ℯFastQC Report

Mon 28 Aug 2017
Sample9_reverse_paired.fq.gz

Summary

✅ Basic Statistics

✅ Per base sequence quality

⚠️ Per tile sequence quality

✅ Per sequence quality scores

⚠️ Per base sequence content

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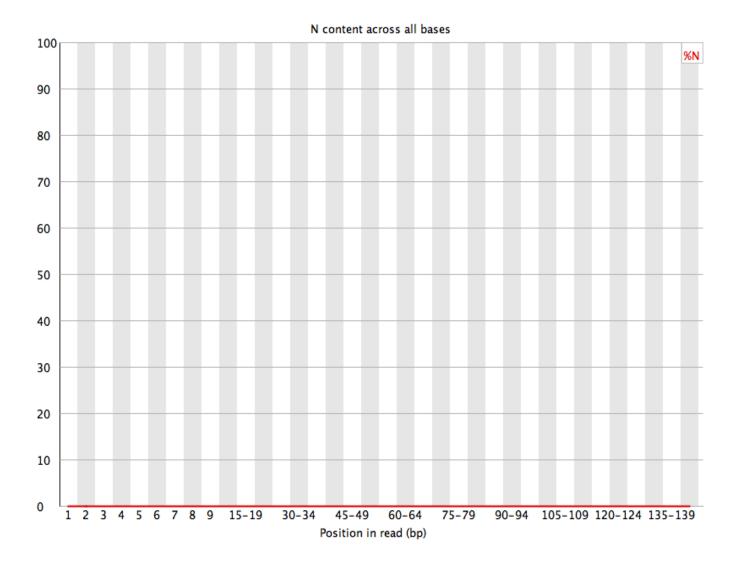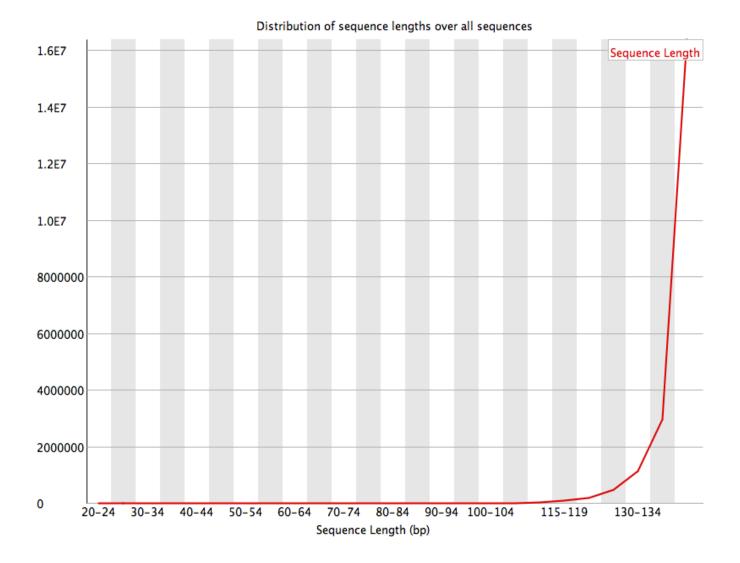
✅ Per base N content
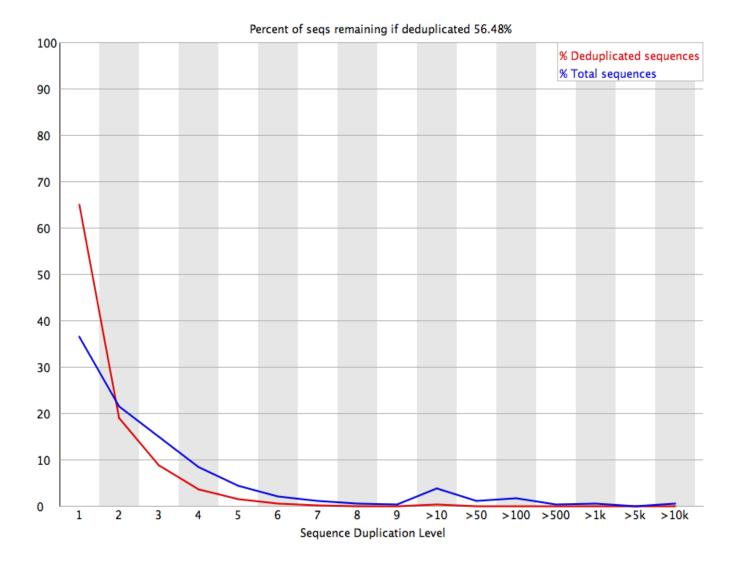
⚠️ Sequence Length Distribution
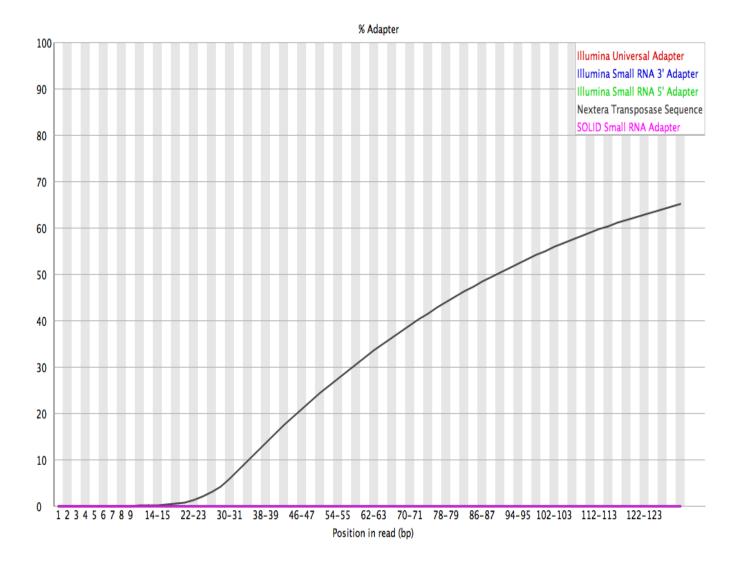
⚠️ Sequence Duplication Levels

