

Pseudomonas aeruginosa website

Eureka Genomics

April 9, 2010



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# Pseudomonas aeruginosa Sample 1

## Sequencing Summary

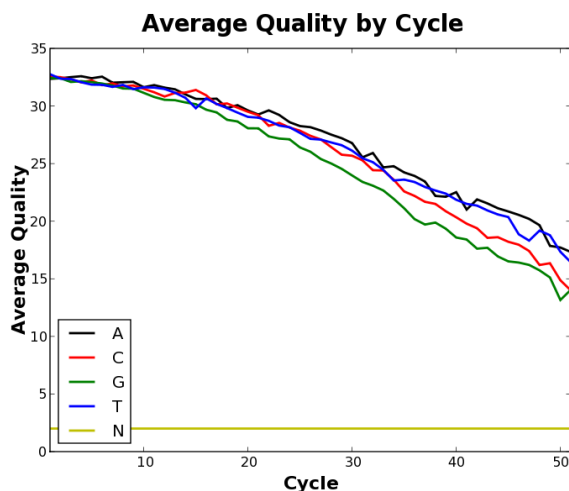
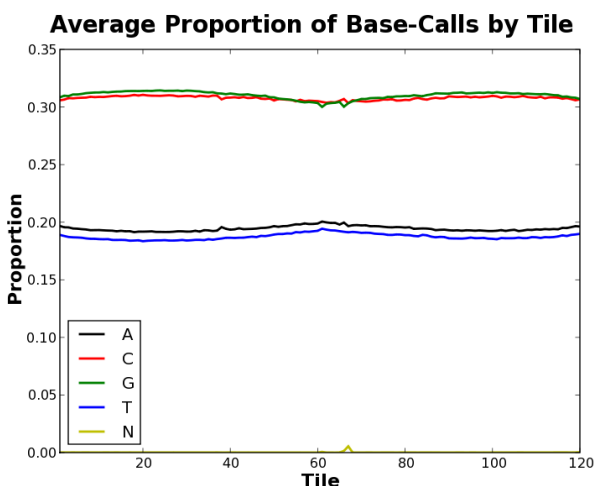
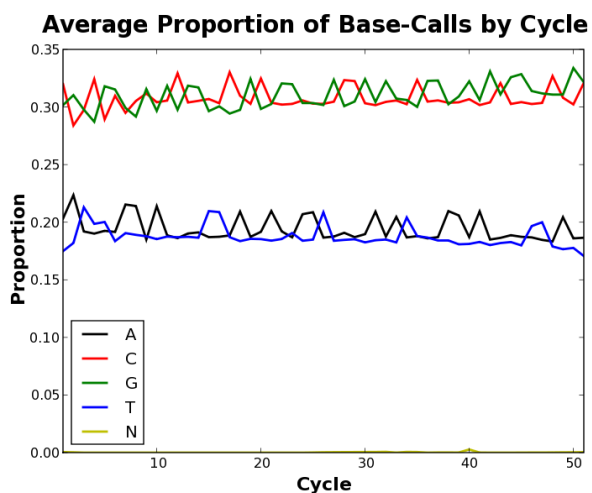
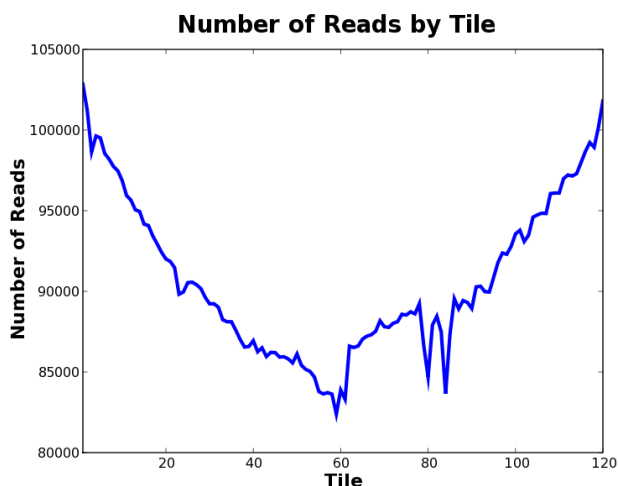
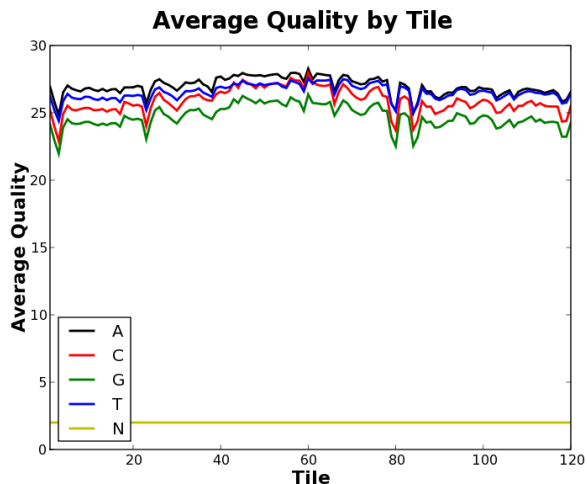
**# of Reads:** 21,778,712  
**GC Content:** 62.16%  
**Total Data:** 1,110 Mbases

	<b>Read Length</b>	<b># of Reads</b>	<b>Unique Reads</b>	<b>Unique %</b>	<b>GC Content</b>
<b>Left 1</b>	51	10,889,356	4,197,627	38.55%	61.82%
<b>Right 1</b>			4,438,090	40.76%	62.51%

### Quality Control

Left 1

File Format:	FASTQ
Unique Reads:	4,197,627
Total Reads:	10,889,356
Percent Unique:	38.55%
Reads Length:	51
GC Content:	61.82%
Reads with Adapters:	0
Percent Adapter Contamination	0.00%

