Data Use Certification Agreement

Multi-Ethnic Study of Atherosclerosis (MESA)

Introduction and Statement of Policy

The National Institutes of Health (NIH) has developed central data repositories to archive and distribute the results of studies provided by Contributing Investigators examining the relationship between genomic data (e.g., genotype, sequence, or epigenetic information) and phenotype. Such studies include genome-wide association studies, medical sequencing, and molecular diagnostic assays. Implicit in the establishment of the NIH data repositories, for example the database of Genotypes and Phenotypes (dbGaP), is the view that scientific progress in this area will be greatly enhanced if the data produced by these studies are readily available to all investigators in the research community.

Dataset access will be provided to research investigators who, along with their institutions, have certified their agreement with the expectations and terms of access detailed below. It is the intent of the NIH and the National Heart, Lung, and Blood Institute (NHLBI) that Approved Users of NIH-provided datasets recognize any restrictions on data use delineated within the original informed consent agreements of contributing studies, as identified by the submitting institutions and stated on database websites.

Definitions of terminology used in this document are found in the Appendix.

The parties to this agreement include: the Principal Investigator (PI) requesting access to the GWAS dataset ("the Approved User"), his/her home institution as represented by the Institutional Signing Official designated through the eRA Commons system ("the Requester"), and the NHLBI, NIH. The effective date of this agreement shall be the Project Approval Date, as specified on the Data Access Committee approval notification.

Study Background

MESA

The Multi-Ethnic Study of Atherosclerosis (MESA) is a study of the characteristics of subclinical cardiovascular disease (disease detected non-invasively before it has produced clinical signs and symptoms) and the risk factors that predict progression to clinically overt cardiovascular disease or progression of the subclinical disease. MESA researchers study a diverse, population-based sample of 6,814 asymptomatic men and women aged 45-84. Thirty-eight percent of the recruited participants are white, 28 percent African American, 22 percent Hispanic, and 12 percent Asian, predominantly of Chinese descent.
Participants were recruited from six field centers across the United States: Wake Forest University, Columbia University, Johns Hopkins University, University of Minnesota, Northwestern University and University of California – Los Angeles. Each participant received an extensive physical exam to determine coronary calcification, ventricular mass and function, flow-mediated endothelial vasodilation, carotid intimal-medial wall thickness and presence of echogenic lucencies in the carotid artery, lower extremity vascular insufficiency, arterial wave forms, electrocardiographic (ECG) measures, standard coronary risk factors, sociodemographic factors, lifestyle factors, and psychosocial factors. Selected repetition of subclinical disease measures and risk factors at follow-up visits allows study of the progression of disease. Blood samples have been assayed for putative biochemical risk factors and stored for case-control studies. DNA has been extracted and lymphocytes cryopreserved (for possible immortalization) for study of candidate genes and genome-wide scanning, expression, and other genetic techniques. Participants are being followed for identification and characterization of cardiovascular disease events, including acute myocardial infarction and other forms of coronary heart disease (CHD), stroke, and congestive heart failure; for cardiovascular disease interventions; and for mortality. In addition to the six Field Centers, MESA involves a Coordinating Center, a

Central Laboratory, and Central Reading Centers for Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Ultrasound, and Electrocardiography (ECG). Protocol development, staff training, and pilot testing were performed in the first 18 months of the study. The first examination took place over two years, from July 2000-July 2002. It was followed by three examination periods that were 17-20 months in length. Participants have been contacted every 9 to 12 months to assess clinical morbidity and mortality. NHLBI funded a renewal of the study in August 2008 (MESA II), which will support a fifth exam of the cohort, starting in April 2010.

MESA Family

The general goal of the MESA Family Study, an ancillary study to MESA funded by a grant from NHLBI, is to apply modern genetic analysis and genotyping methodologies to delineate the genetic determinants of early atherosclerosis. This is being accomplished by utilizing all the current organizational structures of the **Multi-Ethnic Study of Atherosclerosis (MESA)** and Genetic Centers at Cedars-Sinai Medical Center and the University of Virginia. In the MESA Family Study, the goal is to locate and identify genes contributing to the genetic risk for cardiovascular disease (CVD), by looking at the early changes of atherosclerosis within families (mainly siblings). 2128 individuals from 594 families, yielding 3,026 sibpairs divided between African Americans and Hispanic Americans, were recruited by utilizing the existing framework of MESA. MESA Family studied siblings of index subjects from the MESA study and from new sibpair families (with the same demographic characteristics) and is determining the extent of genetic contribution to the variation in coronary calcium (obtained via CT Scan) and carotid artery wall thickness (B-mode ultrasound) in the two largest non-majority U.S. populations. In a small proportion of subjects, parents of MESA index subjects participating in MESA Family were studied but only to have blood drawn for genotyping.