⚠️ Overrepresented sequences

❌ Adapter Content

❌ Kmer Content

✅ Basic Statistics

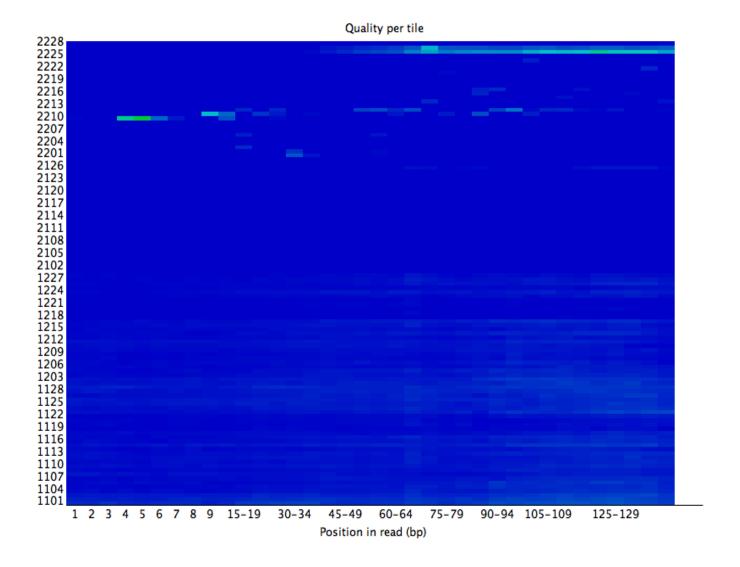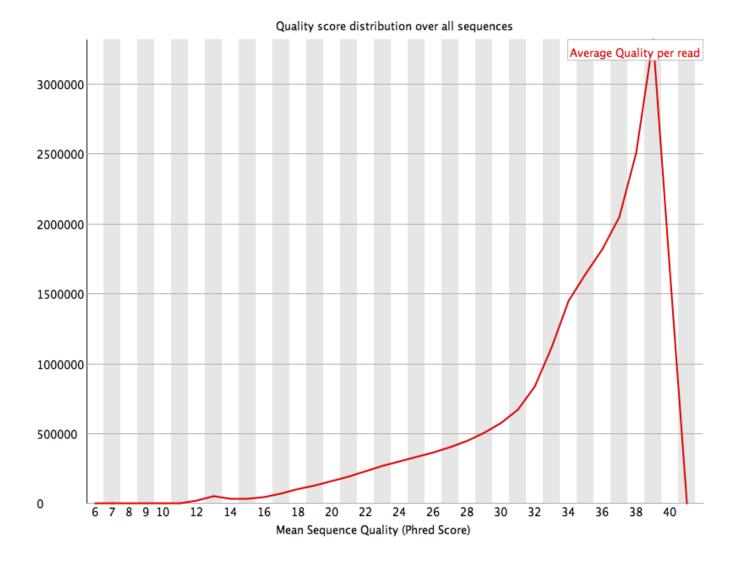| Measure	Value
Filename	Sample9_reverse_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	21369905
Sequences flagged as poor quality	0
Sequence length	21-143
%GC	51

