FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

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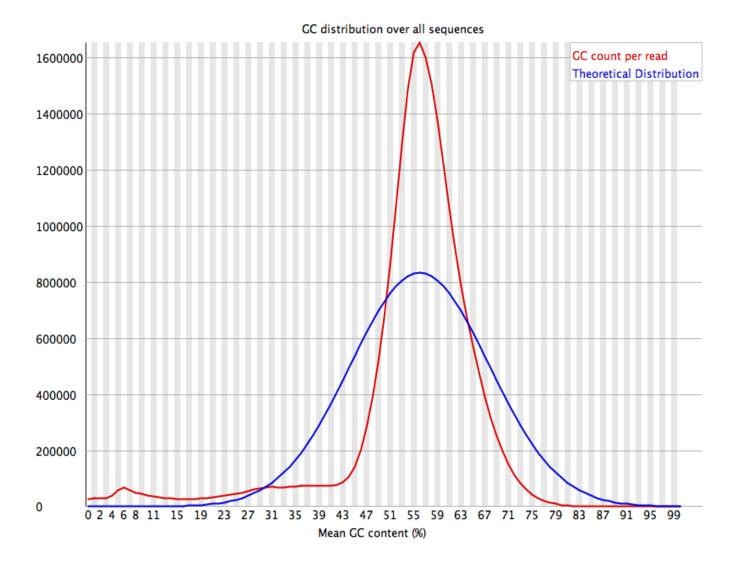
✅ Per sequence quality scores
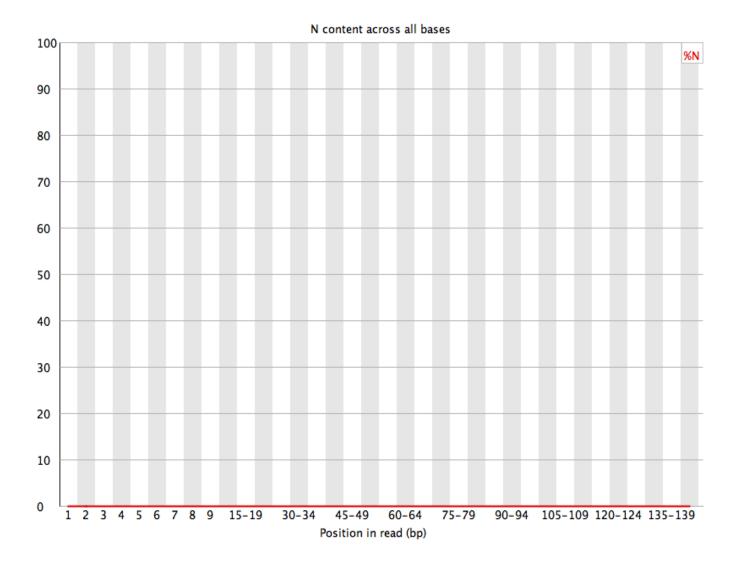
⚠️ Per base sequence content

