BAYLOR GENETICS

BAYLOR GENETICS
2450 HOLCOMBE BLVD.
GRAND BLVD. RECEIVING DOCK
HOUSTON, TX 77021-2024

PHONE
1.800.411.4363
FAX
1.800.434.9850

CONNECT

WHOLE EXOME SEQUENCING (WES) REQUISITION

PATIENT INFORMATION (COMPLETE ONE FORM FOR EACH PERSON TESTED)

Patient Last Name | Patient First Name | MI | Date of Birth (MM / DD / YYYY)

Address | City | State | Zip | Phone

Genetic Sex:
◯ Female ◯ Male ◯ Unknown

Accession # | Hospital / Medical Record #

Gender identity (if different from above):

Note: All reports will be sent via fax except for international recipients.

ORDERING PHYSICIAN

Ordering Physician | Institution Code

Institution Name

Email (Required for International Clients)

Phone | Fax

ADDITIONAL REPORTS

Name | Email | Phone | Fax

Name | Email | Phone | Fax

Note: Reports will be sent by FAX except for international recipients

PAYMENT (FILL OUT ONE OF THE OPTIONS BELOW)

◯ **SELF PAYMENT**

☐ Pay With Sample ☐ Bill To Patient

◯ **INSTITUTIONAL BILLING**

Institution Name | Institution Code | Institution Contact Name | Institution Phone | Institution Contact Email

◯ **INSURANCE**

☐ Do Not Perform Test Until Patient is Aware of Out-Of-Pocket Costs (excludes prenatal testing)

REQUIRED ITEMS
1. Copy of the Front/Back of Insurance Card(s)
2. ICD10 Diagnosis Code(s)
3. Name of Ordering Physician
4. Insured Signature of Authorization

ICD10 Diagnosis Code(s) (Required)

Primary Insurance Co. Name	Secondary Insurance Co. Name
Primary Insurance Co. Phone	Secondary Insurance Co. Phone
Primary Member Policy #	Secondary Member Policy #
Primary Member Group #	Secondary Member Group #
Name of Insured	Name of Insured
Insured Date of Birth (MM / DD / YYYY)	Insured Date of Birth (MM / DD / YYYY)
Patient's Relationship to Insured	Patient's Relationship to Insured
Phone of Insured	Phone of Insured
Address of Insured	Address of Insured
City / State / Zip	City / State / Zip

By signing below, I hereby authorize Baylor Genetics to provide my insurance carrier any information necessary, including test results, for processing my insurance claim. I understand that I am responsible for any co-pay, co-insurance, and unmet deductible that the insurance policy dictates. If self-pay is selected, I agree to pay for the cost of testing ordered and billed by Baylor Genetics as outlined in the Good Faith Estimate I received. I understand that I am responsible for sending Baylor Genetics any and all payments that I receive directly from my insurance company in payment for this test. Please note, Medicare may not cover certain screening tests.

Patient / Guardian Printed Name | Patient / Guardian Signature | Date (MM / DD / YYYY)

STATEMENT OF MEDICAL NECESSITY AND CONSENT TO TERMS & CONDITIONS FOR TEST ORDER (REQUIRED)

This requisition hereby incorporates the Terms and Conditions of the Laboratory Services found at https://www.baylorgenetics.com/lab-terms-conditions/ or, in the case of international entities, https://www.baylorgenetics.com/terms-conditions-of-the-laboratory-services-international/. This test is medically necessary for the risk assessment, diagnosis, or detection of a disease, illness, impairment, symptom, syndrome, or disorder. The results will determine my patient's medical management and treatment decisions. The person listed as the Ordering Physician is authorized by law to order the test(s) requested herein. I confirm that I have provided genetic testing information to the patient, and they have consented to genetic testing.

Physician's Printed Name | Physician's Signature | Date (MM / DD / YYYY)

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WHOLE EXOME SEQUENCING (WES) REQUISITION

Patient Last Name | Patient First Name | MI | Date of Birth (MM / DD / YYYY) | Genetic Sex

INSTRUCTIONS FOR ORDERING

Any combination of Chromosomal Microarray Analysis (CMA), mtDNA Analysis, or Global MAPS® can be ordered along with a WES test, however the turnaround time for results will differ from exome sequencing.

TRIO WES TEST OPTIONS

- ☐ 1600 Trio Whole Exome Sequencing
- ☐ 1532 Trio Whole Exome Sequencing + Comprehensive mtDNA Analysis
- ☐ 1722 Rapid Trio Whole Exome Sequencing
- ☐ 1533 Rapid Trio Whole Exome Sequencing + Comprehensive mtDNA Analysis

CORRESPONDING PARENTAL TESTS (Both Biological Parents Are Required)

- ☐ 1550 Parental WES - Maternal
- ☐ 1550 Parental WES - Paternal
- ☐ 1602 WES - Additional Affected Sibling

NOTE: Please use separate *Additional Affected Sibling for Trio* requisition for additional family members.

