FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per tile sequence quality
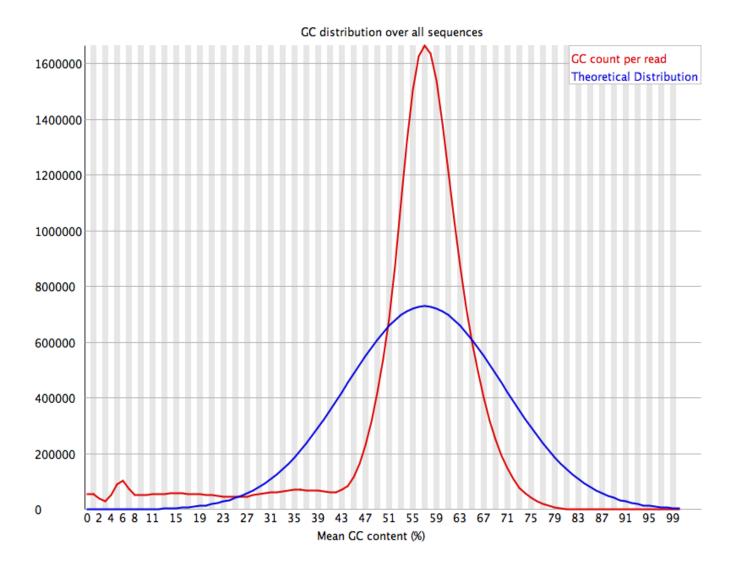
✅ Per sequence quality scores
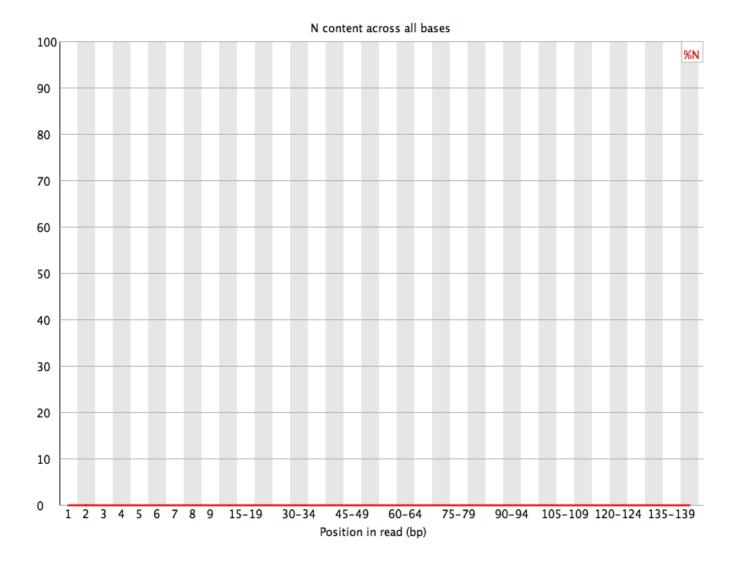
⚠️ Per base sequence content

❌ Per sequence GC content
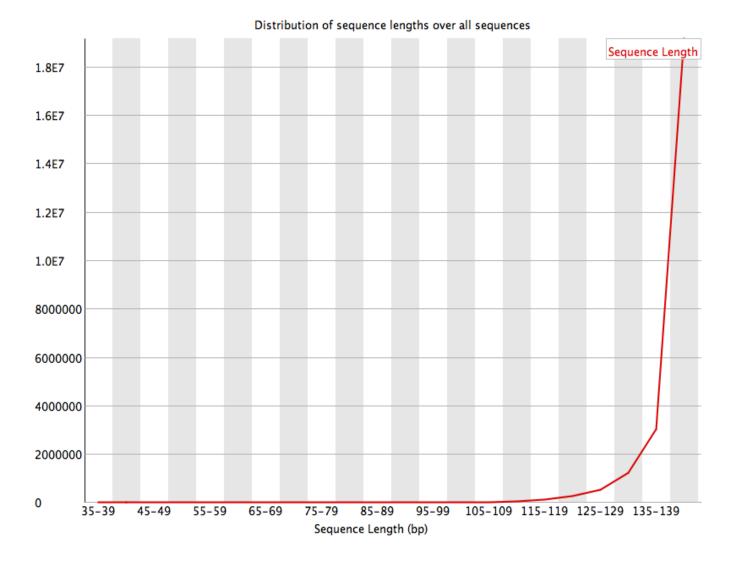
✅ Per base N content
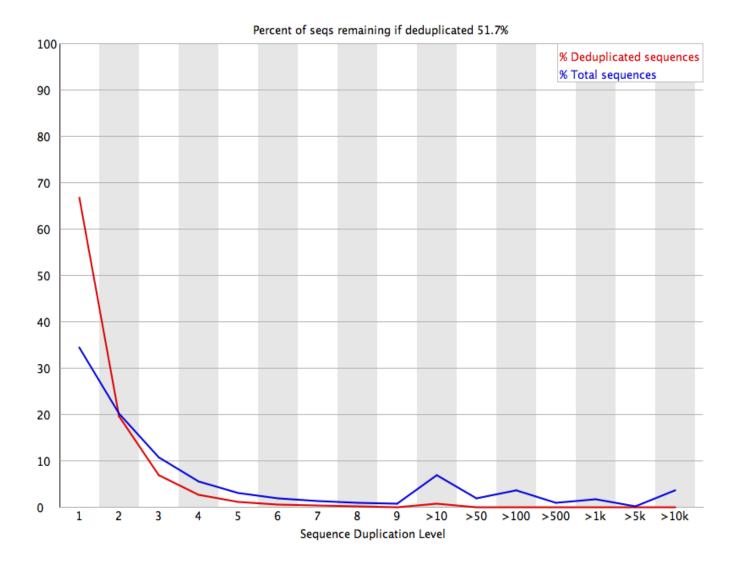
⚠️ Sequence Length Distribution
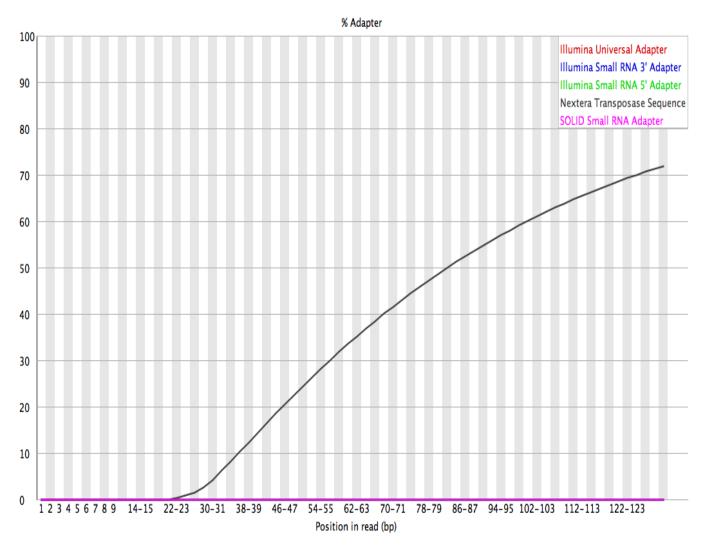
⚠️ Sequence Duplication Levels

