

# Evaluating Metagenome Assembly on a Complex Community

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## Abstract

### NEEDS ENHANCEMENTS

**Motivation:** With the emergence of de novo assembly, several work have been to done to assemble metagenomic data from de novo. Several assemblers exist that are based on different assembly techniques. However, we still lack a study that analyze different assemblers behavior on metagenomic data .

**Problem statement:** In this paper, we performed analytical study for metagnome assembly using different assemblers and different preprocessing treatments. The aim of the analysis is studying how well metagenome assembly works, and which assembly works best. In addition, the study analyzes the resource requirements of the assembly.

**Approach:** We used a mock community dataset for the analysis, and used its reference genome for benchmark evaluation. We quality filtered the reads, then we applied 2 other preprocessing steps: digital normalization and partitioning. We used 4 different assembler: Velvet, IDBA-UD, SPAdes, and megahit to assemble the reads using each treatment. We used Quast to analyze assemblies accuracy.

**Results:** Results show that assembly works well. Velvet is the worst assembler in terms of accuracy and recourses utilizations. The results also showed that assembly counts to most of the reads.

**Conclusions:** Except for Velvet, assemblers works well. Further analysis is required to study which assembler is better used with each specific dataset. This step is left for our future work,

## Author Summary

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## Introduction

Metagenome is the sequencing of DNA in an environmental sample. While whole genome sequencing (WGS) usually targets one genome, metagenome targets several ones which introduces complexity to metagenome analysis due to genomic diversity and variable abundance within populations. Metagenomic assembly means the assembly of multiple genomes from mixed sequences of reads of multiple species in a microbial community. Most approaches for analyzing metagenomic data rely on mapping to reference genomes. However, not all microbial diversity of many environments are covered by reference databases. Hence, the need for de novo assembly of complex metagenomic data rises. Several assemblers exist that can be used for de novo assembly. In order to decide which assembly works best, we need to evaluate metagenome assembly generated by each assembler. In this paper, we provide, an evaluation for metegnome assembly generated by several assemblers and using different preprocessing treatments. We use a reference genome as a benchmark for the evaluation. The evaluation is based on assembly accuracy, and time and memory requirements. This evaluation shed light on doability of metagenome assembly and the minimum requirements needed for the assembly. In addition, knowing how each assembler works, helps deciding which assembler to use prior to assembly. However, the later point is left for our future work.

The comparative study in this paper is based on four different assemblers; Velvet [1], SPAdes [2], IDBA-UD [3], and Megahit [4].

Velvet [1] is a group de Bruin graph-based sequence assembly methods for very short reads that can both remove errors. It also uses read pair information to resolve a large number of repeats. The

error correction algorithm merges the sequences that belongs together. Then the repeat solver algorithm separates parts that share overlaps.

Spades [2] is an assembler for both single-cell and standard (multicell) assembly. SPAdes generates single-cell assemblies and provides information about genomes of uncultivable bacteria that vastly exceeds what may be obtained via traditional metagenomics studies.

IDBA-UD [3] is a de Bruijn graph approach for assembling reads from single cell sequencing or metagenomic sequencing technologies with uneven sequencing depths. IDBA-UD uses multiple depth-relative thresholds to remove erroneous k-mers in both low-depth and high-depth regions. It also uses paired-end information to solve the branch problem of low-depth short repeat regions. It applies an error correction step to correct reads of high-depth regions that can be aligned to high confident contigs.

Megahit [4] is a new approach that constructs a succinct de Bruijn graph using multiple k-mers, and uses a novel "mercy k-mer" approach that preserves low-abundance regions of reads. It also uses GPUs to accelerate the graph construction.

## Materials and Methods

### Datasets

We used a diverse mock community data set [5]. Raw reads contains 5536.29 megabases and 54,814,748 sequences for each file. In total, 11072.58 megabases and 109,629,496 sequences. The set also has a reference genome downloaded from XX. Using a reference genome makes the evaluation process easier and much better in terms of accuracy measures.

