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## Abstract

We performed whole genome sequencing to assess the specificity of colony forming units derived from three different plating media's: Potato Dextrose Agar (PDA), PDA with chloramphenicol and Dichloran Rose Bengal with chloramphenicol (DRBC). Colonies were isolated from each media type and whole genome sequenced to identify the diversity of microbes presented with each media selection. ITS3 and 16S qPCR was performed to correlate these CFUs with fungi and bacterial specific qPCR. The plating mediums each displayed a log scale different colony forming unit count. PDA with chloramphenicol demonstrated the highest diversity and the highest concordance with whole genome sequencing. According to ITS3 and 16S qPCR DRBC under counts yeast and mold while PDA without chloramphenicol over counts CFUs due to bacterial growth without selection.

# Introduction

Total yeast and mold testing is required in many states for safety testing cannabis prior to sale of cannabis flowers and cannabis infused products. Cannabis is an inhaled product and cases of cannabis acquired Aspergillosis exist in the clinical literature (Bal et al. 2010; Gargani et al. 2011; McKernan et al. 2015; Remington et al. 2015; Ruchlemer et al. 2015; McKernan et al. 2016). Cannabis is a unique matrix in that antibiotic cannabinoids can make up to 20% of the flowers weight and many fungi that infect cannabis are endophytes. Endophytes are not easily cultured from the plant without lysing open plant cell walls. Conditions which lyse open plant cells walls also lyse open fungal cell walls thus impacting the viability of the microbes in the lysis and homogenization process required for testing. Cannabis flowers contain both bacteria and fungi, further complicating fungal quantitation with colony forming units that lack speciation. Antibiotic selections are often utilized to reduce background bacteria but many of these antibiotics (chloramphenicol) inhibit the growth of the most pathogenic fungi found on cannabis (Fusarium, Pythium and Aspergillus)(Smith and Marchant 1968; Day et al. 2009; Joseph et al. 2015).

As part of an AOAC Emergency response validation (ERV) in the State of Michigan, we investigated the impact of media selection on surveying total yeast and mold on cannabis. Cured cannabis flowers were homogenized and tested on 3 different plating medias. These data were compared to ITS3 and 16S based qPCR and whole genome sequencing. To further complement these cannabis flower samplings, organisms were acquired from ATCC and plated as pure monocultures on different plating mediums to confirm the differential growth on each media.

# Methods

### Plating

Samples originated from Steadfast Analytical Laboratories (Hazel Park, MI) and were tested independently at a laboratory within the Michigan Coalition of Independent Cannabis Testing Laboratories. Briefly, 10 grams of dried cannabis flowers were sampled from three lots of homogenized cannabis containing high, medium and low quantities of CFUs as measured using



culture-based techniques with chloramphenicol selection. 10 grams of homogenized flower were soaked with 90ml of Tryptic Soy Broth (TSB) in a filtered Whirl-Pak bag. Samples were hand homogenized, and then 0.1 mL plated onto 3 plates (1:100 dilution). Two additional dilutions were prepared (10 mL into 90 mL) and same plating protocol was followed. All plates were incubated for 5 days at 25°C.

#### qPCR

ITS3 qPCR was performed as described in McKernan *et al.* with 2 modifications. Briefly, 1ml of homogenate from a WhirlPak bag if collected and briefly micro-centrifuged to enrich for live organisms. This pellet was resuspended in 200µl ddH20 and lysed with the addition of 12µl of Thaumatin-like protein (TLP) and incubated at 37°C for 30 minutes. This enzymatic lysis step (glucanase) ensures more complete lysis of fungal cell walls (MGC part #420206)(McKernan et al. 2015; McKernan et al. 2016). 12.5µl of MGC Lysis buffer was added, vortexed and incubated for 5 minutes at 25°C. Lysed sample were micro-centrifuged and 200µl of supernatant was aspirated and added to 250µl of MGC binding buffer (MGC part# 420001) for magnetic bead isolation. The samples were incubated with the bead mixture for 10 minutes, magnetically separated and washed 2 times with 70% ethanol. The beads were dried at 37°C for 5 minutes to remove excess ethanol and eluted with 25µl of ddH20. qPCR was performed according to the manufacturers' instructions on a BioRad CFX instrument.

#### DNA isolation from colonies for whole genome sequencing.

Colonies were picked with a pipette tip and introduced into 200µl of ddH20 with 12.5µl of MGC TLP (MGC part #420206). TLP is a glucanase active at 37°C. Samples were digested for 30 minutes at 37°C and 12.5µl of MGC Lysis buffer was added, vortexed and incubated for 5 minutes at 25°C. Lysed sample were micro-centrifuged and 200µl of supernatant was aspirated and added to 250µl of MGC binding buffer (MGC part# 420001) for magnetic bead isolation. The samples were incubated with the bead mixture for 10 minutes, magnetically separated and washed 2 times with 70% ethanol. The beads were dried at 37°C for 5 minutes to remove excess ethanol and eluted with 25µl of ddH20.

#### Library construction for whole genome sequencing.

#### Fragmentation

gDNA was quantitated with a Qubit (Thermo Fisher Scientific) and normalized to reflect 4-8ng/µl in 13µl of TE buffer. Libraries were generated using enzymatic fragmentation with the NEB Ultra II kits (NEB part # E7103). Briefly,  $3.5\mu$ l of 5X NEB fragmentation buffer and 1µl of Ultra II fragmentation enzyme mix are added to 13µl of DNA. This reaction was tip mixed 10 times, vortexed, and quickly centrifuged. Fragmentation is performed in a thermocycler at 3.5 minutes at 37°C, 30 minutes at 65°C. The reaction was kept on ice until ready for adaptor ligation.



#### Adaptor ligation

1) Prepare master mix on ice

Component	Volume (µl)
SureSelect Adaptor Oligo Mix (brown cap)	0.75
ddH2O	0.5
Ultra II Ligation Master Mix	15
Ligation enhancer	0.5
Total Volume	16.75

2) Add 16.75µl Master Mix to the 17.5µl Fragmentation/End Prep DNA reaction mixture, incubate for 15 minutes at 20°C.

#### 3. Cleanup step to remove excess adaptors and adaptor dimers

- 1) Vortex room temp AMPure XP beads (Beckman Coulter) to resuspend
- 2) Add 16µl (approximately 0.45X) of resuspended AMPure XP beads to the ligation reactions. Mix well by pipetting up and down at least 10 times.
- 3) Incubate for 5 minutes at  $25^{\circ}$ C.
- 4) Put the PCR plate on an appropriate magnetic stand to separate beads from supernatant. After the solution is clear (about 5 minutes), carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.
- 5) Add 200µl of 70% ethanol to the PCR plate while in the magnetic stand. Incubate at room temperature for 30 seconds, and then carefully remove and discard the supernatant.
- 6) Repeat Step 5 once for a total of 2 washes. Remove trace amount of EtOH
- 7) Air dry beads for ~ 7 minutes while the PCR plate is on the magnetic stand with the lid open.
- 8) Remove PCR plate from magnet and elute DNA target from beads into 10µl of H20, transfer 9µl cleaned DNA to a fresh well.

#### 4. PCR amplification

 Add 12.5µl 2x NEBNext Q5 Hot Start Master Mix to 9µl ligated DNA, then add 3.5µl NEB 8bp index primer/universal primer, run the following program

STEP	TEMP	TIME	Cycle
Initial denaturation	98°C	30 sec	1
Denaturation Annealing/Extension	98°C 65°C	10 sec 75 sec	6
Final extension	65°C	5 min	1
Hold	4°C	forever	1

Please adjust total PCR volume to 25µl on Thermocycler



#### 5. PCR reaction cleanup

- 1) Vortex room temp AMPure XP beads to resuspend
- Add 15µl of resuspended AMPure XP beads to the PCR reactions (~ 25µl). Mix well by pipetting up and down at least 10 times.
- 3) Incubate for 5 minutes at room temperature.
- 4) Put the PCR plate on an appropriate magnetic stand to separate beads from supernatant. After the solution is clear (about 5 minutes), carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.
- 5) Add 200µl of 70% ethanol to the PCR plate while in the magnetic stand. Incubate at room temperature for 30 seconds, and then carefully remove and discard the supernatant.
- 6) Repeat Step 5) once.
- 7) Air dry beads for ~ 7 minutes while the PCR plate is on the magnetic stand with the lid open.
- Elute DNA target from beads into 15µl of nuclease free H2O, transfer 15µl into a fresh well.

#### Sample quality control

Libraries were evaluated on an Agilent Tape Station prior to pooling for Illumina sequencing. Sequencing was performed by GeneWiz, Cambridge MA. 473 million read pairs (2 x 150bp) were generated, averaging over 10 million read pairs per sample and 141Gb of total sequence.

## Analysis

Fastq files were uploaded to OneCodex for Kmer analysis and Simpson's diversity index of each genome (Supplementary Table 1, sheet Summary). Reads were also assembled with MegaHit v.1.2.9 (Li et al. 2015; Li et al. 2016). The Nextflow mapping and assembly pipeline is published in GitHub (<u>https://github.com/mclaugsf/mgc-public/tree/master/AOAC\_TYM\_ERV</u>). Quast 5.0 was used to calculate the assembly quality statistics (Gurevich et al. 2013). Sequencing data is deposited in NCBI under Project ID PRJNA725256.

# Results

Each colony that was imaged on plates and picked for whole genome sequencing and OneCodex analysis is displayed in Table 1 (DRBC), Table 2 (PDA-CAMP) and Table 3(PDA no CAMP). A link to each OneCodex analysis and its' respective NCBI submission ID is available in Supplementary Table 1- Sheet Summary. Some of the colonies from the plate merged with other colonies producing mixtures of genomes as evident in the OneCodex pie charts. These merged colonies were further evidenced with the display of bimodal sequence coverage (clusters of contigs at 1000X and 10X coverage) and compared with the plating images (Figure 1). A heatmap of sequencing read speciation and purity is seen in Figure 2. While merged colonies can be difficult to resolve visually, whole genome sequencing can resolve simple metagenomes and still extract additional diversity information for the samples. Colonies that were noticeably mixed according to sequence analysis and colony visual inspection were more prevalent with the PDA without selection colonies (Table 4).



A Simpson's diversity index analysis demonstrated PDA with CAMP provides the highest diversity score (Figure 3.) While the DRBC had 100-fold lower CFU counts than PDA without selection, it predominantly displayed fungal colonies (80%) while PDA without selection was biased toward bacteria (22%). PDA with chloramphenicol displayed more fungi (55%) than bacteria and also produced a half log more fungal colonies than DRBC with chloramphenicol (Table 5).

One fungal sample (*Cladosporum*) presented delayed Ct (31.79) with TYM qPCR primers. Scrutiny of the primer sequences against the *Cladosporum* genome demonstrates proper primer binding locations but missing probe sequence. The coverage of this genome is only 10X and the ITS regions are often in copy number flux resulting in assembly breaks in the ITS regions. This may explain the missing probe sequence in the low coverage fragmented assembly. Additionally, some significantly delayed TAC signal was observed in fungal colonies. This is the result of the use of a Thaumatin-like protein which is cloned and expressed in *E.coli* and is utilized to lyse the fungal cells. This background TLP expression vector *E.coli* signal can be seen in blank preps. In some cases this signal is elevated due to mixed colonies observed in the sequencing data.

The qPCR data represents an increased selectivity compared to DRBC delivering 80% fungal colonies. Even if we discount the mixed colonies and count only a single bacterial colony out of 13 on DRBC we obtain 92% fungal colonies on DBRC. Quantitative PCR demonstrated over 10 Cts (1024 fold) differences between the TYM and TAC primer sets and the majority of the residual TAC Ct can be discounted due to the background *E.coli* TLP DNA.

To confirm these observations several Aspergillus species and Botrytis cinerea were ordered from ATCC and plated on various plating medias in absence of background cannabis matrix (Table 6 and Figure 4). In all cases DRBC shows reduced CFU counts.



#### Table 1. DRBC with Chloramphenicol:

Colony Image (Left), Assembly sequence coverage (Y) compared with contig Length (X) where the contigs are sorted largest to smallest from left to right (Mid-Left). Assembly statistics calculated with Quast 5.0 (Mid Right). OneCodex speciated kmer count (Right).









#### Table 2. PDA with Chloramphenicol:

Colony Image (Left), Assembly sequence coverage (Y) compared with contig Length (X) where the contigs are sorted largest to smallest from left to right (Mid-Left). Assembly statistics calculated with Quast 5.0 (Mid Right). OneCodex speciated kmer count (Right).

