

SNPmplexViewer

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)

Submit the target file (.fsa format)

25-plex bovine traceability

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

uploaded_reference_file -> C:\VirtualMarker160707.fsa

uploaded_target_file -> C:\EyalNoMarker.fsa

25-plex bovine traceability -> 25PLEX

norm -> 200

action -> align

RESULTS

This file originated from 310 sequencer.

This file originated from 310 sequencer.

b peak at 2951 g peak at 2903 y peak at 2935 r peak at 2881 start 2666

b peak at 2948 g peak at 2901 y peak at 2899 r peak at 2878 start 2663

Alignment and differences

Following alignment the marker channel of reference file was added to the modified target file target67673_M.fsa

[Download Modified Trace](#)

