**Setup**

1. Setup AWS server
   1. Mount EFS from EC2
   2. Create GitHub repository for project
      1. Connect GitHub repo cloud with local documents
   3. Setup FastQ file processing pipeline
   4. Generate gVCFs
      1. So I can know the exact regions that have been sequenced (with coverage)
2. Install required analysis tools
   1. ANNOVAR
      1. Load ANNOVAR databases
         1. Follow startup guide
         2. <https://annovar.openbioinformatics.org/en/latest/user-guide/startup/>
      2. Test ANNOVAR with an exome
         1. Prepare input files
         2. Follow gene-based annotation process
         3. Follow filter-based annotation process
      3. Assign variant annotations found in ClinVar and gnomAD databases
         1. Do I need to install the independently?
   2. VEP
      1. Assess differences with ANNOVAR
      2. Assess whether it is worth installing

**Requests**

1. Need to know regions captured for the exome. Please can they send them to me?
2. With regards to the delivery of datasets, can I have VCF and VCF files?
3. Get hold of the gene panels we need
   1. Infection susceptibility (ACE2 polymorphisms)
   2. Immunological response
   3. Direct determinants of disease severity