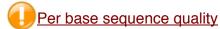
Report

Wed 16 Aug 2017 Carnea1-L06-i12_S83_L006_R2_001.fastq

Summary





- 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
- Kmer Content

Basic Statistics

Measure Value

Filename Carneal-L06-i12_S83_L006_R2_001.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

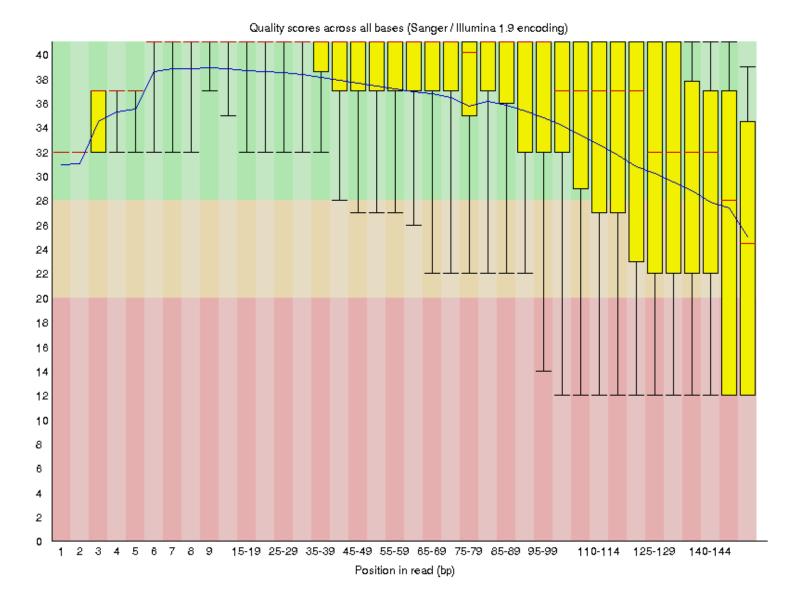
Total Sequences 339953040

Sequences flagged as poor quality 0

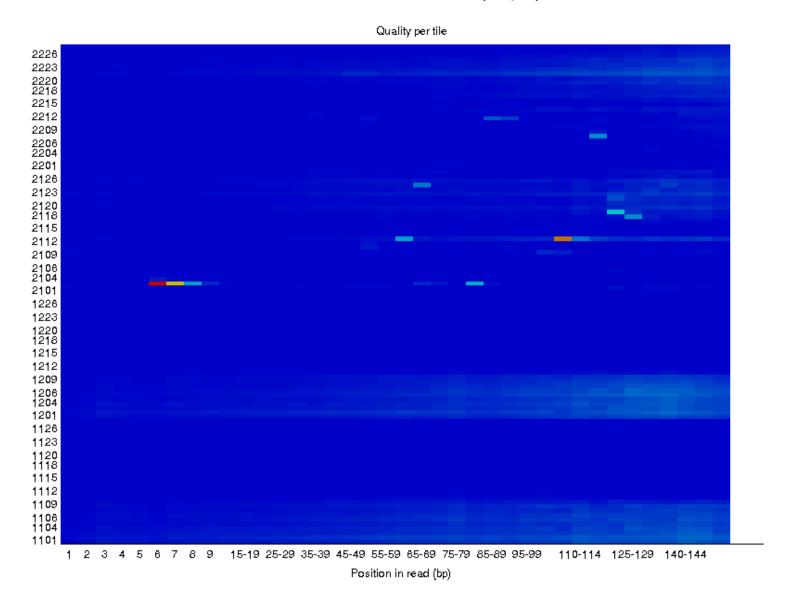
Sequence length 151

%GC 35