The MESA Family cohort was recruited from the six MESA Field Centers. MESA Family participants underwent the same examination as MESA participants, during May 2004 – May 2007. DNA was extracted and lymphocytes immortalized for study of candidate genes, genome-wide linkage scanning, and analyzed for linkage with these subclinical cardiovascular traits. While linkage analysis is the primary approach being used, an additional aspect of the MESA Family takes advantage of the existing MESA study population for testing a variety of candidate genes for association with the same subclinical traits. Genotyping and data analysis will occur throughout the study.

MESA Air

The general goal of the Multi-Ethnic Study of Atherosclerosis and Air Pollution ('MESA Air') is to prospectively examine the relation between an individual level assessment of long-term ambient air pollution exposures (including $PM_{2.5}$ and gaseous co-pollutants) and the progression of subclinical cardiovascular disease in a multi-city, multi-ethnic cohort. MESA Air will also prospectively examine the relationship between an individual level assessment of long-term ambient air pollution exposures and the incidence of cardiovascular disease, including myocardial infarction and cardiovascular death. MESA Air is funded by a grant from the United States Environmental Protection Agency to the University of Washington, and subcontracts from UW to other participating institutions.

MESA Air will assess if ambient air pollution is associated with changes over time in subclinical measures of atherosclerosis and plasma markers of inflammation, oxidative damage, and endothelial activation in a longitudinal data model, adjusting for age, race/ethnicity, socioeconomic status, and specific cardiovascular risk factors (such as diabetes, hypertension, smoking, and diet). The study will similarly assess if the incidence of cardiovascular events is associated with long-term exposure to ambient air pollution, using a proportional

hazards model. The study includes refinement of statistical tools, and explores joint/independent effects of acute and long-term pollutant exposure in the occurrence of cardiovascular disease.
The MESA Air study is built on the foundation of the ongoing MESA study. The parent MESA Study cohort is located in six geographic areas ('Field Centers') that capture tremendous exposure heterogeneity, comparable to or greater than the variability in locations of prior U.S. cohort studies. In addition to the six Field Centers, the study involves a Coordinating Center, a Central Laboratory, and Reading Centers for Computed Tomography (CT), ultrasound and air pollution data.
The cohort for the MESA Air study currently includes 6226 subjects: 5479 enrolled in the parent MESA study; 257 recruited specifically for this study, and 490 recruited from the MESA Family study. The entire MESA Air cohort will be followed over a 10-year project period for the occurrence of cardiovascular disease events.
On two occasions over the ten-year study period, 3600 subjects from the MESA Air cohort, residing in nine locales, will undergo computed tomography scanning to assess presence and extent of coronary artery calcification (CAC), and ultrasound of the carotid artery to determine intima-media thickness (IMT). We will also repeatedly assess plasma markers of inflammation, oxidative damage, and endothelial function in 720 subjects.

MESA Air adds state-of-the-art air pollution exposure assessment information to the MESA cohort study, and introduces new subjects and outcome measures to achieve our aims. The study will assess long-term individual-level exposure to ambient air pollutants for each subject using community-scale monitoring, outdoor spatial variation, subject proximity to pollution sources, pollutants' infiltration efficiency, and personal time-activity information. The exposure models will be validated using detailed monitoring in a subset of subjects.

Terms of Access

1. Research Use

The Requester agrees that if access is approved, the Principal Investigator named in the Data Access Request (DAR) submitted to the NIH, those named in the “Senior/Key Person Profile” portion of the DAR, which should include the Information Technology Director or his/her designee, and any trainee or employee working on the proposed research project under the direct supervision of these individuals, shall become Approved Users of the requested dataset(s). Research use will occur solely in connection with the research project described in the DAR, which includes a 1-2 paragraph description of the research objectives and design. New uses of these data outside those described in the DAR will require submission of a new DAR; modifications to the research project will require submission of an amendment to this application (e.g., the addition of new aims related to the approved project, adding or deleting collaborators from the same institution, and the potential addition of new NIH GWAS datasets to an approved project). The Requester and all Approved Users may use the dataset(s) only in accordance with the parameters described on the NIH database Web site for the appropriate research use, and any limitations on such use, of the dataset(s) and as required by law.

