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Sequence data for *Clostridium autoethanogenum* using three generations of sequencing technologies

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During the past decade, DNA sequencing output has been mostly dominated by the second generation sequencing platforms which are characterized by low cost, high throughput and shorter read lengths for example, Illumina. The emergence and development of so called third generation sequencing platforms such as PacBio has permitted exceptionally long reads (over 20 kb) to be generated. Due to read length increases, algorithm improvements and hybrid assembly approaches, the concept of one chromosome, one contig and automated finishing of microbial genomes is now a realistic and achievable task for many microbial laboratories. In this paper, we describe high quality sequence datasets which span three generations of sequencing technologies, containing six types of data from four NGS platforms and originating from a single microorganism, *Clostridium autoethanogenum*. The dataset reported here will be useful for the scientific community to evaluate upcoming NGS platforms, enabling comparison of existing and novel bioinformatics approaches and will encourage interest in the development of innovative experimental and computational methods for NGS data.

Design Type(s)	parallel group design • protocol optimization design
Measurement Type(s)	Whole Genome Sequencing
Technology Type(s)	DNA sequencer
Factor Type(s)	protocol
Sample Characteristic(s)	Clostridium autoethanogenum

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Background & Summary

It has been a decade since the release of the initial Next Generation Sequencing (NGS) platform by 454 Life Sciences (now Roche)[1]. During these ten years several NGS platforms including 454, Illumina, SOLiD, Ion Torrent and Pacific Biosciences (PacBio) have been released and improved[2]. Currently, Illumina offers the highest throughput and the lowest per base cost[3], while third generation sequencing technology provider Pacific Biosciences (PacBio) has median read lengths in range of 4–5 kb and reads length >20 kb[4]. A performance comparison of various NGS platforms and recent advances are summarised[2,3,5]. In general, the second generation sequencing platforms are characterized by shorter read lengths while third generation platforms generate significantly longer, but fewer and more error prone reads.

The majority of published draft genomes have been sequenced using second generation sequencing technologies (Illumina and 454) and this data is readily available[6]. Since its introduction, the PacBio sequencing platform has become more widely used due to the utility of its longer read lengths[7] and range of applications[8]. A limitation for earlier versions of PacBio technology for producing accurate genome assemblies was high error rates (> 15%) combined with lower sequence output (100 Mb)[9]. To address this, efficient algorithms were developed[9,10], which require either >100x PacBio sequence coverage or accurate Illumina reads for error correction. Therefore, development of hybrid approaches which utilize previous sequencing data and also provide an option to employ long-read data remains as the major scientific focus area. An evaluation of various hybrid assembly strategies was recently published in mid-2014 (ref. 11) and within a short time frame the field continued to progress with the release of newer hybrid algorithms[12–16] and updates to existing ones[17,18]. This underlines the requirement and utility of hybrid approaches to the scientific community. The long-read PacBio platform was speculated to be increasingly used to produce finished microbial genome assemblies[4,6], supported by several recent examples[19–23] and the utility of long-read sequencing for microbial genomes has been reviewed recently[24]. Combined developments of greater sequence output and longer reads, together with the random nature of PacBio errors have facilitated improved *de novo* assembly outputs. PacBio has the ability to detect DNA base modifications such as 4-methylcytosine (4-mC), 5-methylcytosine (5-mC) or 6-methyladenine (6-mA)[25]. This methylome information can be useful to understand biological processes such as gene expression and to aid development and optimization of transformation protocols[26–28].

Examples of former NGS platforms include Helicos Biosciences[29], and upcoming platforms include examples such Qiagen-intelligent Biosystems[30], Oxford Nanopore[31], and Quantum Biosystems[32] platforms. Oxford Nanopore has released its portable sequencer MinION, and a recent publication describes the nature of data produced[33]. Many of these newer platforms are still in the initial development stages and especially for customized methods for alignment, consensus, variant calling, *de novo* assembly and scaffolding. During the maturation of these upcoming platforms, evaluations and assessments for sequence data error rates, accuracy, length, output, cost and performance will be critical, as will the development and assessment of bioinformatics tools. Therefore, datasets which contain high-quality data from various generations of sequencing platforms for a single microorganism will be useful for others to test, compare and contrast existing and novel experimental and computational advances and benchmark automated bioinformatics pipelines.

