





Per tile sequence quality

Per sequence quality scores

Per base sequence content

Per sequence GC content

Per base N content

Sequence Length Distribution

Sequence Duplication Levels

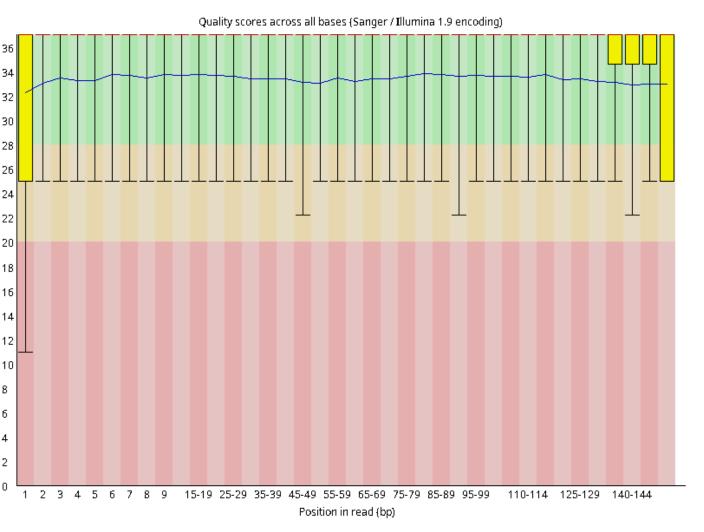
Overrepresented sequences

Adapter Content

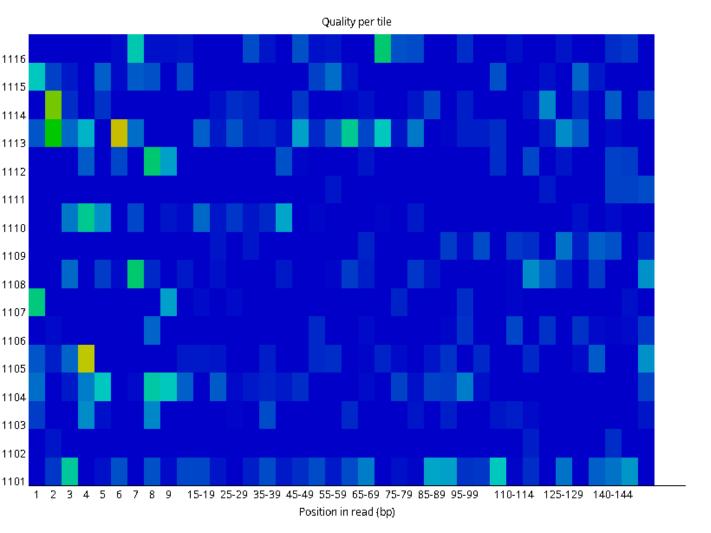
Basic Statistics

Measure	Value		
Filename	SRR33784444_2_unpaired.fastq		
File type	Conventional base calls		
Encoding	Sanger / Illumina 1.9		
Total Sequences	1511		
Sequences flagged as poor quality	0		
Sequence length	50-151		
%GC	48		

