

Acknowledgment Statements for eMERGE GWAS Dataset(s)

(March 28, 2012, Version)

Please use one or more the following Acknowledgment Statements relevant to the datasets used in your analysis:

Group Health Cooperative/University of Washington

Funding support for Alzheimer's Disease Patient Registry (ADPR) and Adult Changes in Thought (ACT) study was provided by a U01 from the National Institute on Aging (Eric B. Larson, PI, U01AG006781). A gift from the 3M Corporation was used to expand the ACT cohort. DNA aliquots sufficient for GWAS from ADPR Probable AD cases, who had been enrolled in Genetic Differences in Alzheimer's Cases and Controls (Walter Kukull, PI, R01 AG007584) and obtained under that grant, were made available to eMERGE without charge. Funding support for genotyping, which was performed at Johns Hopkins University, was provided by the NIH (U01HG004438). Genome-wide association analyses were supported through a Cooperative Agreement from the National Human Genome Research Institute, U01HG004610 (Eric B. Larson, PI). Assistance with phenotype harmonization and genotype data cleaning was provided by the eMERGE Administrative Coordinating Center (U01HG004603) and the National Center for Biotechnology Information (NCBI). The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000234.v1.p1.

Mayo Clinic

Samples and associated genotype and phenotype data used in this study were provided by the Mayo Clinic. Funding support for the Mayo Clinic was provided through a cooperative agreement with the National Human Genome Research Institute (NHGRI), Grant #: U01HG004599; and by grant HL75794 from the National Heart Lung and Blood Institute (NHLBI). Funding support for genotyping, which was performed at The Broad Institute, was provided by the NIH (U01HG004424). Assistance with phenotype harmonization and genotype data cleaning was provided by the eMERGE Administrative Coordinating Center (U01HG004603) and the National Center for Biotechnology Information (NCBI). The datasets used for analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000203.v1.p1.

Marshfield Clinic Research Foundation

Funding support for the Personalized Medicine Research Project (PMRP) was provided through a cooperative agreement (U01HG004608) with the National Human Genome Research Institute (NHGRI), with additional funding from the National Institute for General Medical Sciences (NIGMS) The samples used for PMRP analyses were obtained with funding from Marshfield Clinic, Health Resources Service Administration Office of Rural Health Policy grant number D1A RH00025, and Wisconsin Department of Commerce Technology Development Fund contract number TDF FYO10718. Funding support for genotyping, which was performed at Johns Hopkins University, was provided by the NIH (U01HG004438). Assistance with phenotype harmonization and genotype data cleaning was provided by the eMERGE Administrative Coordinating Center (U01HG004603) and the National Center for Biotechnology Information (NCBI). The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000170.v1.p1.

Northwestern University

Samples and data used in this study were provided by the NUGene Project (www.nugene.org). Funding support for the NUGene Project was provided by the Northwestern University's Center for Genetic Medicine, Northwestern University, and Northwestern Memorial Hospital. Assistance with phenotype harmonization was provided by the eMERGE Coordinating Center (Grant number U01HG04603). This study was funded through the NIH, NHGRI eMERGE Network (U01HG004609). Funding support for genotyping, which was performed at The Broad Institute, was provided by the NIH (U01HG004424). Assistance with phenotype harmonization and genotype data cleaning was provided by the eMERGE Administrative Coordinating Center (U01HG004603) and the National Center for Biotechnology Information (NCBI). The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000237.v1.p1.

Vanderbilt University

Funding support for the Vanderbilt Genome-Electronic Records (VGER) project was provided through a cooperative agreement (U01HG004603) with the National Human Genome Research Institute (NHGRI) with additional funding from the National Institute of General Medical Sciences (NIGMS). The dataset and samples used for the VGER analyses were obtained from Vanderbilt University Medical Center's BioVU, which is supported by institutional funding and by the Vanderbilt CTSA grant UL1RR024975 from NCR/NH. Funding support for genotyping, which was performed at The Broad Institute, was provided by the NIH (U01HG004424). Assistance with phenotype harmonization and genotype data cleaning was provided by the eMERGE Administrative Coordinating Center (U01HG004603) and the National Center for Biotechnology Information (NCBI). The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000188.v1.p1.

