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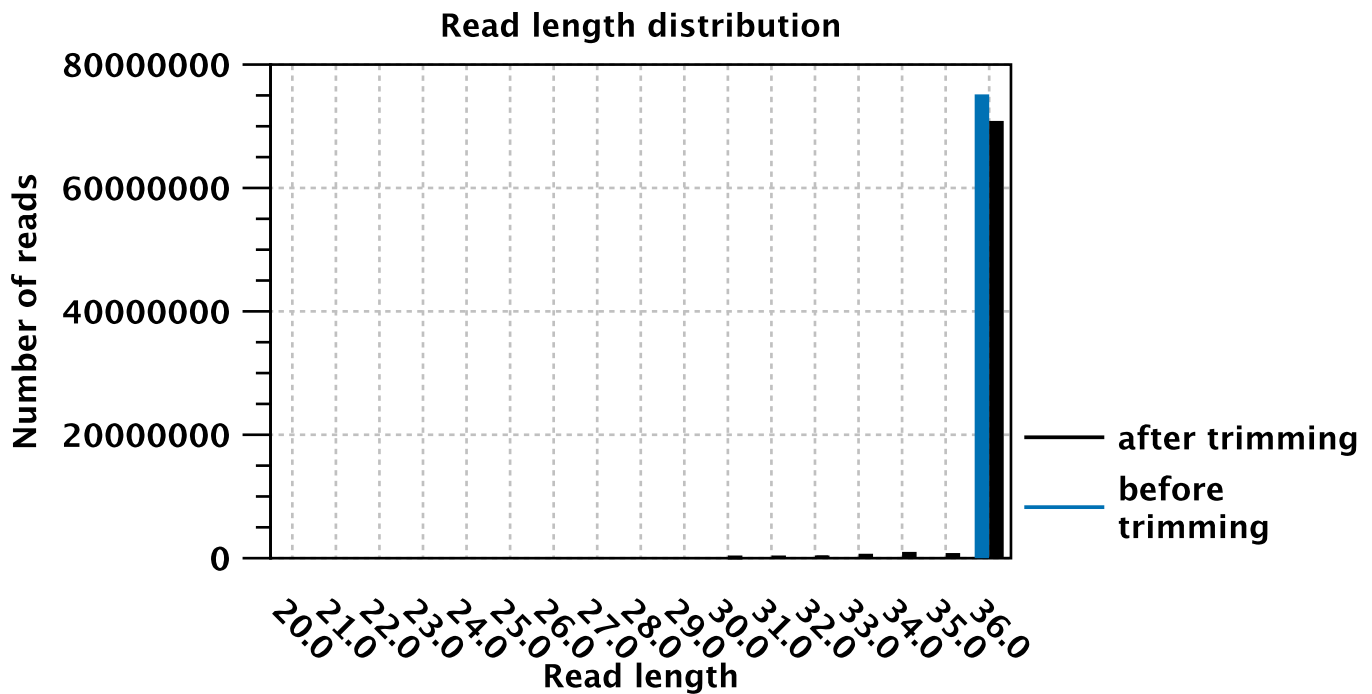
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1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
filtered_QPX_ATCC_10C_CGTACG_L001_R1	45,110,836	36.0	45,082,610	99.94%
filtered_QPX_ATCC_RT_GAGTGG_L001_R1	30,055,835	36.0	30,035,397	99.93%

Avg.length after trim
35.8
35.8

2. Read length before / after trimming



3. Trim settings

- Removal of low quality sequence. (limit = 0.05).
- Removal of ambiguous nucleotides: maximal 2 nucleotides allowed.
- 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	75,166,671	70,865,038	4,293,571	8,062
Ambiguity trim	75,158,609	75,148,360	10,249	0
Filter on length	75,158,609	75,118,007	0	40,602