Colony Image	Assembly Coverage (Y) Large->Small Contigs (X)	Assembly Statistics (Quast 5.0)	OneCodex Kmer Classification	TAC CE TYM CE
PC-E-2-2-A 001.fastg.gz	Pseudomonas oryzihabitans Bacteria	https://app.onecodex.com/analysis/public/4215767e704f4341	Name Estimated Abundance	18.27 ND
	BCE33A	Assembly PC E 2 2 A	Pseudomonas sryshabitans     S2.65%	
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	10000	# contigs (>= 50000 bp) 17	<ul> <li>Pseudomonas putida</li> <li>12.16%</li> </ul>	
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	some of the state	Total length (>= 50000 hp) 4864257	Partoes anaratis 0.94%	
	100	# contins 1802	Pseudomonas colleoptarorum 0.42%	
	Sand Street A	Largest contig 676 208	Barllus adatation 0.20%	
	10	Total length 6 194 697	Preudomonias swimmare 0.25%	
	1	CC (%) 62.05	III Fusarium fujkuroj 0.12%	
	0 50 100 150	GC (%) 02.85	III (Remaining) 0.43%	
	0 30 100 130	N50 331094		
PC-E-2-2-B_001.fastq.gz	Pseudomonas putida Bacteria	https://app.onecodex.com/analysis/public/a903ec0941a6466c	Name Estimated Abundance	17.04 13.48
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and the second se	10000	# contigs (>= 25000 bp) 26	Pseudomonas psychrotolerans 17.20%	
and the second se		# contigs (>= 50000 bp) 22	Pseudomonas oryphabitans 19,93%	
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		Total length (>= 50000 bp) 4994836	The dependence of 1946/67 0.516	
	100	# contigs 193	Bacilus veizenos 0.54%	
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		Total length 5,420,450	Pantoea ananatis 0.09%	
	1	GC (%) 65.11	IIII Kosekonia covanii 0.05%	
	0 20 40 60	N50 296382	III (Remaining) 0.20%	
PC-E-2-2-C 001 fasto oz	Pseudomonas coleopteronum Bacteria	https://ann.onecodex.com/analysis/mublic/fd9dca39c6464007	Name Estimated Abundance	14.41 ND
1 0 2 2 2 0_001.123(q.gz	- acted and a consumer of a citeria	Assembly DCF22C	Pseudomonas coleopterorum     62.39%	44.44 NO
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	10000	# contings (>= 50000 bp) 13	Pseudomonas cannabina 0.17%	
		# contrigs (>= 50000 bp) 1/	Pseudomonas sp. UBA6562 0.16%	
	1000 ********************	Total length (>= 25000 bp) 4541//0	Pantoes aggiomerans 0.15%	
	100	lotal length (>= 50000 bp) 4453469	III Enterobacter cloacae 0.03%	
		# contigs 152	Bacilius velezensis 0.03%	
	10	Largest contig 703,285	Putarlum fujikuroi 0.01%	
		Total length 4,688,673	Personan obran 0.01%	
	1 20 20 20 10	GC (%) 62.04	The demonstration 0.01%	
	0 10 20 30 40	N50 304475		
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Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-D 10000 100 100 10 10 10 10 10 10 10 PC-E-2-E 10000 100 100 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           http://ass.onceder.com/sadva/pdd//ddd/2004/Bach           Assembly $PC_E_2_2_D$ # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         4877180           Total length (>= 50000 bp)         4877180           Total length (>= 50000 bp)         4877473           # contigs         157           Largest contig         927,974           Total length         4,987,292           GC (%)         65.40           NS0         524142           http://pasoecede.com/ast/side/beccede/5864fm           Assembly         PC_E_2_2_E           # contigs (>= 25000 bp)         24           # contigs (>= 50000 bp)         24           # contigs (>= 50000 bp)         24           # contigs (>= 50000 bp)         4641789           Total length (>= 50000 bp)         4537931           # contigs         (>= 50000 bp)         4537931           # contigs         (>= 50000 bp)         4537931           # contigs         (>= 3000 bp)         4537931           # contigs         (>= 3000 bp)         4537931           # contigs <t< th=""><th>Image: Second Second</th><th>15.64 ND</th></t<>	Image: Second	15.64 ND
Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 1000 100 10 10 10 10 10 10 10 Pantoea agglomerans Bacteria PC-E-2-2-E 10000 100 100 100 100 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           PC_E_2_2_D           # contigs (>= 25000 bp)         PC_E_2_2_D           # contigs (>= 25000 bp)         13           # contigs (>= 50000 bp)         12           Total length (>= 25000 bp)         487180           Total length (>= 50000 bp)         487173           # contigs         157           Largest contig         927,974           Total length         4,987,292           GC (%)         65.40           N50         524142           http://assensecoks.com/asinis/add//dcc0005atMsfm           Assembly         PC_E_2_2_E           # contigs (>= 25000 bp)         24           # contigs (>= 25000 bp)         21           Total length (>= 25000 bp)         24           # contigs         3066           Largest contig         641,210           Total length         4,225,766	Encodex Kmer Classification           Izme         Estimate Andrea           Produces inplation         134           Produces inplation         134           Produces inplation         134           Produces inplation         134           Produces inplation         0.04           Produces inplation         0.04<	15.64 ND
Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 10 10 10 10 200 300 Pantoes agglomerans Bacteria PC-E-2-2-E 10000 100 10 1 1 1 1 1 1 1 1 1 1 1 1 1	Assembly Statistics (Quast 5.0)           https://seconcede.com/sec/sec/secon	Interdet Kmer Classification           Interdet Research         Extensit Mondare           Productiona Signification         15 36           Production Obset         15 36           Production Obset <t< th=""><th>TAC Ct. TYM Ct 15.68 ND 15.64 ND 15.64 ND</th></t<>	TAC Ct. TYM Ct 15.68 ND 15.64 ND 15.64 ND
Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           https://aconcende.com/achig/achig/th/th/200584ch           Assembly         PC_E_2_2_D           # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         4871180           Total length (>= 50000 bp)         4877473           # contigs         157           Largest contig         927,974           Total length         4,987,292           GC (%)         65.40           N50         524142           https://aconcede.com/aship/in/ac//dec0005/044fm           Assembly         PC_E_2_2_E           # contigs (>= 25000 bp)         24           # contigs (>= 50000 bp)         21           Total length (>= 50000 bp)         24           # contigs         366           Largest contig         641,210           Total length         4,925,766           GC (%)         53.80           N50         247445	Image: Second	15.64 ND
Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           Http://aconcode.com/nat/nat/nat/nat/nat/nat/nat/nat/nat/nat	Encodex Kmer Classification           Encodex Kmer Classification           Encodex Kmer Classification           Productions signification           Production signification	TAC Ct. TYM Ct 15.68 ND 15.64 ND
Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           https://seconceder.com/nat/nat/ndt//dt/2005Mach           Assembly $PC_E_2_2_D$ # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         13           # contigs         157           Total length (>= 50000 bp)         1877100           Total length         4,987,292           GC (%)         65.40           NS0         524142           http://zeconcedes.com/nath/nat//bet/bet/0005304fm         Assembly           Assembly         PC_E_2_2_E           # contigs (>= 25000 bp)         24           # contigs (>= 50000 bp)         4641789           Total length (>= 50000 bp)         4537931           # contigs (>= 3000 bp)         4537931	Terms filteration           Image filteration         Envasion           Productional filteration         Existing filteration           Producto	TAC Ct. TYM Ct 15.68 ND 15.64 ND 15.64 ND 18.20 ND
Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-0 1000 100 10 10 100 200 200 200	Assembly Statistics (Quast 5.0)           Http://accentes.com/action/public/lick/HV720548enh           Assembly $PC_E_2_2_D$ # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         4877180           Total length (>= 50000 bp)         4877473           # contigs         157           Largest contig         927,974           Total length         4,987,292           GC (%)         65.40           N50         524142           http://accence.com/assin/a/dx//refc0005.stMcMa           Assembly $PC_E_2_2_E$ # contigs (= 25000 bp)         24           # contigs (= 25000 bp)         24           # contigs (= 25000 bp)         21           Total length (>= 25000 bp)         23           Total length (>= 25000 bp)         4641789           Total length (>= 25000 bp)         306           Largest contig         641,210           Total length (>= 50000 bp)         257,766           GC (%)         53.80           N50         247445           http://accencedex.com/assis/s/public/scicle/c104cd1444           Assembly $PC_D_2_2_2_B$	Enclodest Kmer Classification           Image: State of the second state of t	15.64 ND
Colony Image PC-E-2-2-D_001.fastq.gz PC-E-2-2-E_001.fastq.gz PC-E-2-2-E_001.fastq.gz PC-D-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           https://seconcede.com/sec/ns/ns/ns/ns/ns/ns/ns/ns/ns/ns/ns/ns/ns/	Interface         Extrastification           Image: Second Seco	TAC Ct. TYM Ct 15.68 ND 15.64 ND 15.64 ND 18.20 ND
Colony Image           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-0 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           Http://account.gs         PC_E_2_2_D           # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         4877180           Total length (>= 50000 bp)         4877473           # contigs         157           Largest contig         927,974           Total length         4,9877,292           GC (%)         65.40           N50         524142           Http://acconcode.com/asinis/add//dcCOMSatMcMB           Assembly         PC_E_2_2_E           # contigs (>= 25000 bp)         24           # contigs (>= 25000 bp)         24           # contigs (>= 25000 bp)         21           Total length (>= 25000 bp)         24           # contigs (>= 50000 bp)         24           Total length (>= 25000 bp)         247445           http://acconcode.com/asis/s/add/dcCodeAcdMcSt12441           Assembly         S25,766           GC (%)         53.80           N50         247445           http://acconcode.com/asis/s/add/dcd/dcd/dcd/dcd/dcd/dcd/dcd/dcd/dcd	Encodest Kmer Classification           Image: Strate and Andrease           Produces significant         334           Produces significant         334           Produces significant         344           Produces significant         344           Produces significant         346           Produces significant         347           Produces signitant	15.64 ND
Colony Image           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 100 10 100 100 100 1	Assembly Statistics (Quast 5.0)           http://seconcede.com/sec/ind/Wid/Wid/Wid/Wid/Wid/Wid/Wid/Wid/Wid/Wi	Enclodest Kmer Classification           Termstellation         Extension Advances                – Produces signification         32.95                – Produces sig	TAC Ct. TYM Ct 15.68 ND 15.64 ND 15.64 ND 18.20 ND
Colony Image           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-0 10000 100 10 10 10 10 10 10 1	Assembly Statistics (Quast 5.0)           http://acorecode.com/achin/achi/chi/th/200584ch           Assembly $PC_E_2_2_D$ # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         4877180           Total length (>= 50000 bp)         4877180           Total length (>= 50000 bp)         4877473           # contigs         157           Largest contig         927,974           Total length         4,9877,292           GC (%)         65.40           N50         524142           http://acorecode.com/achin/ach//be/Contention         437931           # contigs (>= 25000 bp)         24           # contigs (>= 25000 bp)         247445           http://acorecode.com/achin/ach//be/Coldor/16401444           Assembly $PC_D_2_2_2_B$ # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         247445           http://acorecode.com/achin/ach//be/Coldor/16444           Asse	NetCodex Kmer Classification           Image: Strate Classtration           Image: Str	15.64 ND
Colony Image           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           Http://aconcode.com/nat/nat/nat/nat/nat/nat/nat/nat/nat/nat	Image: Second	15.68 ND
Colony Image           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-E_001.fastq.gz           PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           http://aconsector.com/pach/sit/sit/sit/sit/sit/sit/sit/sit/sit/sit	Encodex Kmer Classification           Image: State of the st	TAC CC TYM CC 15.68 ND 15.64 ND 15.64 ND 18.20 ND
Colony Image           PC-E-2-2-D_001.fastq.gz           Image: PC-E-2-2-D_001.fastq.gz           PC-E-2-2-E_001.fastq.gz           PC-D-2-2-B_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-D 10000 100 100 10 10 100 200 200	Assembly Statistics (Quast 5.0)           Http://accorecte.com/nat/nat/nat/nat/nat/nat/nat/nat/nat/nat	Interface         Entertal Advance           Termine         Entertal Advance           Produces signification         3.36           Produces signification         3.37           Produces signification         3.36           Produces signification         3.37           Produces signification         3.37           Produces signification         3.37           Produces signification         3.37           Produces signification         3.38           Pr	TAC Ct. TYM Ct           15.68         ND           15.64         ND           15.64         ND           18.20         ND
PC-E-2-2-D_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-D 10000 100 100 10 10 100 100 10	Assembly Statistics (Quast 5.0)           https://aconcender.com/ach/ach/200584ch           Assembly         PC_E_2_2_D           # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         13           # contigs (>= 25000 bp)         12           Total length (>= 25000 bp)         4877180           Total length (>= 50000 bp)         4877170           Total length (>= 50000 bp)         4877473           # contigs         157           Largest contig         927,974           Total length         4,987,292           GC (%)         65.40           N50         524142           httm://aconcode.com/ash/si/ba//bd//bd/00005184ffs           Assembly         PC_E_2_2_E           # contigs (>= 25000 bp)         24           # contigs (>= 50000 bp)         21           Total length (>= 50000 bp)         21           Total length         4,925,766           GC (%)         53.80           N50         247445           httm://aconcode.com/ash/si/si/si/si/si/si/si/si/si/si/si/si/si/	Interaction         Extrastification           Image: Second Se	TAC Ct. TYM Ct           15.68         ND           15.64         ND           18.20         ND
Colony Image           PC-E-2-2-D_001.fastq.gz           PC-E-2-2-E_001.fastq.gz           PC-E-2-2-E_001.fastq.gz	Assembly Coverage (V) Large-Small Contigs (X) Pseudomonas fluorescens Bacteria PC-E-2-2-0 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           Http://accorectes.com/school/school/1200546/http://school/sch	Interface         Enterface           Terming         Extension           Produces inplations         334           Produces inplations	TAC Ct. TYM Ct           15.68         ND           15.64         ND           18.20         ND



