

Class 11: Genome Informatics

Andrew Sue

We are reading in the Mexican American Ancestry data for the SNPs associated with childhood asthma.

Q1. What are those 4 candidate SNPs?

rs12936231, rs8067378, rs9303277, and rs7216389

Q2. What three genes do these variants overlap or effect?

ZPBP2, IKZF3, GSDMB

Q3. What is the location of rs8067378 and what are the different alleles for rs8067378?

Location: Chromosome 17:39895095

Q4: Name at least 3 downstream genes for rs8067378?

Genes GSDMB, GSDMA and PSMD3.

```
mxn_data <- read.csv("Asthma_genotypes.csv", row.names = 1)
mxn_data
```

	Genotype..forward.strand.	Population.s.	Father	Mother
NA19648 (F)	A A	ALL, AMR, MXL	-	-
NA19649 (M)	G G	ALL, AMR, MXL	-	-
NA19651 (F)	A A	ALL, AMR, MXL	-	-
NA19652 (M)	G G	ALL, AMR, MXL	-	-
NA19654 (F)	G G	ALL, AMR, MXL	-	-
NA19655 (M)	A G	ALL, AMR, MXL	-	-
NA19657 (F)	A G	ALL, AMR, MXL	-	-
NA19658 (M)	A A	ALL, AMR, MXL	-	-
NA19661 (M)	A G	ALL, AMR, MXL	-	-

NA19663 (F)	A A ALL, AMR, MXL	-	-
NA19664 (M)	G A ALL, AMR, MXL	-	-
NA19669 (F)	A A ALL, AMR, MXL	-	-
NA19670 (M)	A A ALL, AMR, MXL	-	-
NA19676 (M)	G G ALL, AMR, MXL	-	-
NA19678 (F)	A A ALL, AMR, MXL	-	-
NA19679 (M)	A G ALL, AMR, MXL	-	-
NA19681 (F)	A G ALL, AMR, MXL	-	-
NA19682 (M)	A G ALL, AMR, MXL	-	-
NA19684 (F)	A G ALL, AMR, MXL	-	-
NA19716 (F)	G A ALL, AMR, MXL	-	-
NA19717 (M)	A G ALL, AMR, MXL	-	-
NA19719 (F)	G G ALL, AMR, MXL	-	-
NA19720 (M)	G G ALL, AMR, MXL	-	-
NA19722 (F)	G A ALL, AMR, MXL	-	-
NA19723 (M)	G G ALL, AMR, MXL	-	-
NA19725 (F)	A G ALL, AMR, MXL	-	-
NA19726 (M)	A A ALL, AMR, MXL	-	-
NA19728 (F)	A A ALL, AMR, MXL	-	-
NA19729 (M)	A G ALL, AMR, MXL	-	-
NA19731 (F)	A A ALL, AMR, MXL	-	-
NA19732 (M)	A G ALL, AMR, MXL	-	-
NA19734 (F)	G A ALL, AMR, MXL	-	-
NA19735 (M)	G G ALL, AMR, MXL	-	-
NA19740 (F)	A A ALL, AMR, MXL	-	-
NA19741 (M)	A A ALL, AMR, MXL	-	-
NA19746 (F)	A A ALL, AMR, MXL	-	-
NA19747 (M)	G A ALL, AMR, MXL	-	-
NA19749 (F)	A G ALL, AMR, MXL	-	-
NA19750 (M)	A G ALL, AMR, MXL	-	-
NA19752 (F)	A G ALL, AMR, MXL	-	-
NA19755 (F)	A A ALL, AMR, MXL	-	-
NA19756 (M)	G A ALL, AMR, MXL	-	-
NA19758 (F)	A G ALL, AMR, MXL	-	-
NA19759 (M)	G A ALL, AMR, MXL	-	-
NA19761 (F)	G A ALL, AMR, MXL	-	-
NA19762 (M)	A A ALL, AMR, MXL	-	-
NA19764 (F)	A A ALL, AMR, MXL	-	-
NA19770 (F)	A G ALL, AMR, MXL	-	-
NA19771 (M)	A A ALL, AMR, MXL	-	-
NA19773 (F)	A A ALL, AMR, MXL	-	-
NA19774 (M)	A G ALL, AMR, MXL	-	-
NA19776 (F)	A G ALL, AMR, MXL	-	-

NA19777 (M)	A A ALL, AMR, MXL	-	-
NA19779 (F)	G A ALL, AMR, MXL	-	-
NA19780 (M)	A A ALL, AMR, MXL	-	-
NA19782 (F)	G A ALL, AMR, MXL	-	-
NA19783 (M)	A G ALL, AMR, MXL	-	-
NA19785 (F)	A A ALL, AMR, MXL	-	-
NA19786 (M)	G A ALL, AMR, MXL	-	-
NA19788 (F)	A G ALL, AMR, MXL	-	-
NA19789 (M)	G G ALL, AMR, MXL	-	-
NA19792 (M)	A A ALL, AMR, MXL	-	-
NA19794 (F)	G A ALL, AMR, MXL	-	-
NA19795 (M)	A G ALL, AMR, MXL	-	-

Q5. What proportion of the Mexican Ancestry in Los Angeles sample population (MXL) are homozygous for the asthma associated SNP (G|G)?

14% G|G phenotype.

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

A A	A G	G A	G G
34.3750	32.8125	18.7500	14.0625

Q6. Back on the ENSEMBLE page, use the “search for a sample” field above to find the particular sample HG00109. This is a male from the GBR population group. What is the genotype for this sample?

The genotype of this sample is G/G

We are reading in now the GBR dataset and finding the HG00109 sample.

```
gbr <- read.csv("Asthma_genotypes_gbr.csv", row.names = 1)

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

A A	A G	G A	G G
25.27473	18.68132	26.37363	29.67033

To compare the gene expression of the entire population, we will take the population data.

```
expr <- read.table("gene_expression.txt")
head(expr)
```

	sample	geno	exp
1	HG00367	A/G	28.96038
2	NA20768	A/G	20.24449
3	HG00361	A/A	31.32628
4	HG00135	A/A	34.11169
5	NA18870	G/G	18.25141
6	NA11993	A/A	32.89721

```
nrow(expr)
```

```
[1] 462
```

```
table(expr$geno)
```

A/A	A/G	G/G
108	233	121

Lets make a summary plot (boxplot) of the data

```
library(ggplot2)

ggplot(expr) + aes(geno, exp, fill = geno) + geom_boxplot(notch = TRUE)
```