### Quality Filtering

We trimmed low-quality bases using trimmomatic-0.30.jar [6] and using PE and using TruSeq3 adapter. We also used Fastq quality filter from FASTX-Toolkit to filter sequences with low qualities with these parameters -Q33 -q 30 -p 50. The fastx utilities that are not paired-end aware; they're removing individual sequences. Because the paired-end files are interleaved, this means that there may now be some orphaned sequences in there. Downstream, we will want to pay special attention to the remaining paired sequences, so we use "extract-paired-reads.py" script in khmer/scripts to separate out the paired-end and single-end files.

### Mapping

To find out chimeric reads to evaluate initial reads (see Results Section), we used bwa-mem aligner with the default parameters. To estimate unaligned reads, we used the default parameters for bwa aln and bwa samse. We aligned paired-end reads and single-end reads separately and we aligned each as single reads using samse. We also used samtools import to convert sam files to bam files for each paired-end and single-end reads separately.

### Digital Normalization

First, we normalize everything to a coverage of 20, starting with the (more valuable) paired-ended reads by running "normalize-by-median.py" script in khmer/scripts. We used -p to keep pairs, k=20 for k-mer size, cutoff of coverage C=20, N=4 for number of k-mer counting tables, x=1e9 for lower bound on table size and with option savetable for further use. Then we used the same script to normalize the single-ended reads. We then use "filter-abund.py" script in khmer/scripts to trim off any k-mers that are abundance-1 in high-coverage reads. The -V option is used for variable coverage. We ran "extract-paired-reads.py" in khmer/scripts to separate paired-ended and single-ended reads.

## Partitioning

First, eliminate highly repetitive k-mers that could join multiple species using "filter-below-abund.py" script found in khmer/sandbox. Then we run partitioning using do-partition script found in khmer/scripts. We used  $k=32$  for k-mer size,  $x=1e9$  for lower bound on table size to use and  $threads=4$  for number of simultaneous threads to execute. We then extracted partitions to groups using "extract-partitions.py" script in khmer/scripts/ with  $X=100000$  for maximum group size. We finally, ran "extract-paired-reads.py" in khmer/scripts to separate paired-ended and single-ended reads.

## Metagenomes Assembly and evaluation

We assembled the reads using four different assemblers; Velvet [1], Idba [3], Spades [2], and Megahit [4]. For Velvet [1], we used kmers values from 19 to 51 incremented by 2. We also used -fastq.gz for fastq format, -shortPaired for the pe files and -short for the se files. Also, we used exp\_cov auto cov\_cutoff auto. For Idba [3], we also used -pre\_correction and -r for the pe files.

We examined the assembly quality of each assembler and treatment using Quast [7] using quast.py with these parameters -R for the reference genome and -o for the output and we use the default min contig length equal to 500.

## Results

### Quality filtering did not change the number of reads

We performed quality filtering to remove primers and poor-quality sequences. After trimming, we got 11024.50 megabases and 109,153,498 sequences for the pair-end reads and 14.86 megabases and 235,966 sequences for the single-end reads. In total, 11039.36 megabases and 109,389,464 sequences. After fastx, we got 10547.80 megabases and 104,433,622 sequences for the pair-end reads and 184.44 megabases and 106,326,865 sequences for the single-end reads. In total, 10732.23 megabases and 106,326,865 sequences. In summary, the quality filtering eliminates 3.01% of the reads.

### Initial Reads Evaluation

To evaluate initial reads, we mapped quality filtered reads using bwa aln [8] [XX CHECK THIS REFERENCE] to the reference genome. We then, extracted the unaligned sequences. There are 3,664,869 unaligned reads which represents 3.45% of the quality filtered reads. These unaligned reads are either errors and/or new sequences. We also used bwa mem [8] to look for chimeric reads where a read spans two different genes, we found X310,128X chimeric reads. [REMINDER TO ASK TITUS]

### Digital normalization and partitioning resources utilizations

To examine if digital normalization and partitioning are doable treatments, we evaluated the resource utilization for each of them. Digital normalization utilized 74.93 GB of memory and took around 3 hours and 53 minutes to run. Partitioning utilized 21.78 GB and around 2 hours and 57 minutes to run.

### Digital normalization and partitioning decreased the total number of reads

To evaluate how many reads digital normalization and partitioning throws away, we estimated number of reads after running each treatment. After digital normalization, the pair ended file contains 1687.59 megabases and 16,853,716 sequences while the single ended file contains 5.86 megabases and 64,638 sequences. After partitioning, we got 28 partitions. The largest partition has 1379.27 megabases. The

smallest partition has 7.14 megabases. The total base pairs in all partitions is 1651.53 megabases. Clearly, digital normalization and partitioning decrease the total number of reads.

