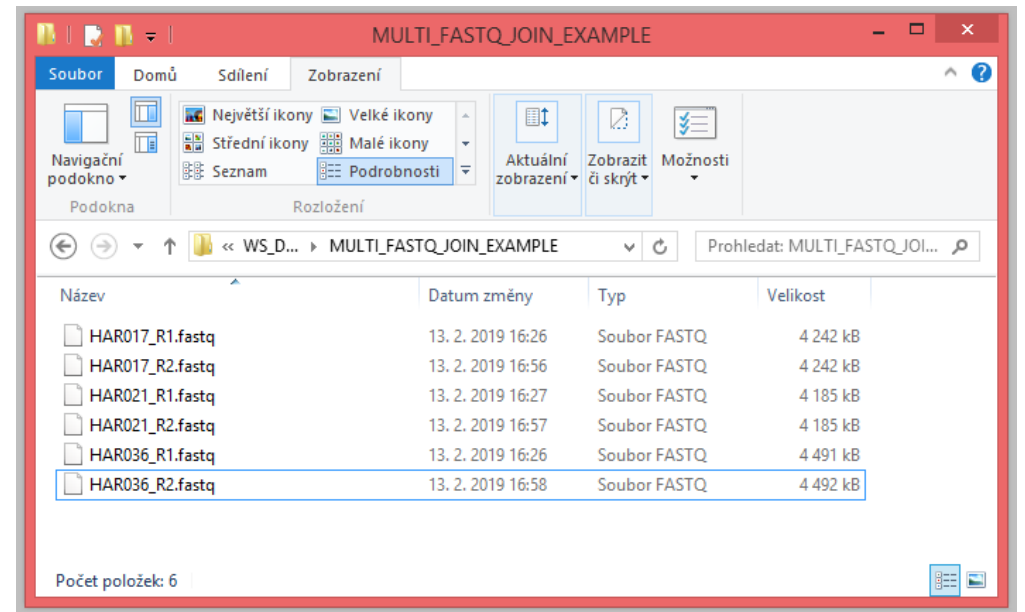
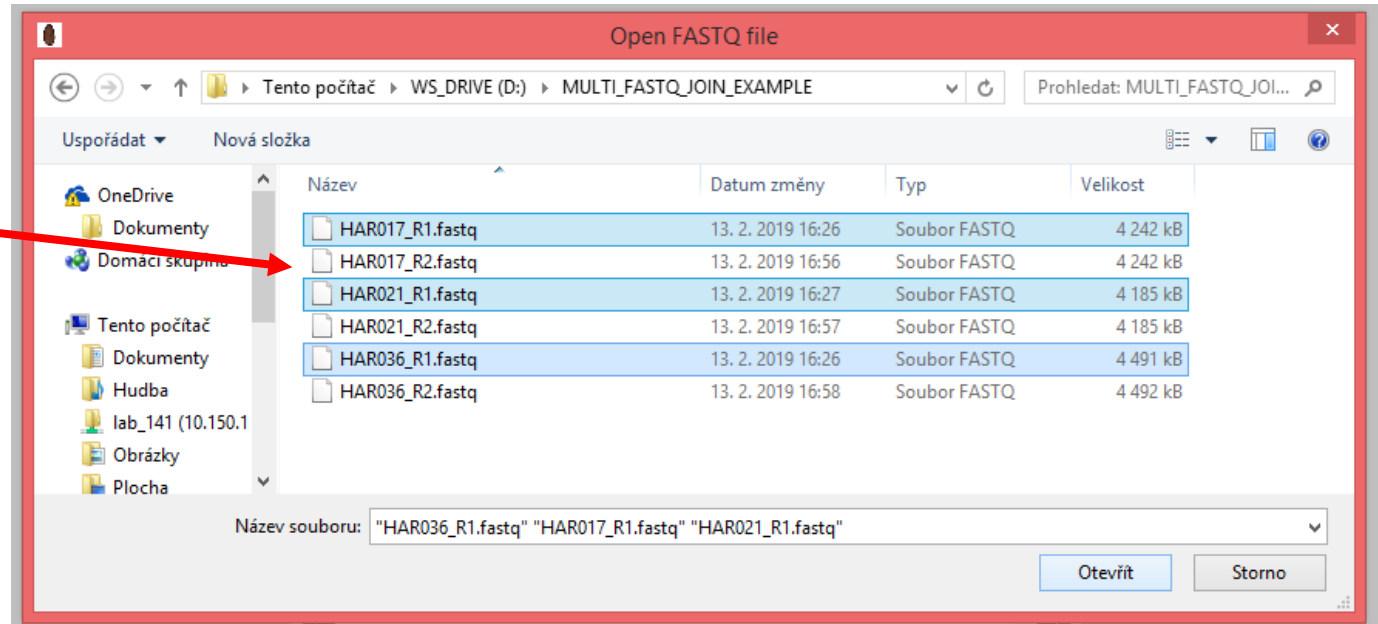
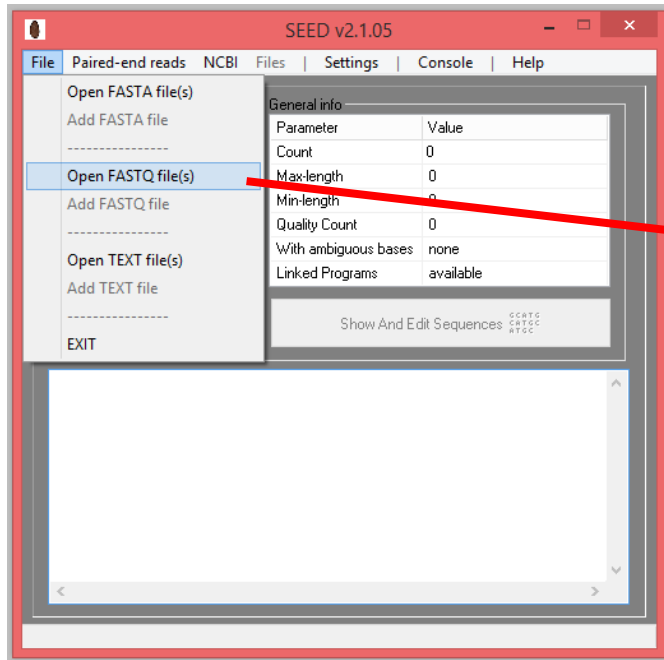


