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Genomic tools for *Cannabis sativa* and *Psilocybe cubensis* propagation

Kevin McKernan
Chief Scientific Officer
Medicinal Genomics

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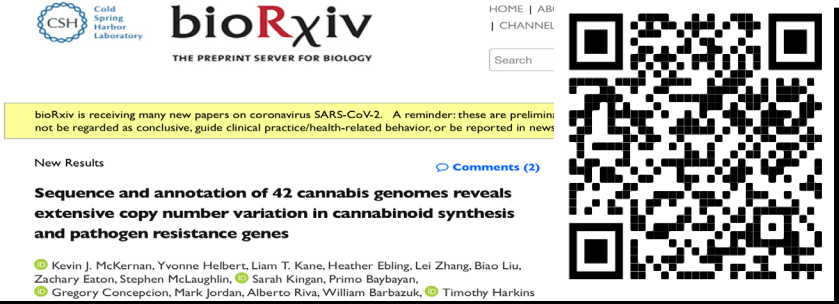
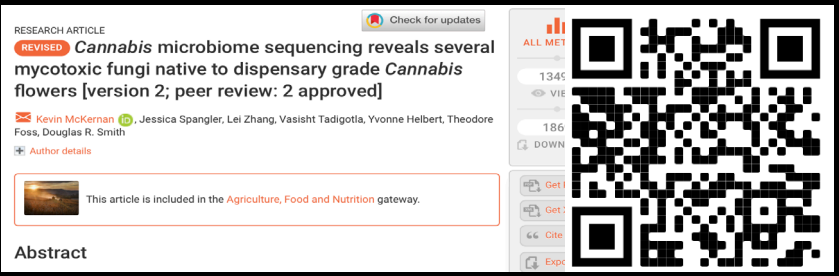
Transparent and Public Data Resources

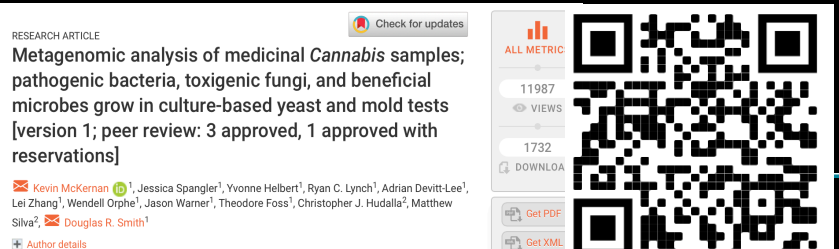
Produced by MJBizScience



42 Cannabis genome public Largest Cannabis DNA sequence repository. 10X larger than all previous submissions



In 2016 we published the first Cannabis Flower Microbiomes studies



Published TYM qPCR primers that navigate cannabis ITS problems

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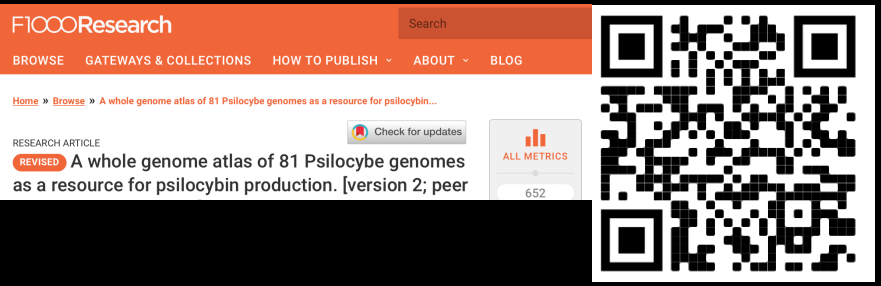
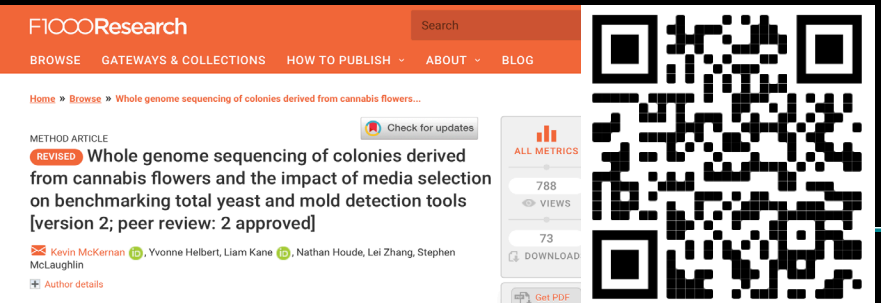
Transparent and Public Data Resources