To facilitate further assessments and tool development for current and future NGS technologies, we report and describe in detail the methods, data and quality measurements for five sequencing technologies used to sequence the biofuel producing *Clostridium autoethanogenum* genome. This dataset represents three generations of sequencing technologies, and contains six types of data from four NGS platforms; 454 GS FLX, Illumina MiSeq, Ion Torrent, and PacBio RS-II; and Sanger sequence data. The PacBio data alone was sufficient to obtain the complete genome assembly of *C. autoethanogenum*. Several datasets were initially released into the NCBI Sequence Read Archive (SRA) with the finished *C. autoethanogenum* genome[4]. At present the NCBI SRA supports deposition of PacBio fastq files, but not the raw files required by certain software. The earlier study showed that assemblies utilizing shorter read DNA technologies were confounded by the nine copies of the 5 kb rRNA gene operons and other repetitive sequences[4]. Raw Ion Torrent and 454 shotgun sequence data for the draft genome sequence were not been previously released[34], nor were *C. autoethanogenum* DNA methylation data.

Methods

Microorganism and genomic DNA preparation

Clostridium autoethanogenum strain JA1-1 (DSMZ 10061) was obtained from the German Collection of Microorganisms and Cell Cultures (DSMZ).

In order to prepare genomic DNA for 454 paired-end (PE), Illumina PE and PacBio sequencing the strain was cultured in PETC medium as described[35]. A single JA1-1 colony was purified and its 16S rDNA sequence confirmed before genomic DNA was prepared for Illumina and PacBio sequencing[35]. Genomic DNA for 454 paired-end, Illumina PE and PacBio sequencing was prepared as described previously[4]. Genomic DNA for 454 shotgun and Ion Torrent shotgun sequencing was prepared using the UltraClean Microbial DNA Isolation kit (catalog# 12224-250) from MoBio Laboratories, Inc (Carlsbad, CA). Prior to library preparation DNA quality was assessed by Nanodrop analysis (Thermo Scientific) and visualization on an agarose gel. Quality samples have an A260/280 ratio above 1.8, and appear on a

gel as a single high molecular weight band. The quantity was determined by Qubit broad range double stranded DNA assay (Life Technologies, Grand Island, NY).

Illumina TruSeq library preparation and sequencing

Illumina TruSeq libraries were prepared as described in the manufacturer's protocols (Part #15005180 RevA) following the low throughput protocol. In short, 3 µg of DNA was sheared to a size between approximately 200 and 1,000 bp by nebulization (using nitrogen as the carrier gas) for 1 min at 30 PSI. Sheared DNA was purified on a QIAquick Spin column (Qiagen). The quantity of sheared material was accessed with a broad range double stranded DNA assay from Qubit (Life Technologies) and visualized on an Agilent Bioanalyzer DNA 7500 chip (Agilent). One microgram of sheared DNA was used in the end repair reaction, and subsequently cleaned up by Agencourt AMPure XP bead purification (Beckman Coulter). The ends of the DNA were modified by adenylation of the 3′ ends and Illumina adapters were then ligated to the DNA. The DNA was cleaned up using Agencourt AMPure XP beads, and samples were then run for 2 h at 120 Volts on a 2% agarose gel containing SYBR Gold (Life Technologies). Ligation products were then purified from the sample by excising a band from the gel from approximately 350–450 bp. The DNA from the gel slice was then purified using a MinElute Gel Extraction kit (Qiagen) for each library/band. The DNA fragments were enriched by performing 10 cycles of amplification [98 °C–30 s, 10 cycles of: 98 °C for 10 s, 60 °C for 30 s, 72 °C for 30 s, followed by a final extension at 72 °C for 5 min. Amplified products were then cleaned up using Agencourt AMPure XP beads. Final libraries were validated by Qubit (Life Technologies) and visualized by Agilent Bioanalyzer for appearance and size determination. Samples were normalized using the Illumina's Library dilution calculator to a 10 nM stock, and subsequently run on an Illumina MiSeq Instrument (M02014R).

