

# 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 containing 64 known species, sequenced with Illumina HiSeq, yielding 109,629,496 paired-end sequences with an untrimmed length of 11.07 Gbp and an estimated insert size of  $\sim 380$  [5]. The two unfiltered read files each contained 5.5 Gbp of sequence data.

In total, the data set contained 11.1 Gbp of DNA sequence in 109,629,496 reads. We received the reference genomes from the original authors (posted on FigShare at 10.6084/m9.figshare.1506873) and the original reads are available through the NCBI Sequence Read Archive at Accession SRX200676.

### Quality Filtering

We removed adapters with Trimmomatic v0.30 in paired-end mode with the Truseq [6]. We next used the fastq-quality\_filter from the FASTX-Toolkit v0.0.13.2 [7] to remove sequences using the parameters -Q33 -q 30 -p 50, which keeps all sequences with 50% or more bases with quality score greater than or equal to 30.

### Mapping

We aligned all quality-filtered reads to the reference metagenome with bwa aln (v0.7.7.r441) [8]. We aligned paired-end and orphaned reads separately, and we aligned each as single reads using bwa samse. We then used samtools (v0.1.19) [9] to convert SAM files to BAM files for both paired-end and orphaned reads. To find the unaligned reads, we count the records with the "4" flag in the SAM files [9].

We found chimeric alignments with the bwa mem aligner using the default parameters (v0.7.7.r441). Chimeric alignments cut reads in two (or more). For each chimeric alignment, in the SAM file, there will be a primary alignment and at least one secondary alignment tagged SA. To count the chimeric alignments, we count the records with the "SA" flag in the SAM file [9].

### Reference Coverage

To evaluate how much of the reference genome was contained in the read data, we used bwa aln to map quality filtered reads, digitally normalized reads and partitioned reads to the reference genome, generating a SAM file from each. We then calculated how many reference bases are contained in at least one mapped read (script `sam-calc-refcov-cmp.py`).

## Digital Normalization

We applied the `normalize-by-median.py` script from khmer v1.1 to execute abundance normalization (“digital normalization”, [10]) on the data, retaining paired reads and using a k-mer size of 20 (`-p -k 20`). We executed digital normalization with 4 hash tables, each 1 GB in size (`-N 4 -x 1e9`). After read normalization, we used the `filter-abund.py` script to trim high-abundance reads (estimated k-mer coverage  $\geq 20$ ) at low-abundance k-mers (k-mer abundance  $\leq 2$ ) to remove erroneous k-mers [11] [12].

## Partitioning

We next applied partitioning to the data [13,14]. We first eliminated high-abundance k-mers that could join multiple species bins using the `filter-below-abund.py` script from khmer v1.1 using an abundance cutoff of 50 or higher. We then ran `do-partition.py` with a k-mer size of 32 and 4 Bloom filters each of size 1 GB for partitioning (`-k 32 -N 4 -x 1e9`). After partitioning, partitions were extracted to groups using the `extract-partitions.py` script with a maximum group size of 100,000 (`-X 100000`).

## Metagenomes Assembly and evaluation

We assembled the reads using four different assemblers: Velvet [1], IDBA-UD [3], SPAdes [2], and MEGAHIT [4].

For Velvet v1.2.07 [1], we used k-mer 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 asked Velvet to automatically calculate expected coverage and coverage cutoff (`-exp_cov auto -cov_cutoff auto`). From among the many assemblies, one for each k-mer size, we then chose the assembly that had the most bases in contigs longer than 500 bp (script `calc-best-assembly.py`).

For IDBA-UD v1.1.1 [3], we used `-pre_correction` to perform pre-correction before assembly and `-r` for the pe files. For SPAdes v3.1.1 [2], we used `-sc -pe1-12` where `-sc` is required for MDA (single-cell) data and `-pe1-12` for file with interlaced reads for the first paired-end library.

For MEGAHIT [4], we used `-l 101 -m 3e9 -cpu-only` where `-l` is for maximum read length, `-m` is for max memory in byte to be used, and `-cpu-only` to use CPU not GPU.

We examined the assembly quality of each assembler and treatment using QUAST v2.3 [15] using `quast.py` and we use the default minimum contig length equal to 500.

