic disorders.

The current paradigm for genetic diagnosis rests on PCR and microarray-based detection of specific mutations of known significance and/or Sanger sequencing that allows detection of previously described, as well as novel mutations, in genes that have been well established to play a role in a specific disease. These methods work well for screening for specific mutations or for demonstration of mutations in a small number of genes, if the gene(s) to test can be largely ascertained based on the clinical phenotype. However, they fall short in cases where the phenotype and genotype correlation is not strong enough to efficiently guide the decision-making process as to what mutation in which gene should be tested for. In cases like congenital hearing loss in which over 100 loci have been implicated, it is often impossible to establish in what order to perform the review of genes linked to the phenotype. Even if a more logical phenotype based approach is available, like in the case of muscular dystrophies, the diagnostic odyssey is often too painful and expensive to undertake. Since genetic information is changing at a rapid pace, clinicians may be unaware of all known genes and, therefore, fail to order the appropriate tests. NGS allows for simultaneous sequencing of large number of genes that might carry mutations causing the symptoms of a patient at an affordable price. This prevents individual clinician bias in testing decisions and improves diagnostic success rate.

We offer four clinical NGS tests at the Personalized Genomic Medicine Laboratories at Columbia University Medical Center. These are full mitochondrial genome sequencing (MGS), the Columbia Combined Genetic Panel (CCGP), whole exome sequencing (WES) and whole genome sequencing (WGS) tests. The MGS and CCGP tests are for patients whose disease shows a very characteristic phenotype strongly associated with mutations in the mitochondrial genome, or in a few dozen candidate genes. The WES and WGS tests are to be used in situations where one cannot generate a credible list of candidate genes to be tested. These tests interrogate all coding regions or the entire genome, respectively. In addition to identifying known disease causing mutations and probable disease causing mutations in disease-associated genes they can also identify entirely new private mutations in genes previously not linked to the disease. Confirmation of the disease causing nature of these novel mutations is based on segregation of the mutation in families and structural and functional characteristics of the mutation and the gene itself.

Indication for testing

- The presence of a congenital developmental abnormality of presumed genetic origin
- Development of symptoms that suggest the presence of a genetic disorder with mitochondrial or Mendelian inheritance

Methodology

- Hardware: Illumina sequencing instruments: MiSeq for MGS and CCGP tests and HiSeq2500 for WES and WGS tests.
- Capture reagents: We use PCR to capture the mitochondrial genome and Agilent SureSelect technology to capture the regions of interest (ROI) for the CCGP and WES studies. The WGS does not require capture, since the entire genome is sequenced.

Specimen requirements

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- All specimens should carry two independent identifiers.
- Blood > 300microliters, should be anti-coagulated, preferably with citrate or EDTA and should be less than a week old.
- Muscle biopsy specimens (>50mg) should be refrigerated from the time of biopsy to arrival to the lab.
- DNA should be greater than 10kb median length. We optimally need 3 micrograms of genomic DNA at concentrations 50-200ng/microliter.