FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

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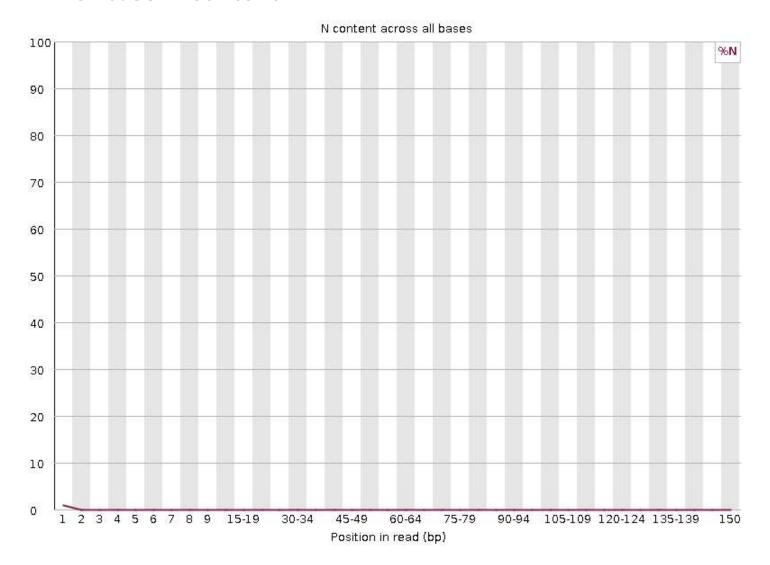
✅ [Per sequence quality scores](#)

❌ [Per base sequence content](#)

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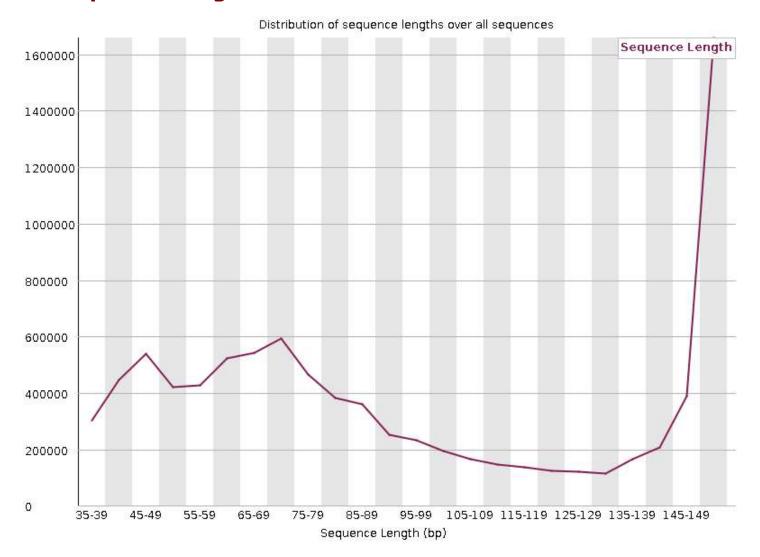
⚠️ [Sequence Length Distribution](#)

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✅ Basic Statistics

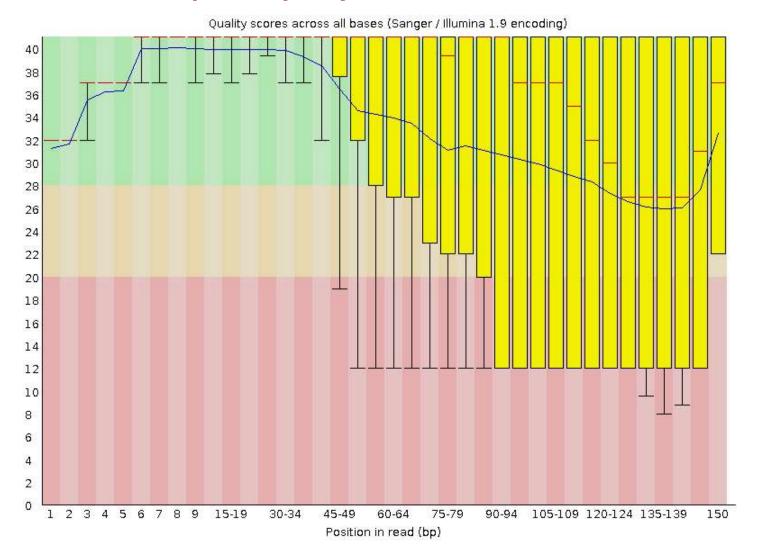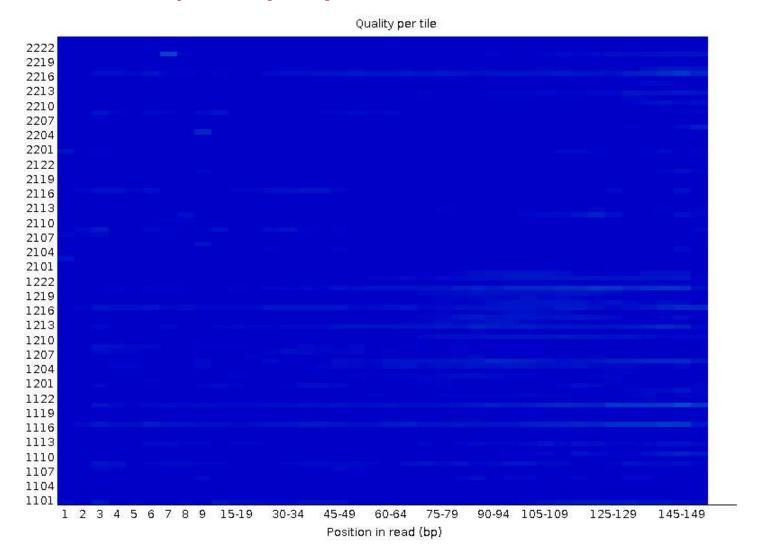| Measure	Value
Filename	SRR17656263_2_val_2.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	8955276
Total Bases	835.4 Mbp
Sequences flagged as poor quality	0
Sequence length	36-150
%GC	37

