

Large Scale Analysis and Sequencing Center (LSAC) Capacity

- Each of the LSACs was asked for their capacity to complete WGS before the end of this fiscal year (Sept 30, 2016)
 - Each responded that they could take about 1,000 samples
 - Samples need to be at the LSAC not later than the end of June 2016 in order to meet production schedules

Prioritization of samples for initial WGS

- WGS will need to be performed in waves based on capacity at the LSACs
- Select the initial ~3,000 samples and distribute equally across the 3 LSACs
- Prioritize racial diversity (AA, Hispanic, EA)
- European American samples cannot have previous WES or WGS (exceptions were made for ACT samples); for Hispanic and African American, samples with previous WES are acceptable for this new WGS initiative
- Minimize inter-LSAC variation by placing each racial/ethnic group at a separate LSAC

Sample requirements

- Site/study must have GDS approval
- Sample must have successful GWAS available
- LCL-derived DNA
 - Broad - will not accept LCL-derived DNA
 - WashU, Baylor – will/could accept LCL-derived DNA

Phenotypic Requirements

- AD cases: prioritize autopsy confirmed, especially if omics data are available, or probable AD; no age restrictions
- Healthy controls: must be between 60 and 90 at last normal assessment; start with autopsy confirmed normal subjects then select individuals between the ages of 60-90 at their last normal assessment
- Preferential selection of samples with longitudinal data

Reference samples

- Include reference samples to help bridge across the 3 LSAC and datasets to include the three samples that were sequenced across all the LSACs in the Discovery and Discovery Extension Phase. Include at least one new replicate from each of the 3 races being sequenced in the Discovery Extension phase.