

FastQC Report

Tue 8 Apr 2014

2831_4902_8529_H8PNLADXX_GS061B_R1.fastq

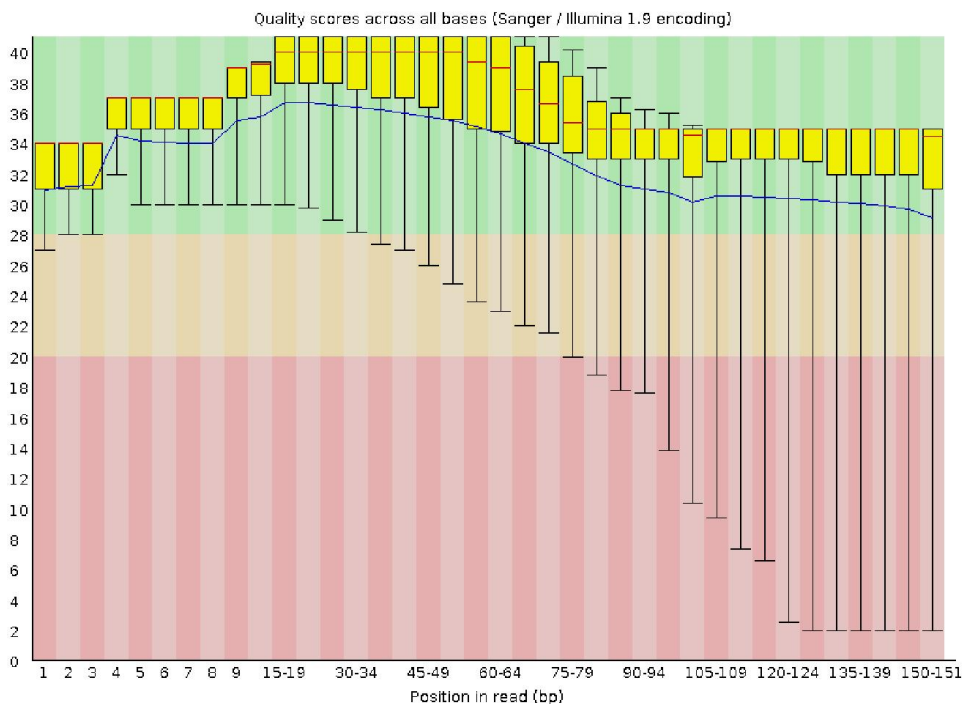
Summary

- ✓ [Basic Statistics](#)
- ✓ [Per base sequence quality](#)
- ✓ [Per sequence quality scores](#)
- ⚠ [Per base sequence content](#)
- ⚠ [Per base GC content](#)
- ⚠ [Per sequence GC content](#)
- ✓ [Per base N content](#)
- ✓ [Sequence Length Distribution](#)
- ✓ [Sequence Duplication Levels](#)
- ✓ [Overrepresented sequences](#)
- ⚠ [Kmer Content](#)

