













FastQC Report

Summary

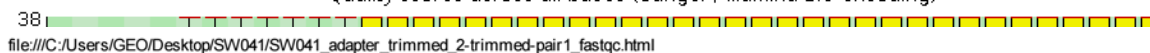
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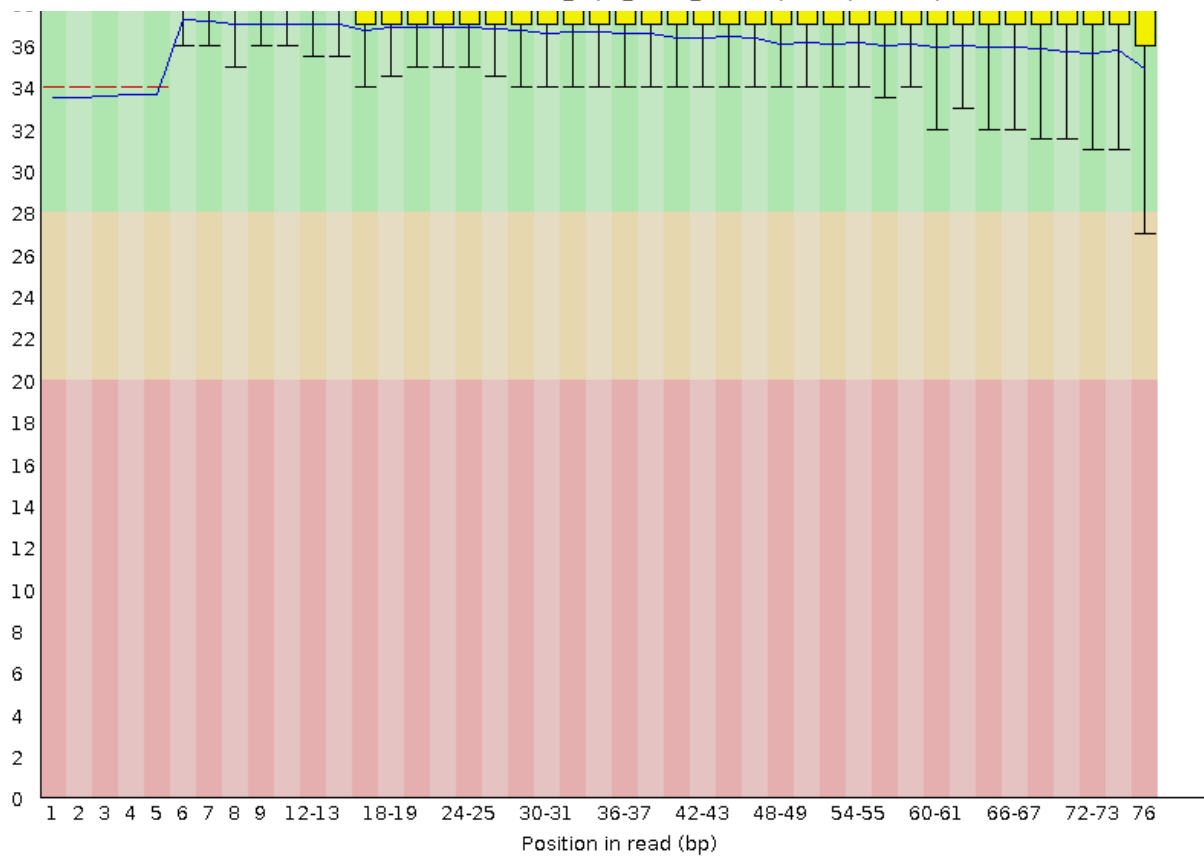
Basic Statistics

Measure	Value
Filename	SW041_adapter_trimmed_2-trimmed-pair1.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)

