

FastQC Report

Tue 8 Apr 2014

2831_4902_8529_H8PNLADXX_GS061B_R1.fq

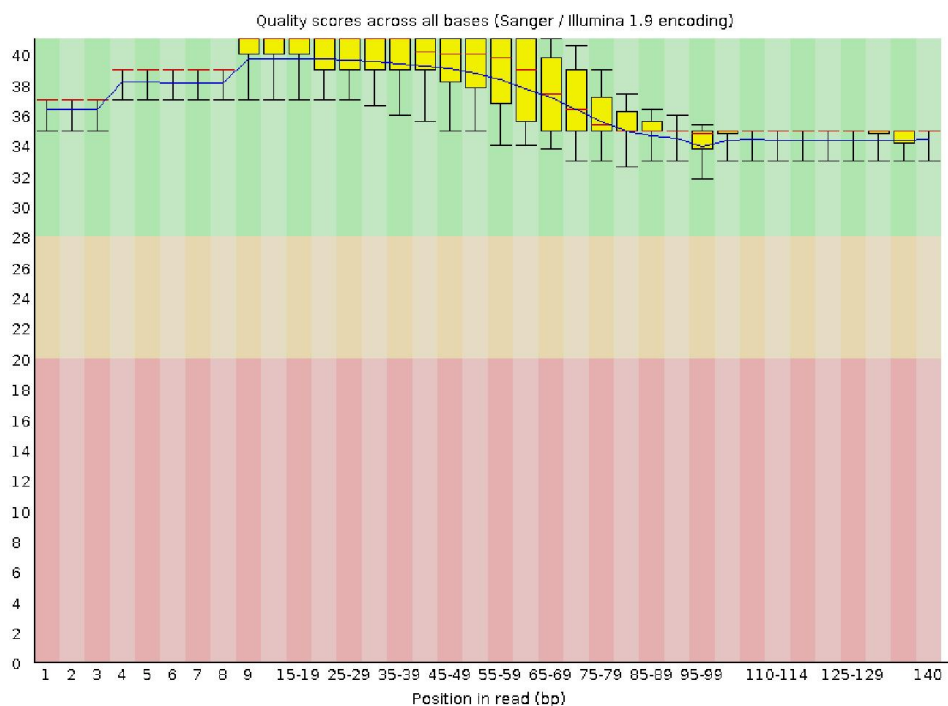
Summary

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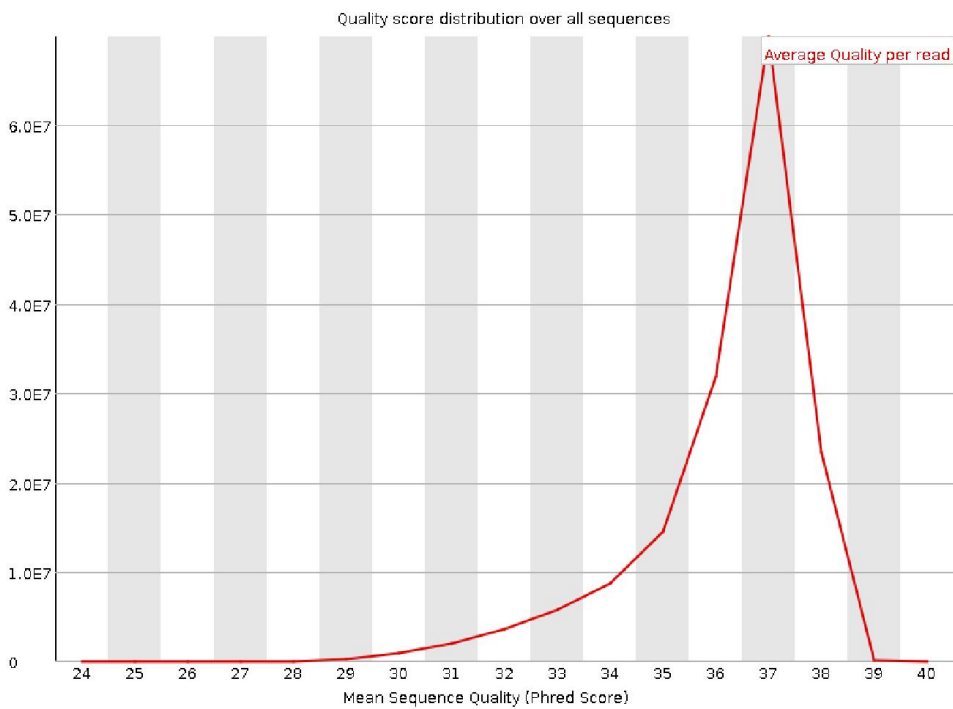
Basic Statistics

