

# Sequence assembly with Codoncode aligner

Open files in codoncode aligner or you can also drag the file

CodonCode Aligner untitled project

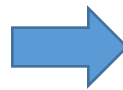
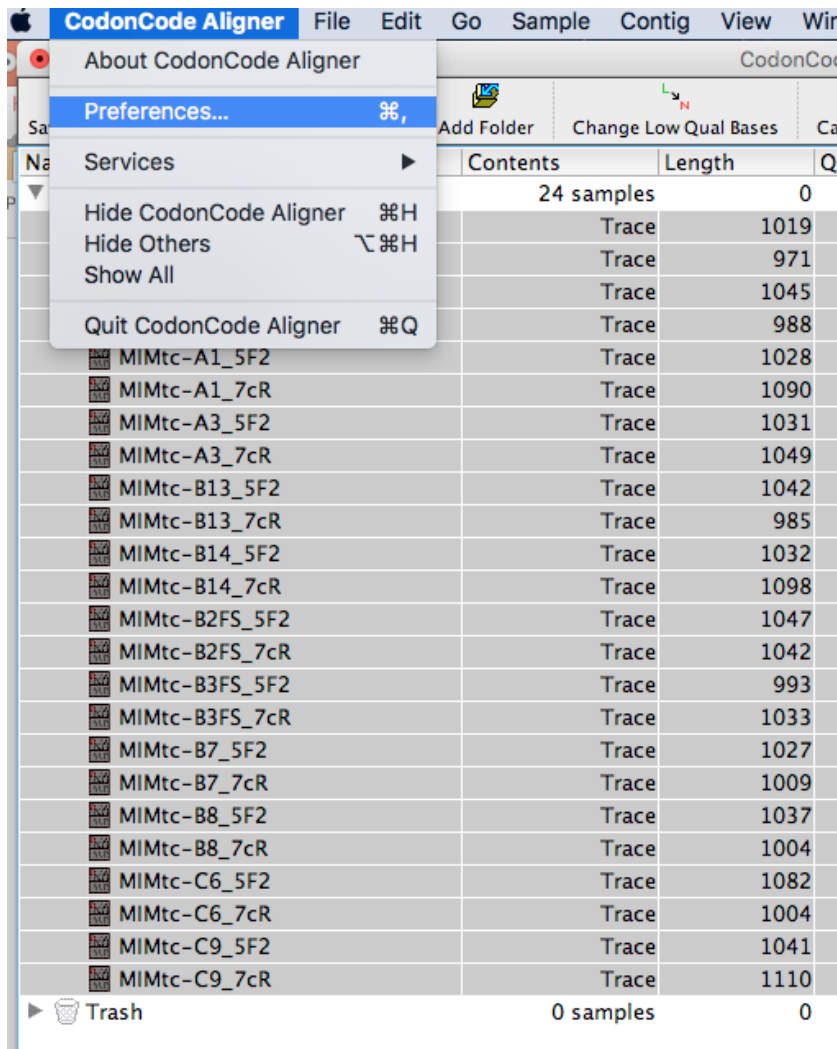
Save Project Save Project As Add Samples Add Folder Change Low Qual Bases Call Bases Clip Ends Assemble Assemble with Preprocessing Assemble in Groups Compare Contigs

Name	Contents	Length	Quality	Position	Added	Modified	Comments
Unassembled Samples	24 samples	0	0		- 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A11_5F2	Trace	1019	945		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A11_7cR	Trace	971	240		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A12_5F2	Trace	1045	948		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A12_7cR	Trace	988	179		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A1_5F2	Trace	1028	945		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A1_7cR	Trace	1090	926		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A3_5F2	Trace	1031	937		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A3_7cR	Trace	1049	824		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B13_5F2	Trace	1042	945		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B13_7cR	Trace	985	800		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B14_5F2	Trace	1032	934		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B14_7cR	Trace	1098	202		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B2FS_5F2	Trace	1047	927		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B2FS_7cR	Trace	1042	181		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B3FS_5F2	Trace	993	535		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B3FS_7cR	Trace	1033	283		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B7_5F2	Trace	1027	933		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B7_7cR	Trace	1009	754		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B8_5F2	Trace	1037	934		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B8_7cR	Trace	1004	511		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C6_5F2	Trace	1082	548		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C6_7cR	Trace	1004	379		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C9_5F2	Trace	1041	913		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C9_7cR	Trace	1110	184		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
Trash	0 samples	0	0		- 6/7/16, 10:27 AM	6/7/16, 10:27 AM	

