













# FastQC Report

## Summary

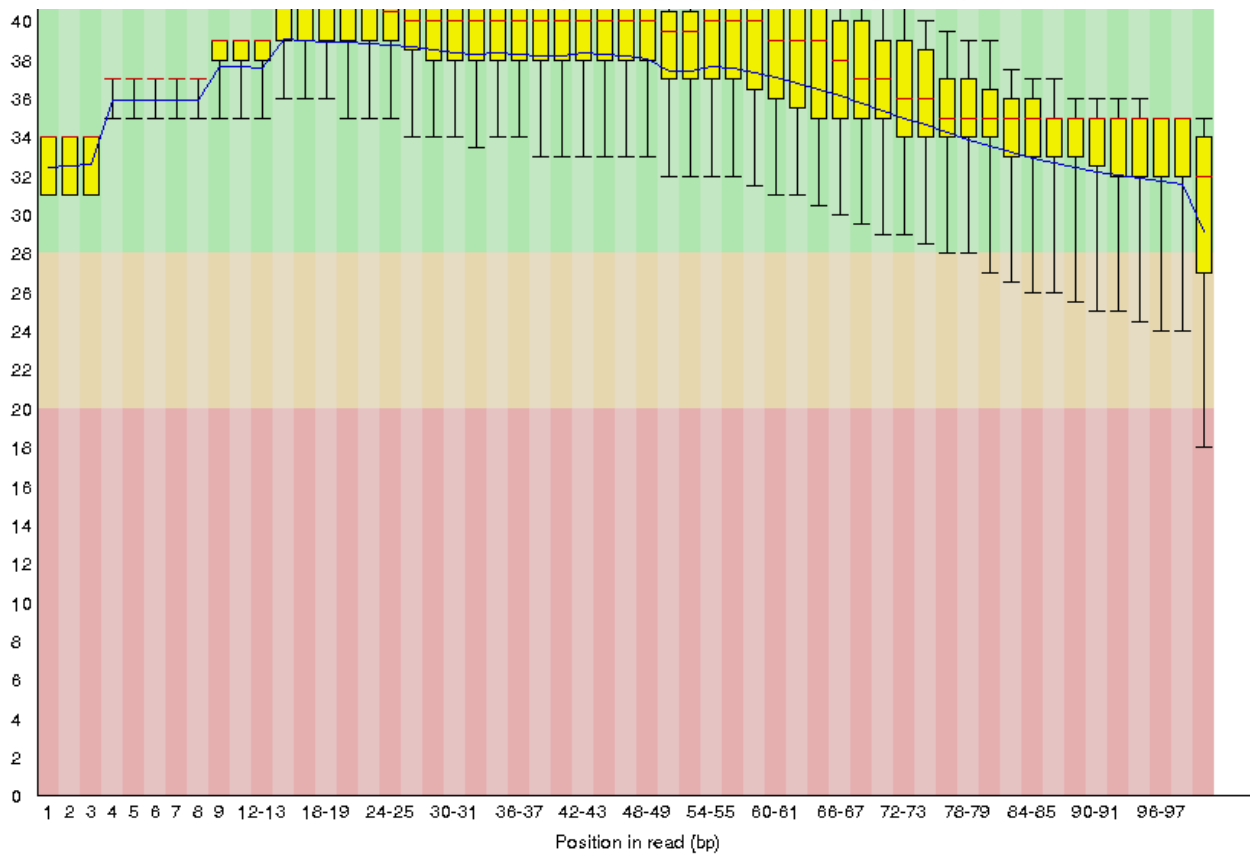
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## Basic Statistics

Measure	Value
Filename	SW018_adapterTrimmed_dupRemoved_150424_R2.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