## Metagenome assemblers recover the great majority of the known content

We used four assemblies and run each one using each treatment; quality filtering, digital normalization, and partitioning. The unaligned length for assembly is 8,977,149 bp, 10,709,716 bp, 10,597,529 bp, and 10,686,421 bp using quality filtered reads for Velvet, IDBA, SPAdes, and Megahit respectively. The genome fraction % is the percentage of aligned bases in the reference. A base in the reference is aligned if there is at least one contig with at least one alignment to this base. The genome fraction percentage is 72.949 %, 90.969 %, 90.424%, and 90.358% using quality filtered reads for Velvet, IDBA, SPAdes, and Megahit respectively. Misassembled contigs length is the total number of bases in misassembled contigs. Misassemblies contigs length is 631, 1032, 752, and 648 using quality filtered reads for Velvet, IDBA, SPAdes, and Megahit respectively. Clearly, SPAdes, IDBA, and Megahit have fairly similar results and they all outperformed Velvet.

Table 1 shows various quality metrics for the results of the assembly using combinations of four different assemblers and different preprocessing treatments. Figure 1 shows total length of different assemblies using different min contig length. Increasing the min contig length slightly decreased the total assembly length.

## Digital normalization and partitioning reduced memory and time requirements for assembly

In this section, we aim to explore time and memory requirements of metagenome assembly using each preprocessing treatments.

Table 2 shows the running time and memory utilizations for four assemblers and different reads treatments.

For Velvet assemblies, it took  $\sim 60$  hours using quality filtered reads, while it took only  $\sim 6$  hours using digital normalizations and  $\sim 4$  hours using partitioning. For IDBA assemblies, it took  $\sim 33$  hours using quality filtered reads, while it took  $\sim 6$  hours using digital normalization and  $\sim 8$  hours using partitioning. SPAdes assemblies utilized  $\sim 67$  hours using quality filtered reads while it took  $\sim 15$  hours and  $\sim 7$  hours using digital normalization and partitioning respectively. Finally, for megahit, it took  $\sim 2$  hours,  $\sim$  half an hour, and  $\sim$  hour and a half using quality-filtered reads, digital normalization, and partitioning respectively.

For Velvet assemblies, it used 98.40 GB of memory using quality filtered reads, while it used one 52.67 GB and 35.23 GB of memory when applying digital normalization and partitioning respectively. For IDBA assemblies, it used 123.84 GB of memory using quality filtered reads, while it used one 99.88 GB and 76.53 GB of memory when applying digital normalization and partitioning respectively. For SPAdes assemblies, it used 381.79 GB of memory using quality filtered reads, while it used one 121.52 GB and 94.70 GB of memory when applying digital normalization and partitioning respectively. For megahit, it utilizes 33.41 GB, 18.89 GB, 13.17 GB for quality-filtered reads, digital normalization, and partitioning respectively. See Table 2 for more details. Clearly, Megahit is the best assembler in terms of memory and time utilization. We also conclude that Digital normalization and partitioning treatments reduced time and memory requirements of assembly while they didn't affect assemblies quality. This means that digital normalization throws unnecessary reads.

## Something about misassemblies

As shown in Table 1, using quality filtered reads, misassemblies contigs length are 16,566,891, 21,777,032, 28,238,787 and 11,927,502 for Velvet, SPAdes, IDBA, and Megahit respectively. Clearly, Velvet and

Megahit has fewer misassemblies.

Velvet/quality filtering shows the least mismatches percentage 0.06%. IDBA/quality filtering, SPAdes/quality filtering, and Megahit/quality filtering have 0.08%, 0.09%, and 0.08% mismatches percentages respectively. Digital normalization and partitioning slightly increased the mismatches percentages. For Velvet, mismatches increased from 0.06% using quality filtering to 0.09% and 0.12% using digital normalization and partitioning respectively. For IDBA, the percentage increased from 0.08% using quality filtering, to 0.12% for both digital normalization and partitioning. For SPAdes, the percentage increased from 0.09% using quality filtering to 0.12% for both digital normalization and partitioning. For Megahit, it increased from 0.08% using quality filtering to 0.10% for both digital normalization and partitioning. Indels percentage is 0.03%, 0.01%, 0.01%, and 0.01% for Velvet, IDBA, SPAdes, and Megahit respectively. Clearly, the mismatches percentage is very low. Digital normalization and partitioning insignificantly increased the mismatches.

