













FastQC Report

Summary

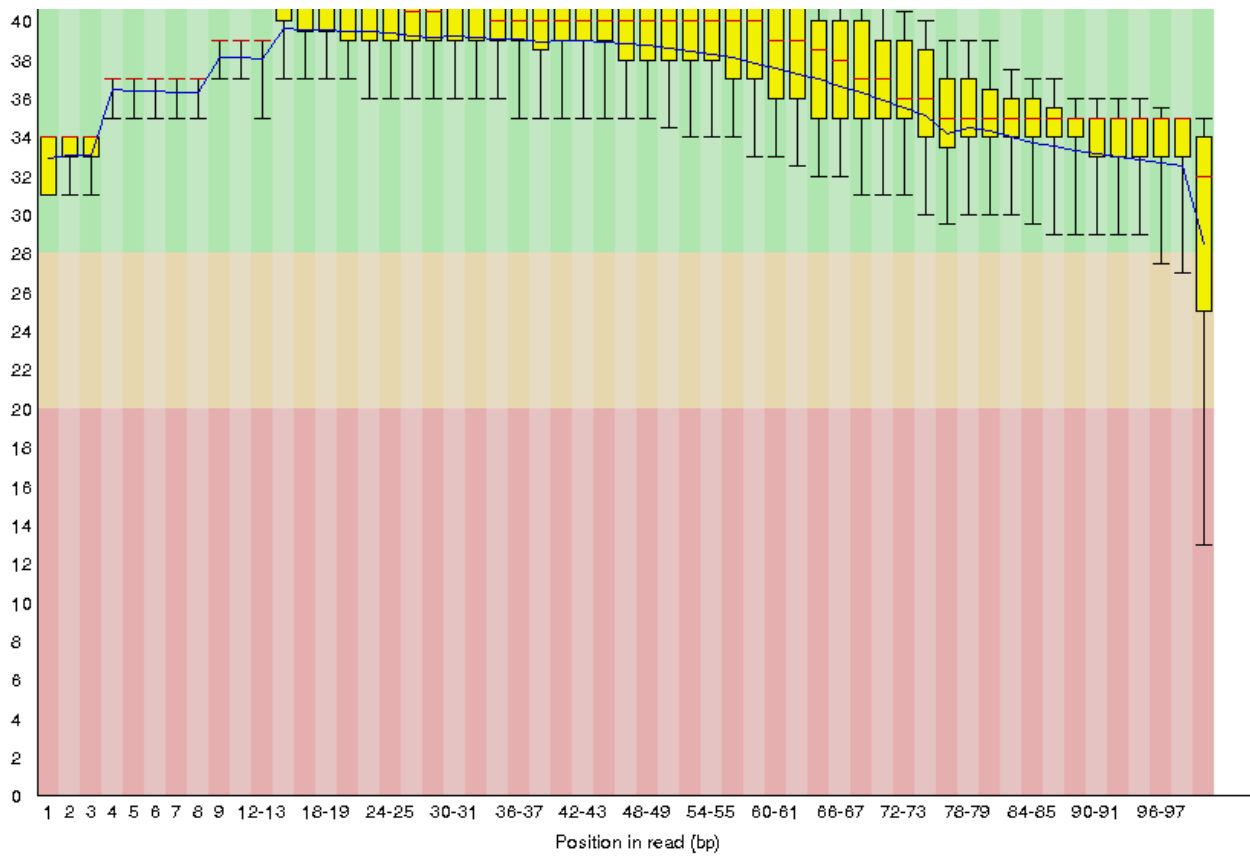
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Basic Statistics

Measure	Value
Filename	SW018_adapterTrimmed_dupRemoved_150424_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	138864653
Sequences flagged as poor quality	0
Sequence length	25-100
%GC	42