Geisinger Health System

Samples and data in this obesity study were provided by the non-alcoholic steatohepatitis (NASH) project. Funding for the NASH project was provided by a grant from the Clinic Research Fund of Geisinger Clinic. Funding support for the genotyping of the NASH cohort was provided by a Geisinger Clinic operating funds and an award from the Clinic Research Fund. The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000380.v1.p1.

Samples and data in this study were provided by the abdominal aortic aneurysm (AAA) project. Funding for the AAA project was provided by a grant from the Clinic Research Fund of Geisinger Clinic. Funding support for the genotyping of the AAA cohort was provided by a Geisinger Clinic operating funds and an award from the Clinic Research Fund. The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000387.v1.p1

Samples and data in this study were provided by the Geisinger MyCode[®] Project. Funding for the MyCode[®] Project was provided by a grant from Commonwealth of Pennsylvania and the Clinic Research Fund of Geisinger Clinic. Funding support for the genotyping of the MyCode[®] cohort was provided by a Geisinger Clinic operating funds and an award from the Clinic Research Fund. The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000381.v1.p1

Mount Sinai School of Medicine

Samples and data used in this study were provided by the Mount Sinai School of Medicine (MSSM) Biobank Project funded by The Charles R. Bronfman Institute for Personalized Medicine (IPM) at Mount Sinai School of Medicine. The Coronary Artery Disease study (IPM BioBank GWAS) is a genome-wide association study funded by the Charles R. Bronfman Institute for Personalized Medicine. The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number phs000388.v1.p1

The Children's Hospital of Philadelphia (CHOP)

Samples and associated genotype and phenotype data used in this study were provided by the Center for Applied Genomics at the Children's Hospital of Philadelphia. Genotyping for this project was performed at the Center for Applied Genomics and supported by an Institutional Development Award from The Children's Hospital of Philadelphia. We gratefully thank all the children and their families who enrolled in this study, and all individuals who donated blood samples for research purposes. The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number [INSERT ACCESSION NUMBER].

Children's Hospital Boston (CHB)

Samples and data used in this study are provided by The Gene Partnership (TGP) (<http://www.genepartnership.org/>) a prospective longitudinal study to study the genetic and environmental contributions to childhood health and diseases, collect genetic information on a large number of children who have been phenotyped, and implement the Informed Cohort and the Informed Cohort Oversight Board (ICOB). Children's Hospital Boston (CHB) has committed \$10 million for the start-up of the TGP. The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number [INSERT ACCESSION NUMBER].

Cincinnati Children's Hospital Medical Center (CCHMC)

CCHMC is a participating Pediatric Institution for Phase II of the eMERGE network, a national consortium formed for the purpose of integrating electronic medical records with DNA and sera repositories for large scale, high throughput genetic research. Multiple CCHMC PIs have contributed genome wide association data with various funding support mechanisms. These support mechanisms can be categorized into two groups: disease specific awards (PI initiatives) which focus on particular samples and phenotypes and non-specific awards which contributed to a clinical service.

Disease specific awards: 1. Juvenile idiopathic arthritis (JIA): Samples were collected and genotyping was performed by Dr. David Glass with funding support from N01AR42272 and P01AR048929 (PI: Glass). Additional support and genotyping for systemic JIA has been provided by Dr. Dan Kastner's laboratory at the NIH. As of the date of submission, the JIA GWAS data have not been published. 2. Absence seizures: Samples were collected by Dr. Tracy Glauser and genotyping was performed with the support of 5 U01 NS045911 (PI: Glauser) from the National Institute of Neurological Disorders and Stroke. 3. Autism Spectrum Disorder (ASD): Samples were collected by Drs. Cynthia Molloy and Patricia Manning-Courtney and genotyping was performed with the support of Award 1984, Genome-wide Association Study of Autism Characterized by Developmental Regression (PIs: Molloy & Manning), from Autism Speaks Inc. 4. Eosinophilic Esophagitis: Samples were collected and genotyping was performed by Dr. Marc Rothenberg with funding support of 5 U19 AI066738 Project 3, Eosinophilic esophagitis and food allergy (PI: Sampson, Co-PI & Project 3 PI: Rothenberg). As of the date of the submission, the