✅ Per base sequence quality

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

⚠️ Per tile sequence quality

Quality per tile

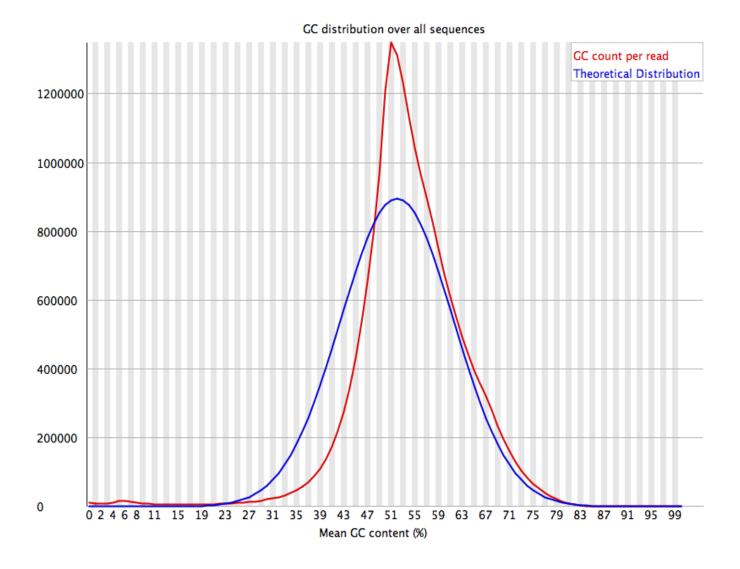✅ **Per sequence quality scores**

⚠️ 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 56.48%

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	48155	0.22534026239236907	No Hit
CACACACACACACACACACACACACACACACACACACACACACACACA	42256	0.19773602175582905	No Hit
GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	21933	0.10263499065625234	No Hit

❌ Adapter Content

Kmer Content

Log2 Obs/Exp

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	56130	0.0	65.91276	1
CAGAGTA	75950	0.0	48.96929	2
AGAGTAC	80030	0.0	46.355587	3
CGCAGAG	54390	0.0	46.00575	1
AGTACGG	74440	0.0	44.41351	5
GAGTACG	74715	0.0	44.371883	4
GTACGGG	74860	0.0	43.927357	6
TACGGGG	31405	0.0	42.61306	7
TACGGGT	19420	0.0	40.766064	7
TACGGGC	20000	0.0	38.341606	7
TACGGGA	10800	0.0	37.677586	7
GTACTTT	10670	0.0	37.375595	6
AGTACTT	12470	0.0	31.869154	5

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACGGGGG	15840	0.0	31.84334	8
GAGTACT	12765	0.0	31.760897	4
TACTTTT	12535	0.0	31.391169	7
ACGGGTG	14685	0.0	31.146341	8
ACTTTTT	12970	0.0	30.863142	8
ACGGGGT	10570	0.0	29.864601	8
ACGGGGA	12010	0.0	25.724604	8

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