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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
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| **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*** |