## Results

### Initial Evaluation of the Reads

We removed primers and poor-quality sequences as described in Methods. We retained 11.00 Gbp in 109,153,498 paired-end sequences, and 14.9 Mbp in 235,966 orphaned reads. After quality filtering, 10.7 Gbp of sequence remained in 106,134,639 paired-end sequences, with 12.6 Mbp in 2,226 orphan sequences. In total, only 3.01% of the reads were removed (3302631 reads, 340345361 bp), indicating that the original reads are high quality (see also [12], where an independent analysis of error rates in this data set using k-mer abundances found a very low error rate).

We mapped quality filtered reads to the metagenome reference. We found 3,664,869 unaligned reads which represent 3.45% of the total quality filtered reads. These unaligned reads are either highly erroneous reads that cannot be mapped, or are from sequences not present in the reference genomes. For mapped reads, the quality of mapping was high, with 92.0m reads (86.49% of the quality filtered reads) having a MAPQ  $\geq 30$ .

We then evaluated the fraction of the reference genome covered by at least one read (see Methods for details). Quality filtered reads cover 203,030,147 (98.75%) bases of the reference genome (205,603,715 bp total)

## Effect of Digital normalization and partitioning

After digital normalization, we retained 1687.59 Mbp in 6,853,716 paired-end sequences, and 5.86 Mbp in 64,638 orphaned reads. After partitioning, we got 29 partitions. For paired-end sequences, the largest partition has 1.38 Gbp, and the smallest partition has 7.14 Mbp, in total, 1651.53 Mbp. For orphaned sequences, the largest partition has 13.90

Mbp, the smallest partition has 2.52 Mbp, in total 24.6 Mbp. Digital normalized reads and partitioned reads covered 202,201,168 and 201,193,779 bases of the reference genome (205,603,715), or 98.34%, and 97.85% of the reference respectively.

For mapped reads, the quality of mapping was high, with 15.25m reads and 15.16m reads having  $\text{MAPQ} \geq 30$ , using digital normalized reads, and partitioned reads respectively.

We have 28,969 and 26,960 chimeric reads using digital normalized reads and partitioned reads respectively. Digital normalization and partitioning decreased chimeric alignments which is less than the chimeric reads found using quality filtered reads (310,131).

## Compute Cost of Assembly

We estimated time and memory requirements for each of them. We also estimated the running time and memory utilization for each assembler under both treatments and compared to assemblers time and memory requirements using quality filtered reads.

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 a half to run.

For Velvet assemblies, table 2 row 3, 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-UD assemblies, table 2 row 6, 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, table 2 row 9. 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, table 2 row 12.

For Velvet assemblies, table 2 row 4, 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-UD assemblies, table 2 row 7, it used 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, table 2 row 10, 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, table 2 row 13 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 (see above).

## Assembly Comparisons

All of the assembler/treatment comparisons (with the exception of Velvet/QC, which will not be considered further) recovered approximately 90% of the reference genome. IDBA/QC yielded the best assembled length (as measured by N50), but also had the largest number of bases in misassembled contigs; however,

MEGAHIT (when compared treatment-to-treatment) had the fewest number of bases in misassembled contigs, while still retaining a high N50.

IDBA/QC again performed best in both assembly length and genome recovery when looking at small contigs: Figure 1 and Figure 2 show that IDBA/QC has more data in long contigs than do any of the other assembler/treatment pairs.

Digital normalization increased the number of bases in misassembled contigs, in general, while the partitioning treatment always had the fewest number of bases in misassembled contigs. Digital normalization always decreased the N50, and partitioning after digital normalization also always decreased the N50.

All assemblies have approximately the same number of unaligned bases, suggesting that data missing from the reference is being assembled. We will examine this below.

