ReportSummary

Sun 21 Sep 2014 SRR1033798.fastq









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

Kmer Content



Measure Value

Filename SRR1033798.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

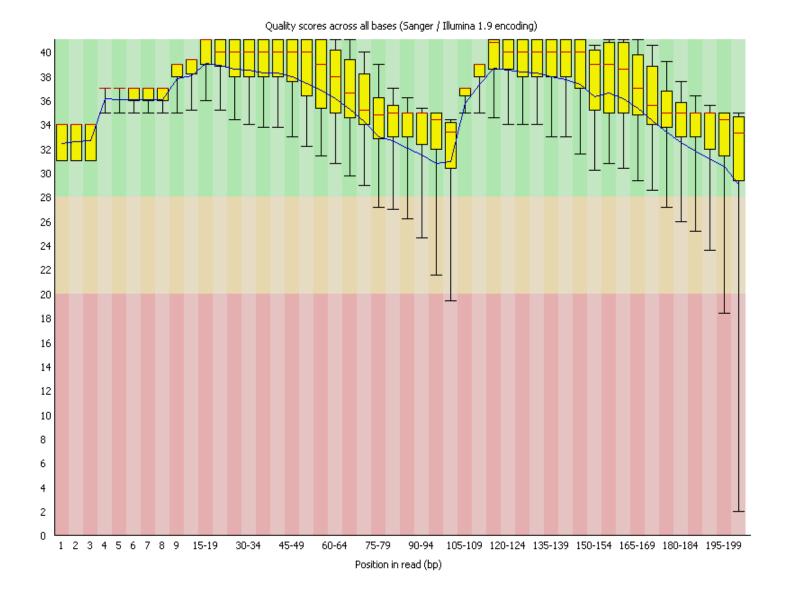
Total Sequences 31073094

Sequences flagged as poor quality 0

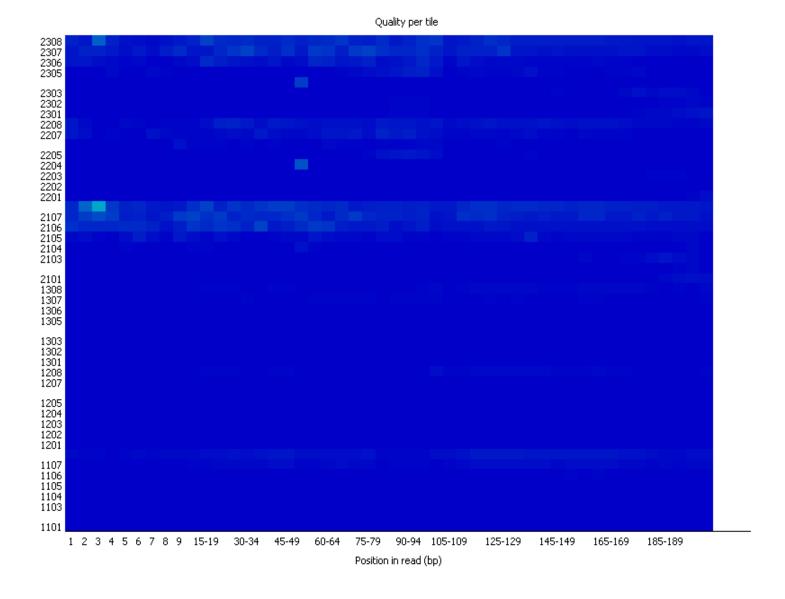
Sequence length 202

%GC 48

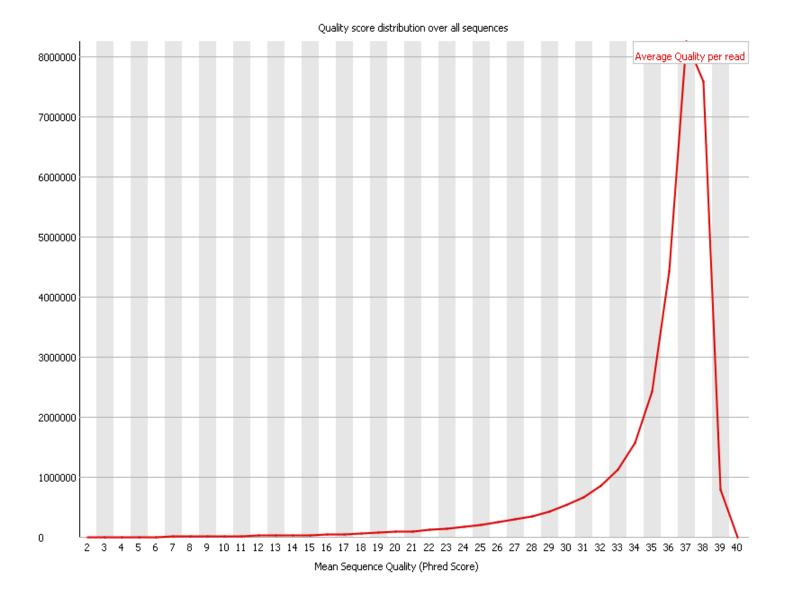