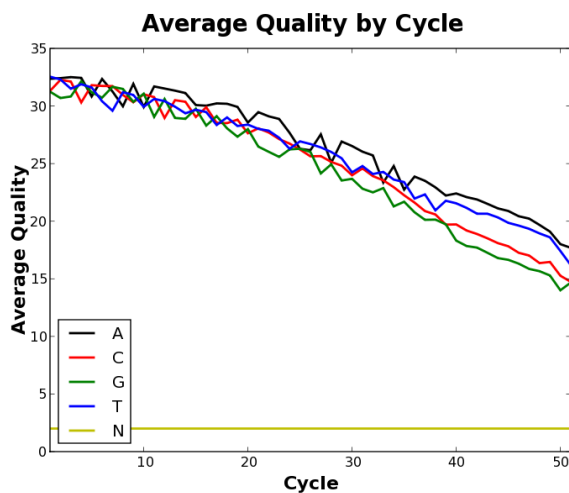
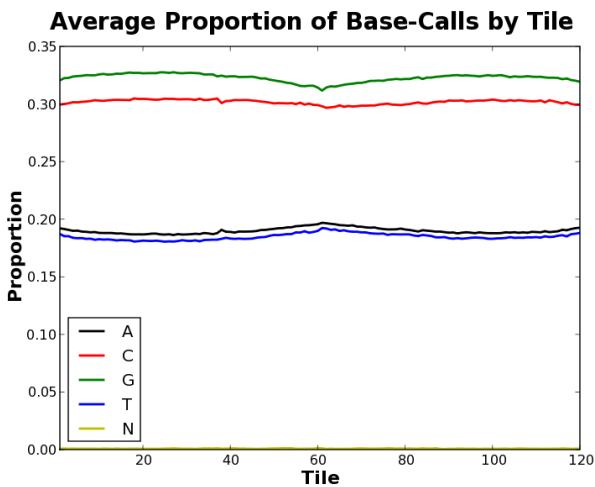
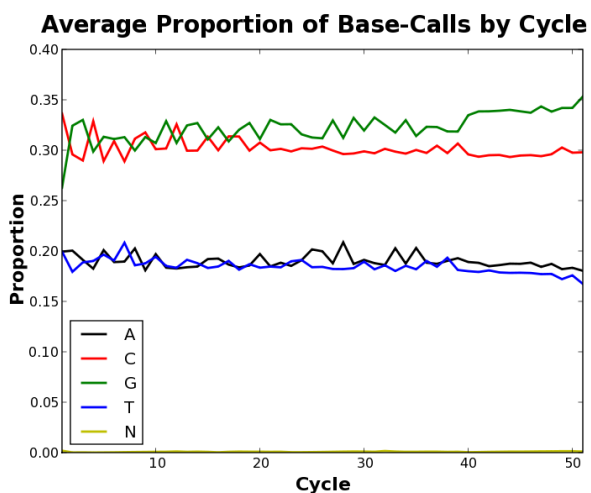
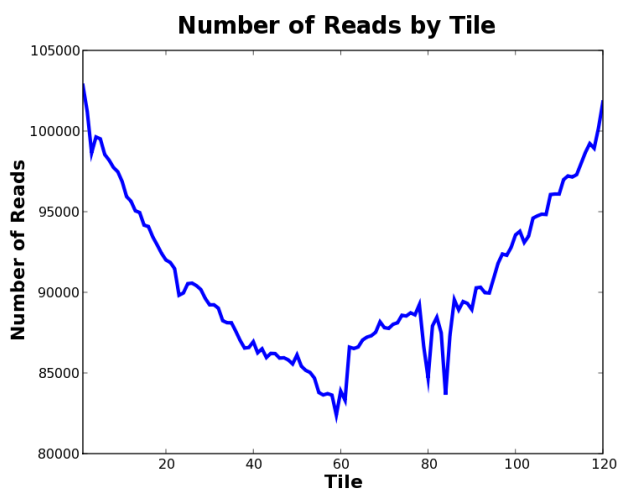
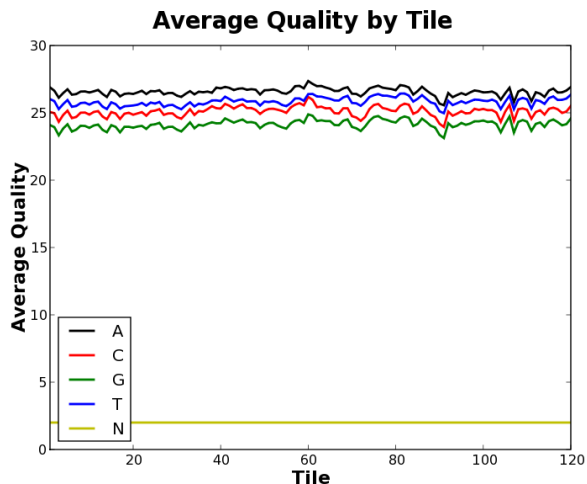


