

NCI dbGaP Data Submission Information

(Basic Study Information form)

In order for the **NIH NATIONAL CANCER INSTITUTE** to register your data into the dbGaP Submission System, please provide the information listed below and return to your NIH Program Officer (PO), or intramural Genomic Program Administrator (GPA). You may use the sample documents or any other format.

Checklist for required documents:

- Institutional Certification
- dbGaP Data Submission Information

PART I – Study Registration Information

Study name:		
Is this a multi-center study? Yes No		
If YES, please list participating sites:		
Target data delivery date: (YYYY-MM-DD)	Target public release date: (YYYY-MM-DD)	
Estimated number of study participants:		
Is data submission expected to the following repositories? (Description of repositories)	Sequence Read Archive (SRA): (Y/N)	Trusted Partner (e.g. Bionimbus, GDC) (Y/N/NA)

PART II – Principal Investigator (PI) and Funding Information

PI name:	PI e-mail:
PI institution:	
PI assistant/submitter name:	PI assistant/submitter e-mail:
Do you have an eRA Commons or an NIH account? (Y/N) Yes No	
If YES , go to next question. If NO , please register at https://commons.era.nih.gov/commons/registration/registrationInstructions.jsp .	
NIH Intramural Project (Z01), Grant or Contract Number:	NIH PO (if applicable):
NIH Institutes/Centers supporting the study:	

PART III – Policy

Do you have Institutional Certification (IC) to submit these data? Yes No	
<p>The IC should include the Data Use Limitations (DUL), which are based on the informed consent given by each research subject. For every research subject, his/her corresponding data will be tagged with the appropriate DUL. Each study may have multiple DULs, based on the informed consent in the study.</p> <p>If YES, send attachment to NIH PO or intramural GPA, along with this form.</p> <p>If NO, please obtain the Institutional Certification from your Institutional Official. dbGaP requires that the sponsoring IC verifies that this certification has been met. A description of the requirements for the Institutional Certification and an example may be found in the accompanying “Submission into the NIH Database of Genotypes and Phenotypes (dbGaP)” guide.</p>	

PART IV – Study Description

Study type(s) (e.g., longitudinal, case-control, case set, control set, parent-offspring trios, cohort):

Is aggregate-level data appropriate for General Research Use? Yes No

If **YES**, aggregate data will be included in the [Compilation of Aggregate Genomic Data](#), a collection of analyses across many dbGaP studies that can be accessed with a single Data Access Request.

NOTE: This should be consistent with the Institutional Certification

Samples genotyped/sequenced:

Please check all data types expected for this study:	General <input type="checkbox"/> Individual Phenotype <input type="checkbox"/> Individual Genotype <input type="checkbox"/> Individual Sequencing <input type="checkbox"/> Supporting Documents <input type="checkbox"/> Metagenomic <input type="checkbox"/> Protomic/Metabolomic <input type="checkbox"/> Images	Sample Types <input type="checkbox"/> Germline <input type="checkbox"/> Tumor/Normal <input type="checkbox"/> DNA <input type="checkbox"/> RNA <input type="checkbox"/> Mitochondria <input type="checkbox"/> Microbiome <input type="checkbox"/> From Repository	Array Data <input type="checkbox"/> SNP Array <input type="checkbox"/> Expression Array <input type="checkbox"/> Methylation Array
	Genotypes <input type="checkbox"/> Array derived Genotypes <input type="checkbox"/> CNV calls from miroarray <input type="checkbox"/> CNV calls derived from Sequencing <input type="checkbox"/> Genotype calls derived from Sequence <input type="checkbox"/> Somatic SNV (.MAF) <input type="checkbox"/> Array CGH CNVs	Sequencing <input type="checkbox"/> Whole Genome <input type="checkbox"/> Whole Exome <input type="checkbox"/> Targeted Genome <input type="checkbox"/> Targeted Exome <input type="checkbox"/> Whole Transcriptome <input type="checkbox"/> Targeted Transcriptome <input type="checkbox"/> Epigenomic Marks <input type="checkbox"/> Sanger <input type="checkbox"/> 16S rRNA	Analyses <input type="checkbox"/> Association/Linkage Results <input type="checkbox"/> Array derived Expression <input type="checkbox"/> RNA Seq derived Expression <input type="checkbox"/> Array derived Methylation

Genotype/Sequence platform information

Name and version	Vendor	# Probes	URL	Description (optional)
<i>Example: [GenomeWideSNP_6] Affymetrix Genome-Wide Human SNP 6.0 Array</i>	<i>Affymetrix</i>	<i>1880794</i>	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL6801	

PART V – Acknowledgement Statement(s)***

The submitting PI should provide specific points that should be included in an acknowledgement, such as sources of support or collaborators who have made subjects or samples available. Any NIH support must be specifically acknowledged by including the grant number. Consider citing a specific publication that comprehensively describes the origin of the dataset.

The suggested Acknowledgement Statement to accompany the dataset is:

[Click here to enter text.](#)

PART VI – Original Summary of Study

Please provide an original description of the study.¹

[Click here to enter text.](#)

¹ If the submitting institution certifies that aggregate data from a project can be included in the Compilation, then a study description for the aggregate data should be provided in addition to a description for the individual data.