seqs

5-7Rename.sh  
file\_naming  
MIMtc-A1\_5F2.ab1  
MIMtc-A1\_7cR.ab1  
MIMtc-A3\_5F2.ab1  
MIMtc-A3\_7cR.ab1  
MIMtc-A11\_5F2.ab1  
MIMtc-A11\_7cR.ab1  
MIMtc-A12\_5F2.ab1  
MIMtc-A12\_7cR.ab1  
MIMtc-B2FS\_5F2.ab1  
MIMtc-B2FS\_7cR.ab1  
MIMtc-B3FS\_5F2.ab1  
MIMtc-B3FS\_7cR.ab1  
MIMtc-B7\_5F2.ab1  
MIMtc-B7\_7cR.ab1  
MIMtc-B8\_5F2.ab1  
MIMtc-B8\_7cR.ab1  
MIMtc-B13\_5F2.ab1  
MIMtc-B13\_7cR.ab1  
MIMtc-B14\_5F2.ab1  
MIMtc-B14\_7cR.ab1  
MIMtc-C6\_5F2.ab1  
MIMtc-C6\_7cR.ab1  
MIMtc-C9\_5F2.ab1  
MIMtc-C9\_7cR.ab1

raw



Select **preferences** to adjust parameters as needed (usually default parameters are fine):

- Clipping parameters (removed bad sequences)
- Assembly parameters
- Other adjustments

## Assembly parameters

Assembly

Algorithm: End to end alignments

Min. percent identity:

Min. overlap length:

Min. score:

Max. unaligned end overlap:

Bandwidth (max. gap size):

Word length:

Max. successive failures:

Match score:

Mismatch penalty:

Gap penalty:

Additional first gap penalty:

Defaults

## Clipping parameters

End clipping

☒ Maximize region with error rate below

☐ Use separate criteria for start and end:

Trim from start until

☒ Error rate is below  in a  base window

☐ There are fewer than  bases with quality below  in a  base window

Trim from end until

☒ Error rate is below  in a  base window

☐ There are fewer than  bases with quality below  in a  base window

After end clipping

☒ Move all sequences shorter than  bases to trash.

☒ Move all sequences with fewer than  Phred 20 bases to trash.

## Phred quality score

$$Q = -10 \log_{10} P$$

or

$$P = 10^{\frac{-Q}{10}}$$

For example, if Phred assigns a quality score of 30 to a base, the chances that this base is called incorrectly are 1 in 1000.

### Phred quality scores are logarithmically linked to error probabilities

Phred Quality Score	Probability of incorrect base call	Base call accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1000	99.9%
40	1 in 10,000	99.99%
50	1 in 100,000	99.999%
60	1 in 1,000,000	99.9999%



```
S - Sanger           Phred+33, raw reads typically (0, 40)
X - Solexa           Solexa+64, raw reads typically (-5, 40)
I - Illumina 1.3+ Phred+64, raw reads typically (0, 40)
J - Illumina 1.5+ Phred+64, raw reads typically (3, 40)
  with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)
  (Note: See discussion above).
L - Illumina 1.8+ Phred+33, raw reads typically (0, 41)
```

Click on **call bases**, if necessary. files will be removed and new files will be generated with the corrected quality values

**CodonCode Aligner** File Edit Go Sample Contig View Window Script Help

CodonCode Aligner untitled project

Save Project Save Project As Add Samples Add Folder Change Low Qual Bases **Call Bases** Clip Ends Assemble Assemble with Preprocessing Assemble in Groups Compare Contigs

