# **Report**

Wed 16 Aug 2017 Carnea1-L06-i12\_S83\_L006\_R1\_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\_R1\_001.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

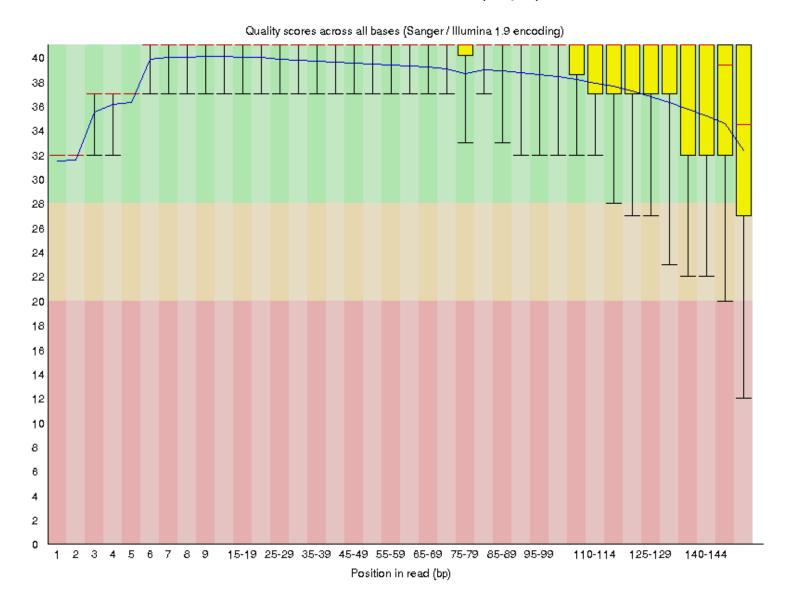
Total Sequences 339953040

Sequences flagged as poor quality 0

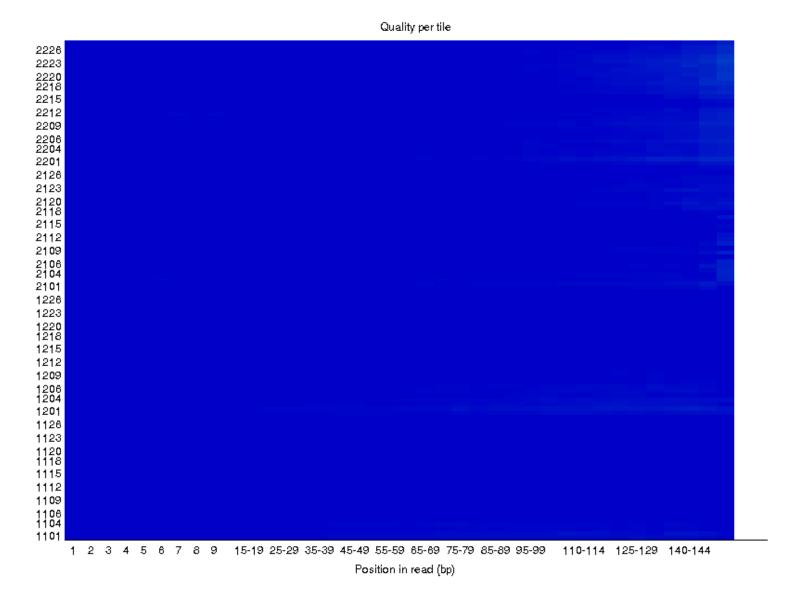
