**Minutes from AFGen call on February 10, 2016**

**Attending:**

|  |  |
| --- | --- |
| **AGES** |  |
| **AFNET/KORA** |  |
| **ARIC** | **Alvaro** |
| **CHS** | **Susan, Nona** |
| **WGHS** | **Christine,** |
| **FHS** | **Emelia, Honghuang, Josee** |
| **Gutenberg** |  |
| **HABC** |  |
| **Ship** |  |
| **Cleveland Clinic** | **John, Mina, Johnathan** |
| **WHI** |  |
| **Luric** |  |
| **Malmo** | **Gustav** |
| **MESA** | **Henry** |
| **Rotterdam** |  |
| **MGH** | **Ingrid, Carolina, Patrick, Lu-Chen, Steve** |
| **Prevend** | **Bastiaan** |
| **Prosper** |  |
| **Vanderbilt** | **Ben, Darbar** |
| **Korean AF network** |  |
| **Generation Scotland** | **Caroline, Archie** |
| **Beat-AF** | **David** |
| **BioMe** |  |
| **ULSAM/Epihealth/ Pivus/Twingene** |  |
| **FINCAVAS** |  |
| **Heinz Nixdorf** |  |
| **DDCHS** |  |
| **Sao Paulo** |  |
| **Munich WTCC stroke** |  |
| **Metastroke** |  |
| **Geisinger** | **Scott** |
| **Mayo** |  |

**Agenda**

**New projects**

* Myocardial Genetics Consortium – Presentation by Chris Newton-Cheh (pdfs enclosed)
  + Chris Newton-Cheh and Niek Verweij
  + Perform multivariate GWAS on ***summary level results*** from different myocardial phenotypes – PheWas, with Myocardial phenotypes as the Phenome evaluated.
  + Only targeting already published GWAS results
  + Aims:
    1. Can unbiased genetic correlation of myocardial traits using genome-wide common variant association identify biologically informative clusters?
    2. Can specific genetic variants associated with such clusters be identified using multivariate GWAS?
       - Potentially identify novel genetic variants that fail to achieve genome-wide significance for individual trait association
       - Cross-phenotype associations of novel/established variants
  + Presented to different consortia
    - ECG LV Mass, EchoGen, CHARGE Echo LV MASS, eQTL in LV tissue and CM GWAS (Tom Coppola), Hypertrophic CM (Gordon Huggins), ST-T wave measures (unpublished)
  + One representative from each Consortium
    - Each onsortium has one vote
  + Initially intended for one joint paper, but if collaboration is successful, may continue to exome chip and other platforms
  + Generally positive attitude towards participating with AFGen results from 2012 meta-analysis
  + Think about it until our next call – then we’ll pick up on it again

**Ongoing projects**

* 1000G AF meta / Exome chip – Ingrid/Carolina
  + Accepted for HRS 2016 – oral presentation
  + Meta QC underway – hopefully completed by next call
  + Two less common variants (MAF 2-4%) identified in AA samples in ~500 individuals
* Ablation GWAS – Ben
  + Moving forward – many studies have completed phenotype files.
* AF WGS / NIH – Steve, Patrick
  + Production – 20 samples left for sequencing
  + Transfer of data to Goncalo’s group has been successfully going on in the background
  + Carolina is working on cleaning up the phenotype files
  + Honghuang is working on refining QC on a subset; 1200 AF genomes including multiple sites, 1400 referents from FHS
  + Cloud based QC and analytical methods are being evaluated as well
  + Anticipate complete calling of 20K samples in June-July

**Next call:** February 24, 2016