DUO WES TEST OPTIONS

- ☐ 1603 Duo Whole Exome Sequencing
- ☐ 1723 Rapid Duo Whole Exome Sequencing

CORRESPONDING PARENTAL TESTS (One Parent Is Required)

- ☐ 1550 Parental WES - Maternal
- ☐ 1550 Parental WES - Paternal
- ☐ 1602 WES - Additional Affected Sibling

NOTE: Please use separate *Additional Affected Sibling for Trio* requisition for additional family members.

PROBAND WES TEST OPTIONS

- ☐ 1500 Proband Whole Exome Sequencing
- ☐ 1530 Proband Whole Exome Sequencing + Chromosomal Microarray Analysis (CMA) (Comprehensive)
- ☐ 1531 Proband Whole Exome Sequencing + Comprehensive mtDNA Analysis
- ☐ 1729 Rapid Proband Whole Exome Sequencing

CORRESPONDING PARENTAL TESTS

- ☐ 6997 Optional Parental Control

NOTE: See consent for for the control will be used.

GLOBAL MAPS® TESTS

- ☐ 4900 Global Metabolomic Assisted Pathway Screen - Plasma from EDTA
  Was plasma extracted from EDTA? ◯ Yes ◯ No
- ☐ 4901 Global Metabolomic Assisted Pathway Screen - Urine

ADD-ON TESTS

- ☐ 8665 Chromosomal Microarray Analysis (CMA)-HR+SNP Screen (Comprehensive)
- ☐ 2055 Comprehensive mtDNA analysis by NGS
- ☐ 9815 Exome Raw Data Release

ADDITIONAL REPORTING OPTIONS

If a box is not checked the lab will default to No / Not Report.

☐ Opt-In for Other Incidental Findings ☐ Opt-In for Research Findings

PROBAND SAMPLE(S)

Please refer to www.baylorgenetics.com for full sample requirements.

- ◯ Whole Blood in EDTA
- ◯ Buccal Swab
- ◯ Saliva
- ◯ Cord Blood
- ◯ Cultured Skin Fibroblast
- ◯ Extracted DNA from _____

mtDNA analysis only

- ◯ Skeletal Muscle
- ◯ Liver
- ◯ Tissue

Global MAPS® only

- ◯ Plasma from EDTA
- ◯ Urine

_____ / _____ / _____
Date of Collection (MM / DD / YYYY)

NOTE: Extracted DNA/RNA will only be accepted if the isolation of nucleic acids for clinical testing occurs in a CLIA-certified laboratory or a laboratory meeting equivalent requirements as determined by the CAP and/or the CMS.

BIOLOGICAL PARENTS INFORMATION

BIOLOGICAL PARENTS SAMPLES ARE REQUIRED FOR TRIO WES; Other family members cannot be substituted for either parent. Be sure to label parental samples with full name and date of birth - DO NOT LABEL WITH CHILD'S NAME. Must sign parental testing authorization on consent.

MATERNAL INFORMATION

☐ Asymptomatic ☐ Symptomatic (Attach summary of findings)

Maternal Last Name | Maternal First Name | MI

Maternal Date of Birth (MM / DD / YYYY) ____/____/____

Date of Collection (MM / DD / YYYY) ____/____/____

Sample Type:
- ◯ Blood in EDTA (preferred)
- ◯ Buccal Swab
- ◯ Saliva

PATERNAL INFORMATION

☐ Asymptomatic ☐ Symptomatic (Attach summary of findings)

Paternal Last Name | Paternal First Name | MI

Paternal Date of Birth (MM / DD / YYYY) ____/____/____

Date of Collection (MM / DD / YYYY) ____/____/____

Sample Type:
- ◯ Blood in EDTA (preferred)
- ◯ Buccal Swab
- ◯ Saliva

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WHOLE EXOME SEQUENCING (WES) REQUISITION

Patient Last Name | Patient First Name | MI | Date of Birth (MM / DD / YYYY) | Genetic Sex

ITEM CHECKLIST FOR TESTING

- ☐ Proband Sample (Required)
- ☐ Maternal Sample (Required for Trio WES)
- ☐ Paternal Sample (Required for Trio WES)
- ☐ Signed WES Consent Form
- ☐ Clinical Note/Summary
- ☐ Requisition
- ☐ Indication for Study
- ☐ Pedigree (Optional)

INDICATION FOR TESTING (REQUIRED)

Please provide the following clinical information regarding the patient to be tested. Please also submit a clinic note and pedigree, if available. Phenotypes listed are in HPO terms with the corresponding HPO number (http://human-phenotype-ontology.github.io/). This information is needed to facilitate interpretation of whole exome sequencing results. If the laboratory requires additional information, please indicate the health care provider to be contacted:

PRE/PERINATAL HISTORY

- ☐ 0001622 Prematurity - GA at birth _____
- ☐ 0001511 Intrauterine Growth Restrictions
- ☐ 0001562 Oligohydramnios
- ☐ 0001561 Polyhydramnios
- ☐ 0000476 Cystic Hygroma
- ☐ 0000776 Congenital Diaphragmatic Hernia
- ☐ 0001508 Failure to Thrive
- ☐ 0001539 Omphalocele
- ☐ 0002084 Encephalocele
- ☐ 0010880 Increased Nuchal Translucency
- ☐ _____

