SeqTrimNext
Statistics of pre-processing

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1 Output Files

SeqTrimNext provides several files, the most interesting ones are in the following directories:

- output_files
  - `output.less`, containing an extensive information about the trimming of each sequence. It can be visualised on terminal using the command `less -R`.
  - `used_params.txt`, containing the complete set of parameters used for execution of SeqTrimNext with your data
  - `rejected.txt`, containing a list of rejected sequences together with the reason for their removal.
  - `initial_stats.json`, containing statistics for raw sequences.
  - `stats.json`, containing the statistics of the cleaning process.
  - There is a collection of `folders` that gather sequences with the same MID; each folder contains a `sequences` file (in FastQ format) with useful reads. There may also exists a file with reads containing low complexity regions. If you want to reconstruct a SFF with the useful segment of each pre-processed read, use `sff_info` file in combination with the original SFF file for the `sfffile` tool.
- graphs
  - `size_stats.png`, a graph with the distribution of read lengths in raw data (see Fig. **??**).
  - `qualities.png`, a graph to inspect read qualities in raw data (see Fig. **??**).
  - `PluginExtractInserts_insert_size.png`, a graph with the distribution of read lengths after SeqTrimNext pre-processing (see Fig. 1).
  - There are other graphs (mostly bar plots) that illustrate the quality of pre-processed reads. All are in PNG format.
- latex
  - It is provided as a compressed file `latex.zip` containing all ".tex" files required to compile this document. Graphs are taken from the `graph` folder

2 Relevant parameters

In this section, the relevant parameters used in your experiment are shown. Full information about the parameters can be obtained from file `used_params.txt`

2.1 General

Plugins applied to every sequence, separated by commas. Order is important

1. PluginIndeterminations
2. PluginFindPolyAt
3. PluginAbAdapters
4. PluginUserContaminants
5. PluginContaminants
6. PluginVectors
7. PluginLowQuality
8. PluginLowComplexity
9. PluginExtractInserts

Remove duplicated (clonal) sequences (using CD-HIT 454)

`remove_clonality: false`

Minimum insert size for every trimmed sequence

`min_insert_size_trimmed: 30`

Minimum insert size for each end of paired-end reads; true paired-ends have both single-ends longer than this value

`min_insert_size_paired: 40`

Seqtrim version

`seqtrim_version: 2.0.67`

`min_sequence_size_raw:`

2.2 Quality

Minimum quality value for every nucleotide

`min_quality: 20`

`window_width:`

2.3 Contaminants

Blast E-value used as cut-off when searching for contaminations

`blast_evalue_contaminants: 1.0e-10`

Minimum required identity (%) for a reliable contamination

`blast_percent_contaminants: 85`

Minimum hit size (nt) for considering a true contamination

`min_contam_seq_presence: 40`

Genus of input data: contaminations belonging to this genus will be ignored

`genus:`

Is a contamination considered a source of sequence rejection? (setting to false will only trim contaminated sequences instead of rejecting the complete read)

`contaminants_reject: true`

Path for contaminants database

`contaminants.fasta`

`cont_ribosome.fasta`

3 Pre-processing statistics

Next figure is equivalent to Figure **??** but using output reads (useful sequences). The mode is expected to decrease but the shape of the plot should be similar.

