Report

Wed 28 Dec 2022 K7-DMS-NEB_S3_L001_R1_001.fastq.gz

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

Basic Statistics

Measure Value

Filename K7-DMS-NEB_S3_L001_R1_001.fastq.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

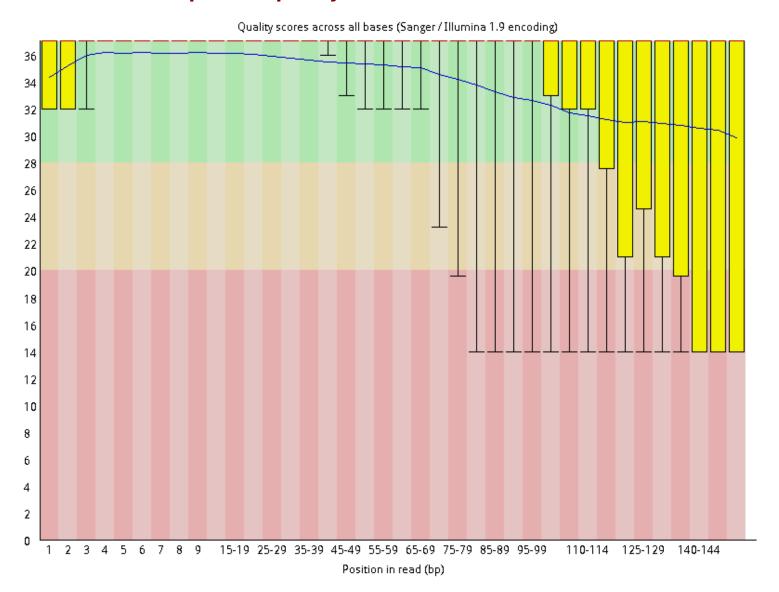
Total Sequences 2232898

Sequences flagged as poor quality 0

Sequence length 151

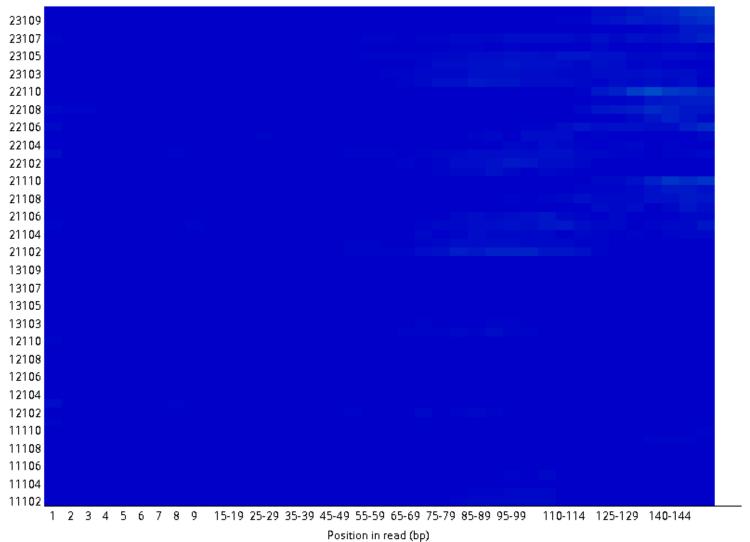
%GC 43

Per base sequence quality



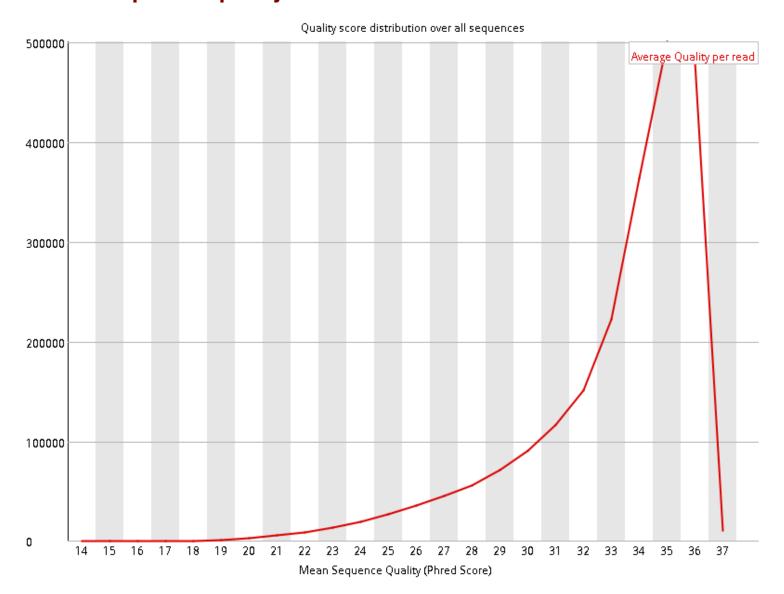
Per tile sequence quality



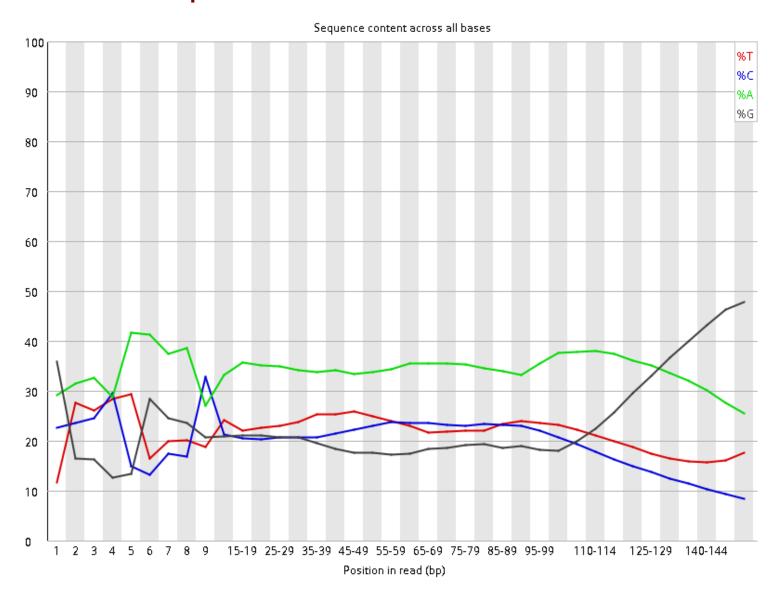


file:///Users/herber4/Desktop/SF3B1/DMS_Seq/mutliqc/K7-DMS-NEB_S3_L001_R1_001_fastqc.html

