**Analysis plan**

Step 1: QC and SNP set

We recommend using HapMap3 SNPs and filter those with a MAF>1% in your sample.

Step 2: Create per-chromosome GRM

Example for chromosome 22:

[prompt]$ **gcta64** --bfile AA\_chrom22 --make-grm-bin --out myGRMfolder/AA.chrom22

GCTA will produce three type of files: \*.grm.bin, \*.grmN.bin and \*.grm.id

Step 3: Calculate “within-chromosomes” and “between-chromosomes” GRMs

1. Create a file with prefixes of per-chromosome GRMs.

[prompt]$ cat mgrm.prepare-data.txt

myGRMfolder/AA.chrom1

myGRMfolder/AA.chrom2

myGRMfolder/AA.chrom3

…

myGRMfolder/AA.chrom21

myGRMfolder/AA.chrom22

1. Run **makeBCgrm** program

[prompt]$ ./**makeBCgrm** --help

--mgrm : list of genetic relationship matrices (GRM).

--out : Specify prefix for output GRM.

[prompt]$ ./**makeBCgrm** --mgrm mgrm.prepare-data.txt --out myGRMfolder/AA

**makeBCgrm** will produce four files (+ a \*.makeBCgrm.log file):

within-chromosome GRM: \*.within.grm.bin, \*.within.grm.id

between-chromosome GRM: \*.between.grm.bin, \*.between.grm.id

Step 4: Analyse trait with GCTA (recommended to include Principal Components as fixed effects)

1. Create “mgrm” file with prefix corresponding to within- and between-chromosomes GRMs

[prompt]$ cat mgrm.analyse-data.txt

myGRMfolder/AA.within

myGRMfolder/AA.between

1. Single GRM analysis

[prompt]$ **gcta64** –grm myGRMfolder/AA.within \

--pheno myPhenotype-file.txt --mpheno 1 –reml \

--qcovar myQuantitativeCovariates.txt \

--reml-no-constrain --out myResultsFolder/AA.singleGRM

1. Two-GRM analysis

[prompt]$ **gcta64** –mgrm mgrm.analyse-data.txt \

--pheno myPhenotype-file.txt --mpheno 1 –reml \

--qcovar myQuantitativeCovariates.txt \

--reml-no-constrain--out myResultsFolder/AA.twoGRM

Step 5: Share results:

* All log files from Step 4
* All \*.hsq files from Step 4

Traits: height, BMI, education, blood pressure, etc.