

Week12 lab genomics

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#Section1

```
mxl <- read.csv("373531-SampleGenotypes-Homo_sapiens_Variation_Sample_rs8067378.csv")
head(mxl)
```

```
##      Sample..Male.Female.Unknown. Genotype..forward.strand. Population.s. Father
## 1              NA19648 (F)                      A|A ALL, AMR, MXL      -
## 2              NA19649 (M)                      G|G ALL, AMR, MXL      -
## 3              NA19651 (F)                      A|A ALL, AMR, MXL      -
## 4              NA19652 (M)                      G|G ALL, AMR, MXL      -
## 5              NA19654 (F)                      G|G ALL, AMR, MXL      -
## 6              NA19655 (M)                      A|G ALL, AMR, MXL      -
##      Mother
## 1      -
## 2      -
## 3      -
## 4      -
## 5      -
## 6      -
```

```
table(mxl$Genotype..forward.strand.)
```

```
##
## A|A A|G G|A G|G
## 22 21 12 9
```

```
table(mxl$Genotype..forward.strand.)/nrow(mxl)*100
```

```
##
##      A|A      A|G      G|A      G|G
## 34.3750 32.8125 18.7500 14.0625
```

Different population GBR

```
gbr <- read.csv("373517-SampleGenotypes-Homo_sapiens_Variation_Sample_rs8067378.csv")
```

Find proportion of G|G

```
round(table(gbr$Genotype..forward.strand.)/nrow(gbr)*100,2)
```

```
##
##      A|A      A|G      G|A      G|G
## 35.11 26.60 26.60 11.70
```

This variant that is associated with childhood is more frequent in GBR population than MKL