Research access to the requested dataset(s) is granted for a period of one (1) year as defined below.

Contributing Investigators, or their direct collaborators, who provided the data or samples used to generate an NIH genomic dataset and who have appropriate IRB approval, if applicable, for broader use of the data are exempt from the limitation on the scope of the research use as defined in the DAR.

NHLBI Specific Terms

DATA USE LIMITATION FOR MESA:

“Data may not be used to investigate individual pedigree structures or individual participant genotypes for the purpose of identifying individuals or families; assess variables or proxies that

could be considered as stigmatizing an individual or a group; perform phenotype-only analyses (note: investigators may request data for such phenotype-only analyses through the NHLBI's BioLINCC); or explore issues such as non-maternity and non-paternity and perceptions of racial/ethnic identity. All research must be related to the etiology and prevention of morbidity and mortality of the U.S. Population consistent with the demographic distribution in MESA."

Two consent groups are available from MESA: Health/Medical/Biomedical (HMB) Research Use and HMB Non-profit Use Only.

2. Institutional and Approved User Responsibilities

The Requester agrees through the submission of the Data Access Request (DAR) that the PI named in the DAR has reviewed and understands the principles for responsible research use and data handling of the genomic datasets as defined in the NIH GWAS Data Sharing Policy and detailed in this Data Use Certification agreement. The Requester and Approved Users further acknowledge that they are responsible for ensuring that all uses of the data are consistent with federal, state, and local laws and regulations and any relevant institutional policies. Through submission of the DAR, the Principal Investigator also agrees to submit annual data use reports to the appropriate NIH Data Access Committee (DAC) describing the research use of the Approved Users as described under *"Research Use Reporting"* below.

Approved Users who may have access to personal identifying information for research participants in the original study at their institution or through their collaborators, may be required to have IRB approval. By approving and submitting the attached Data Access Request, the Institutional Signing Official provides assurance that relevant institutional policies and applicable federal, state, or local laws and regulations (if any) have been followed, including IRB approval if required. The Institutional Signing Official also assures through the approval of the Data Access Request that other organizations within the institution with relevant authorities (e.g., the Office of Human Subjects Research, the Office of Information Technology, the Office of Technology Transfer, etc.) have reviewed the relevant sections of the NIH GWAS Data Sharing Policy and the associated procedures and are in agreement with the principles defined.

It is anticipated that, at least in some cases, these datasets will be updated with additional information. Unless otherwise indicated, all statements herein are presumed to be true and applicable to the access and use of all versions of these datasets.

3. Public Posting of Approved User's Research Use Statement

The Principal Investigator agrees that, if he or she becomes an Approved User, information about the PI and the approved research use may be posted on a public, US government web site that describes approved research projects. The information may include the Approved User's name and institution, project name, Research Use Statement, and a Non-technical Summary of the Research Use Statement. In addition, citations resulting from the use of NIH genomic datasets may be posted on NIH data repository websites.

4. Non-Identification

Approved Users agree not to use the requested datasets, either alone or in concert with any other information, to identify or contact individual participants from whom phenotype data and DNA samples were collected. This provision does not apply to research investigators operating with specific IRB approval, pursuant to 45 C.F.R. 46, to contact individuals within datasets or to obtain and use identifying information under an approved IRB research protocol. All investigators conducting "human subjects research" within the scope of 45 C.F.R. 46 must comply with the requirements contained therein.

5. Non-Transferability

The Requester and Approved Users agree to retain control over the data and further agree not to distribute data obtained through this Data Access Request to any entity or individual not covered

in the submitted Data Access Request. If Approved Users are provided access to NIH genomic datasets for inter-institutional collaborative research described in the Research Use Statement of the Data Access Request, and all members of the collaboration are also Approved Users through their home institution(s), data obtained through this Data Access Request may be securely transmitted within the collaborative group. All data security practices and other terms of use defined in this agreement and the *dbGaP Security Best Practices* for the raw data are expected to be followed for the derived data, including any transmission of the data.

The Requester and Approved Users acknowledge responsibility for ensuring the review and agreement to the terms within this Data Use Certification and the appropriate research use of NIH genomic data by research staff associated with any approved project, subject to applicable laws and regulations. NIH genomic datasets obtained through this Data Access Request, in whole or in part, may not be sold to any individual at any point in time for any purpose.