❌ Overrepresented sequences

❌ Adapter Content

❌ Kmer Content

✅ Basic Statistics

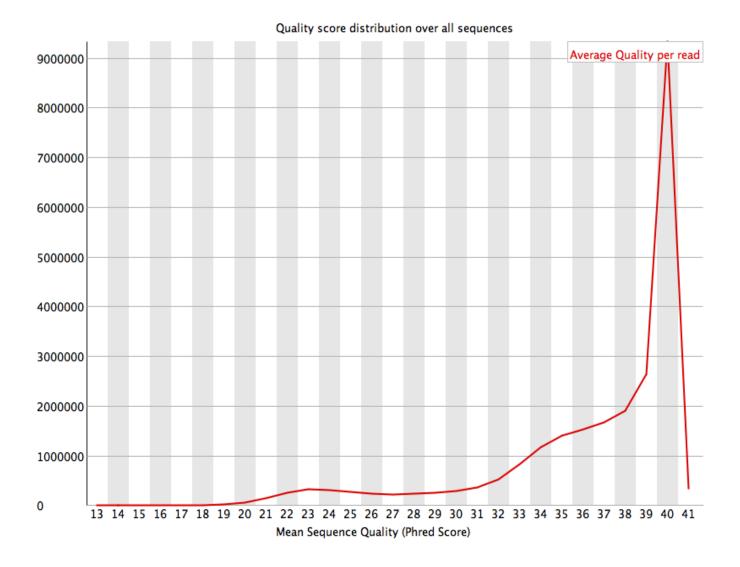| Measure	Value
Filename	Sample10_forward_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	24435292
Sequences flagged as poor quality	0
Sequence length	38-143
%GC	50

✅ Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

✅ Per tile sequence quality

Quality per tile

✅ **Per sequence quality scores**

Quality score distribution over all sequences

⚠️Per base sequence content

Sequence content across all bases

❌ **Per sequence GC content**

GC distribution over all sequences

✅ Per base N content

N content across all bases

⚠️ Sequence Length Distribution

Distribution of sequence lengths over all sequences

⚠️ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 51.7%

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	264997	1.0844846871484082	No Hit
CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	174961	0.71601763547577	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	146095	0.5978852227343958	No Hit
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	122092	0.4996543524014364	No Hit
TACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	87525	0.3581909313790889	No Hit
AGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	30709	0.12567478219617756	No Hit
CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	28782	0.11778864766584332	No Hit

❌ Adapter Content

❌ Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGCAGAG	94765	0.0	84.21058	1
GCAGAGT	183170	0.0	73.09822	1
CAGAGTA	241255	0.0	55.496395	2
AGAGTAC	252935	0.0	52.859203	3
GAGTACT	114575	0.0	52.367348	4
AGTACTT	120330	0.0	49.969234	5
GTACTTT	120505	0.0	49.829662	6
AGTACGG	149555	0.0	49.22993	5
GTACGGG	149505	0.0	49.124874	6
TACGGGG	109935	0.0	48.83014	7
GAGTACG	151405	0.0	48.61931	4
TACGGGT	19525	0.0	42.836105	7
ACGGGGG	54035	0.0	42.11418	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACTTTT	144490	0.0	41.543743	7
ACGGGGT	30810	0.0	41.363586	8
TACGGGA	18690	0.0	41.149715	7
ACTTTTT	150715	0.0	39.881435	8
ACGGGGA	32065	0.0	39.76563	8
ACGGGTA	7090	0.0	32.3622	8
ACGCAGA	19775	0.0	31.270203	2

Produced by [FastQC](#) (version 0.11.5)