emerge network

eMERGE Network: Manuscript Concept Sheet

Reference Number *(to be assigned by CC)*	NT400
Submission Date	7/15/2020
Project Title	A phenome-wide association study to evaluate other effects of SARS-CoV-2 infection
Tentative Lead Investigator *(first author)*	TBD
Tentative Senior Author *(last author)*	Wei-Qi Wei
All Other Authors	Todd Edwards, Josh Peterson, Digna Velez Edwards, Dan Roden
Sites Participating	Open to all sites Current participants: Vanderbilt
Background / Significance	Since January 2020, novel coronavirus has spread to nearly every country and territory in the world. As of 04/27/2020, more than 3 million Covid-19 cases have been confirmed throughout the United States. Besides well documented the catastrophic pulmonary effects, accumulated reports suggest that COVID-19 damages multiple other organ systems, such as the heart, kidneys, and liver, in both children and adults.
Outline of Project	We will explore other clinical outcomes of a COVID-19 infection within the eMERGE network. We plan to perform a 2-stage PheWAS to compare the individuals being infected by COVID-19 with the individuals being tested only negative. We will define cases as individuals who were either confirmed positive by a SARS-CoV-2 PCR test or had a COVID-19 ICD10 code (U07.1) after April 1st, 2020. We will define controls as individuals who were confirmed negative by a SARS-CoV-2 PCR test and had not been tested positive. We will collect their new-onset ICD codes, i.e., which earliest diagnosis dates are at least 7 days after the first test date. We will aggregate all ICD codes into up to phecodes for the analysis. We will run a PheWAS using the data from each site independently, followed by a meta-analysis. We will adjust our findings for covariates such as age, gender, race, and other candidate confounders for COVID-19 infection outcomes. We also plan to perform post hoc analyses and stratify the data by race, gender, age, etc.
Desired Data - Common Variables* *(Available from the CC)*	☒Demographics ☒ICD9/10 codes ☐CPT codes ☐Common Variable Labs ☐Common Variable Meds

	☒Phecodes ☒BMI	☐Other: Case/Control status on Phase I and ☐Phase II phenotypes
Other Desired Data *(Available from participating sites)*		
Desired Genetic Data	☐eMERGE I-III Merged set (HRC imputed, GWAS) ☐eMERGE PGx/PGRNseq data set ☐eMERGEseq data set (Phase III) ☐eMERGE Whole Genome sequencing data set ☐eMERGE Exome chip data set ☐eMERGE Whole Exome sequencing data set ☐Other (not listed above):	
Does project pertain to an existing eMERGE Phenotype?	☒Yes, if so please list: Phecodes and other COVID outcomes ☐No	
Planned Statistical Analyses	1) PheWAS for COVID outcomes 2) Meta-analysis with the data from all sites.	
Ethical Considerations	None noted	
Target Journal	Related clinical journal	
Milestones *(This section should include the key dates for completion of project, including approval, project duration, draft completion, and submission.)*	1. phenotype data collection from participating sites: by the end of 2020 2. Conduct PheWAS and meta-analysis: 2 months 3. Result explanation and manuscript preparation: 2-3 months	