## Example of Basic Study Information for Non-NIH-Funded Studies

In order for NIH to consider your data for deposition in dbGaP, the following information will need to be submitted to <u>GDS@mail.nih.gov</u> . To submit the required information, you may use this sample document or any other format.											
PART I – Study Registration Information											
Study name:											
Is this a multi-center study?											
Target data delivery date: (YYYY-MM-DD)				Target public release date: (YYYY-MM-DD)							
Estimated number of study participants:				Sequence Read Archive:							
NIH Institute or Center most closely aligned with your project:											
Has this study been accepted for publication? (Y/N) (if yes please attach documentation)											
PART II – Principal Investigator (PI) and Funding Information											
PI name:				PI e-mail:							
PI institution:											
Secondary contact name:				Secondary contact e-mail:							
Source of funding:											
PART III – Study Description											
Study type(s) (e.g., longitudinal, case-control, case set, control set, parent-offspring trios, cohort):											
Submission expected for: Ph (Y/N)		Phenotype	(	Genotype /		s Gene Expressio Omnibus		Trac e			
Is aggregate-level data appropriate for General Research Use1? (Y/N)											
Please check all data types expected for this study:	General Individual Phenotype Individual Genotype Individual Sequencing Supporting Documents Metagenomic Protomic/Metabolomic Images			Sample Types Germline Tumor/Normal DNA RNA Mitochondria Microbiome From Repository		Array Data SNP Array Expression Array Methylation Array					
	Genotypes Array derived Genotypes CNV calls from miroarray CNV calls derived from Sequencing Genotype calls derived from Sequence Somatic SNV (.MAF) Array CGH CNVs			Sequencing Whole Genome Whole Exome Targeted Genome Targeted Exome Whole Transcriptome Targeted Transcriptome Epigenomic Marks Sanger 16S rRNA		Analyses Association/Linkage Results Array derived Expression RNA Seq derived Expression Array derived Methylation					
PART IV – Genotype platform information Name and version Vendor # Probes URL Description (optional)											
Name and version		Vendor	# Pr	obes	URL		Description (opt	tional)			

<sup>1</sup> To be included in the <u>Compilation of Aggregate Genomic Data</u>, a collection of analyses across many dbGaP studies that can be accessed with a single Data Access Request.

Example	Affymetrix	1880794	http://www.ncbi.nlm.nih.gov/							
[GenomeWideSNP_6]			<u>qeo/query/acc.cqi?acc=GPL68</u>							
Affymetrix Genome-			<u>01</u>							
Wide Human SNP 6.0										
Array										
PART V – Acknowledgement Statement(s)***										
The suggested Acknowledgement Statement to accompany the dataset is:										
*** 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. Consider citing a specific publication that comprehensively describes the origin of the dataset.										
PART VI – Original Summary of Study										
Please provide a description of the study.										