See Table 3 for more details about misassemblies contigs, the types of misassembly events, mismatches and indels lengths.

## Assemblies contain most of the reference

We aligned the reference genome to each assembly to find out what exists in the reference genome and not found in the assemblies. Aligning the reference genome to IDBA and SPAdes and IDBA quality filtered assemblies, we got zero unaligned contigs, in addition to 29,776,904, 2,062,384, 2,063,510, and 2,063,473 partially unaligned length for Velvet, IDBA, SPAdes, and Megahit respectively which represent 18.11%, 1.03%, 1.03%, and 0.97% of their corresponding assemblies length respectively.

Using digital normalization, we got also zero unaligned contigs, with partial unaligned length 2,046,452, 2,067,700, 2,063,803, and 2,063,457 for Velvet, IDBA, SPAdes, and Megahit respectively which represent 1.02%, 1.03%, 1.03%, and 1.03% of their corresponding assemblies length respectively.

Using partitioning, we got also zero unaligned contigs, with partial unaligned length 2,053,035, 2,071,046, 2,069,811 and 2,068,118 for Velvet, IDBA, SPAdes, and Megahit respectively which represent 1.02%, 1.04%, 1.04%, and 1.04% of their corresponding assemblies length respectively.

## Assembly Statistics

Contig or scaffold N50 is a weighted median statistic such that 50% of the entire assembly is contained in contigs or scaffolds equal to or larger than this value. Using quality filtering, N50 is 38,028, 49,773, 42,773, and 35,136 for Velvet, IDBA, SPAdes, and Megahit respectively. The NG50 statistic is the same as N50 except that it is 50% of the known reference genome size that must be achieved. Using quality filtered reads, NG50 is 22,223, 45,748, 38,841, and 32,251 for Velvet, IDBA, SPAdes, and Megahit respectively. N50 and NG50 decreases with digital normalization and partitioning. For diginorm assemblies, N50 is 18,944 47,828, 35,580, and 35,427 for Velvet, IDBA, SPAdes, and Megahit respectively. For partitioning, N50 is 8,504, 26,575, 22,319, and 17,492, for Velvet, IDBA, SPAdes, and Megahit respectively. See Table 1 for more details.

## Metagenome assemblies account for the majority of reads

To further evaluate assemblies, we mapped the quality filtered reads to each assembly using bwa [8]. Then we extracted the unaligned sequences. Table 4 shows the number and percentages of unaligned sequences from mapping quality filtered reads to each assembly. For all treatments assemblies, the full set of trimmed reads were used for mapping. Default parameters were used, and both paired ends and singletons were mapped. Samtools [9] was used for format conversion from SAM to BAM format, and also to calculate the percentage of mapped reads. We conclude that assemblies account for the majority of reads. For quality-filtered assembly, the number of unaligned reads is 6,801,329, 1,490,609 and 2,100,555,

and 1,559,300 for Velvet, IDBA, SPAdes, and megahit respectively. This represents 4.26 %, 0.75%, 1.06%, and 0.79% of the quality filtered sequences. These percentages reflect errors or low coverage reads. See Table 4 for more details.

We then aligned the unaligned contigs of each assembly with different treatments to the unaligned contigs of IDBA assembly using quality filtered treatment. Using quality filtered reads, the genome fraction equals 80.613%, 91.922%, and 92.715% for Velvet, SPAdes, and Megahit respectively. The unaligned length is 2,475,529, 2,174,574, and 916,247 for Velvet, SPAdes, and Megahit respectively using quality filtered reads, representing 31.45%, 26.22% and 12.74% of the reference length which is IDBA unaligned contigs using quality filtered reads. See Table 5 for more details. We conclude that unalignments are almost common among assemblers. [XX Needs better explanation]

Figure 2 shows genome fraction percentages using different min contig length.

To further analyze what are these unknowns, ADD STUFF OF FUNGENES HERE.