## Evaluation against Reference Genome

We aligned each assembly to the reference genome using Quast [15]. To evaluate the quality of the assembly, we used different quality metrics, including the unaligned length and genome fraction percentage. 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 unaligned length 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-UD, SPAdes, and MEGAHIT respectively. The genome fraction percentage is 72.949 %, 90.969 %, 90.424%, and 90.358% using quality filtered reads for Velvet, IDBA-UD, SPAdes, and Megahit respectively. Using digital normalization, the genome fraction is 89.043%, 91.003%, 90.173%, and 89.92% for Velvet, IDBA-UD, SPAdes, and Megahit respectively. Using partitioning, the genome fraction is 88.879%, 90.082%, 89.272%, and 88.769% for Velvet, IDBA-UD, SPAdes, and MEGAHIT respectively. Except for Velvet assemblies, digital normalization and partitioning did not effect genome fraction percentatge. However, for Velvet assemblies, digital normalization and partitioning increased the genome fraction percentage. 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 [16]. 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 assemblies, the full set of trimmed reads were used for mapping. Default parameters were used, and both paired ends and singletons were mapped. Samtools [17] was used for format conversion from SAM to BAM format, and also to calculate the percentage of mapped 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-UD, SPAdes, and MEGAHIT respectively. This represents 6.40%, 1.40%, 1.97%, and 1.47% of the total number of reads respectively. These percentages reflect errors or low coverage reads. See Table 4 for more details.

## Decreasing Coverage did not effect assembly quality

We extracted random samples of size 25%, 50%, and 75% of the raw reads . We quality filtered each sample, then applied digital normalization and partitioning. For quality filtered reads, Velvet assembly genome fraction decreased from 72.95% using all reads to 71.31%, 70.09%, and 63.53% using 75%, 50%, and 25% of reads respectively. IDBA assembly genome fraction decreased from 90.97% using all reads to 86.90%, 84.66%, and 76.98% using 75%, 50%, and 25% of reads respectively. SPAdes assembly genome fraction decreased from 90.42% using all reads to 87.54%, 86.00%, and 80.05% using 75%, 50%, and 25% of reads respectively. Megahit assembly genome fraction decreased from 90.36% using all reads to 86.00%,

83.87%, and 76.19% using 75%, 50%, and 25% of reads respectively. Figure 3 shows genome fraction percentages for different assemblies using different coverage. We conclude that decreasing coverage did not highly affect assemblies qualities.

## Assembly Errors

Misassembled contigs length is the total number of bases in misassembled contigs. As shown in Table 1, using quality filtered reads, mis-assemblies contigs length are 16,566,891, 21,777,032, 28,238,787 and 11,927,502 for Velvet, SPAdes, IDBA-UD, and MEGAHIT respectively which represents 8.057%, 10.59%, 13.73% and 5.801% of the reference genome respectively.

Using digital normalization, mis-assemblies contigs length are 25,594,315, 27,668,818, 23,103,154, and 17,319,534 for Velvet, SPAdes, IDBA-UD, and MEGAHIT respectively which represents 12.45%, 13.46%, 11.24% and 8.42% of the reference genome respectively.

Using partitioning, mis-assemblies contigs length are 16,922,852, 18,440,791, 14,338,099, and 11,814,070 for Velvet, SPAdes, IDBA-UD, and MEGAHIT respectively which represents 8.23%, 8.97%, 6.97% and 5.75% of the reference genome respectively.

Although IDBA-UD has the highest NG50 (see above), IDBA-UD shows the highest mis-assemblies contigs length using digital normalization and partitioning. It also shows a high mis-assemblies contigs length using quality filtering but not the highest.

Using quality filtering, mismatches percentages are 0.05%, 0.08%, 0.09%, and 0.07% for Velvet, IDBA-UD, SPAdes, and MEGAHIT respectively. Indels percentages are 0.02%, 0.014%, 0.013%, and 0.007% using Velvet, IDBA-UD, SPAdes, and MEGAHIT respectively. Percentages are computed with respect to the reference genome. See Table 3 for more details about mis-assemblies contigs, the types of misassembly events, mismatches and indels lengths.

## More about misassemblies

We looked for the genomes that has 10 regions or more that are misassembled by all the assemblers. Using quality filtering, *Enterococcus faecalis\_V583*, *Desulfovibrio vulgaris\_DP4*, *Sulfurihydrogenibium yellowstonense\_SS-5*, *Thermus thermophilus\_HB27*, and *Pyrococcus furiosus\_DSM.3638* has 70, 26, 22, 56, and 11 regions that are misassembled by all the assemblers. The misassembled regions are scattered with average gap length equal to 548,867, 875,212, 229,042, 305,389, and 284,824 for *Enterococcus faecalis\_V583*, *Desulfovibrio vulgaris\_DP4*, *Sulfurihydrogenibium yellowstonense\_SS-5*, *Thermus thermophilus\_HB27*, and *Pyrococcus furiosus\_DSM.3638* respectively. This shows that these genomes contain problematic regions, however, the regions are not localized.

