FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per tile sequence quality
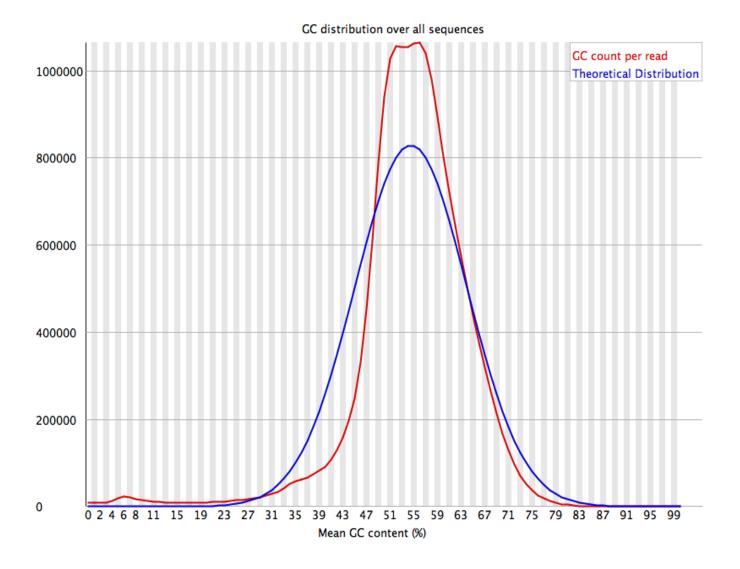
✅ Per sequence quality scores

⚠️ Per base sequence content

⚠️ Per sequence GC content

✅ Per base N content
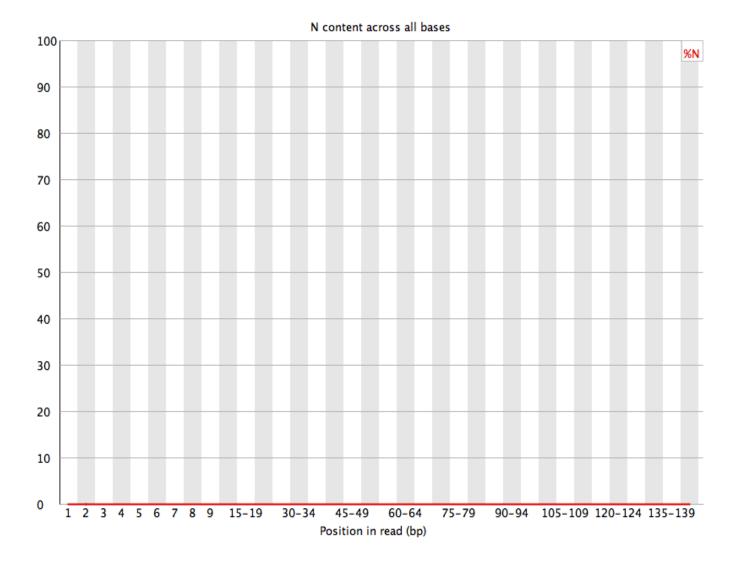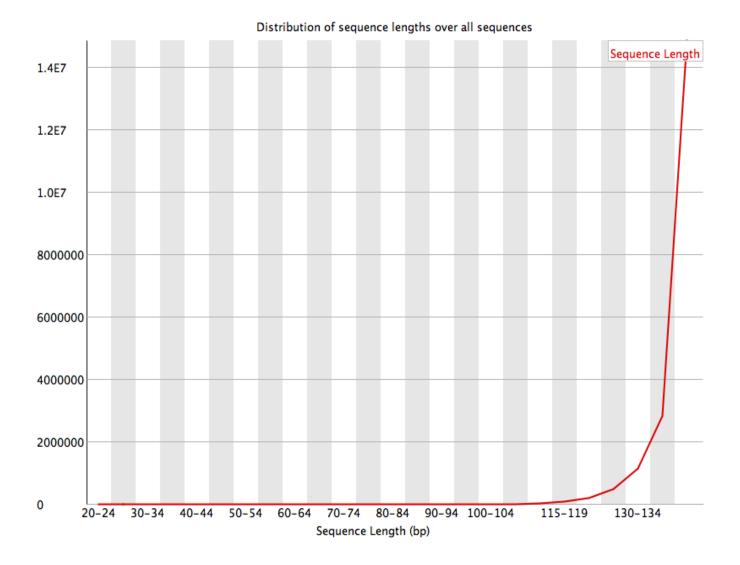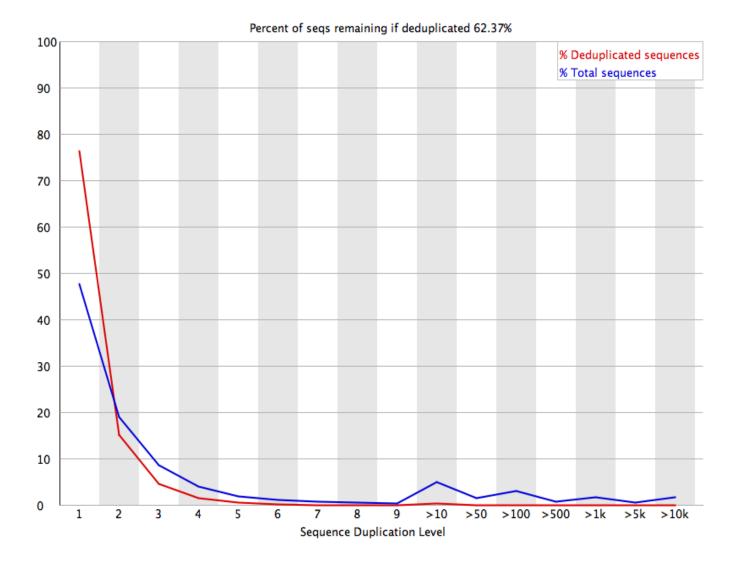
⚠️ Sequence Length Distribution
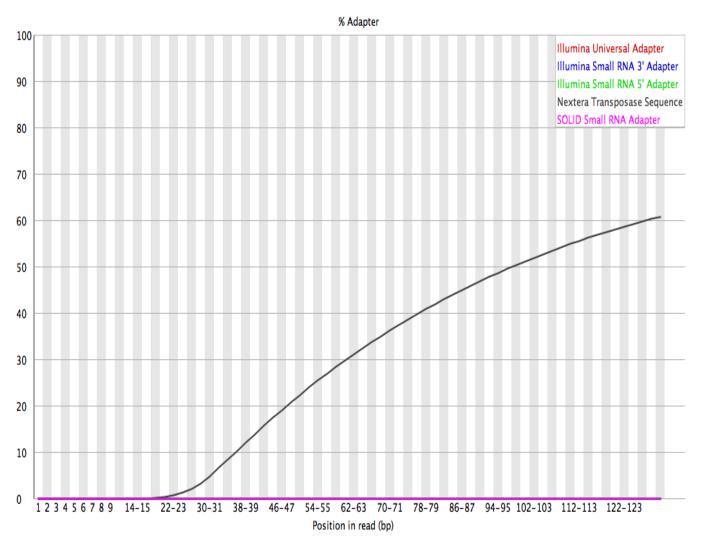
⚠️ Sequence Duplication Levels