## Discussion

### Assembly works pretty well

Except for Velvet assembly using quality filtered reads, the genome fraction percentage is 88% or higher. Unaligned length is less than 1% for all assemblers and using different treatments. Misassembled length is less than 1.3% for all assemblers and using different treatments. We conclude that assembly works well although there are some rooms for improvements including enhancing accuracy, and decreasing time and memory requirements. Velvet shows the least performance in terms of accuracy and time, and memory utilizations. However, the difference between other assemblers are not significant. Hence, more investigations are needed to decide what assembler to use prior assembly. Such analysis is left for our future work.

### Digital normalization and partitioning significantly reduce running time and memory utilizations

The difference between genome fraction percentage using quality filtered reads versus digital normalizations and partitioning doesn't exceed 1%. However, the time and memory resource are reduced a lot using digital normalization and partitioning. We conclude that digital normalization and partitioning are beneficial steps for assembly to reduce time and memory utilities.

### Digital normalization and partitioning do not affect misassemblies and unalignments

Except for Velvet assemblies, misassemblies are not affected by digital normalization and partitioning. Mapping the unaligned contigs of different assemblies and different treatments to the unaligned contigs of IDBA assembly using quality filtered , shows genome fraction percentage is 91% or higher. This means the unaligned contigs are common among assemblers with various treatments and they are likely to be unknowns, new assemblies, or contamination. This indicates that digital normalization and partitioning enhance assembly time and memory requirements without affecting assembly accuracy.

## Acknowledgments

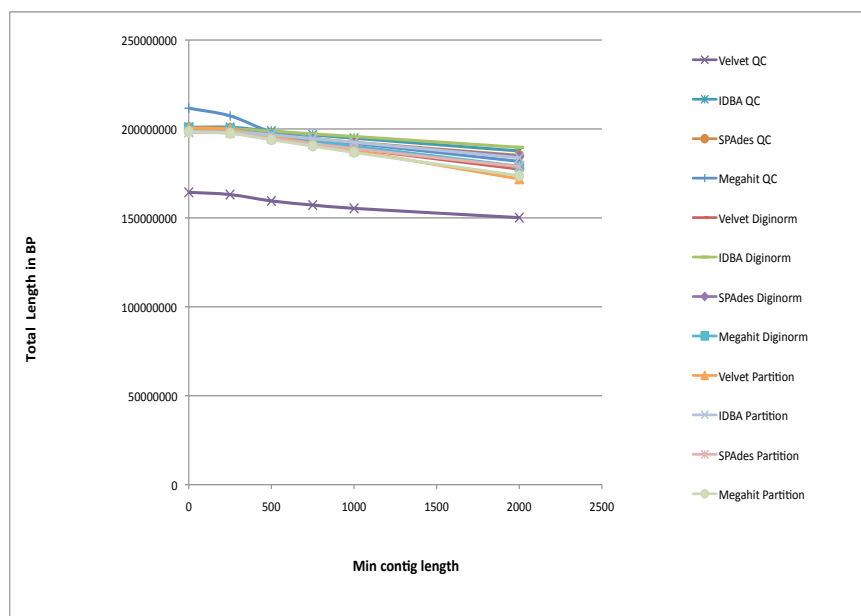
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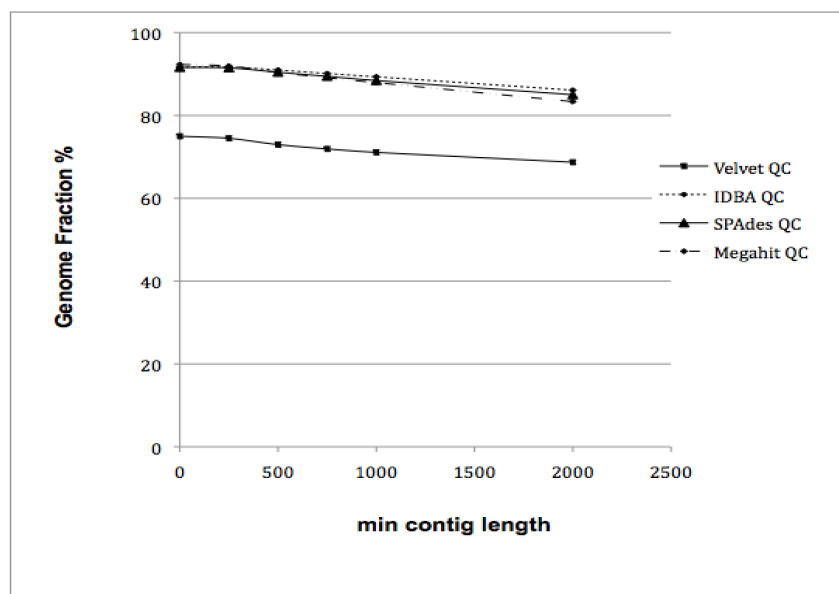
## Figure Legends