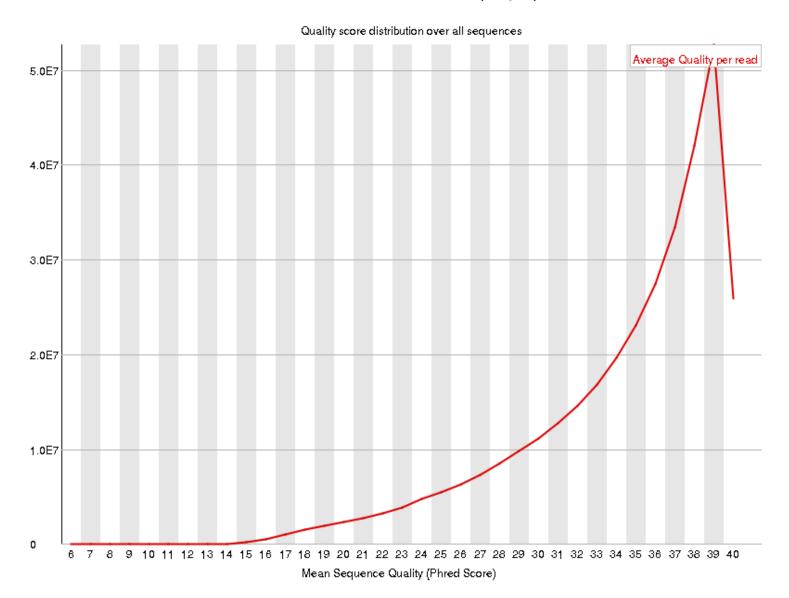
Per base sequence quality



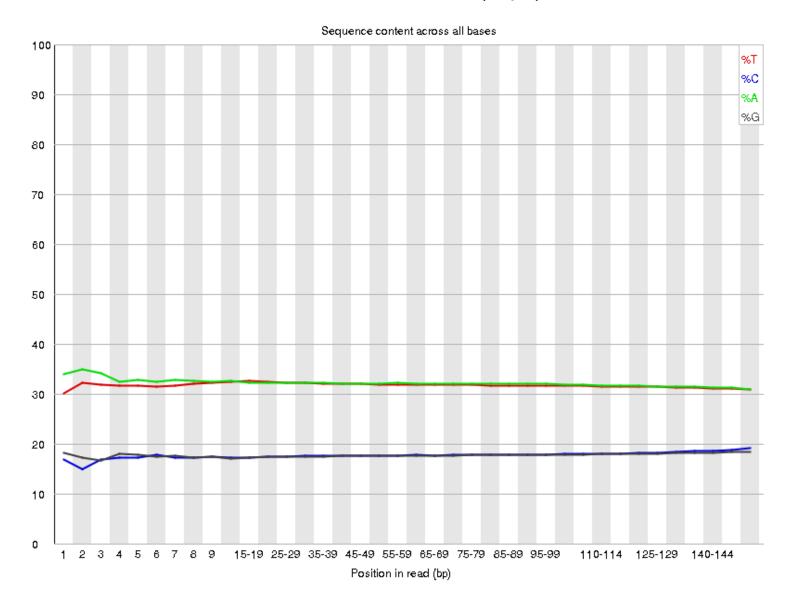
Per tile sequence quality



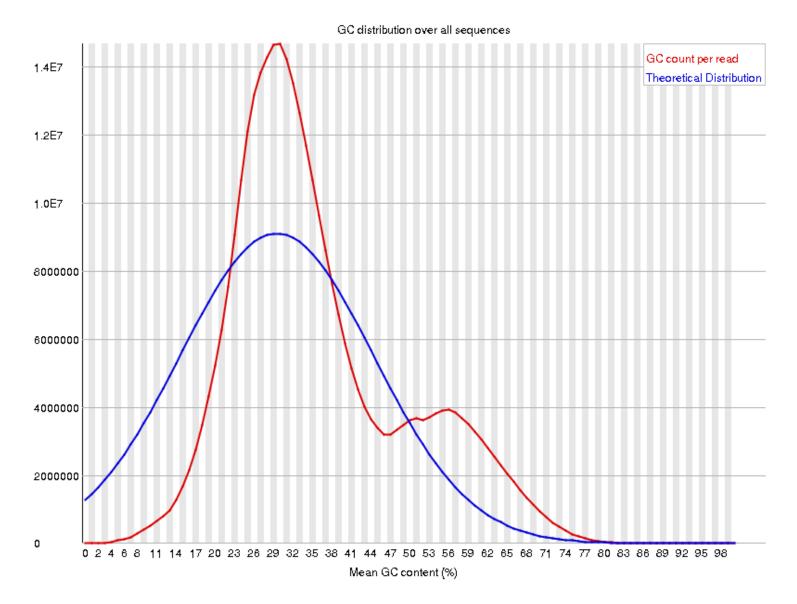
Per sequence quality scores



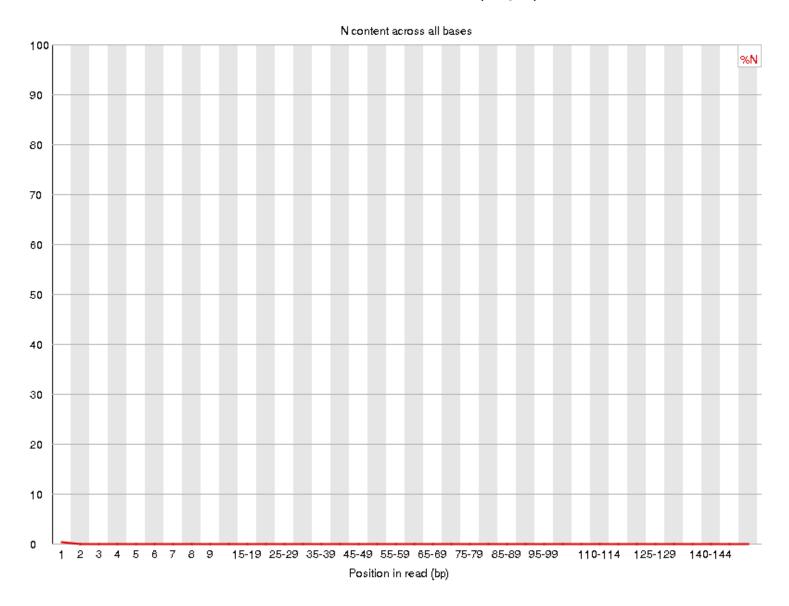
Per base sequence content



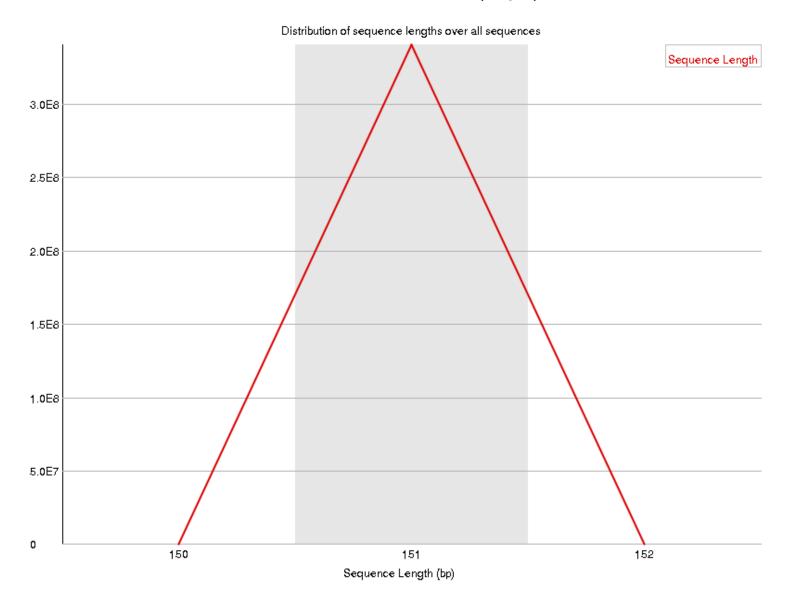
Per sequence GC content



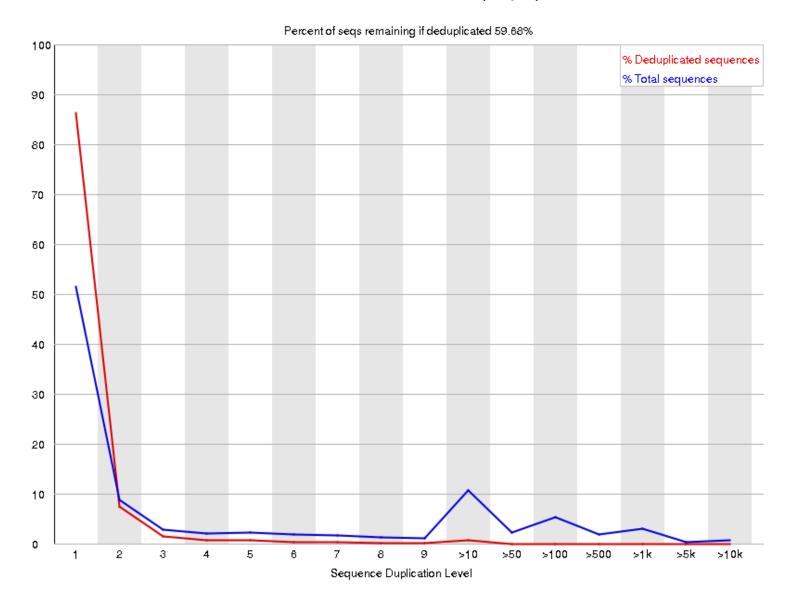








Sequence Duplication Levels

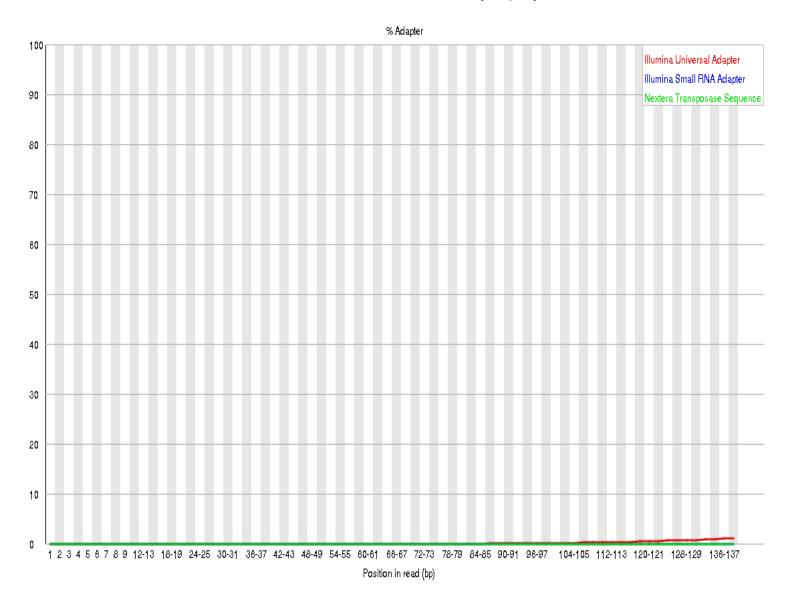


Overrepresented sequences