EYE DEFECTS & VISION

- ☐ 0000505 Visual Impairment
- ☐ 0000618 Blindness
- ☐ 0000589 Coloboma
- ☐ 0000526 Aniridia
- ☐ 0000528 Anophthalmia
- ☐ 0000568 Microphthalmia
- ☐ 0000508 Ptosis
- ☐ 0000486 Strabismus
- ☐ 0000519 Cataract Congenital Bilateral
- ☐ _____
- ☐ _____

MOTOR/COGNITIVE DEVELOPMENT

- ☐ 0000750 Delayed Speech & Language Development
- ☐ 0001270 Delayed Motor Milestones
- ☐ 0002376 Developmental Regression
- ☐ Intellectual Disability
  - ☐ 0001256 Mild
  - ☐ 0002342 Moderate
  - ☐ 0010864 Severe
- ☐ 0000729 Autistic Spectrum Disorder
- ☐ _____
- ☐ _____

STRUCTURAL BRAIN ABNORMALITIES

- ☐ 0001360 Holoprosencephaly
- ☐ 0001339 Lissencephaly
- ☐ 0002084 Encephalocele
- ☐ 0000238 Hydrocephalus
- ☐ 0002119 Ventriculomegaly
- ☐ 0001273 Abnormality of Corpus Callosum
- ☐ 0002539 Cortical Dysplasia
- ☐ 0012444 Brain Atrophy
- ☐ 0002352 Leukoencephalopathy
- ☐ 0002269 Abnormality of Neuronal Migration
- ☐ 0002126 Polymicrogyria
- ☐ 0001302 Pachgyria
- ☐ 0002500 Abnormality of Cerebral White Matter
- ☐ 0007266 Cerebral Dysmyelination
- ☐ 0006808 Cerebral Hypomyelination
- ☐ 0002134 Abnormality of the Basal Ganglia
- ☐ 0002363 Abnormality of the Brainstem
- ☐ 0007360 Aplasia/Hypoplasia of the Cerebellum
- ☐ 0006817 Aplasia/Hypoplasia of the Cerebellar Vermis
- ☐ _____

NEUROLOGICAL

- ☐ 0001284 Areflexia
- ☐ 0200134 Epileptic Encephalopathy
- ☐ 0001250 Seizures
  - ☐ 0002373 Febrile Seizures
  - ☐ 0012469 Infantile Spasms
  - ☐ 0002123 Generalized Myoclonic Seizures
  - ☐ 0002069 Generalized Tonic-clonic Seizures
  - ☐ 0010818 Generalized Tonic Seizures
  - ☐ 0010819 Atonic Seizures
  - ☐ 0002121 Absence Seizures
  - ☐ 0011169 Generalized Clonic Seizures
  - ☐ 0001251 Ataxia
  - ☐ 0001332 Dystonia
  - ☐ 0002072 Chorea
  - ☐ 0001257 Spasticity
  - ☐ 0009830 Neuropathy
- ☐ _____
- ☐ _____

CRANIOFACIAL

- ☐ 0000256 Macrocephaly
- ☐ 0000252 Microcephaly
- ☐ 0001363 Craniosynostosis
- ☐ 0000204 Cleft Upper Lip
- ☐ 0000175 Cleft Palate
- ☐ 0000316 Hypertelorism
- ☐ 0000601 Hypotelorism
- ☐ 0008050 Abnormality of the Palpebral Fissures
- ☐ 0000286 Epicanthal Folds
- ☐ 0000288 Abnormality of the Philtrum
- ☐ 0010938 Abnormality of the External Nose
- ☐ _____
- ☐ _____

Indications continued on next page

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INDICATION FOR TESTING (REQUIRED) - CONTINUED

HAIR & SKIN

- ☐ 0000957 Cafe-Au-Lait Spots
- ☐ 0001034 Hypermelanotic Macule
- ☐ 0001010 Hypopigmentation of the Skin
- ☐ 0008066 Abnormal Blistering of the Skin
- ☐ 0008064 Ichthyosis
- ☐ 0000988 Skin Rash
- ☐ 0001581 Recurrent Skin Infections
- ☐ 0005306 Capillary Hemangiomas
- ☐ 0001597 Abnormality of the Nail
- ☐ 0004554 Generalized Hypertrichosis
- ☐ 0001596 Alopecia
- ☐ 0002208 Coarse Hair
- ☐ 0002299 Brittle Hair
- ☐ _____
- ☐ _____

CARDIAC

- ☐ 0001631 Atria Septal Defect
- ☐ 0001629 Ventricular Septal Defect
- ☐ 0001655 Patent Foramen Ovale
- ☐ 0001713 Abnormality of Cardiac Ventricle
- ☐ 0001636 Tetralogy of Fallot
- ☐ 0001680 Coarctation of Aorta
- ☐ 0001647 Bicuspid Aortic Valve
- ☐ 0002616 Aortic Root Dilatation
- ☐ 0001638 Cardiomyopathy
- ☐ 0011675 Arrhythmia
- ☐ _____
- ☐ _____