## Top 50 Read Sequences

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CGGTTCCAGCA	GGAATGCCGA	GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	A	18,530
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTTCCAG	A	10,933
CGGAAGAGCG	GTTCCAGCAGG	AATGCCGAGA	TCGGAAGAGC	GGTTCAGCAG	G	6,794
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTTCCAG	G	5,078
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGGTCCAG	A	4,153
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTTCCG	C	3,607
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGGGGTTCCAG	C	3,496
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGGTCCAG	G	2,863
GATCCCTTCT	GCCGCTGCCCT	CGGCCTCAGC	GCGCTTCTCC	TCCGCCCGTG	T	2,274
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGGTCCG	C	2,023
CGGAAGAGCG	GTTCCAGCAGG	AATGCCGAGA	TCGGAAGAGC	GGTTCAGCAG	G	1,805
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTTTAG	C	1,731
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGGGGGTCCAG	C	1,399
CGGTTCCAGCA	GGAATGCCGA	GATCGGAAGA	GCGGGTCCAGC	AGGAATGCCG	A	1,273
AGCTTAAAAG	ATGACACCGA	ACAGGGCGGG	GATGGCGCAG	GCGGCGCAA	C	1,092
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGGGGTTCCAG	G	1,086
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTTAAG	C	1,079
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	GGCGGTTCCAG	C	1,074
CGGTTCCAGCA	GGAATGCCGA	GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	G	1,051
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	GATCGGAAGA	GCGGTTCCAGC	A	1,043
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGGGGTTCCAG	A	1,009
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTGCAG	C	896
CAGCAGGAAT	GCCGAGATCG	GAAGAGCGGT	TCAGCAGGAA	TGCCGAGACC	G	817
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGGTTAG	C	699
AGCTTAAAAG	ATGACACCGA	ACAGGGCGGG	GATGGCGCAG	GCGGCGCAA	A	696
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	GGCGGGTCCAG	C	670
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGAGGTTCCAG	C	631
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	CGCGGTTCCAG	C	603
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGGGGGTCCAG	G	593
TCGAGACTCC	GGTAGCCATG	GGCGCGATGG	GACGGGTGGT	GGGCAGGCCT	T	586
GATCGGAAGA	GCGGTTCCATC	AGGAATGCCG	AGATCGGAAG	AGCGGTTCCAG	C	494
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGGTAAG	C	471
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GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTTGAG	C	409
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGGGGGTCCAG	A	407
CGGTTCCAGCA	GGAATGCCGA	GATCGGAAGA	GCGGTTCCAGC	AGGAAAGCCG	A	386
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TCGAGAAACT	TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	T	376
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GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	AGCGGTTTAG	A	374
CACCCCTCG	TTGAGCAGGT	CGACCCGGCG	GGGGGTGAGG	GGGGTGTCCC	G	373
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGAAG	CGCGGGTCCAG	C	358
GATCGGAAGA	GCGGTTCCAGC	AGGAATGCCG	AGATCGGACG	AGCGGTTCCAG	C	346
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CGGTTCCAGCA	GGAATGCCGA	GATCGGAAGA	GCGGTTCCAGC	AGGAATGGCG	A	338

Right 1

File Format:	FASTQ
Unique Reads:	4,438,090
Total Reads:	10,889,356
Percent Unique:	40.76%
Reads Length:	51
GC Content:	62.51%
Reads with Adapters:	0
Percent Adapter Contamination	0.00%

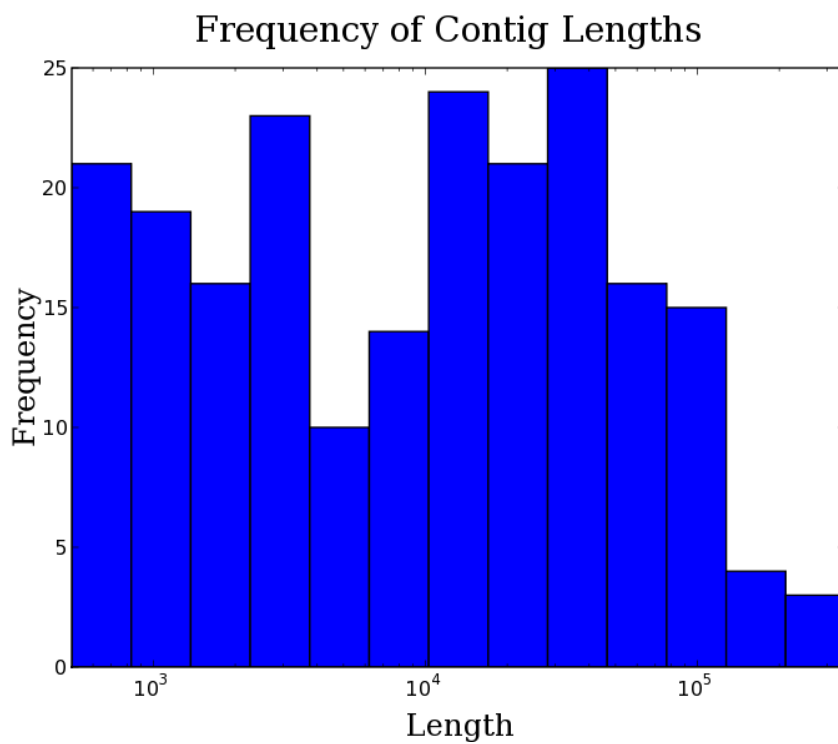
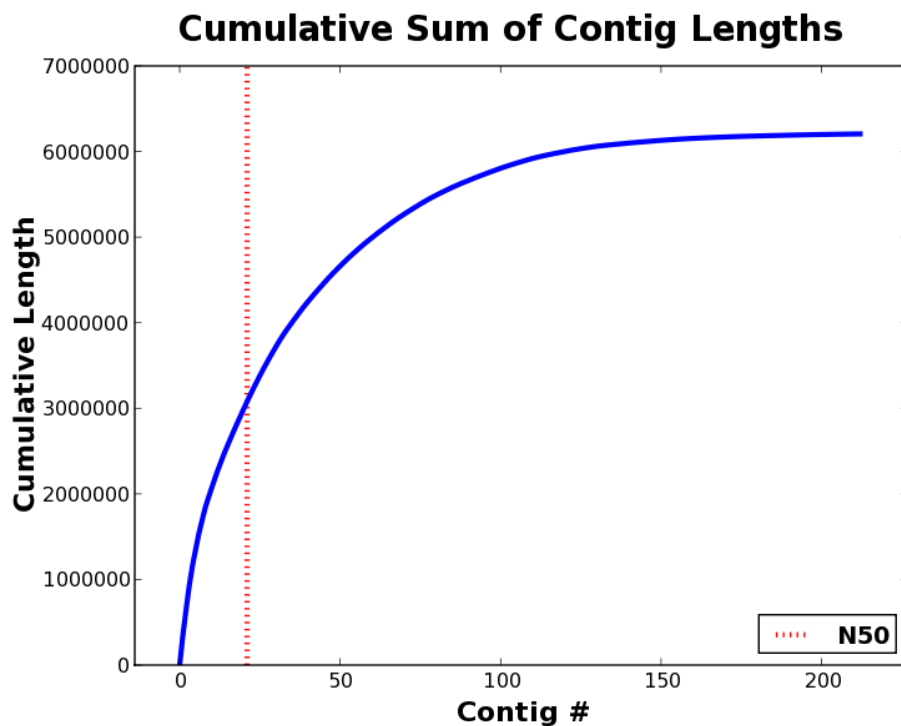