454 shotgun library preparation and sequencing

The 454 shotgun library was prepared using Roche's GS FLX Titanium Rapid Library Preparation Kit and was run on the Titanium platform according to manufacturer's specifications. Briefly, DNA was fragmented under gas pressure and the ends repaired. Adapters were ligated onto the fragments and then small fragments were selected out of the library. The library was then assessed for quality and concentration (including size length assessment and contaminating fragments of inappropriate size) using an Agilent Bioanalyzer 2100 prior to running on the 454 instrument.

454 3 kb library preparation and sequencing

A 454 3 kb paired end library was prepared following the manufacturer's instructions (Roche- Paired End Library Preparation Method Manual—3 kb Span GS FLX Titanium Series- Oct 2009)[36]. Five micrograms of high quality, high molecular weight DNA was sheared to an average fragment size of 3 kb using a HydroShear apparatus (Genomic Solutions). The sheared material was then purified using Angencourt AMPure XP magnetic beads (Beckman Coulter). A portion of the sheared DNA was run on an Agilent Bioanalyzer 2100 to verify the size of the fragments. The fragment ends were polished and purified. The circularization adapters were appended and the product was again purified. Size selection of the material was completed followed by a fill in reaction and circularization. The sample was sheared by nebulization, purified, and checked for size on an Agilent Bioanalyzer 2100. The fragment ends were again polished and purified. The library was immobilized on Dynal M270 Streptavidin beads (Life Technologies) and the library adapters were ligated and gaps were filled. The library was amplified and a final purification step yielded a single stranded paired end library. The final library was amplified using emulsion PCR (emPCR); the products were purified, and then sequenced on a Roche 454 GS FLX system using Titanium chemistry according to the manufacturer's instructions (Roche).

SMRTbell library preparation and PacBio sequencing

Ten micrograms of DNA were sheared using G-tubes (Covaris, Inc., Woburn, MA, USA), targeting 20 kb fragments. SMRTbell libraries were prepared with the DNA Template Kit 1.0 (Pacific Biosciences, Menlo Park, CA, USA) and library fragments above 4 kb were isolated using the BluePippin system (Sage Science, Inc., Beverly, MA, USA). The average SMRTbell library insert size (including adapters) was approximately 19 kb. Sequencing primers were annealed to the SMRTbell template and samples were sequenced on a PacBio RS II system (2013) using Magbead loading, C2 chemistry, Polymerase version P4, and SMRT analysis software version 2.2. DNA base modifications analysis was performed by 'RS Modification and Motif Analysis' workflow with default settings. Detailed information about detection of DNA base modifications workflow is available as online documentation[37].

Ion torrent library preparation and sequencing

Genomic libraries were prepared separately for each genomic sample from 100 ng of DNA. DNA was fragmented with Ion Shear Plus Reagents, Ion Torrent specific adapters Ion Xpress P1 (5′—CCTCTCTATGGGCAGTCGGTGAT-3′) and Ion Xpress Barcode X Adapters (5′-CCATCTCAT CCCTGCGTGTCTCCGACTCAG-3′) were ligated to DNA using DNA ligase (Life Technologies, Grand Island, NY). The Ion Xpress Barcode X Adapters contain a 10 bp sequence, Ion Xpress Barcode (Life Technologies) unique to each of the samples. Ligated DNA was nick repaired using Nick Repair Polymerase (Life Technologies) and purified with Agencourt AMPure XP Reagent (Beckman Coulter,

Sequencing Platform	Data type	SRA Accession/ Dryad doi	Size
Accession linking all SRA data for this project		SRP030033	—
Roche 454 shotgun	Raw data in SFF format	SRR1748017	1.5 Gb
Roche 454 3 kb	Raw data in SFF format	SRR989497	1.4 Gb
Illumina	Raw data in fastq format	SRR989790	(669x2) Mb*
Ion Torrent	Raw data in SFF format	SRR1748018	858 Mb
PacBio RS II	Filtered subreads in fastq format	SRR1740585	1.2 Gb
Dryad doi linking all depositions for this project		doi: 10.5061/dryad.6fm1p	—
PacBio RS II	Raw PacBio data in tar.gz format	doi:10.5061/dryad.6fm1p/4	8.5 Gb
PacBio RS II	DNA methylation motifs in gff format	doi:10.5061/dryad.6fm1p/2	1.99 Mb
Sanger Sequencing	Chromatogram files in ABI format	doi:10.5061/dryad.6fm1p/1	4.39 Mb

Table 1. Summary of datasets. Datasets described in this manuscript, which can be accessed using the accession numbers provided. *There are two files for Illumina data corresponding read_1 and read_2. Detailed instructions for downloading data from SRA are provided in the Supplementary Information.

