**Application for a protocol to participate in the Intramural Secondary Genomic Findings Service (SGFS)**

Is this a new application to the SGFS?

[ ]  Yes – Please complete all fields below

[ ]  No – This is a submission of a new batch of data, all details from original application are unchanged → remainder of application does not need to be filled out

[ ]  No – This is a submission of a new batch of data but some project details have changed → complete only portions of application that have changed

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Protocol Title/Number (if available):

IRB-reviewed version of protocol and consent forms are included with this application

[ ]  Yes [ ]  No – explain:

PI:

Precis:

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Sequencing methodology: [ ]  ES [ ] GS

Proposed file format of submitted variants: [ ]  VarSifter [ ]  VCF

Which reference sequence were your data aligned to? [ ]  GRCh37 [ ]  GRCh38

Will your submitted data be redacted in any way?

[ ]  No, we will submit full files

[ ]  Yes, we will only submit data pertaining to the current SGFS gene list

[ ]  Other – explain:

Is the disorder under investigation related to a gene on the current ACMG list?

[ ]  No [ ]  Yes – explain:

Description of genotype quality assessment (e.g., GATK quality score):

Naming convention for individual identifiers (e.g., “6 digit coded identifier”):

Source DNA: [ ]  peripheral blood [ ]  tissue other

Total number of sequenced samples:

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Where does your cohort **primarily** reside?

[ ]  Most participants live in the US [ ]  Most participants live outside of the US - country:

Estimated number of samples per year:

Person(s) to notify if a secondary variant is present and contact information:

Will SGFS return secondary findings per the protocol outlined in the SGFS Guidance Memo?

[ ]  Yes [ ]  No

**If Yes, please complete information below**

Person(s) consenting participants to protocol and contact information:

Any characteristics of your cohort/population that may have special relevance with respect to the return of secondary findings?

[ ]  High proportion of non-English speaking participants (Language:      )

[ ]  Many participants unlikely to have access to healthcare

[ ]  Anticipate difficulty re-contacting participants

[ ]  Other:

Questions?

Please visit [ <http://www.genome.gov/sgfs>] for more information.

Contact Kate Driscoll at (301) 594-1754 or Julie Sapp at (301) 435-6689 with any remaining questions.

Please send completed application along with an electronic version of the draft protocol and consent form to:

Kate Driscoll [ kate.driscoll@nih.gov ] and Julie Sapp [ sappj@mail.nih.gov ].