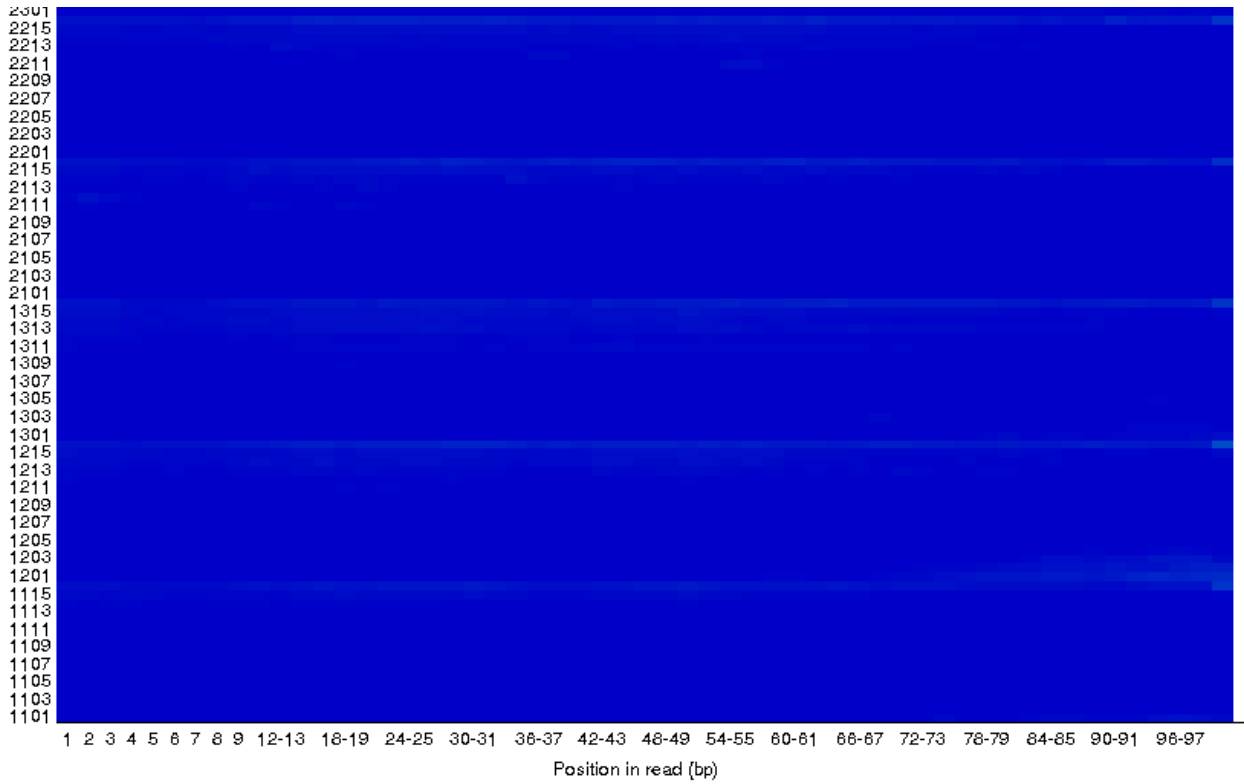
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