Per base sequence quality



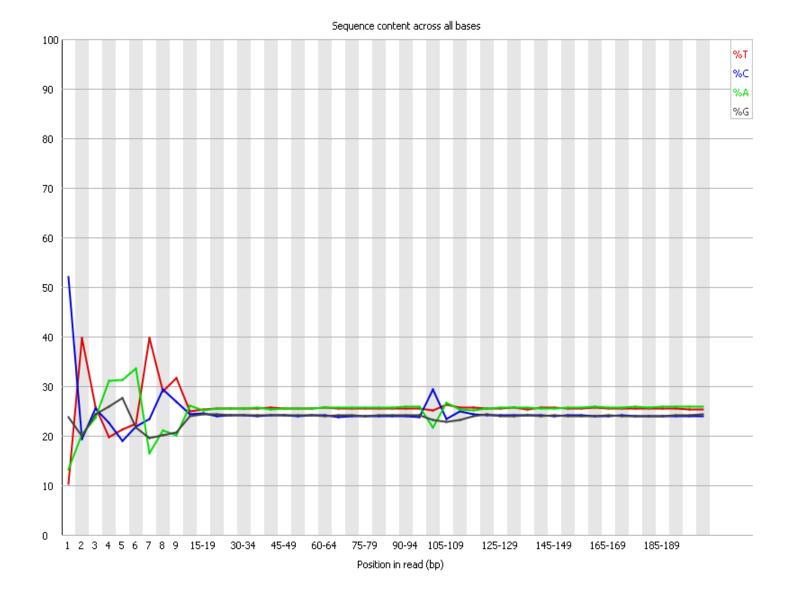




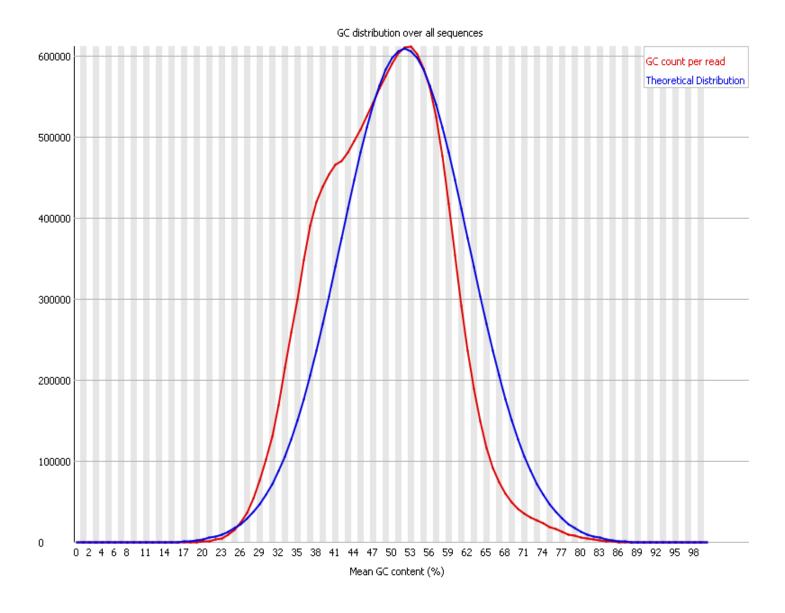
Per sequence quality scores



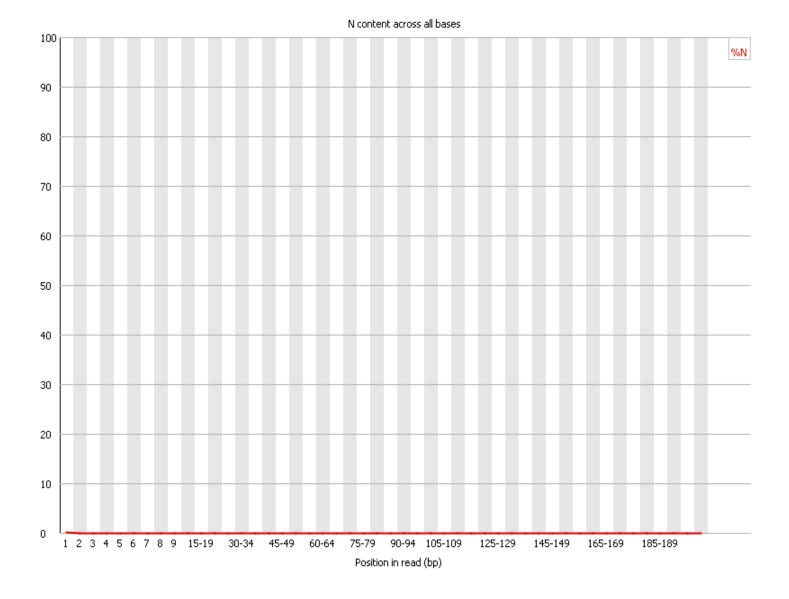
Per base sequence content



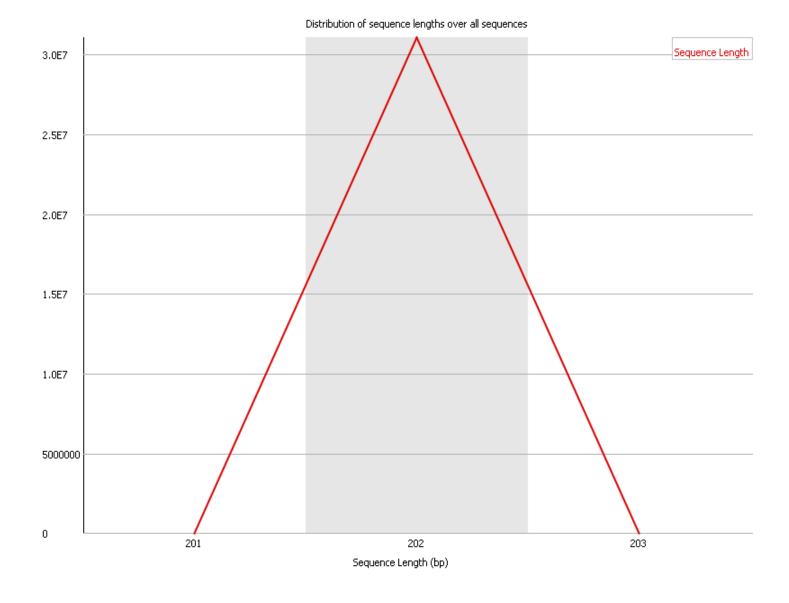
Per sequence GC content



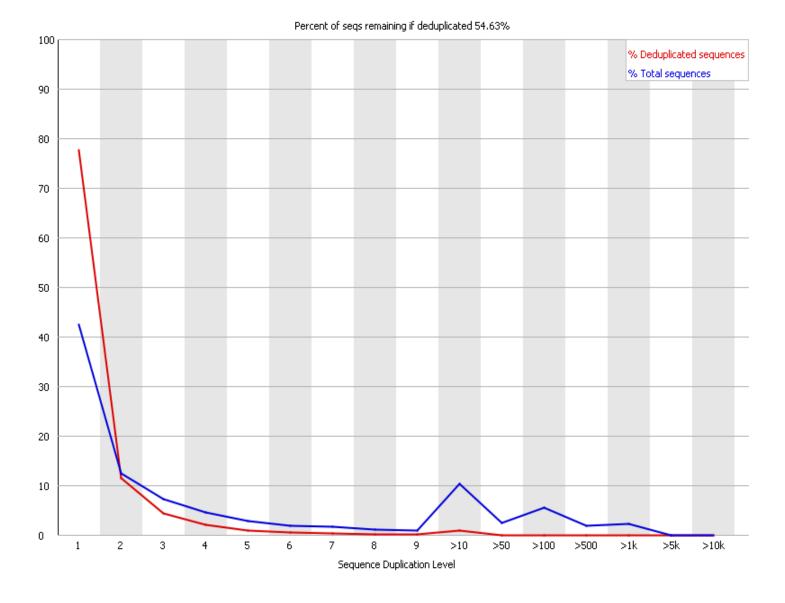








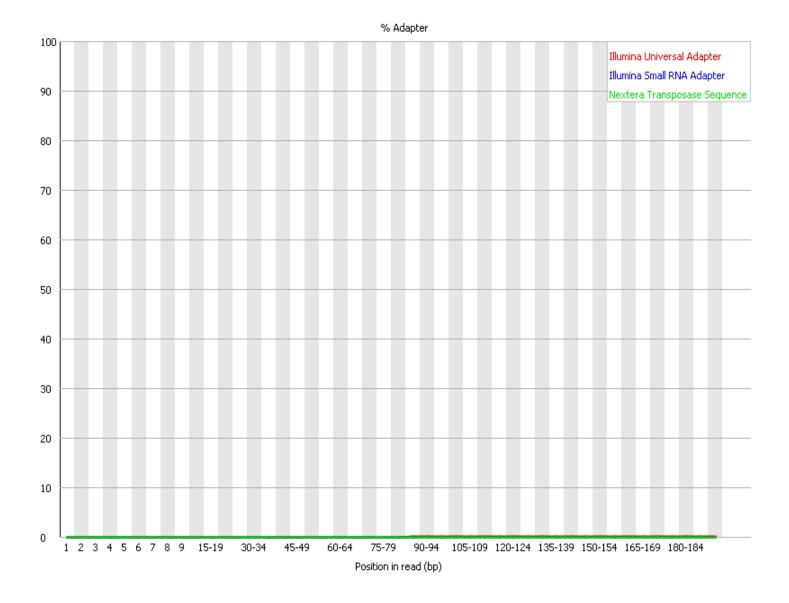
Sequence Duplication Levels