✅ Per base sequence quality

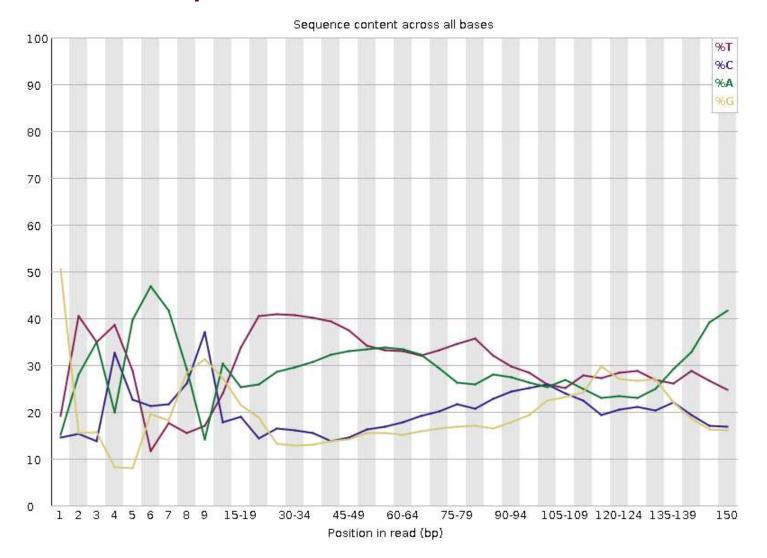Quality scores across all bases (Sanger / Illumina 1.9 encoding)
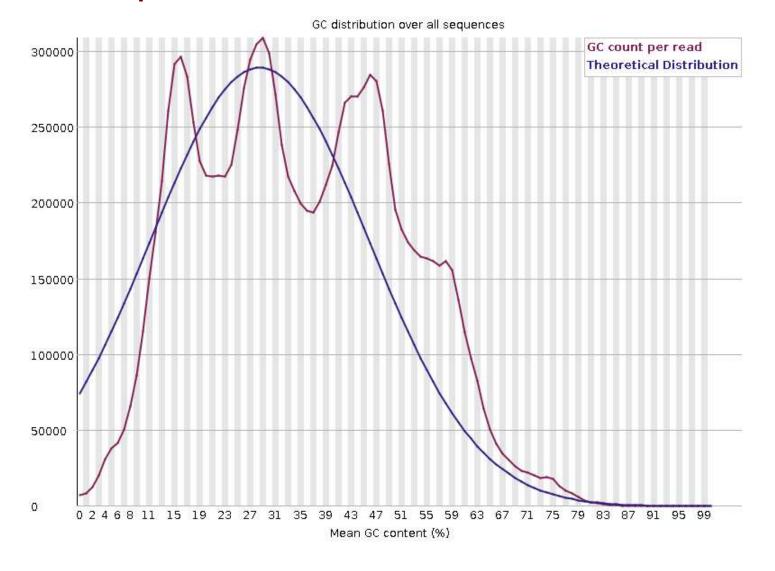
✅Per tile sequence quality