Name	Contents	Length	Qual	Modified	Comments
▼ Unassembled Samples	24 samples	0	0	- 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A11_5F2	Trace	1019	945	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A11_7cR	Trace	971	240	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A12_5F2	Trace	1045	948	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A12_7cR	Trace	988	179	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A1_5F2	Trace	1028	945	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A1_7cR	Trace	1090	926	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A3_5F2	Trace	1031	937	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-A3_7cR	Trace	1049	824	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B13_5F2	Trace	1042	945	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B13_7cR	Trace	985	800	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B14_5F2	Trace	1032	934	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B14_7cR	Trace	1098	202	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B2FS_5F2	Trace	1047	927	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B2FS_7cR	Trace	1042	181	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B3FS_5F2	Trace	993	535	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B3FS_7cR	Trace	1033	283	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B7_5F2	Trace	1027	933	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B7_7cR	Trace	1009	754	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B8_5F2	Trace	1037	934	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-B8_7cR	Trace	1004	511	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-C6_5F2	Trace	1082	548	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-C6_7cR	Trace	1004	379	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-C9_5F2	Trace	1041	913	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
MIMtc-C9_7cR	Trace	1110	184	0 6/7/16, 10:27 AM	6/7/16, 10:27 AM
▶ Trash	0 samples	0	0	- 6/7/16, 10:27 AM	6/7/16, 10:27 AM

Then select all the sequences and click on **clip bases**

The screenshot shows a software interface with a menu bar at the top containing: Save Project, Save Project As, Add Samples, Add Folder, Change Low Qual Bases, Call Bases, **Clip Ends** (circled in red), Assemble, Assemble with Preprocessing, Assemble in Groups, and Compare Contigs.

Below the menu is a table with the following columns: Name, Contents, Length, Quality, Position, Added, Modified, and Comments.

Name	Contents	Length	Quality	Position	Added	Modified	Comments
▼ Unassembled Samples	24 samples	0	0		- 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A11_5F2	Trace	1019	945		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A11_7cR	Trace	971	240		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A12_5F2	Trace	1045	948		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A12_7cR	Trace	988	179		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A1_5F2	Trace	1028	945		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A1_7cR	Trace	1090	926		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A3_5F2	Trace	1031	937		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-A3_7cR	Trace	1049	824		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B13_5F2	Trace	1042	945		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B13_7cR	Trace	985	800		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B14_5F2	Trace	1032	934		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B14_7cR	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B2FS_5F2	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B2FS_7cR	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B3FS_5F2	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B3FS_7cR	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B7_5F2	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B7_7cR	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B8_5F2	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-B8_7cR	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C6_5F2	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C6_7cR	Trace				0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C9_5F2	Trace	1041	913		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
MIMtc-C9_7cR	Trace	1110	184		0 6/7/16, 10:27 AM	6/7/16, 10:27 AM	
► Trash	0 samples	0	0		- 6/7/16, 10:27 AM	6/7/16, 10:27 AM	

A 'Clipping Preview' dialog box is open in the foreground, showing the following information:

- Preview of clipping results:
- Number of samples clipped: 24
- Average length before clipping: 1033
- Average length after clipping: 625
- Average number of 5' bases clipped: 192
- Average number of 3' bases clipped: 215
- Number of samples moved to Trash: 6

The dialog box has three buttons at the bottom: Cancel, Change parameters, and Clip.