Approved Users agree that if they change institutions during the access period, they will submit a new Data Access Request and Data Use Certification in which the new institution agrees to the NIH GWAS data use policy before data access resumes. Any versions of data stored at the prior institution for the approved use will be destroyed and documented through a final Data Use Report as described below. However, if advance written notice and approval by the NHLBI Data Access Committee is obtained to transfer responsibility for the approved research project to another Approved User within the same institution the data may not need to be destroyed.

6. Data Security and Data Release Reporting

The Requester and Approved Users, including the institutional Information Technology Director or his/her designee, acknowledge the intent of the NIH that they have reviewed and agree to handle the requested dataset(s) according to the current *dbGaP Security Best Practices*, including its detailed description of requirements for security and encryption. These include, but are not limited to:

- all Approved Users have completed all required computer security training required by their institution, for example, the http://irtsectraining.nih.gov/, or the equivalent;
- the data will always be physically secured (for example, through camera surveillance, locks on doors/computers, security guard);
- servers must not be accessible directly from the internet, (for example, they must be behind a firewall or not connected to a larger network) and unnecessary services should be disabled;
- use of portable media, e.g., on a CD, flash drive or laptop, is discouraged, but if necessary then they should be encrypted consistent with applicable law;
- use of updated anti-virus/anti-spyware software;
- security auditing/intrusion detection software, detection and regular scans of potential data intrusions;
- use of strong password policies for file access.
- all copies of the dataset should be destroyed, as permitted by law, whenever any of the following occurs:
  - the DUC expires and renewal is not sought;
  - access renewal is not granted;
  - the NHLBI requests destruction of the dataset;
  - the continued use of the data would no longer be consistent with the DUC.

In addition, the Requester and Approved Users agree to keep the data secure and confidential at all times and to adhere to information technology practices in all aspects of data management to assure that only authorized individuals can gain access to NIH genomic datasets. This agreement includes the maintenance of appropriate controls over any copies or derivatives of the data obtained through this Data Access Request.

Requesters and Approved Users agree to notify the NHLBI Data Access Committee of any unauthorized data sharing, breaches of data security, or inadvertent data releases that may compromise data confidentiality within 24 hours of when the incident is identified. As permitted

by law, notifications should include the known information regarding the incident and a general description of the activities or process in place to fully define and remediate the situation. Within 3 business days of the NHLBI Data Access Committee notification, the Requester, through the Approved User and the Institutional Signing Official, agree to submit to the NHLBI Data Access Committee a more detailed written report including the date and nature of the event, actions taken or to be taken to remediate the issue(s), and plans or processes developed to prevent further problems, including specific information on timelines anticipated for action.

All notifications and written reports of data security incidents should be sent to:
NHLBI Data Access Committee
Email: nhlbigeneticdata@mail.nih.gov

The NHLBI, the NIH, or another entity designated by the NIH may, as permitted by law, also investigate any data security incident. Approved Users and their associates agree to support such investigations and provide information, within the limits of applicable local, state and federal laws and regulations. In addition, Requesters and Approved Users agree to work with the NHLBI and the NIH to assure that plans and procedures developed to address identified problems are mutually acceptable consistent with applicable law.

7. Intellectual Property

By requesting access to genomic dataset(s), the Requester and Approved Users acknowledge the intent of the NIH that anyone authorized for research access through the attached Data Access Request follow the intellectual property principles within the NIH GWAS Policy for Data Sharing as summarized below:

> Achieving maximum public benefit is the ultimate goal of data distribution through the NIH genomic data repositories. The NIH believes that these data should be considered as pre-competitive, and urges Approved Users to avoid making IP claims derived directly from the genomic dataset(s). However, the NIH also recognizes the importance of the subsequent development of IP on downstream discoveries, especially in therapeutics, which will be necessary to support full investment in products to benefit the public.
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> It is expected that these NIH-provided data, and conclusions derived therefrom, will remain freely available, without requirement for licensing. The NIH encourages broad use of genomic datasets coupled with a responsible approach to management of intellectual property derived from downstream discoveries in a manner consistent with the NIH's Best Practices for the Licensing of Genomic Inventions and the NIH Research Tools Policy.

8. Research Dissemination and Acknowledgement of NIH GWAS Datasets

[Example below assumes standard 12-month publication exclusivity]

It is the intent of the NIH to promote the dissemination of research findings from NIH genomic dataset(s) as widely as possible through scientific publication or other appropriate public dissemination mechanisms. Approved Users are strongly encouraged to publish their results in peer-reviewed journals and to present research findings at scientific meetings, etc.