Per base sequence quality

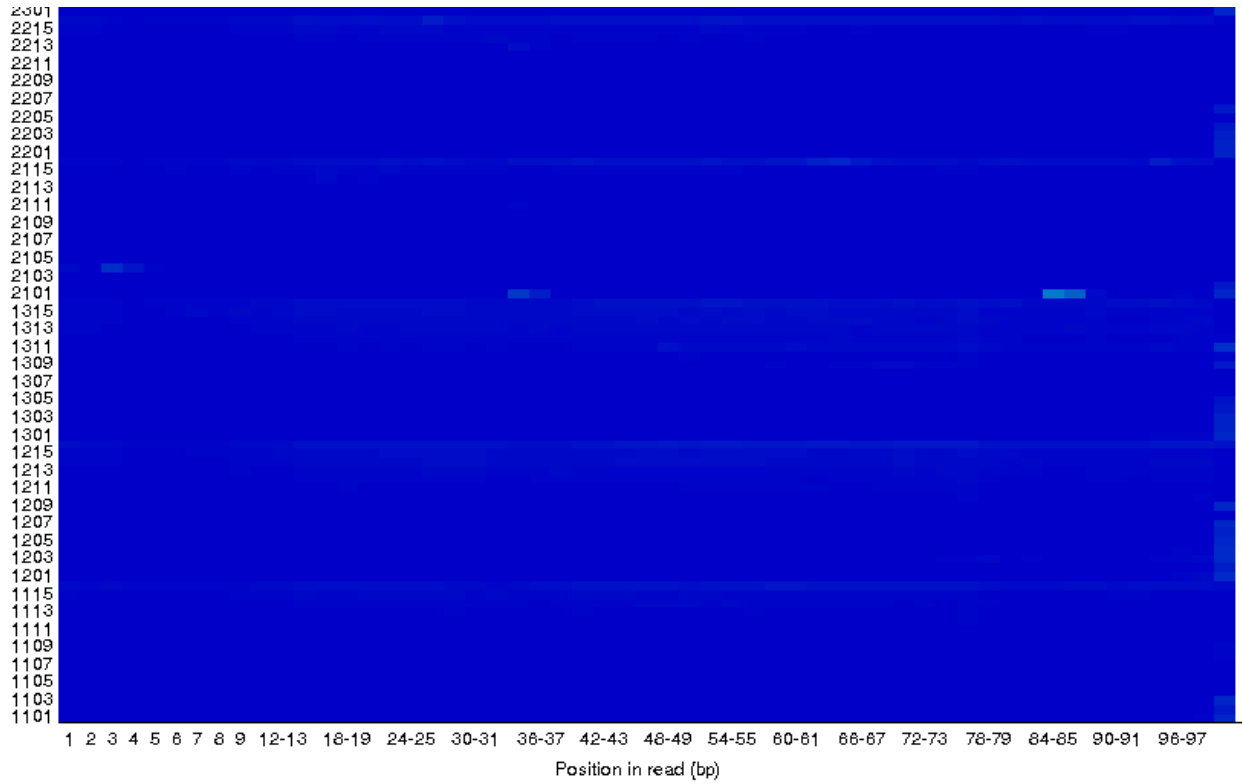
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