Measure	Value
Filename	2831_4902_8529_H8PNLADXX_GS061B_R1.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	161852368
Filtered Sequences	0
Sequence length	60-140
%GC	42

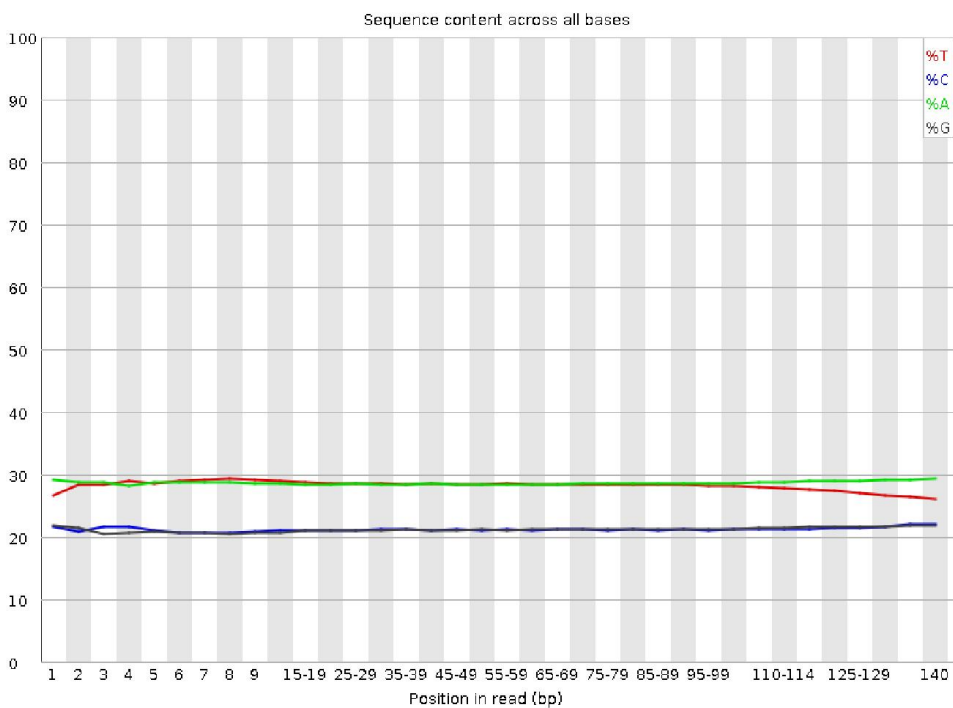