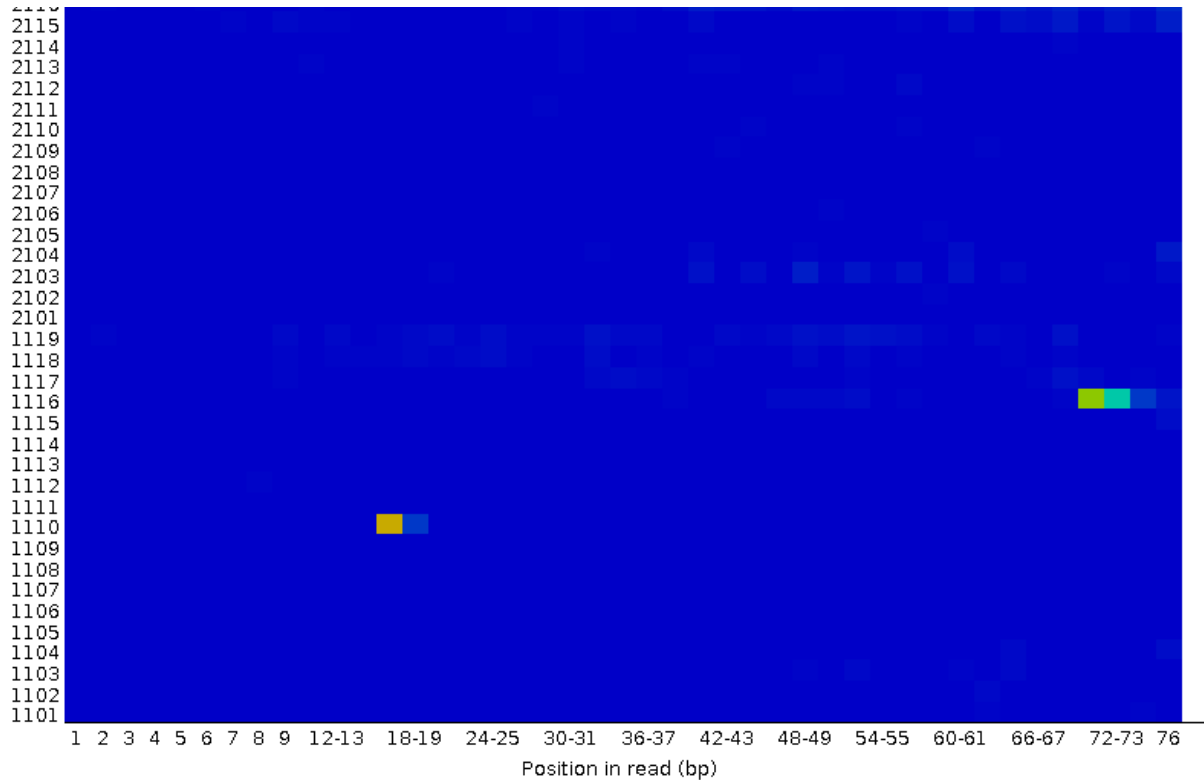




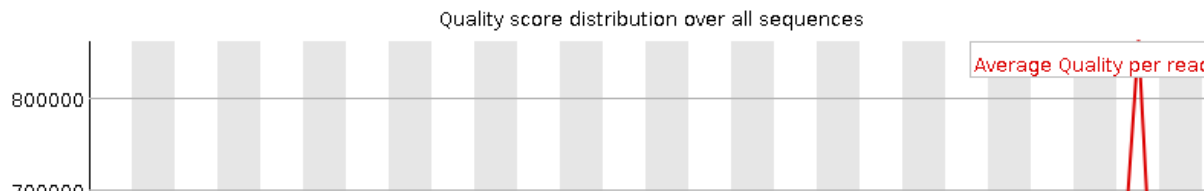
 **Per tile sequence quality**

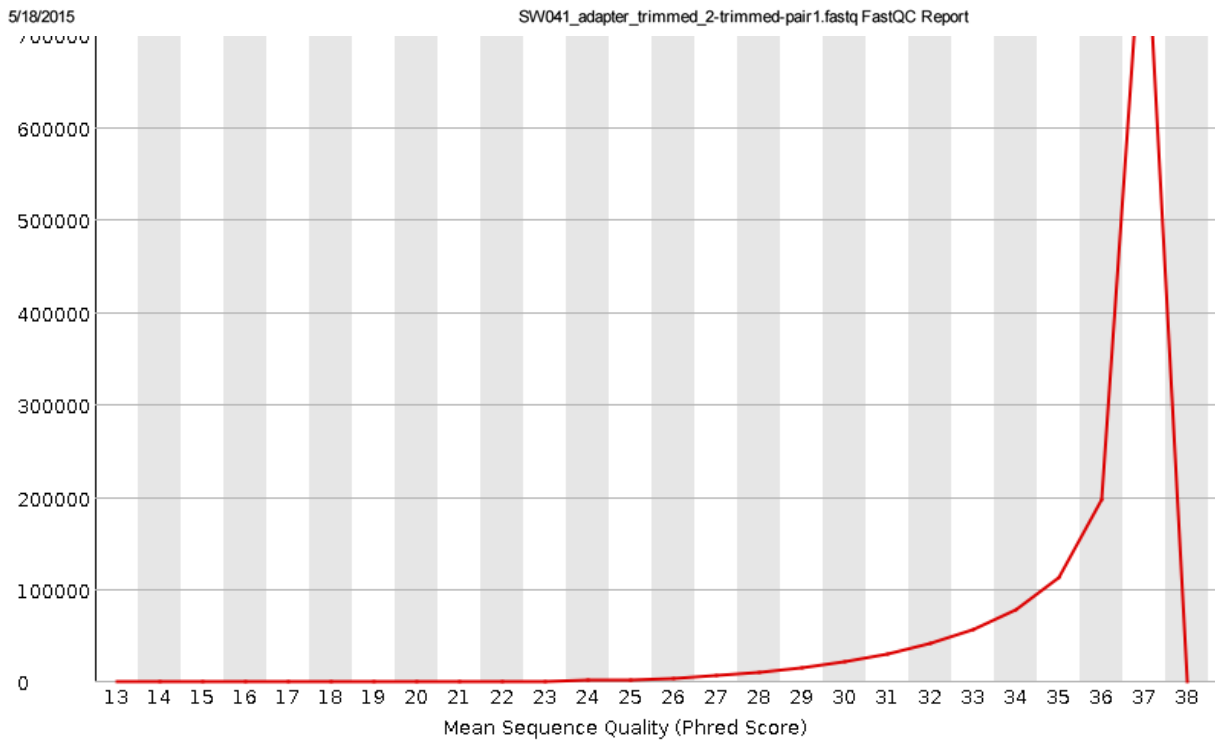
Quality per tile

2119
2118
2117
2116

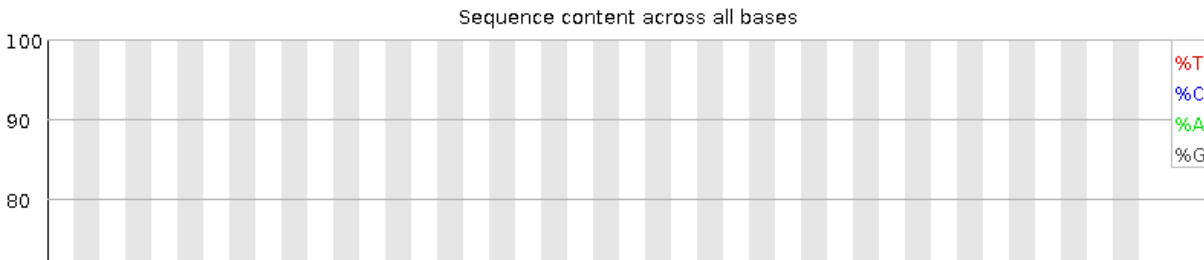