Most complete Psilocybe cubensis genome reference



81 additional Psilocybe genomes

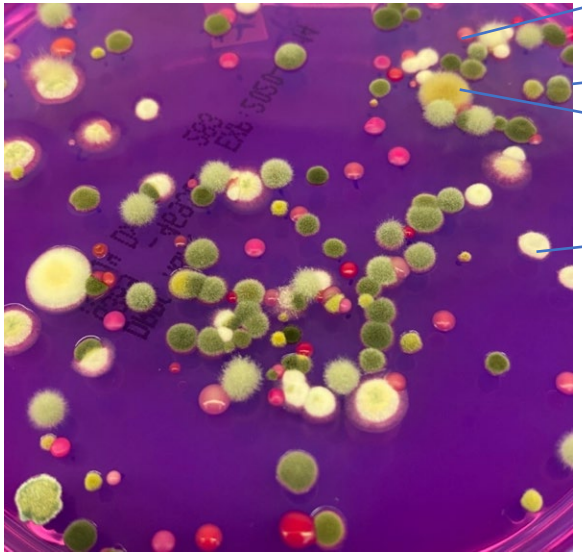


Comparison of TYM qPCR to PDA, PDA with CAMP, DRBC via Whole Genome sequencing of 45 genomes

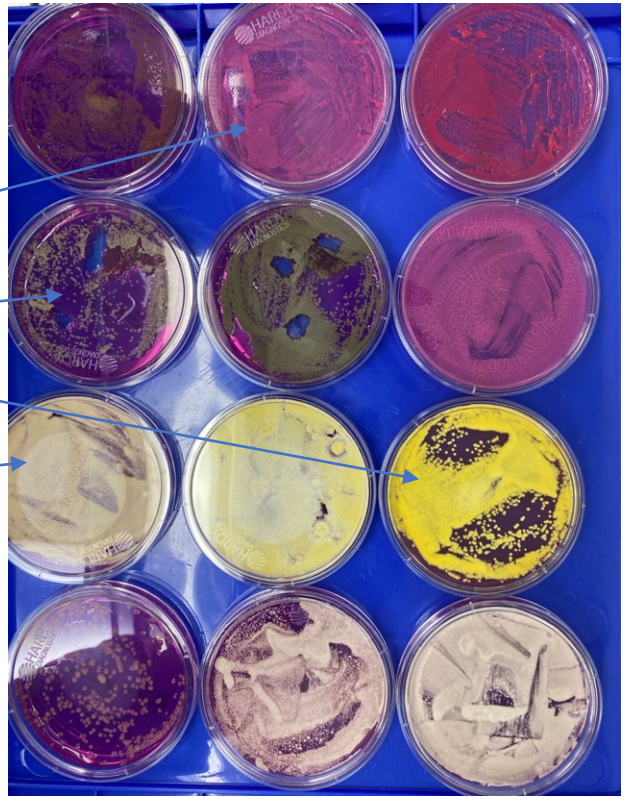
AOAC certified Aspergillus and Sal/STEC Flowers and MIPs

DRBC 5 day plating
>100 inclusion organisms on TYM
>40 exclusion organisms

Recalibrate on new media



Enumeration Tests in Validation



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PeerJ. 2021 May 13;9:e11446. doi: 10.7717/peerj.11446. eCollection 2021.