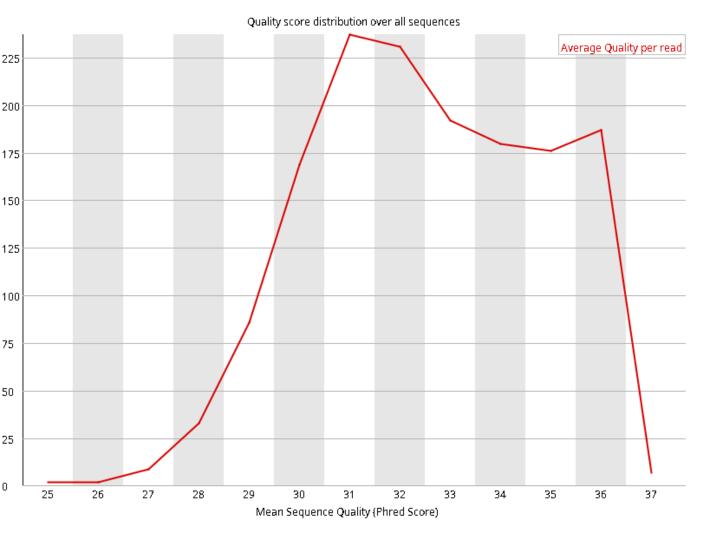
Per base sequence quality



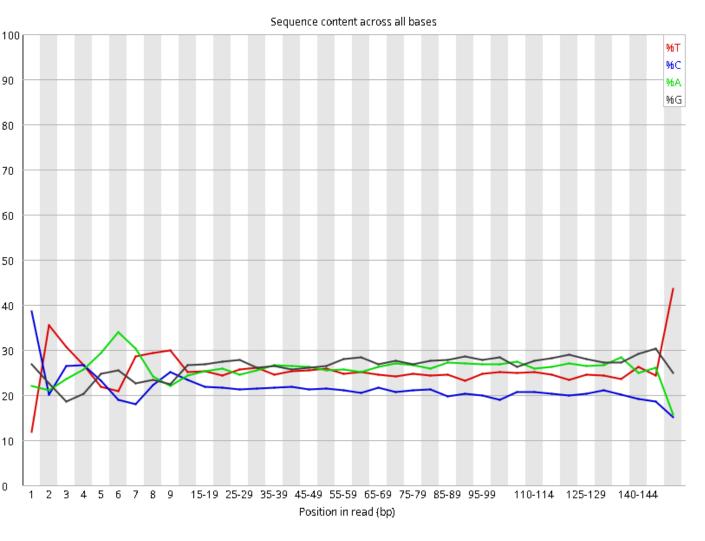
Per tile sequence quality



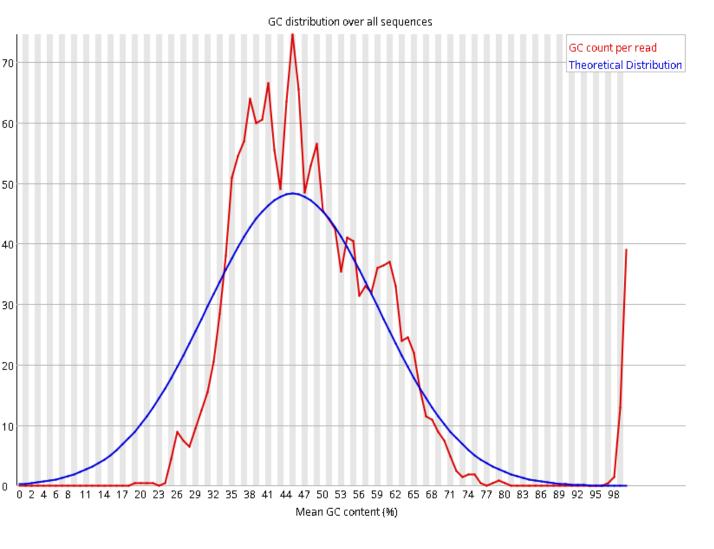
Per sequence quality scores



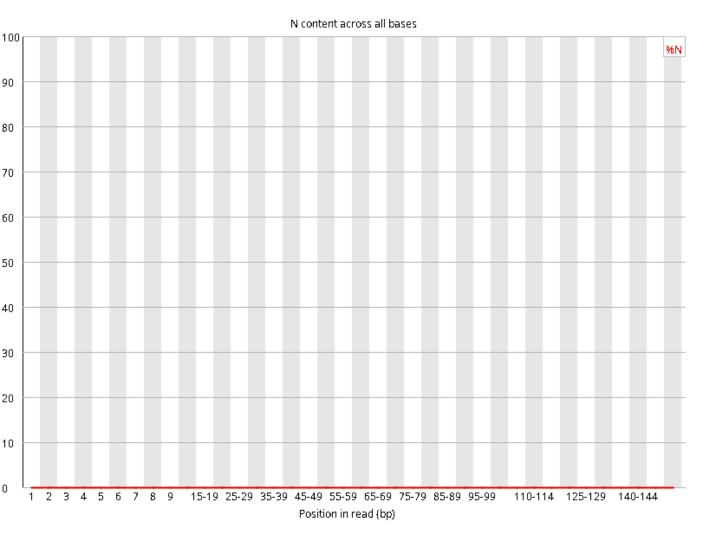
Per base sequence content



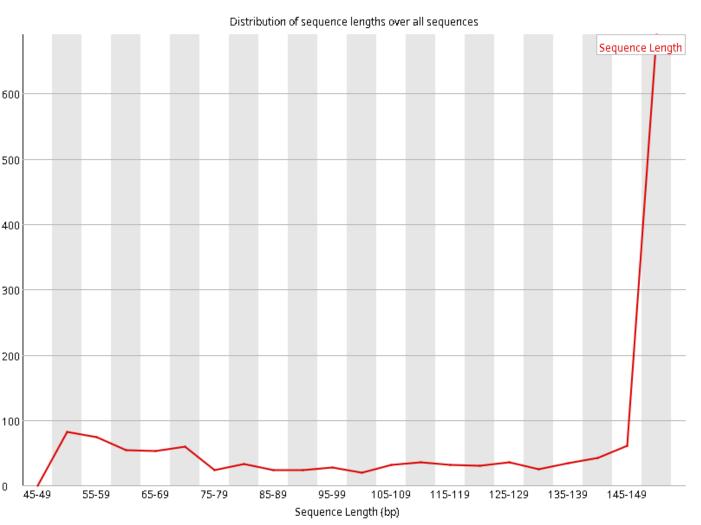
Per sequence GC content



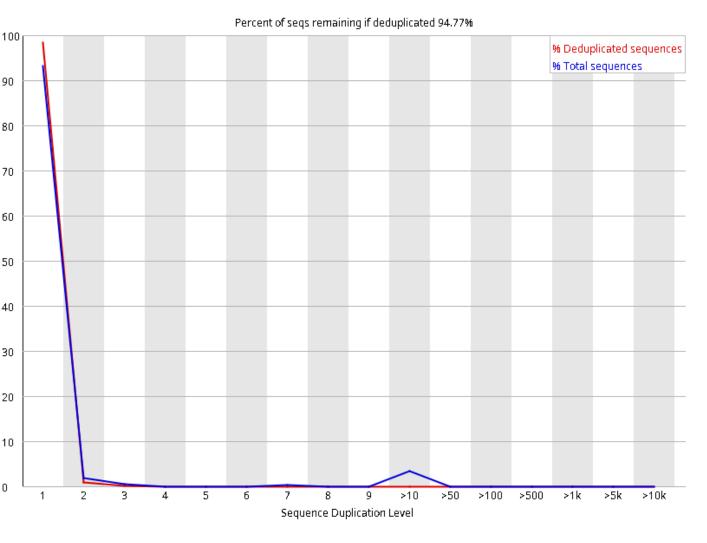




Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
000000000000000000000000000000000000000	39	2.5810721376571806	No Hit
GATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTACACGCAGTGTAGATCT	15	0.9927200529450696	Illumina Single End PCR Primer 1 (96% over 32bp)
999999999999999999999999999999999999999	7	0.4632693580410324	No Hit
CTCTTTGGCAGCGACCCCTAGTCACAGTAAAAATAGGGGGACAGCTAATA	3	0.1985440105890139	No Hit
${\tt GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG$	3	0.1985440105890139	No Hit
TTAAAAGAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3	0.1985440105890139	No Hit
CAGCTATTTGGGAAGCTGAGGCAAGAGAATCACTTAAACCTGGGAGGTGG	2	0.13236267372600927	No Hit
GTTCAATACAATGTACACATGGAATTAAGCCAGTGGTATCAACTCAATTA	2	0.13236267372600927	No Hit
