SNPmplexViewer

This program compares an old reference file with a similar target file, and aligns chromatograms showing the difference between them.

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INPUT

Submit a reference file you wish to compare as (like format)

Browse...

Submit the target file (like format)

Browse...

* 10 bps before mismatch

Normalize signal strength to (100 default) * A: * 100 * T: * 100 * G: * 100 * C: * 100

Align

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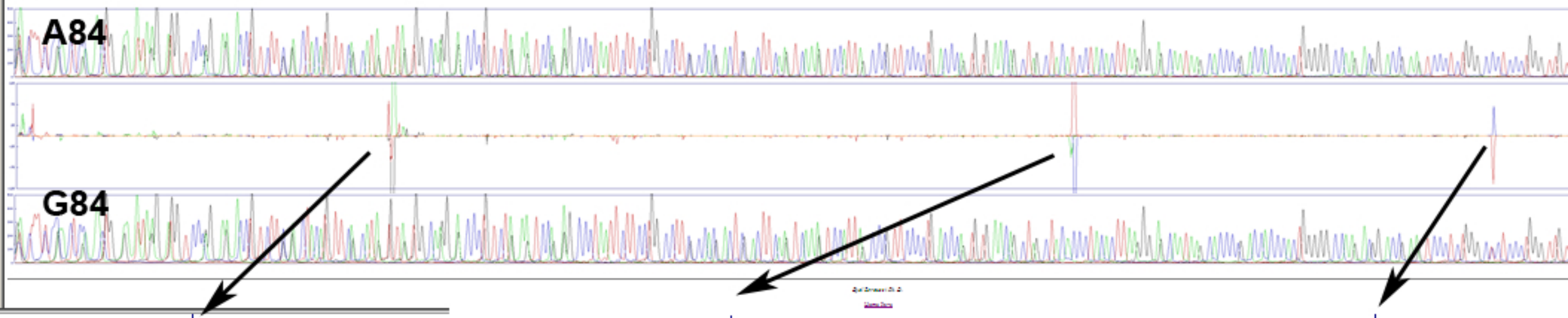
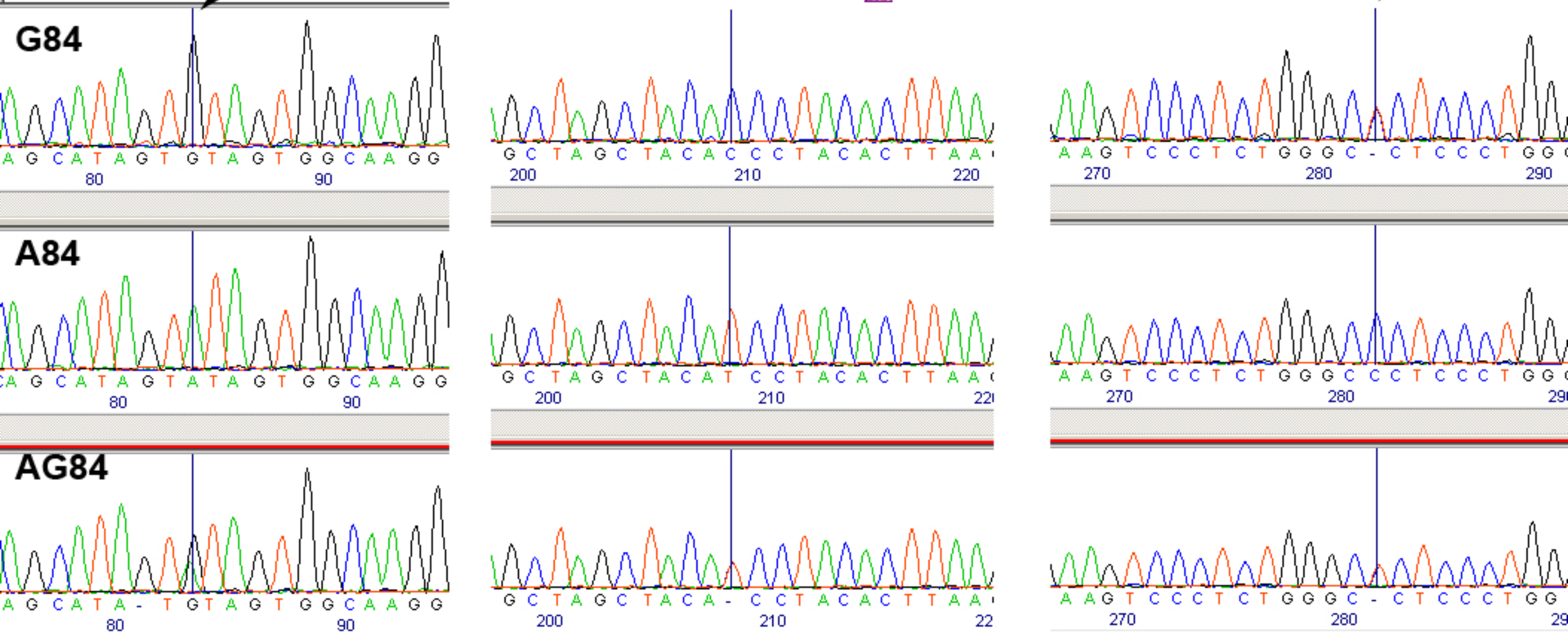
reference_file = C:\Documents and Settings\nathan.fish\Desktop\SNPmplexViewer\Data\Seq1710 A84.ab1
target_file = C:\Documents and Segings\nathan.fish\Desktop\SNPmplexViewer\Data\Seq1710 G84.ab1
range = 100
marker = align

RESULTS

This file aligned from 1710 sequences
This file aligned from 1710 sequences
A peaks at: 1014 , T peaks at: 1024 , G peaks at: 1034, C peaks at: 1042, score: 1014
A peaks at: 1024, T peaks at: 1014 , G peaks at: 1042, C peaks at: 1032, score: 1024

Alignment and difference:

Below is alignment, the reference chromat. file was added to the modified target file target1710_G1.ab1
Save aligned Chromat Files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