## Top 50 Read Sequences

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GATCCCTTCT	GCCGCTGCC	CGGCCTCAGC	GCGCTTCTCC	TCCGCCCGTG	T	2,122
AGCTTAAAAG	ATGACACCGA	ACAGGGCGGG	GATGGCGCAG	GCGGCGGCAA	C	1,526
CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GTCGTGGAGG	G	928
CGGCATTCT	GCTGAGATCG	GAAGAGCGTC	GTGTAGGGAA	AGAGTGTAGA	T	786
TCGAGACTCC	GGTAGCCATG	GGCGCGATGG	GACGGGTGGT	GGGCAGGCCT	T	744
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGTGTA	GGGAAAGAGG	G	712
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGTGGA	GGGAAAGAGT	G	580
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CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GTCGGGTAGG	G	532
CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GGCGTGTAGG	G	513
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGTGTA	GGGAAAGAGT	G	506
TCGAGAAACT	TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	T	423
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CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GTCGTGTGGG	G	368
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CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGGGTA	GGGAAAGAGT	G	343
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AATCCGTCA	GGTGGCCTGG	AGCGGGGAAA	TGTGCGCGGA	ACCCCTATTT	G	327
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGTGTA	GGGAAAGGGT	G	315
CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GGCGTGGAGG	G	292
TCGAGTGATA	ACACTGCGGC	CAACTTACTT	CTGACAACGA	TCGGAGGACC	G	269
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGGGTA	GGGAAAGAGG	G	260
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGGCGTGTA	GGGAAAGAGT	G	243
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGGCGTGTA	GGGAAAGAGG	G	239
GATCCTCGGG	AAACCTGTCG	TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	G	216
CGGCATTCT	GCTGAGATCG	GAAGAGCGTC	GTGTAGGGAA	AGAGGGTAGA	T	202
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGTGGA	GGGAAAGAGG	G	191
CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GGCGGGTAGG	G	181
CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GTCGGGGAGG	G	177
TCGAGATATA	CTTTAGATTG	ATTTAAAACT	TCATTTTTAA	TTTAAAAGGA	T	171
GATCCCTTCT	GCCGCTGCC	CGGCCTCAGC	GCGCTTCTCC	TCCGCCCGTG	G	158
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGGCGTGTA	GGGAAAGAGG	G	154
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TCGAGGTTAT	GGCAGCACTG	CATAATTCTC	TACTGTTCAT	GCCATCCGTA	A	143
AGCTTGATCC	CGCCCTCCC	GTAGAGGAGC	CTCCACCGGC	CGGGGGACA	G	135
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGTGTG	GGGAAAGAGT	G	133
CCTGCTGAAC	CGCTCTCCG	ATCAGATCGG	AAGAGCGTCG	TGTAGGGAAA	G	124
AGCTTTCCTT	TCGCAGCGCC	GCCTCTGCCT	GCTCGCGCTG	TTGCAACTCT	A	123
CGGCATTCT	GCTGAACCGC	AGATCGGAAG	AGCGTCGTGT	AGGGAAAGAG	G	122
CGGCATTCT	GCTGAACCGC	TCTTCCGAGA	TCGGAAGAGC	GGCGGGGAGG	G	119
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGGGTA	GGGAAAGAGG	G	112
CGGCATTCT	GCTGAACCGA	GATCGGAAGA	GCGTCGTGGA	GGGAAAGAGT	G	112
CGGCATTCT	GCTGAACCGC	AGATCGGAAG	AGCGTCGTGT	AGGGAAAGAG	T	110
AGCTTAAAAG	ATGACACCGA	ACAGGGCGGG	GATGGCGCAG	GCGGCGGCCA	C	105
ACGTACGTAC	GTACGTACGT	AGATCGGAAG	AGCGTCGTGT	AGGGAAAGAG	G	104

