SGFS Data Submission Form

Instructions for Teams Submitting Data:

A completed Data Submission Form must accompany EACH batch of data submitted to SGFS. When you submit your application, you will receive a copy of this form specific to your project. Data will not be accepted/processed unless accompanied by a signed and completed form.

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 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. Please check and/or 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 ACMG73 gene list per the BED file supplied by SGFS

   e.   The data set is restricted to only "PASS"/high quality 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

3. Approximate date you plan to submit this data set via secure email or Globus:

It is **extremely important** that the data you submit to the SGFS comprises sequence data derived ONLY from the participant population reflected in your approved 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 submitter initial below:

Submitter Initials: **PI Intitials:**

Form v2.0 (March 2022)