In accord with the NIH GWAS Policy for Data Sharing, and as expressed through the submission of the DAR, Approved Users acknowledge the NIH's expectation **that they will not *submit* findings using the MESA dataset(s), or updated versions thereof, for publication or presentation for a period of exclusivity for Contributing Investigators concluding with the Embargo Date identified on the dbGaP or other NIH genomic data repository homepage. Please note that different variables may have different embargo dates.**

Approved Users agree to acknowledge the NIH data repository, the Contributing Investigator(s) who contributed the phenotype data and DNA samples from his/her original study, and the primary funding organization that supported the contributing study in all oral and written presentations, disclosures, and publications resulting from any analyses of the data. Approved

Users further agree that the acknowledgment shall include the dbGaP accession number to the specific version of the dataset(s) analyzed.

A sample statement for the acknowledgment of the MESA dataset(s) can be found at the following link: MESA dbGaP Acknowledgment Statements

9. Research Use Reporting

To assure that NIH policies and procedures for genomic data use are adhered to, Approved Users agree to provide to the NHLBI Data Access Committee annual feedback on how these data have been used and any results that have been generated as a result of access to the data, including patents and publications. This information will be used by the NHLBI Data Access Committee staff for program evaluation activities, and may be considered by the NIH GWAS Governance committees as part of the NIH effort to provide ongoing oversight and management of all NIH genomic data sharing activities.

Approved Users thus agree to provide a brief Annual Data Use Report on the research specified within the DAR submitted with this DUC. Approved Users who are seeking renewal agree to provide specific information in a renewal DAR. Those not seeking renewal agree to provide specific information to the Data Access Committee via the contact information below. Annual Data Use Reports will provide information regarding potentially significant findings and publications or presentations that resulted from the use of the requested dataset(s), a summary of any plans for future research use, any violations of the terms of access described within this Data Use Certification and the implemented remediation, and information on any downstream intellectual property generated as a result of the data. Approved Users also may include general comments regarding topics such as the effectiveness of the NIH genomic data access process (e.g., ease of access and use), appropriateness of data format, challenges in following the policies, and suggestions for improving data access or the program in general if desired.

Approved Users agree to send the Annual Data Use Report prior to the anniversary of the Approved Access Date assigned by the DAC and specified within the manifest file provided to Approved Users by the NIH Data Repository at the time that data access is provided. It is agreed that the Annual Data Use Report will be shared with the NIH within the context of a renewal Data Access Request, or via a letter signed by the Institutional Signing Official and the Approved User.

Annual Data Use Reports should be submitted to:

NHLBI Data Access Committee Chair
Email: nhlbigeneticdata@mail.nih.gov

Note that any inadvertent or inappropriate data release incidents should be reported to the NHLBI Data Access Committee according to the agreements and instructions under Term 6.

10. Non-Endorsement, Indemnification

The Requester and Approved Users acknowledge that although all reasonable efforts have been taken to ensure the accuracy and reliability of NIH genomic data, the NIH, the NHLBI Data Access Committee, and Contributing Investigators do not and cannot warrant the results that may be obtained by using any data included therein. The NIH, the NHLBI Data Access Committee, and all contributors to these datasets disclaim all warranties as to performance or fitness of the data for any particular purpose.

No indemnification for any loss, claim, damage or liability is intended or provided by any party under this agreement. Each party shall be liable for any loss, claim, damage, or liability that said party incurs as a result of its activities under this agreement, except that the NIH, as an agency of the United States, may be liable only to the extent provided under the Federal Tort Claims Act, 28 U.S.C. 2671 et seq.

11. Termination and Violations

This Data Use Certification will be in effect for a period of one (1) year from the date the

dataset(s) are made accessible to the Approved User ("Approved Access Date"). At the end of the access period, Approved Users agree to destroy all copies of the requested dataset(s), except as required by publication practices or law to retain them.

Consideration will be given to a renewal of this agreement upon submission of a new DAR. Copies of NIH genomic dataset(s) may not need to be destroyed if, with advance notice and approval by the NHLBI Data Access Committee, the project has been transferred to another Approved User. In this case, documentation must be provided that other Approved Users are using the dataset(s) under an active DAC approved research project at the same institution.

The Requester and Approved User acknowledge that the NIH or the NHLBI may terminate this agreement and immediately revoke access to all NIH genomic datasets at any time if the Requester is found to be no longer in agreement with the policies, principles and procedures of the NIH and the NHLBI.