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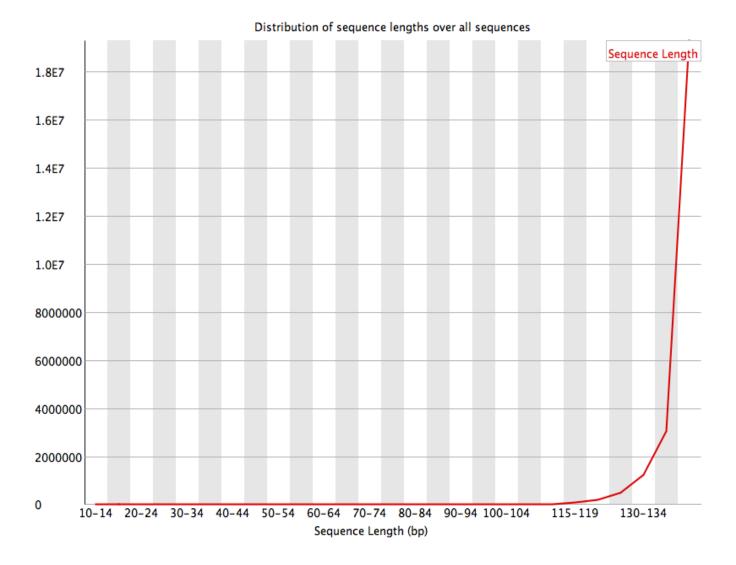
✅ Per base N content
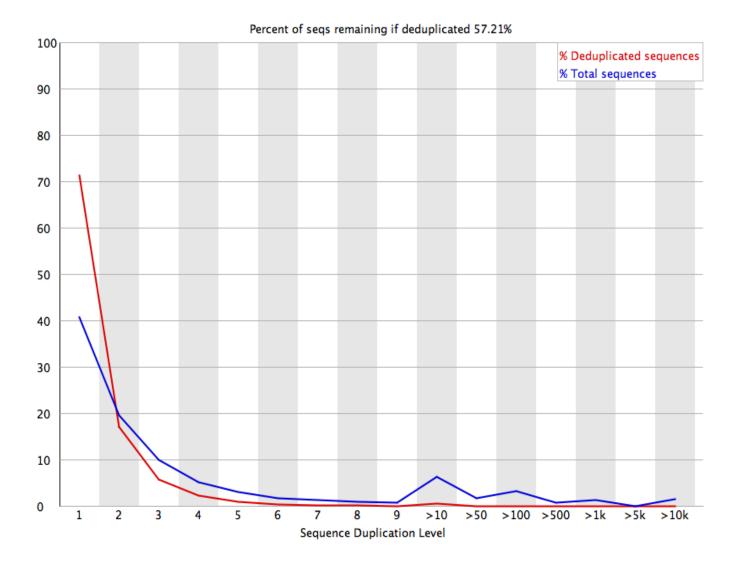
⚠️ Sequence Length Distribution
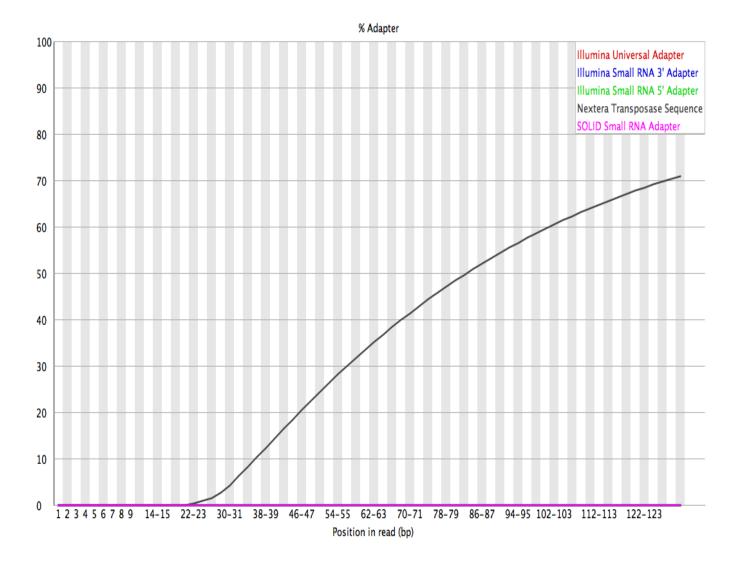
⚠️ Sequence Duplication Levels

⚠️ Overrepresented sequences

❌ Adapter Content

❌ Kmer Content

✅ Basic Statistics

Measure	Value
Filename	Sample10_reverse_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	24435292
Sequences flagged as poor quality	0
Sequence length	12-143
%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 57.21%

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	113568	0.46477038211779914	No Hit
CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	76143	0.3116107636446497	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	59629	0.24402818677182167	No Hit
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	49745	0.20357849621768384	No Hit
TACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	40365	0.16519139611673148	No Hit

Adapter Content

❌ Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	134725	0.0	68.39007	1
CGCAGAG	87860	0.0	66.12349	1
CAGAGTA	173710	0.0	53.301556	2
AGAGTAC	182405	0.0	50.631775	3
AGTACGG	148655	0.0	48.78331	5
GTACGGG	147950	0.0	48.758835	6
TACGGGG	109590	0.0	48.398483	7
GAGTACG	151155	0.0	48.017242	4
GAGTACT	42960	0.0	45.470592	4
GTACTTT	44980	0.0	43.108906	6
ACGGGGG	54420	0.0	42.324757	8
ACGGGGT	31480	0.0	41.394596	8
TACGGGT	19300	0.0	41.21226	7

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGTACTT	47255	0.0	41.14169	5
TACGGGA	18680	0.0	40.814953	7
TACTTTT	48495	0.0	39.949463	7
ACTTTTT	50530	0.0	38.35	8
ACGGGGA	32990	0.0	36.439476	8
TAATCCG	2240	0.0	31.84831	9
CGGGGGA	23390	0.0	30.788042	9

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