## Assemblies contain most of the reference

To find what exists in the reference genome and is missed by the assemblies, we aligned the reference genome to each assembly. Using quality filtering, 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-UD, SPAdes, and MEGAHIT respectively which represent 14.48%, 1.003%, 1.003%, and 1.003% of the reference genome.

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-UD, SPAdes, and MEGAHIT respectively which represent 1.0%, 1.005%, 1.003%, and 1.003% of the reference genome.

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-UD, SPAdes, and MEGAHIT respectively which represent 1.0%, 1.007%, 1.006%, and 1.005% of the reference genome.

In conclusion,  $\sim 1.01\%$  of the reference genome is missed by the assemblies, except for Velvet/QC, which missed 14.48% of the reference.

## **The de novo assemblies recover unexpected genomic sequence from the mock community**

We aligned the unaligned contigs of each assembly to the unaligned contigs of IDBA-UD quality filtered assembly. Using quality filtered reads, the reference fraction (the reference here is the unaligned contigs of IDBA-UD quality filtered assembly) equals to 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 37.06%, 32.56% and 13.72% of the reference length. See Table 5 for more details. Velvet unalignments show the highest percentages of IDBA-UD QC unalignments. IDBA-UD diginorm unalignments shows the less percentage of IDBA-UD QC unalignments.

\*\*To further explore the unalignment, we downloaded fusa seeds from Fungenes. We used blast to map the unaligned reads to fusa seeds, using IDBA-UD/digital normalized assemblies, and no hits found.

## **Discussion**

### **Dataset has a high quality**

Having almost all reads aligned to the reference, shows that the data has a high quality. The high quality of the data is one reason the assemblers work the same (see below). However, understanding the behaviors of assemblers on less quality data is essential to decide which assembler is best to use. Analyzing the behaviors of assemblers on different datasets, using different quality and signatures is left for our future work.

### **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 assemblies. Misassembled length is less than 1.3% for all assemblies. Velvet shows the least performance in terms of accuracy and time, and memory utilizations. Some genomes contain problematic regions that causes misassemblies. We conclude that assembly works well although there are some rooms for improvements including enhancing accuracy, and decreasing time and memory requirements.

### **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. This also means that digital normalization throws unnecessary reads. We conclude that digital normalization and partitioning are beneficial steps for assembly to reduce time and memory utilities while not affecting quality.

### **Digital normalization and partitioning do not affect mis-assemblies and un-alignments**

Except for Velvet assemblies, misassemblies are not affected by digital normalization and partitioning. Mapping the unaligned contigs of different assemblies to the unaligned contigs of IDBA-UD assembly using quality filtered , shows genome fraction percentage is 91% or higher. This means the unaligned contigs are common among assemblies. These common unaligned contigs are likely to be unknowns, new assemblies, or contamination. This indicates that digital normalization did not throw necessary reads. In

addition, digital normalization and partitioning enhance assembly time and memory utilizations without affecting assembly accuracy.