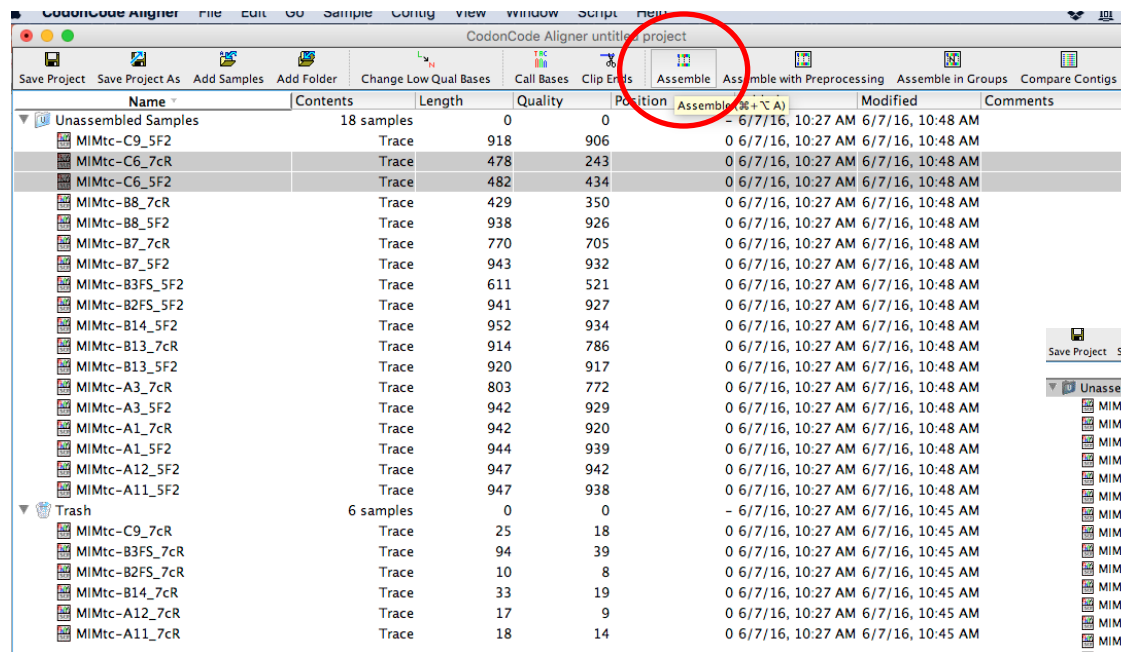
Some sequences did not pass the quality threshold, so they were moved to the trash

<div>  Save Project            Save Project As            Add Samples            Add Folder            Change Low Qual Bases            Call Bases            Clip Ends            Assemble            Assemble with Preprocessing            Assemble in Groups            Compare C         </div>							
Name	Contents	Length	Quality	Position	Added	Modified	Comments
▼ Unassembled Samples	18 samples	0	0	0	- 6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A11_5F2	Trace	947	938	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A12_5F2	Trace	947	942	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A1_5F2	Trace	944	939	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A1_7cR	Trace	942	920	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A3_5F2	Trace	942	929	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A3_7cR	Trace	803	772	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B13_5F2	Trace	920	917	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B13_7cR	Trace	914	786	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B14_5F2	Trace	952	934	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B2FS_5F2	Trace	941	927	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B3FS_5F2	Trace	611	521	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B7_5F2	Trace	943	932	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B7_7cR	Trace	770	705	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B8_5F2	Trace	938	926	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B8_7cR	Trace	429	350	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-C6_5F2	Trace	482	434	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-C6_7cR	Trace	478	243	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-C9_5F2	Trace	918	906	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
▼ Trash	6 samples	0	0	0	- 6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A11_7cR	Trace	18	14	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-A12_7cR	Trace	17	9	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B14_7cR	Trace	33	19	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B2FS_7cR	Trace	10	8	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-B3FS_7cR	Trace	94	39	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MIMtc-C9_7cR	Trace	25	18	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	

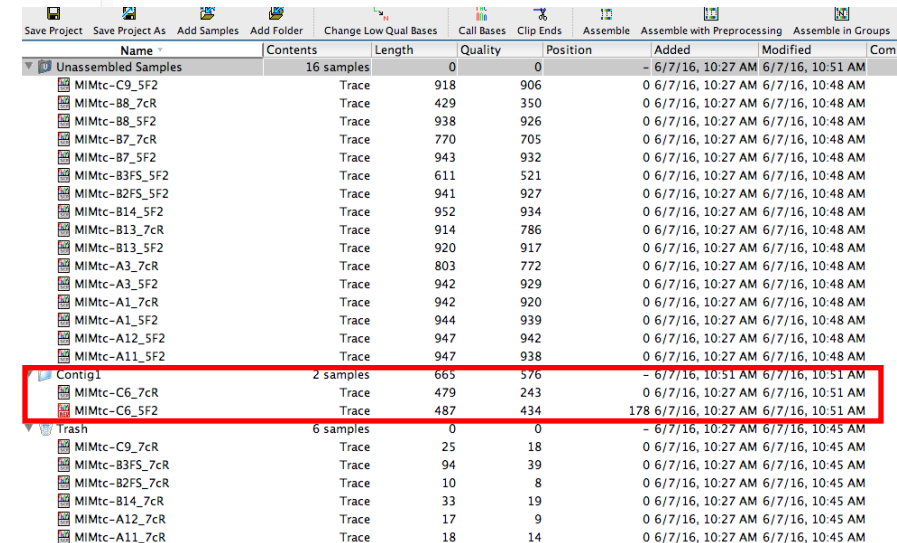


To assemble sequences there are two options, the first is to assemble manually:

1. Select the corresponding sequences
2. Hit assemble and it will generate a contig
3. The resulting contig will be labeled as contig1, make sure that you rename to the actual isolate name



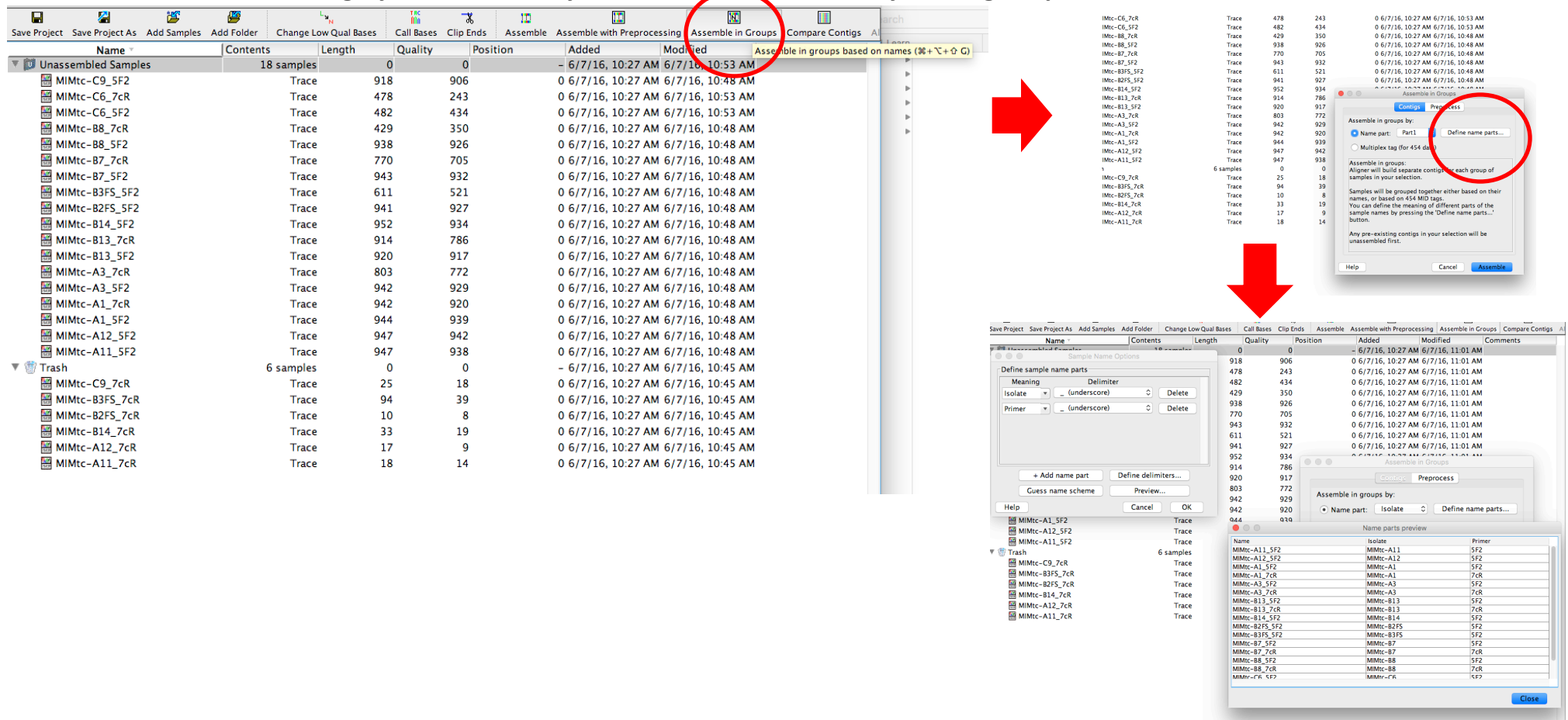
Name	Contents	Length	Quality	Position	Modified	Comments
Unassembled Samples	18 samples	0	0	-	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-C9_SF2	Trace	918	906	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-C6_7cR	Trace	478	243	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-C6_SF2	Trace	482	434	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B8_7cR	Trace	429	350	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B8_SF2	Trace	938	926	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B7_7cR	Trace	770	705	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B7_SF2	Trace	943	932	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B3FS_SF2	Trace	611	521	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B2FS_SF2	Trace	941	927	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B14_SF2	Trace	952	934	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B13_7cR	Trace	914	786	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-B13_SF2	Trace	920	917	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-A3_7cR	Trace	803	772	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-A3_SF2	Trace	942	929	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-A1_7cR	Trace	942	920	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-A1_SF2	Trace	944	939	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-A12_SF2	Trace	947	942	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
MI-Mtc-A11_SF2	Trace	947	938	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM
Trash	6 samples	0	0	-	6/7/16, 10:27 AM	6/7/16, 10:45 AM
MI-Mtc-C9_7cR	Trace	25	18	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM
MI-Mtc-B3FS_7cR	Trace	94	39	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM
MI-Mtc-B2FS_7cR	Trace	10	8	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM
MI-Mtc-B14_7cR	Trace	33	19	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM
MI-Mtc-A12_7cR	Trace	17	9	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM
MI-Mtc-A11_7cR	Trace	18	14	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM



Name	Contents	Length	Quality	Position	Added	Modified	Comments
Unassembled Samples	16 samples	0	0	-	6/7/16, 10:27 AM	6/7/16, 10:51 AM	
MI-Mtc-C9_SF2	Trace	918	906	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B8_7cR	Trace	429	350	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B8_SF2	Trace	938	926	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B7_7cR	Trace	770	705	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B7_SF2	Trace	943	932	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B3FS_SF2	Trace	611	521	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B2FS_SF2	Trace	941	927	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B14_SF2	Trace	952	934	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B13_7cR	Trace	914	786	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-B13_SF2	Trace	920	917	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-A3_7cR	Trace	803	772	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-A3_SF2	Trace	942	929	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-A1_7cR	Trace	942	920	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-A1_SF2	Trace	944	939	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-A12_SF2	Trace	947	942	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
MI-Mtc-A11_SF2	Trace	947	938	0	6/7/16, 10:27 AM	6/7/16, 10:48 AM	
Contig1	2 samples	665	576	-	6/7/16, 10:51 AM	6/7/16, 10:51 AM	
MI-Mtc-C6_7cR	Trace	479	243	0	6/7/16, 10:27 AM	6/7/16, 10:51 AM	
MI-Mtc-C6_SF2	Trace	487	434	178	6/7/16, 10:27 AM	6/7/16, 10:51 AM	
Trash	6 samples	0	0	-	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MI-Mtc-C9_7cR	Trace	25	18	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MI-Mtc-B3FS_7cR	Trace	94	39	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MI-Mtc-B2FS_7cR	Trace	10	8	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MI-Mtc-B14_7cR	Trace	33	19	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MI-Mtc-A12_7cR	Trace	17	9	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	
MI-Mtc-A11_7cR	Trace	18	14	0	6/7/16, 10:27 AM	6/7/16, 10:45 AM	

To assemble sequences there are two options, the first is to assemble manually:

1. Select assemble in groups
2. A window will pop up and the select define name parts to establish your naming system
3. Define the naming system and verify it before you continue by clicking on preview



The screenshot shows the software interface with the 'Assemble in Groups' menu item circled in red. A red arrow points from this menu item to a 'Sample Name Options' dialog box. Another red arrow points from the dialog box to a 'Name parts preview' dialog box.