Indianapolis, IN). The ligated and nick repaired DNA was size-selected individually with the E-GelR SizeSelect Agarose Gel (Life Technologies). The size selected libraries were amplified using PlatinumR PCR SuperMix High Fidelity and Library Amplification Primer Mix (Life Technologies). The thermal profile for the amplification of each sample had an initial denaturing step at 94 °C for 5 min, followed by a cycling of denaturing of 95 °C for 15 s, annealing at 58 °C for 15 s and a 1 min extension at 70 °C (5 cycles) and a final hold at 4 °C. Each sample was again purified individually using Agencourt AMPure XP Reagent (Beckman Coulter, Indianapolis, IN) and standardized prior to pooling. Template-Positive Ion OneTouch 200 Ion Sphere Particles were prepared from the library pool using the Ion OneTouch DL system (Life Technologies, Invitrogen division). Prepared template was sequenced on an Ion Torrent PGM instrument (Microbiome Core Facility, Chapel Hill NC) using the Ion PGM 300 Sequencing reagents and protocols (Life Technologies). Initial data analysis, base pair calling and trimming of each sequence was performed on an Ion Torrent browser to yield high quality reads.

Sanger sequencing

Prior to PacBio sequencing, limited manual finishing of *C. autoethanogenum* was performed using PCR and Sanger sequencing. PCR reactions were performed using Phusion High-Fidelity PCR Kit (New England Biolabs, Ipswich, MA) following the standard protocol. Sanger sequencing was performed at Molecular Biology Research Facility, University of Tennessee, Knoxville using ABI 3730 Genetic Analyzer Instrument (Life Technologies).

Data Records

Raw data from each sequencing platform was submitted to the Sequence Read Archive (SRA) at NCBI under Project ID SRP030033 (Data Citation 1). Raw data deposited at the SRA and Dryad repository is organized by the type of sequencing platforms and corresponding accessions and file sizes are provided in Table 1. Data deposited in Dryad (Data Citation 2) are available under a project deposition and details for different datasets are summarized (Table 1).

Illumina sequencing instruments generate raw image files which are automatically processed through instrument control software to output sequence data in fastq format. More details about different types of data files generated by the instrument and fastq conversion steps are described in online documentation[38]. The 150 bp paired-end (PE) Illumina reads in fastq format were deposited to SRA with run ID SRR989790. The fastq is standard file format which can be directly used to perform several downstream applications such as *de novo* assembly or mapping to a reference genome. The 454 Pyrosequencing and Ion Torrent instrument generates the sequencing data in Standard Flowgram Format (SFF). The SRA deposition for 454 shotgun, 454 3 kb PE and Ion Torrent data was made in SFF format under run ID SRR1748017, SRR989497 and SRR1748018, respectively. For validation purposes, quality statistics were determined for each short-read dataset using CLC Genomics Workbench (CLC) software version 7.5.1 and a complete report is provided as Supplementary Information.

The PacBio sequencing was performed using two SMRT cells. Each SMRT cell generates a metadata.xml file which contains information about run conditions and barcodes. Three bax.h5 files containing base calls and quality information of actual sequencing data and one bas.h5 file that acts as a pointer to consolidate three bax.h5 files[8]. A typical raw read from PacBio sequencing is composed of DNA insert with both ends flanked by the adapter sequences[8]. During downstream processing through SMRT Analysis software, the adapter sequences are removed and subreads are created which contains only the DNA sequence of interest. The PacBio filtered subreads were deposited at SRA in fastq format under run ID SRR1740585. Additionally, all the primary analysis data in the original formats as provided by the

Motif	Modified Position	Modification Type	% Motifs Detected	No. of Motifs Detected	No. of Motifs In Genome	Mean Modification QV	Mean Motif Coverage
CAAAAAR	6	m6A	95.44	4,190	4,390	68.4	56.8
GWTAAT	5	m6A	93.87	7,975	8,496	78.5	58.1
SNNGCAAT	7	m6A	85.27	3,242	3,802	75.9	57.8

Table 2. Summary of DNA methylation motif patterns discovered across the *C. autoethanogenum* genome. Modified base within each motif is shown in bold.