How to join pair-ends of multiple fastq when you have renamed R1 and R2 of individual samples already with the barcodes trimmed...

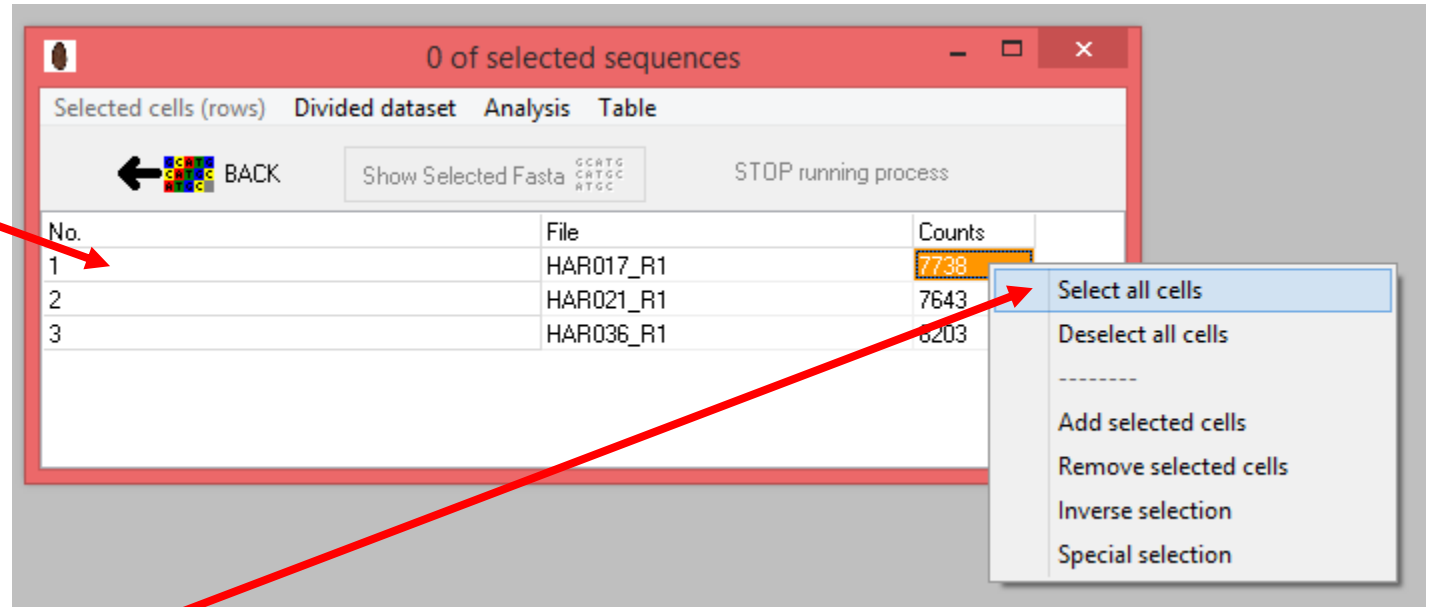
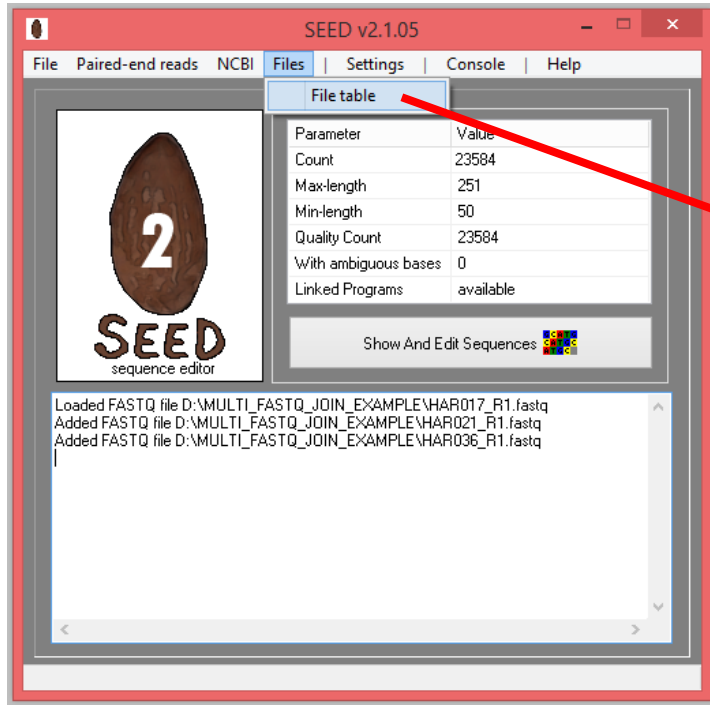
Imagine those input files:



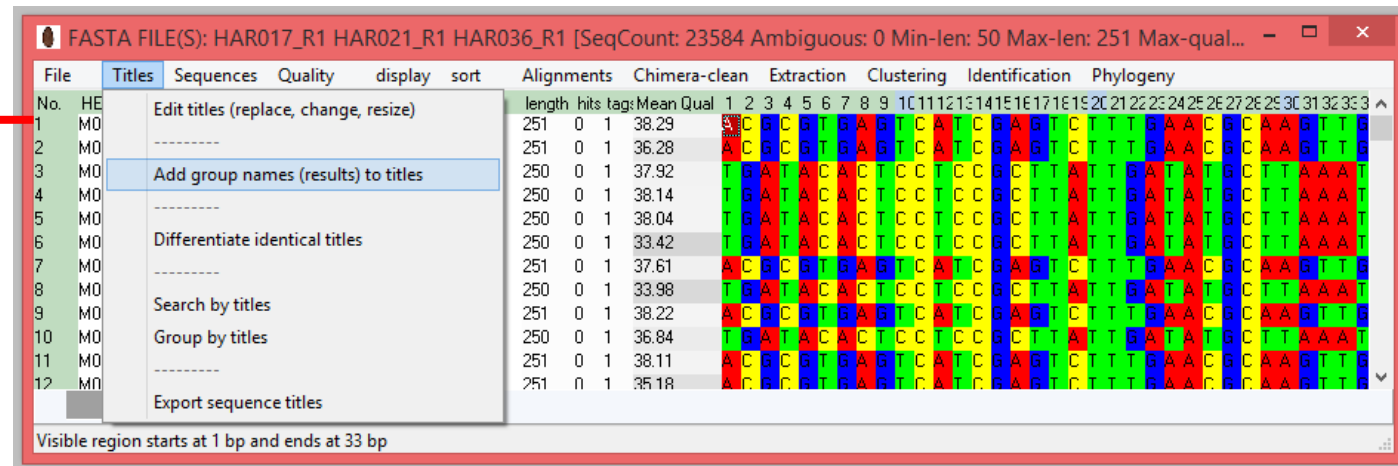
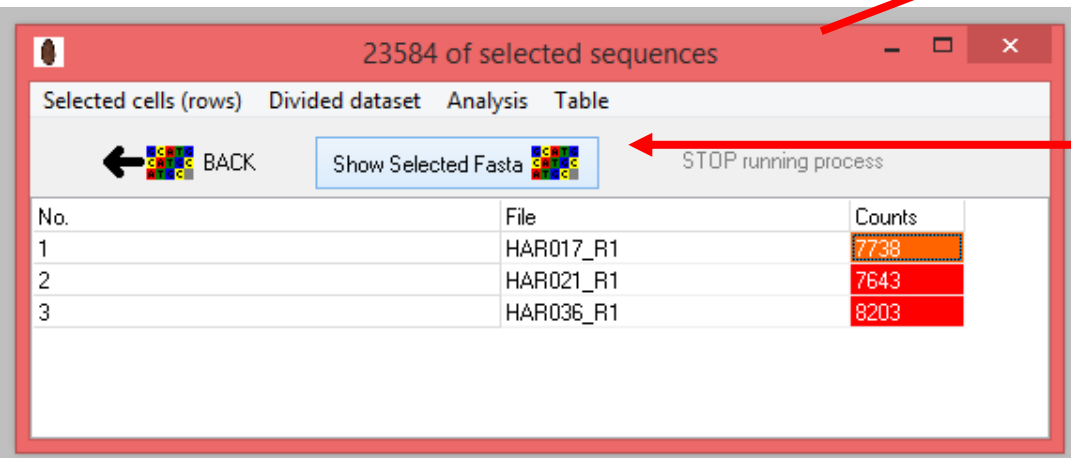
Step 1 – open multiple R1 files from folder... select them by Ctrl or copy them to separate folder (Ctrl+A)



