













FastQC Report

Summary

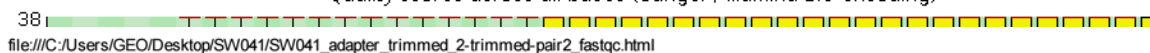
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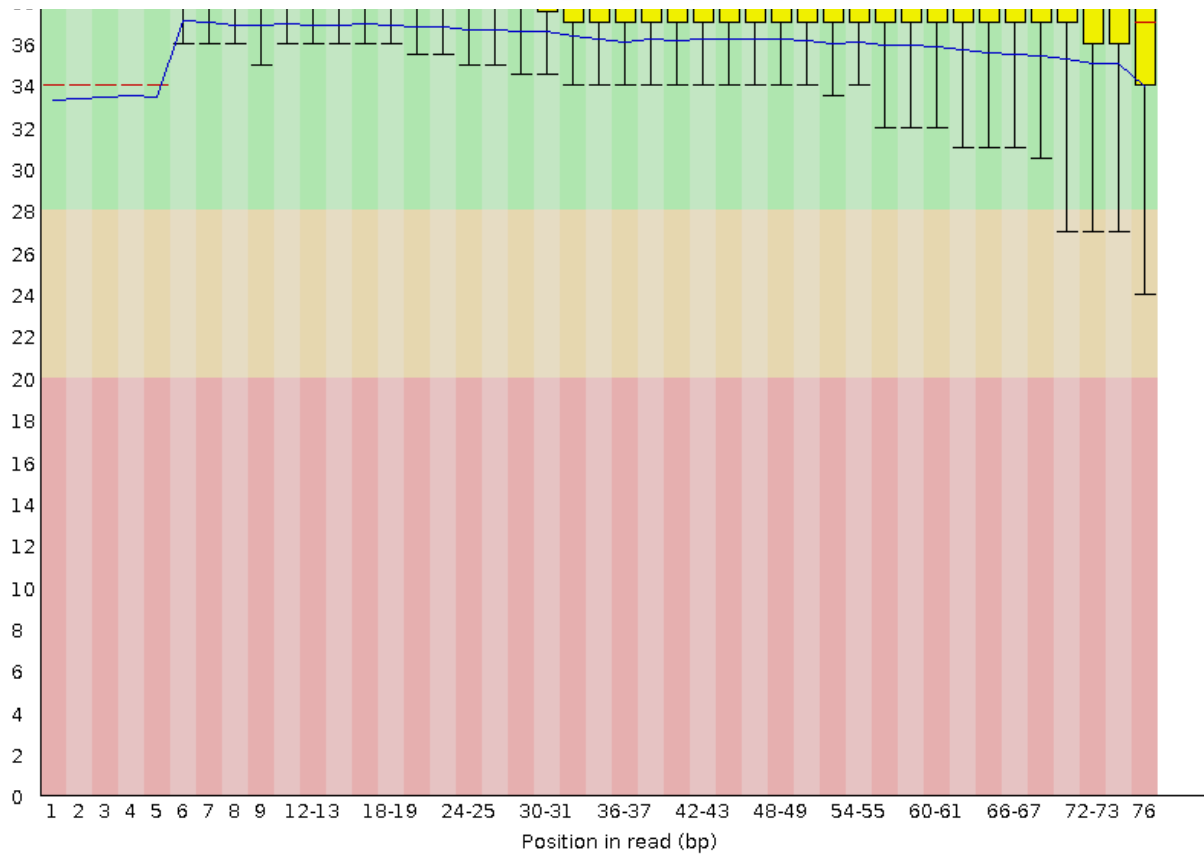
Basic Statistics

Measure	Value
Filename	SW041_adapter_trimmed_2-trimmed-pair2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1449417
Sequences flagged as poor quality	0
Sequence length	18-76
%GC	43