Sequencing Platform	Type	No. of reads	Average length	No. of reads after Trim	Average length after Trim	Total Trimmed bases	Fold Coverage
Roche 454	Singletons* Paired end reads Shotgun Data	128,856 764,756 462,052	275 151 289	128,806 764,744 458,340	261 144 249	33,631,416 110,124,864 114,126,660	46x 26x
Ion Torrent	Single end reads	453,686	215	419,010	188	78,773,880	18x
Illumina	Paired end reads	3,689,644	150	3,682,655	149	549,756,956	126x

Table 3. Summary of quality trimming statistics for Illumina, 454 and Ion Torrent data. *The singleton sequences are generated from 454 3 kb sequencing run.

Sequencing Platform	Type	No. of filtered subreads	N50 filtered subread length	Maximum filtered subread length	Total filtered bases	Fold Coverage
PacBio RSII	Single end reads	94,408	9,196	26,777	631,598,400	145x

Table 4. Post-filter quality statistics for PacBio data.

PacBio RS-II instrument are now made available on an external server (Table 1). Methylation in bacteria generally occurs at specific sequence motifs that are recognized by methyltransferases. Genome wide analysis of DNA base modifications was performed and a high level summary of the motifs discovered is provided in Table 2. Additionally, a 'motifs.gff' file is provided (Table 1), which shows all of the sites in the genome that are methylated, all the sites with one of the discovered motifs and the overlap between the methylation and the motifs as detected by SMRT analysis software version 2.2. Prior to PacBio sequencing, a manual finishing strategy for *C. autoethanogenum* generated high-quality Sanger sequence data and it is available to download (Table 1).

Raw reads represent the actual output from sequencing instruments. However, quality based trimming of Illumina and 454 data is recommended and often yields better results with downstream applications such as *de novo* assembly[11,39]. On the other hand, PacBio raw read filtering to generate subreads is a necessary step to remove adapter sequences[8]. Quality based trimming of Illumina and 454 data was performed using CLC software while PacBio filtering and mapping was performed using SMRT analysis version 2.2. The post-filter summary statistics for Illumina, 454 and Ion Torrent datasets are listed in Table 3 and for PacBio dataset in Table 4. The Illumina and PacBio datasets were sequenced to higher coverages (>100x), while 454 and Ion Torrent datasets had lower coverages (< 50x). See the Technical Validation section for details on quality statistics and filtering parameters used.

Technical Validation

DNA and sample preparation

All samples were required to pass a quantity and quality assessment using a Qubit (Life Technologies), Nanodrop (ThermoFisher) and gel electrophoresis. Samples were required to have readings indicative of pure DNA and of sufficient quantity to move forward with library preparations. DNA was visualized by gel electrophoresis and was required to be high molecular weight DNA without shearing or RNA contamination.

Each sequencing library preparation method includes specific technical validation to determine quality and quantity of the final libraries to ensure high quality output from the various sequencing platforms. This technical validation typically involves assessment of the final libraries with a Qubit assay (Life Technologies) to determine quantity and visualization of the final libraries on an Agilent Bioanalyzer chip to determine quality.

Quality determination and analysis

To assess the quality of the libraries sequenced, we determined basic quality statistics for Illumina, 454 and Ion Torrent datasets using CLC software. This includes the calculation of sequence lengths