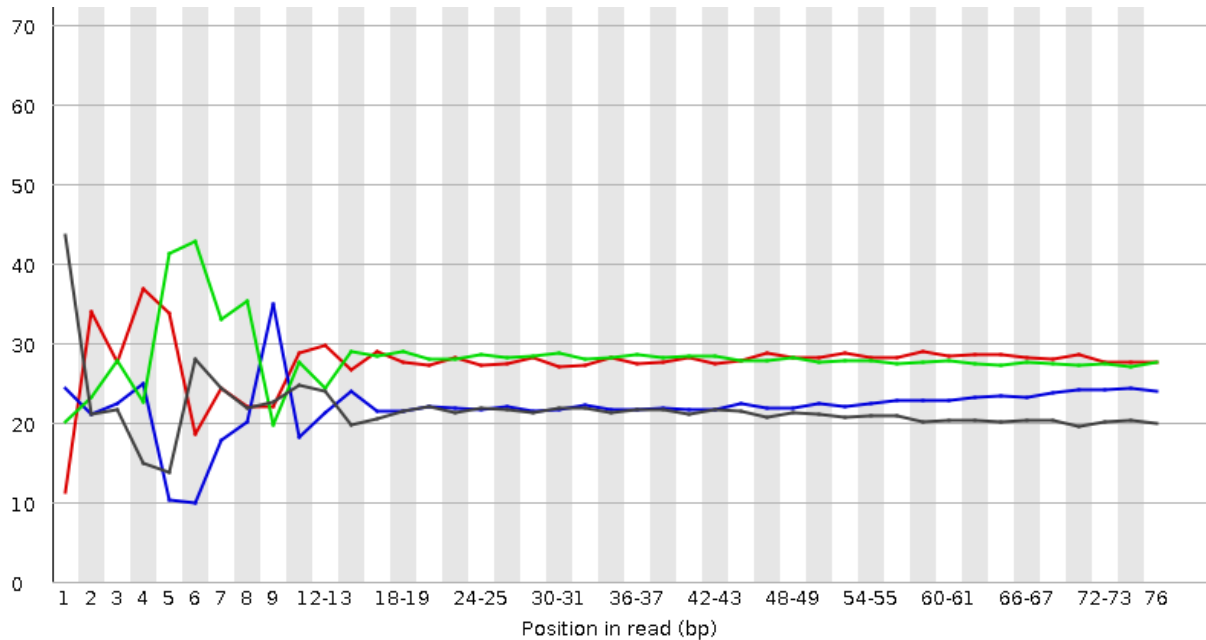
Per sequence quality scores



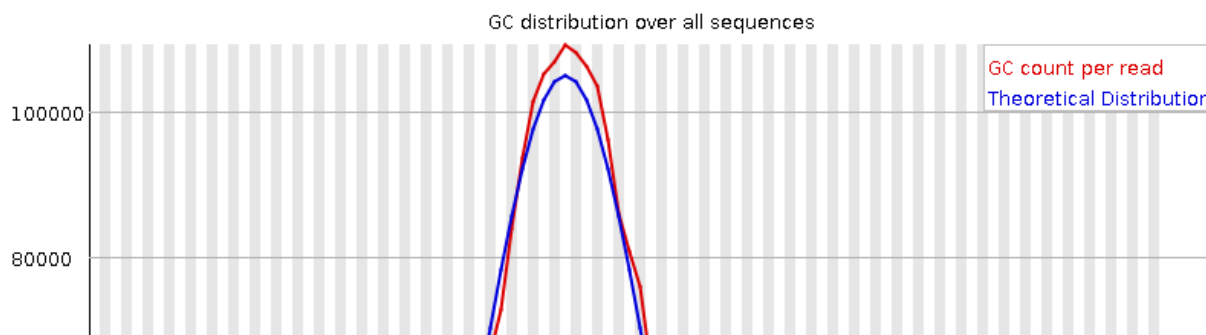


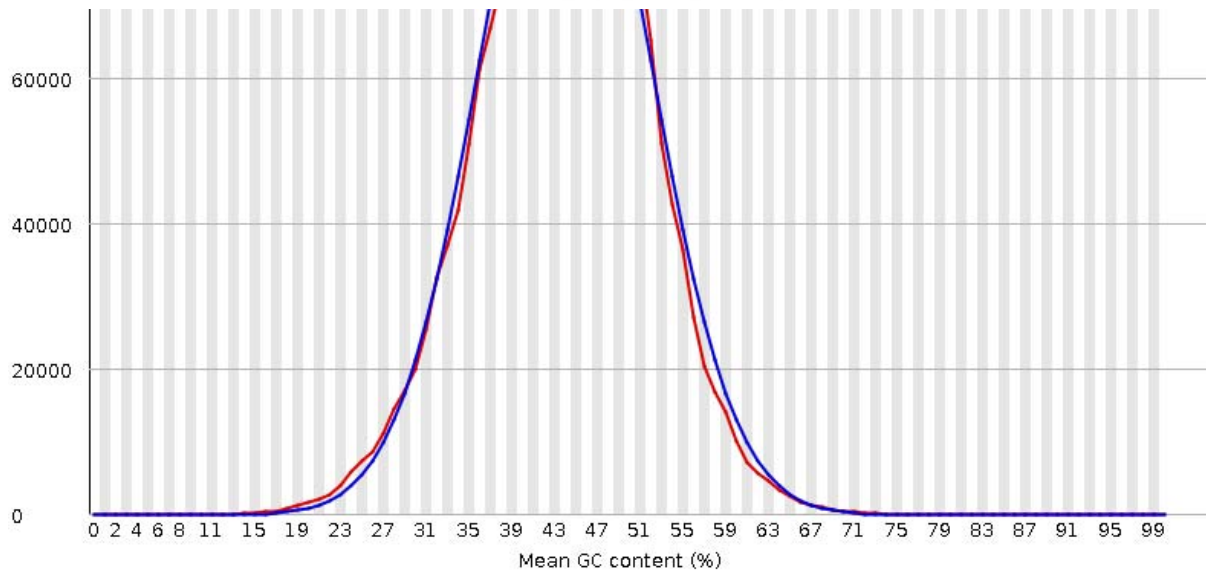
✖ Per base sequence content



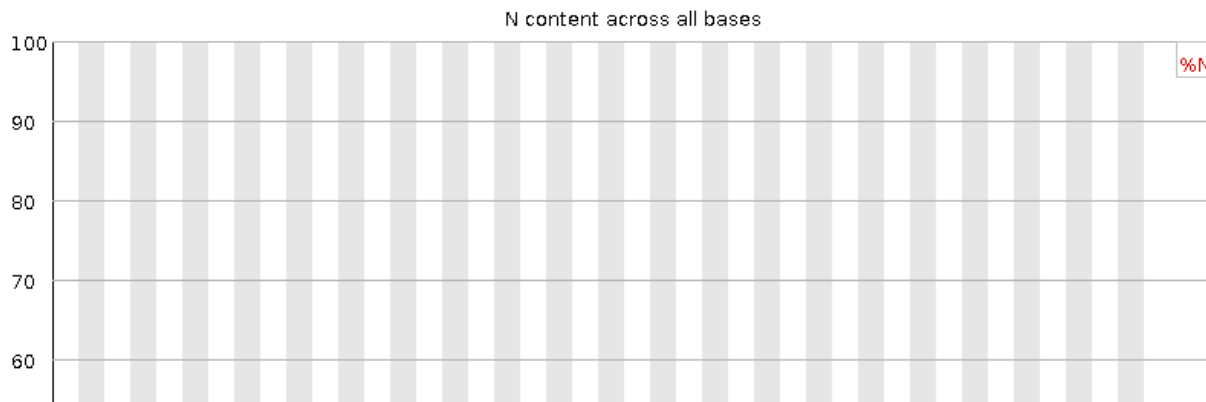