Per base sequence quality

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

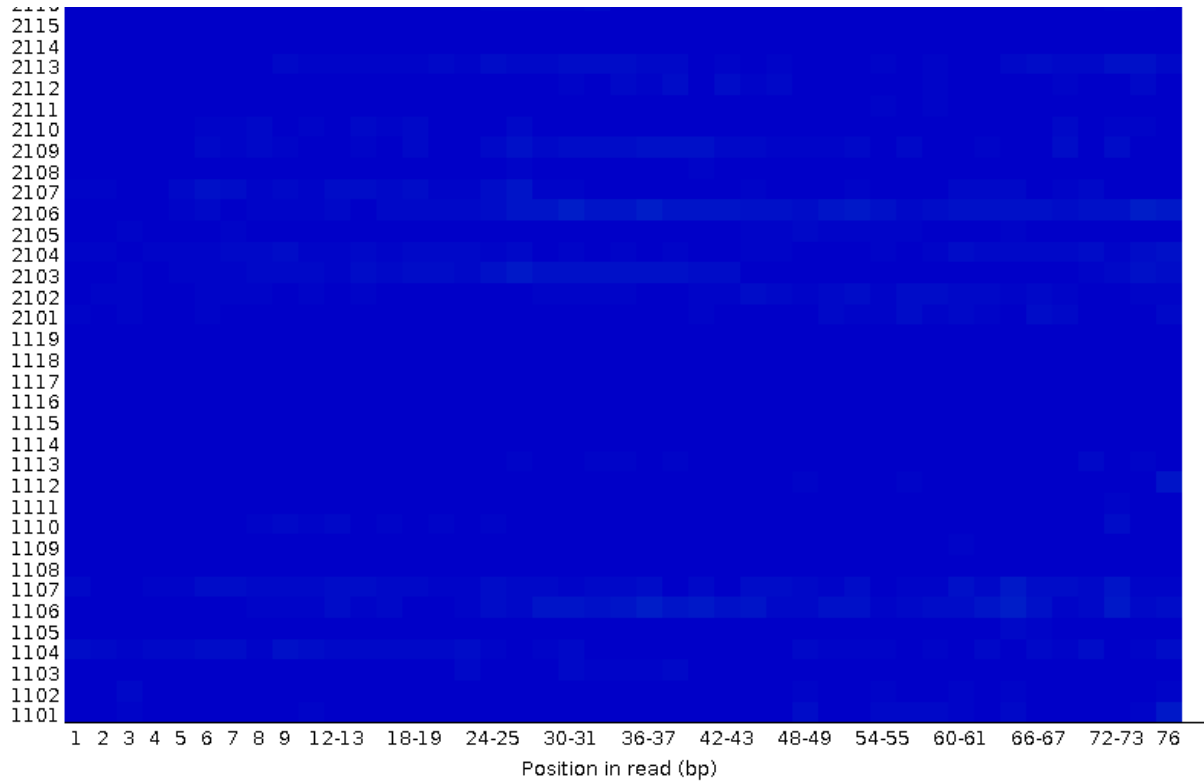




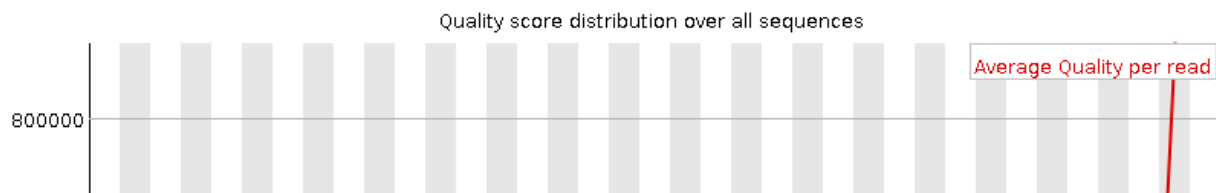
 **Per tile sequence quality**

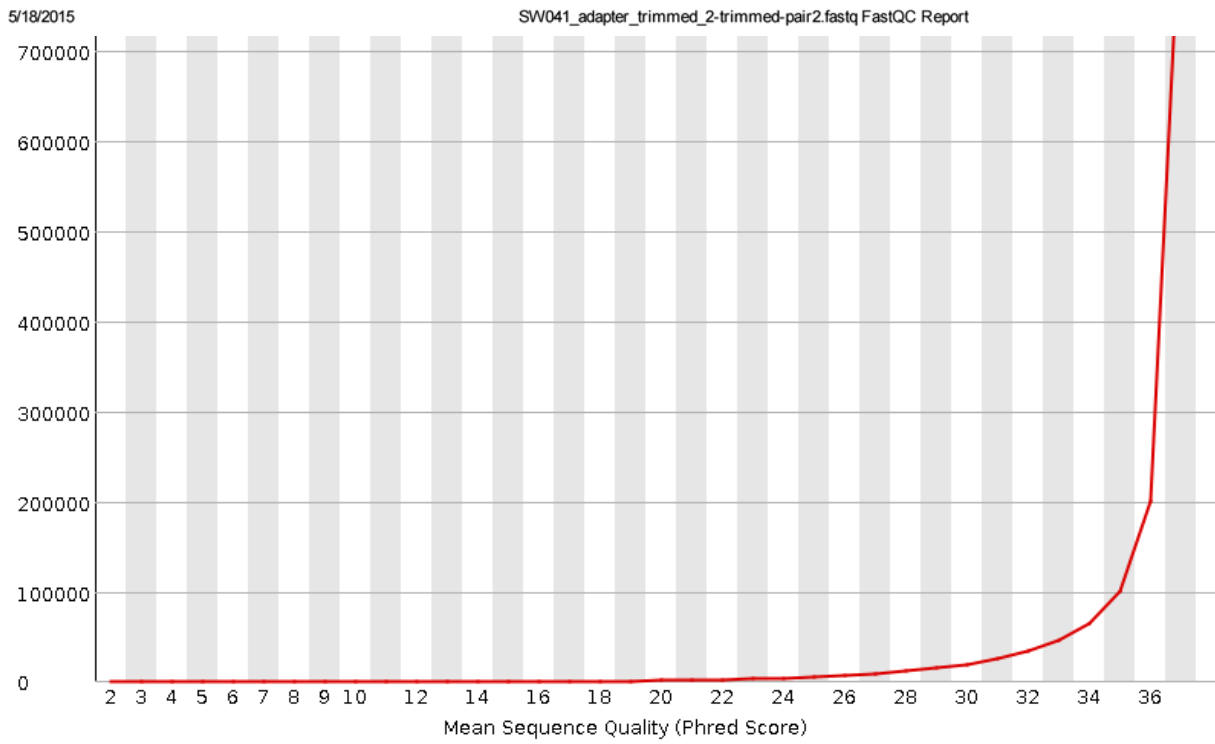