GENITOURINARY

- ☐ 0000113 Polycystic Kidney Dysplasia
- ☐ 0000107 Renal Cyst
- ☐ 0008738 Partially Duplicated Kidney
- ☐ 0000104 Renal Agenesis
- ☐ 0000085 Horseshoe Kidney
- ☐ 0000069 Abnormality of the Ureter
- ☐ 0000795 Abnormality of the Urethra
- ☐ 0000047 Hypospadias
- ☐ 0000028 Cryptorchidism
- ☐ 0000035 Abnormality of the Testis
- ☐ 0000062 Ambiguous Genitalia
- ☐ _____
- ☐ _____

RESPIRATORY

- ☐ 0002093 Respiratory Insufficiency
- ☐ 0002878 Respiratory Failure
- ☐ 0002104 Apnea
- ☐ 0002791 Hypoventilation
- ☐ 0002883 Hyperventilation
- ☐ 0002788 Recurrent Upper Respiratory Tract Infections
- ☐ _____
- ☐ _____

METABOLIC

- ☐ 0001946 Ketosis
- ☐ 0003074 Hyperglycemia
- ☐ 0001943 Hypoglycemia
- ☐ 0001941 Acidosis
- ☐ 0003128 Lactic Acidosis
- ☐ 0003215 Dicarboxylic Aciduria
- ☐ 0002490 Increased CSF lactate
- ☐ 0001992 Organic Aciduria
- ☐ 0030085 Abnormal CSF Lactate Level
- ☐ 00003542 Increased Serum Pyruvate
- ☐ 0003535 3-Methylglutaconic aciduria
- ☐ 0001942 Metabolic acidosis
- ☐ 0100493 Hypoammonemia
- ☐ 0001987 Hyperammonemia
- ☐ 0004923 Hyperphenylalaninemia
- ☐ 0003234 Decreased Plasma Carnitine
- ☐ 0003236 Elevated Serum Creatine Phosphokinase
- ☐ Abnormal Newborn Screen
- ☐ Unusual Color/Odor
- ☐ _____
- ☐ _____

MUSCULOSKELETAL

- ☐ 0011398 Hypotonia
- ☐ 0001276 Hypertonia
- ☐ 0000098 Tall Stature
- ☐ 0004322 Short Stature
- ☐ 0001382 Joint Hypermobility
- ☐ 0001371 Flexion Contracture
- ☐ 0002804 Arthrogryposis Multiplex Congenita
- ☐ 0001161 Hand Polydactyly
- ☐ 0001829 Foot Polydactyly
- ☐ 0006101 Finger Syndactyly
- ☐ 0001770 Toe Syndactyly
- ☐ 0100490 Camptodactyly of Finger
- ☐ 0012165 Oligodactyly
- ☐ 0001762 Talipes Equinovarus
- ☐ 0002757 Recurrent Fractures
- ☐ 0002650 Scoliosis
- ☐ 0002808 Kyphosis
- ☐ 0003307 Hyperlordosis
- ☐ 0001528 Hemihypertrophy
- ☐ 0001513 Obesity
- ☐ 0001548 Overgrowth
- ☐ 0002652 Skeletal Dysplasia
- ☐ _____
- ☐ _____

GASTROINTESTINAL

- ☐ 0002021 Pyloric Stenosis
- ☐ 0002575 Tracheoesophogeal Fistula
- ☐ 0002032 Esophageal Atresia
- ☐ 0002020 Gastroesophageal Reflux
- ☐ 0001733 Pancreatitis
- ☐ 0002014 Diarrhea
- ☐ 0002019 Constipation
- ☐ 0002037 Inflammatory Bowel Disease
- ☐ 0004389 Intestinal Pseudo-Obstruction
- ☐ 0001399 Hepatic Failure
- ☐ 0002572 Episodic Vomiting
- ☐ 0001744 Splenomegaly
- ☐ 0002240 Hepatomegaly
- ☐ 0001508 Postnatal Failure to Thrive
- ☐ 0002578 Gastroparesis
- ☐ _____
- ☐ _____

Indications continued on next page

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WHOLE EXOME SEQUENCING (WES) REQUISITION

Patient Last Name | Patient First Name | MI | Date of Birth (MM / DD / YYYY) | Genetic Sex

INDICATION FOR TESTING (REQUIRED) - CONTINUED

ENDOCRINE

- ☐ 0000819 Diabetes Mellitus
- ☐ 0000873 Diabetes Insipidus
- ☐ 0000821 Hypothyroidism
- ☐ 0000829 Hypoparathyroidism
- ☐ 0000834 Abnormality of the Adrenal Glands
- ☐ 0001738 Exocrine Pancreatic Insufficiency
- ☐ 0002721 Immunodeficiency
- ☐ _____
- ☐ _____