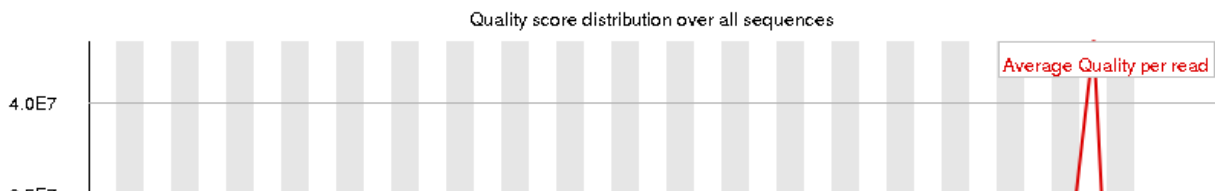
 **Per tile sequence quality**

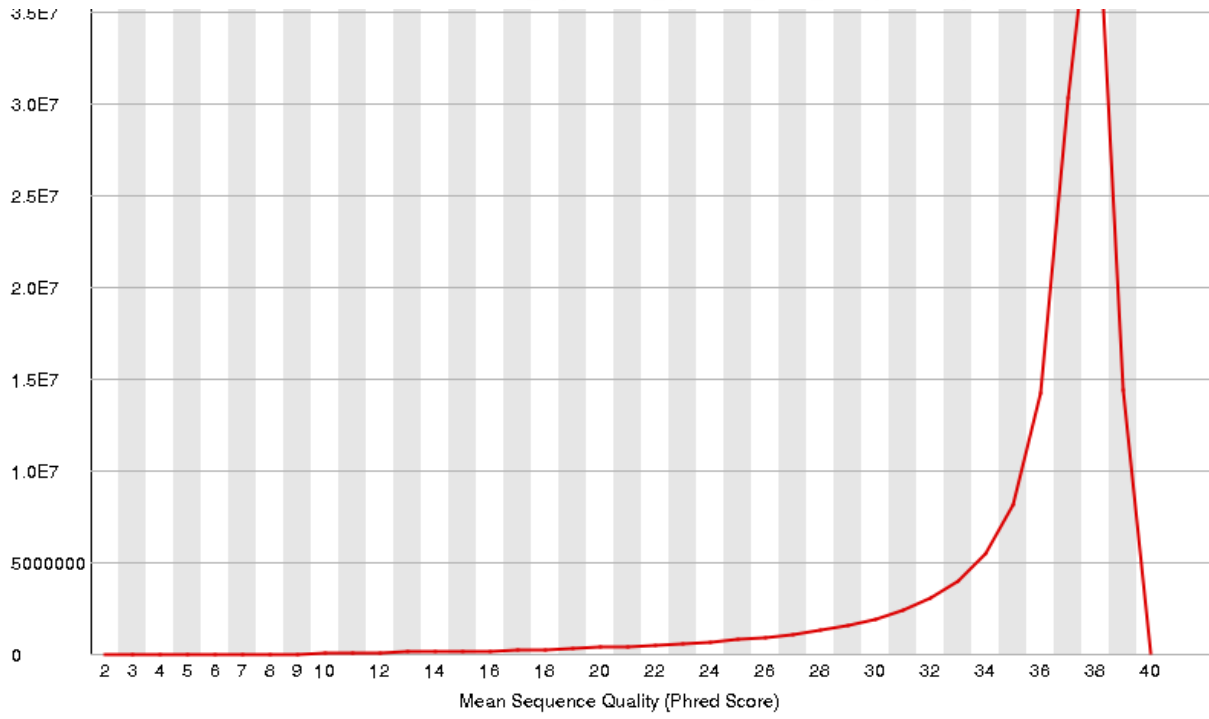
Quality per tile

2315  
2310  
2305  
2303  
2299

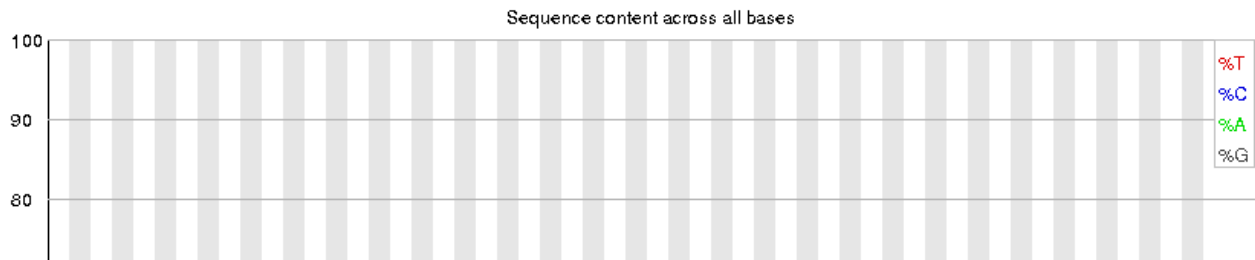


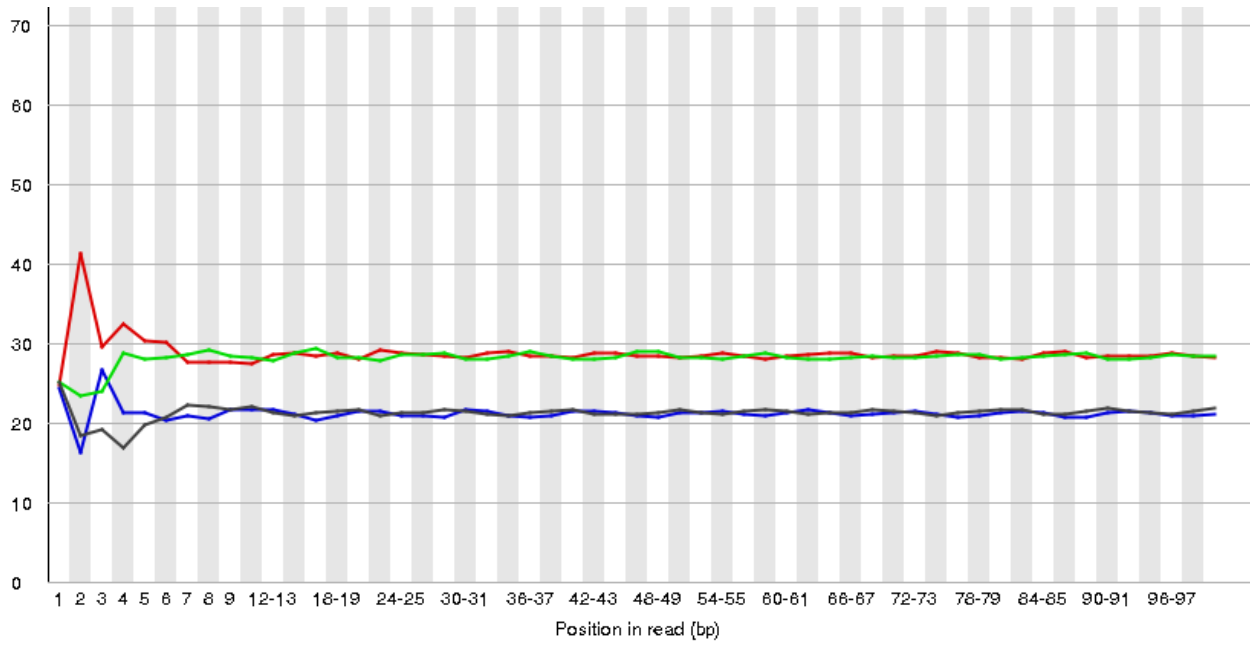
