

## SGFS Data Submission Form

Project ID: \_\_\_\_\_

Application Acceptance Date: \_\_\_\_\_

Maximum number of samples approved to submit for this protocol: \_\_\_\_\_

Number of previously submitted samples: \_\_\_\_\_

Date returned to submitting team: \_\_\_\_\_

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### Instructions:

Please complete this form for each new batch of sequence data and email this form to Julie Sapp [sappj@mail.nih.gov] prior to submitting data. Data will not be accepted until this form is received and approved.

Before submitting sequence data please review the instructions regarding data submission on the [SGFS website](#).

We can accept batches of sequence data as follows:

- Up to 200 participants every 6 months for prospective data submissions
- Up to 300 participants per year for retrospective data submissions

Please contact us or come to SGFS office hours if the data you are submitting exceed these parameters.

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### 1. How many samples are in this batch of data?

*Please double check that this submission does not put your total sample count over the maximum number approved for this protocol as stated above.*

### 2. What date will you submit this data set via secure email or Globus?

### 3. Please check and confirm the following:

- a. Reference genome:      GRCh37              hg19
  - b. Aligner used to align reads:
  - c. Variant caller used to call variants:
  - d. The data set is restricted to the ACMG 59 gene list, per this [BED file](#)
  - e. The data set is restricted to only "PASS" variants
  - f. The data set is a single, multi-sample VCF file
  - g. The number of samples in the VCF equals the number of samples in question #1
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It is **extremely important** that the data you submit to the SGFS comprises sequence data derived ONLY from the participant population reflected in the SGFS application. It is not uncommon for sequence data from healthy volunteers, biobank participants, additional cohorts, etc. to be submitted to the SGFS in error. Because of this, we ask that both the PI and the data submitter initial below:

The sequence data submitted to SGFS is restricted to the participant population referenced in our SGFS application.

Submitter Initials:

PI Initials: