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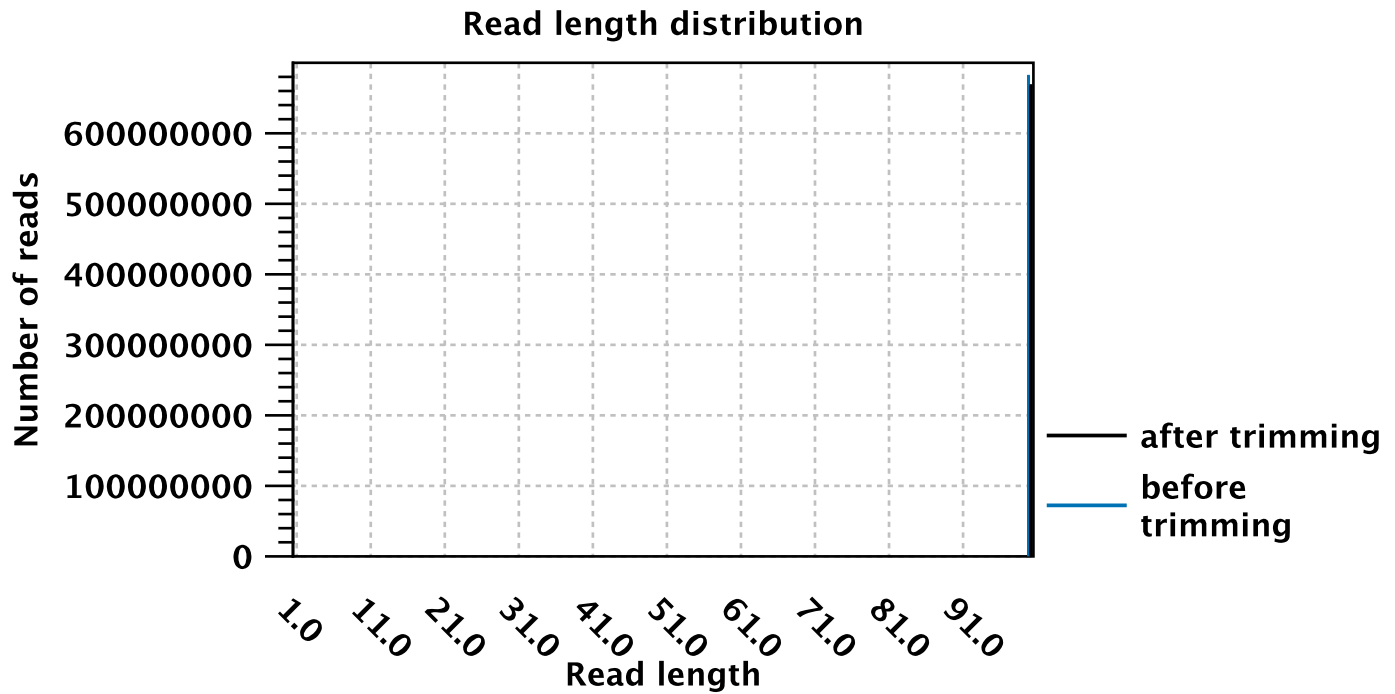
1. Trim summary

Name	Number of reads	Avg.length	Number of reads after trim	Percentage trimmed
Oct_11__SF_8_ACTT GA_R1 (paired)	56,789,390	100.0	56,789,390	100%
Mar_11__SF_8_TTAG GC_R1 (paired)	47,378,256	100.0	47,378,256	100%
Mar_11__SF_14_TTA GGC_R1 (paired)	43,025,554	100.0	43,025,554	100%
Mar_11__SF2_ATCA CG_R1 (paired)	98,430,410	100.0	98,430,410	100%
Nov_10__SF_2_TAG CTT_R1 (paired)	54,655,338	100.0	54,655,338	100%
Jul_10__SF2_GATCA G_R1 (paired)	55,650,668	100.0	54,306,684	97.58%
Nov_10__SF_14_AT CACG_R1 (paired)	60,540,366	100.0	60,540,366	100%
Jul_10__SF14_GATC AG_R1 (paired)	60,916,064	100.0	60,916,064	100%
Jul_10__SF8_GATCA G_R1 (paired)	46,044,438	100.0	46,044,438	100%
Oct_11__SF_14_ACT TGA_R1 (paired)	90,638,860	100.0	90,638,860	100%
Nov_10__SF_8_ATC ACG_R1 (paired)	21,467,972	100.0	21,467,972	100%
Oct_11__SF_2_TTAG GC_R1 (paired)	47,348,974	100.0	47,348,974	100%

Avg.length after trim
100.0
100.0
99.9
99.9
99.9
93.8
99.9
99.9
99.9
99.9

Avg.length after trim
100.0
99.9

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.

4. Detailed trim results

Trim	Input reads	No trim	Trimmed	Nothing left or Discarded
Trim on quality	682,886,290	671,018,545	10,537,004	1,330,741
Ambiguity trim	681,555,549	680,132,268	1,410,038	13,243