EAR DEFECTS & HEARING

- ☐ 0000407 Sensorineural Hearing Impairment
  - ☐ 0008619 Bilateral
- ☐ 0000405 Conductive Hearing Impairment
- ☐ 0000410 Mixed Hearing Impairment
- ☐ 0004467 Preauricular Pit
- ☐ 0000384 Preauricular Skin Tag
- ☐ 0000369 Low-set Ears
- ☐ 000037 Abnormality of the Pinna
- ☐ _____
- ☐ _____

HEMATOLOGY

- ☐ 0001875 Neutropenia
  - ☐ 0005549 Congenital
  - ☐ Chronic
  - ☐ Cyclic
- ☐ 0001873 Thrombocytopenia
- ☐ 0040185 Macrothrombocytopenia
- ☐ 0005537 Decreased Mean Platelet Volume
- ☐ 0005518 Erythrocyte Macrocytosis
- ☐ 0004444 Spherocytosis
- ☐ 0012410 Pure Red Cell Aplasia
  - ☐ Aplastic
  - ☐ Hypoplastic
- ☐ 0001903 Anemia
- ☐ 0005528 Bone Marrow Hypocellularity
- ☐ _____
- ☐ _____

CANCER

- ☐ Type of Cancer _____
- ☐ Age of Diagnosis _____
- ☐ Family History of Cancer and Affected Relatives

_____

_____

OTHER

- ☐ Organomegaly
- ☐ Chronic Infections
- ☐ 0004311 Abnormality of Macrophages
- ☐ 0001954 Episodic Fever
- ☐ 0004313 Hypogammaglobulinemia
- ☐ 0010701 Abnormal Immunoglobulins
- ☐ 0002721 Immunodeficiency
- ☐ 0012088 Abnormal urinary odor
- ☐ 0012537 Food intolerance
- ☐ 0008067 Abnormally lax or hyperextensible skin
- ☐ Abnormal Movements
- ☐ Family History of Similar Disorder
- ☐ 0001254 Lethargy
- ☐ 0002415 Leukodystrophy
- ☐ _____
- ☐ _____

GENES OF INTEREST

_____

_____

_____

_____

ADDITIONAL CLINICAL INFORMATION

DIFFERENTIAL DIAGNOSIS

Consent on next page

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WHOLE EXOME SEQUENCING (WES) CONSENT

Patient Last Name	Patient First Name	MI	Date of Birth (MM / DD / YYYY)	Genetic Sex
			/ /	

INFORMATION AND CONSENT FOR TESTING

DESCRIPTION OF WHOLE EXOME SEQUENCING (WES) TEST

The Whole Exome Sequencing (WES) test identifies changes, called variants, in a person's DNA that cause genetic disorders or medical conditions. The WES test provides a comprehensive analysis of the exome, which is the part of the human genome that helps the body make important proteins. The WES test will analyze the important regions of thousands of genes at the same time. Based on the symptoms that are known, genes with changes associated with these symptoms will be reported. WES results are very accurate, but no test is perfect. There is a small chance that DNA changes may not be detected due to limitations of technology or information known about the genes being tested. Results are based on the information available at the time of the testing and may change in the future as medical knowledge changes. It is possible that even if WES identifies the underlying genetic cause for a disorder in a family this information may not help in predicting medical outcomes or change medical management or treatment of disease. WES testing may also identify information about genes and diseases that have clear and immediate medical significance to your health or the health of your family members, even if that information is not related to currently known symptoms. You may consider discussing the significance of your results with your healthcare provider or genetic counselor.

TEST RESULTS

You may receive any of the following types of results:

- Positive: Positive results mean there are one or more changes in the genetic material related to your medical issues.
- Negative: Negative results mean no relevant genetic change could be detected using WES. Genetic testing, while highly accurate, might not detect a change present in the genes tested. This can be due to limitations of the information available about the genes being tested, or limitations of the testing technology. In addition, WES does not test all of the genes in the genome due to technical limitations.
- Results of Unclear Significance: WES can detect change(s) in DNA that do not have clear meaning. These changes are also referred to as variants of uncertain significance (VUS). Additional studies may be indicated if a VUS is identified in a gene that may be associated with your medical condition.

INCIDENTAL FINDINGS

This test may also find changes in genes that cause symptoms or diseases not related to the reason for having the test. These are called Secondary Findings and are associated with clear and immediate medical significance to your health or the health of your family members.

Category I: ACMG Secondary Findings

The American College of Medical Genetics (ACMG) has published guidelines for the reporting of these types of medically actionable or secondary findings (PMID: 34012068). These guidelines include a list of genes, which are updated occasionally, that are considered medically actionable and indicate laboratories should report pathogenic (disease-causing) findings in these genes. In accordance with an update to this policy statement (PMID: 25356965), you may choose to opt-in to receive this information.

Category II: Other Incidental Findings

Medically actionable variants are changes found in genes known to be associated with disease but not associated with your current symptoms or clinical presentation. These variants are reported as they may cause severe, early-onset disease or may have implications for treatment and prognosis. You may choose to opt-in to receive this information.

ADDITIONAL REPORTING CONSIDERATIONS

The interpretation of the test results is based on information available at the time of testing. As medical knowledge advances, our interpretation of these results may change in the future. We expect to find hundreds of changes when testing a person's DNA, and most of these changes do not relate to disease and therefore will not be reported. The raw sequence data generated by WES is available for request once a WES report has been issued. Please see our website for further information.

