

Purpose: To be able to analyze the SNP RS7903146 to understand my genotype and its clinical significance

Materials:

- Computer

Conclusion:

I loaded both my new primers sample (N) and my old primer sample (O). The N-sample was loaded into two different wells B7 & D7, whereas the O-sample was loaded into one, C7. I loaded the N-sample into two different wells because I believed that I had not pipetted correctly and did an extra well just to be sure. Based on the results below, all my wells produced mostly successful results, with a few off-peaks, but nevertheless, still distinguishable.

D7& B7 both produced shorter sequences, which both utilized the same new primers, compared to the longer sequence of the old primers found in well C7. Based on the given data, I obtained the following sequences for each.

N-B7:

TTTCTCTGCCTCAAAACCTAGCACAGCTGTTATTTACTGAACAATTAGAGAGCTAAG
CACTTTTATAGATACTATATAATTTAATTGCCGTATGAGGWA

O-C7:

AGAGCTAAGCACTTTTTAG[A*]ATACCTAYCMTWWTTTAATTGCCGTATGAGGCACC
CTTAGTTTTTCAGACGAGAAACCACAGTTACAGGGAAGGCAAGTAAGTCAATG
TCAGATAACTAGGAAAAGGTTAGAGGGGCCCTGGACACASGCCTGTGTGACTGAGA
AGCTTGGGCACTTCACYA

N-D7:

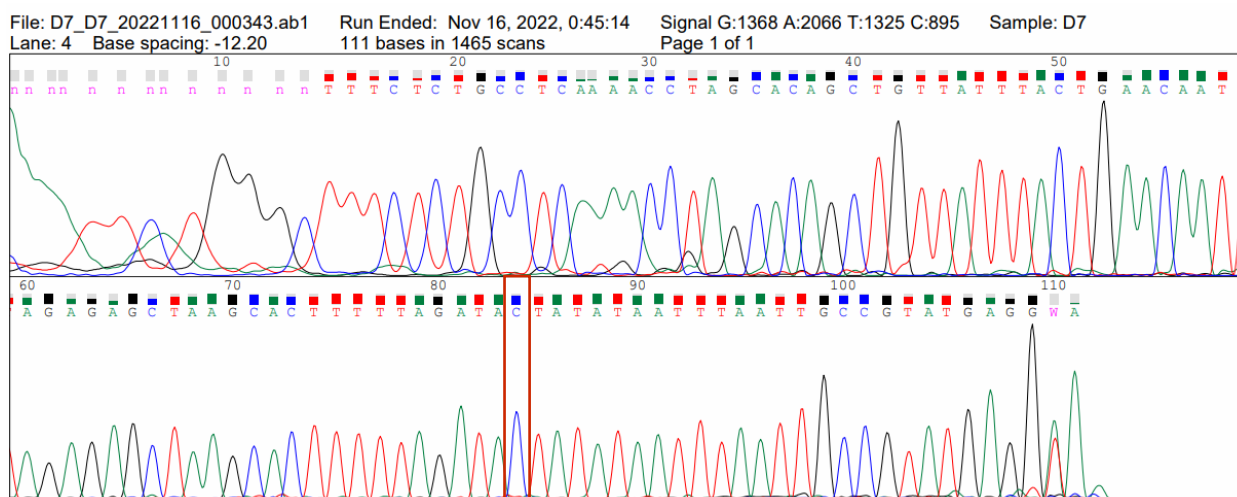
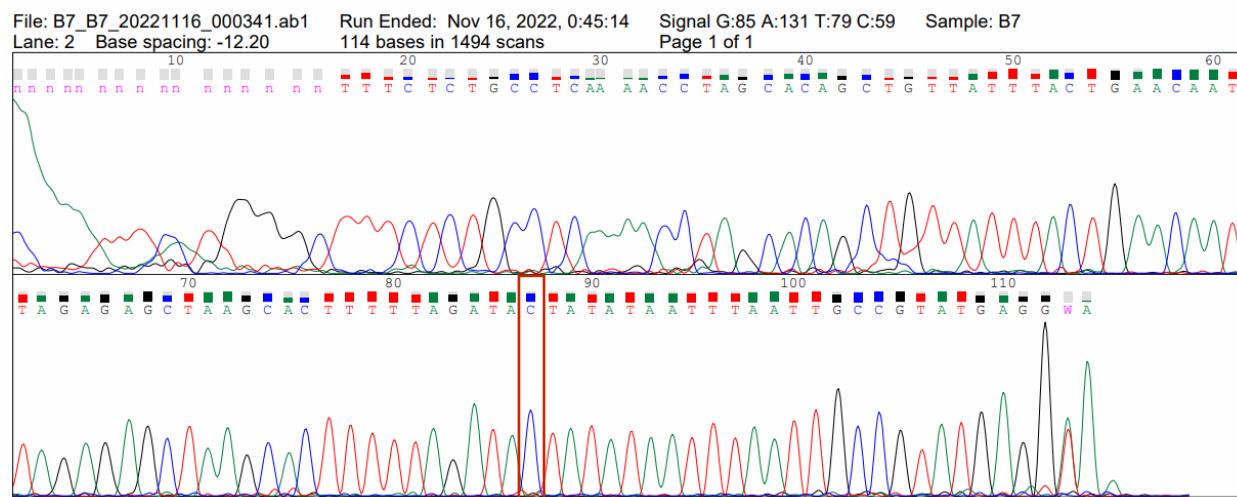
TTTCTCTGCCTCAAAACCTAGCACAGCTGTTATTTACTGAACAATTAGAGAGCTAAG
CACTTTTATAGATACTATATAATTTAATTGCCGTATGAGGWA