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By submission of the attached Data Access Request, the Requester through the Institutional Signing Official attests to the Approved Users' qualifications for access to and use of NIH genomic dataset(s) and certifies their agreement to the NIH principles, policies and procedures for the use of the requested datasets as articulated in this document, including the potential termination of access should a violation of any of these agreement terms be identified.

Requesters and the Principal Investigator further acknowledge that they have shared this document and the NIH GWAS data sharing policies and procedures for access and use of genomic datasets with any Approved Users, appropriate research staff, and all other Key Personnel identified in the DAR.

Institutional Signing Officials acknowledge that they have considered the relevant NIH GWAS policies and procedures, that they have shared this document and the relevant policies and procedures with appropriate institutional organizations, and have assured compliance with local institutional policies related to technology transfer, information technology, privacy, and human subjects research.

Appendix

Definitions of Terminology

Annual Data Use Report: A report submitted to the DAC on the anniversary of access approval summarizing the analysis of NIH genomic datasets obtained through the Data Access Request and any significant findings derived from the work.

Approved User: Post-DAC approval will include the PI, collaborators at the home institution who are named in the "Senior/Key Person Profile" portion of the DAR, the IT Director or designee named in the "Senior/Key Person Profile" portion of the DAR, and trainees or staff to these investigators.

Contributing Investigator: The researcher who submitted the genomic dataset to dbGaP.

Data Access Request: SF 424 (R&R) cover pages and requested attachments, if any.

Data Derivative: any data including individual-level data or aggregate genomic data that stems from the original dataset obtained through dbGaP. Excepted from this term is summary information that is expected to be shared through community publication practices.

Final Data Use Report: A final report submitted to the DAC at the conclusion of the approved access period when no additional access is sought, or when leaving an institution. This report should summarize the analysis of GWAS datasets obtained through the Data Access Request and any significant findings derived from the work.

Information Technology Director: Someone with the authority to vouch for the IT capacities at an institution, or higher-level division of an institution (e.g., the School of Medicine).

Institutional Signing Official: Someone with the authority to sign on behalf of the Requester and credentialed through the eRA system as such.

Requester: The home institution/organization for the Primary Investigator (PI) that will use the requested data.

Senior/Key Persons: Collaborators at the home institution, and the IT Director or designee.

Addendum to the Data Use Certification Agreement
Modification of Data Security Terms and Best Practices

Effective for all dbGaP Data Access Requests submitted on or after March 23, 2015,
Section 6 of the Data Use Certification Agreement is replaced in its entirety by the following:

6. Data Security and Data Release Reporting

The Requester and Approved Users, including the institutional IT Director, acknowledge NIH's expectation that they have reviewed and agree to manage the requested dataset(s) according to the current NIH Security Best Practices for Controlled-Access Data Subject to the GDS Policy and the institutional IT security requirements and policies, and that the institution's IT security requirements and policies are sufficient to protect the confidentiality and integrity of the NIH controlled-access data entrusted to the Requester.

If approved by NIH to use cloud computing for the proposed research project, as outlined in the Research and Cloud Computing Use Statements of the Data Access Request, the Requester acknowledges that the IT Director has reviewed and understands the cloud computing guidelines in the NIH Security Best Practices for Controlled-Access Data Subject to the GDS Policy.

Requesters and PIs agree to notify the NHLBI DAC of any unauthorized data sharing, breaches of data security, or inadvertent data releases that may compromise data confidentiality within 24 hours of when the incident is identified. As permitted by law, notifications should include any known information regarding the incident and a general description of the activities or process in place to define and remediate the situation fully. Within 3 business days of the NHLBI DAC notification, the Requester, through the PI and the Institutional Signing Official, agree to submit to the NHLBI Data Access Committee a detailed written report including the date and nature of the event, actions taken or to be taken to remediate the issue(s), and plans or processes developed to prevent further problems, including specific information on timelines anticipated for action.

All notifications and written reports of data security incidents should be sent to:
NHLBI Data Access Committee URGENT: nhlbigeneticdata@nhlbi.nih.gov
GDS mailbox: gds@mail.nih.gov

NIH, or another entity designated by NIH may, as permitted by law, also investigate any data security incident. Approved Users and their associates agree to support such investigations and provide information, within the limits of applicable local, state, and federal laws and regulations. In addition, Requesters and Approved Users agree to work with the NHLBI and NIH to assure that plans and procedures that are developed to address identified problems are mutually acceptable and consistent with applicable law.