**For Mahmuda code to filter a VCF file by SNP location using VCF tools**

***Opening a connection with the MacColl lab server using PUTTY:***

Open a PUTTY session with the following configuration:

Host Name: maccolllab.life.nottingham.ac.uk

Port: 22

Connection type: SSH

Leave everything else as it is in the PUTTY configuration and click open

Type your university username (not your email just your username) in the shell, click enter. When prompted enter your password (don’t worry, it won’t show any text when you type your password, that’s normal). Then click enter and it should log you in.

***On the maccolllab.life.nottingham.ac.uk server:***

cd path/to/where/your/vcf/file/is

e.g. :

cd /home/mbzlld/lauras\_files/Post-doc\_work\_2018/Mahmuda\_VCF\_filtering

vcftools \

--vcf batch\_1.haplotypes.vcf \

--chr groupI \

--from-bp 21700112 \

--to-bp 21730178 \

--recode \

--recode-INFO-all \

--out mahmuda\_Atp1a1\_SNPs

vcftools \

--vcf batch\_1.haplotypes.vcf \

--chr groupII \

--from-bp 13035298 \

--to-bp 13239947 \

--recode \

--recode-INFO-all \

--out mahmuda\_CSMD1\_SNPs

Each time you run vcftools two files will be produced a log file and a .recode.vcf file which contains the SNP information you want. This file can be opened in a text editor and the chromosome and position of each SNP is at the beginning of each line.