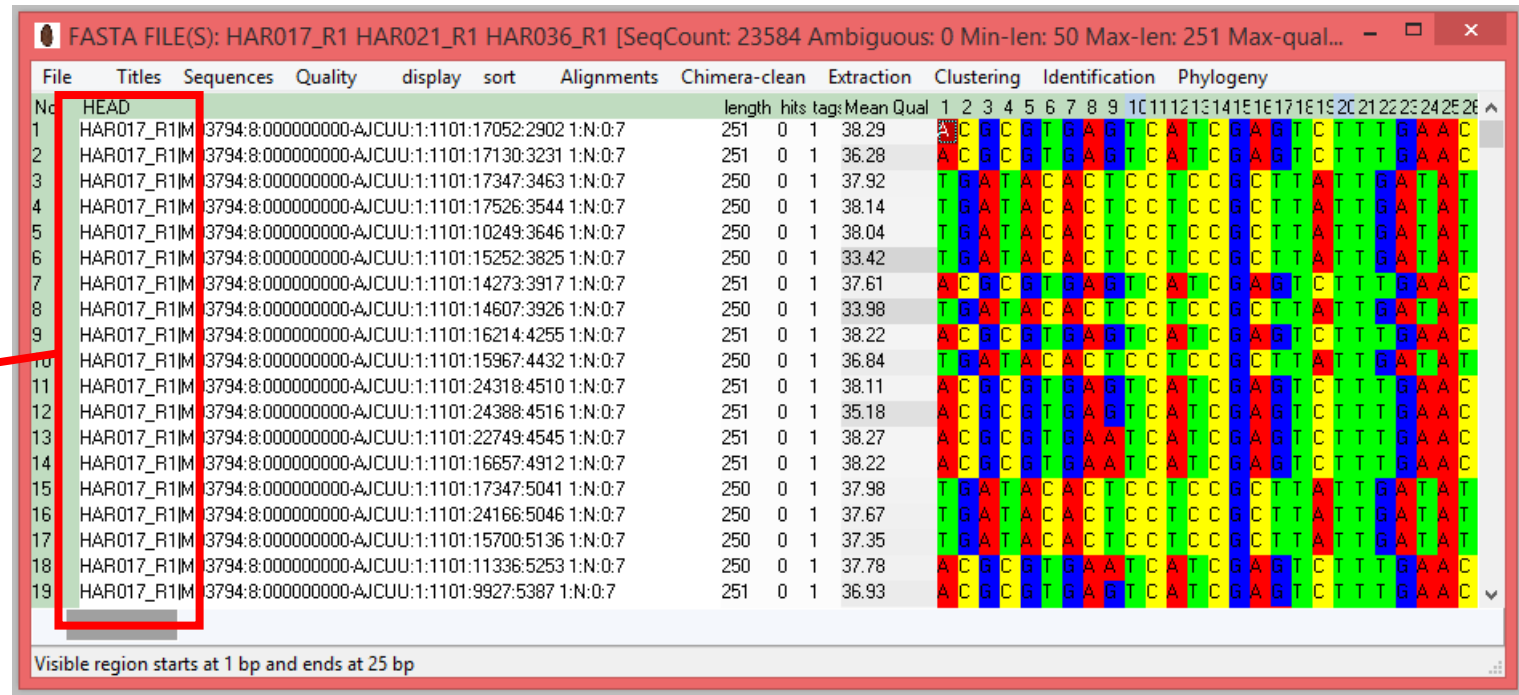
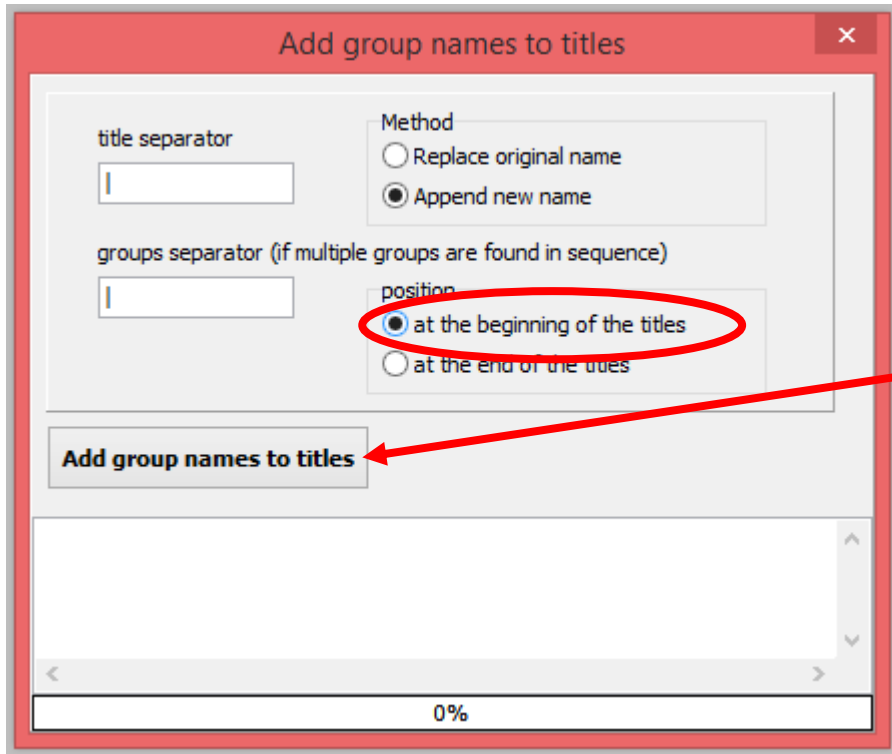
Step 2 – Put sample names (file names) at the beginning of the sequence titles....