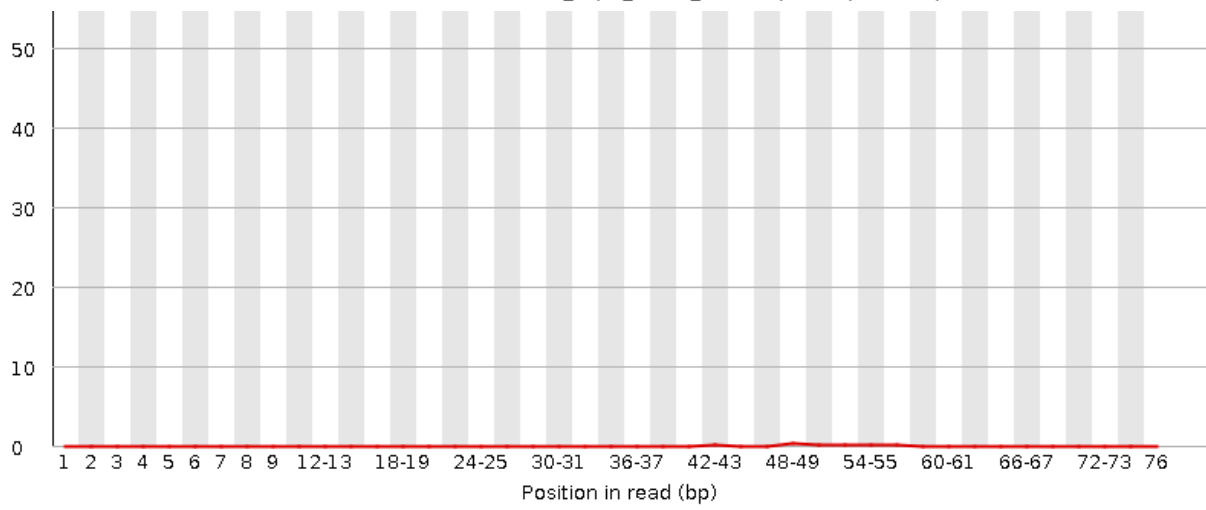
Per sequence GC content



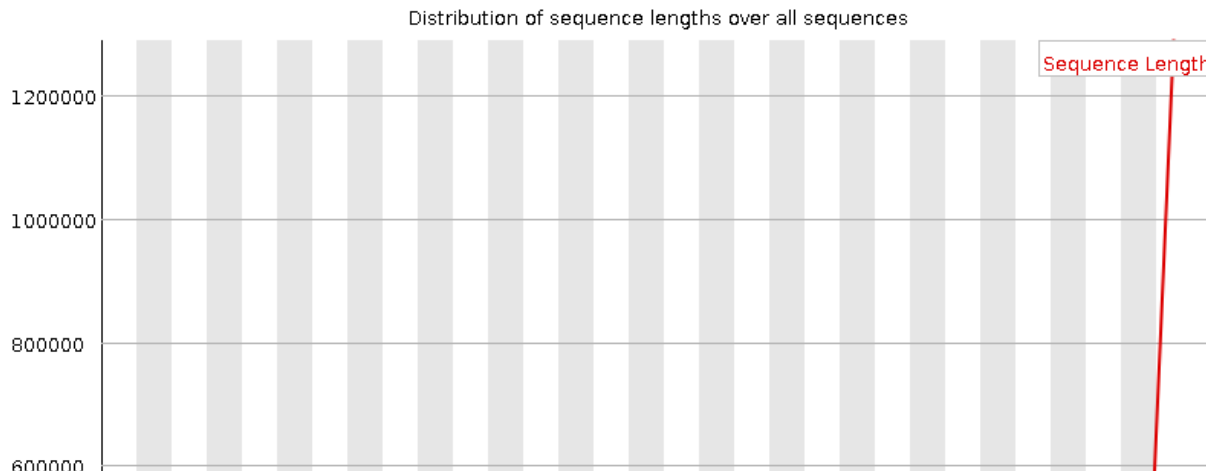


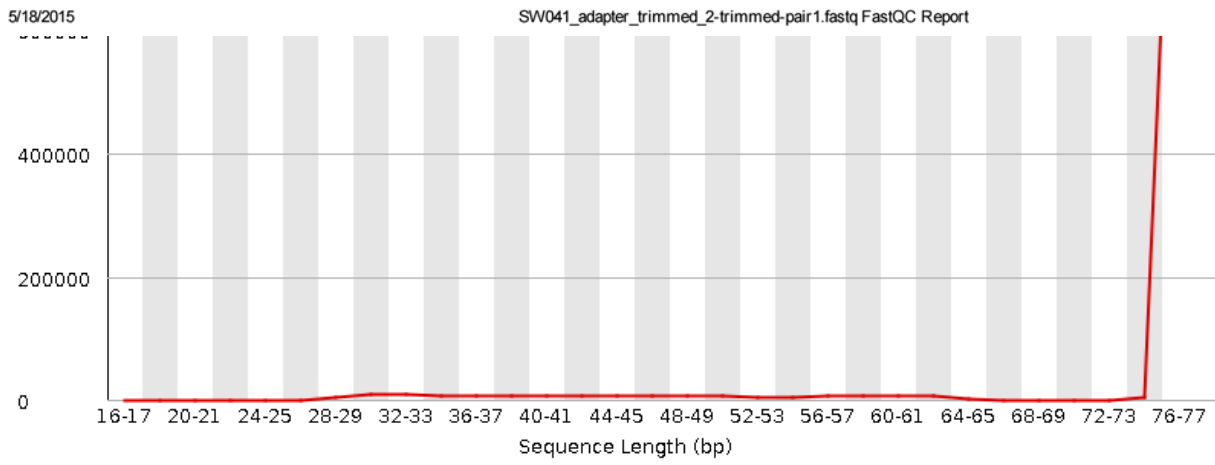
 **Per base N content**



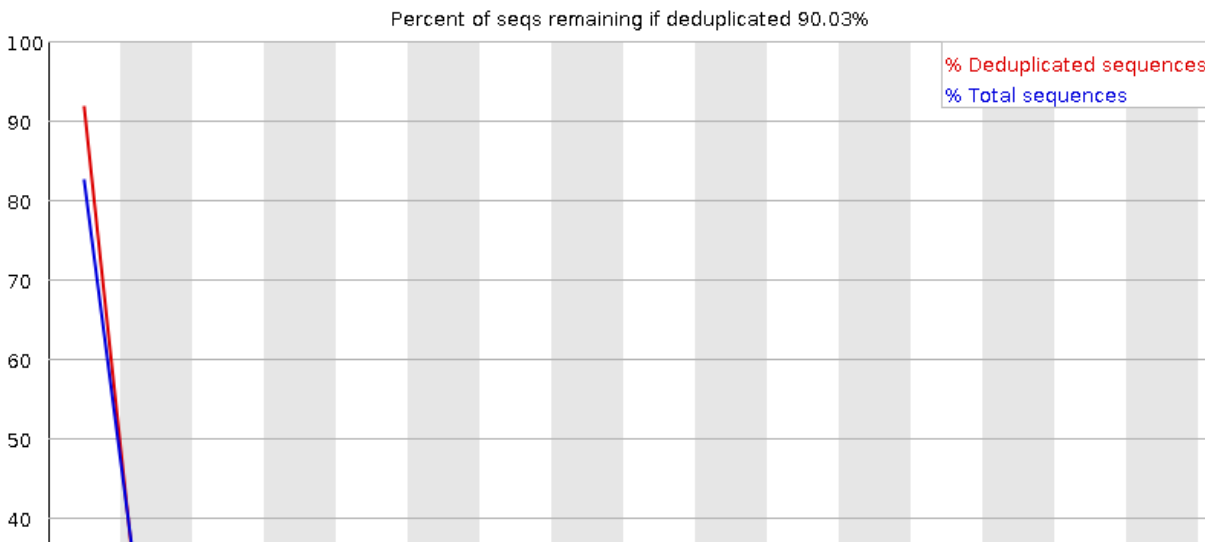