 **Per sequence quality scores**



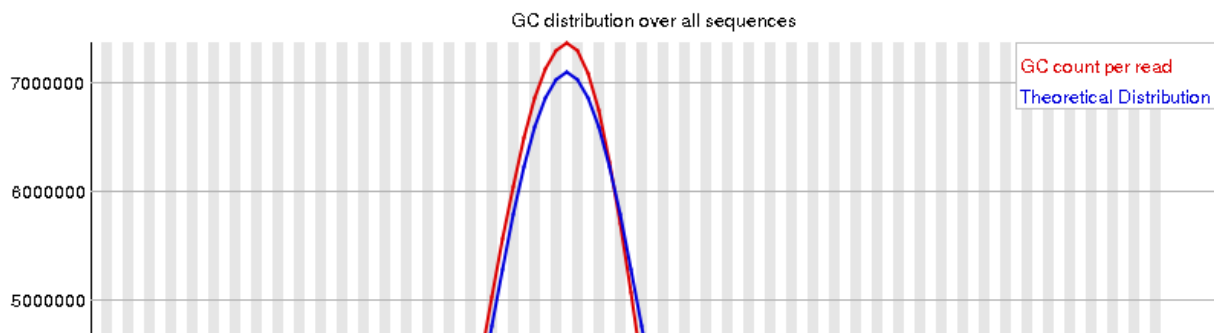


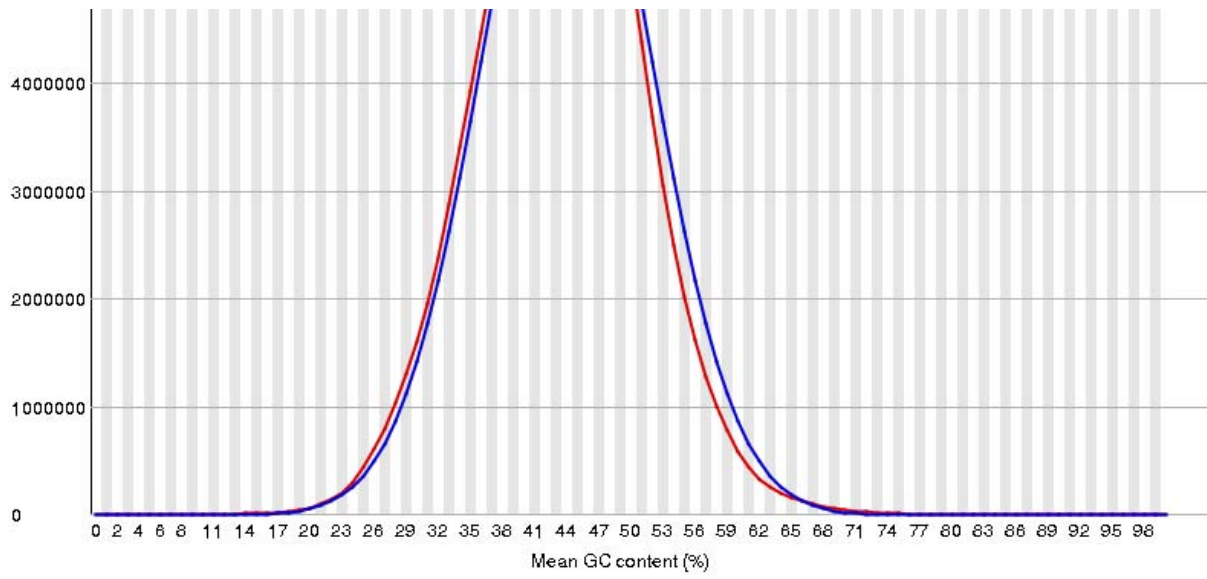
### ❌ Per base sequence content



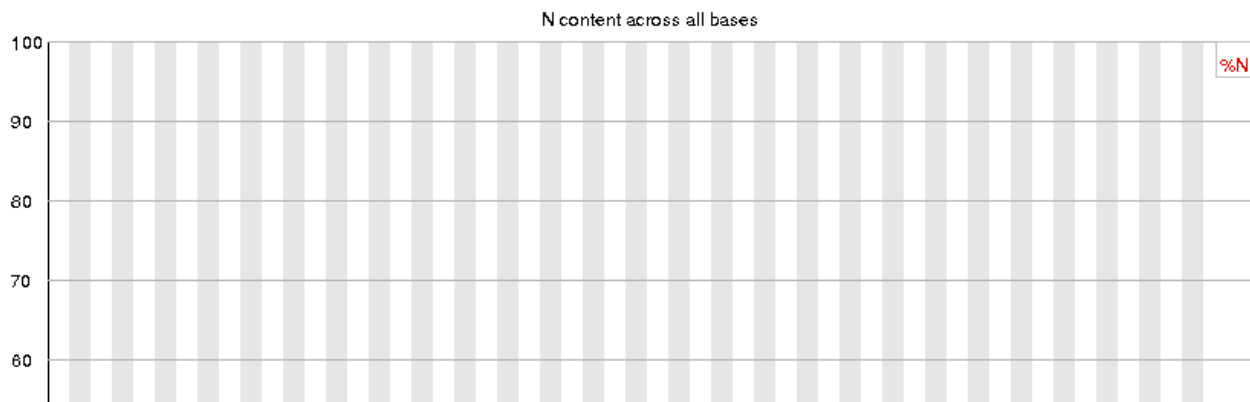


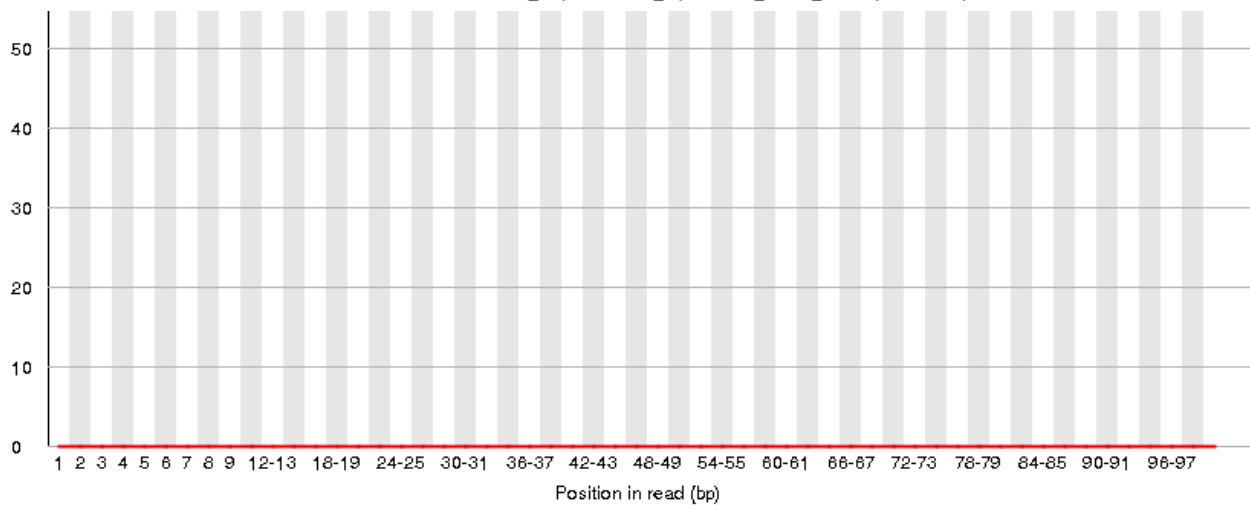
 **Per sequence GC content**



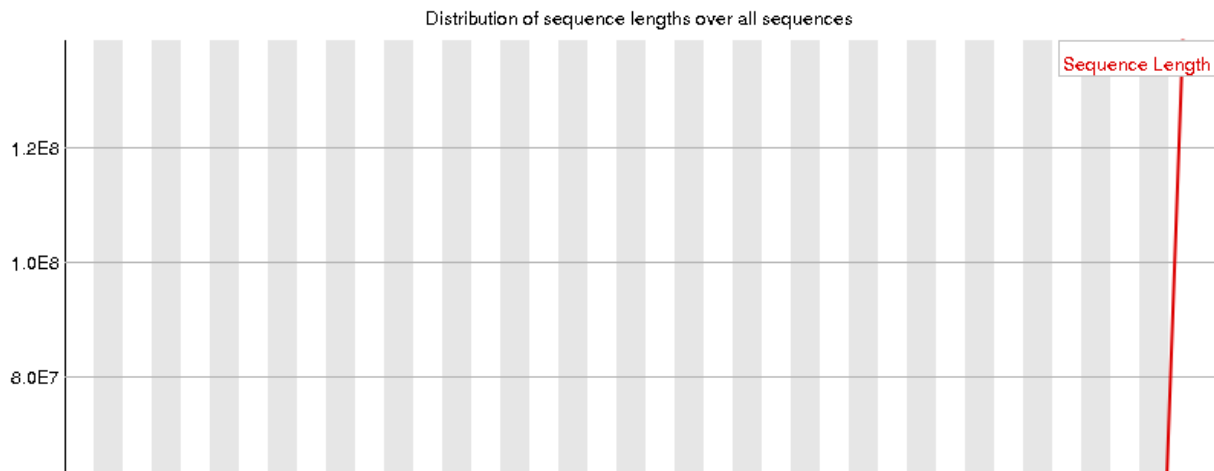