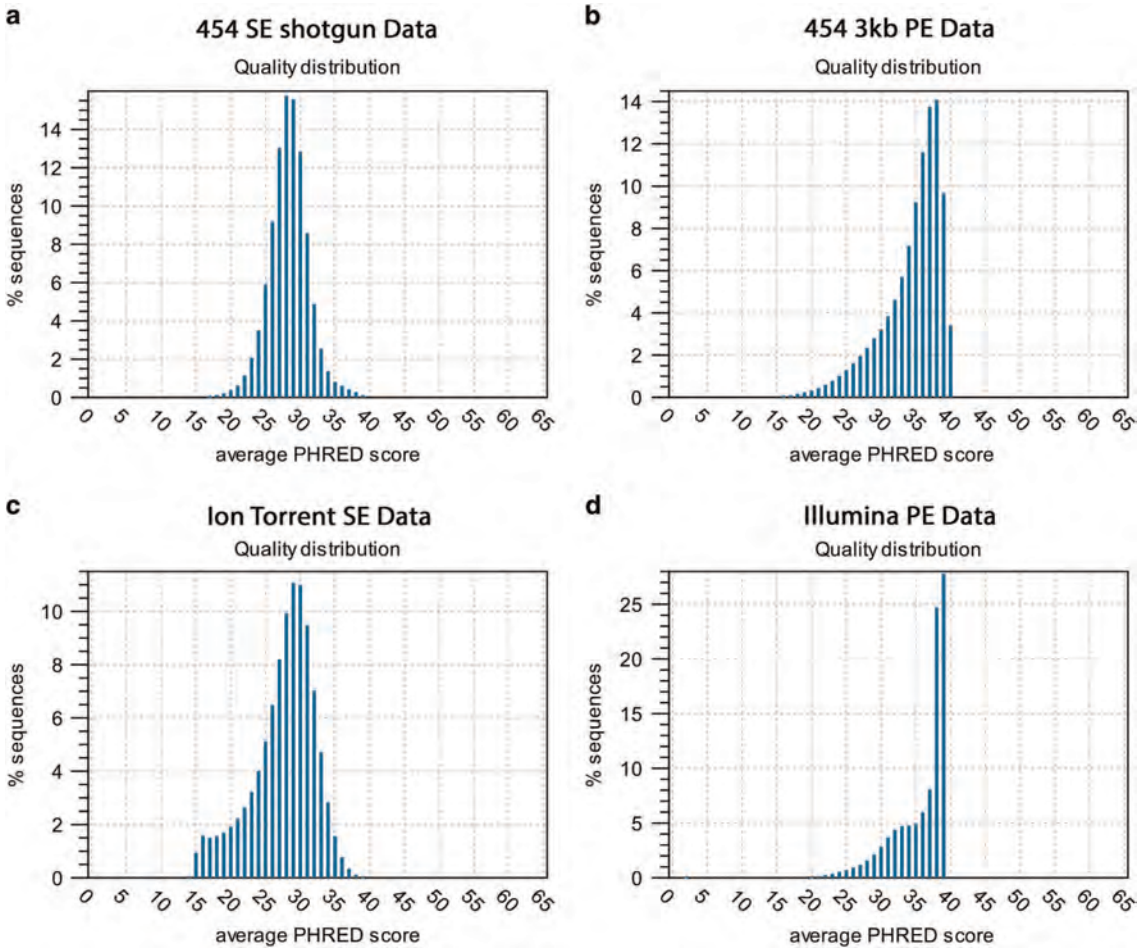

Figure 1. PHRED quality score distribution. The distribution of average PHRED quality score is plotted on X-axes and percentage of sequences on Y-axes for (**a**) 454 single end shotgun data (**b**) 454 3 kb paired end data (**c**) Ion Torrent single end data and (**d**) Illumina paired end data. Quality distribution shows that more than 95% reads from each dataset have average PHRED scores above 20.

distribution, GC-content, Ambiguous base-content, PHRED quality score distribution, nucleotide contributions, kmer distribution analysis and sequence duplication levels. The quality statistics are calculated for every read, averaged for each dataset and provided in a complete quality report (Supplementary Information). More than 95% of the Illumina, 454 and Ion Torrent reads have PHRED scores above 20 (Fig. 1) with a very low percentage of ambiguous bases and sequence duplication levels detected (See section 2.3 and 4.2 for each dataset—Supplementary Information). Quality based trimming of these short-read datasets was performed at a stringent cut-off value of 0.02. More details about the trimming algorithm used by CLC and an example can be found in online documentation[40]. After quality trimming, only a few reads were discarded and minor changes in average read lengths were observed (Table 3). The PacBio data was processed through SMRT analysis software version 2.2. Filtering conditions applied were read quality score>0.8, read length >500 bp, subread length >500 bp. In addition, adapter sequences were removed and ends of the reads were removed when found outside of the high-quality region[8,41]. PacBio data retained 72% of the bases after filtering. The PacBio data by itself was sufficient to generate finished genome sequence. The complete genome sequence of *C. autoethanogenum* strain DSM10061 and *de novo* and hybrid assembly comparison using QUAST, REAPR, CGAL and Mauve tools have been described previously[4]. The Sanger sequencing data were found to be in agreement with the finished genome sequence of strain DSM10061 and provide additional validation for the high quality of PacBio dataset[4].