The 'Sample Name Options' dialog box has the following fields:

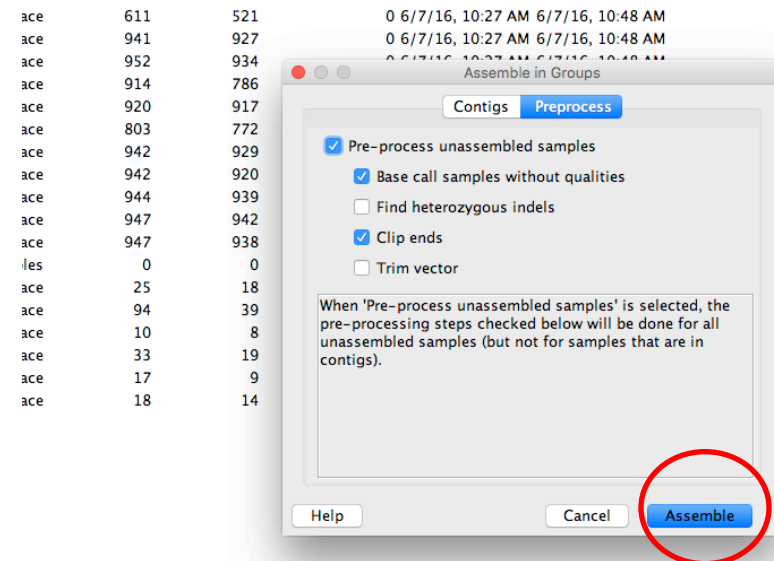
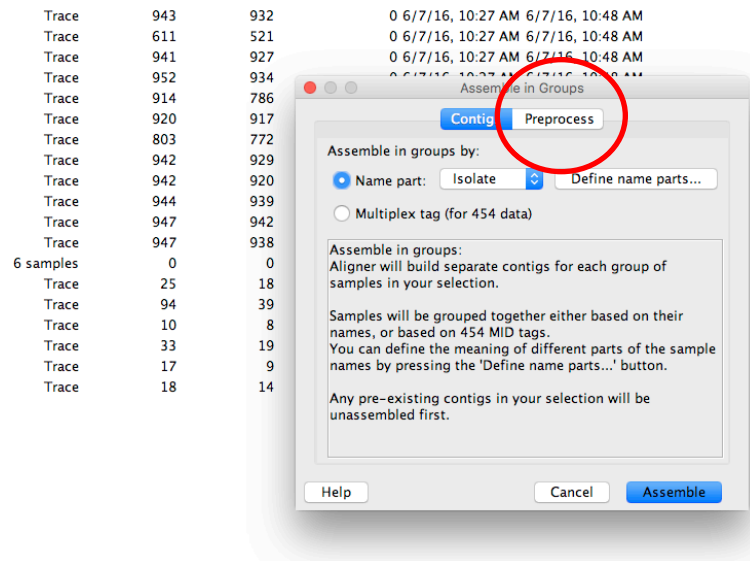
- Meaning: Isolate
- Delimiter: underscore
- Primer: underscore

The 'Name parts preview' dialog box shows a table of sample names and their corresponding parts:

Name	Isolate	Primer
MIMtc-A11_SF2	MIMtc-A11	SF2
MIMtc-A12_SF2	MIMtc-A12	SF2
MIMtc-A1_SF2	MIMtc-A1	SF2
MIMtc-A1_7cR	MIMtc-A1	7cR
MIMtc-A3_SF2	MIMtc-A3	SF2
MIMtc-A3_7cR	MIMtc-A3	7cR
MIMtc-B13_SF2	MIMtc-B13	SF2
MIMtc-B13_7cR	MIMtc-B13	7cR
MIMtc-B14_SF2	MIMtc-B14	SF2
MIMtc-B2FS_SF2	MIMtc-B2FS	SF2
MIMtc-B3FS_SF2	MIMtc-B3FS	SF2
MIMtc-B7_SF2	MIMtc-B7	SF2
MIMtc-B7_7cR	MIMtc-B7	7cR
MIMtc-B8_SF2	MIMtc-B8	SF2
MIMtc-B8_7cR	MIMtc-B8	7cR
MIMtc-C9_SF2	MIMtc-C9	SF2

