℮FastQC Report

Summary

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❌ [Per base sequence quality](#)

✅ [Per tile sequence quality](#)
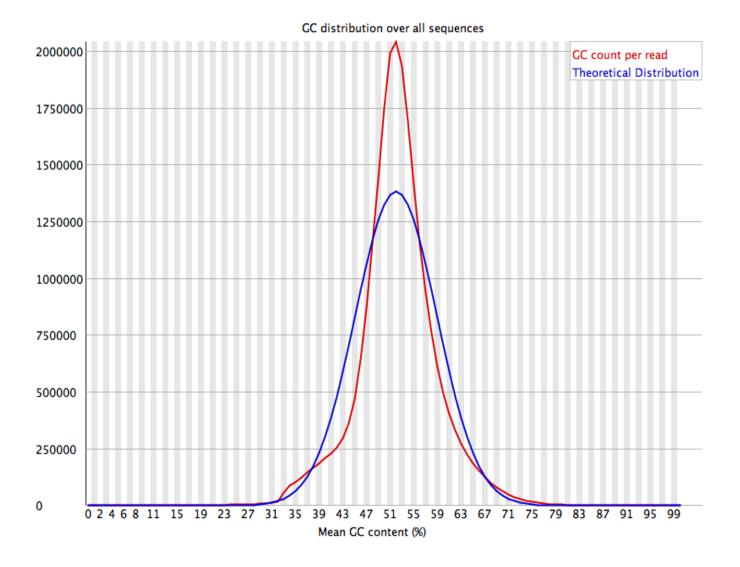
✅ [Per sequence quality scores](#)

⚠️ [Per base sequence content](#)

⚠️ [Per sequence GC content](#)

✅ [Per base N content](#)
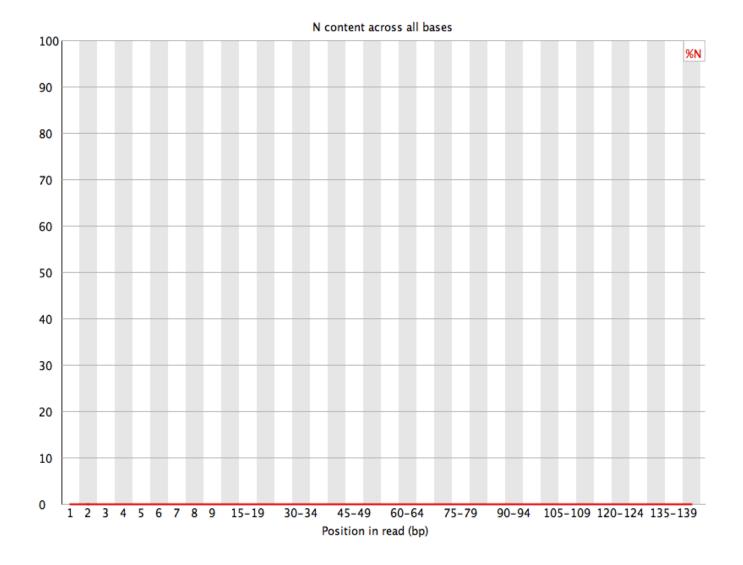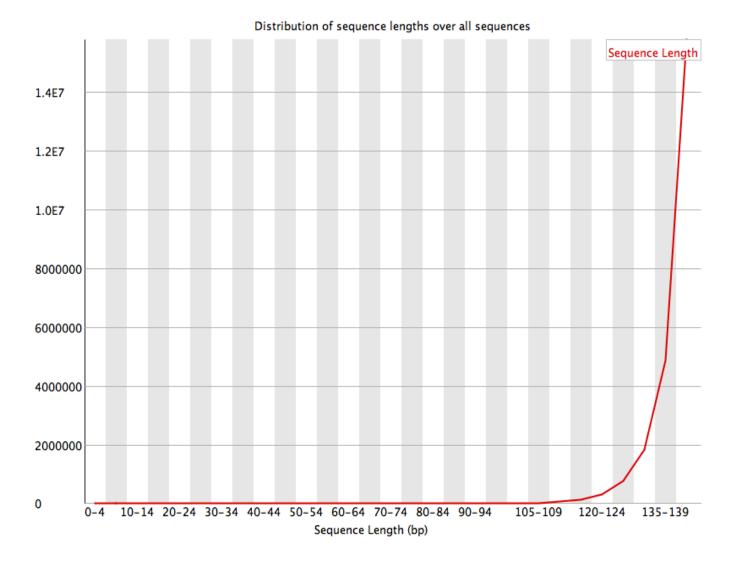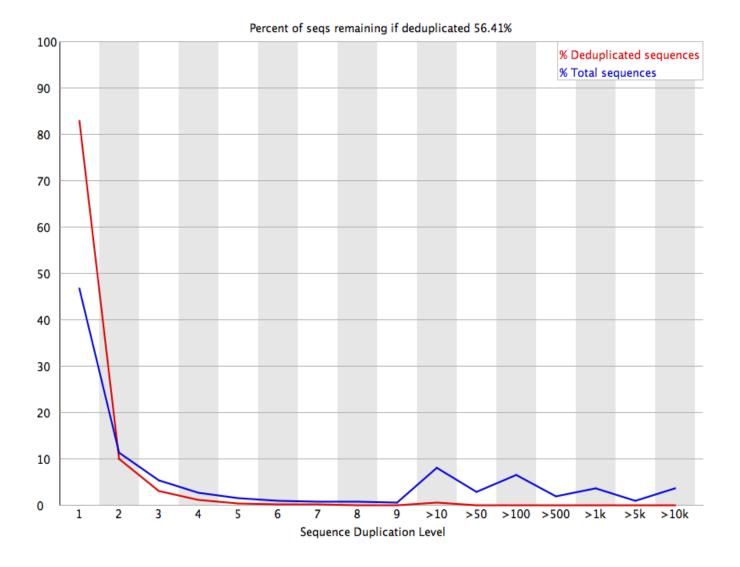
⚠️ [Sequence Length Distribution](#)
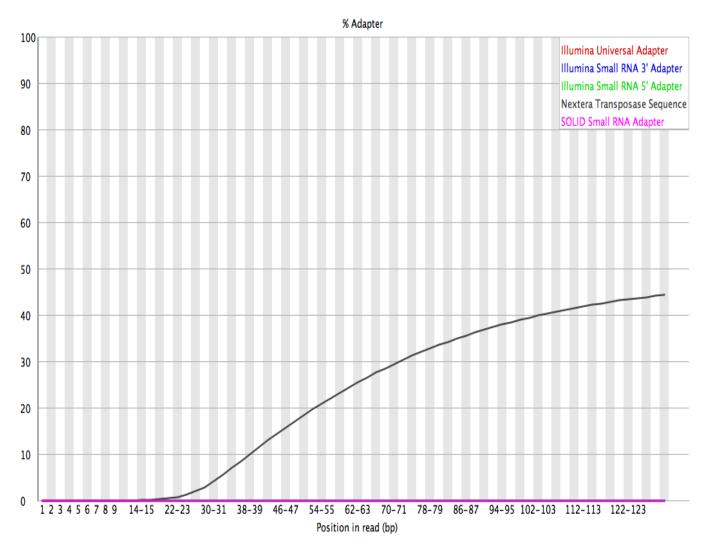
⚠️ [Sequence Duplication Levels](#)