Sequence length 151

%GC 35

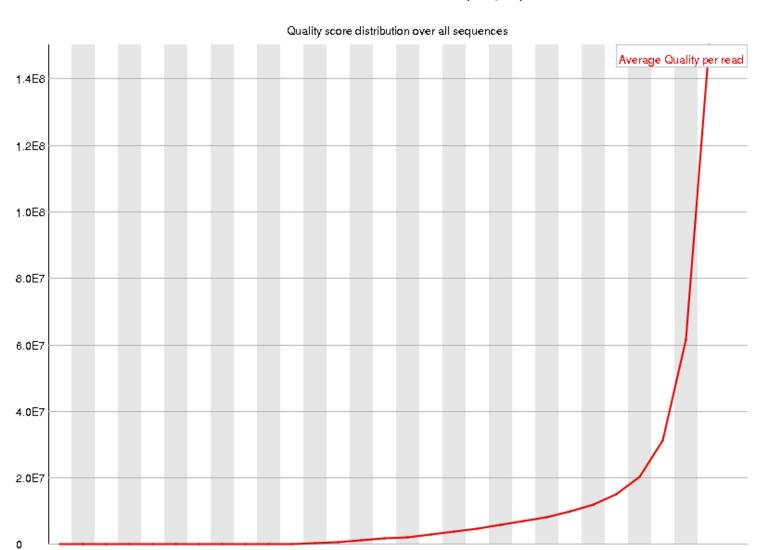
### Per base sequence quality



### Per tile sequence quality



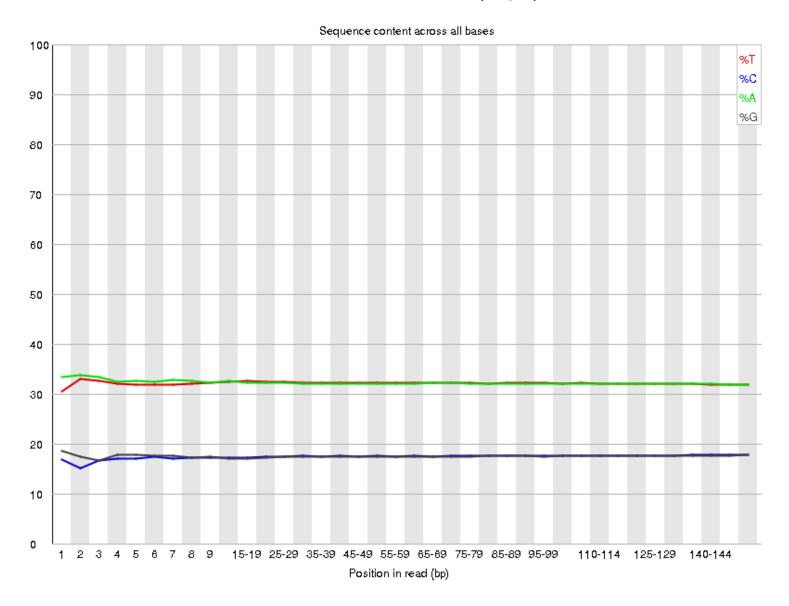




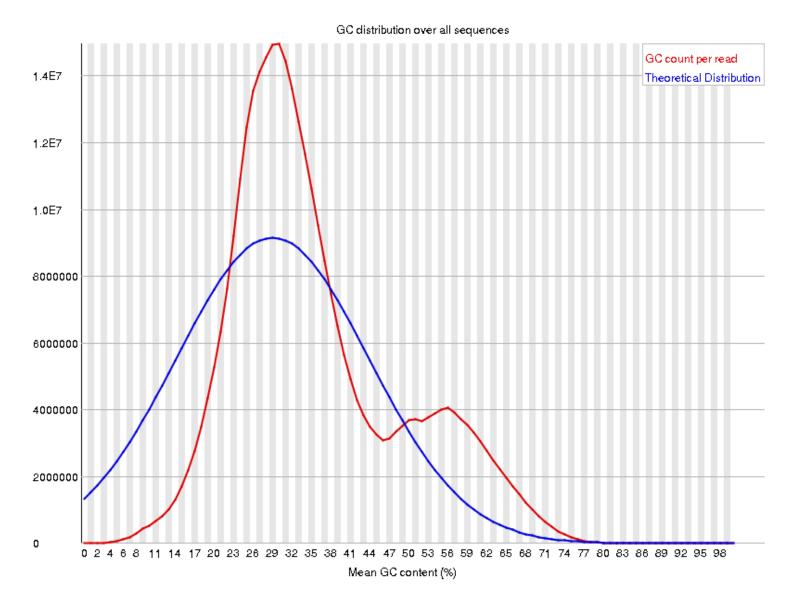
12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40

Mean Sequence Quality (Phred Score)