**Assembly recovers content not in the reference**

**Assemblies account for the majority of reads**

## Acknowledgments

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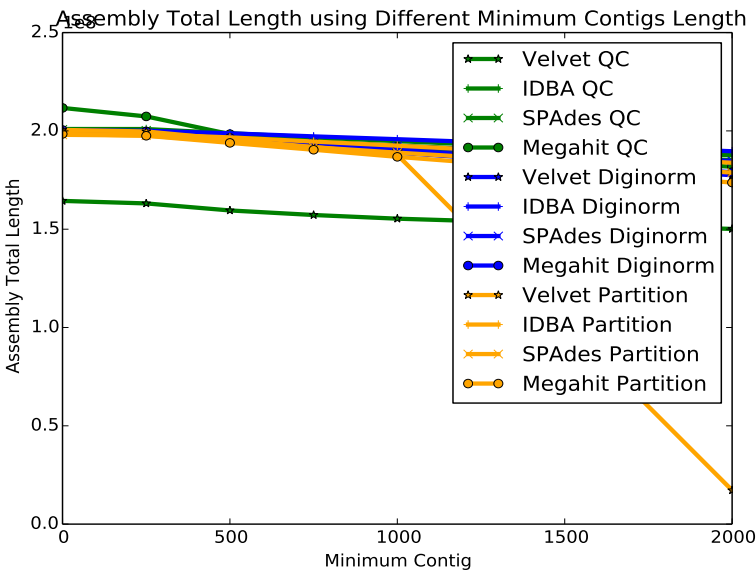
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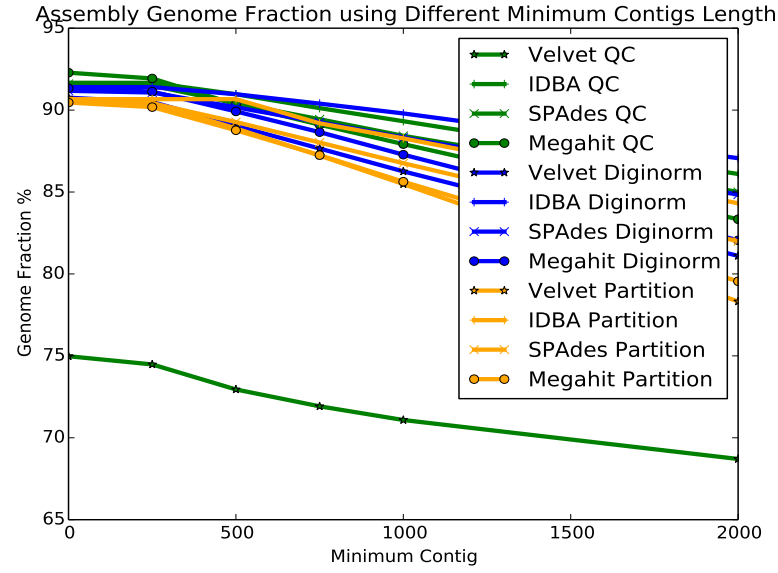
Figure Legends



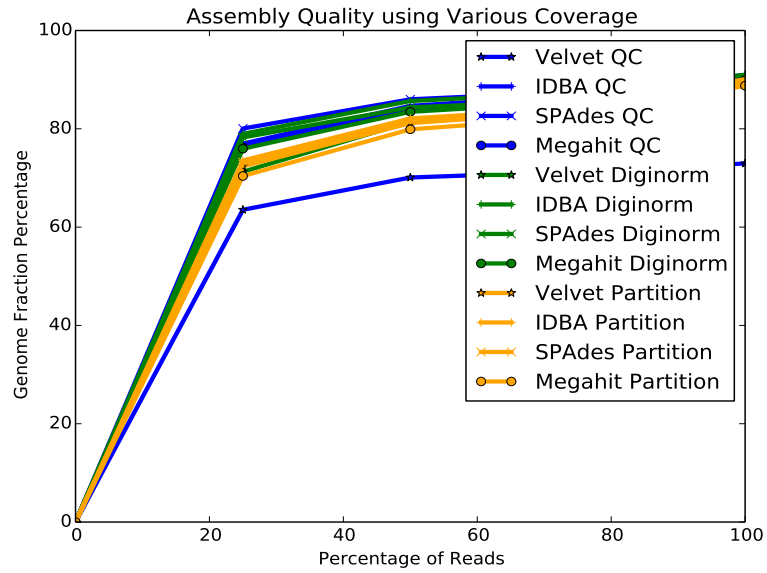
**Figure 1.** Total Length of assemblies in basepairs based on different min contigs length.

Tables

Supporting Information Legends



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



**Figure 3.** Genome Fraction of assemblies using different read coverage.

**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-UD</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>	35,136	27,302	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-UD</b>			
<b>Running Time</b>	33:53:46	6:34:24	8:30:29
<b>Memory Utilization in GB</b>	123.84	99.88	89.25
<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	123.7
<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	189.55

