

A

ACHLO	RBNII
Achl_ACHLO006-09_1.F.ab1	Achl_RBNII396-13_1.F.ab1
Achl_ACHLO006-09_2.R.ab1	Achl_RBNII396-13_2.R.ab1
Achl_ACHLO007-09_1.F.ab1	Achl_RBNII397-13_1.F.ab1
Achl_ACHLO007-09_2.R.ab1	Achl_RBNII397-13_2.R.ab1



B

sangeranalyseR

SangerAlignment Overview Page

Save S4 instance | Close UI

Input Parameters:

Re-calculate Contigs Alignment

Output Directory: /var/folders/33/7v38jdd2874jcx6l71m00h0000gn/T//RtmpZy72rk

Raw ABI Parent Directory: /Users/chaokuan-hao/Desktop/Allolobophora_chlorotica/

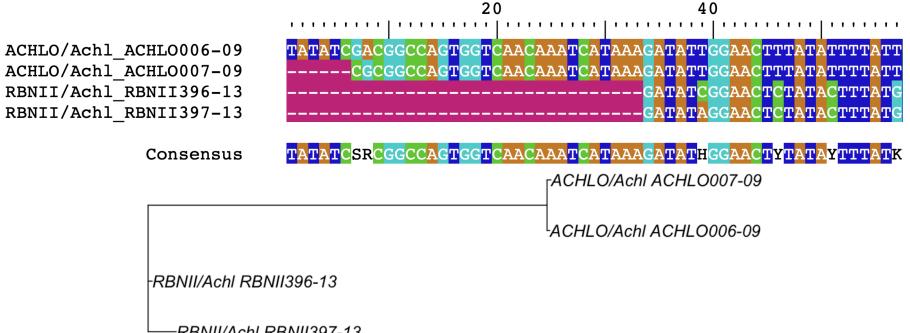
Trimming Method: Method 1: 'Modified Mott Trimming'

Forward Suffix RegEx: _[0-9]*_F.ab1

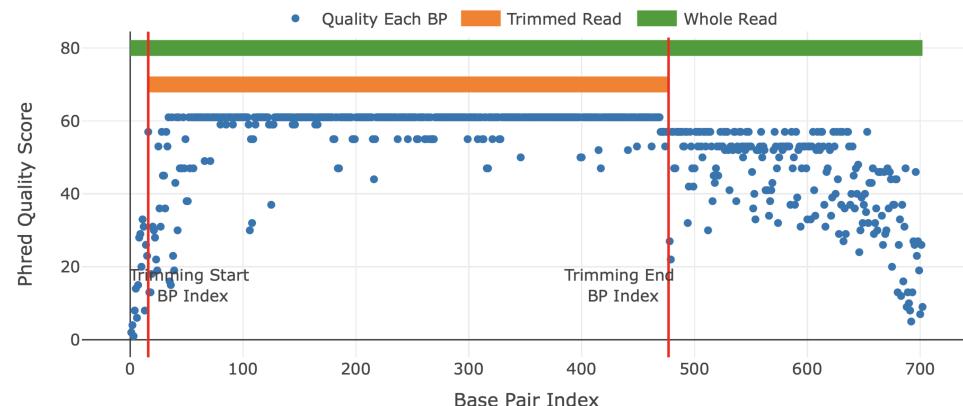
Reverse Suffix RegEx: _[0-9]*_R.ab1



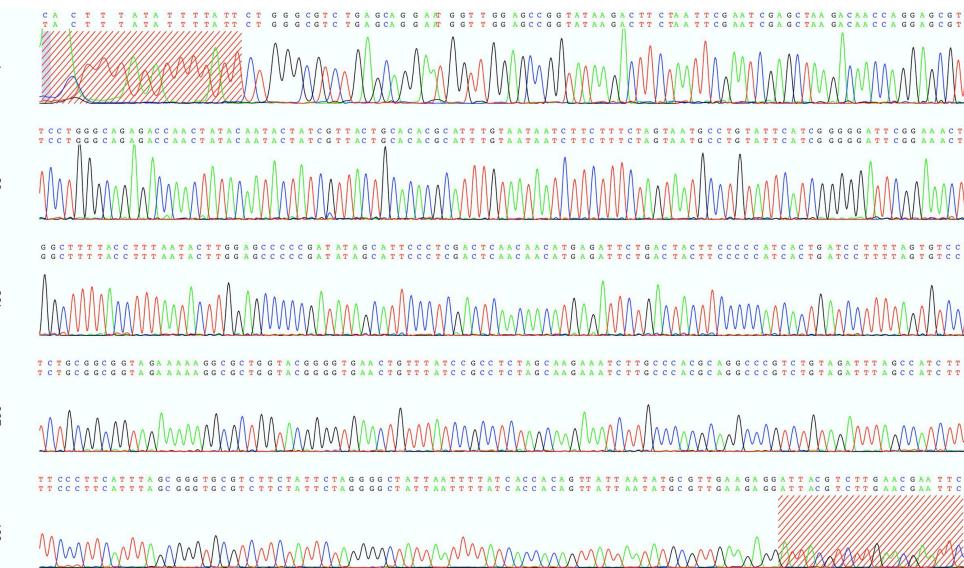
C



D



E



F

```

parentDir <- "/Users/chaokuan-hao/Desktop/Allolobophora_chlorotica/"
suffixForwardRegEx <- "[0-9]*_F.ab1"
suffixReverseRegEx <- "[0-9]*_R.ab1"
myAlignedContigs <- new("SangerAlignment",
  inputSource = "ABIF",
  parentDirectory = parentDir,
  suffixForwardRegEx = suffixForwardRegEx,
  suffixReverseRegEx = suffixReverseRegEx)
launchApp(myAlignedContigs)
generateReport(myAlignedContigs)

```