Assembly

# Contigs	Total	Min	Max	Average	Median	N50	Sum
212	6,205,268	501	349,482	29,270	11,540	77,919	6,205,268



# Pseudomonas aeruginosa Sample 2

## Sequencing Summary

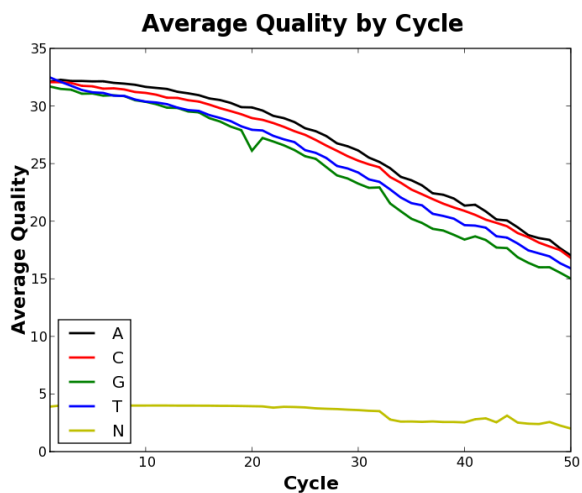
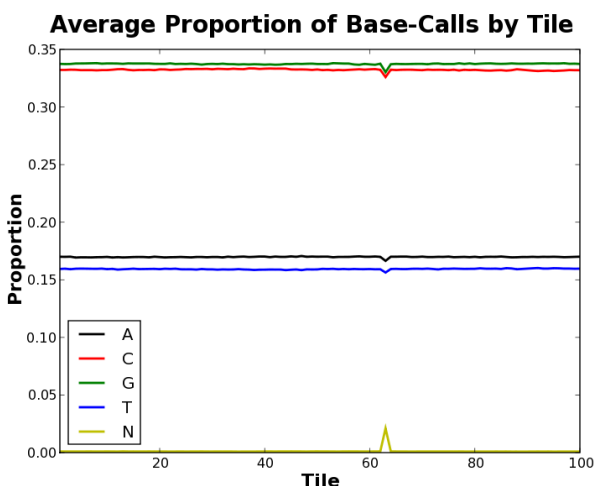
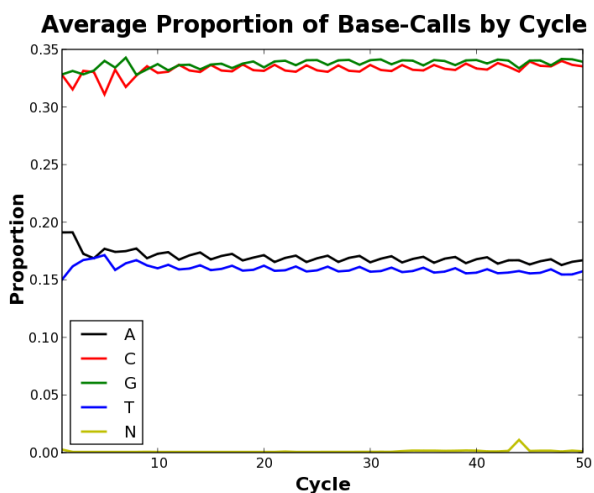
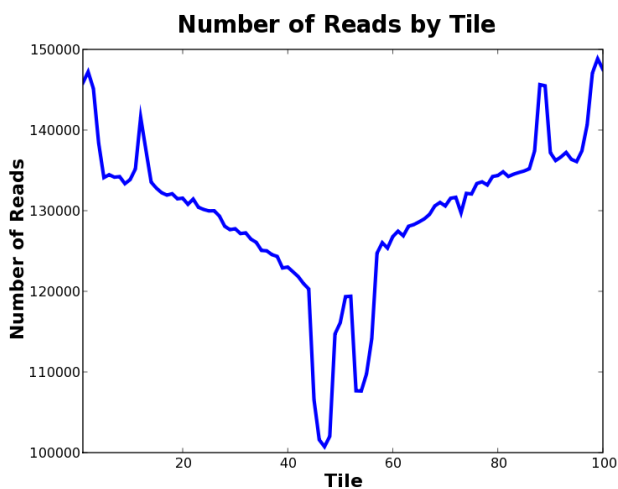
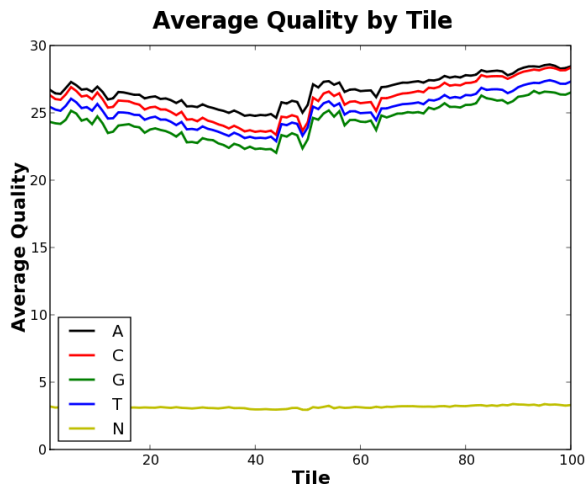
**# of Reads:** 25,940,318  
**GC Content:** 67.71%  
**Total Data:** 1,297 Mbases

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<b>Left 1</b>	50	12,970,159	7,702,557	59.39%	67.05%
<b>Right 1</b>			8,242,692	63.55%	68.38%

Quality Control

Left 1

File Format:	FASTQ
Unique Reads:	7,702,557
Total Reads:	12,970,159
Percent Unique:	59.39%
Reads Length:	50
GC Content:	67.05%
Reads with Adapters:	0
Percent Adapter Contamination	0.00%