eosinophilic esophagitis data have not been published. 5. Bicuspid Aortic Valve: Samples were collected and genotyping was performed by Dr. Woodrow Benson with funding support from NIH/NHLBI award HL69712, Genetic mechanisms of cardiac disease in the young (PI: Benson), and NIH/NHLBI award HL74728, SCCOR in Pediatric Heart Development and Disease titled Molecular mechanisms of valve development and disease (PI: Benson).

Non-specific awards: 1. The Cincinnati Control Cohort is a collection of biological samples that have been collected and genotyped through a multidisciplinary approach and with collaboration of more than twenty divisions within CCHMC, supported by the Cincinnati Children's Research Foundation. Lead PIs responsible for this collection are Drs. David Glass and Ardythe Morrow. 2. Clinical cytogenetics samples. Since 2007, more than 2000 samples, enriched for developmental delay, autism and various rare or common genetic diseases as well as specific chromosomal abnormalities such as deletions and duplications, have been genotyped for the purpose of uncovering chromosomal abnormalities.

The extraction of data from the EPIC electronic medical record into the de-identified data warehouse, i2b2, was made possible by institutional resources and 1UL1RR026314, Cincinnati Center for Clinical and Translational Sciences and Training Grant (PI: Heubi).

The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number [INSERT ACCESSION NUMBER].

Please use the following Acknowledgment Statements relevant to the eMERGE Network datasets (phs000297.v1.p1, and/or phs000360.v1.p1) used in your analysis:

Group Health Cooperative/University of Washington – Funding support for Alzheimer's Disease Patient Registry (ADPR) and Adult Changes in Thought (ACT) study was provided by a U01 from the National Institute on Aging (Eric B. Larson, PI, U01AG006781). A gift from the 3M Corporation was used to expand the ACT cohort. DNA aliquots sufficient for GWAS from ADPR Probable AD cases, who had been enrolled in Genetic Differences in Alzheimer's Cases and Controls (Walter Kukull, PI, R01 AG007584) and obtained under that grant, were made available to eMERGE without charge. Funding support for genotyping, which was performed at Johns Hopkins University, was provided by the NIH (U01HG004438). Genome-wide association analyses were supported through a Cooperative Agreement from the National Human Genome Research Institute, U01HG004610 (Eric B. Larson, PI).

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Northwestern University – Samples and data used in this study were provided by the NUgene Project (www.nugene.org). Funding support for the NUgene Project was provided by the Northwestern University's Center for Genetic Medicine, Northwestern University, and Northwestern Memorial Hospital. Assistance with phenotype harmonization was provided by the eMERGE Coordinating Center (Grant number U01HG04603). This study was funded through the NIH, NHGRI eMERGE Network (U01HG004609). Funding support for genotyping, which was performed at The Broad Institute, was provided by the NIH (U01HG004424).

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Assistance with phenotype harmonization and genotype data cleaning was provided by the eMERGE Administrative Coordinating Center (U01HG004603) and the National Center for Biotechnology Information (NCBI). The datasets used for the analyses described in this manuscript were obtained from dbGaP at <http://www.ncbi.nlm.nih.gov/gap> through dbGaP accession number **phsXXXXXX.vX.pX**. (**Note:** Please add the corresponding phs number(s) of the dataset(s), phs000297.v1.p1. and/or phs000360.v1.p1. used in your analysis here.)