

Starling-May18

Projects/Katarina Stuart/KStuart.Starling-Aug18/Sv6\_Morphology/Analysis/2021.05.24.GCTA\_7pheno

PDF Version generated by

Katarina Stuart (z5188231@ad.unsw.edu.au)

on

Feb 12, 2022 @03:42 PM AEDT

## Table of Contents

2021.05.24.GCTA_7pheno .....	2
------------------------------	---



## Chromosome partitioning analysis

<https://cnsgenomics.com/software/gcta/#Overview>

<https://www.nature.com/articles/hdy201729>

<https://www.nature.com/articles/ng.823>

```
module load gcta/1.93.2beta
```

```
cd /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv6_Morphology/analysis/GCTA212_7pheno
```

### Trying out with the starling data;

```
VCF=/srv/scratch/z5188231/KStuart.Starling-Aug18/Sv6_Morphology/analysis/GenoPhenoVariation/sv6_Phenofilter_14pop_Tarsus_maf005_miss50_r2_missind50/Stacks_filtered_baypass_128217s
```

```
module add vcftools/0.1.16
module load plink/1.90b6.7
module load samtools/1.9
```

### Prepare the data:

```
awk '{gsub(/^starling/, ""); print}' $VCF > no_chr.vcf
bgzip no_chr.vcf
bcftools index no_chr.vcf.gz
```

```
bcftools view no_chr.vcf.gz --regions 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31 > no_chr_cut.vcf
```

```
vcftools --vcf no_chr_cut.vcf --plink --out no_chr_cut.plink
```

```
awk 'FNR==NR{a[FNR]=$1;next}{$1=a[FNR]}1' no_chr_cut_famlist.txt no_chr_cut.plink.ped > no_chr_cut2.plink.ped
cp no_chr_cut2.plink.ped no_chr_cut.plink.ped
```

```
mkdir plink_files
```

```
plink --file no_chr_cut.plink --make-bed --noweb --allow-extra-chr --out plink_files/no_chr_cut --chr-set 30
```

```
for PHENO in mass tarsus head beak wing spleen heart
do
```

```
plink --file no_chr_cut.plink --keep GCTA_${PHENO}_subset.txt --make-bed --noweb --allow-extra-chr --out plink_files/no_chr_cut_${PHENO} --chr-set 30
done
```

### Pheno PCA axis runs:

```
DIR=/srv/scratch/z5188231/KStuart.Starling-Aug18/programs/gcta_1.93.2beta
GCTA=/srv/scratch/z5188231/KStuart.Starling-Aug18/programs/gcta_1.93.2beta/gcta64
```

### Split chrom runs:

```
cd /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv6_Morphology/analysis/GCTA212_7pheno
```

```
mkdir gcta_grm
```

```

for PHENO in mass tarsus head beak wing spleen heart
do
${GCTA} --bfile plink_files/no_chr_cut_${PHENO} --autosome --make-grm --out gcta_grm/no_chr_cut_${PHENO} --thread-num 4 --autosome-num 30
done

mkdir chrom_split

for PHENO in mass tarsus head beak wing spleen heart
do
for NUM in 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
do
${GCTA} --bfile plink_files/no_chr_cut_${PHENO} --chr ${NUM} --make-grm --out chrom_split/no_chr_cut_${PHENO}_chr${NUM} --thread-num 16 --autosome-num
${GCTA} --bfile plink_files/no_chr_cut_${PHENO} --chr 31 --make-grm-xchr --out chrom_split/no_chr_cut_${PHENO}_chr31 --thread-num 16 --autosome-num 30
done
done

```

### Pheno runs

```

for PHENO in mass tarsus head beak wing spleen heart
do
for NUM in 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31
do
mkdir Pheno_${PHENO}
cd Pheno_${PHENO}
${GCTA} --grm ../chrom_split/no_chr_cut_${PHENO}_chr${NUM} --pheno ../GCTA_${PHENO}_pheno.txt --reml --out GCTA_${PHENO}_pheno_chr${NUM} --threa
${GCTA} --grm ../gcta_grm/no_chr_cut_${PHENO} --pheno ../GCTA_${PHENO}_pheno.txt --reml --out GCTA_${PHENO}_pheno_chrall --thread-num 4
grep "^V(G)" GCTA_${PHENO}_pheno_chr*.hsq | sed '/^Vp/d' > hsq.outsummary.${PHENO}.txt
grep "^V(G)/" GCTA_${PHENO}_pheno_chr*.hsq > hsq.outsummary.${PHENO}.proportions.txt
cd ../
done
done

```

### Grab chromosome sizes:

```

GENOME=/srv/scratch/z5188231/KStuart.Starling-
Aug18/Sv3_Genome/Sv3.2_Starling10x/chromosome_alignment/satsuma2/Chromosome.L_RNA_scaffolder.polished.tidy.purge.fasta/Sturnus_vulgaris_

module load samtools/1.10

cut -f1,2 $GENOME > sizes.genome

```

### Grabbing genes per chromosome:

```
cd /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv6_Morphology/analysis/GCTA212_7pheno
```

```

awk ' $3=="gene"' /srv/scratch/z5188231/KStuart.Starling-Aug18/Sv4_Historic/analysis/outlier_analysis/mapping_variants/myFile_lociMerged_longe
total_genes_annotation.txt

```