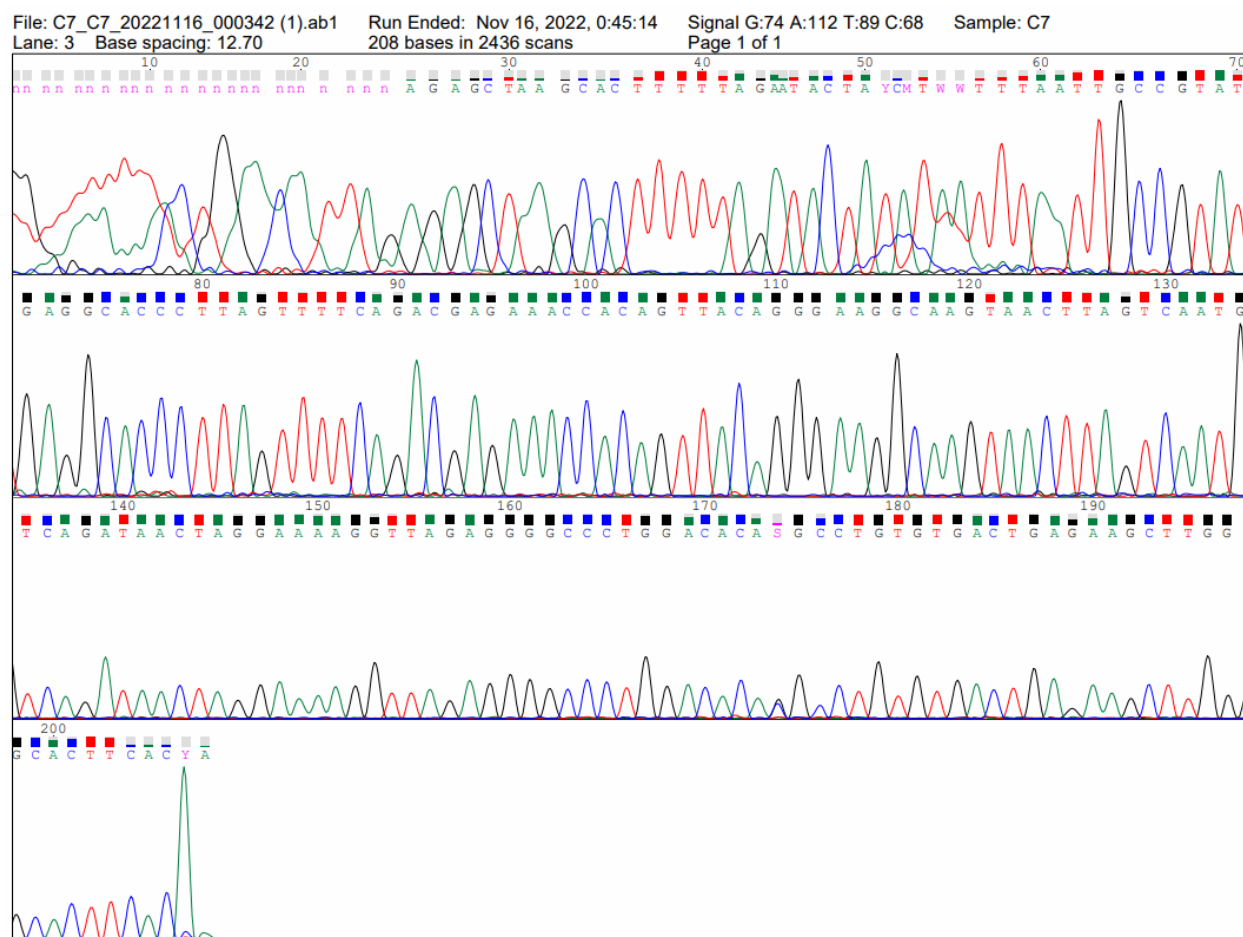
Now comparing the above sequences (they are all for the same SNP) to the flanking region surrounding SNP RS7903146 (given below), I am able to locate the SNP region and highlight it in my sequences and in my peak's graphs. I am homozygous CC, which is associated with lower risk of Type 2 Diabetes and Gestational Diabetes. The results were obtained from my new primer sequence set, and I was not able to exactly pinpoint the flanking regions in my old primer set. I put an asterisk to indicate an additional A that might have been attached by accident to the sequence, which interfered with my results.