The report will NOT include findings in genes causing adult-onset neurodegenerative syndromes for which there is presently no prevention or cure. If the reason for testing includes features that clearly indicate such a disorder, we recommend pursuing targeted testing based on specific symptoms and not WES testing. However, if the reason for testing includes a clinical presentation that could include such a disorder, then results may be reported in the proband (patient) and the parents for genes that have an allelic association with dementia or is a component of the phenotype.

Additional considerations for Trio WES (test codes 1600, 1722, 1532, 1533): As part of the Trio WES test, blood samples from the biological parents of the proband are required. Trio WES will be performed on the proband and parental samples at the same time and the sequence data will be analyzed in the context of the family relationships. The parental data will be used to help interpret the proband's data. We will report changes in genes that are present in the affected individual, but not in the asymptomatic parents. This category of results caused by new (de novo) findings may be significant in determining the cause of the medical condition. Thus, this category of changes will be reported for genes with a known current association with disease. We will also report changes in genes where each parent has one change and the affected individual has inherited both changes. Custom Family Sequence Analysis (test code 1580) is available for other family members at an additional charge. Free testing for variants of unknown significance is available with prior approval. A separate parental report will be issued regarding ACMG secondary findings.

continue on next page

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WHOLE EXOME SEQUENCING (WES) CONSENT

Patient Last Name	Patient First Name	MI	Date of Birth (MM / DD / YYYY)	Genetic Sex
			/ /	

ADDITIONAL REPORTING CONSIDERATIONS

Additional considerations for Duo WES (test codes 1603, 1623): As part of the Duo WES test, a sample from one biological parent is required. Duo WES will be performed on the proband and parental sample at the same time and the sequence data will be analyzed in the context of the family relationships. The parental data will be used to help interpret the proband's data. Custom Family Sequence Analysis (test code 1580) is available for family members at an additional charge. Free testing for variants of unknown significance is available with prior approval. A separate parental report will be issued regarding secondary findings.

Additional reporting for Proband WES (test codes 1500, 1530,1531): Biological parental samples may help facilitate interpretation of Proband WES results. After the proband report is issued, the parental samples received will be tested by Whole Exome Sequencing (test code 1551) for the entire exome, or will be tested by targeted methods such as Sanger sequencing (test code 1580) for changes in genes that are highly likely to be causative of disease in the affected individual to confirm mode of inheritance, de novo status, etc. as determined necessary by the laboratory. Testing of parental status will ONLY be initiated if there is a variant identified in the proband. For targeted testing on the variants detected in the proband's exome data, test code 1580 is available for all family members. Free testing for variants of unknown significance in the immediate family members is available if approved by Baylor Genetics.

Your physician may order additional tests along with WES. Further test code specific information is as follows:

Test codes 1531, 1532 and 1533: In addition to WES analysis as detailed above, this order will also include a separate analysis of the mitochondrial DNA.

Test code 2055: This order is an analysis of the Mitochondrial DNA (mtDNA). This will be reported separately from the WES results with a turnaround time of 14-28 days. If a change in the mtDNA is identified, the report will indicate recommendations for familial follow-up. Baylor Genetics will NOT automatically initiate testing on the maternal sample. If this is desired, please contact client services for assistance.

Test code 1530: This order will also include a separate Chromosomal Microarray Analysis for the detection of deletions and duplications (missing or extra regions of DNA) plus a screen for uniparental disomy (UPD) and absence of heterozygosity (AOH), which are changes that can be associated with an increased risk for certain genetic conditions.

Test code 8665: The result of this Chromosomal Microarray Analysis (including copy number changes and UPD/AOH detection) will be reported separately from the WES results with a turnaround time of 14 days. If a copy number change is identified, the report will indicate recommendations for familial follow-up. Baylor Genetics will NOT automatically initiate testing on the parental sample(s). If this is desired, please contact client services for assistance.

Test codes 4900 and 4901: This is a large scale, semi-quantitative screening test that looks at changes related to biochemical and metabolic conditions. This is a screening tool for individuals who have symptoms that are not clearly associated with a known disease or as supportive evidence in individuals with results of unclear significance in genes related to biochemical and metabolic conditions. It is not intended to replace current diagnostic testing for specific conditions, nor is it intended for monitoring therapy of a diagnosed condition. Any abnormalities detected using Global MAPS® should be confirmed by diagnostic biochemical or molecular diagnostic testing.

This is the consent for WES testing and does not need to be completed if only Chromosomal Microarray Analysis, Mitochondrial DNA Analysis, or Global MAPS® is ordered. Please visit the Baylor Genetics website for further information about these tests and their associated consent forms.

