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1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
RI0307_S10_L007_R 1_001 (paired)	44.726.310	100,0	43.442.435	97,13%

Avg.length after trim
96,6

2. Read length before / after trimming



3. Trim settings

- Automatic removal of read-through adapter sequences.
- Removal of low quality sequence. (limit = 0,05).
- Removal of ambiguous nucleotides: maximal 2 nucleotides allowed.
- Removal of adapter sequences, using the following adapters :

19 # TruSeq Adapter. Index (GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAAACGATCTCGTATGCCGTCTTCTGCTTG), Reads: First read, When an adapter is found: Trim 5' end, For reads without adapters: Keep the read, Score: [2:3:10:4] # TruSeq Adapter, Index 3 (GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAGGCATCTCGTATGCCGTCTTCTGCTTG), Reads: First read, When an adapter is found: Trim 5' end, For reads without adapters: Keep the read, Score: [2 : 3 : 10 : 4] 7 # TruSeq Adapter, Index (GATCGGAAGAGCACACGTCTGAACTCCAGTCACCAGATCATCTCGTATGCCGTCTTCTGCTTG), Reads: First read, When an adapter is found: Trim 5' end, For reads without adapters: Keep the read, Score: [2:3:10:4] # TruSeq Adapter, Index 6 (GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCCAATATCTCGTATGCCGTCTTCTGCTTG), Reads: First read, When an adapter is found: Trim 5' end, For reads without adapters: Keep the read, Score: [2:3:10:4] 8 # TruSeq Adapter, Index (GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTGAATCTCGTATGCCGTCTTCTGCTTG), Reads: First read, When an adapter is found: Trim 5' end, For reads without adapters: Keep the read, Score: [2:3:10:4] Illumina # Single End PCR Primer 1 (AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT), Reads: Second read, When an adapter is found: Trim 3' end, For reads without adapters: Keep the read, Score: [2:3:10:4] 1 # TruSeq Adapter, Index (GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCACGATCTCGTATGCCGTCTTCTGCTTG), Reads: First read, When an adapter is found: Trim 5' end, For reads without adapters: Keep the read, Score: [2:3:10:4] adapter is found: Trim 3' end, For reads without adapters: Keep the read, Score: [2:3:10:4] an adapter is found: Trim 5' end, For reads without adapters: Keep the read, Score: [2:3:10:4]

• Removal of sequences on length: minimum length 20 nucleotides.

4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	44.726.310	33.112.620	11.613.684	6
Ambiguity trim	44.726.304	44.716.022	10.052	230
Adapter trimming	44.726.074	40.231.033	3.497.452	997.589

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Filter on length	43.728.485	43.442.435	0	286.050

Notice: Automatic adapter read-through statistics are found in the next section.

5. Automatic adapter read-through trimming

Processed read pairs	22363155
Read pairs trimmed	267013
Read pairs trimmed (percent)	1,19%

Statistics for read 1

Read 1 trimmed	267013
Read 1 trimmed (percent)	1,19%
Detected read-through sequence	AGATCGGAAGAGCACACGTCTGAACTCCAGTCACT

Statistics for read 2

Read 2 trimmed	267013
Read 2 trimmed (percent)	1,19%
Detected read-through sequence	AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGGA TAG

