Q1: What are those 4 candidate SNPs?

[HINT, you will may want to check the first few links of search result]

In association studies of 4 candidate SNPs (rs12936231, rs8067378, rs9303277, and rs7216389) in 3 family-based childhood asthma cohorts, all 4 SNPs demonstrated significant evidence for association

Q2: What three genes do these variants overlap or effect? ZPBP2

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

[HINT, alleles and location are listed at the top of the the Ensemble page. You may

search in a genome browser to find this information]  
Chromosome **17:39895095**

Q4: What are the downstream genes for rs8067378? Any genes named ZPBP2,

GSDMB, and ORMDL3?

Q5: What proportion of the Mexican Ancestry in Los Angeles sample population (MXL) are homozygous for the asthma associated SNP (G|G)? [HINT: You can download a CVS file for this population from ENSEMBLE and use the R functions read.csv(), and table() to answer this question] 14%

Q6. Back on the ENSEMBLE page, search for the particular sample HG00109. This is a male from the GBR population group. What is the genotype for this sample? G|G

Q7: How many sequences are there in the first file? What is the file size and format of the data? Make sure the format is fastqsanger here!

3863

Q8: Q8: Does the first sequence have good quality?

Good

Q9: What is the GC content and sequence length of the second fastq file? [HINT, you may check “Basic Statistics”]

54%GC, 3863 sequences

Q10: How about per base sequence quality? Does any base have a mean quality score below 20?

Good. No base has mean quality below 20