**Table 3.** mis-assemblies

Assembly	Quality Filtering	Digital Normalization	Partition
<b>(1) Velvet</b>			
mis-assemblies	917	5271	5202
Relocations	592	998	1036
Translocations	309	4262	4153
Inversions	16	11	13
Misassembled Contigs Length	16,566,891	25,594,315	16,922,852
Mismatches	104,740	174,446	178,348
Percentage of Mismatches	0.05%	0.08%	0.09%
Indels Length	50,190	181,453	346,988
Indels Percentage	0.02%	0.09%	0.17%
<b>(3) IDBA-UD</b>			
mis-assemblies	1223	1094	960
Relocations	613	668	578
Translocations	580	398	350
Inversions	30	28	32
Misassembled Contigs Length	21,777,032	27,668,818	18,440,791
Mismatches	162,733	231,432	230,840
Percentage of Mismatches	0.08%	0.11%	0.11%
Indels Length	30,433	43,358	42,523
Indels Percentage	0.01%	0.02%	0.02%
<b>(2) SPAdes</b>			
mis-assemblies	894	997	753
Relocations	608	613	496
Translocations	267	368	239
Inversions	19	16	18
Misassembled Contigs Length	28,238,787	23,103,154	14,338,099
Mismatches	184,630	244,849	235,396
Percentage of Mismatches	0.09%	0.12%	0.11%
Indels Length	27,328	32,783	21,516
Indels Percentage	0.01%	0.02%	0.01%
<b>(4) MEGAHIT</b>			
mis-assemblies	738	880	748
Relocations	448	593	513
Translocations	172	274	222
Inversions	118	13	13
Misassembled Contigs Length	11,927,502	17,319,534	11,814,070
Mismatches	152,964	207,349	203,515
Percentage of Mismatches	0.07%	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

<b>Treatment</b>	<b>Quality Filtering</b>	<b>Digital Normalization</b>	<b>Partition</b>
<b>(1) Velvet</b>			
<b>No. of Unaligned Sequences</b>	6,801,329	3,375,222	3,890,205
<b>Percentage</b>	6.40%	3.17%	3.66%
<b>(2) IDBA-UD</b>			
<b>No. of Unaligned Sequences</b>	1,490,609	1,738,371	2,297,377
<b>Percentage</b>	1.40%	1.63%	2.16%
<b>(3) SPAdes</b>			
<b>No. of Unaligned Sequences</b>	2,100,555	2,439,158	2,804,006
<b>Percentage</b>	1.98%	2.29%	2.64%
<b>(4) MEGAHIT</b>			
<b>No. of Unaligned Sequences</b>	1,559,300	2,082,881	2,747,427
<b>Percentage</b>	1.47%	1.96%	2.58%

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

<b>Treatment/Quality Metric</b>	<b>Quality Filtering</b>	<b>Digital Normalization</b>	<b>Partition</b>
<b>(1) Velvet</b>			
<b>Unaligned IDBA Fraction</b>	80.613 %	92.03%	92.982%
<b>Unaligned Length</b>	2,475,529	3192491	3,868,558
<b>Percentage of unaligned</b>	37.06%	47.8%	57.92%
<b>(2) IDBA-UD</b>			
<b>Unaligned IDBA Fraction</b>	-	91.53%	94.72%
<b>Unaligned Length</b>	-	498,299	1,320,036
<b>Percentage of unaligned</b>	-	7.46%	19.76%
<b>(3) SPAdes</b>			
<b>Unaligned IDBA Fraction</b>	91.92%	93.959%	94.826%
<b>Unaligned Length</b>	2,174,574	1,951,911	2,398,664
<b>Percentage of unaligned</b>	32.56%	29.22%	35.91%
<b>(4) MEGAHIT</b>			
<b>Unaligned IDBA Fraction</b>	92.715%	91.838%	92.219%
<b>Unaligned Length</b>	916,247	1,569,436	3,832,050
<b>Percentage of unaligned</b>	13.72%	23.5%	57.37%

**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-UD</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>(2) SPAdes</b>			
<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

**Table 7.** Comparision between N50 and NG50

<b>Treatment</b>	<b>Quality Filtering</b>	<b>Digital Normalization</b>	<b>Partition</b>
<b>(1) Velvet</b>			
<b>N50</b>	38,028	18,944	8,504
<b>NG50</b>	22,223	17,212	7,905
<b>(2) IDBA-UD</b>			
<b>N50</b>	49,773	47,828	26,575
<b>NG50</b>	45,748	44,351	24,326
<b>(3) SPAdes</b>			
<b>N50</b>	42,773	35,580	22,319
<b>NG50</b>	38,841	32,598	19,909
<b>(4) MEGAHIT</b>			
<b>N50</b>	35,136	27,302	17,492
<b>NG50</b>	32,251	25,248	15,393