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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 | Normalized Pooled library | | Non-pooled library | |
| Library must be quantified by the recommended library prep recommended means (qPCR , Fluorometric) prior to submission | | | | |

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| **ORDERING PHYSICIAN/PROVIDER** | | | |
| Name: Email:  Phone: | | Clinic/Hospital/Institution name:  Department:  Address: | | |
| **CLINICAL INFORMATION – For Human Clinical Samples** | | | |
| **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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| **NGS Application** |  | | | | |
| **Paired end or single reads** |  | | | | |
| **Number of libraries** |  | | | | |
| **Library prep kit** |  | | | | |
| **Are libraries pooled** |  | | | | |
| **If pooled. Concentration of pooled library (in nM)\*** |  | | | | |
| **for non-pooled libraries, provide Each library nM Conc & Average fragment length (1) (5)** | **Library ID** | | **fragment length** | | **nM Conc.** |
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| **Final Pooled library loading concentration (In nM, Please Refer to Genomic Requisition for SBS Sequencing Requirements) (2)** |  | | | | |
| **Internal control added (PhiX, Inline, Coriell gDNA…etc)** |  | | | | |
| **If custom internal control, please specify** |  | | | | |
| **Flow cell request (Novaseq SP, S1 and Novaseq S2 available) (3)** |  | | | | |
| **Coverage Request \*\*\*** |  | | | | |
| **Dual or Single Flowcell Configuration (3)** |  | | | | |
| **Desired Sample per flowcell throughput (3) & (4)** |  | | | | |
| **Average amplicon length per library before pooling (Use the Following** |  | | | | |
| **Indexing used (Single, dual, combinatorial), Name, type and Cat. No of Index Kit** |  | | | | |
| **Library ID, Illumina index ID and Sequence for each library** | **Library ID** | **Index ID** | | **Sequence** | |
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| **For non-pooled libraries: Additional Kappa qPCR Quantification or Qubit Quantification of libraries prior to pooling (qPCR is default & highly recommended when performing WGS)** |  | | | | |
| **Inline Control DNA (default is No, IC will not be analyzed if a Bioinformatics service is requested)** |  | | | | |
| **Expected Gb output** |  | | | | |
| ***1: Table can be Cut, pasted and expanded if more libraries are included***  ***2: Additional dilution might be needed based on recommended loading nM concentration***  ***3: Pricing may change depending on if your preference differs from default***  ***4: Might Affect Coverage Requested***  ***5: Provide Size & Conc. files (Agilent Bioanalyzer, Tapestation, Fragment Analyzer Graphs, Qubit and qPCR tables in ng/ul and nM conversion )*** | | | | | |