FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per tile sequence quality
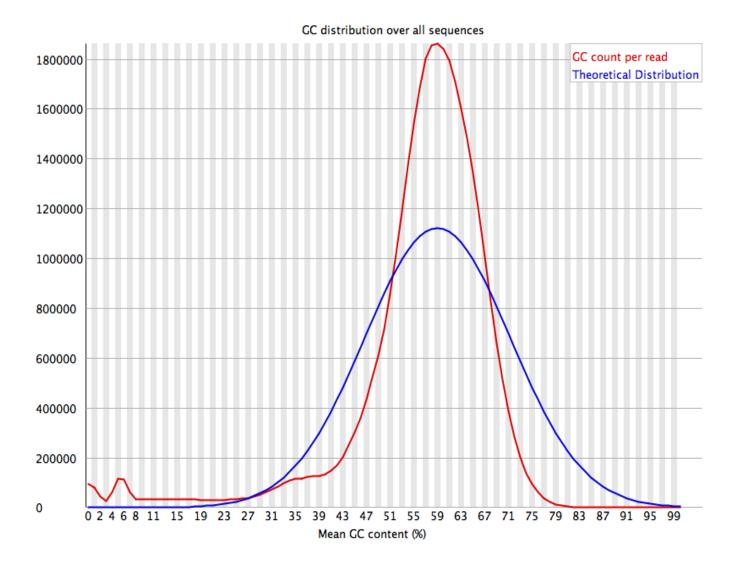
✅ Per sequence quality scores

⚠️ Per base sequence content

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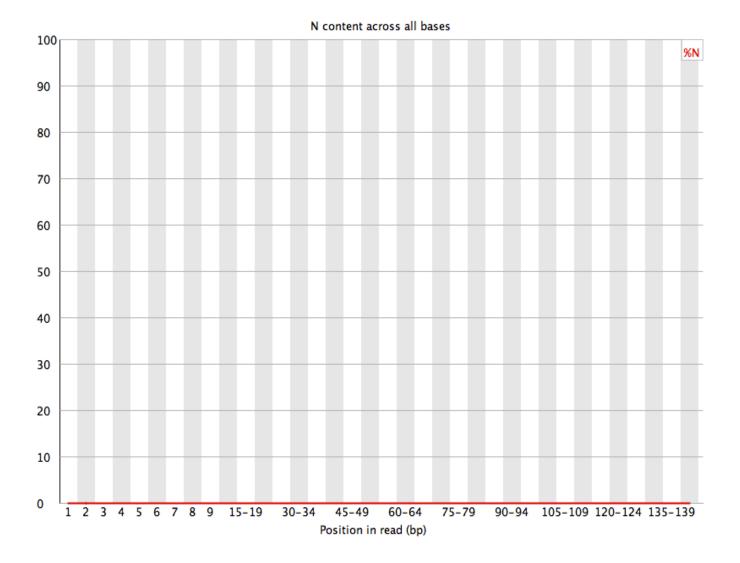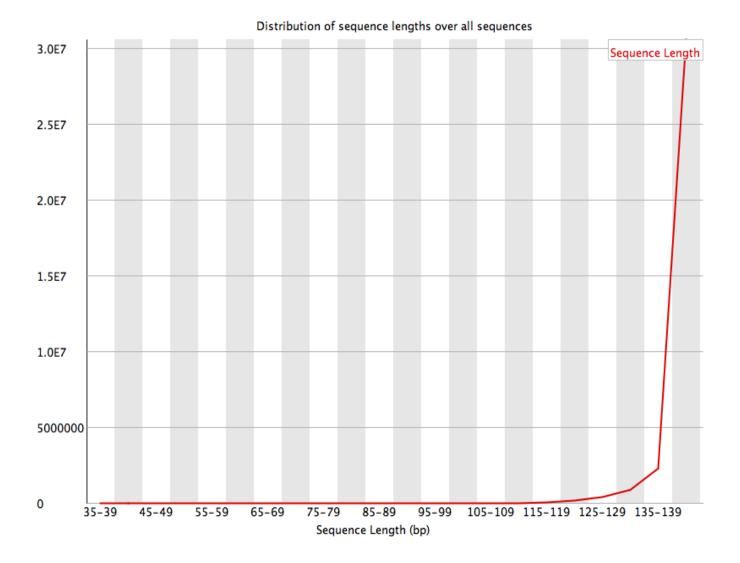
✅ Per base N content
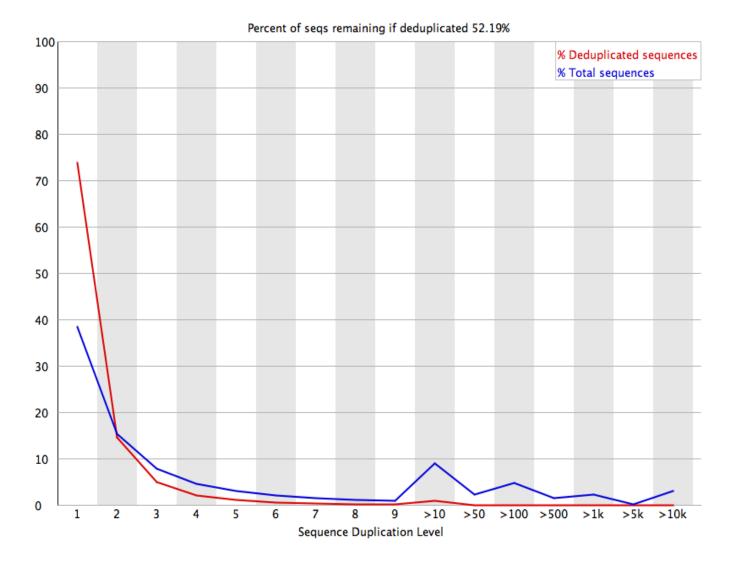
⚠️ Sequence Length Distribution