CONSIDERATIONS AND LIMITATIONS

1. It is possible that you could have a change in a gene included in the WES test, but the WES test was unable to detect the change. Therefore, it is possible that you may be affected with one of the conditions tested by WES, but that the test did not detect the change associated with this condition.
2. The WES test does not analyze all of the genes in the human genome. There are some genes that cannot be included in the test due to technical limitations.
3. Results may be unclear or indicate the need for further testing on other family members
4. It is possible that additional information may come to light during these studies regarding family relationships. For example, data may suggest that family relationships are not as reported, such as non-paternity (the father of the individual is not the biological father) or consanguinity (reproductive partners are blood relatives). Since the accurate assignment of family relationships is critical to the analysis of WES, we may perform a separate genetic test to confirm that the samples that were submitted from the parents were correctly identified. If a discrepancy is identified, we will proceed with testing for the individual(s) who are correctly identified.
5. If you sign the consent form, but you no longer wish to have your samples tested by WES, you can contact your doctor to cancel the test. If testing is complete, but you have not received your results yet, you can inform your doctor that you no longer wish to receive the results. However, if you withdraw consent for testing after 5:00 p.m. CST the next business day following sample receipt by the laboratory, you will be charged for the full cost of the test.
6. Changes identified by WES may be submitted to public databases, such as ClinVar, to contribute knowledge to the medical profession. Usually limited clinical information is also required for the submission. However, it is unlikely that contents of the database submissions will include any information that will identify you personally.
7. Because many different genes and conditions are being analyzed, there is a risk that you will learn genetic information about yourself or your family that is not directly related to the reason for ordering the WES. This information might relate to diseases with symptoms that may develop in the future in yourself or other family members as well as conditions that have no current treatment.
8. It is possible that even if WES identifies the underlying genetic cause for the disorder in your family, this information may not help in predicting prognosis or change management or treatment of disease.

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CONNECT

WHOLE EXOME SEQUENCING (WES) CONSENT

Patient Last Name | Patient First Name | MI | Date of Birth (MM / DD / YYYY) | Genetic Sex

PATIENT CONFIDENTIALITY AND SPECIMEN RETENTION

Results will only be released to a licensed healthcare provider, to those allowed access to test results by law, and to those authorized in writing.

In rare cases, persons with genetic diagnoses have experienced problems with insurance coverage and employment. The U.S. Federal Government has enacted several laws that prohibit discrimination based on genetic test results by health insurance companies and employers. In addition, these laws prohibit unauthorized disclosure of this information. For more information, you can visit www.genome.gov/10002077.

Samples will be retained in the laboratory in accordance with the laboratory retention policy.

After testing is complete, the de-identified submitted specimen may be used for test development and improvement, internal validation, quality assurance, and training purposes. DNA specimens are not returned to individuals or to referring healthcare providers unless specific prior arrangements have been made.

Samples from residents of New York State will not be included in the de-identified research studies described in this authorization and will not be retained for more than 60 days after the sample was collected, unless specifically authorized by your selection. No tests other than those authorized shall be performed on the biological sample.

Information including results, indications for testing, and clinical status obtained from the hereditary cancer gene testing may be shared with healthcare providers, scientists, and healthcare databases or used in scientific publications or presentations, but the personal identifying information of all persons studied will not be revealed in such data sharing or publications/presentations.

PATIENT REPORTING OPTIONS AND AUTHORIZATION

Please read the statements below carefully and check the appropriate box and initial. Due to the nature of the methodology of this testing we are unable to guarantee that all pathogenic (disease-causing) variants in each option will be detected by the WES testing. Please refer to the Baylor Genetics website for up-to-date information on the detectable range of the WES test.

DNA Prep (test code 6997): At the discretion of Baylor Genetics, select parental analyses may be performed and reported under Sequential Trio Whole Exome Sequencing (test code 1551) or Custom Family Sequence Analysis (test code 1580) per the additional reporting for Proband WES protocol in the consent below.

For Options 1 & 2: If neither box is checked, or if the form is not signed, consent is interpreted as "NO."

INITIAL 1. SECONDARY FINDINGS

Pathogenic and likely pathogenic variants in genes included in the ACMG policy statement regarding recommendations for reporting of secondary findings will be reported as medically actionable on the WES report.

_____ ◯ **YES** Please report pathogenic and likely pathogenic variants in genes determined to be medically actionable by the ACMG policy statement.

_____ ◯ **NO** Please do NOT report pathogenic or likely pathogenic variants in genes included in the ACMG policy statement.

INITIAL 2. OPTION TO ALLOW RELEASE OF UPDATED RESULTS

If a possible diagnosis can be made with this information we would like to issue an updated report to the physician who ordered your WES test. This review does NOT include a complete review of all of your data.

_____ ◯ **YES** If new information regarding the clinical significance of changes in my WES testing becomes known, I would like Baylor Genetics to issue an updated report which includes this information to my physician who ordered this WES testing.

_____ ◯ **NO** Please do NOT issue an updated report if there is new information regarding the clinical significance of my WES testing that becomes known.

I hereby authorize Baylor Genetics to conduct genetic testing for myself (or my child) for the Whole Exome Sequencing test as recommended by my physician.