⚠️ Overrepresented sequences

❌ Adapter Content

❌ Kmer Content

✅ Basic Statistics

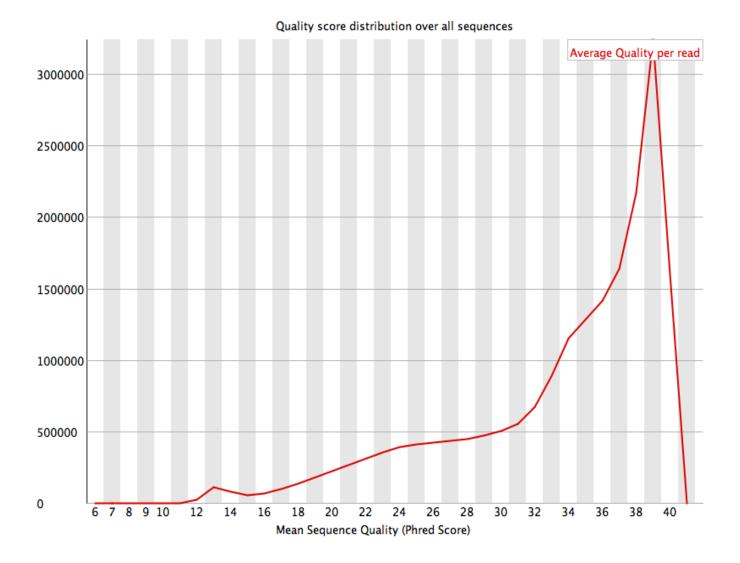| Measure	Value
Filename	Sample8_reverse_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	19702055
Sequences flagged as poor quality	0
Sequence length	22-143
%GC	51

✅ 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**

Sequence Length Distribution

Distribution of sequence lengths over all sequences

⚠️ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 62.37%

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	62482	0.317134430900736	No Hit
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	43591	0.22125103193550116	No Hit
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	40075	0.20340517778475392	No Hit
GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	38187	0.19382242106216838	No Hit
CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	27619	0.1401833463565095	No Hit
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	24060	0.12211924086091526	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	19843	0.1007153822278945	No Hit

Adapter Content

Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	45465	0.0	62.317608	1
CAGAGTA	55715	0.0	50.92526	2
CGCAGAG	37205	0.0	48.395416	1
AGAGTAC	59190	0.0	47.81097	3
GTACGGG	46735	0.0	45.953968	6
TACGGGG	33250	0.0	45.293617	7
AGTACGG	48210	0.0	44.696037	5
GAGTACG	49095	0.0	44.06546	4
GTACTTT	16770	0.0	39.675514	6
GAGTACT	17585	0.0	37.906628	4
TACGGGA	6960	0.0	37.87875	7
AGTACTT	17640	0.0	37.37235	5
ACGGGGG	21950	0.0	34.909634	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACTTTT	19080	0.0	34.807205	7
TACGGGT	5475	0.0	33.694645	7
ACTTTTT	23100	0.0	29.337505	8
TACGGGC	7545	0.0	27.828989	7
ACGGGGA	13610	0.0	26.425331	8
ACGGGGT	9215	0.0	26.067623	8
CTTGTTA	2880	0.0	17.92914	1

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