Per base sequence quality



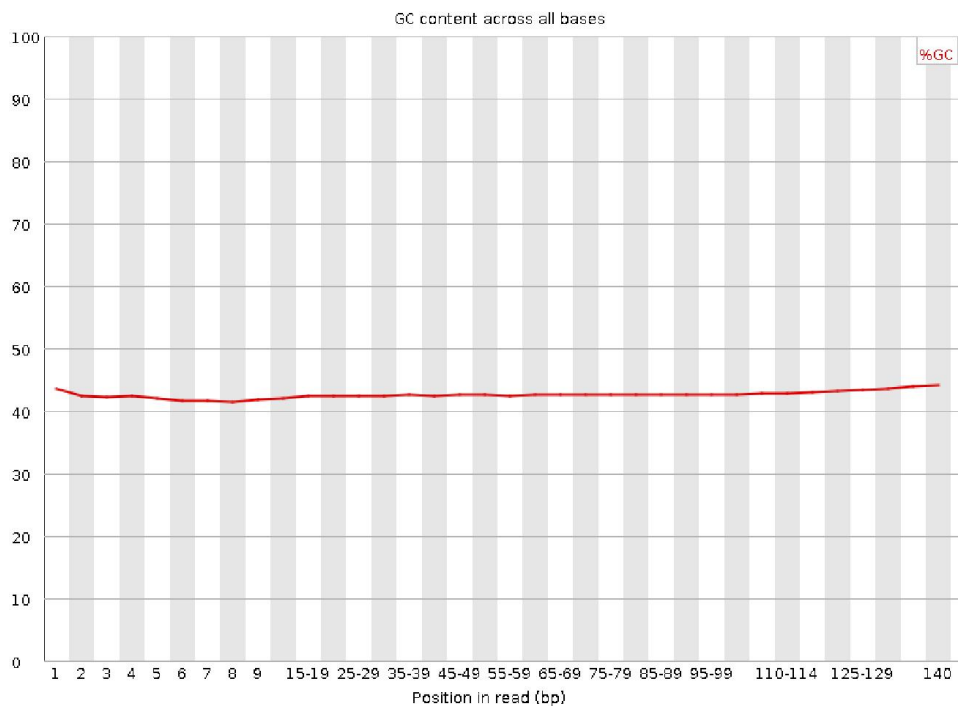
✓ Per sequence quality scores



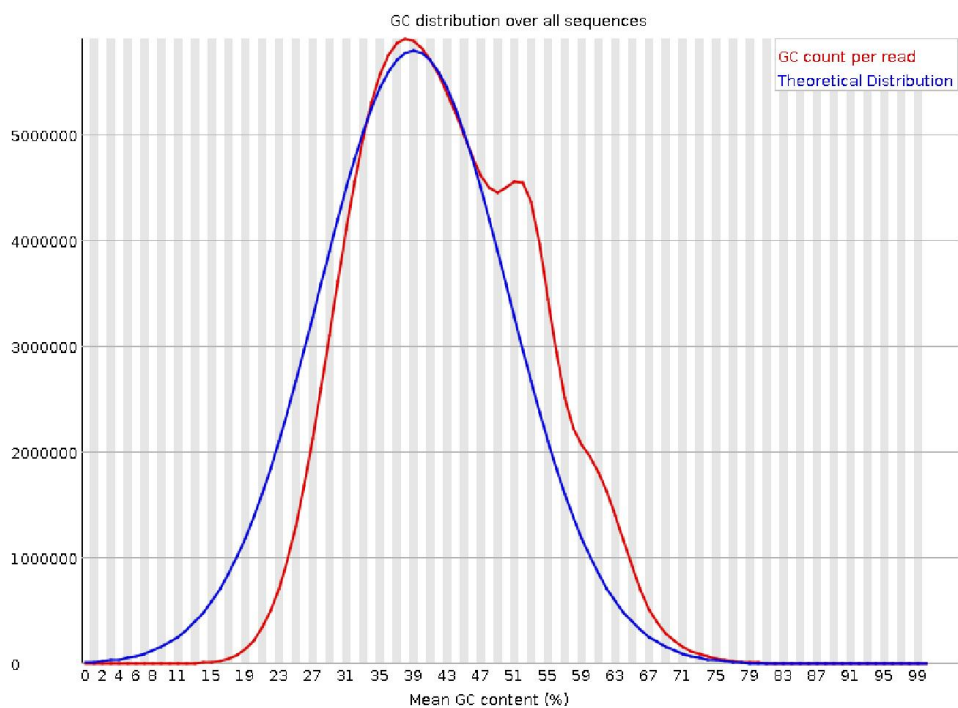
✓ Per base sequence content



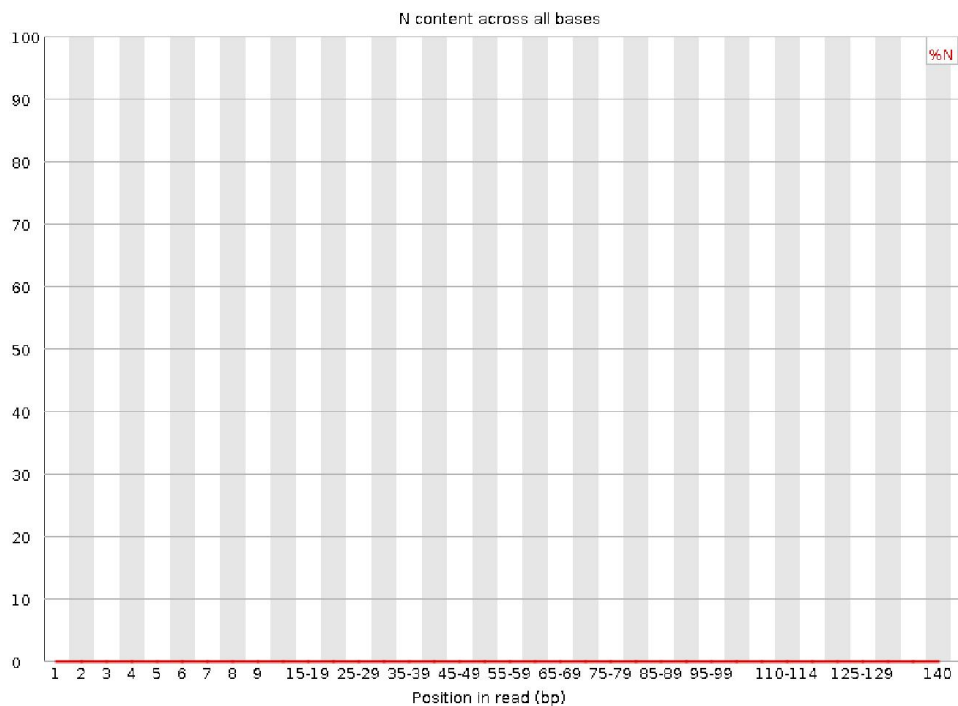