Colony Image	Assembly Coverage (Y) Large->Small	Contigs (X)	Assembly Statistics (Quast 5.0)	One	Codex Kmer Classific	ation		
PC-D-2-2-D 001.fasto.oz	Penicillium citrinum	Fungi	https://app.onecodex.com/analysis/public/f4f7a05888bS4ca4	Name		Estimated Abundance		28.78 16.27
			Assembly PC D 2 2		Pericilium obtinum	77.99%		
	PC-D-2-2-D		# conting (>= 25000 hp) 402		Paritosa applomerans	5.228		
	10000	_	# contrigs (>= 25000 bp) 402	-	Partona anaratis	1.526		
		•	# contigs (>= 50000 bp) 211	-	Pseudomonas montella	3.14%		
	1000	•	lotal length (>= 25000 bp) 26589484	-	Escherichia celi	1.73%		
	100	2	Total length (>= 50000 bp) 19786523		Pseudomonas coleopteronam	1.42%		
		19B	# contigs 2324	-	Bacilus anyioliquefacienti	1.29%		
	10		Largest contig 355,055		Pseudomonas oryzihabitans	1,10%		
and the second se			Total length 32,726,848	-	Bacillus velezensis	1.02%		
	1		GC (%) 46.46	-	Fusarium fujikurol	0.78%		
	0 500	1000	N50 66412		(Remaining)	2.79%		
				-				and the second second second
PC D 2 2 E 001 feete ez	Des leillium eiteinum	Fund						27.05 17.19
PC-D-2-2-E_001.iastq.gz	Fencingin cicingin	rungi	Accombly PC D 2 2	E T	Restored an objector	ESCIMACED ADUINDANCE		27.05 17.10
	PC-D-2-2-E				Percinami comami	80.80%		
	10000		# contigs (>= 25000 bp) 436	-	Paradomonia mostali	6.71%		
		Charles 1	# contigs (>= 50000 bp) 217	-	Pantnea anaratis	4.90%		
	1000		Total length (>= 25000 bp) 26450972		Bacillus velezensis	3,439		
	100		Total length (>= 50000 bp) 18441260		Pseudomonas coleopterorum	3.17%		
	100 A State of Land	1.55	# contigs 7634	-	Escherichia coli	1.82%		
	10		Largest contig 268,477		Pseudomonas oryphabitans	1.60%		
	and the second se		Total length 36,552,780		Pantoea vagans	1.45%		
	1		GC (%) 47.46		Fostarium fojikumoj	1.28%		
	0 500 1000	1500	N50 50555		(Remaining)	6.98%		
			9000		100000			
PC D 2 2 E 001 facto on	Depicillium sitelaum	Fund			1993			21 66 20.01
FG-D-2-2-F_001.tastq.gz	Penicillum citrinum	Fungi	https://app.onecodex.com/analysis/public/36bb541f014c437f	Name	Readcour	nt (% of classified reads)		51.66 30.91
	Fusarium fujikuroi	MIX	Assembly PC_D_2_2_	-	Ustilago maydis	33661 (2,64%)		
and the second second	PC-D-2-2-F		# contigs (>= 25000 bp) 429	-	Penicillium citrinum	16863 (1.32%)		
and the second s	10000		# contigs (>= 50000 bp) 297	-	Fusarium fujikuroi	16724 (1.3196)		
and all the second			Total length (>= 25000 bp) 44070909	-	Trichoderma harzianum	9119 (0.71%)		
ALC: NOT THE P	1000		Total length (>= 50000 bp) 39227038	-	Pseudomonas coleopterorum	8262 (0.65%)		
Contraction 1	100		# contigs 2392		Epicoccum nigrum	7871 (0.62%)		
Renovation	and the second s		Largest contig 709,629	-	Pseudomonas oryzihabitaris	7355 (0.58%)		
and the second	10	1	Total length 47 801 658		Fantoea aggiomerans	5866 (0.46%)		
and have been and the	1				Atemana atemata	3718 (0.29%)		
Contraction of the second	0 200 400 60	00 800	SC (%) 50.00		Aspergerus sp. MA 6041	2670 (0.21%)		
			N30 1280/8	1 C C C C C C C C C C C C C C C C C C C	(vacuationg)	27272323480		
					construction of the second second second second			
Colony Image	Assembly Coverage (Y) Large->Small	Contigs (X)	Assembly Statistics (Quast 5.0)	One	Codex Kmer Classifie	ation		TAC Ct TYM Ct
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)	One	Codex Kmer Classifie	Estimated Abundance		TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G	Contigs (X) Fungi	Assembly Statistics (Quast 5.0) https://app.onecodex.com/analysis/public/02509f1971b94c1d Assembly PC_D_2_2_	G One	Codex Kmer Classifie	Estimated Abundance		TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           https://app.onecodex.com/anahois/public/02509/1971b94-1d           Assembly         PC_D_22           # contigs (>= 25000 bp)         464	G Cone	Abernaria alternata Methylobacterium phyliophaerae	Estimated Abundance (8.2%) 10.44%		TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 1000	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           https://app.anecodex.com/ana/sis/public/00509/1971/04-cld           Assembly         PC_D_2_2	G S	Alternaria alternata Merkylobacterium phyliophaerae Alternaria arborescen	Estimated Abundance (8.2%) 10.4% 6.12%	$\sim$	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           http://sec.onscodex.com/sabsid/sobic/0509107104518           Assembly         PC_D_2.2_2           # contigs (>= 25000 bp)         464           # contigs (>= 56000 bp)         257           Total length (>= 25000 bp)         33602944	G =	Codex Kmer Classifie Aternatis aternata Methylobacterium phyliospherse Aternatia atborescens Methylobacterium brachiatum	Estimated Abundance (8.2%) 10.46% 6.12% 5.38%	$\bigcirc$	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 1000 100	Contigs (X) Fungi	$\label{eq:constraints} \begin{array}{l} \mbox{Assembly Statistics (Quast 5.0)} \\ \mbox{htm://www.mc/makes/public/00509/197198-tid} \\ \mbox{Assembly} & PC_D_2_2_2 \\ \mbox{# contigs (>= 25000 bp)} & 464 \\ \mbox{# contigs (>= 50000 bp)} & 257 \\ \mbox{Total length (>= 25000 bp)} & 33602944 \\ \mbox{Total length (>= 25000 bp)} & 26097287 \\ \mbox{Total length (>= 2500 bp)} & 260$	G G	Codex Kmer Classifie Alternalis alternata Methylobcarium phylopherae Alternalis altoreson Methylobcarium trachiatum Pastoea aggiomerans	Estimated Abundance (8.299) 10.46% 6.12% 5.38% 1.27%	0	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.g2	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 1000 100	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           https://seconcodex.com/subsit/obl/CVS09197148418           Assembly PC_D_2.2.           # contigs (>= 25000 bp) 464           # contigs (>= 25000 bp) 257           Total length (>= 25000 bp) 3662944           Total length (>= 55000 bp) 2697287           Total length (>= 55000 bp) 3662944           Total length (>= 55000 bp) 3662944	G S	Codex Kmer Classifie Alteraria alternata Mehylobatarium phyliospharae Alteraria arborescen Wehylobaterium bachatum Pattoea aggionezas Stretorores purporgenesiderotoa	Estimated Abundance (8.2%) 10.4% 6.1% 5.5% 1.7% 1.3% 1.3%	0	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 1000 100 10	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           http://www.news.colspan="2">http://www.news.colspan="2"           http://www.news.colspan="2">http://wwww.news.colspan="2"         http://wwww.news.colspan="2"         http://www.news.colspan="2"         http://www.news.colspan="2"         http://wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww	G C C C C C C C C C C C C C C C C C C C	Codex Kmer Classifie Aternata aternata Methylokaterium phylogherse Aternata atoresen Methylokaterium franklaum Pantosa aggionetas Pantosa aggionetas Pantosa atanatas Pantosa atanatas	Estimated Abundance 62.2% 13.4% 5.5% 1.7% 1.3% 1.3%	0	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           http://spacescolscol/spacee/spaceeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee	G Cone	Aberraria alternaza Mehylabacerium phylioghaerae Aternada arboreseen Mehylabacerium phylioghaerae Aternada arboreseen Mehylabacerium toxihoum Partose arangionerans Singtoniynes jungunegenesideratus Partosea arandis Partosea arandis	Estimated Abundance (8.23%) 10.44% 6.12% 5.55% 1.27% 1.27% 1.25% 1.27% 1.25% 1.27% 1.25% 1.25% 1.27% 1.25% 1.25% 1.27% 1.25% 1.27% 1	0	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           http://spacescodec.com/sabai/spai/spai/spai/spai/spai/spai/spai/sp	G G	Codex Kmer Classifie Ateraia densa Menjalacrim pilophene Ateraia doreces Menjalacress pilophene Sciptores paragenedetoca Petera annos Petera anos Petera anos Petera anos Petera anos Petera anos	Estimated Abundance (8.2%) 19.4% 6.12% 5.3% 1.37% 1.37% 0.32% 0.32%	0	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           http://spacescols.com/subsid/spat/c030/137108418           Assembly         PC_D_2_2_1           # contigs (>= 25000 bp)         464           # contigs (>= 55000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         395,256,281           GC (%)         53.75	G G	Attradic Almera Classified Attradic almosta Merglubaction phylosphares Attradia toroneen Merglubaction toolutan Pateoa agioneens Simpromyne public Pateoanara politik Pateoanara politik Pateoanara simplemens Pateoanara simplemens	Estimated Abundance (8.2%) 15.46% (8.2%) 1.57% (8.2%) 1.57%{	0	TAC Ct. TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G	Contigs (X) Fungi	Assembly Statistics (Quast 5.0)           https://sec.nocdex.com/subsit/sol/CVSDSUSTUP14810           Assembly         PC_D_2.2_#           # contigs (>= 25000 bp)         464           # contigs (>= 50000 bp)         257           Total length (>= 50000 bp)         26097287           Total length (>= 50000 bp)         3602944           Total length (>= 50000 bp)         26097287           Largest contig         384,610           Total length         39,526,281           GC (%)         53.75           NS0         77385	G	Codex Kmer Classifie Attradu dense Verplaksenin pångkanes Verplaksenin program Verplaksenin tradikan Pattera agtimens protores anals Pattera agtimens Pattera agtimens Pattera agtimens Pattera agtimens Backomma Stepfansm Benkomma	Estimated Abundance 64.29% 13.44% 4.32% 1.37% 1.37% 1.37% 0.35% 0.35% 0.35% 0.35%	0	TAC Ct TYM Ct 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large-Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contigs (X) Fungi 6000	Assembly Statistics (Quast 5.0)           http://spacescolec.com/spacee/space/space/space/space/space/space/space/space/space/space/space	G Cone	Codex Kmer Classifie Attradu atmaz Mahlatorum philosphare Attradu atoresen Mahlatorum bashdum Pattea agamesis promonose puorgenetabeticos Patea aransis Pasadamena pida Bashamena (depatrasm Pasadamena (depatrasm) Pasadamena (depatrasm)	Estimated Abundance (4.37%) (3.34%)	0	TAC Ct. TYM Ct. 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz PC-D-2-1-A_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 0 2000 4000 Pseudomonas oryzihabitans	Contigs (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           http://spacescolscol/spatia	G A Name	Codex Kmer Classifie Atmas atmas Weyblacture policipares Atmas atmas Weyblacture tooluce Atmas agenes Singenges policipared Singenges policipared Singenges policipared Reading website Reading website Beating Participares Attooluces installate	Estimated Abundance 62.2% 19.4%19.4% 19.4% 19.4% 19.4% 19.4	0	TAC C: TYM C: 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-A	Contigs (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           http://spacescolec.com/satistic/space/0509107194518           Assembly         PC_D_2.2_2           # contigs (>= 25000 bp)         464           # contigs (>= 55000 bp)         257           Total length (>= 25000 bp)         3662944           Total length (>= 50000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         39,526,281           Total length         39,526,281           MS0         77385           http://ssomecofec.com/satisf/sbdc/sdf2553eet6484         Assembly           # contig         2800 bp)         260_2_1_1	G Name	Codex Kmer Classifie Atmats Immus Verbibschung Johophane Atmats Internet Methyloschung trachuson Pastaa agionean Methyloschung sopragenetidetics Pastaanaras Pastamara pola Beckung sopragenetidetics Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atmats Atm	Extinuited Adundance Extinuited Adundance (2278) (2	0	TAC Ct. TYM Ct. 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contigs (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           http://spacesodec.com/subsid/pat/US09197194518           Assembly         PC_D_2_2_           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         2697287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           N50         77385           http://spacesodec.com/space/space/space/space         4           Assembly         PC_D_2_1_           # contigs (>= 25000 bp)         18	One	Codex Kmer Classifie Aternala atensa Weyhäcksnin printpalarens Meryhäcksnin printpalarens Meryhäcksnin straduum Areatea generes Srepronge proceedentoo Areatea areans Arachmena print Arachmena (Stephenson Benaring) Prodomoras (Stylhalters Prodomoras (Stylhalters Prodomoras (Stylhalters	Ections Howleave 622% 13.4% 13.4% 13.5% 13.7%13.7% 13.7%13.7% 13.7% 13.7% 13.7%13.7% 13.7% 13.7%13.7% 13.7% 13.7%13.7% 13.7% 13.7%13.7% 13.7% 13.7%13.7% 13.7% 13.7%13.7% 13.7% 13.7%13.7% 13.7%13.7% 13.7% 13.7%13.7% 13.7%13.7% 13.7%14% 13.7%14%	0	TAC C: TYM C: 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-A	Contigs (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           https://sec.org/sec	A Name	Codex Kmer Classifie Attrasta atmaz Veryhdestania phytoplanes Partial a drovenia Partial a gronzenia Partial agrimens Partial agrimens Partial agrimens Partial ands Partial and Partial Partial and Partial Partial and Partial Partial and Partial Partial agriphical Partial agriphical Partial Partial agriphical Partial	Cations Edinated Abundance (229) (	0	TAC Ct. TYM Ct. 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternata alternata Mk PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contigs (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           http://spacesodec.com/swipsi/point/000/007/000/007/000/000           Assembly         PC_D_2_2_1           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         260           # contigs (>= 50000 bp)         33602944           Total length (>= 50000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         39,526,281           GC (%)         53.75           NS0         77385           http://spacesodec.com/swisis/solic/sol	C Nama	Codex Kmer Classifie Attracts atmas Merphässim philophane Merphässim philophane Merphässim philophane Attracta agrones Promose provenendentos Protos anno Protos anno Attracta agrones Protos anno Protos	Ections 444 447 447 447 447 447 447 447 447 447	0	TAC C: TYM C: 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-A	Contigs (X) Fungi 6000 Bacteria	$\label{eq:constraints} \begin{array}{ c c c c c c } \hline Assembly Statistics (Quast 5.0) \\ \hline \mbox{trass}//ise consoles con/salasi/sal$	C One	Codex Kmer Classifie Attrasts atmaz Veryhässenin prönspärers Veryhässenin prönspärers Veryhässenin trastalian Parstal agternen Parstale agternen Parstale agternen Parstalenna Berlander Parstalenna Parst	Cations Advantance Extinuited Advantance (229) (	0	TAC Ct. TYM Ct. 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternatia alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contigs (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           http://spacesodec.com/subsid/pol/c0309137108418           Assembly         PC_D_2_2_1           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         395,56,281           GC (%)         53.75           N50         77385           http://spacesodec.com/subsid/sdd/sd3555ccf484           Assembly         PC_D_2_1_1           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         17           Total length (>= 25000 bp)         17           Total length (>= 25000 bp)         4871673           Total length (>= 50000 bp)         483662           Total length (>= 50000 bp)         483662           Total length (>= 50000 bp)         483662	A Normal State	Codex Kmer Classifie Attracta atmaza Merghalacsiun philoplanes Attracta atoesan Merghalacsiun shaduan Attracta agenesis Singtongos pupungenediotoco Patena aranto Patena aranto P	Cations Adventions Extinuited Adventions 10,27% 10,	0	TAC C: TYM C: 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-A 10000 100 100 100 100 100 100 100 100	Contigs (X) Fungi 6000 Bacteria	$\label{eq:constraints} \begin{array}{ c c c c c c } \hline & & & & & & & & & & & & & & & & & & $	A Name	Codex Kmer Classifie Attrasta atmaz Veryhäcstnin pyhoplanes Veryhäcstnin pyhoplanes Attrasta zaposen Singrompo pupingenes Singrompo pupingenes Singrompo pupingenes Pettos pano Pettos pano Pettos sensis Pettos sensis	Cations Advantage Extinuited Advantage (22%) (23	0	TAC Ct. TYM Ct. 