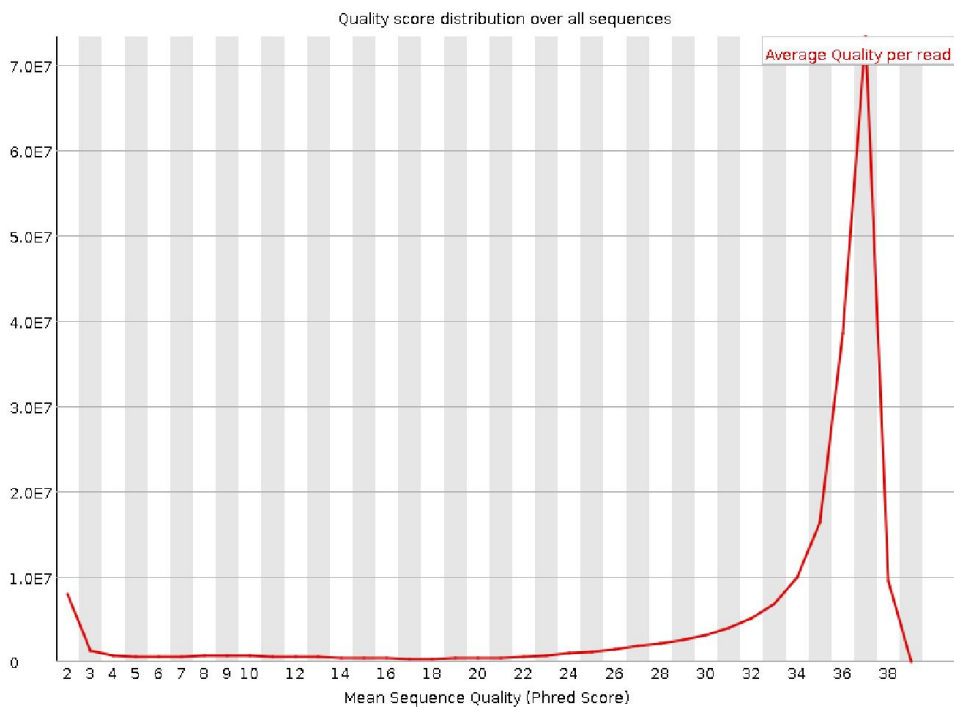
Basic Statistics

Measure	Value
Filename	2831_4902_8529_H8PNLADXX_GS061B_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	198749393
Filtered Sequences	0
Sequence length	151
%GC	43