✓ Per base GC content



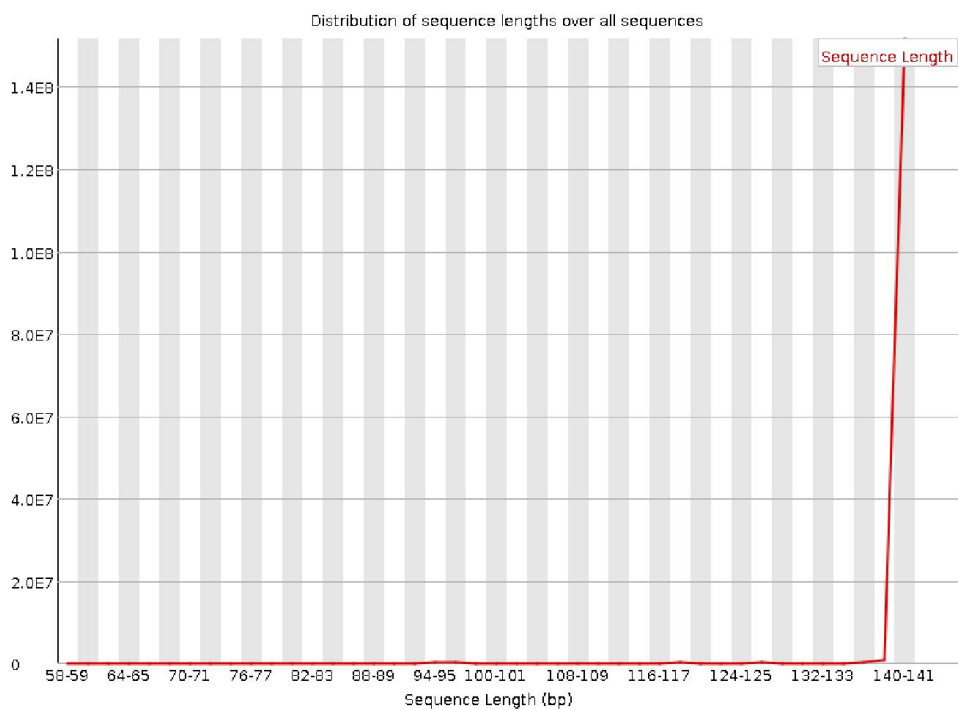
Per sequence GC content



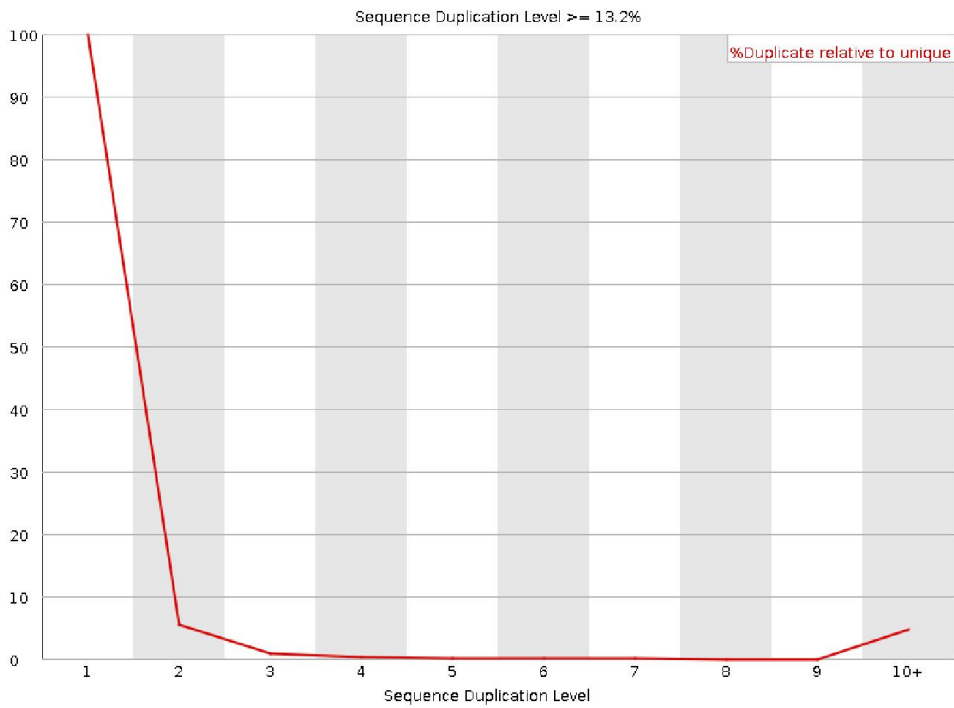
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