 **Per tile sequence quality**

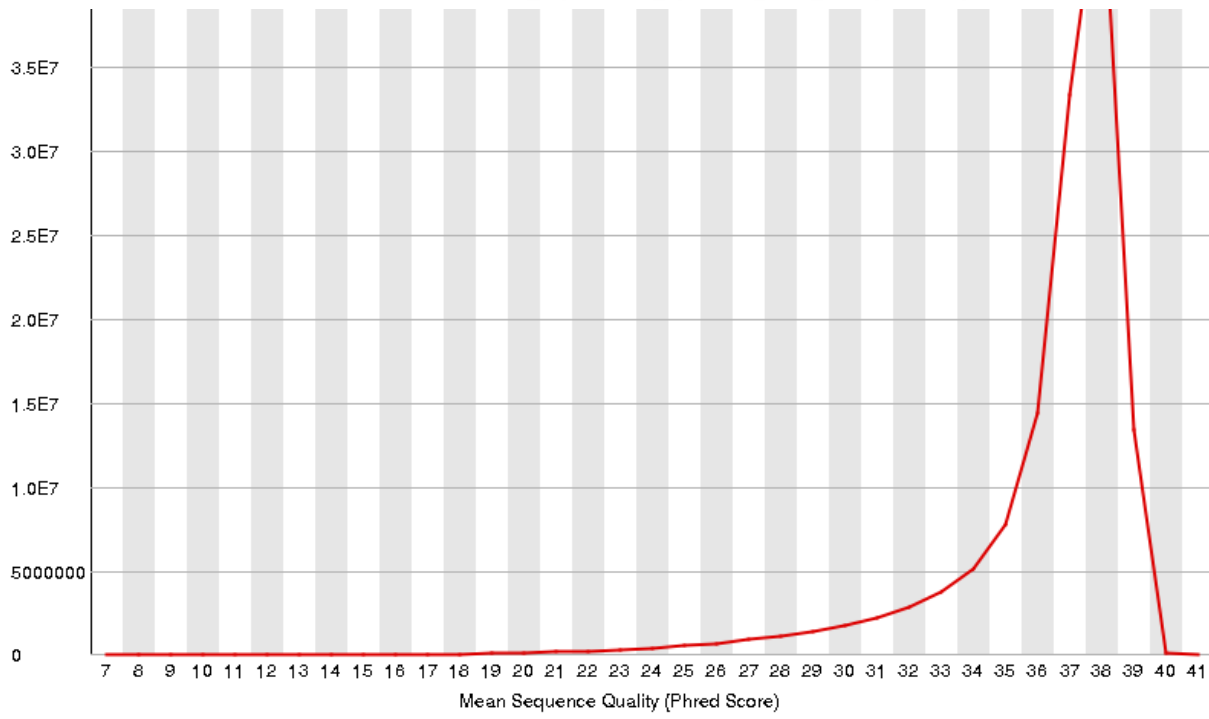
Quality per tile

2315
2310
2305
2303
2299

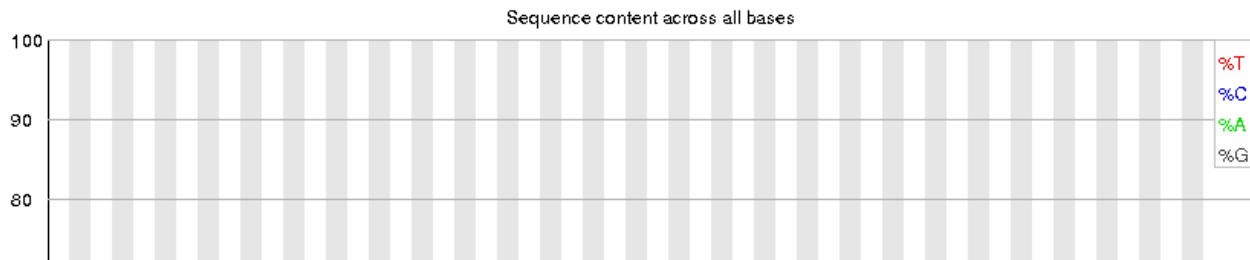


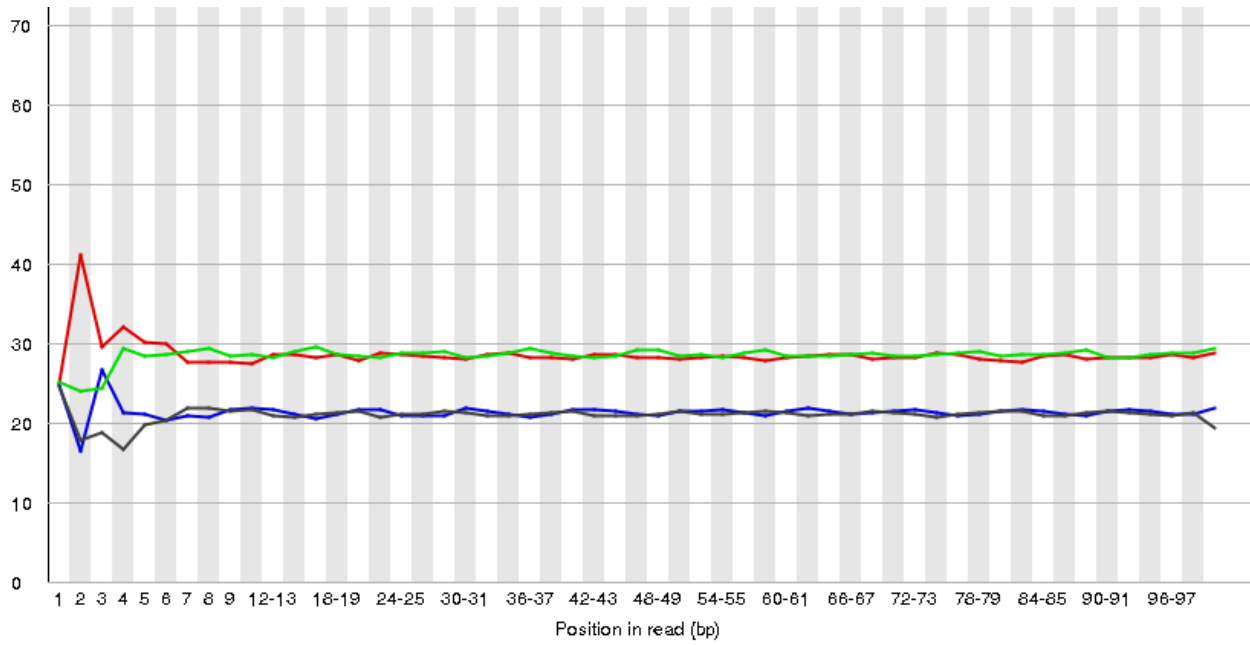
Per sequence quality scores



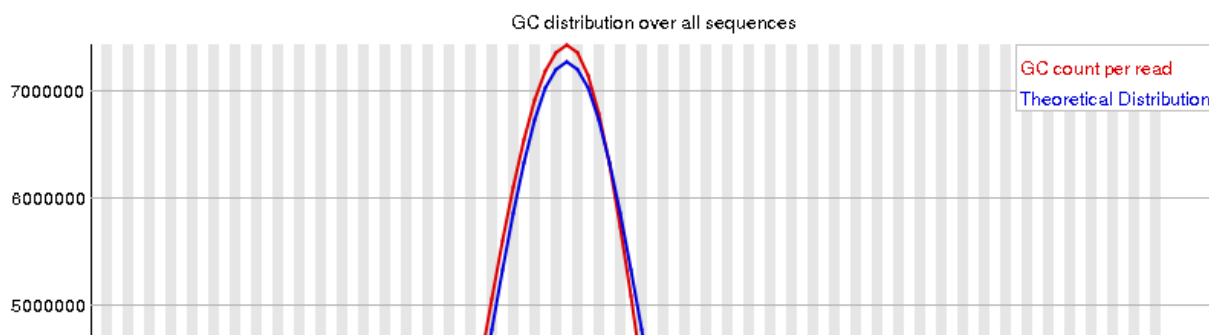