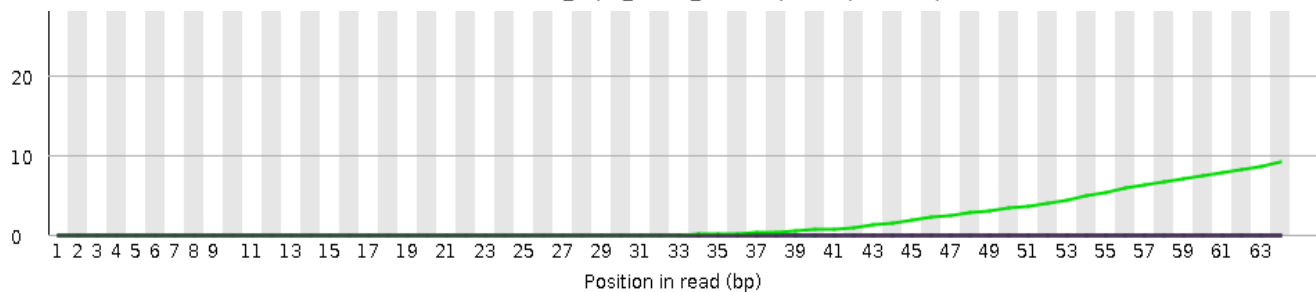
Sequence Length Distribution



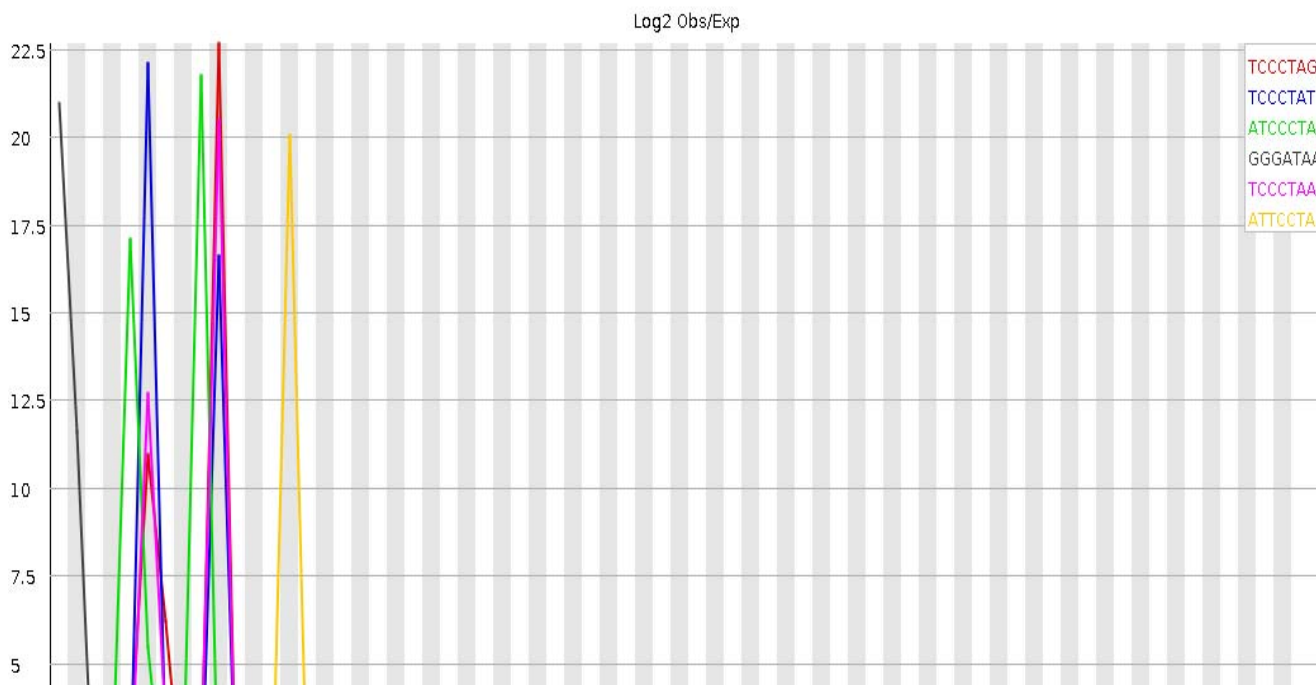


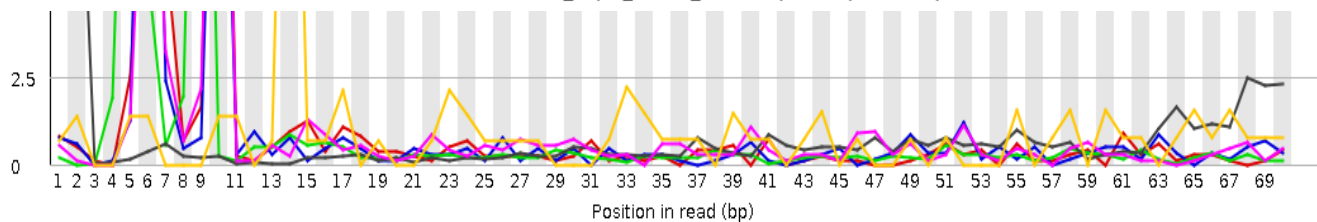
 **Sequence Duplication Levels**





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCCCTAG	2370	0.0	22.639704	10
TCCCTAT	2065	0.0	22.110252	6
ATCCCTA	7205	0.0	21.739876	9
GGGATAA	10550	0.0	20.951693	1
TCCCTAA	2260	0.0	20.497437	10
ATTCCTA	465	0.0	20.06773	14
GCGTCCC	100	5.4607814E-4	20.003653	1
CCCTAGA	950	0.0	19.99606	11
ATAACAG	11175	0.0	19.861174	4
CCGCGAT	85	0.005032986	19.604656	2
AGGGTAA	10915	0.0	19.602184	9
CAGGGTA	11075	0.0	19.499542	8
GGCCGAG	140	1.2594341E-5	19.044523	2
GGATAAC	11815	0.0	18.730204	2
GATAACA	11820	0.0	18.722282	3
CCCTATG	750	0.0	18.66299	7
GGTAATT	3095	0.0	18.62853	11
TCCGCGA	90	0.0069878837	18.5219	1
ACAGGGT	12155	0.0	17.958893	7
TATCCCT	8825	0.0	17.937922	8

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