To further ensure that the sequences matched with the model organism of interest, we mapped the post-filtering reads from each dataset to the model organism of interest. We used *C. autoethanogenum* DSM 10061 genome from NC_022592.1 (Data Citation 3) and *C. ljungdahlii* DSM 13528 from NC_014328.1 (Data Citation 4) at the NCBI GenBank as reference sequences. Since a finished genome sequence for *C. autoethanogenum* was obtained using the PacBio reads from the current dataset, we used another independent reference *C. ljungdahlii* DSM 13528 to avoid any bias. These two genomes have an

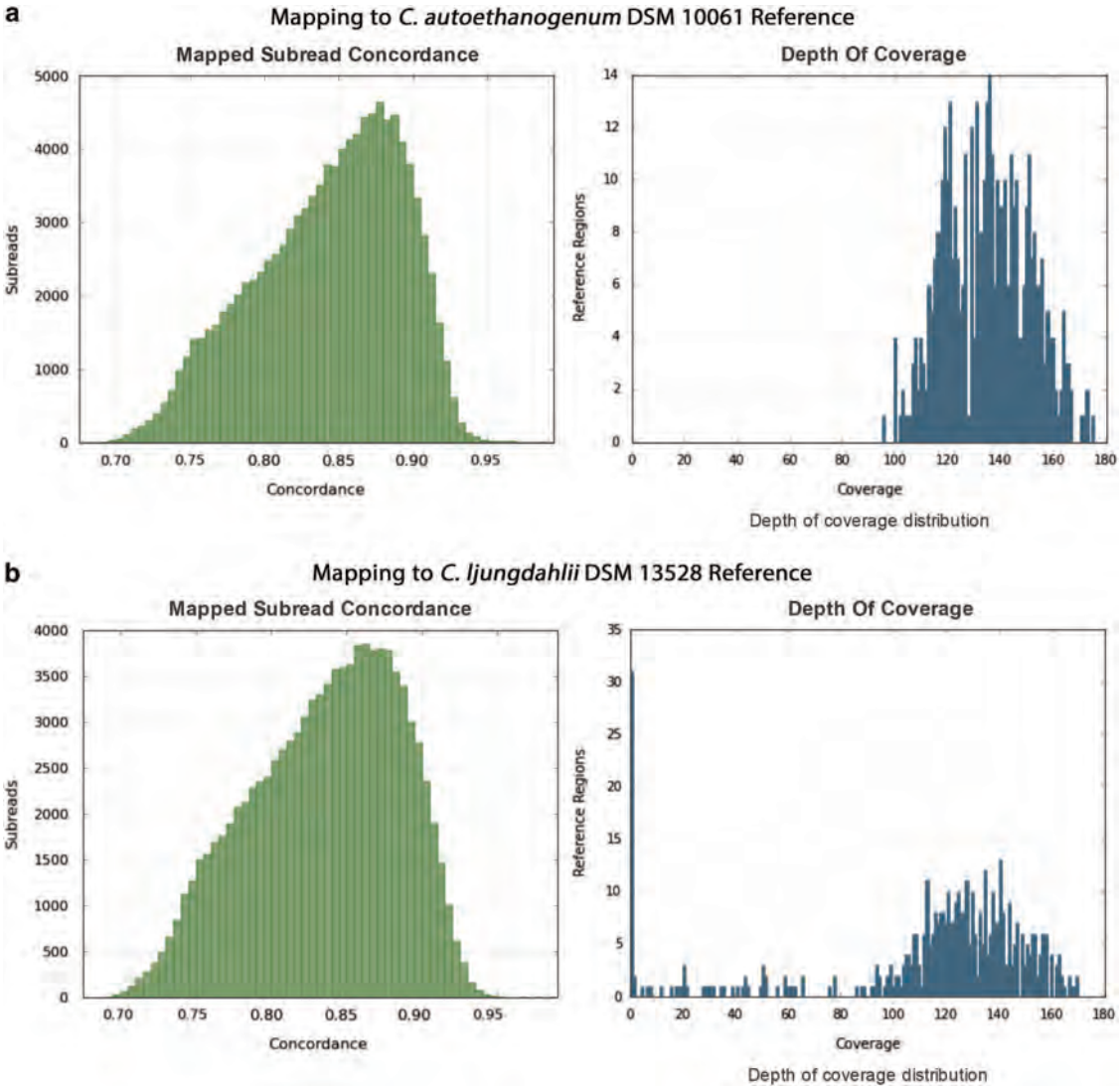

Figure 2. Mapped subread concordance and coverage. The distribution of mapped subread concordances and mapped subread coverages are plotted with (**a**) *C. autoethanogenum* DSM 10061 finished genome and (**b**) *C. ljungdahlii* DSM 13528 as reference. These graphs suggest good agreement between reads and reference genomes.

average nucleotide identity score over 99%. Illumina and 454 reads were mapped to reference using the bowtie2 algorithm[42] while PacBio reads were mapped using the BLASR algorithm[43] from the SMRT Analysis software. The Illumina and 454 datasets have mapping rates above 90% with *C. ljungdahlii* and above 97% with the finished genome of *C. autoethanogenum*. Ion Torrent data have a comparatively lower mapping rate, 86% with *C. ljungdahlii* and 91% with *C. autoethanogenum*. For the PacBio dataset, plots showing the distributions of mapped subread concordances and coverage are shown in Fig. 2 and provide an estimate of read agreement with reference genomes. Therefore, the data quality statistics, trimming reports and mapping results articulate the high quality of the datasets described in this manuscript.

Usage Notes

The five NGS datasets described can be downloaded from the SRA with accession numbers provided in Table 1. Detailed instructions for downloading each dataset from NCBI SRA and md5 checksum values are provided in the Supplementary Information. The fastq/SFF formatted files from second generation sequencing data are sufficient to use for any downstream analysis using most third-party tools. On the other hand, original data formats are necessary for analysing the PacBio data through SMRT analysis software or other algorithms and these are provided (Table 1). Currently the SRA allows depositions of fastq formatted PacBio reads only. Therefore, all the primary analysis data in original formats as generated by the PacBio RS II instrument (*.metadata.xml, *.bas.h5, *.bax.h5 files), as well as DNA

