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
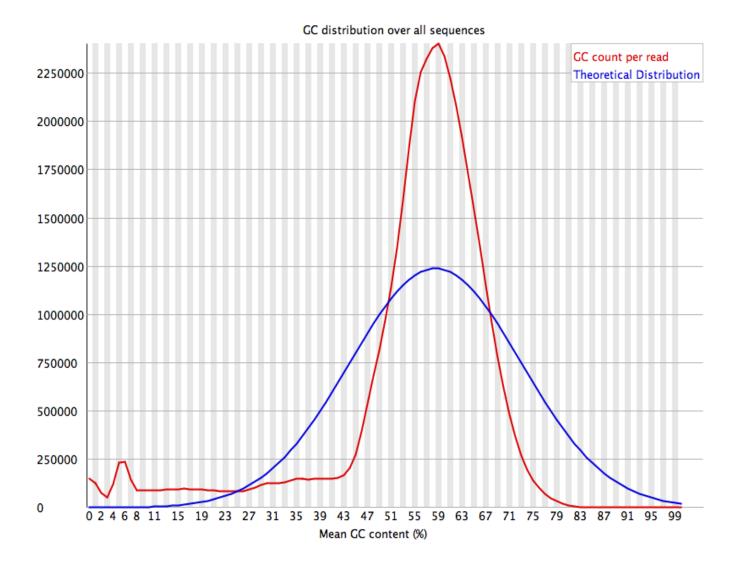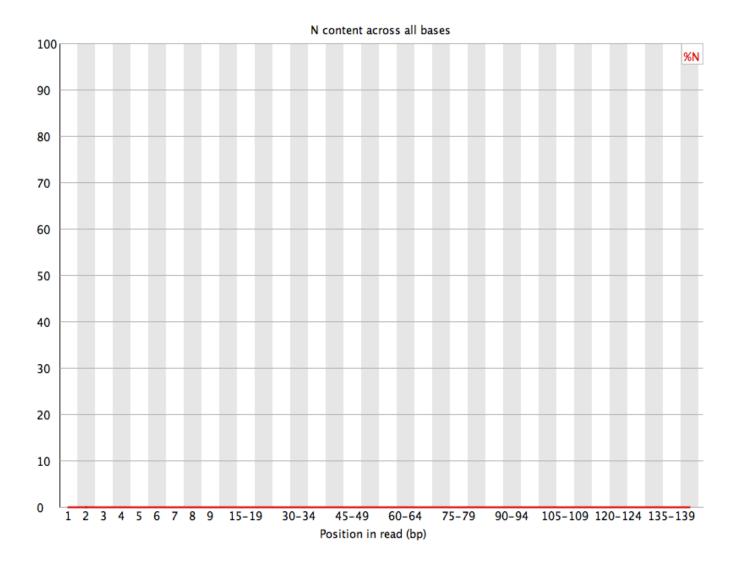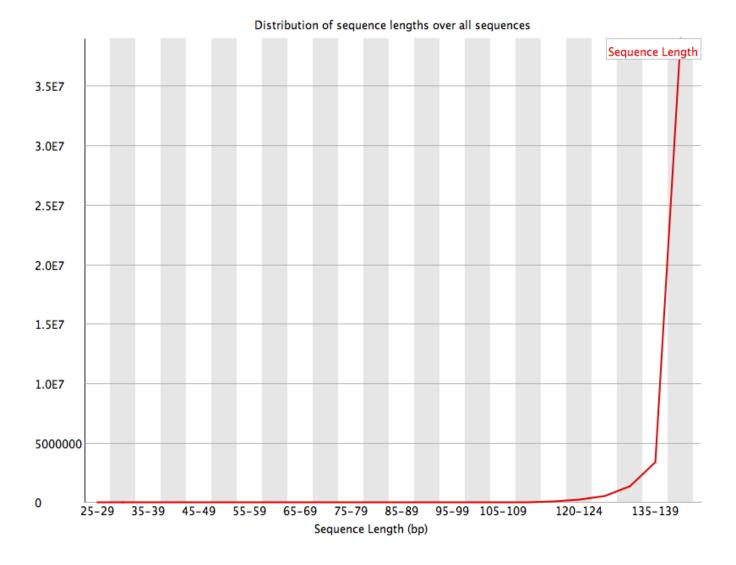
✅ Per base N content
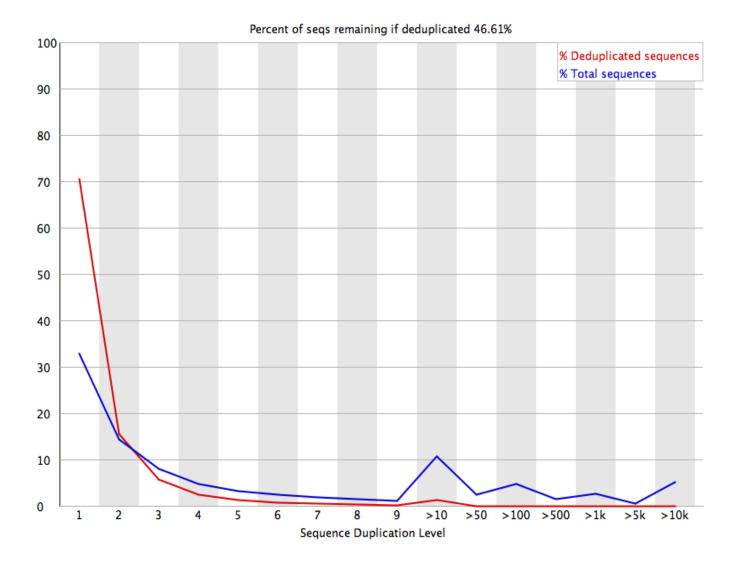
⚠️ Sequence Length Distribution