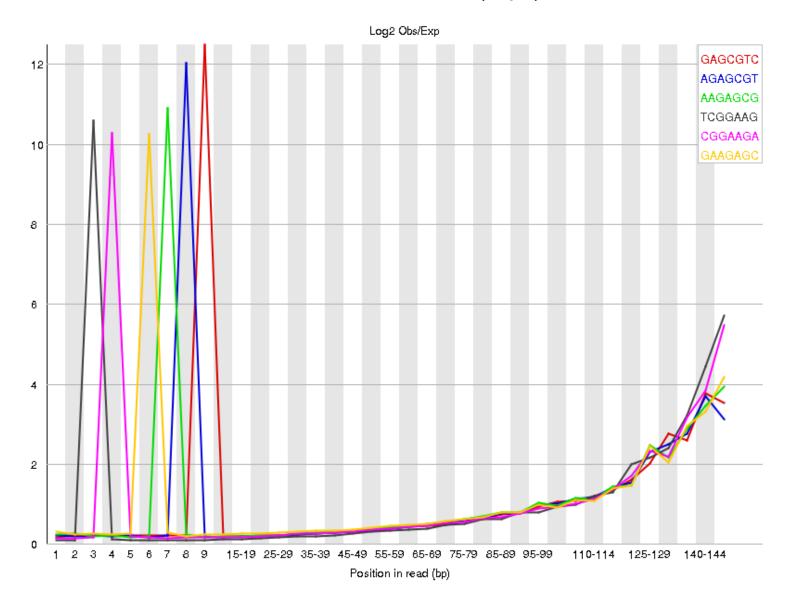
Sequence Count Percentage Possible Source

GATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATCTCGGTGGTCGCCG 508819 0.1496733195855522 PCR Primer 1 (100% over 50bp)









Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GAGCGTC	626905	0.0	12.472189	9
AGAGCGT	650290	0.0	12.023601	8
AAGAGCG	720825	0.0	10.912491	7
TCGGAAG	733710	0.0	10.589493	3
CGGAAGA	761870	0.0	10.276502	4
GAAGAGC	765950	0.0	10.260721	6
GGAAGAG	783145	0.0	10.031676	5
GATCGGA	789430	0.0	9.883904	1
ATCGGAA	913000	0.0	8.7474785	2
CGTATCA	295635	0.0	5.681889	45-49
TGGTCGC	296475	0.0	5.6508484	40-44
GCCGTAT	303615	0.0	5.5741057	45-49

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTGGTCG	302000	0.0	5.5537086	40-44
CCGTATC	309345	0.0	5.514923	45-49
CGCCGTA	307680	0.0	5.475952	45-49
AGATCGG	782180	0.0	5.15312	140-144
GGTCGCC	330840	0.0	5.1423216	40-44
TCTCGGT	327595	0.0	5.085212	35-39
GGTGGTC	334605	0.0	5.0658293	40-44

Produced by FastQC (version 0.11.2)