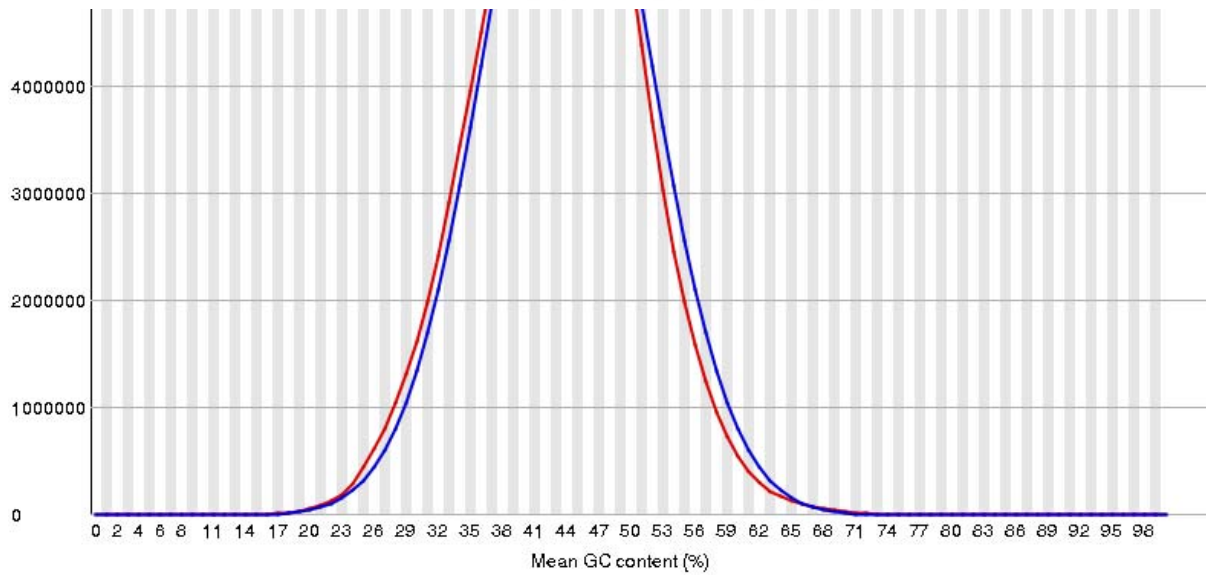
❌ Per base sequence content



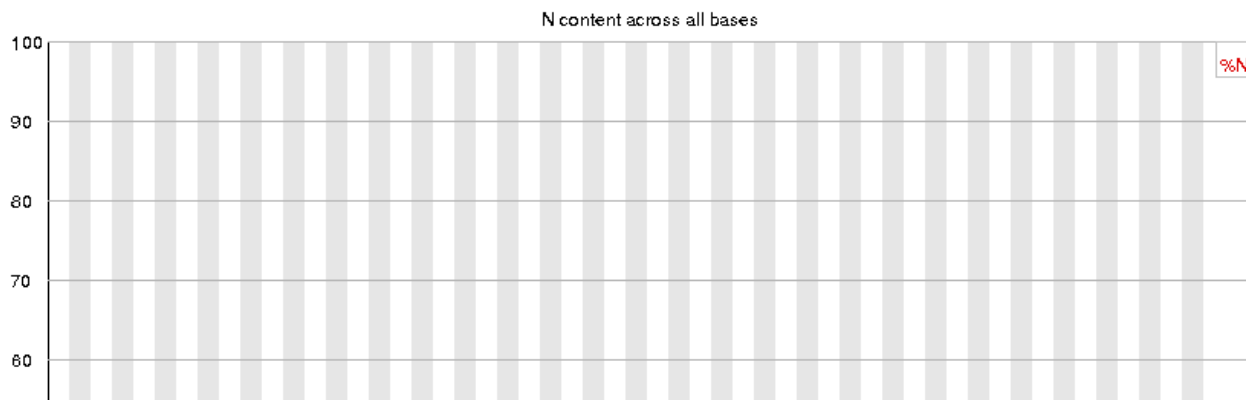


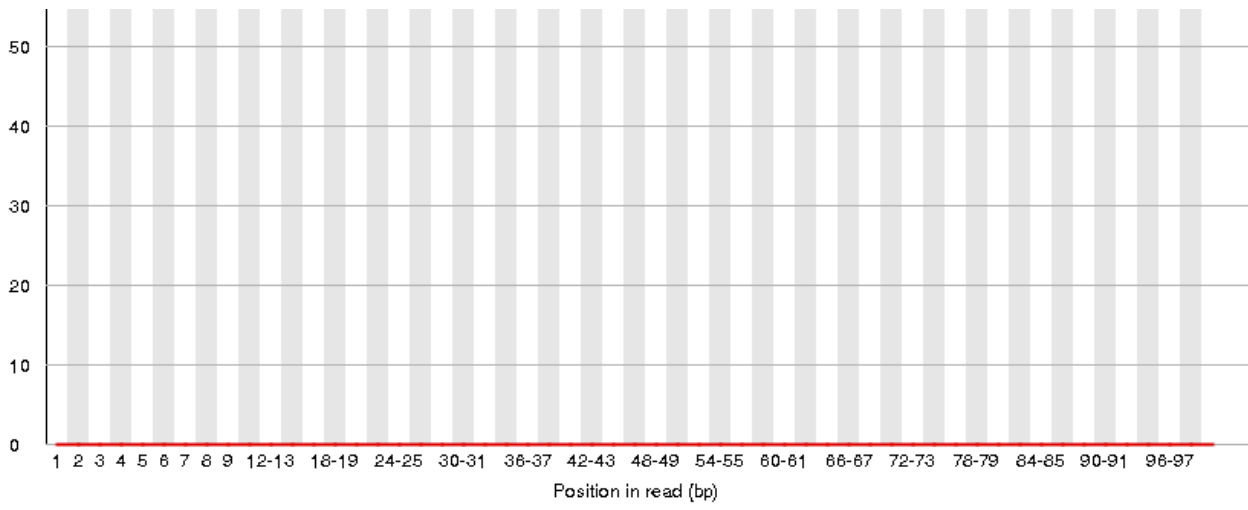
 **Per sequence GC content**



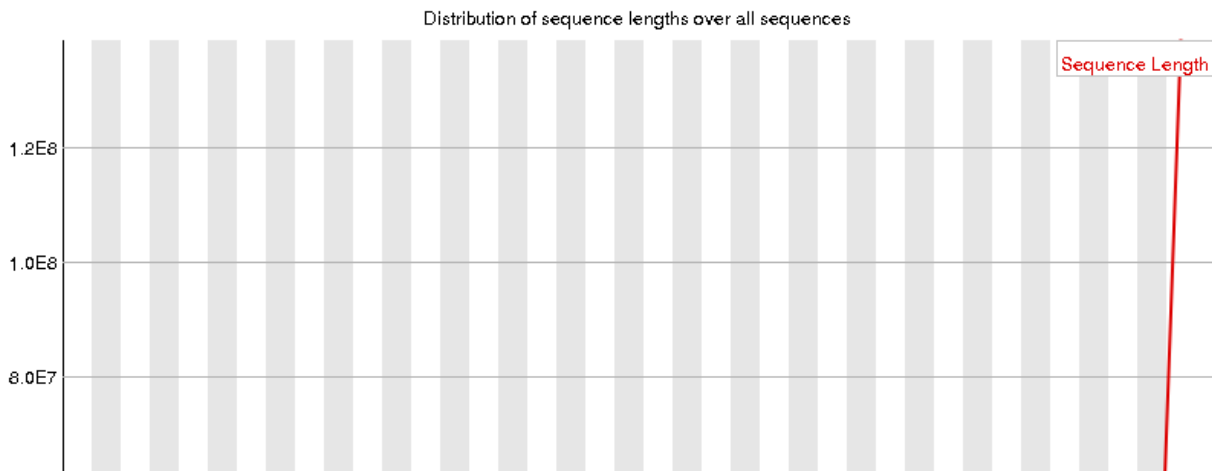