Quality per tile

2119
2118
2117
2116

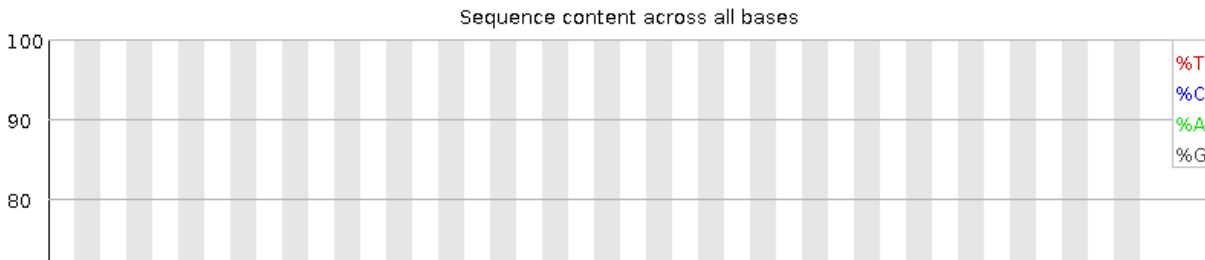


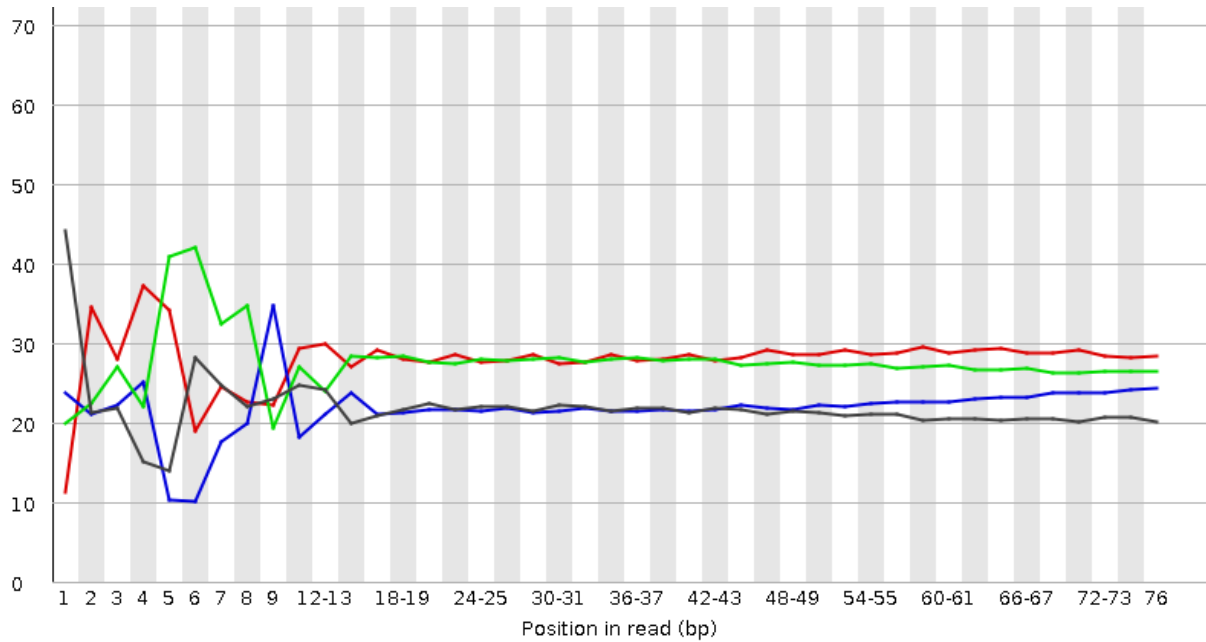
✔ Per sequence quality scores



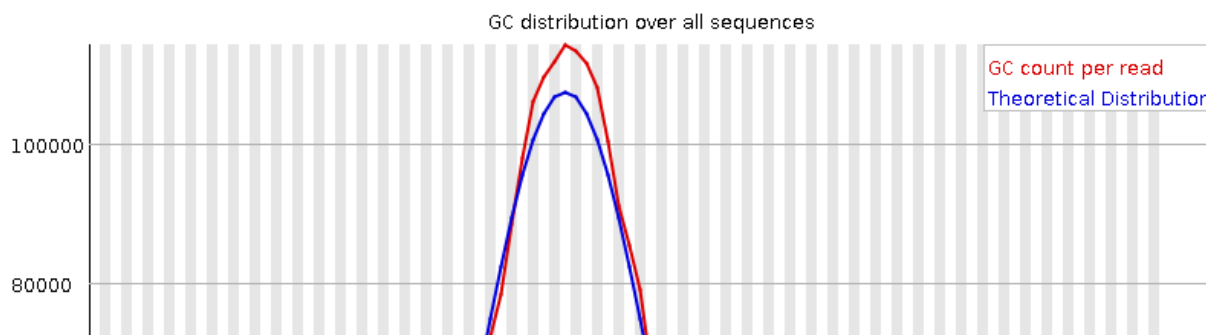


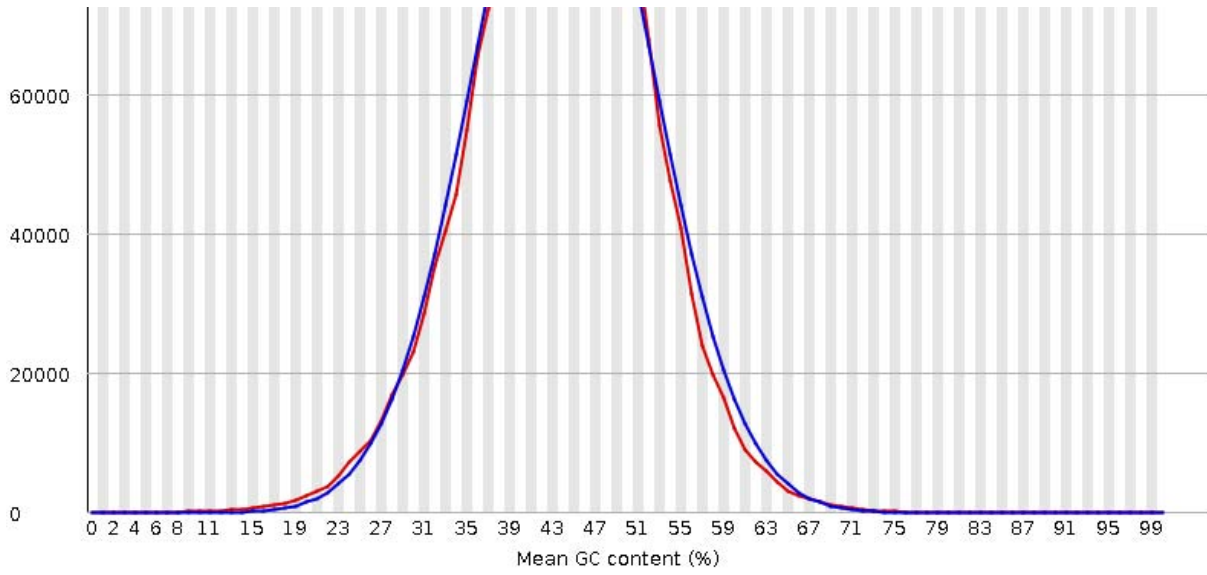