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternatia alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           http://sponsecodes.com/subsid/polic/0309137304514           Assembly         PC_D_2_2_1           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           N50         77385           http://sponsecies.com/subsid/sddf/sddf/sdsf253teci6484           Assembly         PC_D_2_1_1           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         17           Total length (>= 25000 bp)         17           Total length (>= 25000 bp)         4831662           # contigs (>= 25000 bp)         128           Largest contig         128           Largest contig         128           Largest contig         4,965,263	A Name	Codex Kmer Classifie Attracts atmas Merphässim philophane Attracta stream Merphässim philophane Attracta stream Attracta stream Attract	lection Extinuited Adundates Extensional Ad	0	TAC C: TYM C: 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi	Assembly Statistics (Quast 5.0)           http://www.ordex.com/walkid/bal/COSOUSTID-104-104           Assembly $PC_D 2_2_2$ # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         26097287           Total length (>= 55000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         39,526,281           GC (%)         53.75           NS6         77385           http://www.orecodes.com/wahrd/public/sdf255tecd484           Assembly $PC_D_2_1_1$ # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         18           # contigs (>= 55000 bp)         18           # contigs (>= 55000 bp)         4833662           # contigs         128           Largest contig         1,466,263           Total length (>= 55000 bp)         4833662           # contigs         128           Largest contig         1,466,263           Total length         4,982,481           Cottal length         4,982,481	A Normal A	Codex Kmer Classifie Attrasta almaa Weyhlacariun pylooplanes Heyhlacariun pylooplanes Attrasta agenes Singenope pup:regeneticity Pacationage public Basilia viteensis Pacationes public Pacationes to pylooplanes Pacationes to pylooplanes Pacationes to pylooplanes Pacationes agenesis Pacationes agenesis Pacationes agenesis Pacationes applications Pacationes applications Pacatione	Cations Hardians Extinuite Markanse Extension 2014 Extension 2014 Extensio	0	TAC Ct. TYM Ct. 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternatia alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria	Assembly Statistics (Quast 5.0)           Interview Colspan="2">Interview Colspan="2">Interview Colspan="2">Interview Colspan="2"           Assembly         PC_D_2_2_1           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         35602544           Total length (>= 25000 bp)         35602544           Total length (>= 50000 bp)         25607287           # contigs         1387           Largest contig         384,610           Total length         39,526,281           GC (%)         53.75           N50         77385           Muto//woonscoles.com/www.inst/pub/c/pdf/2531ecf644           Assembly         PC_D_2_1_1           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         17           Total length (>= 50000 bp)         128           Largest contig         1,066,263           Total length         4982,481           GC (%)         65.59           N50         3408055	G A Rama	Codex Kmer Classifie Attrada atmaa Merphäsenin philopäane Attrada saloesenin Merphäsenin tradisationen Attrada saloesenin Attrada saloesenin Singenopos pupurgenödetotois Pastonense publik Pastonense publik Paston	Lettion Linute Alumine Linute Alumine 19.42% 19.4% 19.5% 19.	0	TAC C: TYM C: 25.06 24.57
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300	Assembly Statistics (Quast 5.0)           http://sqc.orecodex.com/salphit/pabl/10509137108418           Assembly         PC_D_2_2_           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         2697287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           NS0         77385           http://ssc.orecides.com/sslati/ssdi/sdi/2535ecf481           Assembly         PC_D_2_1_1           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         18           # contigs (>= 58000 bp)         17           Total length (>= 59000 bp)         18           # contigs         128           Largest contig         1,066,263           Total length         4,982,481           GC (%)         65.59           NS0         340805	G A Name	Codex Kmer Classifie Atmais atmas Weyblacking pipepting Weyblacking pipepting Weyblacking pipe Atmas atwares Presentation	Cations Extinuite Monitorie 622% 13.4% 13.5% 13.5% 13.5% 13.5% 2.5% Extinuite Autoence 14.5% 14.	0	TAC C:         TYM C:           25.06         24.57           17.48         ND
Colony Image PC-D-2-2-G_001.fastq.gz PC-D-2-1-A_001.fastq.gz PC-D-2-1-A_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-A 10000 100 100 10 10 10 10 10 10 10 10 1	Contigs (X) Fungi 6000 Bacteria 300	Assembly Statistics (Quast 5.0)           http://isponsore.org/subject/pair/colspan="2">Coll Colspan="2">Coll Colspan="2">Coll Colspan="2">Coll Colspan="2">Coll Colspan="2"           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         3602944           Total length (>= 50000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         39,526,281           GC (%)         53,75           NS0         77385           http://sponsodec.com/selsi/sbd//sdd/2552ecf581           Assembly         PC_D_2_1_           # contigs (>= 25000 bp)         18           # contigs (>= 50000 bp)         4833662           # contigs         128           Largest contig         1,665,263           Total length         4,982,481           GC (%)         65.59           NS0         340805	A Mana	Codex Kmer Classifie Attrasts atmas Veryhäckning pålogikans Veryhäckning pålogikans Veryhäckning pålogikans Strattas atrastes Strattas atrastes Strattas atrastes Attrasta attrastes Pettos analos Pettos analos Pettos attrastes Pettos a	Cations Advances Editions of Advances (22%) (23%	0	TAC Ct. TYM Ct. 25.06 24.57 17.48 ND
Colony Image PC-D-2-2-G_001.fastq.gz PC-D-2-1-A_001.fastq.gz PC-D-2-1-A_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternata alternata Mk PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300	Assembly Statistics (Quast 5.0)           http://sponsecodec.com/subsid/pob/cUS050137304544           Assembly         PC_D_2_2_           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         26997287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           NS0         77385           http://sponsecoles.com/subsis/solic/so	S A Name	Codex Kmer Classifie Attracts atmas Merghalssnin piptinghame Attracta atwas Attracta atwas Attracta atwas Attracta atwas Attracta attractor Attracta attractor Attracta attractor Attracta attractor Attracta attractor Att	Ections Ections Markers Ections Advances Extension	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           17.48         ND           32.00         23.49
Colony Image PC-D-2-2-G_001.fastq.gz PC-D-2-1-A_001.fastq.gz	Assembly Coverage (Y) Large-Small Alternaria alternata Mix PC-D-2-2-G 0 0 0 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-A 1000 100 100 100 100 100 100 100 100 1	Contigs (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           http://wp.oncodex.com/walkid/bal/(2005/05/05/05/05/05/05/05/05/05/05/05/05/	A Mana A	Codex Kmer Classifie Attrasts almast Weyklacturum photoplanes Attrasta agrones Attrasta agrones Attrasta Attrasta agrones Attrasta Attrast	Cational Advances Edinated Advances 13.444 13.474 13.474 13.7788 13.77888 13.7788 13.77888 13.77888 13.7788 13.7788	0	TAC Ct. TYM Ct. 25.06 24.57 17.48 ND 32.00 23.49
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternata alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           http://wp.onsodex.com/walmid/pab/cUS09137104514           Assembly         PC_D_2_2_           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         2697287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           N50         77385           http://wp.onecodex.com/walmid/pab/c/s518ccf484           Assembly         PC_D_2_1_           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         17           Total length (>= 25000 bp)         17           Total length (>= 25000 bp)         17           Total length (>= 50000 bp)         17           Total length (>= 50000 bp)         128           Largest contig         1,066,263           Total length         4,982,481           GC (%)         65.59           N50         340805           http://wp.oncodex.com/walmid/pab/c/12431818124314           Assembly         PC_D_2_1_           # conti	S Cone	Codex Kmer Classifie Attracts atmas Merphässinn philophane Attracts assesses Singeorges proceedings Singeorges proceedings Practice games Practice games Practice and philo Practice games Practice and philo Practice and philo Practice and philophane Practice	Lettion Etimista Alavitation 10.27%	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2:2-G_001.fastq.gz C-D-2:1-A_001.fastq.gz PC-D-2:1-A_001.fastq.gz	Assembly Coverage (Y) Large-Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-R 1000 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           http://wp.oncodex.com/walkid/bal/(2005/05/05/05/05/05/05/05/05/05/05/05/05/	A Mana A Man A Mana A Man A Mana A Ma	Codex Kmer Classifie Atmas atmas Weyklacturun paloglams Atmas atmas Singengen papargenetik Singengen papargenetik Singengen papargenetik Readon velannis Readon velannis	Cations Advantage Extinuited Advantage (22%) (23	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2-2-G_001.fastq.gz PC-D-2-1-A_001.fastq.gz PC-D-2-1-A_001.fastq.gz PC-D-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternata alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           http://wp.orecodex.com/walkid/pdf/US091971904514           Assembly         PC_D_2_2_           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         33602944           Total length (>= 50000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           N50         77385           http://wp.orecodex.com/walkit/pdf/cdf/253bccf484           Assembly         PC_D_2_1_           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         17           Total length (>= 25000 bp)         17           Total length (>= 25000 bp)         128           Largest contig         1,066,263           Total length         4,982,481           GC (%)         65.59           N50         340005           http://wp.orecodex.com/walkit/pdf/1210131314144           Assembly         PC_Q_2_1_           # contigs (>= 25000 bp)         1           # contigs (>= 25000 bp)         1           # contigs (>=	S Cone	Codex Kmer Classifie Attracts atmas Merphässim philophane Attracts assesses Attracts assessesses Attracts assesses Attracts assesses Attracts assesses Attracts assesses Attracts assesses Attracts assessesses Attracts assessesses Attracts assesses Attracts assesses Attracts assesses Attracts assesses Attracts assesses Attracts assesses Attracts assessessessessessesses Attracts assessessessessessessessessessesses Attracts assessessessessessessessessessessessesse	Lettion Extinuted Abundance 10,27%	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2:2:G_001.fastq.gz	Assembly Coverage (Y) Large-Small Alternaria alternata Mix PC-D-2-2-G 100 100 100 100 2000 4000 Pseudomonas oryzihabitans PC-D-2-1-A 1000 100 100 100 100 100 2000 Cercospora nicotianae PC-D-2-1-8 1000 100 100 100 100 100 100 1	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           http://wp.oncodex.com/walkid/bal/(2003/03/03/03/03/03/03/03/03/03/03/03/03/	A A A A A A A A A A A A A A A A A A A	Codex Kmer Classifie Aternata atenata Weryhäkastina pythophanes Aternata atenata Weryhäkastina pythophanes Aternata atenata Singroupes purchagenes Atenation atenation Atenation atenation Reachtmine (Stepplerson Bendring) Produmines (Stepplerson Produmines (St	cation Internet Aluminer 12,255 13,454 13,454 13,458 13,558 13,558 13,558 13,558 13,558 14,	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2-2-G_001.fastq.gz PC-D-2-1-A_001.fastq.gz PC-D-2-1-A_001.fastq.gz PC-D-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternata alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           Http://www.ordex.com/walkid/pdf/0309197109414           Assembly         PC_D_2_2_1           # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         35602944           Total length (>= 25000 bp)         35602944           Total length (>= 50000 bp)         25607287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           NSØ         77385           Mttp://www.onecodes.com/walkits/bdf/2ddf/253tecf644           Assembly         PC_D_2_1_           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         17           Total length (>= 25000 bp)         483662           # contigs         128           Largest contig         1,066,263           GC (%)         65.59           NSO         340005           Mttp://www.onecesces.com/walkis/bdf/2ddf/3df/3df/3df/3df/3df/3df           Mttp://www.onecesces.com/walkis/bdf/2df/3df/3df<	S Normal S N	Codex Kmer Classifie Attrada alemaa Merjulacisum pipiloplaame Attrada astoesen Attrada salesen Attrada salesen Attrada salesen Attrada salesen Singenopos pupungenöötetöö Pastoese pupungenööte	Cations Extinuits Alaminetics Extinuits Ala	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2:2:G_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 100 100 100 2000 4000 Pseudomonas oryihabitans PC-D-2-1-A 1000 100 100 100 100 100 2000 Cercospora nicotianae PC-D-2-1-8 1000 100 100 100 100 100 100 1	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           Intro //wap.org/subject/pat/050/05709000000000000000000000000000000	A Name	Codex Kmer Classifie Attrasta almaa Merjahastania pidoplama Merjahastania pidoplama Merjahastania pidoplama Sergenges purungenetidettos Partasa agenera Partasa agenera Partasa agenera Partasa agenera Partasa agenera Partasa agenera Partasa agenera Sergengen Alastania Partasa agenera Sergengen Alastania Sergengen Alastania Serg	cation Internet Aluminet 12,255 13,455 13,455 13,455 13,455 13,455 13,455 13,455 13,455 13,455 13,455 13,455 13,455 13,455 14,	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2-2-G_001.fastq.gz	Assembly Coverage (Y) Large-Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           Intro //www.order.com/water/pat/050/05709000000           Assembly $P_{CD_2}Z_2$ # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         35602944           Total length (>= 55000 bp)         257           Total length (>= 50000 bp)         256097287           # contigs         1387           Largest contig         384,610           Total length         395,526,281           GC (%)         53.75           NSO         77365           Mttp://www.encedex.com/water/stat/stat/stat/stat/stat/stat/stat/sta	S Normal S N	Codex Kmer Classifie Attrada shmaa Merjulacisun pipiloplame Attrada streame Merjulacisun pipiloplame Attrada streame Simponyos pupurgentolitetoia Pastana gaina Pastana pilola Pastana pilola Pastan	Ections Aborder Ections Aborder 1999 19	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2:2:G_001.fastq.gz PC-D-2:1-A_001.fastq.gz PC-D-2:1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 2000 4000 Pseudomonas oryihabitans PC-D-2-1-A 10000 10 10 10 10 10 10 10 10 10 10 10	Contige (X) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           Inter/Jag consolex com/sales/dpd/(USOSUSUSUSUSUSUSUSUSUSUSUSUSUSUSUSUSUSU	A A A A A A A A A A A A A A A A A A A	Codex Kmer Classifie Atmaia atmaa Menjabacsina piptinghame Atmaia atwane Menjabacsina piptinghame Sengroups purchagene Sengroups purchagene Partana arans Partana a	Retinotal Alumines Terinstat Alumines 19,244 19,244 19,247 19,447	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49
Colony Image PC-D-2-2-G-001.fastq.gz PC-D-2-1-A.001.fastq.gz PC-D-2-1-A.001.fastq.gz	Assembly Coverage (Y) Large-Small Alternaria alternata Mix PC-D-2-2-G 100 10 10 10 10 10 10 10 10 10 10 10 10	Contige (N) Fungi 6000 Bacteria 300 Fungi	Assembly Statistics (Quast 5.0)           http://www.ordex.com/walkid/shif(2050197704416           Assembly $PC_D_2_2_2$ # contigs (>= 25000 bp)         464           # contigs (>= 25000 bp)         257           Total length (>= 25000 bp)         3602944           Total length (>= 55000 bp)         26097287           # contigs         1387           Largest contig         384,610           Total length         39,526,281           GC (%)         53.75           NS0         77385           http://www.orecodes.com/wahshi/public/sdl255tecd188           Assembly $PC_D_2_1_2$ # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         18           # contigs (>= 25000 bp)         4871673           Total length (>= 25000 bp)         483662           # contigs (>= 50000 bp)         483665           http://www.orecodes.com/wahshi/sobic/17431813744164           Assembly $PC_D_2_2_1_4$ # contigs (>= 25000 bp)         1           Total length (>= 25000 bp)         6           Total length (>= 25000 bp)         0           Total length (>=	S A A A A A A A A A A A A A A A A A A A	Codex Kmer Classifie Attrasta ahmaa Weykhacsina pideqlaams Weykhacsina pideqlaams Attrasta atorese Strasta genera Strasta genera Packamana pide Packamana pide Packamana pide Packamana sitegeraran Packamana sitegeraran	Ections Aluminor Ections Aluminor 1949	0	TAC C:         TYM C:           25.06         24.57           17.48         ND           32.00         23.49