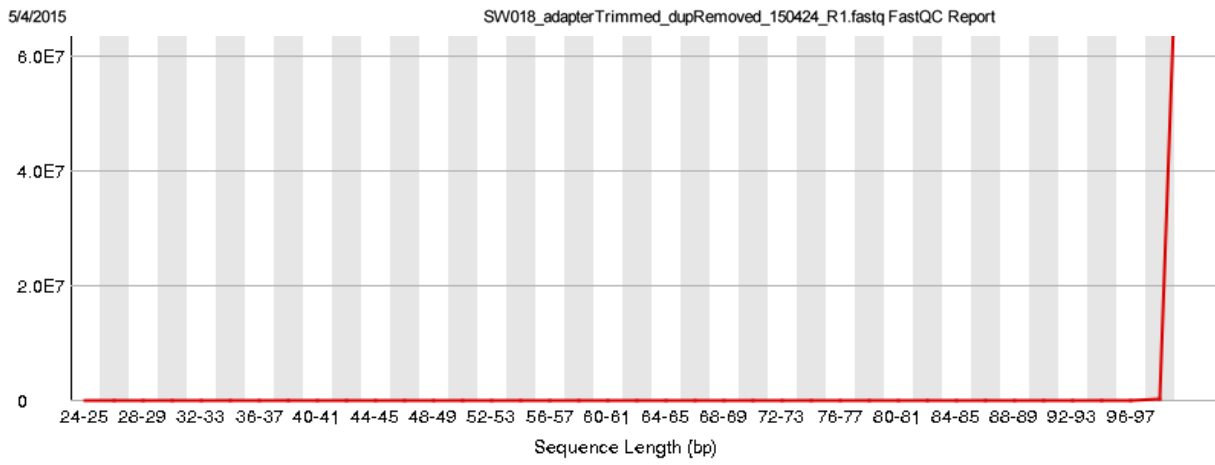
Per base N content



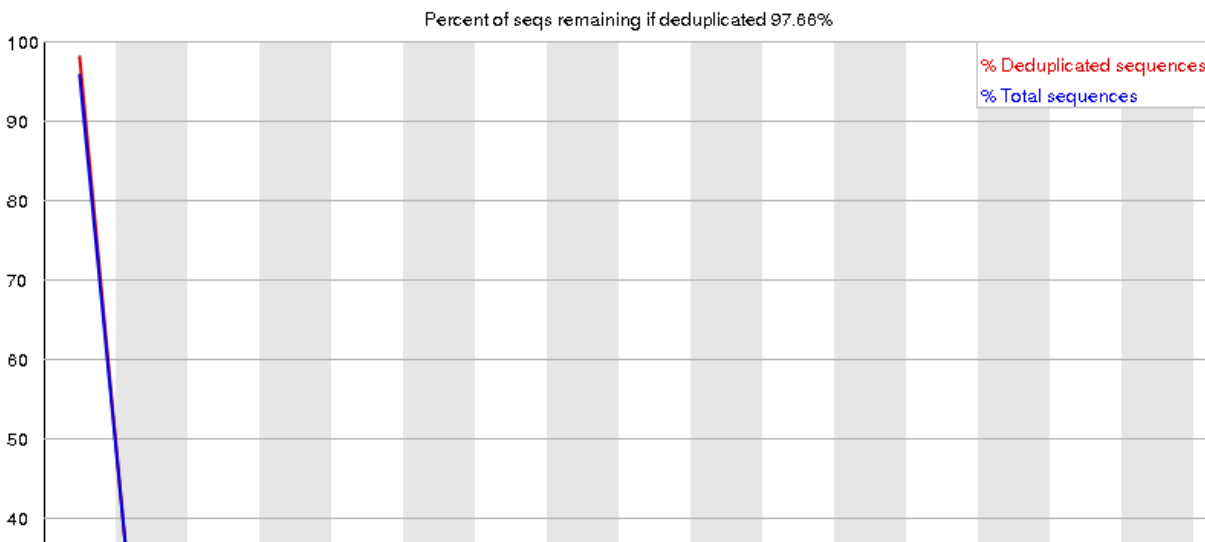


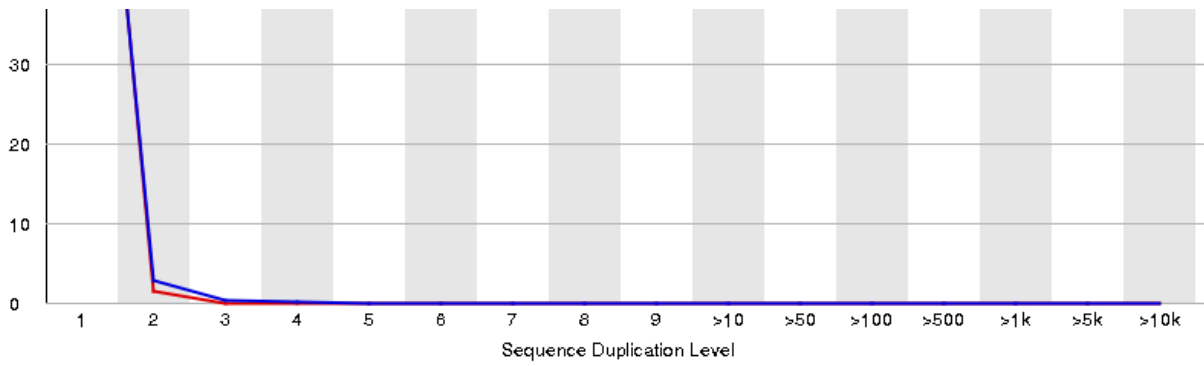
Sequence Length Distribution





✔ Sequence Duplication Levels



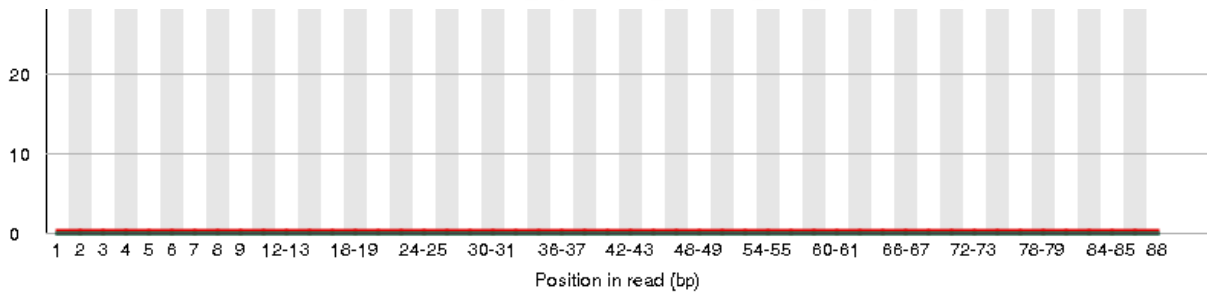


✔ Overrepresented sequences