CCTTTTAAATGGTGACAAATTCATGGGCTTTCTCTGCCTCAAAACCTAGCACAGCT
GTTATTTACTGAACAATTAGAGAGCTAAGCACTTTTATAGATA

[C/G/T]

TATATAATTTAATTGCCGTATGAGGCACCCTTAGTTTTTCAGACGAGAAACCACAGTT
ACAGGGAAGGCAAGTAACTTAGTCAATGTCAGATAACTAGGAA



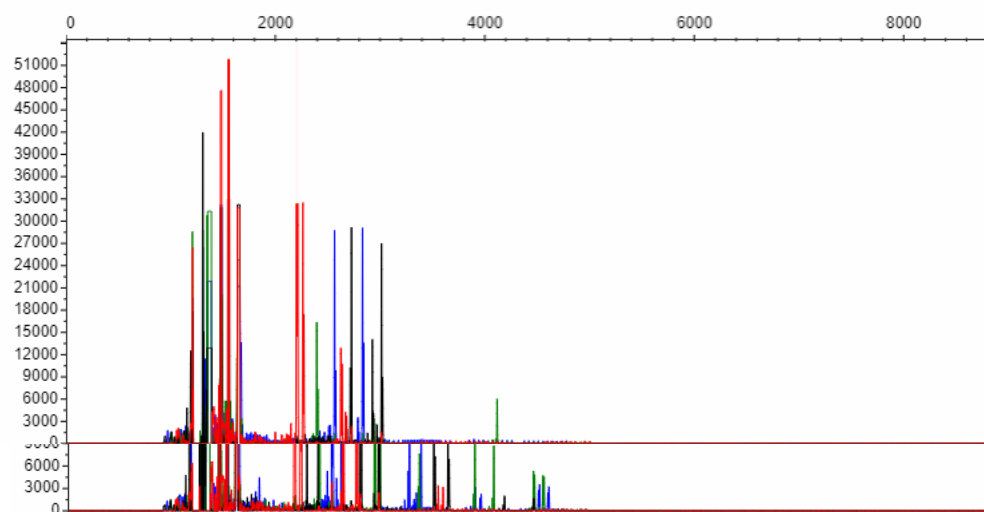