✅Per sequence quality scores

❌Per base sequence content

❌Per sequence GC content
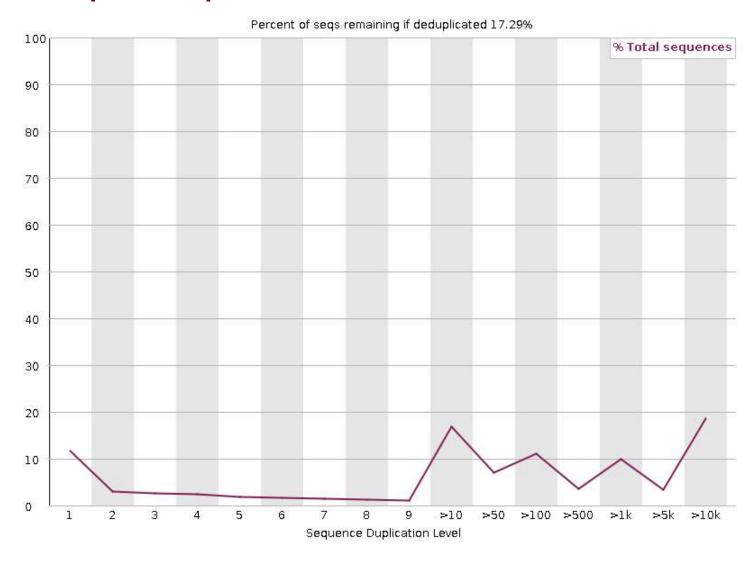
✅ Per base N content

⚠️Sequence Length Distribution

Distribution of sequence lengths over all sequences

❌Sequence Duplication Levels

❌Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	335047	3.741336392088865	No Hit
TATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	202396	2.260075513027181	No Hit
GGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	202371	2.259796347985255	No Hit
ACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	70251	0.7844649344140817	No Hit
GTATCAACGCAGAGTACGGGGAACAACAACAACAACAACAGAAAAAAAAA	63251	0.7062987226747673	No Hit
GTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	56811	0.6343858078745982	No Hit
TATCAACGCAGAGTACGGGGAACAACAACAACAACAACAGAAAAAAAAAA	50675	0.5658675399842507	No Hit
GTATCAACGCAGAGTACGGGGAACAACAACAACAACAACAAAAAAAAAAAA	46154	0.5153833338023306	No Hit
GGTATCAACGCAGAGTACGGGGAACAACAACAACAACAGAAAAAAAAA	42031	0.4693434350878744	No Hit

Sequence	Count	Percentage	Possible Source
GAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	39859	0.44508957624533296	No Hit
TATCAACGCAGAGTACGGGGAACAACAACAACAACAACAAAAAAAAAAAA	35936	0.40128299786628574	No Hit
GAGTACGGGGAACAACAACAACAACAACAGAAAAAAAAAAAAAAAAAAAA	30476	0.34031335270962054	No Hit
GGTATCAACGCAGAGTACGGGGAACAACAACAACAACAACAAAAAAAAAA	30469	0.34023518649788126	No Hit
ATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	30402	0.33948702418551924	No Hit
GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	30295	0.33829219780607545	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG	30218	0.337432369476943	No Hit
GTATCAACGCAGAGTACGGGGAACAACAACAACAACAACACAAAAAAAAA	24947	0.2785732120372393	No Hit
GAGTACGGGGAACAACAACAACAACAACAAAAAAAAAAAAAAAAAAAAAA	20784	0.232208664925570133	No Hit
TATCAACGCAGAGTACGGGGAACAACAACAACAACAACACAAAAAAAAAA	20007	0.22341019975263746	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	19291	0.21541491295187326	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	17950	0.20044050010295608	No Hit
TATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG	16966	0.18945256405274388	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGT	16489	0.18412609505279345	No Hit
GGTATCAACGCAGAGTACGGGGAACAACAACAACAACAACACAAAAAAAA	16132	0.18013961825408845	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	14791	0.1651652054051712	No Hit
GGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG	13914	0.15537209573440283	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	13137	0.14669564623133893	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTC	13136	0.14668447962966188	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTT	13087	0.14613731614748668	No Hit
TATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGT	12989	0.1450429891831363	No Hit
TATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	12922	0.14429482687077427	No Hit
GTACGGGGAACAACAACAACAACAACAGAAAAAAAAAAAAAAAAAAAAAA	12908	0.14413849444729565	No Hit
GTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	12411	0.13858869341380434	Clontech SMART CDS Primer II A (100% over 21bp)
TATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	12150	0.13567421037609562	No Hit
GAGTACGGGGAACAACAACAACAACAACACAAAAAAAAAAAAAAAAAAAA	11467	0.12804742143067394	No Hit
ATCAACGCAGAGTACGGGGAACAACAACAACAACAACAGAAAAAAAAAAA	10772	0.12028663326512773	No Hit
TATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	10319	0.11522816270542638	No Hit
CAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	9856	0.11005802612895459	No Hit
AACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	9345	0.10435189267198465	No Hit
GTACGGGGAACAACAACAACAACAACAAAAAAAAAAAAAAAAAAAAAAAA	9255	0.10334689852105061	No Hit
GTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGG	9048	0.10103541197390231	No Hit
TATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTT	8987	0.10035424927160258	No Hit

❌Adapter Content

Produced by FastQC (version 0.12.1)