

SNPplexViewer

This program compares an ABI reference fsa file with a similar target file, and outputs chromatograms showing the difference between them.

[Source code](#)

[Example Data Set](#)

INPUT

Submit a reference file you wish to compare to (.fsa format)

Browse...

Submit the target file (.fsa format)

Browse...

25-plex bovine traceability

Normalize signal strength to (100 default) 50 100 200 400 800

align

uploaded_reference_file -> C:\VirtualMarker3100pop7.fsa

uploaded_target_file -> C:\3100pop7_3noStandard.fsa

25-plex bovine traceability -> 25PLEX

norm -> 100

action -> align

RESULTS

This file originated from 3100 sequencer.

This file originated from 3100 sequencer.

b peak at 270, g peak at 269, y peak at 456, r peak at 2075, start 1845

b peak at 2080, g peak at 2086, y peak at 2058, r peak at 2099, start 1868

Alignment and differences

Following alignment the marker channel of reference file was added to the modified target file target14854_M.fsa