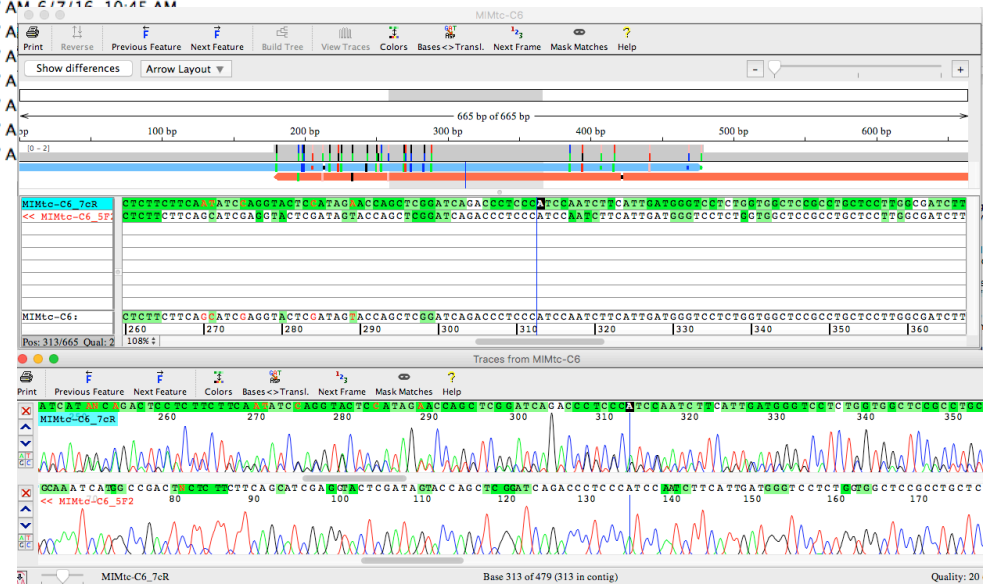
To assemble sequences there are two options, the first is to assemble manually:

1. Make sure that the “name part” is the correct one
2. There is an option for pre-processing that does what it was done in the previous steps
3. Click assemble and you will get contigs named with the name part selected



The project will look like this and you can double click the contig folder to see chromatograms

Name	Contents	Length	Quality	Position	Added	Modified	Comments
Unassembled Samples	6 samples	0	0		- 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-C9_5F2	Trace	918	906		0 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-B3FS_5F2	Trace	611	521		0 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-B2FS_5F2	Trace	941	927		0 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-B14_5F2	Trace	952	934		0 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-A12_5F2	Trace	947	942		0 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-A11_5F2	Trace	947	938		0 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-C6	2 samples	665	576		- 6/7/16, 11:04 AM	6/7/16, 11:04 AM	
MIMtc-C6_7cR	Trace	479	243		0 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-C6_5F2	Trace	487	434	178	6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-B8	2 samples	938	926		- 6/7/16, 11:04 AM	6/7/16, 11:04 AM	
MIMtc-B7	2 samples	943	932		- 6/7/16, 11:04 AM	6/7/16, 11:04 AM	
MIMtc-B13	2 samples	952	937		- 6/7/16, 11:04 AM	6/7/16, 11:04 AM	
MIMtc-A3	2 samples	942	929		- 6/7/16, 11:04 AM	6/7/16, 11:04 AM	
MIMtc-A1	2 samples	975	964		- 6/7/16, 11:04 AM	6/7/16, 11:04 AM	
Trash	6 samples	0	0		- 6/7/16, 10:27 AM	6/7/16, 11:04 AM	
MIMtc-C9_7cR	Trace	25	18		0 6/7/16, 10:27 AM		
MIMtc-B3FS_7cR	Trace	94	39		0 6/7/16, 10:27 AM		
MIMtc-B2FS_7cR	Trace	10	8		0 6/7/16, 10:27 AM		
MIMtc-B14_7cR	Trace	33	19		0 6/7/16, 10:27 AM		
MIMtc-A12_7cR	Trace	17	9		0 6/7/16, 10:27 AM		
MIMtc-A11_7cR	Trace	18	14		0 6/7/16, 10:27 AM		



Then you can go to **file** then select **export** and pick the **consensus sequences** and save it as fasta for further analysis