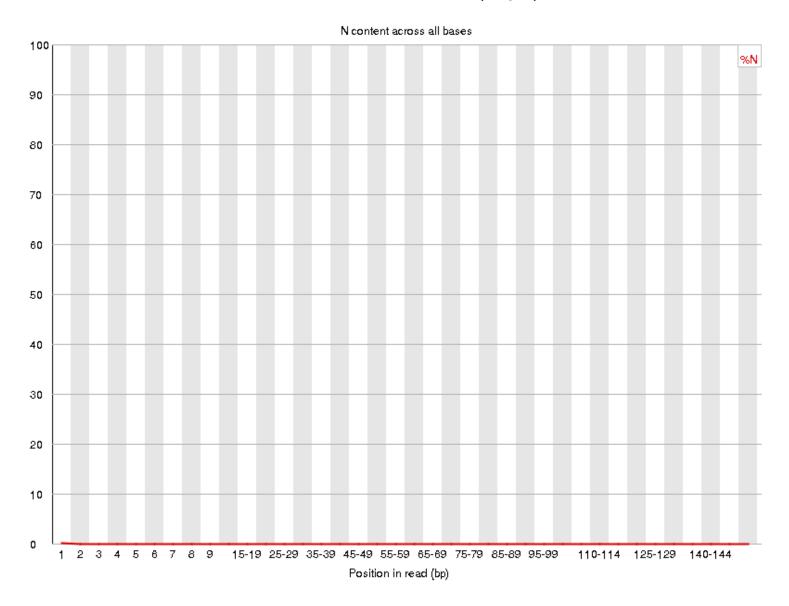
### Per base sequence content



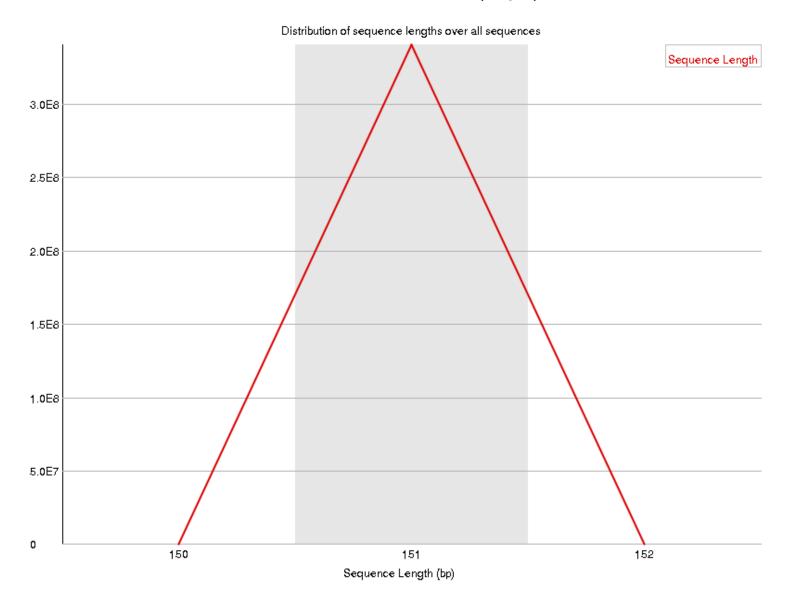
## Per sequence GC content



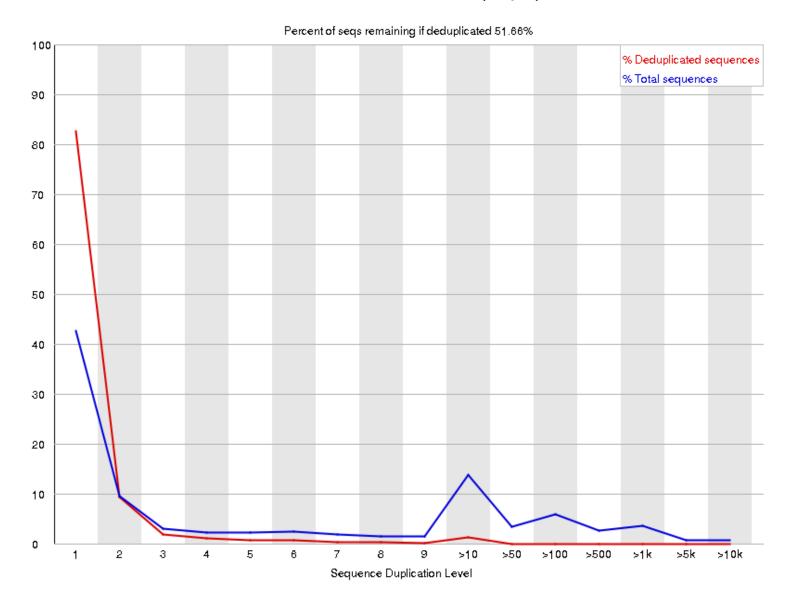








#### Sequence Duplication Levels

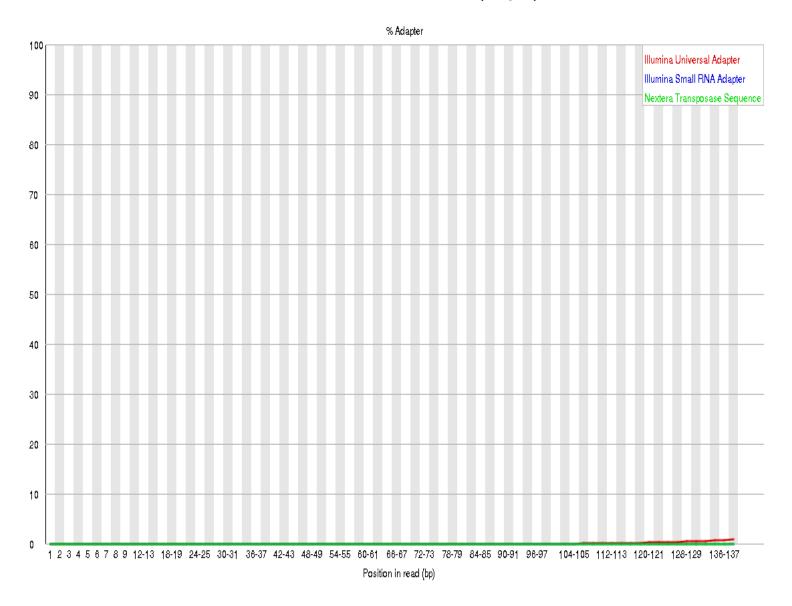


### Overrepresented sequences

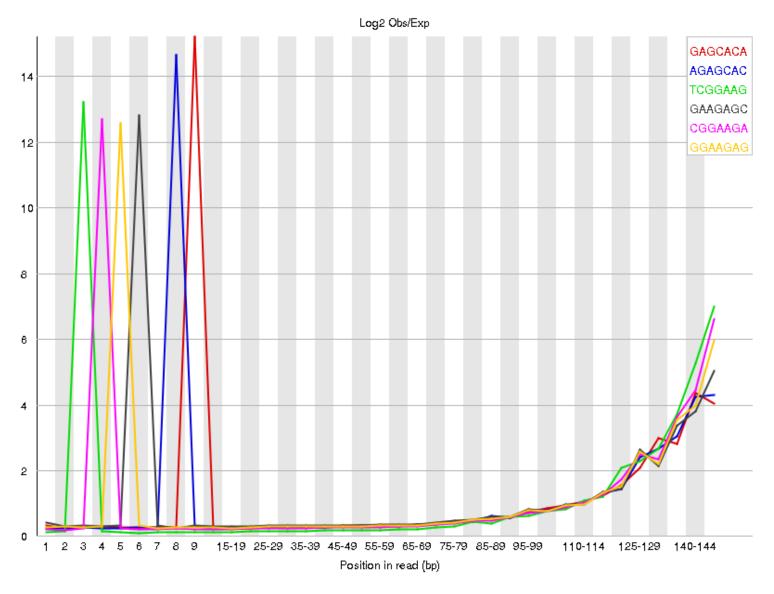
Sequence Count Percentage Possible Source

TruSeq Adapter,
Index 12 (100% over 50bp)









Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GAGCACA	517325	0.0	15.186383	9
AGAGCAC	536500	0.0	14.654459	8
TCGGAAG	592600	0.0	13.216657	3
GAAGAGC	618720	0.0	12.795649	6
CGGAAGA	620905	0.0	12.675461	4
GGAAGAG	629115	0.0	12.563481	5
GATCGGA	648755	0.0	12.122357	1
AAGAGCA	693550	0.0	11.566011	7
ATCGGAA	783600	0.0	10.261626	2
CGTATGC	201380	0.0	8.142435	40-44
CTCGTAT	215230	0.0	7.668322	40-44
GCCGTCT	213025	0.0	7.66333	45-49

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGTCTTC	218285	0.0	7.4890714	50-54
TCGTATG	233895	0.0	7.1642475	40-44
CTTCTGC	238895	0.0	7.0274754	50-54
TCTCGTA	231875	0.0	6.798325	40-44
GTCTTCT	255450	0.0	6.5595574	50-54
GTATGCC	259715	0.0	6.5218153	45-49
ATCTCGT	247680	0.0	6.3528013	40-44
CCGTCTT	265145	0.0	6.3153334	50-54

Produced by FastQC (version 0.11.2)