✖ Per base sequence content



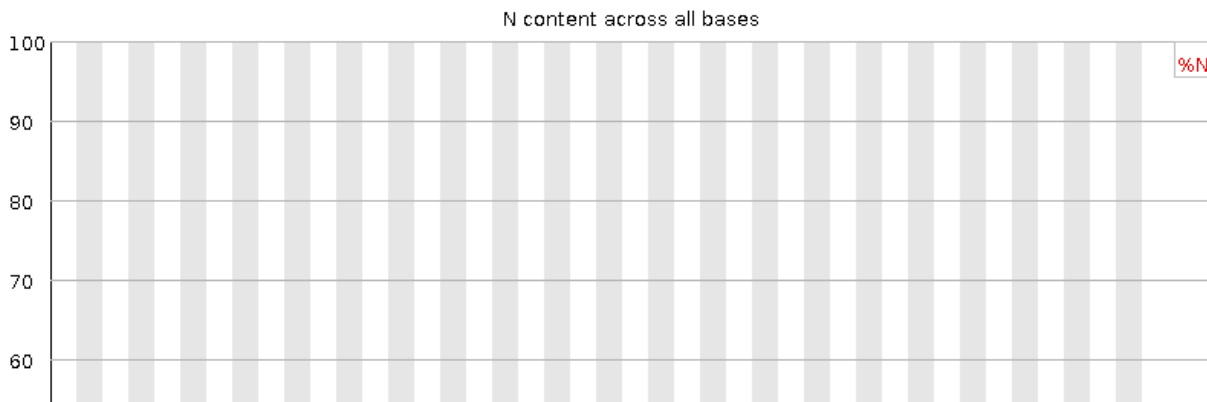


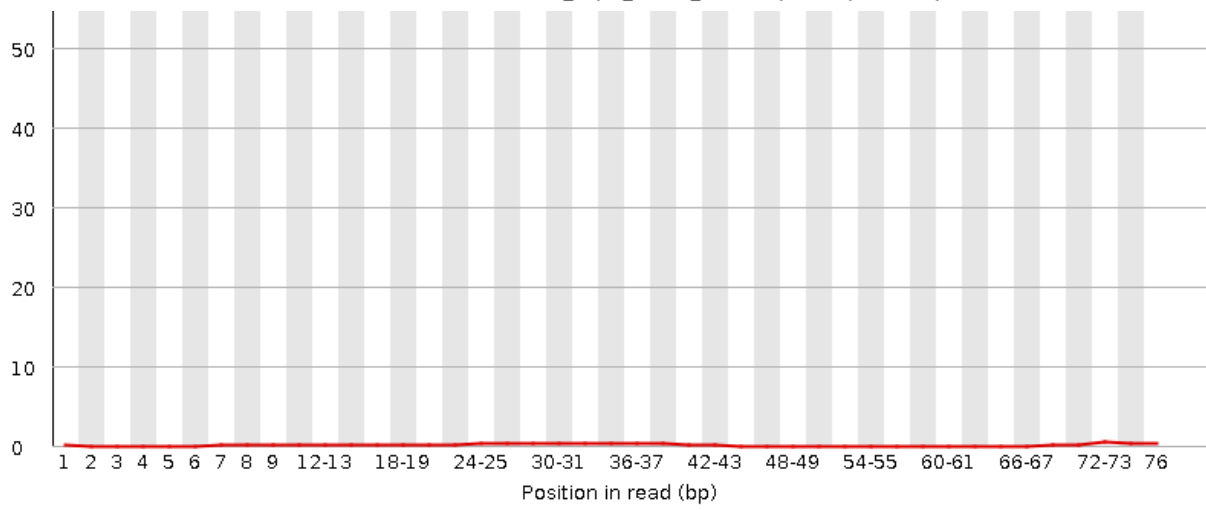
Per sequence GC content



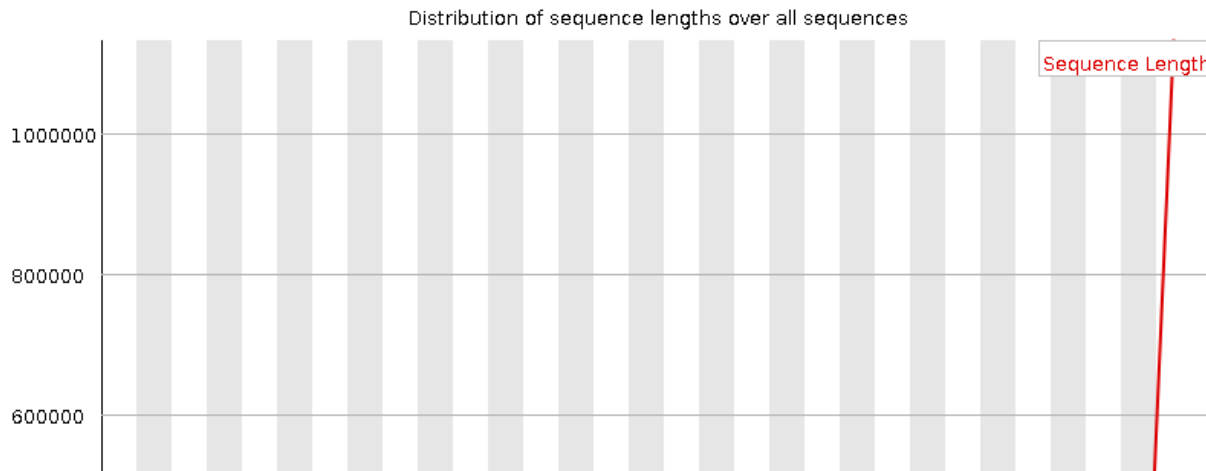


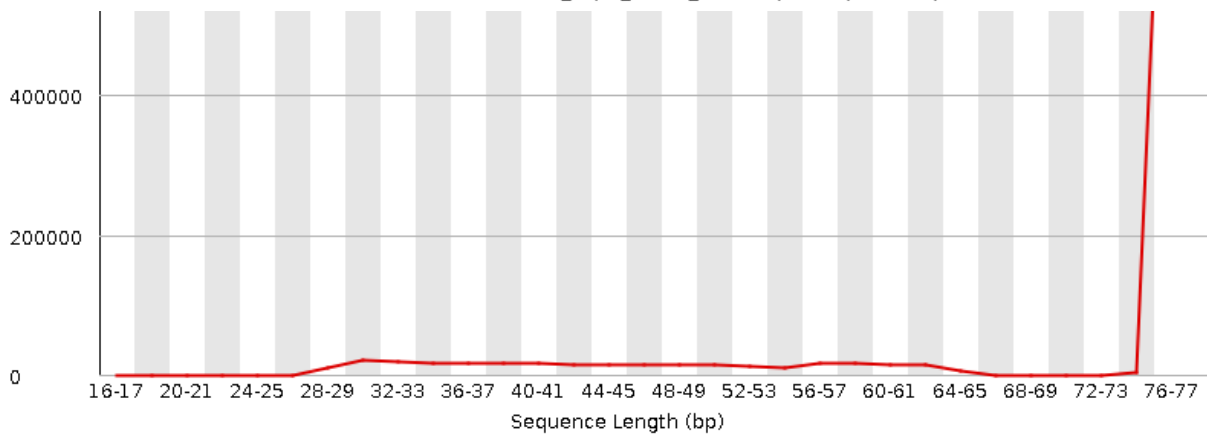
