FastQC Report

Summary

✅ Basic Statistics

⚠️ Per base sequence quality

✅ Per tile sequence quality

✅ Per sequence quality scores
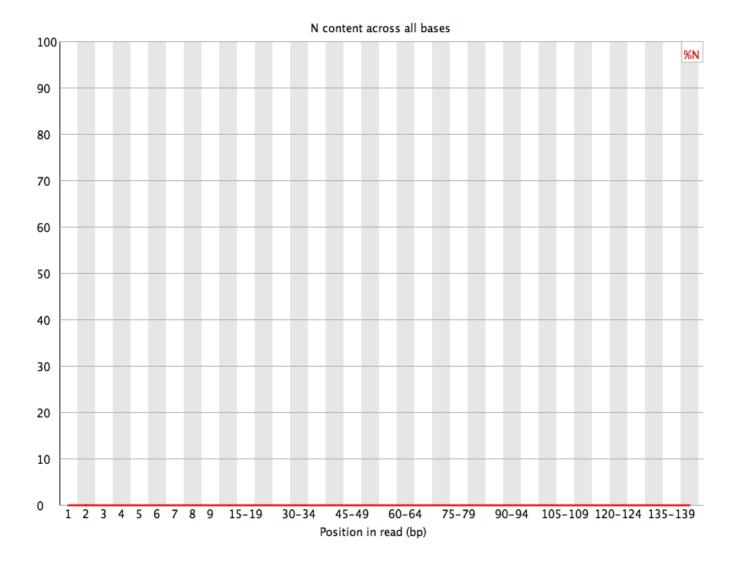
⚠️ Per base sequence content

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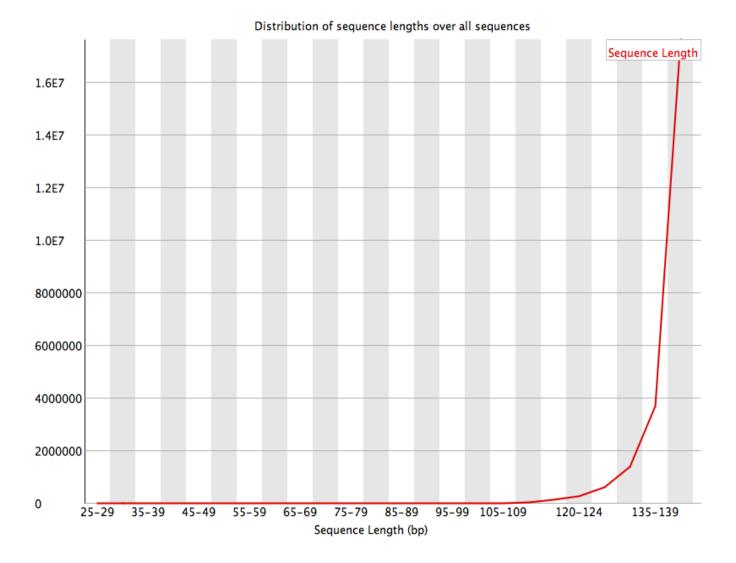
✅ Per base N content
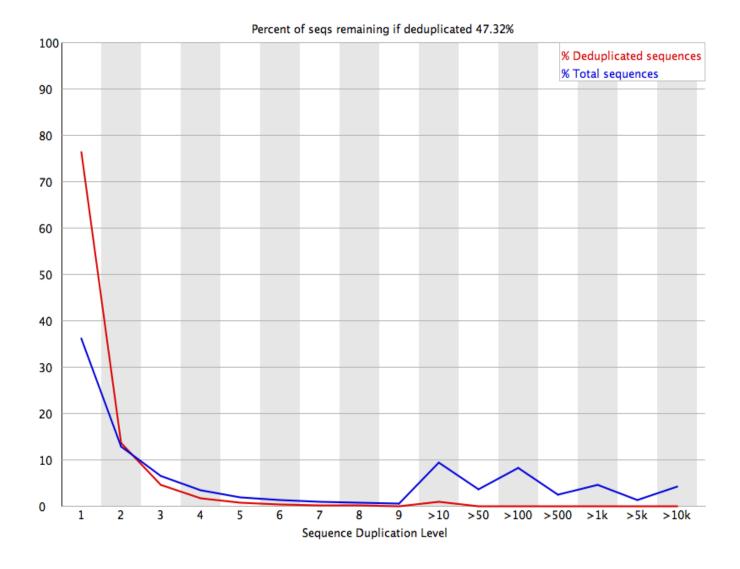
⚠️ Sequence Length Distribution
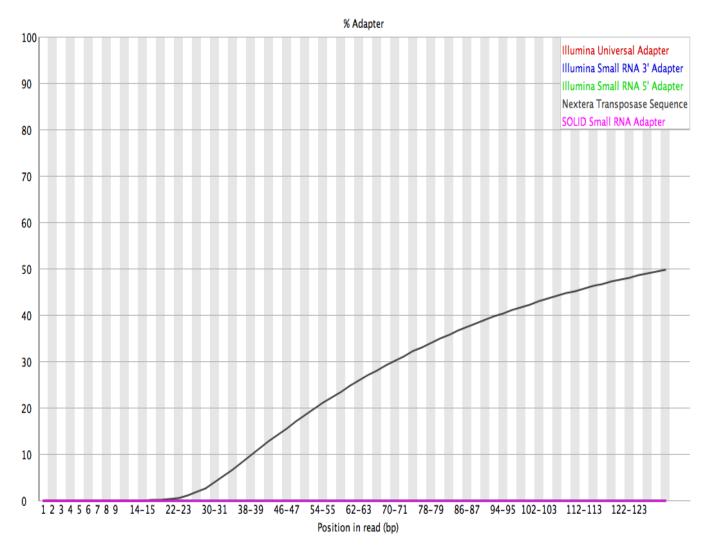
❌ Sequence Duplication Levels