Colony Image	Assembly Coverage (1) Large->Small Contigs (X)	Assembly Statistics (Quast 5.0)	Unecodex Kmer Classification	TAC CE I TIVI CE
PC-D-2-1-C1 001.fastg.gz	Trichoderma harzianum Fungi	https://app.onecodex.com/analysis/public/3127e7a8311b40c8	Name Estimated Abundance	32.17 26.16
		Assembly PC D 2 1 C1	Trichoderma harzianum 77.15%	
Mark States and States	PC-D-2-1-C1	# contigs (>= 25000 bp) 340	Trichoderma atrobrureeum 6.34%	
THE REAL PROPERTY OF THE PARTY	10000	# contrigs (>= 50000 bp) 37	<ul> <li>Trichoderma guzhouense</li> <li>6.19%</li> </ul>	
The Party of the Party of the	1000 • •	Total length (>= 25000 bp) 12261952	Pantoea aggiomerans 2.28%	
		Tetal length (>= 20000 bp) 12501055	Pseudomonas aeruginosa 1.83%	
The second second second	100	Total length (>= 50000 bp) 2316186	Partoea ananatis 1.45%	
	and a start with a set of	# contigs 5131	Bacilus velezensis 1.39%	
State Party of State	10	Largest contig 131,469	Pseudomonas coleopterorum 0.70%	
		Total length 41,502,375	Pseudomonas orychabitans 0.37%	
MOLES -	1	GC (%) 46.82	IIII Fusarium fujikurol 0.31%	
UNIX CONSIGNATION OF THE OWNER	0 1000 2000 3000	N50 16662	(Remaining) 1,38%	
PC-D-2-1-C2_001.fastq.gz	Trichoderma harzianum Fungi	https://app.onecodex.com/analysis/public/fa69f1b1f1324d2e	Name Estimated Abundance	30.47 24.95
S. M. Marker & S. M. Marker	PC-D-2-1-C2	Assembly PC_D_2_1_C2	Trichoderma harpianum 75.59%	
And a state of the state of the	1002102	# contigs (>= 25000 bp) 12	💻 Trichoderna atrobranieum 5.64%	
and all and the second second	10000	# contigs (>= 50000 bp) 0	<ul> <li>Trichaderma guizhouense</li> <li>5.48%</li> </ul>	
- 15 States in state in the	1000	Total length (>= 25000 bp) 346836	<ul> <li>Partoea aggiomerans</li> <li>3.01%</li> </ul>	
The state of the state of the state of the	and the second s	Total length (>= 50000 bp) 0	Pseudomonas oryzihabitans 1.85%	
A REAL PROPERTY AND A REAL	100 200 0 100	# contigs 12671	Partoea ananatts 1.30%	
1 Course of the second second	10	Largest contig 34,730	Bacilus veiezensis 1.20%	
		Total length 41.758.812	Passdomonas companyamini 137%	
and the second se	1	GC (%) 47.09	III Pseudomonas publica 0.62%	
Strange in	0 2000 4000 6000 8000 10000	N50 5262	III (Remaining) 3.09%	
		5202		
BC D 2-1-C2 001 feets	Trickederma harrianum funct	have the second as any local state to be the the second second		22 10 22 22
-0-0-2-1-03_001.1astq.gz	Fungi	Accombly DC D D 1 CD	Name Estimated Abundance	32.18 23.22
	PC-D-2-1-C3	Assembly PC_D_2_1_C3	Trichodernu harstanum 74.87%	
Statistical Statistics	100000	# contigs (>= 25000 bp) 251	Trichoderma atrobrunneum 5.61%	
REMANDING STREET	10000	# contigs (>= 50000 bp) 19	Trichoderma guidhouense 5.49%	
Not the second second	1 1 1 1 1 1 1 1	Total length (>= 25000 bp) 8677054	Particlea aggiomerans 2.19%	
and the second second	1000	Total length (>= 50000 bp) 1137009	Partnes anauris 1606	
	100	# contigs 6487	Bacilus velepensis 1.39%	
60 Martines	10	Largest contig 94,369	<ul> <li>Pseudomonas coleopterorum</li> <li>1,24%</li> </ul>	
A DESIGNATION OF A		Total length 41,771,792	Pseudomonas psychrotolerans 0.91%	
All second second second	1	GC (%) 46.85	Pseudomonas sp. UBA6562 0.51%	
Accessive Total	0 2000 4000	N50 13238	III (Remaining) 2.71%	
Colony Image	Assembly Coverage (Y) Large->Small Contigs (X)	Assembly Statistics (Quast 5.0)	OneCodex Kmer Classification	TAC CT TYM CT
Colony Image	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzibabitans Bacteria	Assembly Statistics (Quast 5.0)	OneCodex Kmer Classification	TAC Ct TYM Ct
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria	Assembly Statistics (Quast 5.0) https://app.onecodex.com/analysis/public/beb700ca5c46431a Assembly PC E 2 1 B	OneCodex Kmer Classification Name Estimated Abundance Prevedences crysthalitars 51.78	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-B	Assembly Statistics (Quast 5.0)           http://spo.orecodes.com/analysis/public/beb700ca5c66531a           Assembly         PC_E_2_1_B           # contrists (s= 25000 hp)         20	OneCodex Kmer Classification           Name         Edinated Number           - handmass organization         51/76           - handmass foresas         63/56	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-B 10000	Assembly Statistics (Quast 5.0)           http://sponecoder.com/ana/sis/public/bb/700cs5c46431a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 56000 bp)         19	OneCodex Kmer Classification           Name         Estimated Abundance           Pouchmus systaatics         547%           Pouchmus fumsters         434%           Pouchmus subjecterum         434%	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000	Assembly Statistics (Quast 5.0)           http://sponcecker.com/subsit/public/beb70004564631a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 50000 bp)         19           Total length (>= 25000 bp)         4033410	OneCodex Kmer Classification           New         Estimate Assurance           Prodomous (Seriess)         63.7%           Prodomous (Seriess)         63.7%           Prodomous (Seriess)         63.7%           Prodomous (Seriess)         63.7%	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large-Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 1000	Assembly Statistics (Quast 5.0)           http://ipp.orecodex.com/ana/ski/public/bb/70003666531a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 50000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 25000 bp)         995124	OneCodex Kmer Classification           Name         Estimate Abundance           Productives crystillatives         \$4.7%           Productives Streams         6.3%           Productives burgersum         6.1%           Productives burgersum         6.1%           Productives burgersum         2.0%           Productives burgersum         2.0%	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 1000 100	Assembly Statistics (Quast 5.0)           http://txp.oncodec.com/subsit/pair/be/D005c46431a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 50000 bp)         19           Total length (>= 25000 bp)         4935124           # contigs         >= 50000 bp)         4925124	OneCodex Kmer Classification           New         Extense Aluminary           Pradmemors syndators         43.06           Pradmemors layersmin         43.06           Press aglements         23.06           Press aglements         32.06           Press aglements         32.06	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 1000 100 100 100 100 100	Assembly Statistics (Quast 5.0)           http://top.oncodex.com/hashid/public/beb70004564531a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 50000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         1895124           # contigs         102           Jaronatic contigs         570	OneCodex Kmer Classification	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 100 10 10	Assembly Statistics (Quast 5.0)           http://top.orcedec.com/subsit/pair/be/D00546431a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 50000 bp)         19           Total length (>= 25000 bp)         4953124           # contigs         102           Largest contig         570,530           Total length         52.42	OneCodex Kmer Classification	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 1000 100 10 10 10 1	Assembly Statistics (Quast 5.0)           http://pair/be/b700364631a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 56000 bp)         19           Total length (>= 25000 bp)         49333410           Total length (>= 56000 bp)         4895124           # contigs         102           Largest contig         570,530           Total length         5,832,442           Contig         5,632,442	OneCodex Kmer Classification           New         Estimate Advances           - Prodomote Synthetics         6178           - Podomote Synthetics         6178           - Prodomote Synthetics         6178           - Podomote Synthetics         6178           - Podomote Synthetics         618           - Podomote Synthetic Synthetics         618           - Podomote Synthetic Syntheti	TAC Ct TYM Ct 16.23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 100 100 100 0 10 20 30 40	Assembly Statistics (Quast 5.0)           http://sponcecdec.com/swiphi/pad/pabe/D00546431a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4995124           # contigs         102           Largest contig         570,530           Total length         582,442           GC (%)         365675	OneCodex Kmer Classification       New     Extract Alundare       • Audomous systatize     43.0       • Prachmens Stores     43.0       • Prachmens systatize     43.0       • Prachmens Stores     43.0       • Prachmens systatize     43.0       • Prachmens Stores     43.0       • Prachmens system     43.0       • Prachmens system     43.0       • Prachmens system     43.0       • Prachmens system     30.0       • Enclasser class     30.0       • Enclassers     30.0       • Prestances statem     30.0       • Prestance     30.0	TAC Ct TYM Ct 16:23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 1000 100 10 1 0 10 20 30 40	Assembly Statistics (Quast 5.0)           http://tsponcecdec.com/subsit/pair/be/DMCB/64631a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 50000 bp)         19           Total length (>= 50000 bp)         4953124           # contigs         102           Largest contig         570,530           Total length         5,832,442           GC (%)         65.69           NS0         3356575	SoneCodex Kmer Classification       New     Extension Syndals       Prachements Syndals     3.36       Prachement Syndals     3.36       Prachement Syndals     3.36       Prachement Syndals     3.36       Prachement Syndals     3.37       Prachement Syndals     3.37       Prachement Syndals     3.37       Prachement Syndals     3.37       Prachement Syndals     3.36       Prachement Syndals <th>TAC Q TYM Q 16:23 ND</th>	TAC Q TYM Q 16:23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas orysihabitans Bacteria PC-E-2-1-8 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           http://pair/be/b700364631a           Assembly         PC_E_2_1_B $\#$ contigs (>= 25000 bp)         20 $\#$ contigs (>= 5000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 5000 bp)         4895124 $\#$ contigs         102           Largest contig         570,530           Total length         5,032,442           GC (%)         65.69           NS0         336575	Decoder Kmer Classification           Image: Status         Estimate Awners           Andreament synthetiker         617, 63           Andreament Synthetiker         618, 63	TAC CT TYM Ct 16:23 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 00000 100 10 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 0 10 1	Assembly Statistics (Quast 5.0)           http://tsp.orecodec.com/subsit/pad/tabe/D00564631a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         495124           # contigs         102           Largest contig         570,530           Total length         5,032,442           GC (%)         65.69           NS0         3356575           http://pp.ape.obj.com/sathsit/pdd/chs6214560498           Accembly         65.212.0	OneCodex Kmer Classification       Term     Extransf Alundar       1     Anadomus sylination	TAC Q TYM Q 16:23 ND 15:31 ND
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Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           https://spacecodec.com/swipsit/pair/bet/Docs/6431a           Assembly $PC \in [2, 1, B]$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4995124           # contigs         102           Largest contig         570,530           Total length         5,832,442           GC (%)         65.69           NS0         356575           http://spacecode.com/swinking/be//cba/24/66/2496           Assembly         PC E_2_1_D           # contigs (>= 25000 bp)         14	OneCodex Kmer Classification       New     Extract Alundare       ***     Paschmans Algerson       ***     ****       ***     *****       ***     ************************************	TAC Q TYM Q 16:23 ND 15:31 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 0000 100 10 1 0 10 1 0 10 20 30 40 Pseudomonas coleopterorum Bacteria PC-E-2-1-0 00000 *	Assembly Statistics (Quast 5.0)           https://tsponcecdec.com/salphil/pall/beh200csC4631a           Assembly $PC_E[2.1]B$ # contigs (>= 25000 bp)         20           # contigs (>= 50000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         495124           # contigs         102           Largest contig         570,530           Total length         5,832,442           GC (%)         65.69           NS0         356575           https://sponecodes.com/salpid/bd/bd/2d76562498e           Assembly $PC_E[2_1]D$ # contigs (>= 25000 bp)         14           # contigs (>= 25000 bp)         14           # contigs (>= 25000 bp)         14	OneCodex Kmer Classification       New     Extension (Application)       Tester     Extension (Application)       Presidences (Application)     43/8       Presidences (Application)	TAC Q TYM Q 16:23 ND 15:31 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           https://spacesedec.com/salphit/pad/tabe/D00546431a           Assembly $PC \in \mathbb{Z}_2 \mathbb{L}_B$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4935124           # contigs         102           Largest contig         570,530           Total length         5,659           N50         356575           http://www.onecodes.com/salphit/pad/tab/tab/tab/tab/tab/tab/tab/tab/tab/tab	OneCodex Kmer Classification       Image: State of the st	TAC QT TYM QT 16:23 ND 15:31 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas coryainabitans Bacteria PC-E-2-1-8 10000 100 10 1 0 10 1 0 10 20 30 40 Pseudomonas coleopterorum Bacteria PC-E-2-1-0 10000 1000 1000 1000 1000 1000 10	$\label{eq:constraints} \begin{array}{ c c c c c c } \hline \textbf{Assembly Statistics (Quast 5.0)} \\ \hline \textbf{Mts://tep.oncodex.com/substit/pdd/zbetXtosc4631a} \\ \hline \textbf{Assembly} & PC_E_2_1_B \\ \# \ contigs (>= 25000 \ bp) & 20 \\ \# \ contigs (>= 25000 \ bp) & 19 \\ \hline \textbf{Total length} (>= 50000 \ bp) & 4933410 \\ \hline \textbf{Total length} (>= 50000 \ bp) & 4995124 \\ \# \ contigs & 102 \\ \hline \textbf{Largest contig} & 570,530 \\ \hline \textbf{Total length} & 5,032,442 \\ GC \ (%) & 65.69 \\ \hline \textbf{NS0} & 356575 \\ \hline \textbf{Mts://spacemodex.com/substit/pdd/zba62476d/6601896 \\ \hline \textbf{Assembly} & PC_E_2_1_D \\ \# \ contigs \ (>= 25000 \ bp) & 14 \\ \# \ contigs \ (>= 25000 \ bp) & 14 \\ \# \ contigs \ (>= 25000 \ bp) & 14 \\ \hline \textbf{Total length} \ (>= 50000 \ bp) & 4591239 \\ \hline \textbf{Total length} \ (>= 50000 \ bp) & 4591239 \\ \hline \textbf{Total length} \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total length \ (>= 50000 \ bp) & 4591239 \\ \hline \ total \ botal \ bot$	Desclodex Kmer Classification           Teinand Runder           Nationaus sylindlase           Pradmenss formania           Pradmenss sylindlase           Pradmense sylindlase           Pradmense sylindlase           Pradmense sylindlase           Pradmense synindlase	TAC Q TYM Q 16:23 ND 15:31 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas coryaihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           Intro //saparts/padr/bet/Tools/6431a           Assembly $PC_E 2_{-1}B$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         20           # contigs (>= 55000 bp)         19           Total length (>= 55000 bp)         4933410           Total length (>= 50000 bp)         493124           # contigs         102           Largest contig         570,530           Total length         5,822,442           GC (%)         65.69           N50         356575           http://www.newcolec.com/wabrit/padr/bad/24/2462496e         Assembly           Assembly         PC_E_2_l_D           # contigs (>= 250000 bp)         14           Total length (>= 250000 bp)         14           Total length (>= 50000 bp)         14           Total length (>= 50000 bp)         14           Total length (>= 50000 bp)         13	OneCodex Kmer Classification       Image: State of the st	TAC QT TYM Qt           16:23         ND           11:23         ND           11:31         ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           Intro //wap.nt/sat/sat/sat/sat/sat/sat/sat/sat/sat/sa	OneCodex Kmer Classification       New     Extrated Renders       **     Pradmenser syndatase       **     **       **	TAC QT TYM Q 16:23 ND 15:31 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large-Small Contigs (X) Pseudomonas oryzinabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 20 30 40 Pseudomonas coleopterorum Bacteria PC-E-2-1-D 10000 100 100 100 100 100 100 100 100	$\label{eq:constraints} \begin{array}{ c c c c c c } \hline \textbf{Assembly Statistics (Quast 5.0)} \\ \hline \textbf{Mts://ise.oncodex.com/salphil/pall/beh200a5c4631a} \\ \hline \textbf{Assembly} & PC_E_2_1_B \\ \# \mbox{ contigs } (>= 25000 \mbox{ bp}) & 20 \\ \# \mbox{ contigs } (>= 50000 \mbox{ bp}) & 19 \\ \hline \textbf{Total length} (>= 50000 \mbox{ bp}) & 4895124 \\ \# \mbox{ contigs } 102 \\ \mbox{ Largest contig } 570,530 \\ \hline \textbf{Total length} & 5,832,442 \\ \mbox{ GC (%)} & 65.69 \\ \hline \textbf{NS0} & 356575 \\ \hline \ \textbf{Mts://seo.oncodex.com/salphil/pall/beh2016562498e} \\ \hline \textbf{Assembly} & PC_E_2_1_D \\ \# \mbox{ contigs } (>= 25000 \mbox{ bp}) & 14 \\ \hline \textbf{Total length} & (>= 25000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 50000 \mbox{ bp}) & 4591239 \\ \hline \textbf{Total length} & (>= 664, 689 \\ \hline \ \textbf{Total length} & (>= 664, 689 \\ \hline \ \textbf{Total length} & (>= 664, 689 \\ \hline \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$	OneCodex Kner Classification       Term     Extension Science       Parademonis Syndalas:     32.33	TAC QT TYM Q 16:23 ND 15:31 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 100 100 100 100 100	Assembly Statistics (Quast 5.0)           http://wp.oncode.com/wwb/it/pad/Deb/D00504631a           Assembly $PC \in \mathbb{Z}_{-1} = \mathbb{B}$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4995124           # contigs         102           Largest contig         570,530           Total length         5,632,442           GC (%)         65.65           NS0         356575           http://www.newnix/solid/bal/Dal/2016/62486           Assembly         PC E_2_1_D           # contigs (>= 25000 bp)         14           # contigs (>= 50000 bp)         14           Total length (>= 50000 bp)         591239           # contigs         113           Largest contig         824,814           Total length         4,664,689           GC         62.21	OneCodex Kmer Classification       Term     Extract Alundare       1     Anadomara syllatlasu     32.3       1     Panadomara syllatlasu     32.3       1     Pan	TAC QT TYM Qt           16:23         ND           15:31         ND
Colony Image PC-E-2-1-B_001.fastq.gz PC-E-2-1-D_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzinabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10	$\label{eq:constraints} \begin{array}{ c c c c c } \hline & \mbox{Statistics}(Quast 5.0) \\ \hline & \mbox{Miss}(Jean Gradewidth (Salisher) & \mbox{Cells}(2,2,1,2,1,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2$	Desclodex Kmer Classification           Image: Second Seco	TAC QT TYM Q 16:23 ND 15:31 ND
Colony Image PC-E-2-1-B_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 100 100 100 100 100	$\label{eq:constraints} \begin{array}{ c c c c c c } \hline track//secondscom/selection/sele$	Second	TAC QT TYM Qt           16:23         ND           15:33         ND
Colony Image PC-E-2-1-B_001.fastq.gz PC-E-2-1-D_001.fastq.gz C-E-2-1-D_001.fastq.gz PC-E-2-1-E_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 100 10 10 10 10 10 1	Assembly Statistics (Quast 5.0)           http://wp.oncodex.com/wahai/cyadt/abs/2006.046431a           Assembly         PC_E_2_1_B           # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         10           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4995124           # contigs         102           Largest contig         570,530           Total length         5,832,442           GC (%)         65.69           NSØ         356575           http://www.oncodex.com/wahai/public/bd/200502006           # contigs (>= 25000 bp)         14           # contigs (>= 50000 bp)         4591239           Total length (>= 50000 bp)         4591239           # contigs         113           Largest contig         824,814           Total length         4,664,669           GC (%)         62.21           NS0         328847	Desclodex Kmer Classification           Image: Status of the stat	TAC Q TYM Q 16:23 ND 15:31 ND 31.91 15:45
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Colony Image PC-E-2-1-B_001.fastq.gz PC-E-2-1-D_001.fastq.gz PC-E-2-1-D_001.fastq.gz PC-E-2-1-E_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas ory inhabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	$\label{eq:constraints} \hline \textbf{Assembly Statistics (Quast 5.0)} \\ \hline \textbf{Miss}/(spacescoles.com/subsit/spal/selex/totalselesselesselesselesselesselesselesse$	Conclodex Kmer Classification       Iver     Extract Alundare       1     Anadomas sylination       2     Anadomas sylination       3     Anadomas sylination       3     Anadomas sylination       3     Anadomasylination       3     Anado	TAC CT TYM Ct 16:23 ND 15:31 ND 31:91 15:45
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-D_001.fastq.gz	Assembly Coverage (V) large-Small Contigs (X) Pseudomonas oryibibitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           http://wp.oncodec.com/wahei/chall.phe/DOcsG4631a           Assembly $PC_E_2_1_B$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4933410           Total length (>= 50000 bp)         495124           # contigs         102           Largest contig         570,530           Total length         5,032,442           GC (%)         65.69           NS0         356575           http://socecodec.com/malexit/pabl/2ba027b60439e           Assembly $PC_E_2_1_D$ # contigs (>= 25000 bp)         14           Total length (>= 25000 bp)         14           Total length (>= 50000 bp)         4591239           Total length         4,664,689           GC (%)         62.21           NS9         228847           Nts://sscencedec.com/malexit/pabl/2bc/2bf18511cd46           Assembly         PC_E_	Desclodex Kmer Classification           Image: Second Seco	TAC CT TYM Ct 16.23 ND 15.31 ND 15.31 ND
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-D_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 100 10 10 10 10 10 10 10 10 1	Assembly Statistics (Quast 5.0)           Introduction (Nathrid (Pablic)/NoteSched31a           Assembly $PC \in \mathbb{Z}_{-1} = \mathbb{B}$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4995124           # contigs         102           Largest contig         570,530           Total length         5,832,442           GC (%)         65.69           NS0         356575           Nts://wso.excodes.com/nathrid/sabil/babl/babl/babl/babl/sabil/babl/babl/sabil/sabil/babl/sabil/babl/sabil/sabil/sabil/babl/sabil/sab	Conclodex Kmer Classification           Image: Second and application of the second application of	TAC Q TYM Q 16:23 ND 15:31 ND 31:91 15:45
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-D_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 D0000 D00 D0	Assembly Statistics (Quast 5.0)           http://wp.orecodec.com/wahchi/padi/be/DX005046431a           Assembly $PC \in [2, 1, B]$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         10           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4953124           # contigs         102           Largest contig         570,530           Total length         5,032,442           GC (%)         65.69           NS0         356575           http://www.aecodec.com/mathi/pdd//ba62476566499           Assembly         PC (= 2, 1, D)           # contigs (>= 25000 bp)         14           # contigs (>= 25000 bp)         14           Total length (>= 25000 bp)         4591239           Total length (>= 50000 bp)         4591239           Mtts://www.contigs         62.21           NS0         328847           Mtts://www.contigs         22.200           # contigs	Desclodex Kmer Classification           Inter         Extransfluenter           Prademons of prima         43.5           Prademons of prima         43.6           Presenting of prima         43.7           Presening of pre	TAC QT TYM Q 16:23 ND 15:31 ND 31.91 15:45
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-D_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           Introduction (Nathrit/Sald/Deb/D00564631a           Assembly $PC \in \mathbb{Z}_2 \mathbb{L}_B$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933418           Total length (>= 50000 bp)         4935124           # contigs         102           Largest contig         570,530           Total length         5,65           No8         356575           Nts://wso.excodex.com/salats/sala/sala/sala/sala/sala/sala/sa	Concloser Kuner Classification           Inter         Extrated Alundare (alundare stylinklas)           Paschmans Systems         3.3.3           Paschmans Systems         3.3.6           Paschmans	TAC QT TYM Q:           16:23         ND           15:33         ND           31:91         15:45
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-D_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           Intro //wp.ord/sold/be/D005046318           Assembly $PC \in [2, 1, B]$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4995124           # contigs         102           Largest contig         570,530           Total length         5,832,442           GC (%)         65.69           NS0         356575           Mms://msomeodes.com/nahei/pad//ba/2005004986           Assembly         PC [= 2 - 1.0]           # contigs (>= 25000 bp)         14           # contigs (>= 25000 bp)         14           Total length (>= 25000 bp)         4591239           # contigs (>= 50000 bp)         13           Largest contig         92847           Mts://msonecodes.com/msoli/padd/kst/tst/1st/1st/1st/1cd4e           Assembly	Desclodex Kmer Classification           Image: Second Seco	TAC QT TYM QL 16:23 ND 15:31 ND 31:91 15:45
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-D_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           Inter/log oncodes con/value/1/pad/Deb/Total6431a           Assembly $PC \in \mathbb{Z}_{-L} \mathbb{B}$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4935124           # contigs         102           Largest contig         570,530           Total length         582,2442           GC (%)         65.69           N50         356575           = 25000 bp)         14           Total length (>= 25000 bp)         4591239           # contigs (>= 25000 bp)         4591239           Total length (>= 25000 bp)         320847           Visc/vsconcodes con/valvals/sdd/ded/sdt/sdt/sdt/sdt/sdt/sdt/sdt/sdt/sdt/sd	Conclose Kune Classification       Inter     Extract Alundare (and more systellate presented as systel	TAC QT TYM Qt           16:23         ND           15:31         ND           15:31         ND           31:91         15:45
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-E_001.fastq.gz	Assembly Coverage (Y) Large->Small Contigs (X) Pseudomonas oryinhabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           Intro //wp.nit/sdit/bet/Distated31a           Assembly $PC_E Z_{-L} B$ # contigs (>= 25000 bp)         20           # contigs (>= 25000 bp)         19           Total length (>= 25000 bp)         4933410           Total length (>= 50000 bp)         4995124           # contigs         102           Largest contig         570,530           Total length         5,832,442           GC (%)         65.69           NSØ         356575           Ntm://me.oncodes.com/natosit/sdit/bd/2d	Desclodex Kmer Classification       Inter     Extrated Renders       Prachments sylination     323       Prachments sylination     323       Prachments sylination     323       Prachments sylination     323       Prachments sylination     325       Prachments sylination     326       Prachments sylination     328       Prachment Sylination     328       Prachment Sylination     328       Prachment Sylination <td< th=""><th>TAC QT TYM Q 16:23 ND 15:31 ND 31:91 15:45</th></td<>	TAC QT TYM Q 16:23 ND 15:31 ND 31:91 15:45
Colony Image           PC-E-2-1-B_001.fastq.gz           PC-E-2-1-D_001.fastq.gz           PC-E-2-1-D_001.fastq.gz	Assembly Coverage (Y) Large-Small Contigs (X) Pseudomonas oryzihabitans Bacteria PC-E-2-1-8 10000 100 10 10 10 10 10 10 10 10 10 10	Assembly Statistics (Quast 5.0)           Inter/Importance	DecCodex Kner Classification       Internet available     Extransfluenter       Packmenns syndalse     43.3       Packmenns syndalse     43.4       Packmenns syndalse     43.6       Packmenne s	TAC QT TYM Q.           16:23         ND           15:31         ND           31:91         15:45