methylation motifs detected by PacBio sequencing are available in Dryad (Data Citation 2). The sequence IDs provided in primary analysis files are different than those available through SRA because SRA uses an internal naming convention which changes existing sequence IDs. The sequence IDs in original format contain information about run and the naming convention is described in detail here[8]. Sanger data are posted in Dryad (Data Citation 2).

Some of the datasets described here were initially released with the manuscripts describing the draft[34] and finished genome of *C. autoethanogenum*[4], with primary focus on genomic features and characteristics of this microorganism. Previous manuscripts did not include Ion torrent/454 shotgun data release and detailed quality evaluation and usage instructions were not provided. In addition, DNA modification data for *C. autoethanogenum* from the PacBio is provided, identifying three m6A adenosine methylation patterns (Table 2). The 'motifs.gff' file is a text file which can be opened in most of the graphical sequence viewer software. This data descriptor in Scientific Data provides an opportunity to present the collection of these five different datasets which are originated from a single microorganism and spans three generations of sequencing technologies. Here we provide the detailed characteristics for each dataset and appropriate instructions to download and use the data. Since sequencing technologies are rapidly evolving, this legacy dataset can be used as a benchmark to compare the data from newer NGS technologies and will encourage the development of new and existing hybrid algorithms.

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Author Contributions

D.M.K. generated the Illumina sequence data. S.M.U. and S.D.B. were responsible for analyzing the PacBio and Sanger data. M.K. was responsible for generating the 454 PE data. J.B., M.C. and A.G. were responsible for generating and analyzing the 454 shotgun and Ion Torrent sequencing datasets. S.M.U. deposited data to the S.R.A. and analysed data. S.D.B. coordinated the project. All authors contributed to the manuscript and approved the final version.

Additional Information

Supplementary information accompanies this paper at http://www.nature.com/sdata

Competing financial interests: LanzaTech has a commercial interest in *Clostridium autoethanogenum*.

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