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| **WHOLE GENOME SEQ REQUISITION FORM** | | | | |
| **PATIENT INFORMATION** | | | | |
| Patient Name |  | MRN | |  |
| Date of Birth |  | Gender | | Male  Female Unknown |
| Nationality |  | Race/Ethnicity | |  |
| Is this patient deceased? | Yes  No | Deceased Date | |  |
| Is this patient: | Symptomatic/Affected  Asymptomatic/unaffected | | | |
| **SAMPLE INFORMATION\*** | | | | |
| Sample submitted as | gDNA | | DNA Extraction Request | |
| Patient has had a blood transfusion | Yes  No | Date of last transfusion | |  |
| \*Only blood in purple/lavender EDTA tubes | | | | |
| **TEST ORDERED** | | | | |
| Whole GENOME sequencing (WGS) | Proband only  TRIO (Proband and parents)  Proband, parents and additional family members | | | |

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| **ORDERING PHYSICIAN/PROVIDER** | |
| Name: Email:  Phone: | Clinic/Hospital/Institution name:  Department:  Address: | |

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| FAMILIAL INFORMATION (FOR TRIOS) |

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| BIOLOGICAL MOTHER:Name (First, Last): **Date of Birth:** | | Symptomatic (clinically affected)? Yes  No  Sample Included  Collection date:  Sample To be sent later | | |
| BIOLOGICAL FATHER:Name (First, Last):Date of Birth: | | Symptomatic (clinically affected)? Yes  No  Sample Included  Collection date:  Sample To be sent later | | |
| ADDITIONAL FAMILY MEMBER:Relationship to patient:Name (First, Last):Date of Birth: | | Symptomatic (clinically affected)? Yes  No  Sample Included  Collection date:  Sample To be sent later | | |
| ADDITIONAL FAMILY MEMBER:Relationship to patient:Name (First, Last):Date of Birth: | | Symptomatic (clinically affected)? Yes  No  Sample Included  Collection date:  Sample To be sent later | | |
| **CLINICAL INFORMATION** | | | |
| **ICD-10 codes (required):** | | | |
| **Clinical diagnosis:** | | | |
| **Age at initial presentation:** | | | |
| **Differential diagnosis:** | | | |
| **Reason for Testing (please include pertinent history and findings, including pathology report)**: | | | |
| * Pre/Perinatal History * Structural Brain Abnormalities * Developmental/Behavioral Findings * Neurological Findings * Craniofacial/Dysmorphism * Eye Defects/ Vision * Hearing Impairment * Endocrine Findings * Respiratory Findings * Hematologic or Immunologic Findings | | | * Skin/Hair Findings * Cardiac Findings * Gastrointestinal Findings * Metabolic findings (Attached relevant lab reports/values) * Vascular System * Genitourinary Findings * Musculoskeletal Findings * Cancer * Vascular System | |
| **Parental consanguinity** Yes  No | | | | |
| **If Yes, specify the relationship:** | | | | |
| **Family History (Attach pedigree if available):** | | | | |
| **Other Tests (Attach reports if available):** | | | | |
| **ECHO:**  **EEG:**  **EMG:**  **MRI:** | | | **Muscle Biopsy:**  **Ultrasound:**  **X-rays:**  **Others:** | |
| **Genetic tests** | **Performed at** | | **Result** | |
| **Karyotyping** |  | |  | |
| **Microarray** |  | |  | |
| **Single gene sequencing** |  | |  | |
| **Gene Panel** |  | |  | |
| **Others, specify** |  | |  | |
| **Any remarkable findings related to the below (Please attach reports):** | | | |

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| **Test Parameters Request** |

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| **Flow cell request (default is Novaseq 6000, S2 Flowcell, 8 Genomes per cell, Dual cell configuration) \*** |  | |
| **Coverage Request (Default is a ~30x coverage) \*** |  | |
| **If Sample was provided as gDNA:** | **Extraction Method** |  |
| **Date of Extraction** |  |
| **Storage Method** |  |
| **A260/280** |  |
| **A230/280** |  |
| **Qubit Conc.**  **(Ng/ul)** |  |
| **Nanodrop Conc. (ng/ul)** |  |
| **Total ng gDNA in sample (please refer to the Sample Submission Guidelines for WGS requirements)** |  |
| **Has the patient received any Intravenous Medication 24-48 hours prior to sample acquisition** |  |
| **Dual or Single Flowcell Configuration (Default is Dual flowcell, 8 Genomes per flowcell)** |  | |
| **Indexing preference, Default is Single indexing for batches bellow 24 samples and combinatorial dual Indexing for batches above 24 samples. \*** |  | |
| **Kappa qPCR Quantification or Qubit Quantification (qPCR is default & highly recommended, if Qubit is selected, we cannot guarantee proper Run metrics)** |  | |
| **Shearing size preference (350bp, 550 bp)** |  | |
| **internal Control (default is No, IC will not be analyzed if Bioinformatics service is requested)**  **PhiX Spike (Default is yes)** |  | |
| ***\*: Pricing may change depending on if your preference differs from default*** | | |