❌ Sequence Duplication Levels

❌ Overrepresented sequences

❌ Adapter Content

❌ Kmer Content

✅ Basic Statistics

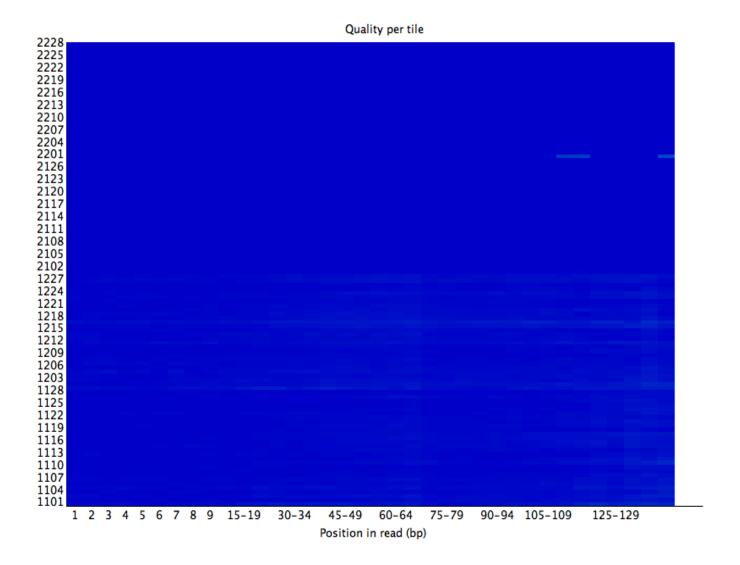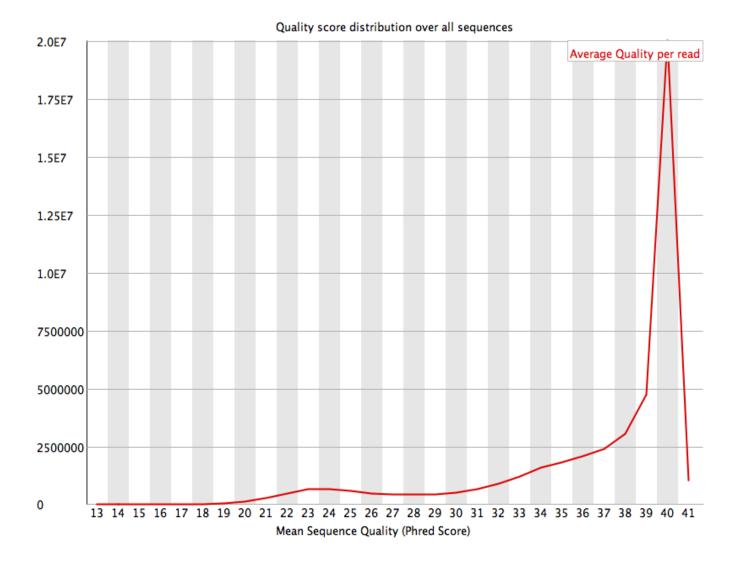| Measure	Value
Filename	Sample6_forward_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	44863497
Sequences flagged as poor quality	0
Sequence length	29–143
%GC	52

✅ Per base sequence quality

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

Position in read (bp)

✅ **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 46.61%

❌ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	540036	1.2037313988251963	No Hit
CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	393331	0.8767283566860604	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	270531	0.6030091680102423	No Hit
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	262343	0.5847582501203595	No Hit
CATCTCCGAGCCCACGAGACTAGGCATGATCTCGTATGCCGTCTTCTGCT	150571	0.33562029281845773	TruSeq Adapter, Index 1 (96% over 26bp)
TACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	124545	0.27760876509470495	No Hit

Sequence	Count	Percentage	Possible Source
CCCACGAGACTAGGCATGATCTCGTATGCCGTCTTCTGCTTGAAAAAAAA	93316	0.2079998355901681	Illumina PCR Primer Index 5 (96% over 27bp)
CTCCGAGCCCACGAGACTAGGCATGATCTCGTATGCCGTCTTCTGCTTGA	92042	0.20516011045683755	RNA PCR Primer, Index 1 (96% over 28bp)
CCGAGCCCACGAGACTAGGCATGATCTCGTATGCCGTCTTCTGCTTGAAA	70508	0.15716117715923927	RNA PCR Primer, Index 1 (96% over 28bp)
CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	53004	0.1181450478548295	No Hit
AGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	46334	0.10327772710183515	No Hit

❌ Adapter Content

Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	293120	0.0	72.71786	1
CGCAGAG	167530	0.0	70.66024	1
CAGAGTA	388955	0.0	54.727947	2
AGAGTAC	404400	0.0	52.58583	3
GAGTACT	227660	0.0	52.074905	4
GTACTTT	231330	0.0	51.201904	6
AGTACTT	236280	0.0	50.155037	5
TACGGGG	143025	0.0	48.055435	7
GTACGGG	195955	0.0	47.93309	6
AGTACGG	196615	0.0	47.81697	5
GAGTACG	206855	0.0	45.49571	4
TACTTTT	261435	0.0	45.315815	7
ACTTTTT	271825	0.0	43.60862	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACGGGGG	77910	0.0	37.963306	8
TACGGGA	27365	0.0	37.818295	7
TACGGGT	27785	0.0	36.174084	7
ACGGGGT	44810	0.0	34.839348	8
ACGGGGA	52580	0.0	32.061092	8
CGGGGGA	38675	0.0	25.900955	9
TAATCCG	3850	0.0	24.101149	9

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