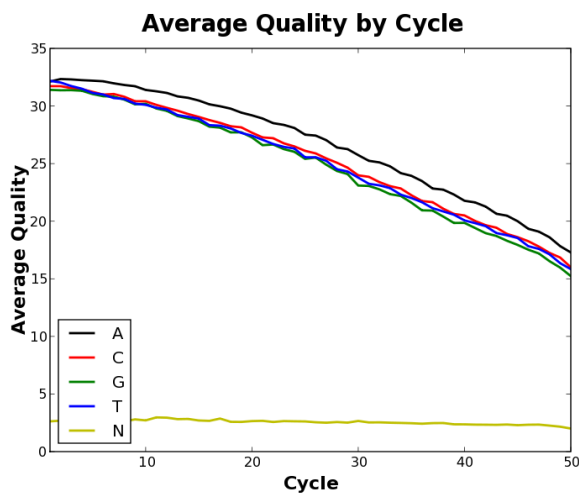
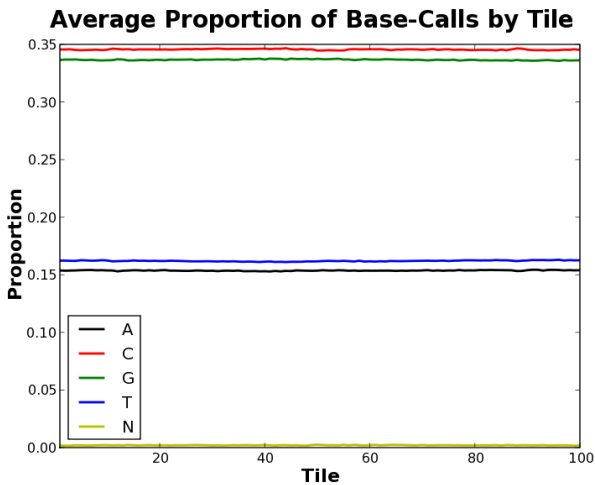
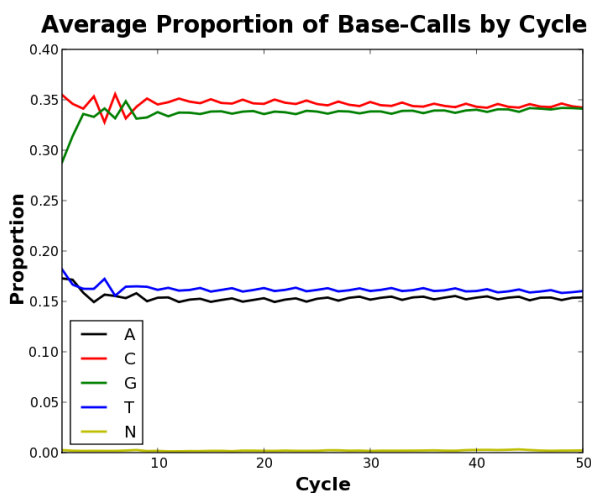
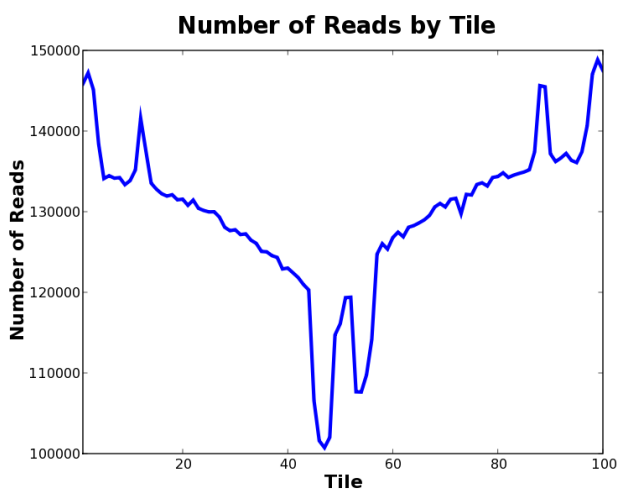
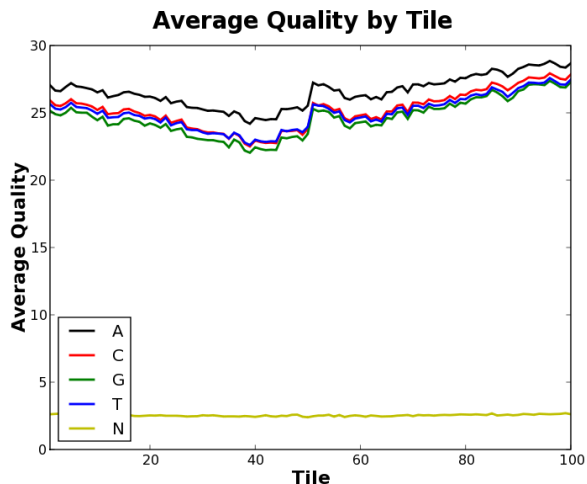