## Tables

## Supporting Information Legends



**Figure 1.** Total Length of assemblies in basepairs based on different min contigs length.



**Figure 2.** Genome Fraction of assemblies in basepairs based on different min contigs length.



**Table 1.** Assembly Quality Metrics

<b>Treatment/Quality Metric</b>	<b>Quality Filtering</b>	<b>Digital Normalization</b>	<b>Partition</b>
<b>(1) Velvet</b>			
<b>Genome Fraction</b>	72.949	89.043	88.879
<b>Unaligned Length</b>	8,977,149	10,909,693	11,317,834
<b>Misassembled contigs length</b>	16,566,891	25,594,315	16,922,852
<b>N50</b>	38,028	18,944	8,504
<b>NG50</b>	22223	17212	7905
<b>(2) Idba</b>			
<b>Genome Fraction</b>	90.969	91.003	90.082
<b>Unaligned Length</b>	10,709,716	10,637,811	10,644,357
<b>Misassembled contigs length</b>	21,777,032	27,668,818	18,440,791
<b>N50</b>	49773	47828	26575
<b>NG50</b>	45748	44351	24326
<b>(3) Spades</b>			
<b>Genome Fraction</b>	90.424	90.173	89.272
<b>Unaligned Length</b>	10,597,529	10,621,398	10,500,235
<b>Misassembled contigs length</b>	28,238,787	23,103,154	14,338,099
<b>N50</b>	42773	35580	22319
<b>NG50</b>	38841	32598	19909
<b>(4) Megahit</b>			
<b>Genome Fraction</b>	90.358	89.92	88.769
<b>Unaligned Length</b>	10,686,421	10,581,435	10,564,244
<b>Misassembled contigs length</b>	11,927,502	17,319,534	11,814,070
<b>N50</b>	35,254	35,427	17,492
<b>NG50</b>	32251	25248	15393

**Table 2.** Running Time and Memory Utilization

<b>Treatment/Quality Metric</b>	<b>Quality Filtering</b>	<b>Digital Normalization</b>	<b>Partition</b>
<b>(1) Velvet</b>			
<b>Running Time</b>	60:42:52	6:48:46	4:30:36
<b>Memory Utilization in GB</b>	98.40	52.67	35.23
<b>(2) Idba</b>			
<b>Running Time</b>	33:53:46	6:34:24	8:30:29
<b>Memory Utilization in GB</b>	123.84	99.88	76.53
<b>(3) Spades</b>			
<b>Running Time</b>	67:02:16	15:53:10	7:54:26
<b>Memory Utilization in GB</b>	381.79	121.52	94.70
<b>(4) Megahit</b>			
<b>Running Time</b>	1:52:55	0:30:23	1:23:28
<b>Memory Utilization in GB</b>	33.41	18.89	13.17