Per base N content



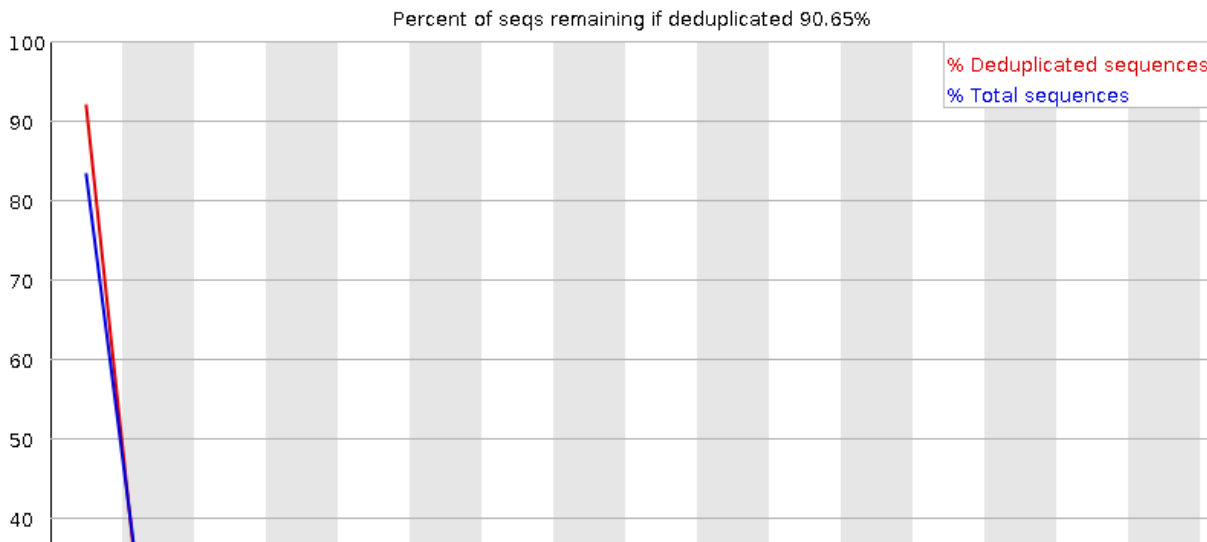


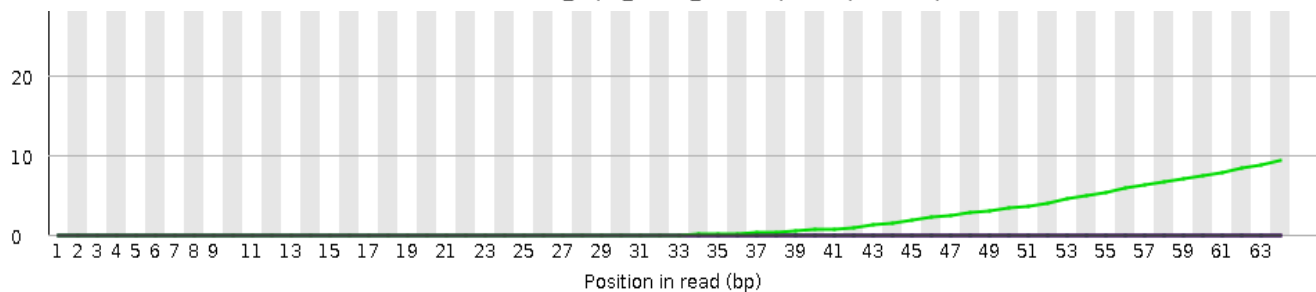
Sequence Length Distribution



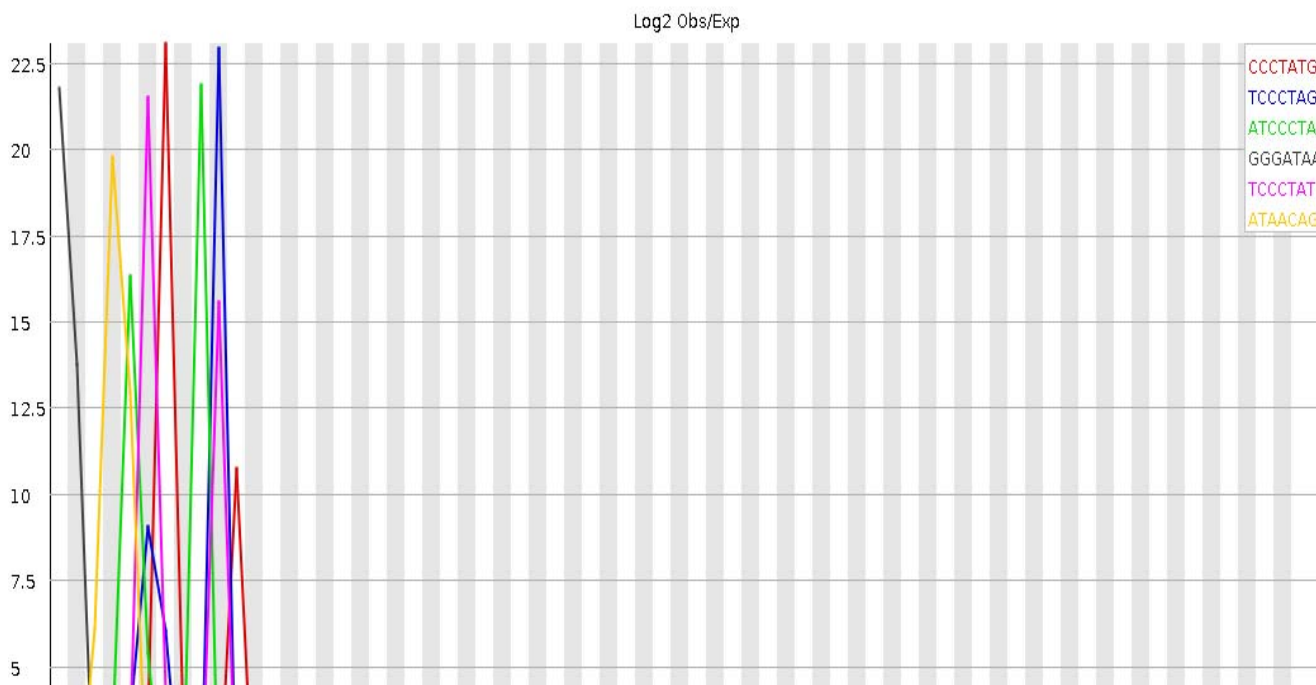


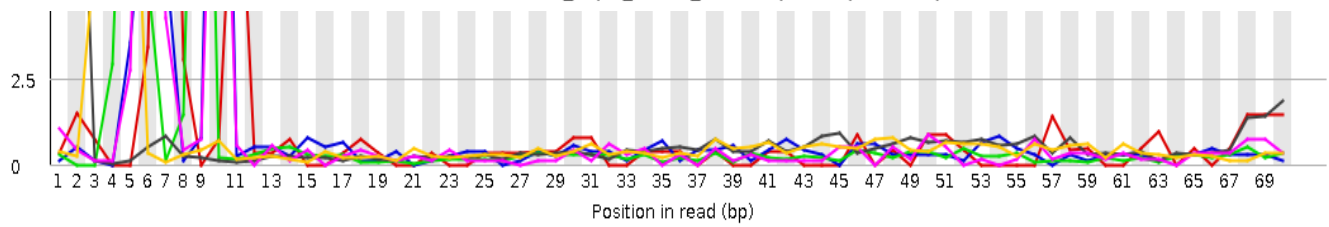
✔ Sequence Duplication Levels





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CCCTATG	825	0.0	23.040506	7
TCCTAG	2310	0.0	22.921597	10
ATCCCTA	7235	0.0	21.867662	9
GGGATAA	9360	0.0	21.77184	1
TCCTAT	2075	0.0	21.526115	6
ATAACAG	10270	0.0	19.803604	4
AGGGATA	6215	0.0	19.785662	1
CCTGTTA	8265	0.0	19.35656	3
TCCTAA	2295	0.0	19.341303	10
CCCTGTT	8390	0.0	19.217878	2
GGATAAC	10555	0.0	19.207523	2
CTGTTAT	8390	0.0	19.105932	4
GATAACA	10830	0.0	18.838097	3
AGGGTAA	10585	0.0	18.631159	9
TATCCCT	8665	0.0	18.509172	8
ACCCTGT	8740	0.0	18.384699	1
CAGGGTA	10795	0.0	18.32175	8
GGTAATT	2995	0.0	17.679092	11
CCCTAGT	1095	0.0	17.373106	11
ACAGGGT	11600	0.0	17.205894	7

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