No overrepresented sequences

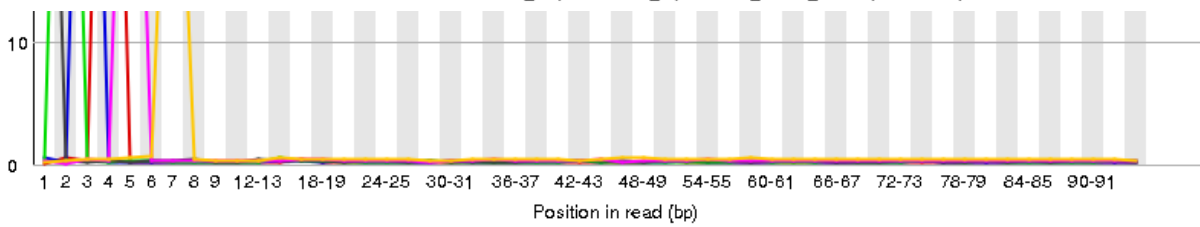
✔ Adapter Content





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	95225	0.0	64.63859	4
ATCGGAA	100310	0.0	61.39935	3
GATCGGA	101820	0.0	60.43805	2
AGATCGG	106535	0.0	57.756805	1
CGGAAGA	116830	0.0	52.86288	5
GAAGAGC	146460	0.0	42.329273	7
CTTCCGA	72005	0.0	36.055737	3
TTCCGAT	76435	0.0	33.929142	4
TCCGATC	78535	0.0	32.888203	5
CCGATCT	84005	0.0	30.75035	6
GGAAGAG	211205	0.0	29.691349	6
TCTTCCG	92130	0.0	28.786629	2
AAGAGCG	58700	0.0	25.396982	8
AAGAGCC	62955	0.0	25.337263	8
AAGAGCT	98230	0.0	17.333817	8
CGATCTA	38945	0.0	17.23975	7
AGAGCGT	41625	0.0	16.47968	9
CTCTTCC	189245	0.0	15.121888	1
AGAGCCT	59340	0.0	13.159325	9
CGATCTT	50700	0.0	13.048037	7

Produced by [FastQC](#) (version 0.11.3)