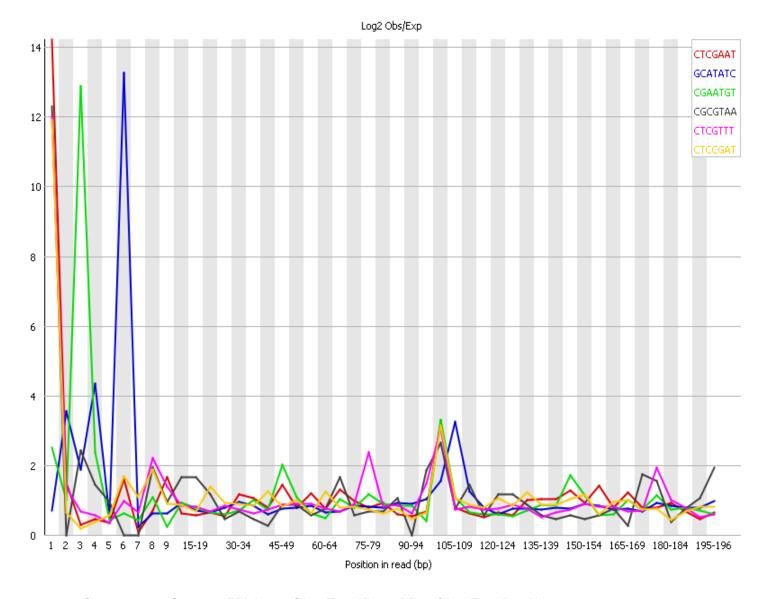


No overrepresented sequences









Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTCGAAT	18800	0.0	14.20412	1
GCATATC	18680	0.0	13.272807	6
CGAATGT	15130	0.0	12.888774	3
CGCGTAA	1995	0.0	12.302699	1
CTCGTTT	23645	0.0	11.999463	1
CTCCGAT	20155	0.0	11.934014	1
GATCGGA	37045	0.0	11.448733	1
CGATTAG	15025	0.0	11.152677	4
TATGCCG	13725	0.0	11.15257	45-49
TCGAATG	17975	0.0	10.685249	2
CCGATTA	14910	0.0	10.581463	3
CCGGTAT	7175	0.0	10.535912	1

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTCGGTT	20095	0.0	10.503976	1
ATATCAC	24545	0.0	10.5005455	8
TTCGATT	12435	0.0	10.481014	2
CTCGGAT	23350	0.0	10.216983	1
CGGAAAT	14845	0.0	10.052329	1
GTTCGAT	11050	0.0	10.03967	1
ATCGGAA	43260	0.0	10.012286	2
AAGACGC	21230	0.0	9.831665	2

Produced by <u>FastQC</u> (version 0.11.2)