GGTCCCTGTTCGGGCGCCACTGCTAGAGATTTTTGTATTCTCACGAGTGG	2	0.13236267372600927	No Hit

Sequence	Count	Percentage	Possible Source
CTCCCATTCCCACTGCTCTTTTTTCTCTCTGCACCACTCTTCTCCTTGCC	2	0.13236267372600927	No Hit
CTAAACACTGTGGGGGGACATCAAGCAGCTATGCAAATGCTAAAGGATAC	2	0.13236267372600927	No Hit
AAGAAGTGAACCCCAATTACATTGCCCACGTGTATACCCAGATCTGCGG	2	0.13236267372600927	No Hit
CTACCACCGATTGAGAGACTTCATATTGATTGCAGCGAGGACAATACAAC	2	0.13236267372600927	No Hit
CTCACAATTTGTTTTATCCTACATGGGAGTGTGACAGTGTCATTCTTGAA	2	0.13236267372600927	No Hit
CAAACATTCTATGCAACAGGTGACATAATAGGAGATATAAGACAAGCACA	2	0.13236267372600927	No Hit
TGGCCTGTACCGTCAGCGCCCGCGAGCTTCGCTGCTAATTGAATGCAAGC	2	0.13236267372600927	No Hit
CCTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	2	0.13236267372600927	No Hit
CTCCAGAGAGCAGTAAGGACATAAGACTCCTGGTTTTAACTGGGGATAAA	2	0.13236267372600927	No Hit
CTCTCACCTTCTCTGTAGCACATGGGCACAGCCCTGGTCCTGATGGGTCA	2	0.13236267372600927	No Hit
CATCACACCTCACCTACCAAGCACAAATTCAAGGAAAGAAA	2	0.13236267372600927	No Hit
CTCCAATTCCCCCTATCATTTTTGGTTTCCACTTCCCTGGTAAATTTATT	2	0.13236267372600927	No Hit

Adapter Content