**Table 3. PDA without Chloramphenicol:** Colony Image (Left), Assembly sequence coverage (Y) compared with contig Length (X) where the contigs are sorted largest to smallest from left to right (Mid-Left). Assembly statistics calculated with Quast 5.0 (Mid Right). OneCodex speciated kmer count (Right).

colony image	Assembly coverage (1) Large-Somali Contigs (A)	Assembly Statistics (Quast 5.0)	Unecodex Kmer classification	TAC CL THIN CL
P-D-2-1-A_001.fastq.gz	Pantoea ananatis Mixed Bacteria	https://app.onecodex.com/analysis/public/bc9df5fe99be4ee7		15.99 ND
	PC-D-2-1-A	Assembly P_D_2_1_A	Name Estimated Abundance	1
,	10000	# contigs (>= 25000 bp) 114	Pantoea ananatis \$1.59%	
		# contigs (>= 50000 bp) 49	Pantoea agglomerans 36.89%	
and the owner of the owner owne	1000	Total length (>= 25000 bp) 7814145	Partosa vagans 5.64%	
and the second second	es************************************	Total length (>= 50000 bp) 5670116	Shigella dysonteriae	
And a local division of the local division o	100	# contins 2129	Pseudomonas oryzihabitans 0.10%	
	10	Largest contin 400.518	Bacillus velezensis 0.06%	
	* * * *	Total length 15,498,447	Pseudomonas coleopterorum 0.06%	
Statement of the local division of the local	1	GC (%) 53.80	Fullenting by control 0.03%	
	0 10 20 30 40	N50 25286	(Remaining) 0.08%	
		1450 25200		
P-D-2-1-B 001 fasta az	Pantona agglomorans Bactoria	https://www.anglang.com/analysis/archis/bdf/0007214/457a	and a second	1851 ND
T D E T D_001.idotq.gE	Tuntocu una line una line una	Assembly PD 2 1 B	Name Estimated Abundance	10.01 110
	P-D-2-1-B	# conting (>= 25000 hp) 26	Partosa aggorieraris 05.04%	
	10000	# contings (>= $50000 \text{ bp}$ ) 20	Pantoea vagans 9.66%	
	1000	Total length ( $>= 25000 \text{ bp}$ ) 4810440	Citrobacter freundi 0.47%	
All and a second	1000	Total length (>= $50000$ bp) $4722027$	Pseudomonas orysthabitans 0.25%	
	100	# contins 886	Enterobacter cloacae 0.23%	
	111. 11. 11.	largest contig	<ul> <li>Pseudomonas putida</li> <li>0.19%</li> </ul>	
	10 50	Total length 5 456 029	Bacillus velezensis 0.18%	
	1		Pseudomonas coleopteronum 0.17%	
	0 20 40 60 80 100	N50 240021	(Remaining) 0.47%	
		N50 249921		
P-D-2-1-C 001 facts at	Pantona andomerans		Ren Portugue	17.77 ND
F-0-2-1-0_001.lastq.gz	Fantoea aggiomerans Bacteria	Accombly D. 2.1.C	Name Estimated Abundance	17.77 ND
	P-D-2-1-C	Assembly $P_U_2_1_C$	Partosa aggiomerans 75.20%	
	10000.0	# contigs (>= 25000 bp) 20	Partoea animato. 15,319 Partoea valeans. 2,524	
		# contrigs (>= 50000 bp) 20	Pseudomonas oryzihabitans 0.27%	
	1000.0	Total length (>= 25000 bp) 4/85028	Enterobacter cloacae 0.23%	
	100.0	lotal length (>= 50000 bp) 4601583	Enterobacteriaceae bacterium UBA4753 0.22%	
and the second s		# contigs 285	Bacilus velezensis 0.21%	
	10.0	Largest contig 557,633	Enterobacteriaceae bacterium UBA3398 0.17%	
	10	Total length 5,026,841	Pseudomonas coleopterorum 0.16%	
	0 100 200 300 400 500	GC (%) 54.46	Pseudomonas psychrotoxerans 0.14%	
		N50 306723		
Colony Image	Assembly Coverage (Y) Large->Small Contigs (X)	Assembly Statistics (Quast 5.0)	Unecodex Kmer Classification	TAC CE TYM CE
			the state of the s	
P-D-2-1-D_001.lasiq.gz	Pantoea aggiomerans. Ivixed Bacteria	https://app.onecodex.com/analysis/public/e1ec0732b319442d	Name Estimated Abundance	17.17 ND
P-D-2-1-D_001.iasiq.g2	P-D-2-1-D	https://app.onecodex.com/analysis/public/e1ec0732b319442d Assembly P_D_2_1_D	Name Estimated Abundance Pantoea aggiorrerans 69.86%	17.17 ND
1-0-2-1-0_001.iasiq.g2	P-D-2-1-D 10000	http://app.onecodex.com/analysis/public/elec0732b319442d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50020 bp)         29	Name Estimated Abundance Pantoea aggionerans 68.86% Pantoea arunatis 18.79% Pentoea suppor 21.45%	17.17 ND
1-0-2-1-0_001.lasid.g2	P-D-2-1-D	http://app.onecodex.com/ana/ytis/public/elec/72b13942d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total / Starb (25000 bp)         28	Name         Estimated Abundance           Im Patose aggiorerans         61.80%           Im Patose anurais         11.70%           Im Patose aggiorerans         7.16%           Im Patose aggiorerans         2.95%	17.17 ND
1-0-2-1-0_001.iasiq.92	P-0-2-1-D	http://spo.oncode.com/analysi/public/elec0732b31942d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total Length (>= 25000 bp)         24271137           Total Length (>= 25000 bp)         242127	Name         Estimated Abundance           P. Antosa aggiorreans         66.30%           P. Pattose annutis         18.70%           P. Antosa agins         7.34%           P. Antosa all         2.93%           9. Singling S-2075         0.23%	17.17 ND
	P-0-2-1-0	Http://spo.encodes.com/ana/wi/SobiC/cleG737311943d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total length (>= 50000 bp)         24277137           Total length (>= 50000 bp)         243250	Name         Estimated Abundance           Partose agrinoran         6.050           Partose agrinoran         6.050           Partose agrinoran         10.704           Partose agrinoran         1.020           Partose agrinoran         2.034           Partose agrinoran         2.034           Partose agrinoran         2.034           Partose agrinorana         2.034           Partose agrinorana         2.034           Partose agrinorana montelli         0.194	17.17 ND
	P-0-2-1-0 10000 1000 100	http://spo.encodes.com/ana/wi/sball/clet0732131942d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total length (>= 25000 bp)         277137           Total length (>= 50000 bp)         3474           # contigs         160 2043450	Name         Estimated Abundance           Pattess aggioreram         63.80           Pattess agrows         15.74           Pattess agrows         7.44           Pattess all         2039           Shighla p. 55-2015         5.224           Paudomoia mortell         0.19           Backdronoia mortell         0.19	17.17 ND
1992110_0011451(492	P-0-2-1-0 10000 1000 100 100	http://spo.oncodes.com/analysi/public/elec07329131942d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total length (>= 25000 bp)         203450           # contigs         3474           Largest contig         169,384	Name         Estimated Abundance           P. Partesa aggiorneram         63.64%           P. Partesa aggiorneram         63.64%           P. Partesa aggiorneram         10.70%           P. Partesa aggiorneram         20.70%           P. Partesa aggiorneram         0.10%           P. Scolenovana montali         0.19%           B. Enchla velazensi         0.16%           B. Enchlaret rolazae         0.4%	17.17 ND
	P-0-2-1-D 10000 1000 100 100 100	http://spo.encodes.com/ana/wi/sbakic/letG733313442d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total length (>= 50000 bp)         24277137           Total length (>= 50000 bp)         243450           # contigs         3474           Largest contig         169,384           Total length         11,841,942           Cf. (f)         15,324	Name         Estimated Abundance           Partese agrinorsin         6.036           Partese agrinorsin         6.037           Partese agrinorsin         10.794           Partese agrinorsin         10.794           Partese agrinorsin         2.034           Partese agrinorsin         2.034           Partese agrinorsin         0.034           Partese agrinorsin         0.194           Partese agrinorsin         0.194           Partese agrinorsin         0.194           Princehoren formali         0.194           Chordscher floatae         0.544	17.17 ND
		http://spo.encodes.com/ana/wi/sball/clac07324313442d           Assembly         P_D_2_1_D           # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total length (>= 25000 bp)         28           Total length (>= 50000 bp)         203450           # contigs         3474           Largest contig         169,384           Total length         11,841,942           GC (%)         53.74	Interaction         Estimated Abundance           Partes aggioreram         63.86           Partes aggioreram         63.86           Partes agrino         10.79           Partes agrino         7.84	17.17 ND
PD-2112_001.iast(g2	P-D-2-1-D 10000 1000 100 100 100 100 100	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Interaction         Estimated Abundance           Partosa agiorneram         63.864           Partosa agiorneram         63.864           Partosa agiorneram         10.704           Partosa agiorneram         2.039           Patosa eali         2.039           Patosa eali         2.039           Patosa eali         2.039           Patosa weeneli         0.104           Chrobator founda         0.104           Prevolutor founda         0.131           Patosano caleogramum         0.844           Pensalona (begramum         0.844           Pensalona (begramum         0.844           Pensalona (begramum         0.844	17.17 ND
P.D.2.1.E. 001 faste as	P-D-2-1-D 10000 100 100 100 100 100 100	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Interest egionecani         Estimated Abundance           Partese agricorecani         64.064           Partese adulti         0.094           Partese adulti         64.064           Conductor floadai         64.064           Conductor floadai         64.064           Partese adultion adultion         64.064	17.17 ND
P-D-2-1-E_001.fastq.gz	P-0-2-1-D P-0-2-1-D 1000 10	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Name         Estimated Abundance                — Partose agrioreram — Partose agrioreram	21.03 27.40
P-D-2-1-E_001.fastq.gz	P-D-2-1-D P-D-2-1-D P-D-2-1-D P-D-2-1-D P-D-2-1-D P-D-2-1-E_R	http://spo.encodes.com/analysi/sobic/telc07324319442           Assembly $PD21D$ # contigs (>= 25000 bp)         95           # contigs (>= 50000 bp)         28           Total length (>= 25000 bp)         2877137           Total length (>= 50000 bp)         2043450           # contigs         3474           Largest contig         169,384           Total length         11,841,942           GC (%)         53.74           NS0         14877           http://spo.oncodes.com/analysis/sodic/Ibse70634694595           Assembly $PD21E$	Instantia         Estimated Abundance           Partosa agromeram         63.80%           Partosa agromeram         63.80%           Partosa agromeram         15.70%           Partosa agromeram         15.70%           Partosa agromeram         15.70%           Partosa agromeram         10.90%           Partosa agromeram         0.91%           Partosa agromeram         0.91%           Partona agromeram         0.91%           Partona collegorarrum         0.91%           Partosa agromeram         6.94%           Pertona agromeram         6.94%           Partona agromeram         6.94%           Partosa agromeram         6.94%           Partona agromeram         6.94%           Partona agromeram         6.94%           Partona agromeram         6.94%	17.17 ND 21.03 27.40
P-D-2-1-E_001.fastq.gz	P-D-2-1-D P-D-2-1-D P-D-2-1-E_R P-D-2-1-E_R	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Instantial Annual Control           Partese agioresmin         64.064           Partese annutis         15.754           Partese annutis         15.754           Partese annutis         15.754           Partese annutis         15.754           Partese annutis         2.034           Partese annutis         0.034           Prisodram mortali         0.994           Bacilla velocenis         0.104           Christer chasae         0.104           Christer finadi         0.374           Prisodramona mortali         0.194           Christer finadi         0.134           Prisodramona contegrity         0.044           Christer finadia         0.574           Prisodramona contegrity         0.044           Prisodramona contegrity         0.044           Prisodramona contegrity         0.044           Partese agiorremain         66.043 (5.515)           Prisodramona contegrity         2.024	21.03 27.40
P-D-2-1-E_001.fastq.gz	P-D-2-1-E_R 10000,0	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Instanta         Estimated Abundance           Particea arunsi         63.08.00           Particea arunsi         15.7%           Particea arunsi         15.7%           Particea arunsi         2.03%           Particea arunsi         2.03%           Particea arunsi         0.03%           Particea arunsi         0.03%           Particea arunsi         0.04%           Conductor floada         0.04%           Conductor floada         0.04%           Conductor floada         0.04%           Conductor floada         0.04%           Conductor fload         0.04%           Conductor floada         0.04%           Conductor floada         0.04%           Conductor floada         0.04%           Conductor floada         0.04%           Conductor fload         0.04%           Partone aginemerain         65.047 (55.01%)           Partone aginemerain         65.047 (55.01%)           Partones aginemerain	21.03 27.40
P-D-2-1-E_001.fastq.gz	P-D-2-1-D P-D-2-1-D P-D-2-1-D P-D-2-1-D P-D-2-1-D P-D-2-1-E_R 10000.0 P-D-2-1-E_R	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Interest annuals         Estimated Abundance           Partisea annuals         63.04           Partisea annuals         10.74           Partisea annuals         10.74           Partisea annuals         10.74           Partisea annuals         10.74           Partisea annuals         0.74           Paudomonias collegiterrun         0.64           Paudomonias collegiterrun         0.64           Paudomonias collegiterrun         0.74           Paudomonias collegiterrun         0.75           Paudomonias diregiterrun         0.75           Paudomonias diterrun <t< th=""><th>17.17 ND 21.03 27.40</th></t<>	17.17 ND 21.03 27.40
P-D-2-1-E_001.fastq.gz	P-D-2-1-D 10000 100 100 100 100 100 100	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Instantial Annual           America Annual	21.03 27.40
P-D-2-1-E_001.fastq.gz	P-0-2-1-D P-0-2-1-D P-0-2-1-D P-0-2-1-D P-0-2-1-D P-0-2-1-E R 10000,0 P-D-2-1-E R 10000,0 1000,0 P-D-2-1-E R	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Interest auroration         Extension Allowation           Partices auroration         10.9%           Partices auroration         10.9%           Partices auroration         10.9%           Partices auroration         10.9%           Partices auroration         0.0%           Partices auroration         0.0% </th <th>21.03 27.40</th>	21.03 27.40
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Figure 1. Plating images. DRBC (Top). PDA with CAMP (Middle). PDA no CAMP (Bottom).