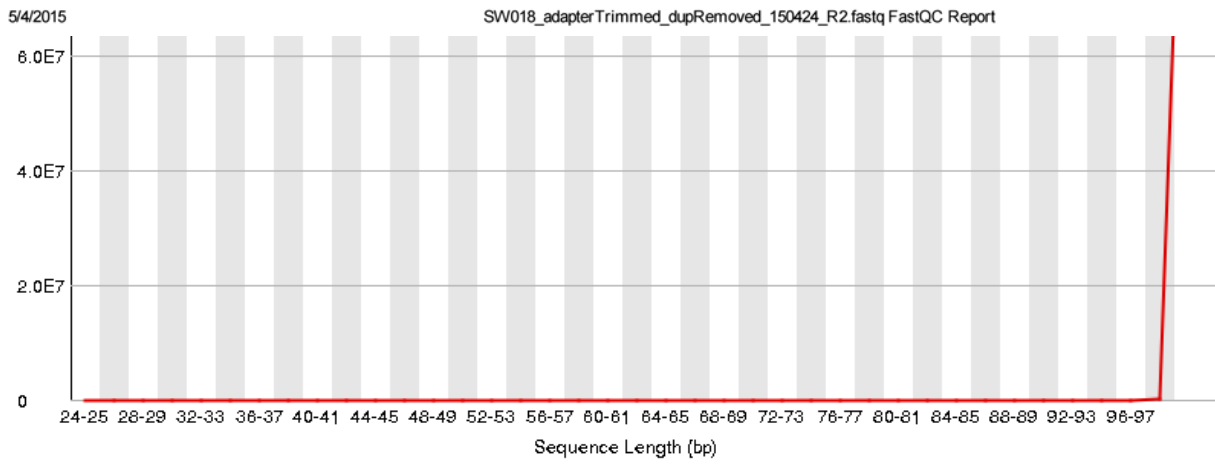
 **Per base N content**



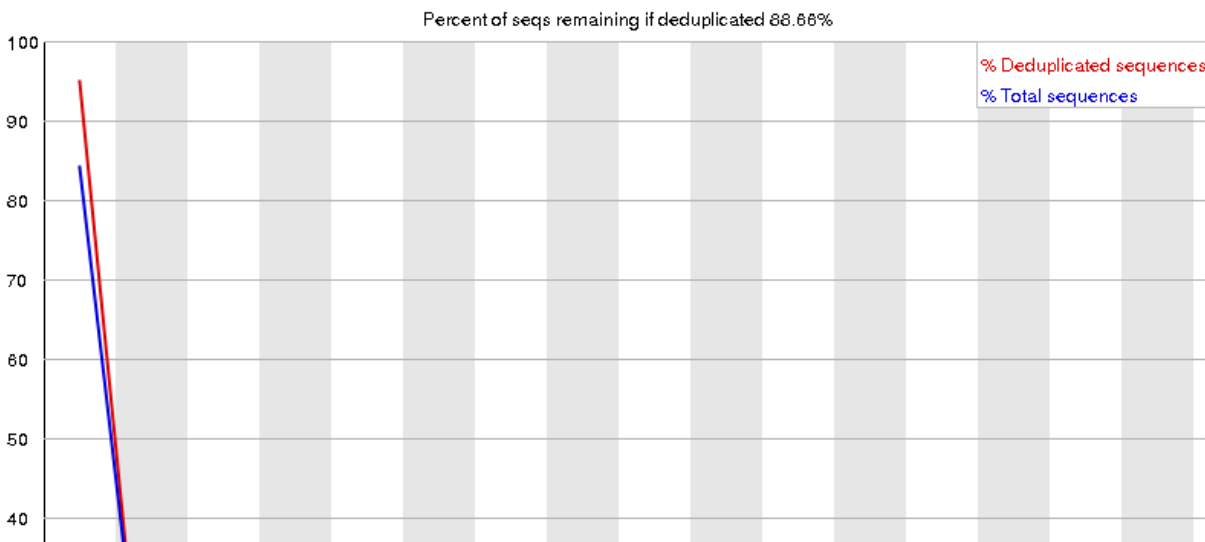


## Sequence Length Distribution

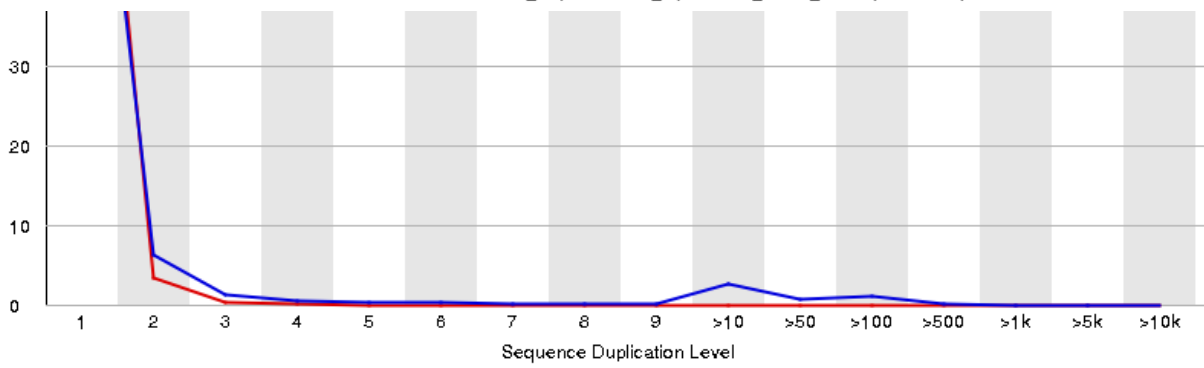




## ✔ Sequence Duplication Levels





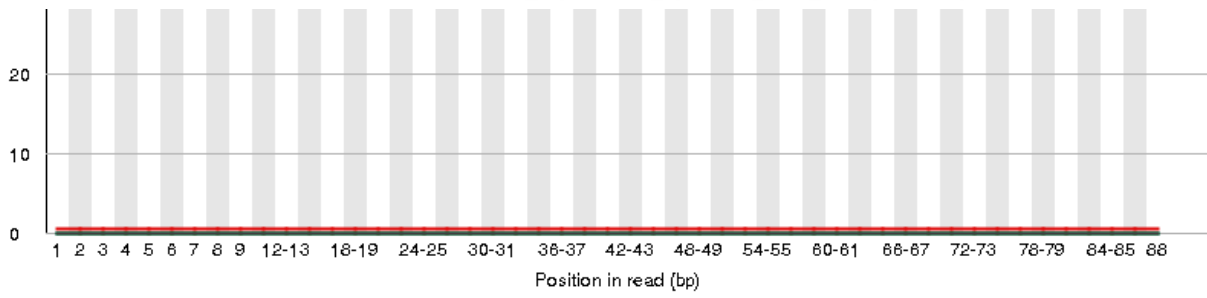


