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| **eMERGE Network: Proposal for Analysis**Project/Manuscript Concept Sheet |
| **Reference Number** | NT280 |
| **Submission Date** | 4/11/2018 |
| **Project Title** | Discovery-Based CNV Analyses of eMERGE-Seq Data  |
| **Tentative Lead Investigator** *(first author)* | Patrick Sleiman |
| **Tentative Senior Author** *(last author)* | Hakon Hakonarson |
| **All Other Authors**  | Frank Mentch, Joseph Glessner, authors from participating eMERGE sites  |
| **Sites Involved** | All sites  |
| **Background / Significance** | Building on our CNV-calling efforts in Phase 2, we propose to recall CNVs from the entire eMERGE-Seq dataset. While CNVs have been called at the clinical sites they are restricted to reporting multi-exon events. The aims of the current proposal are to generate data for discovery research as well as to create a publically accessible CNV map of the most widely tested clinical genes. |
| **Outline of Project** | 1. Call CNVs using multiple software packages on DNAnexus
2. Carry out association analysis of CNVs and record counter phenotypes (ICD9, medications and lab values) on DNAnexus

Deposit the CNVs in a publically accessible database. Unlike SNVs there are currently no high quality CNV frequency resources available. Generating frequency stats broken out by genetic ancestry and potentially phenotype for the ACMG list of genes would be useful for both the research and clinical genetics communities.  |
| **Desired Variables** *(essential for analysis**indicated by* ***\*****)* | NA |
| **Desired Data** | Phenotype data from all eMERGE-Seq participants |
| **Planned Statistical Analyses** | Content analysis and descriptive statistics |
| **Ethical Considerations** | None |
| **Target Journal** | AJHG |
| **Milestones\*\*** | Approval – Spring 2018Winter 2018Submit for publication – Spring 2019 |

***\*\**** *This section should include the timeline for completion of project, including: approval, project duration, first and second draft of the paper and submission.*