Figure 2. Summary heatmap of colony classification by whole genome sequencing.



Table 4. Summary of colony forming unit classification:

	Bacteria	Fungi	Mixed
DRBC CAMP	3	12	2
PDA CAMP	10	9	1
PDA No CAMP	14	4	4



#### Figure 3: Simpson's Diversity Index

Simpson's diversity index is used to quantify the biodiversity of a habitat on a 0 to 1 scale. It takes into account the number of species present, as well as the relative abundance of each species. A diversity index of 1 represent infinite diversity where 0 reflects no diversity. DRBC plating demonstrates the lowest diversity. This is not surprising given DRBC contains 3 different selection agents (Dichloran, Rose Bengal and Chloramphenicol). While this limits bacterial contamination it also limits yeast and mold growth.





#### Table 5: cannabis samples plated on 3 different mediums.

Plating on different media's demonstrates a LOG scale difference in CFU with each plating medium. Sequencing can attribute only half of the colonies as bacteria on PDA with Chloramphenicol. This implies a 5-fold under counting of yeast and mold on DRBC.

Sample	DRBC						
	10 <sup>-2</sup> CFU/g	10 <sup>-2</sup> CFU/g	10 <sup>-2</sup> CFU/g	10 <sup>-3</sup> CFU/g	10 <sup>-3</sup> CFU/g	10 <sup>-3</sup> CFU/g	Final Result CFU/g
Low A	0	4	1	1	0	0	170
Low B	0	3	1	1	1	0	130
Low C	2	1	0	0	0	0	100
Low D	2	5	2	0	2	0	300
Low E	2	0	2	0	0	0	130
			Averag	e CFU/g			170
			PDA wi	th Chloramp	henicol		
	10 <sup>-2</sup> CFU/g	10 <sup>-2</sup> CFU/g	10 <sup>-2</sup> CFU/g	10 <sup>-3</sup> CFU/g	10 <sup>-3</sup> CFU/g	10 <sup>-3</sup> CFU/g	Final Result CFU/g
Low A	8	16	12	1	3	2	1200
Low B	8	12	8	1	0	3	930
Low C	13	19	13	1	2	1	1500
Low D	3	12	21	2	0	1	1200
Low E	9	7	4	0	3	3	670
			Averag	e CFU/g			1100
				PDA			
	10 <sup>-2</sup> CFU/g	10 <sup>-2</sup> CFU/g	10 <sup>-2</sup> CFU/g	10 <sup>-3</sup> CFU/g	10 <sup>-3</sup> CFU/g	10 <sup>-3</sup> CFU/g	Final Result CFU/g
Low A	127	133	124	32	32	21	14000
Low B	151	157	101	26	20	28	15000
Low C	TNTC	TNTC	TNTC	41	45	37	41000
Low D	147	141	123	32	26	26	15000
Low E	138	102	119	23	15	24	13000
			Averag	e CFU/g			20000

#### Table 6. Mono-culture evaluations

Organisms were ordered from ATCC and plated on 2 different medias (PDA and DRBC) to assess growth performance of the organisms in absence of cannabis background bacteria and matrix.

Species	ATCC Number	qPCR	DRBC Plating	PDA
Aspergillus brasiliensis	16404	Amp	5 Day Growth	5 Day Growth
Aspergillus flavus	9643	Amp	Less growth in 7 Days	5 Day Growth
Aspergillus fumigatus	204305	Amp	Less growth in 7 Days	5 Day Growth
Aspergillus niger	16888	Amp	Less growth in 7 Days	5 Day Growth
Aspergillus terreus	1012	Amp	Less growth in 7 Days	5 Day Growth
Aspergillus tubigensis	1004	Amp	Less growth in 7 Days	5 Day Growth
Candida tropicalis	13803	Amp	5 Day Growth	5 Day Growth
Penicillium breviocompactum	9056	Amp	Less growth than PDA	5 Day Growth
Purpureocillium lilacinum	10114	Partial Amp	5 Day Growth	5 Day Growth
Rhizopus oryzae	52748	Partial Amp	Less growth than PDA	5 Day Growth



**Figure 4.** *Aspergillus niger* and *Botrytis cinerea* monocultures plated on 3 different medias: Cultures were plated on PDA, PDA with selection (CAMP or Tartaric acid), and DRBC. Fewer colonies are consistently found on DRBC.

A.niger ATCC#1015 plated on PDA, PDA-TA, DRBC





100ul plated and grown at 25C for 7 days

A.niger on PDA, PDA-CAMP & DRBC



100ul grown 25C 3 days Botrytis cinerea ATCC#204446 plated on PDA, PDA-CAMP, DRBC (red)



100ul plated and grown at 25C for 5 days

# Conclusions

Microbial selection has a significant impact on the diversity index of microbes observed with whole genome sequencing. This has been noted in prior microbiome surveys in cannabis, where the act of culturing the microbes changes the representation of the microbiome as measured by qPCR and sequencing performed directly off of the flower and after culturing (McKernan et al. 2015; McKernan et al. 2016). In this study the DRBC selection reduces bacterial growth more than PDA with chloramphenicol but also reduces the fungal CFU 5-fold in the process. This has important implications for chloramphenicol sensitive cannabis endophytes like *Aspergillus*, *Pythium* and *Fusarium*. Both media types (PDA and DRBC) are referenced in the FDA Bacteriological Analytical Manual (FDA-BAM). States exclusively considering DRBC for ease of colony visualization should be aware of the species-specific sensitivities of using a single media type and consider species specific testing for such pathogenic organisms to complement a partial yeast and mold test offered from a single selection-based media. PCR based techniques can capture more organisms than DRBC alone as no selection is occurring given thorough cell lysis is achieved for qPCR analysis.

Plating also suffers from having a very limited dynamic range. Since it is difficult to count colonies when more than 100 colonies are present on a plate, multiple dilutions are often required to understand the full range of CFU counts one may encounter with a test that is attempting to quantitate 10,000 CFUs/gram. This results in multiplying diluted CFUs by 10, 100 and even a 1,000 fold to back estimate the total CFU count. In this scenario a single colony can swing the CFU count from passing to failing (9 colonies x 1,000 fold dilution vs 10 colonies at 1,000 fold dilution). Quantitative PCR has linear dynamic range over 5-6 orders of magnitude and no such multiplication is required. Thus, qPCR provides a more accurate itemization of actual CFUs counts.



In-vitro inclusion and exclusion testing with ITS3 qPCR on ATCC sourced organisms demonstrated over 96% inclusion (50 yeast and mold) and zero bacterial cross reactivity (30 bacteria) (Supplementary Table 1- Sheet TYM Inclusion & TYM Exclusion). *In-silico* analysis of ITS3 primer sequences, predicts over 1400 yeast and mold should amplify with the described ITS3 primer sequences. All plating media, even with 3 different forms of selection (DRBC), had bacterial contamination and each level of selection reduced fungal CFU counts.

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#### **Conflict Declaration**

The authors are employees of Medicinal Genomics which manufacture qPCR reagents for Cannabis testing.

#### **Author contributions**

KJM- Wrote the manuscript, assisted in experimental design and sequencing analysis YH, LTK, LZ, NH- isolated colonies, constructed sequencing libraries, performed plating and qPCR.

SM- Assembled genomes and performed sequencing analysis.

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