In this homework assignment you will use two files to determine any *known* genetic defects of a particular person given their genetic report.

A few things to note, when one gets their genetic test only certain positions of the genome are measured. The positions are locations where nucleotide changes are known to occur in the population. (The majority of the human genome is identical across all humans) The position and variation is called a SNP (Single Nucleotide Polymorphism), it is pronounced snip. So a SNP is determined by position and a pair of nucleotides (A, G, C, T).

In humans there is a nomenclature for SNPs and it looks something like `rs2240203.` For this SNP `rs2240203,` if the genotype is `AA,` then the person likely has blue eyes, if the genotype is `GG` or `AG`, then the person likely has brown eyes.

Your first task is to take the file from SNPedia and turn it into a dictionary. You will write a function named `readSNP` which takes in the filename as a variable and returns a dictionary.

The key for the dictionary is the SNP name (`rs2240203`) concatenated with the genotype (`AA`). So for this example `rs2240203AA.` The value is the description provided by SNPedia (`blue eye color more likely`).

The challenge is the formatting of the file obtained from SNPedia (they have a new API, but for this assignment, you must use the old file obtained a year ago) It is “somewhat” comma-separated. You may not process the file using anything other than the Python. (Do not convert it using Excel).

It is composed of Name, Position, Chromosome, Summary, Link.

You will need to extract the Name, Summary, and buried within the link the genotype.

```
rs2240203,28249056,15,blue eye color more likely,http://www.snpedia.com/index.php/
Rs2240203(A;A)
```

The second file is a download from 23andMe it contains the measured SNPs for an individual.

The file is tab delimited and consists of

```
rsid chromosome     position  genotype
```

You will write a second function (named `read23`) which takes in a filename, which refers to a file that is structured like a 23andMe report and outputs a dictionary. This time the dictionary key is just the SNP name or `rsID` and the value is the genotype or basepair (`AA`).

Finally, you will write a function named `writeSummary` which takes in both dictionaries generated from the functions above and writes to a file a list of summaries for the given person. The function should take in the full SNP dictionary as the first parameter, and the 23andMe dictionary as the second parameter. The output should give the rsid followed by the genotype followed by the summary. The data should be tab separated.

Ex:

```
rs2240203 AA   blue eye color more likely
```

You should not report summaries which are normal or not tested. In this data set a normal measurement occurs in many formats, you will need to hard code these and determine them given the sample data. Feel free to ask questions.