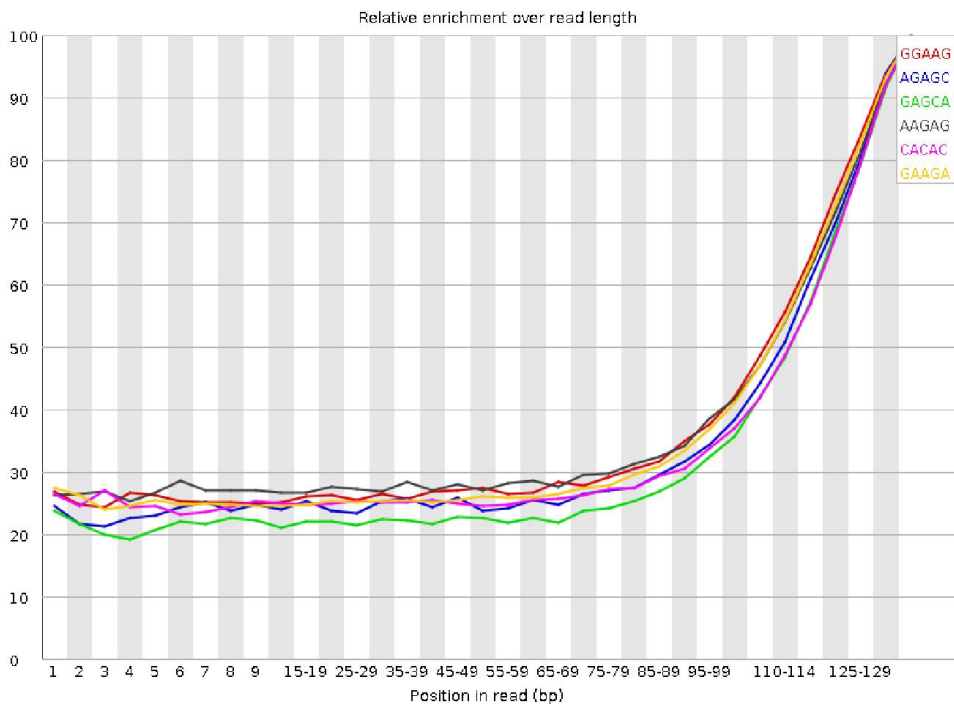


Overrepresented sequences

No overrepresented sequences



Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
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GGAAG	58372995	3.3048606	8.538991	135-136
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AGAGC	49470270	2.8019238	7.717813	135-136
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GAGCA	44263215	2.5070038	7.3930554	135-136
AAGAG	58385320	2.459914	6.312085	135-136
CACAC	43391885	2.4595876	6.836329	135-136
GAAGA	58053260	2.4459233	6.482347	135-136
GCACA	42508840	2.408586	7.006716	135-136
AGCAC	39944155	2.2632687	6.984542	135-136
GTCTG	33839600	1.978432	5.773565	135-136
AGATC	42398890	1.8156558	6.292842	135-136
CGGAA	29658740	1.6798278	7.346067	135-136
GATCG	25329575	1.4575784	7.5178456	135-136
TCGGA	25012795	1.4393494	7.2723413	135-136
CACGT	24933285	1.4353386	5.7209477	135-136
ATCGG	24678695	1.4201237	7.369216	135-136
ACACG	21492105	1.2177604	5.634263	135-136
CGTCT	19247900	1.1257712	5.8096495	135-136
ACGTC	17558405	1.0107876	5.261245	135-136

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