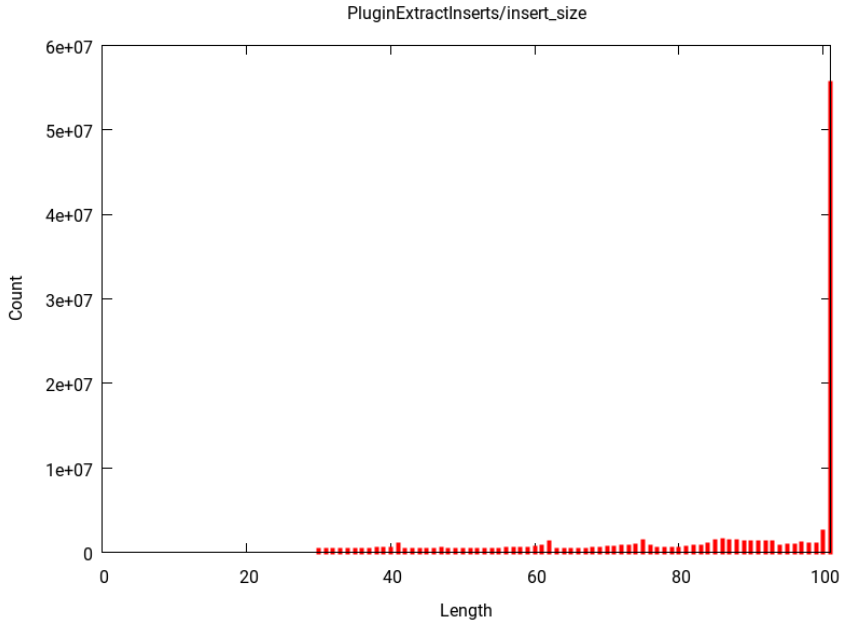

Figure 1: Size distribution of the output sequences. Short sequences (< `min_insert_size_trimmed`) were removed. [PluginExtractInserts_insert_size.png]

Summary statistics of the SeqTrimNext analysis. Be careful and read all warnings that are indicating concerns about your data. In the files `initial_stats.json` and `stats.json` can be found a full statistics of your data and SeqTrimNext pre-processing

Input reads:	total	109866292
	Smallest read (bp)	101
	Largest read (bp)	101
	Mode (bp)	0
	Mean (bp)	0.0
Output results:	total	4592359
	Rejected	13116478
	Low complexity reads	72459
	Mode (bp)	91
	Mean (bp)	90.0
	Output paired reads	92084996
	Total output reads	96677355
Linkers:		

Table 1: List of the most frequent Vectors found among your reads

Vectors	sequences
Cloning vector pKOHPRT complete sequence.	514039
Cloning vector pAAV-MCS, complete sequence.	503089
Enterobacteria phage lambda	150690
Cloning vector pVLH/hsp	49158
Cloning vector pWormgate2, complete sequence.	45975

Table 2: List of the most frequent Adapters found among your reads

Adapters	sequences
ABI_Solid3_Adapter_A	303366
TruSeq_Universal_Adapter	245307
ABI_Solid3_GAPDH_Reverse_Primer	244836
Illumina_Single_End_Adapter_1	215114
ABI_Solid3_GAPDH_Forward_Primer	211445

Table 3: List of the most frequent Contaminants found among your reads

Contaminants	sequences
rRNA_small_subunit_Metazoa_Myotis	98004
rRNA_long_subunit_Metazoa_Dasypus	97101
Saccharomyces cerevisiae S288c chromosome XII, complete sequence	90877
Schizosaccharomyces pombe 972h- chromosome III, complete sequence	65294
Podospora anserina S mat+ unordered scaffolds, whole genome shotgun sequence	64625

Table 4: Summary of nucleotides removed in every plugin.

Plugin	Nucleotides	Percent	Warnings
Low Quality	1771032029	Inf %	OK
Low Complexity	75346562	Inf %	OK
Poly T	34572908	Inf %	OK
Poly A	40513685	Inf %	OK
Contaminants	64049985	Inf %	OK
Adapters	102925604	Inf %	OK
Vectors	60448983	Inf %	OK
Indeterminations	101857	Inf %	OK
Inserts	8709317205	Inf %	iW1

iW1 Warning!, only Inf % of nucleotides are useful

4 Rejected reads

Input sequences	109866292
Output sequences	4592359
Rejected sequences	13116478
Output paired sequences	92084996
Total output sequences	96677355
Low complexity sequences	72459

Table 5: Summary of reads removed in every plugin.

Case	Number of sequences	Percent	Warnings
	13116478	11.939 %	OK
Short inserts	8301987	7.556 %	rdW2
Empty Inserts	4104155	3.736 %	rdW3
Contaminants	686005	0.624 %	OK
No Valid Inserts	17035	0.016 %	OK
Low Complexity	6566	0.006 %	OK
Indeterminations	613	0.001 %	OK
Unexpected Vector	117	0.000 %	OK
Total rejected	13116478	11.939 %	OK

rdW2 Warning!, a 7.556 % of your sequences are too short

rdW3 Warning!, a 3.736 % of your sequences are empty (without an insert)

References

[1] Falgueras et al. SeqTrim: a high-throughput pipeline for preprocessing any type of sequence reads. *BMC Bioinformatics* 11:38 (2010)

[2] Weizhong Li & Adam Godzik. Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. *Bioinformatics* (2006) 22:1658-9

Thanks you for use SeqTrimNext! Send us any comment to scbi support