⚠️ Sequence Duplication Levels

⚠️ Overrepresented sequences

❌ Adapter Content

❌ Kmer Content

✅ Basic Statistics

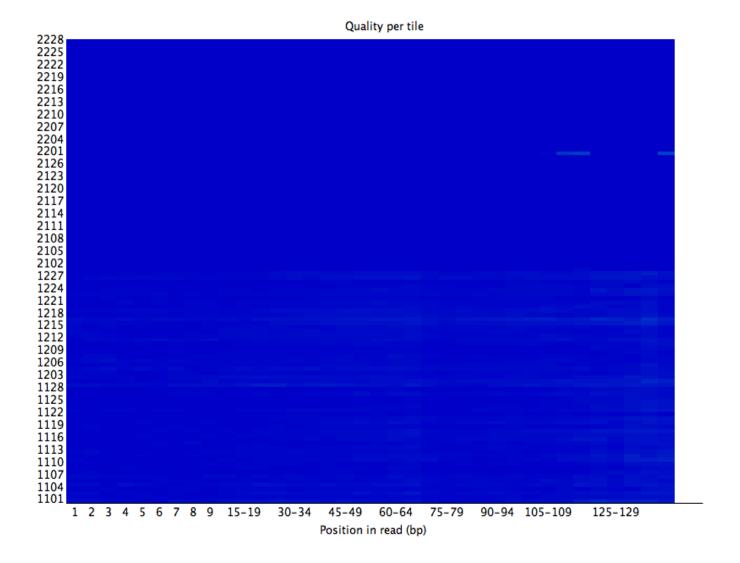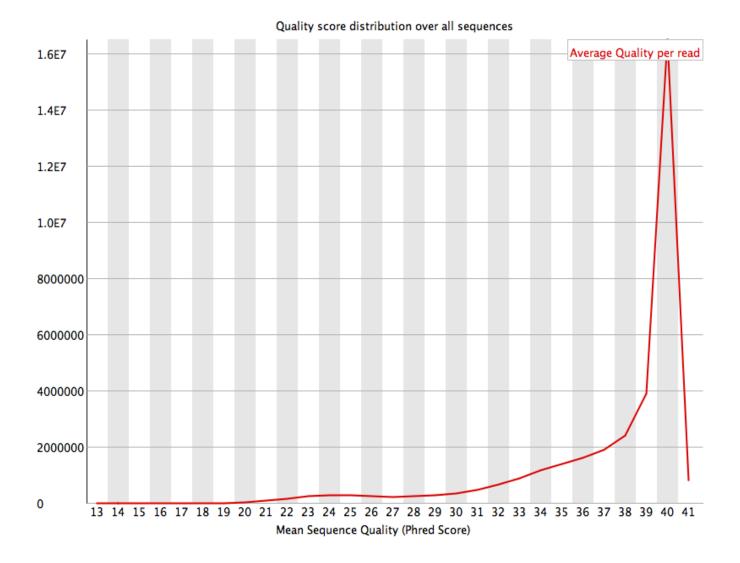| Measure	Value
Filename	Sample1_forward_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	34626514
Sequences flagged as poor quality	0
Sequence length	39-143
%GC	54

✅ Per base sequence quality

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

✅ **Per tile sequence quality**

Quality per tile

Position in read (bp)

✅ **Per sequence quality scores**

Quality score distribution over all sequences

⚠️ Per base sequence content

❌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 52.19%

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	220525	0.6368674594271893	No Hit
CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	163918	0.47338868706217435	No Hit
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	146678	0.4236002503746118	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	106186	0.3066609592868632	No Hit
CATCTCCGAGCCCACGAGACTAAGGCGAATCTCGTATGCCGTCTTCTGCT	90310	0.2608117005367621	RNA PCR Primer, Index 46 (96% over 26bp)
TACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	61229	0.17682692517069434	No Hit

Sequence	Count	Percentage	Possible Source
CCCACGAGACTAAGGCGAATCTCGTATGCCGTCTTCTGCTTGAAAAAAAA	60576	0.17494108705254013	TruSeq Adapter, Index 18 (96% over 27bp)
CTCCGAGCCCACGAGACTAAGGCGAATCTCGTATGCCGTCTTCTGCTTGA	57125	0.1649747358339335	RNA PCR Primer, Index 46 (96% over 28bp)
CCGAGCCCACGAGACTAAGGCGAATCTCGTATGCCGTCTTCTGCTTGAAA	48231	0.13928921635022226	RNA PCR Primer, Index 46 (96% over 28bp)

❌ Adapter Content

❌ Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	119135	0.0	65.26051	1
CAGAGTA	141415	0.0	54.835175	2
AGAGTAC	149505	0.0	51.827045	3
GTACTTT	89570	0.0	49.846554	6
AGTACTT	96055	0.0	46.474186	5
GAGTACT	96950	0.0	46.066135	4
CGCAGAG	92175	0.0	44.296318	1
TACTTTT	100995	0.0	44.153473	7
GTACGGG	75455	0.0	43.38316	6
AGTACGG	78225	0.0	41.872936	5
ACTTTTT	108435	0.0	41.34909	8
GAGTACG	80880	0.0	40.62414	4
TACGGGG	48520	0.0	40.20277	7

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACGGGT	11415	0.0	32.846275	7
TACGGGA	14550	0.0	32.386105	7
TACGGGC	16905	0.0	29.679287	7
ACGGGGG	37195	0.0	25.574669	8
CTTTTTT	213730	0.0	20.981728	9
ACTAGGT	2965	0.0	18.979961	4
ACGGGGT	18570	0.0	18.109509	8

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