...program remembers which sequence belongs to which file....



...put sample name (file name without extension) at the beginning of the titles...



e.g.:

HAR017_R1|M3794:8:000000000-AJCUU:1:1101:14607:3926 1:N:0:7

Step 3 – Remove "_R1" from the titles to make the titles before space (and "1:N:0:7") identical

The image shows a screenshot of a FASTA file editor window titled "FASTA FILE(S): HAR017_R1 HAR021_R1 HAR036_R1 [SeqCount: 23584 Ambiguous: 0 Min-len: 50 Max-len: 251 Max-qual...". The main window displays a table with columns: No., HE, Titles, Sequences, Quality, display, sort, Alignments, Chimera-clean, Extraction, Clustering, Identification, and Phylogeny. A context menu is open over the "Titles" column, with "Edit titles (replace, change, resize)" selected. A red arrow points from this menu item to a dialog box titled "Edit titles (replace, change, resize)".

The dialog box has three tabs: "Rename or change titles", "Append text to titles", and "Resize titles (special replace)". The "Rename or change titles" tab is active. It contains a text area with the text "_R1". A blue box highlights this text with the text "Put just TAB after \"_R1\"". A red arrow points from the "Add Separator (TAB)" button to the text area. Below the text area are "Clear" and "Load from text file..." buttons. There are two main buttons: "Replace titles" and "Find and replace part of title". A red arrow points from the text "Replace it" to the "Find and replace part of title" button. Below these buttons is a checkbox labeled "Ignore multiple KEY values" which is checked. At the bottom, there is a "Method" section with two radio buttons: "Replace original name" (selected) and "Append new name".