### Overrepresented sequences

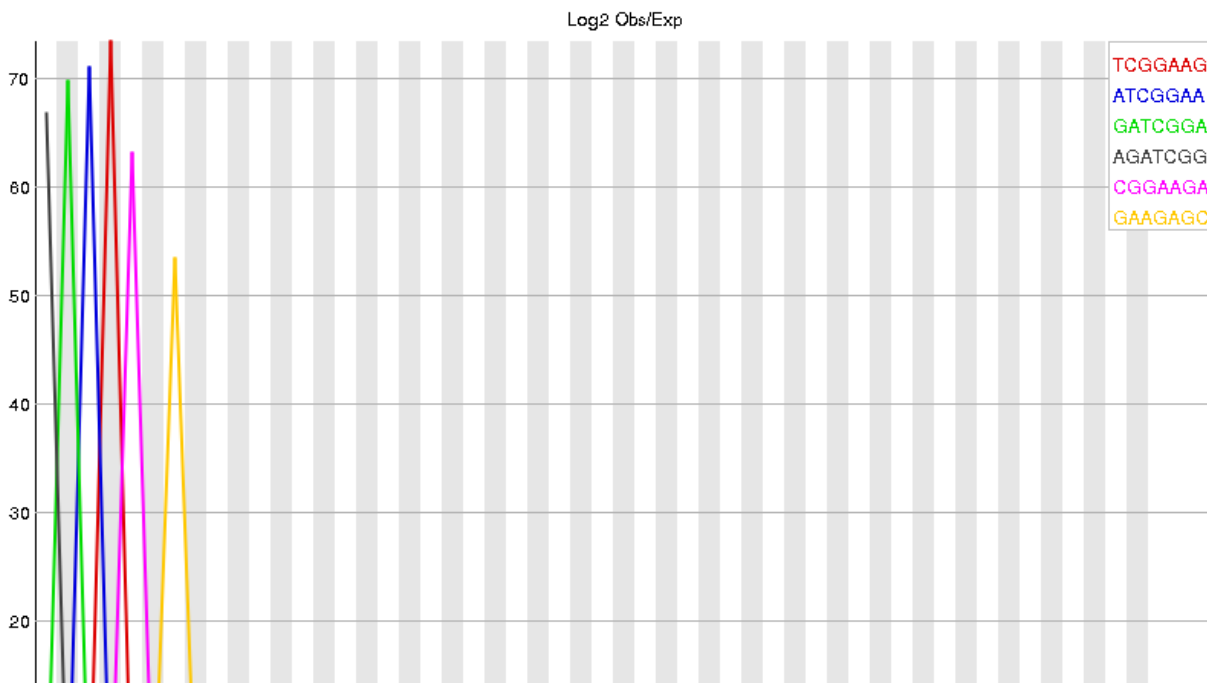
No overrepresented sequences

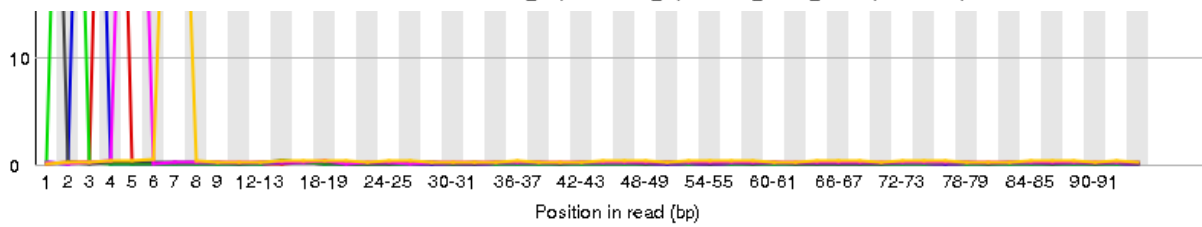
### Adapter Content





## Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	132250	0.0	73.34524	4
ATCGGAA	136660	0.0	71.014496	3
GATCGGA	138885	0.0	69.76089	2
AGATCGG	145105	0.0	66.84381	1
CGGAAGA	153965	0.0	63.06285	5
GAAGAGC	181705	0.0	53.327232	7
GGAAGAG	250980	0.0	38.97542	6
CTTCCGA	74170	0.0	37.2723	3
AAGAGCG	70680	0.0	36.49555	8
TTCCGAT	78980	0.0	34.918205	4
TCCGATC	81370	0.0	33.841175	5
AAGAGCC	71150	0.0	33.203545	8
CCGATCT	86290	0.0	31.868914	6
TCTTCCG	96500	0.0	29.242765	2
AGAGCGT	47330	0.0	26.581116	9
AAGAGCT	106150	0.0	24.526312	8
AGAGCCT	62875	0.0	18.963251	9
CGATCTA	39345	0.0	18.056198	7
CTCTTCC	193290	0.0	15.719371	1
AAGAGCA	157600	0.0	15.088435	8

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