

FastQCFastQC Report

Summary

Wed 19 Mar 2014
Other.fastq

[PASS] [Basic Statistics](#)
[PASS] [Per base sequence quality](#)
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[FAIL] [Per sequence GC content](#)
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[OK] Basic Statistics

Measure	Value
Filename	Other.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	264082
Filtered Sequences	0
Sequence length	50-75
%GC	45

[OK] Per base sequence quality

Per base quality graph

[OK] Per sequence quality scores

Per Sequence quality graph

[FAIL] Per base sequence content

Per base sequence content

[FAIL] Per base GC content

Per base GC content graph

[FAIL] Per sequence GC content

Per sequence GC content graph

[OK] Per base N content

N content graph

[WARN] Sequence Length Distribution

Sequence length distribution

[FAIL] Sequence Duplication Levels

Duplication level graph

[FAIL] Overrepresented sequences

Sequence

Coun

TATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCC	13095
TATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCGTCTTCT	8202
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TATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACA	5360
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GGGGGAGACTTGCTTGCGGCGTCCTACTCTCACAGGGGGAAACCCCGACTACCATCGGCGCTGAAGAGCTTAA	2209
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GGGAA	1634
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GGGGAA	986
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GAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCGTCTTCTGCTTGAAAAA	563
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TATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCGTCTTCTGCTT	470
TATATATATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACA	464
TATATATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACAT	464
ATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCGTCTTCTGCTTGAAAAA	447
GTGGCGATAGCGAAGAGGTCACACCCGTTCCCATACCGAACACGGAAGTTAAGCTCTTCAGCGCCGATGGTAGTC	425

[illegible]

TATATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATC 307

TATATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATG 304

TATATATATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCA 303

TATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCG 301

TATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATC 298

TATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCG 291

CGCTAATT 287

ATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCGTCTT 285

TATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGT 284

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GGGGAGACTTGCTTGGCGGCGTCTACTCTCACAGGGGGGAAACCCCGACTACCATCGGCGCTGAAGAGCTTAAC 274

TATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTA 271

TATATATATATATATATAGATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACAT

266

AGGAAA

266

[FAIL] Kmer Content

Kmer graph

Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
TATAT	732065	29.960512	403.44437	1
ATATA	736285	27.369522	366.09113	2
CGTCT	226005	16.560415	229.39095	30
TTTTT	322300	15.988826	35.720566	71
CGGCT	162490	14.490628	271.43835	47
CACGG	169885	13.760595	251.19255	45
GTCTG	168840	13.667564	253.41403	31
ACGGC	166235	13.464948	250.95837	46
GGAAG	175570	12.95305	232.98418	19
ATCGG	171665	12.621738	232.64209	16
GATCG	171080	12.578728	232.61897	15
TCGGA	168055	12.356312	232.20245	17
AAAAA	384145	11.780394	39.845467	71
GGCTA	158175	11.629881	222.6652	48
CGGAA	171975	11.484825	210.49846	18
AGAGC	171055	11.423388	209.79703	22
GTCAC	170110	11.321519	206.13596	43
TCCAG	169955	11.311202	206.42917	39
GAGCA	169085	11.291825	209.77597	23
ACGTC	168220	11.195731	208.66629	29
CCAGT	167630	11.156465	205.73802	40
CACGT	167535	11.150142	209.02234	28