**Table 3.** Misassemblies

Assembly	Quality Filtering	Digital Normalization	Partition
<b>(1) Velvet</b>			
Misassemblies	917	5271	5202
Relocations	592	998	1036
Translocations	309	4262	4153
Inversions	16	11	13
Misassembled Contigs	631	3104	3337
Mismatches	104,740	174,446	178,348
Percentage of Mismatches	0.06%	0.09%	0.12%
Indels Length	50,190	181,453	346,988
Indels Percentage	0.03%	0.09%	0.18%
<b>(3) IDBA</b>			
Misassemblies	1223	1094	960
Relocations	613	668	578
Translocations	580	398	350
Inversions	30	28	32
Misassembled Contigs	1032	916	828
Mismatches	162,733	231,432	230,840
Percentage of Mismatches	0.08%	0.12%	0.12%
Indels Length	30,433	43,358	42,523
Indels Percentage	0.01%	0.02%	0.02%
<b>(2) SPAdes</b>			
Misassemblies	894	997	753
Relocations	608	613	496
Translocations	267	368	239
Inversions	19	16	18
Misassembled Contigs	752	881	654
Mismatches	184,630	244,849	235,396
Percentage of Mismatches	0.09%	0.12%	0.12%
Indels Length	27,328	32,783	21,516
Indels Percentage	0.01%	0.02%	0.01%
<b>(4) Megahit</b>			
Misassemblies	738	880	748
Relocations	448	593	513
Translocations	172	274	222
Inversions	118	13	13
Misassembled Contigs	648	780	677
Mismatches	152,964	207,349	203,515
Percentage of Mismatches	0.08%	0.10%	0.10%
Indels Length	15,298	18,195	16,517
Indels Percentage	0.01%	0.01%	0.01%

**Table 4.** Mapping quality-filtered reads to assemblies

Treatment	Quality Filtering	Digital Normalization	Partition
<b>(1) Velvet</b>			
No. of Unaligned Sequences	6,801,329	3,375,222	3,890,205
Percentage	4.26%	1.73%	1.99 %
<b>(2) Idba</b>			
No. of Unaligned Sequences	1,490,609	173,871	2,297,377
Percentage	0.75%	0.87%	1.17%
<b>(3) Spades</b>			
No. of Unaligned Sequences	2,100,555	2,439,158	2,804,006
Percentage	1.06%	1.24%	1.44%
<b>(4) Megahit</b>			
No. of Unaligned Sequences	1,559,300	2,082,881	2,747,427
Percentage	0.79%	1.06%	1.42%

**Table 5.** Mapping unaligned contigs to Idba quality-filtered unaligned contigs

Treatment/Quality Metric	Quality Filtering	Digital Normalization	Partition
<b>(1) Velvet</b>			
Genome Fraction	80.613 %	92.03%	92.982%
Unaligned Length	2,475,529	3192491	3,868,558
Percentage of unaligned	31.45%	33.92%	41.11%
<b>(2) Idba</b>			
Genome Fraction	-	91.53%	94.72%
Unaligned Length	-	498,299	1,320,036
Percentage of unaligned	-	7.47%	17.21%
<b>(3) Spades</b>			
Genome Fraction	91.92%	93.959%	94.826%
Unaligned Length	2,174,574	1,951,911	2,398,664
Percentage of unaligned	26.22%	23.64%	27.46%
<b>(4) Megahit</b>			
Genome Fraction	92.715%	91.838%	92.219%
Unaligned Length	916,247	1,569,436	3,832,050
Percentage of unaligned	12.74%	20.33%	38.28%

**Table 6.** Supplementary Table: More Assembly Quality Metrics

<b>Treatment/Quality Metric</b>	<b>Quality Filtering</b>	<b>Digital Normalization</b>	<b>Partition</b>
<b>(1) Velvet</b>			
<b>N75</b>	13301	6084	3771
<b>NG75</b>	1186	4805	3214
<b>L50</b>	1013	2455	6037
<b>LG50</b>	1806	2740	6641
<b>L75</b>	2777	7026	14734
<b>LG75</b>	11087	8460	16867
<b>(2) Idba</b>			
<b>N75</b>	11693	12154	7834
<b>NG75</b>	9617	10221	6461
<b>L50</b>	828	896	1536
<b>LG50</b>	899	970	1712
<b>L75</b>	2986	3025	5062
<b>LG75</b>	3467	3484	6002
<b>N75</b>	11263	10554	6900
<b>NG75</b>	9005	8379	5401
<b>L50</b>	974	1192	1846
<b>LG50</b>	1078	1325	2108
<b>L75</b>	3276	3768	5840
<b>LG75</b>	3908	4495	7198
<b>(4) Megahit</b>			
<b>N75</b>	8166	7230	5271
<b>NG75</b>	6601	5632	4030
<b>L50</b>	1199	1582	2490
<b>LG50</b>	1306	1757	2848
<b>L75</b>	4164	5063	7670
<b>LG75</b>	4907	6147	9581