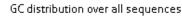
Per sequence quality scores

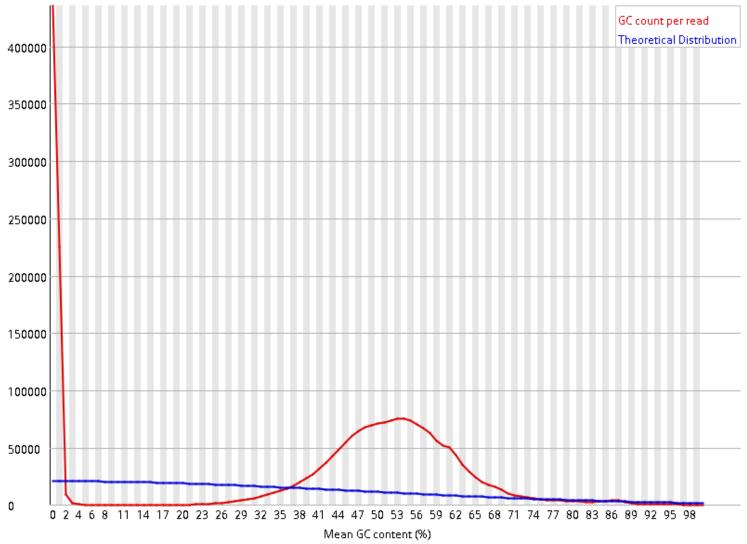


Per base sequence content

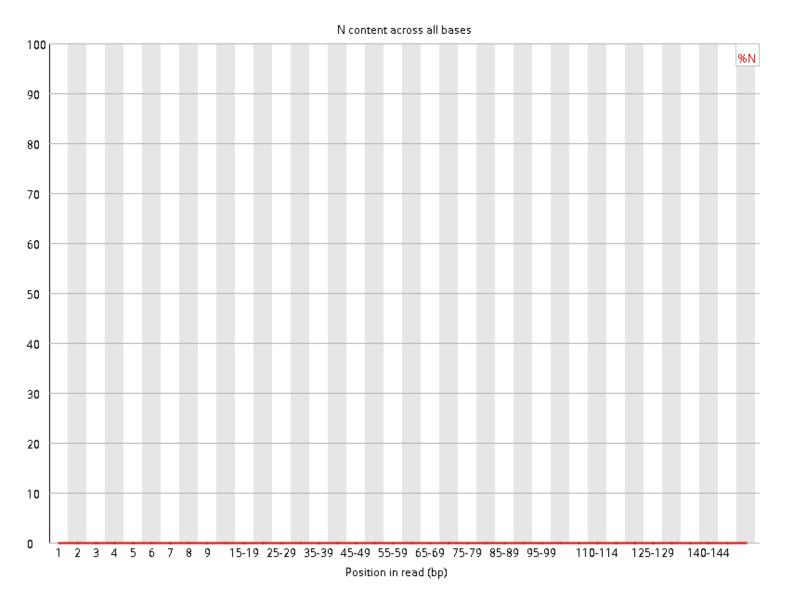


Per sequence GC content

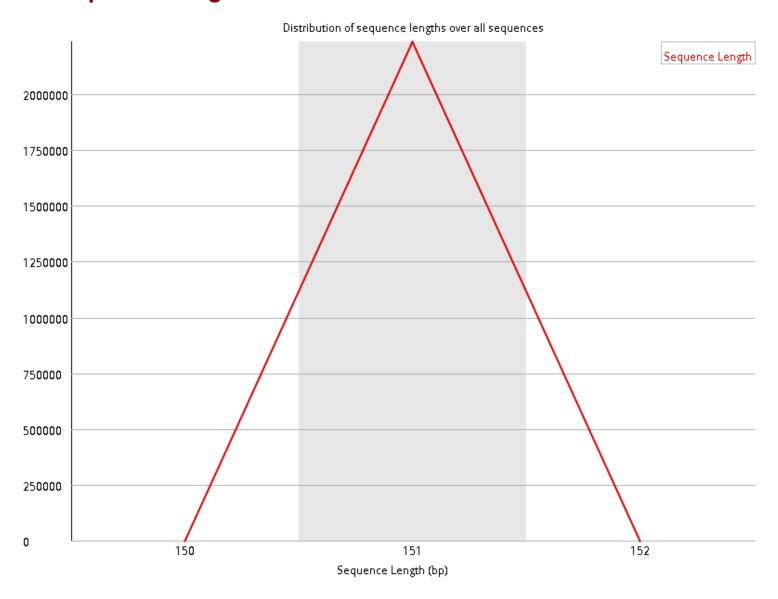




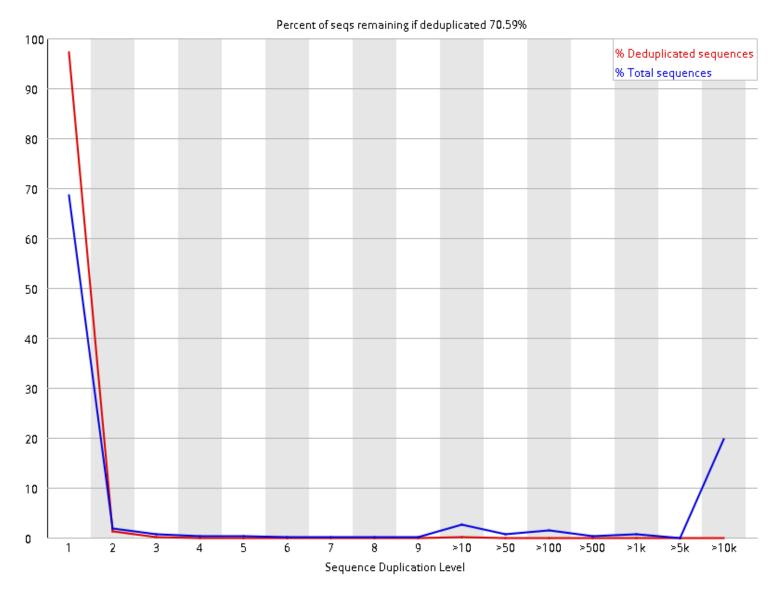
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

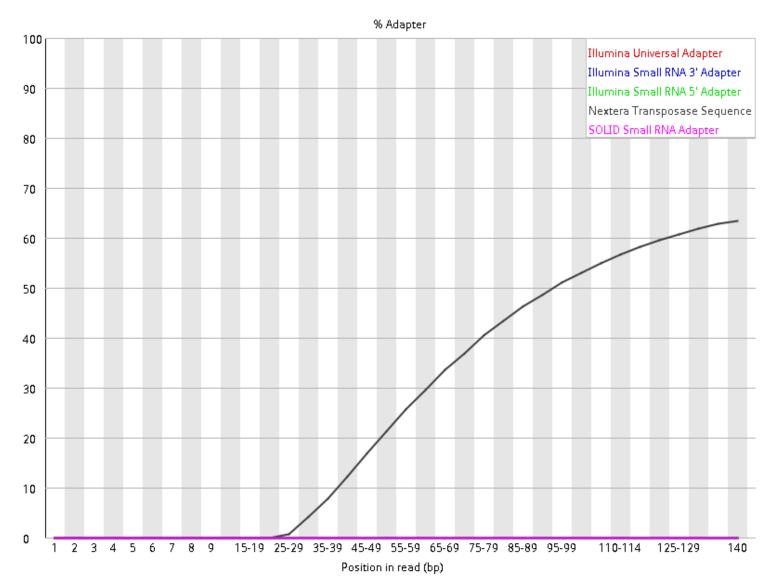


Overrepresented sequences

	Sequence	Count	Percentage	Possible Source
АААААААААА	АААААААААААААААААААААА	348787	15.620373165276694	No Hit
TTTTTTTTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	93721	4.197280843101655	No Hit
CTTATACACAT	CTCCGAGCCCACGAGACTAAGGCGAATCTCGTATGCCGT	11167	0.500112409971257	No Hit
TCTCCGAGCCC	ACGAGACTAAGGCGAATCTCGTATGCCGTCTTCTGCTTG	2948	0.1320257351656905	RNA PCR Primer, Index 46

Sequence	Count	Percentage	Possible Source
			(96% over 28bp)
ATACACATCTCCGAGCCCACGAGACTAAGGCGAATCTCGTATGCCGTCTT	2898	0.1297864927103701	RNA PCR Primer, Index 46 (95% over 21bp)
GTAGTGCGCTATGCCGATCGGGTGTCCGCACTAAGTTCGGCATCAATATG	2298	0.10291558324652537	No Hit

Adapter Content



Produced by FastQC (version 0.11.9)