## Top 50 Read Sequences

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TGCCTGCAGG	TGGTCACCCG	TCCCGGCGAC	CTGGGGGCCA	TCGAGGCGCC	180
GAACAAAAAA	AAAAACAAA	AAAAACAAA	AAAAACAAA	AAAAACAAA	141
GATCGGAAGA	GCACACGTCT	GAAGTCCAGT	CACCAGATCA	TATCGTATGC	87
GATCGGAAGA	GCTCGTATGC	CGTCTTCTGC	TTGGATCGGA	AGAGCACACG	79
CCAGTCACCA	GATCATCTCG	TATGCCGTCT	TCTGCTTGAA	AAAAACAAA	44
GATCGGAAGA	GCACACGTCT	GAAGTCCAGT	CACCAGATCA	TCTCGTATTC	40
GACCGATCCC	ACGGATCCAA	CCGACCCGAC	CACGCCGGGC	AGTGACGGCG	38
AGGATCAGGG	TCTGGAGCGC	GGCGTACATC	GACGCCTTGG	TGGCGACCAC	37
TGGTCGGGAA	CTACCTGCCG	CAAGGCCCGG	ACCGATCCCA	CGGATCCAAC	36
ACCTGCGTCA	AGGCCCCGAC	CGATCCCACG	GATCCAACCG	ACCCGACCAC	35
GGTCGGGAAC	TACCTGCGTC	AAGGCCCGGA	CCGATCCCAC	GGATCCAACC	35
CGTCAAGGCC	CCGACCGATC	CCACGGATCC	AACCGACCCG	ACCACGCCGG	35
GTGGTCGGGA	ACTACCTGCG	TCAAGGCCCG	GACCGATCCC	ACGGATCCAA	34
GGTTCAAGAC	CAAGATGGAG	GCGCAGCAAT	TCGAGGCCAC	CGCGCGTCAG	33
AACTACCTGC	GTCAAGGCCG	CGACCGATCC	CACGGATCCA	ACCGACCCGA	33
GCCCCGCGAC	TTGCGGTAGG	CGTGGGCAAG	GATGGAGATC	CGCCGATCGG	31
TGCCGAGCTA	CGCGGATACG	GAAACCACCT	TCGACGAACT	CCAGTCACCA	31
GGCCGGGCTG	GAAGTGCCGA	GCTACGCGGA	TACGGAAACC	ACCTTCGACG	30
GGTCGTGGTC	GGGAACTACC	TGCGTCAAGG	CCCCGACCGA	TCCCACGGAT	30
GCTGGAAGTG	CCGAGCTACG	CGGATACGGA	AACCACCTTC	GACGAACTCC	30
GCTGACCATC	GTCCCCGATT	CCGAATACGC	CTCGCGGCCG	TGGAGGCAGA	29
TGCGTCAAGG	CCCCGACCGA	TCCCACGGAT	CAAACCGACC	CGACCACGCC	29
CGATCCCACG	GATCCAACCG	ACCCGACCAC	GCCGGGCAGT	GACGGCGGCG	28
GCCCCGGCTG	TCGTGGTCCG	GAAGTACCTG	CGTCAAGGCC	CCGACCGATC	28
TACCTGCGTC	AAGGCCCCGA	CCGATCCCAC	GGATCCAACC	GACCCGACCA	28
TGGAAGTGCC	GAGCTACGCG	GATACGGAAA	CCACCTTCGA	CGAACTCCAG	28
ATTCCGAATA	CGCCTCGCGG	CCCTGGAGGC	AGAAATGATC	GATTGGGAAT	28
GAATAGTGAC	GGAATGAGCA	TGGAAGTGA	AGAGCTTAGC	CCCAGTGCCC	27
TGGTCGTGGT	CGGGAACACT	CTGCGTCAAG	GCCCCGACCG	ATCCCACGGA	27
CCTGCGTCAA	GGCCCCGACC	GATCCCACGG	ATCCAACCGA	CCCGACCACG	27
GATCGGAAGA	GCACACGTCT	GAAGTCCAGT	CACCAGATCA	TCTCCTATTC	27
GATCCCACGG	ATCCAACCGA	CCCGACCACG	CCGGGCAGTG	ACGGCGGGCG	26
ACACCTGCAC	AGCGACAACG	CCTGACATAG	CGATCAGTCC	TCAAACAGCC	26
AAGGGATTTC	AGATCAGCGA	ATACAACATC	GAGCCGACCC	TGCTGGACGC	26
GCGCAACATG	CTGTAGATCA	GGCCGGCAAC	GGCCAGGATC	ACCAGGGCGC	26
GTGCTGAGTC	ACTGCGAAAC	CAACCAAGCC	GCTGTGCATA	TCGCCTTGGA	26
GAGTACGCG	GATACGGAAA	CCACCTTCGA	CGAACTCCAG	TCACCAGATC	26
GCGTCAAGGC	CCCGACCGAT	CCCACGGATC	CAACCGACCC	GACCACGCCG	26
GACCCGGGCT	GCCCGCCCGG	CTGGTCTGGT	TCGGGAACCTA	CCTGCGTCAA	25
ACCTGGGATG	ACGCCATCGC	CACCTGGGAA	AAGAAGGTCG	AGGACGCCAA	25
ACCCGACCAC	GCCGGGCGAG	GACGGCGGCG	GCGATGGCAA	TGGCGGGGGG	25
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AAGGATGGAG	ATCCGCCGAT	CGGCGAAGGG	ATGGGCGTTC	AGATCAACAG	25
GCTGAATGAA	GGCGAAACAG	CCGAATTTGC	AGCAGCGGGA	CAACTACGC	25
GATCGGAAGA	GCACACGTCT	GAAGTCCAGT	CACCAGATCA	TATCGTATTC	25
ATCCCACGGA	TCCAACCGAC	CGACCCACGC	CGGGCAGTGA	CGGCGGGCGC	24
ATACGCCTCG	CGGCCCTGGA	GGCAGAAATG	ATCGATTGGG	AATTCCTCGC	24
ATGCGAGTTC	GCGACACGCC	ATGAAGCCCT	CGGGGGTCGA	GGTCCACGCC	24
AGATCGCCAG	CGACGCCGCC	AAGGGCGCCG	GCGCGGGGCT	GGCCGGGCTG	24

Right 1

File Format:	FASTQ
Unique Reads:	8,242,692
Total Reads:	12,970,159
Percent Unique:	63.55%
Reads Length:	50
GC Content:	68.38%
Reads with Adapters:	0
Percent Adapter Contamination	0.00%



