the undigested and digested samples into the DNA gel because a clear band was present for both individual's results.

Through use of the bioinformatics programs, it was determined that the length of the amplicon for the TAS2R38 gene is about 220 nucelotides. The map location of the gene was between 7q34 and 7q35 on the long arm. Single nucleotide polymorphisms were found at nucleotide 145 which affected the sequencing of 48 codons, nucleotide 785 which affected about 261 codons, and nucleotide 886 which affected about 295 codons. The fragment of the nontaster allele was determined to be 220 nucleotides because it is uncleaved by the restriction enzyme and the DNA fragments for the taster allele were determined to be 43 nucleotides and 176 nucleotides. This information was particularly useful when analyzing my DNA gel results because it pinpointed where a taster or a nontaster's band would form on the DNA gel based upon the calculated base pairs. Longer strands of DNA move a shorter distance on the gel in comparison to shorter strands.

Good

What else did the bioinformatics reveal about the sequence similarity to other primates?

FIGURE 1: DNA gel results from Lab Group 1. My undigested sample is in Lane 3 and my digested sample is in Lane 4. Markers are found in lanes 1 and 2. % gel, voltage run, time