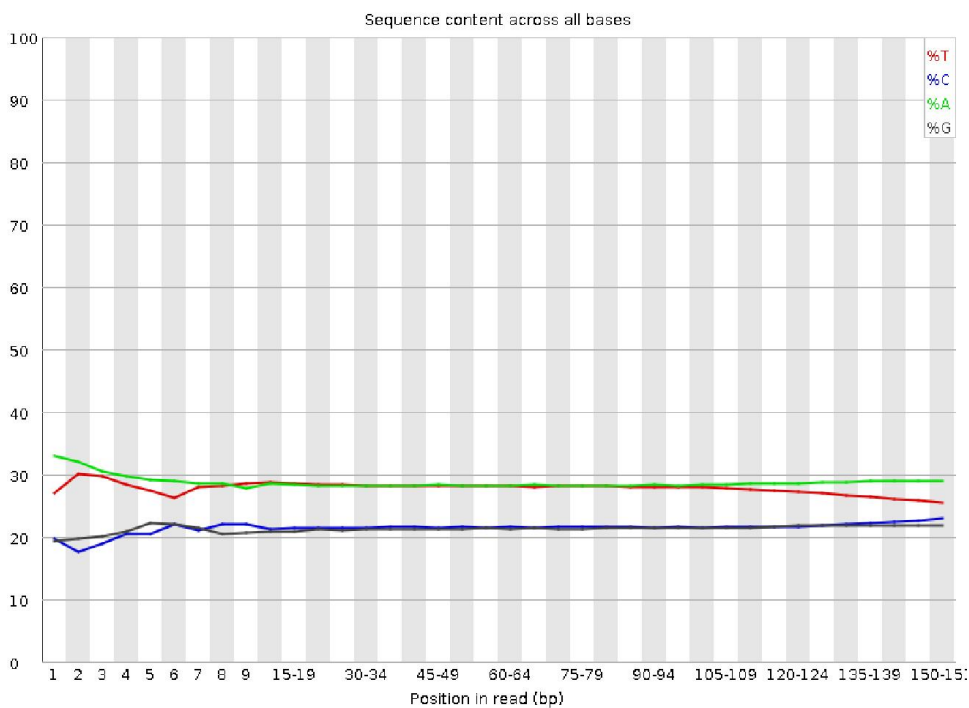
Per base sequence quality



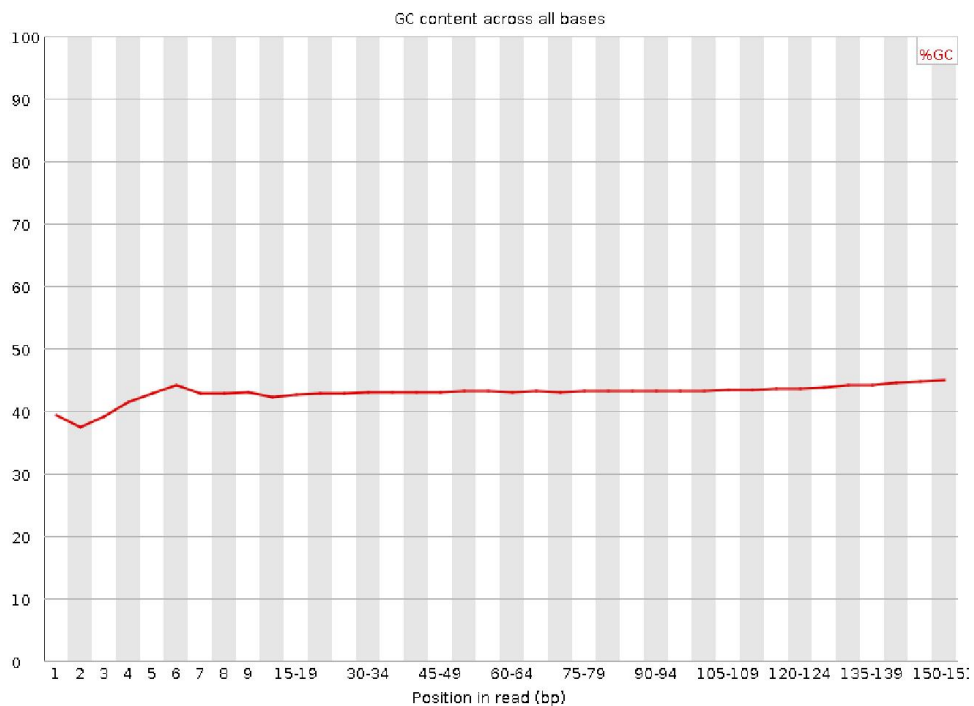
✓ Per sequence quality scores



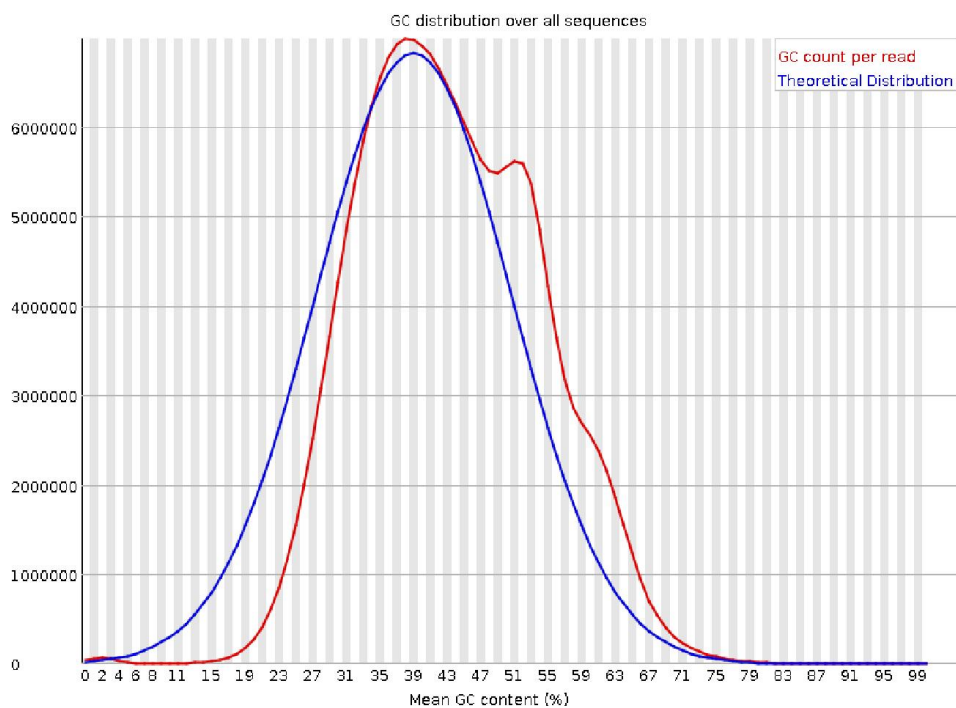
⚠ Per base sequence content



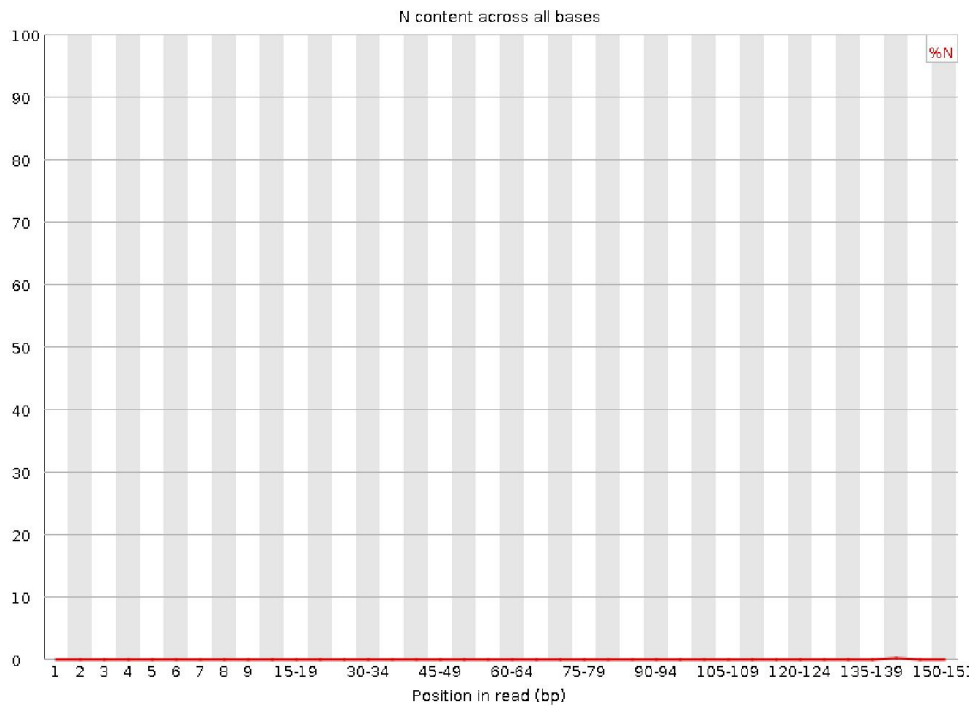
⚠ Per base GC content



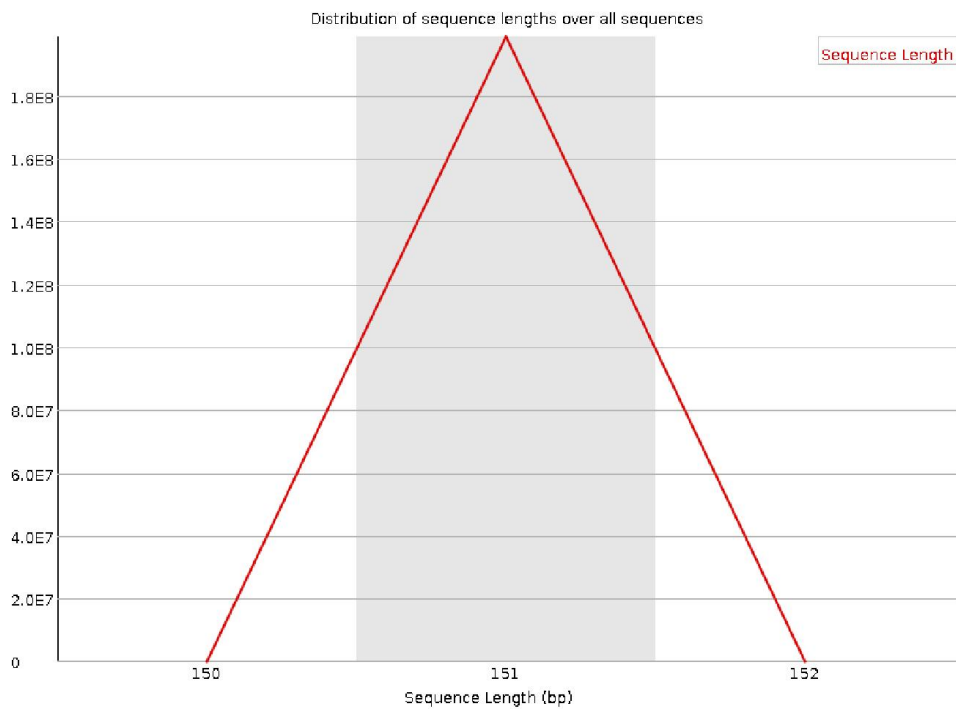
🚩 Per sequence GC content



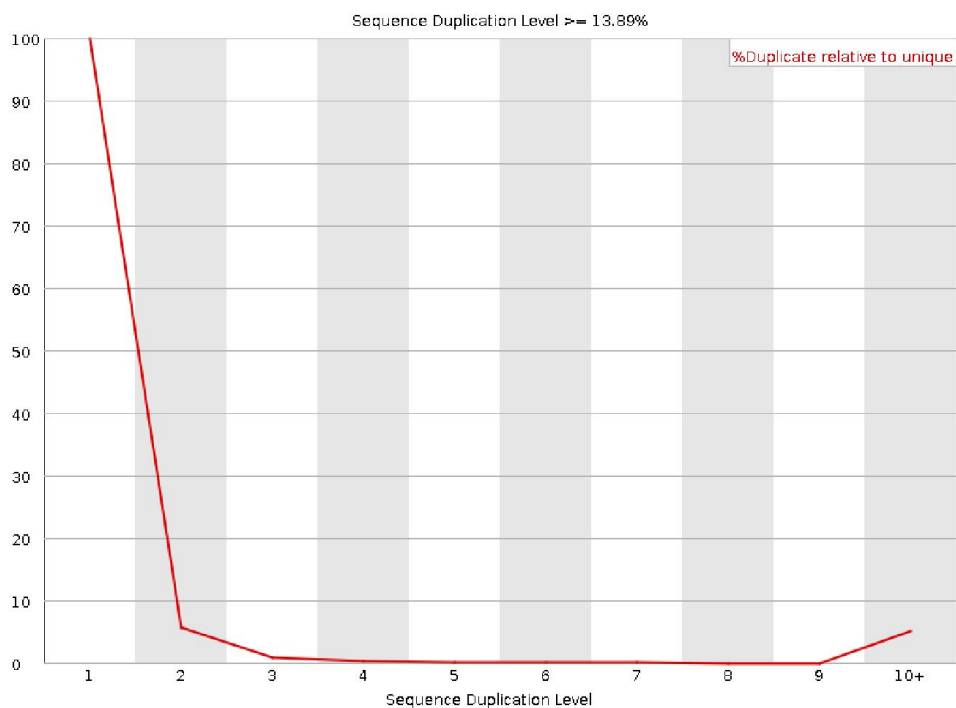
✅ Per base N content



Sequence Length Distribution



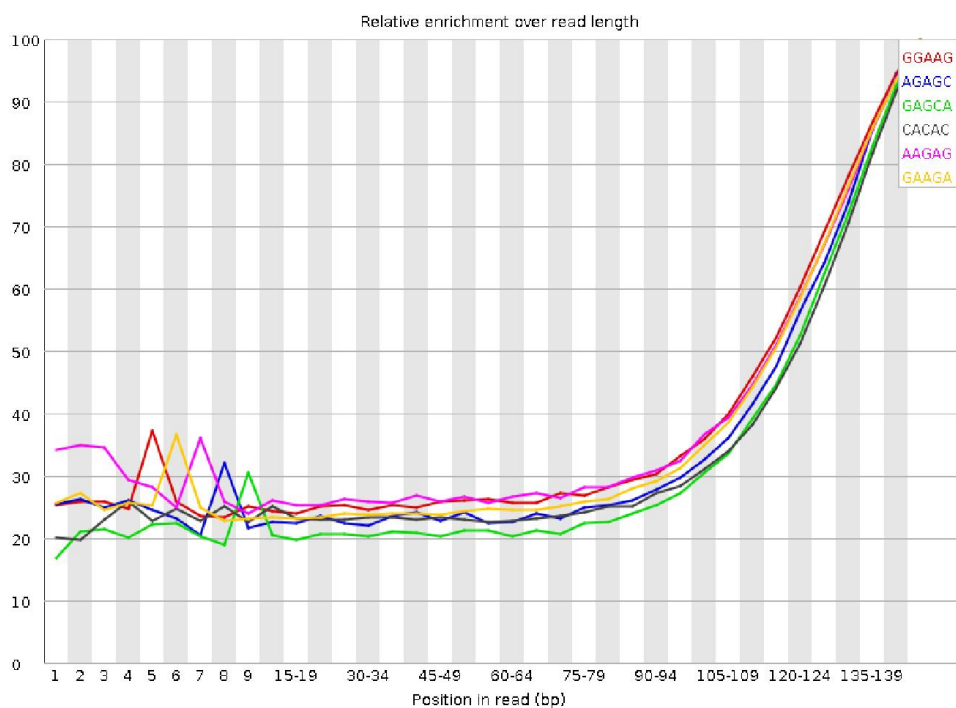
Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