## Top 50 Read Sequences

GTTACGCATC	AACCGGGTGC	GCGAGGACTT	CGAATTCAAC	CTGCATTCCG	415
CCCCCCCCC	CCCCCCCCC	CCCCCCCCC	CCCCCCCCC	CCCCCCCCC	390
TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	103
CGTTGCCATC	GCCGCCCGTG	CCGCTGCCGT	CACCGTCGCC	GCTACCATCG	38
GCCGGGTGCG	AGGTGCCGTT	GCCATCGCCG	CCCGTGCCGC	TGCCGTCACC	38
TCTCTTTCGC	CGGGTCGCAG	GTGCCGTTGC	CATCGCCGCC	CGTGCCGCTG	36
CGCCGGGTGCG	CAGGTGCCGT	TGCCATCGCC	GCCCGTGCCG	CTGCCGTCAC	36
CTGCCGCTGG	CGCTGCTGCT	GATGGCCGCG	CTGATCGCCG	CCCTCATTCT	34
ACCAAGGGCT	CTGCCCTTGT	CATCCCGCTC	TTGCCGCCGA	GGGCTCGGGA	34
AGGTGCCGTT	GCCATCGCCG	CCCGTGCCGC	TGCCGTCACC	GTCGCCGCTA	33
TTGCCATCGC	CGCCCGTGCC	GCTGCCGTCA	CCGTGCCCGC	TACCATCGCC	32
CAGGTGCCGT	TGCCATCGCC	GCCCGTGCCG	CTGCCGTCAC	CGTCGCCGCT	31
TGCCGTTGCC	ATCGCCGCC	GTGCCGCTGC	CGTCACCGTC	GCCGCTACCA	31
GCAGGTGCCG	TTGCCATCGC	CGCCCGTGCC	GCTGCCGTCA	CCGTGCCCGC	31
CCCGCCGCCT	TCCGCCAGGT	TGAGGTCGAA	GCGCCCTTC	ATCTGATCGA	31
CGGGTCGCAG	GTGCCGTTGC	CATCGCCGCC	CGTGCCGCTG	CCGTCACCGT	30
TCCGACTACG	CCGGCCAAT	CTCCAGCCTG	CGCGTGGCGC	TGCTGCTGAT	29
CGTCGCCGCC	GCGACCATGA	TGATGTTTCA	CGCCTGCCGC	ACGCCAAGA	28
CCGGGTCGCA	GGTGCCGTTG	CCATCGCCGC	CCGTGCCGCT	GCCGTCACCG	28
CCTCACGCC	TCGATGGCGC	CGATCCGCGC	ATCCTCCAGG	GCGTGCTGGA	28
CTGGCGACGA	TTGGCGCTCC	GGCTGCTGCG	ACACCTGCCG	ACGTCCTG	28
TTCCGCCGGT	CGCAGGTGCC	GTTGCCATCG	CCGCCCGTGC	CGCTGCCGTC	28
GAGGTATCGC	CTCACGCCCT	CGATGGCGCC	GATCCGCGCA	TCCTCCAGGG	28
AGTTCTCTTT	CGCCGGGTCG	CAGGTGCCGT	TGCCATCGCC	GCCCGTGCCG	28
CAGTTCTCTT	TCGCCGGGTC	GCAGGTGCCG	TTGCCATCGC	CGCCCGTGCC	27
GATCGGAAGA	GCGTCGTGTA	GGGAAAGAGT	GTAGATCTCG	GTGGGGGCG	27
TCCAGCACGC	CCTGGAGGAT	GCGCGGATCG	GCGCCATCGA	GGGCGTGAGG	27
CACCAAGGGC	TCTGCCCTTG	TCATCCCGCT	CTTGCCCGCG	AGGGCTCGGG	27
AGCCAGGGAG	GCCGCTAGGC	CGTCGATCCA	GCCCCAGGCG	TAGCCGGTGG	26
CAGGGCAACG	GCGACGACAT	TGGCAGGACG	CCGTTGCAGC	AGACCTGCA	26
GATCGGAAGA	GCGTCGTGTA	GGGAAAGAGT	GTAGATCTCG	GTGGGGGCG	26
TCAGCCCGGT	CGCCTCGTTC	CGCAACCTGT	GCATCGCCGG	TTCCGTCACT	26
TCTTTCGCCG	GGTCGCAGGT	GCCGTTGCCA	TCGCCGCCCG	TGCCGCTGCC	26
TCGCCGGGTC	GCAGGTGCCG	TTGCCATCGC	CGCCCGTGCC	GCTGCCGTCA	26
TCCTGTTC	ACAGCCAGGT	ACGCAGCAGC	GCGCTATTCA	CCATGCGCAG	26
CATTGCACAA	CGCCGTGCCG	GCCCGCACTA	GACGACTGCG	CACCCGATGC	26
CATCGCCGCC	CGTGCCGCTG	CCGTCACCGT	CGCCGCTACC	ATCGCCCCG	26
CAGCCTGCGC	GTGGCGCTGC	TGCTGATGGC	CGCGTGATC	GCCGCCCTCA	26
CTTTCGCCG	GTCGCAGGTG	CCGTTGCCAT	CGCCGCCCGT	GCCGCTGCCG	26
CCGCCCGTGC	CGCTGCCGTC	ACCGTCGCCG	CTACCATCGC	CCCCGCCGTT	25
CGCAGGGCAG	TTGCCCGCCG	CCTTCGCCA	GGTTGAGGTC	GAAGGCGCCC	25
CACGTACGTG	AGCCTGAATC	TGTCGCTCCA	GTCGAGCGAT	GCGGCCTCC	25
GCGGCCATCA	GCAGCAGCGC	CACGCGCAGG	CTGGAGAGTT	GGCCGGCGTA	25
CGGGTCGCCA	TCGCCGAACG	GATCCCGGTT	CAGGGTCGCC	CACACGCTTT	25
CGCAGGTGCC	GTTGCCATCG	CCGCCCGTGC	CGTGCCGCTC	ACCGTCGCCG	25
TCCGTCACTG	CGCGCACTC	GCTGCCGGCC	TTCCGCCGGG	TGATCGACAC	25
TGCCATCGCC	GCCCGTGCCG	CTGCCGTCAC	CGTCGCCGCT	ACCATCGCCC	25
CACGATTGGC	GCTCCGGCTG	CTGCGACACC	TGCCGACGCT	CCTGGCGACC	25
CGTCCGGGCT	GCTGCGACAC	CTGCCGACGC	TCCTGGCGAC	CCTGCTCAAG	25
GACCTGGTAG	GTCAGGCTCG	GATCGGCATC	GCCGTAGACC	TTGGTCTTGG	24

Assembly

# Contigs	Total	Min	Max	Average	Median	N50	Sum
144	6,155,897	501	344,732	42,749	20,650	112,730	6,155,897