No.	HE	Titles	Sequences	Quality	display	sort	Alignments	Chimera-clean	Extraction	Clustering	Identification	Phylogeny
1	HA	002 1:N:0:7					251	0	1		38.29	
2	HA	031 1:N:0:7					251	0	1		36.28	
3	HA	063 1:N:0:7					250	0	1		37.92	
4	HA	044 1:N:0:7					250	0	1		38.14	
5	HA	046 1:N:0:7					250	0	1		38.04	
6	HA	025 1:N:0:7					250	0	1		33.42	
7	HA	017 1:N:0:7					251	0	1		37.61	
8	HA	026 1:N:0:7					250	0	1		33.98	
9	HA	055 1:N:0:7					251	0	1		38.22	
10	HA	032 1:N:0:7					250	0	1		36.84	
11	HA	010 1:N:0:7					251	0	1		38.11	
12	HA	016 1:N:0:7					251	0	1		35.18	
13	HA	045 1:N:0:7					251	0	1		38.27	
14	HA	HAR017_R1 M03794:8:000000000-AJCUU:1:1101:16657:4912 1:N:0:7					251	0	1		38.22	
15	HA	HAR017_R1 M03794:8:000000000-AJCUU:1:1101:17347:5041 1:N:0:7					250	0	1		37.98	
16	HA	HAR017_R1 M03794:8:000000000-AJCUU:1:1101:24166:5046 1:N:0:7					250	0	1		37.67	
17	HA	HAR017_R1 M03794:8:000000000-AJCUU:1:1101:15700:5136 1:N:0:7					250	0	1		37.35	
18	HA	HAR017_R1 M03794:8:000000000-AJCUU:1:1101:11336:5253 1:N:0:7					250	0	1		37.78	
19	HA	HAR017_R1 M03794:8:000000000-AJCUU:1:1101:9927:5387 1:N:0:7					251	0	1		36.93	

Visible region starts at 1 bp and ends at 25 bp

Replace it

Step 4 – Sort the sequences by title (there must be the same sequence order for joining)

FASTA FILE(S): HAR017_R1 HAR021_R1 HAR036_R1 [SeqCount: 23584 Ambiguous: 0 Min-len: 50 Max-len: 251 Max-qual...

No.	HEAD	File	Titles	Sequences	Quality	display	sort	Alignments	Chimera-clean	Extraction	Clustering	Identification	Phylogeny
1	HAR017 M03794:8:000000000-AJCUU:1:1101:1701						Length						
2	HAR017 M03794:8:000000000-AJCUU:1:1101:1711						Title						
3	HAR017 M03794:8:000000000-AJCUU:1:1101:1731						Hits						
4	HAR017 M03794:8:000000000-AJCUU:1:1101:1751						Mean quality						
5	HAR017 M03794:8:000000000-AJCUU:1:1101:1021						Ambiguous seq.						
6	HAR017 M03794:8:000000000-AJCUU:1:1101:1521						Sequence						
7	HAR017 M03794:8:000000000-AJCUU:1:1101:1421												
8	HAR017 M03794:8:000000000-AJCUU:1:1101:1461												
9	HAR017 M03794:8:000000000-AJCUU:1:1101:16214:4255 1:N:0:7												
10	HAR017 M03794:8:000000000-AJCUU:1:1101:15967:4432 1:N:0:7												
11	HAR017 M03794:8:000000000-AJCUU:1:1101:24318:4510 1:N:0:7												
12	HAR017 M03794:8:000000000-AJCUU:1:1101:24388:4516 1:N:0:7												
13	HAR017 M03794:8:000000000-AJCUU:1:1101:22749:4545 1:N:0:7												
14	HAR017 M03794:8:000000000-AJCUU:1:1101:16657:4912 1:N:0:7												
15	HAR017 M03794:8:000000000-AJCUU:1:1101:17347:5041 1:N:0:7												
16	HAR017 M03794:8:000000000-AJCUU:1:1101:24166:5046 1:N:0:7												
17	HAR017 M03794:8:000000000-AJCUU:1:1101:15700:5136 1:N:0:7												
18	HAR017 M03794:8:000000000-AJCUU:1:1101:11336:5253 1:N:0:7												
19	HAR017 M03794:8:000000000-AJCUU:1:1101:9927:5387 1:N:0:7												