❌ Overrepresented sequences

❌ Adapter Content

❌ Kmer Content

✅ Basic Statistics

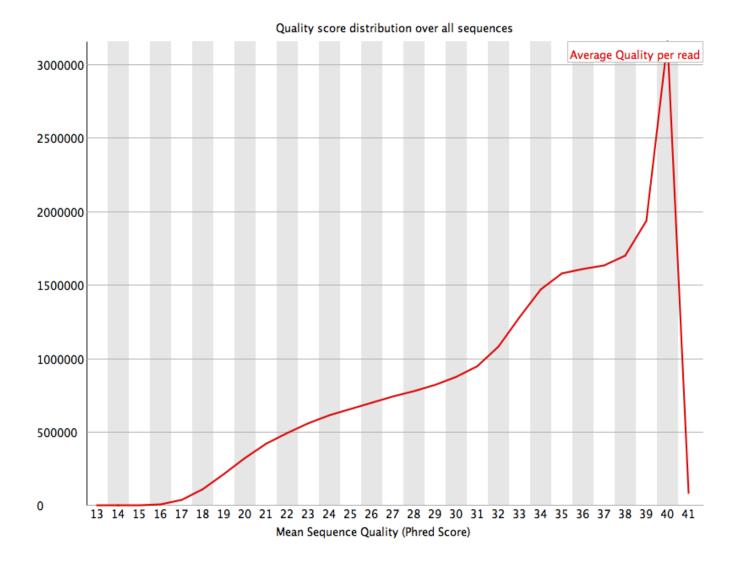| Measure	Value
Filename	Sample11_forward_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23865512
Sequences flagged as poor quality	0
Sequence length	28-143
%GC	49

⚠️ Per base sequence quality

✅ **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 47.32%

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	244342	1.023828862334904	No Hit
TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	121829	0.5104814009437552	No Hit
ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAAC	117969	0.49430743409150407	No Hit
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	106729	0.4472101834647419	No Hit
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	103481	0.4336005864864747	No Hit
GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	38491	0.16128294251554293	No Hit
AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAA	35742	0.1497642288168802	No Hit
CAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA	26081	0.10928322007087046	No Hit

Adapter Content

Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	31215	0.0	63.14486	1
CAGAGTA	39115	0.0	50.30605	2
GAGTACG	34995	0.0	45.62235	4
AGTACTT	8130	0.0	45.32446	5
AGAGTAC	43525	0.0	45.23977	3
AGTACGG	35695	0.0	44.69022	5
GTACGGG	35515	0.0	44.652615	6
GAGTACT	8240	0.0	44.637997	4
TACGGGG	16340	0.0	43.995304	7
TACGGGC	7830	0.0	43.89492	7
GTACTTT	8475	0.0	43.321285	6
ACGGGTC	5695	0.0	41.292583	8
TACGGGT	9145	0.0	39.854176	7

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACGGGA	4150	0.0	38.42267	7
ACGGGGA	11450	0.0	37.097313	8
CGGGTCT	5595	0.0	36.522556	9
TACTTTT	11240	0.0	32.545055	7
ACTTTTT	12200	0.0	29.984133	8
ACGGGGG	5255	0.0	28.940886	7
ACGGGGT	3435	0.0	28.671425	8

Produced by FastQC (version 0.11.5)