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GGAAG	82561105	3.4312346	8.746461	145-147
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AGAGC	71018075	2.9202816	7.981296	145-147
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GAGCA	64055995	2.633999	7.7104115	145-147
CACAC	63804025	2.568418	7.2481503	145-147
AAGAG	81972730	2.5635848	6.488758	145-147
GAAGA	81561510	2.5507243	6.723786	145-147
GCACA	61810510	2.5147748	7.3706794	145-147
AGCAC	58776610	2.3913395	7.324485	145-147
TCCAG	56243955	2.3466096	5.4586563	145-147
CTCCA	53049990	2.189935	5.4179087	145-147
GTCTG	49273435	2.1307147	6.4658794	145-147
TCTGA	61807060	2.0111933	5.1227593	145-147
AGATC	60985910	1.9351603	6.3425994	145-147
CGGAA	46334905	1.9053034	7.418762	145-147
GATCG	38644030	1.6295456	7.577105	145-147
TCGGA	38393130	1.6189656	7.453466	145-147
ATCGG	37872170	1.5969977	7.477632	145-147
CACGT	38210705	1.5942266	6.3501377	145-147
ACTCC	37794980	1.560199	5.017811	145-147
ACACG	34259240	1.3938448	6.2141423	145-147
CGTCT	31094885	1.3304001	6.712797	145-147
ACGTC	27986520	1.1676533	5.831282	145-147

Produced by [FastQC](#) (version 0.10.1)