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✅ Basic Statistics

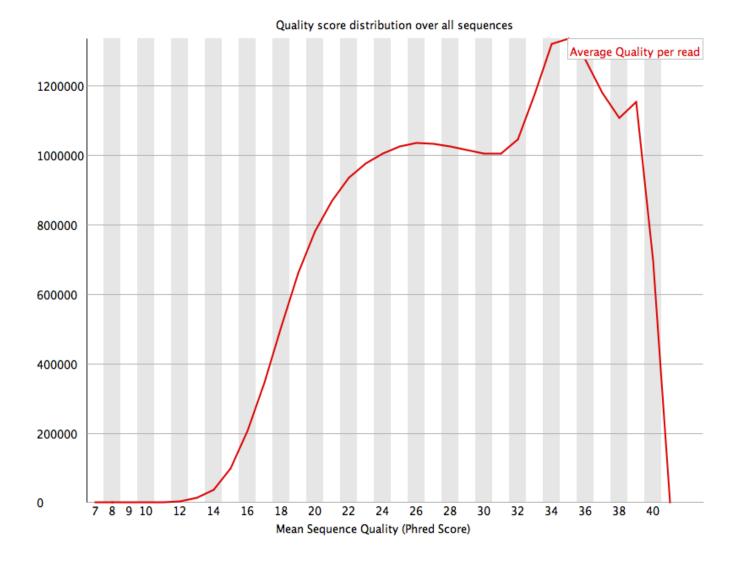| Measure	Value
Filename	Sample11_reverse_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23865512
Sequences flagged as poor quality	0
Sequence length	4-143
%GC	50

❌ 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

✅Per base N content

⚠️ Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Duplication Levels

Percent of seqs remaining if deduplicated 56.41%

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	187310	0.784856407019468	No Hit
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	131370	0.5504595920674151	No Hit
TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	127862	0.53576055690739	No Hit
ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAAC	100934	0.4229282824521008	No Hit
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	79011	0.33106769299565	No Hit
GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	41548	0.17409222144490344	No Hit
AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAA	30805	0.12907747380403992	No Hit
TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	24566	0.10293514758870456	No Hit

Adapter Content

Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	27210	0.0	56.40918	1
CAGAGTA	32015	0.0	47.839363	2
GAGTACG	32295	0.0	44.724667	4
TACGGGG	14355	0.0	43.94531	7
AGTACGG	33500	0.0	43.35736	5
GTACGGG	33235	0.0	43.247635	6
AGAGTAC	35325	0.0	43.225063	3
TACGGGC	7410	0.0	41.802334	7
ACGGGTC	5945	0.0	39.78536	8
TACGGGA	3615	0.0	38.14414	7
TACGGGT	9700	0.0	37.221455	7
ACGGGGA	9430	0.0	36.386673	8
ACGGGCT	6135	0.0	33.448982	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGGGTCT	6420	0.0	32.790833	9
AGTACTT	2710	0.0	29.980751	5
GAGTACT	2755	0.0	29.247356	4
ACGGGTA	950	0.0	28.053251	8
ACGGGGT	3470	0.0	27.643866	7
GTACTTT	3015	0.0	27.172173	6
ACGGGGC	3425	0.0	23.14905	8

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