**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CHARGE Echo LV MASS, eQTL in LV tissue and CM GWAS (Tom Coppola), Hypertrophic CM (Gordon Huggins), ST-T wave measures (unpublished)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