Printed Name | Signature | Date (MM / DD / YYYY)

Relationship to Patient | Proband Name | Proband DOB (MM/DD/YY)

Physician's/Counselor's Signature | Date (MM / DD / YYYY)

FOR SAMPLES SUBMITTED FROM NEW YORK STATE

INITIAL _____ I understand that no genetic test other than those I have authorized shall be performed on my biological sample, and the sample will be destroyed at the end of testing or not more than 60 days after the sample was taken. However, by initialing here, I hereby authorize the lab to retain my sample(s) for longer retention in accordance with the laboratory retention policy for internal laboratory quality assurance studies and possible research testing.

Consent authorization on next page

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WHOLE EXOME SEQUENCING (WES) CONSENT

Patient Last Name | Patient First Name | MI | Date of Birth (MM / DD / YYYY) | Genetic Sex

RAW DATA CONSENT

☐ By checking this box, I agree to allow Baylor Genetics to provide the raw data such as FASTQ or VCF sequencing files from my genetic test, only upon request, to me, my physician, or the requesting laboratory.

RESEARCH & RECONTACT CONSENT

For more information on research at Baylor Genetics, please visit baylorgenetics.com. Please read the below statements carefully and check the appropriate box.

Note: If left blank, consent is interpreted as "NO."

☐ I agree to the use of my de-identified specimen for research to improve genetic testing for all patients and contribute to scientific research.

☐ In addition to agreeing above, I agree to be contacted by Baylor Genetics regarding research opportunities.

☐ I am a New York State Resident, and I give Baylor Genetics permission to store my specimen in accordance to the laboratory retention policy for internal quality assurance and possible research studies.

Authorization and contact information MUST be completed, or we will not be able to reach you regarding these opportunities.

CONTACT INFORMATION

Address | City | State | Zip

Phone # | Alternative Phone # | Email

INFORMATION AND CONSENT FOR TESTING

Trio WES: (test codes 1600, 1722, 1532, 1533) We understand that our samples will be subjected to Trio WES and will be analyzed to help interpret the data from our child. A separate parental report will be issued regarding secondary findings. Testing of parental status for this category of results will be initiated independently of my child's data. It may be possible to infer information about family member's results based on my child's or other family member's results.

Duo WES: (test codes 1603, 1723) I understand that my sample will be subjected to Duo WES and will be analyzed to help interpret the data from my child. A separate parental report will be issued regarding secondary findings. Testing of parental status for this category of results will be initiated independent of my child's data. It may be possible to infer information about family member's results based on my child's or other family member's results.

Proband WES (test codes 1500, 1530, 1531) We understand that our samples will be subjected to targeted testing only (such as Sanger sequencing) and will NOT have WES testing. The laboratory will decide which changes will need parental studies. Testing of the parental status for the category of secondary findings will ONLY be initiated if there is a variant identified in my child.

Please read the statements below carefully and check the appropriate box and initial. Due to the nature of the methodology of this testing we are unable to guarantee that all pathogenic variants in each option will be detected by the WES testing. Note, if neither box is checked, or the form is not signed, consent is interpreted as "NO."

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CONNECT

WHOLE EXOME SEQUENCING (WES) PARENTAL CONSENT

Patient Last Name _____ Patient First Name _____ MI _____ Date of Birth (MM / DD / YYYY) ____ / ____ / ____ Genetic Sex _____

MATERNAL REPORTING OPTIONS AND AUTHORIZATION

INITIAL 1. SECONDARY FINDINGS

Pathogenic and likely pathogenic variants in genes included in the ACMG policy statement regarding recommendations for reporting of secondary findings will be reported as medically actionable on the WES report.

_____ ◯ **YES** Please report pathogenic and likely pathogenic variants in genes determined to be medically actionable by the ACMG policy statement.

_____ ◯ **NO** Please do NOT report pathogenic or likely pathogenic variants in genes included in the ACMG policy statement.

Mother's Printed Name _____ Date of Birth (MM / DD / YYYY) ____ / ____ / ____ Mother's Signature _____ Date (MM / DD / YYYY) ____ / ____ / ____

PATERNAL REPORTING OPTIONS AND AUTHORIZATION

INITIAL 1. SECONDARY FINDINGS

Pathogenic and likely pathogenic variants in genes included in the ACMG policy statement regarding recommendations for reporting of secondary findings will be reported as medically actionable on the WES report.

_____ ◯ **YES** Please report pathogenic and likely pathogenic variants in genes determined to be medically actionable by the ACMG policy statement.

_____ ◯ **NO** Please do NOT report pathogenic or likely pathogenic variants in genes included in the ACMG policy statement.

Father's Printed Name _____ Date of Birth (MM / DD / YYYY) ____ / ____ / ____ Father's Signature _____ Date (MM / DD / YYYY) ____ / ____ / ____

FOR SAMPLES SUBMITTED FROM NEW YORK STATE

MOTHER'S INITIAL _____ FATHER'S INITIAL _____

Specimen Retention: By leaving this section blank, my sample shall be destroyed at the end of the testing process or not more than 60 days after completion of testing. However, by initialing here, I hereby authorize the lab to retain my sample(s) for longer retention in accordance with the laboratory retention policy for internal laboratory quality assurance studies and possible research testing