My Trace Sample vs. A1..._160431

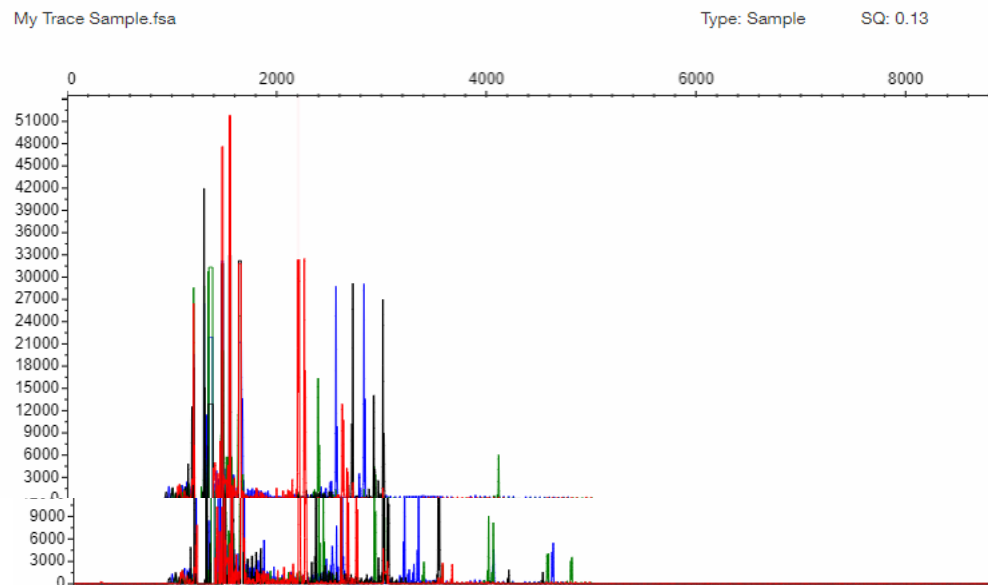
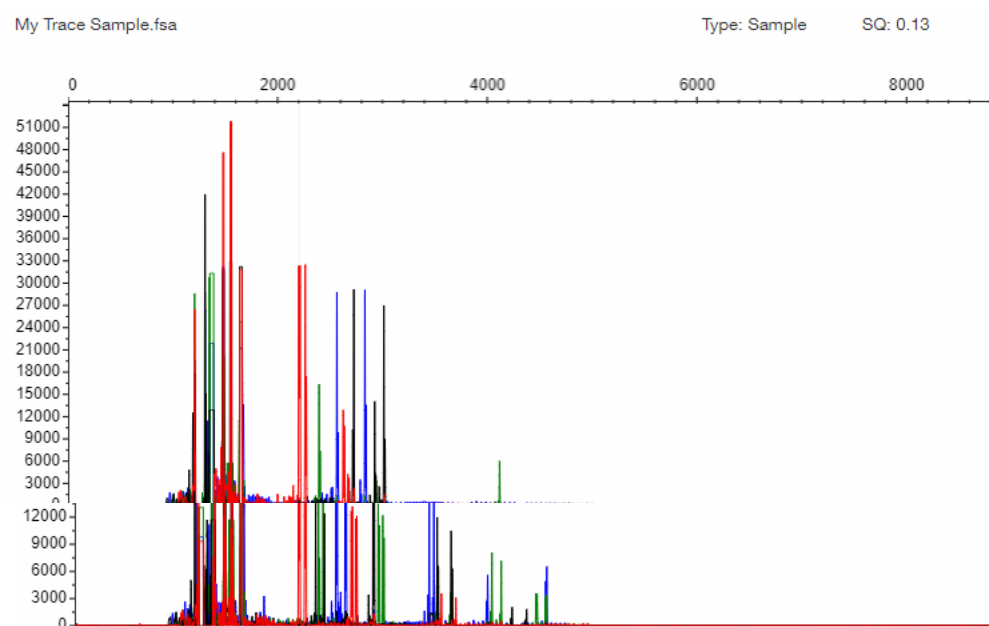
My Trace Sample.fsa

Type: Sample

SQ: 0.13



My Trace Sample vs. F2..._181410



12/6/22

Experiment 23: Blue Pippet of cDNA