Visible region starts at 1 bp and ends at 25 bp

Step 5 – Save it as FASTQ

Step 5 – Save the sequences as FASTQ

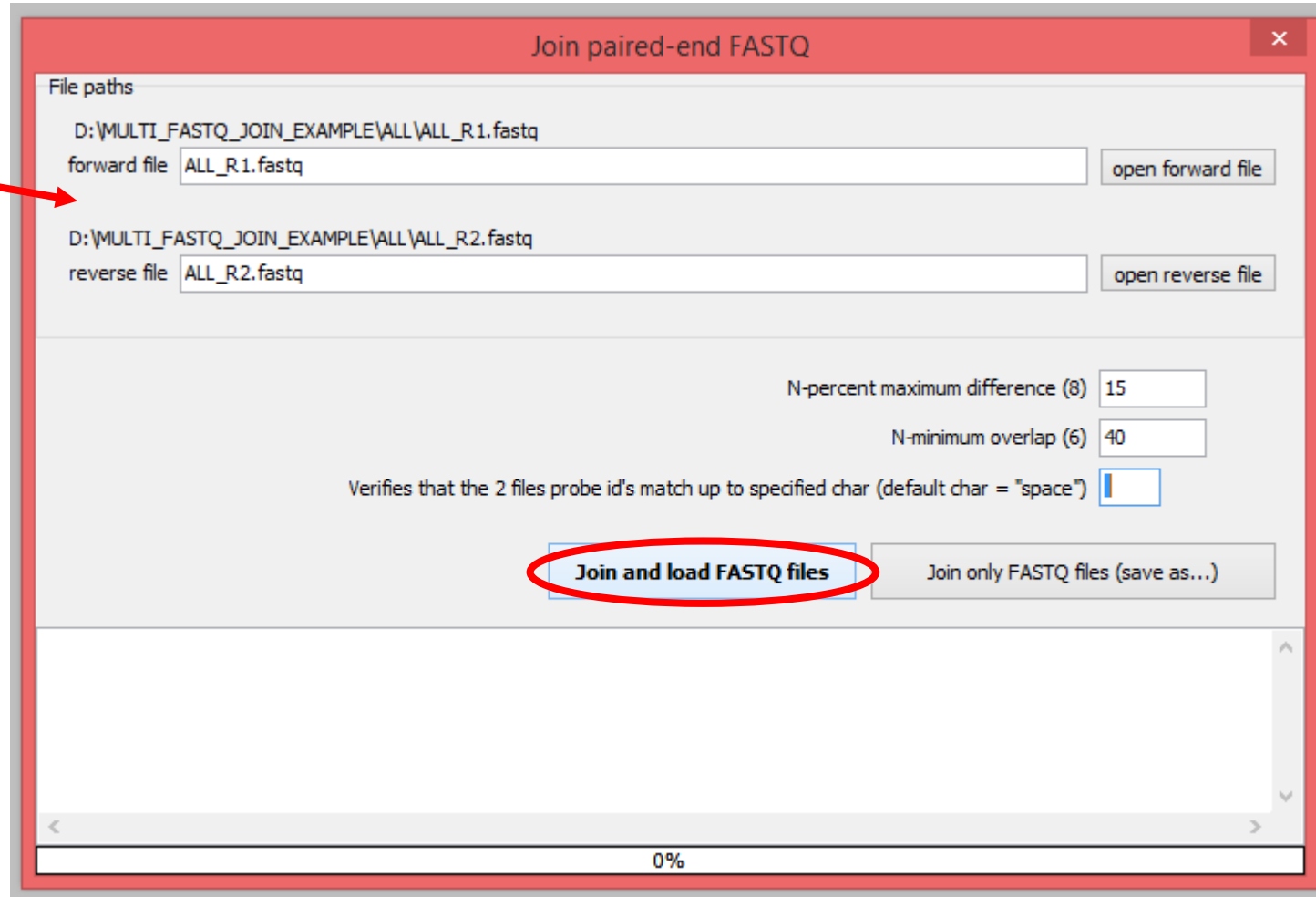
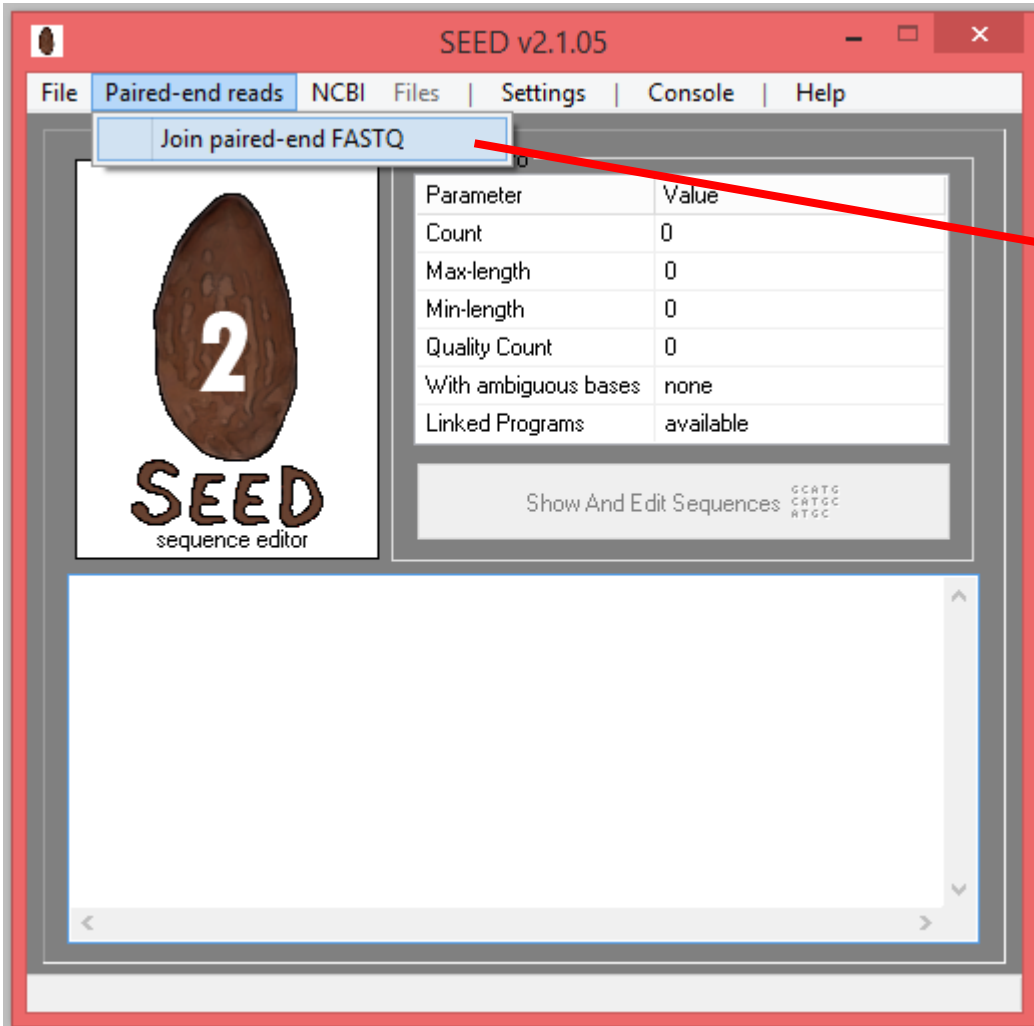
The screenshot shows a software window titled "FASTA FILE(S): HAR017_R1 HAR021_R1 HAR036_R1 [SeqCount: 23584 Ambiguous: 0 Min-len: 50 Max-len: 251 Max-qual...". The main window displays a table of sequence data with columns for "File", "Titles", "Sequences", "Quality", "display", "sort", "Alignments", "Chimera-clean", "Extraction", "Clustering", "Identification", and "Phylogeny". A red arrow points from the "Save as FASTQ" option in the "File" menu to the "Save as FASTQ" dialog box.

The "Save as FASTQ" dialog box is open, showing a file explorer view. The current directory is "MULTI_FASTQ_JOIN_E...". The file name is "ALL_R1". The "Uložit jako typ:" field is empty. The "Uložit" button is highlighted.

File	Titles	Sequences	Quality	display	sort	Alignments	Chimera-clean	Extraction	Clustering	Identification	Phylogeny																						
						length	hits	tag	Mean	Qual																							
						1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		
						250	0	1	37.96																								
						251	0	1	38.11																								
						251	0	1	38.28																								

Step 6 – Do the same for R2 files :)

Step 7 – Join the paired-ends



Then you can continue as described in manual....