Cannabinoids from inflorescences fractions of *Trema orientalis* (L.) Blume (Cannabaceae) against human pathogenic bacteria

Tiwtawat Napiroon [1], Keerati Tanruean [2], Pisit Poolprasert [2], Markus Bacher [3], Henrik Balslev [4], Manop Poopath [5], Wichai Santimaleeworagun [6]

Affiliations + expand

PMID: 34035994 PMCID: PMC8126263 DOI: 10.7717/peerj.11446

Free PMC article

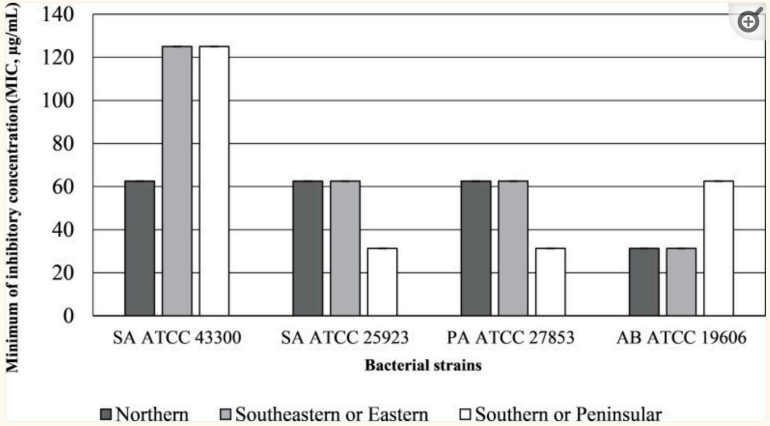
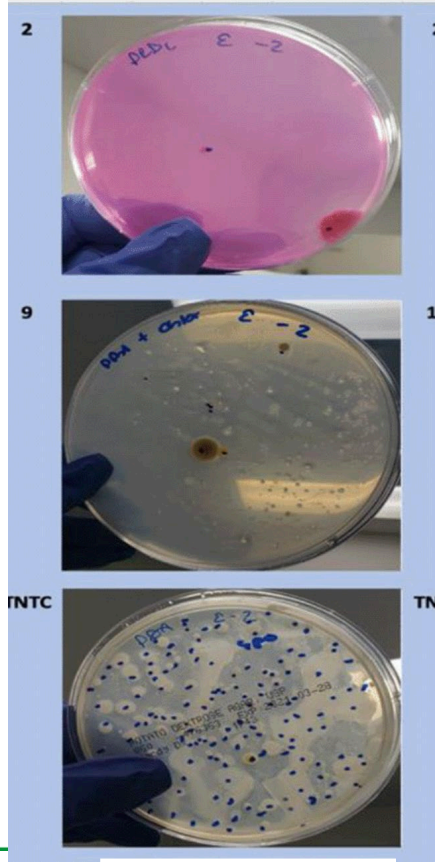


Figure 3

Minimum inhibitory concentration (MIC, µg/mL) of inflorescence fraction (S3).



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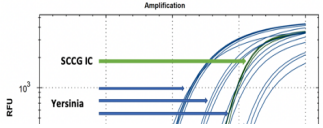
Pathogenic Enterobacteriaceae require multiple culture temperatures for detection in Cannabis sativa L.

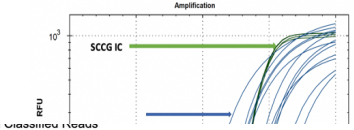
AUTHORS
Kevin McKernan, Yvonne Helbert, Liam T. Kane, Lei Zhang, Nathan Houde, Anne Bennett, Juliana Silva, Heather Ebling, Stephen McLaughlin

AUTHOR ASSERTIONS
Conflict of Interest: Yes ▾ Public Data: Available ▾ Preregistration: Not applicable ▾

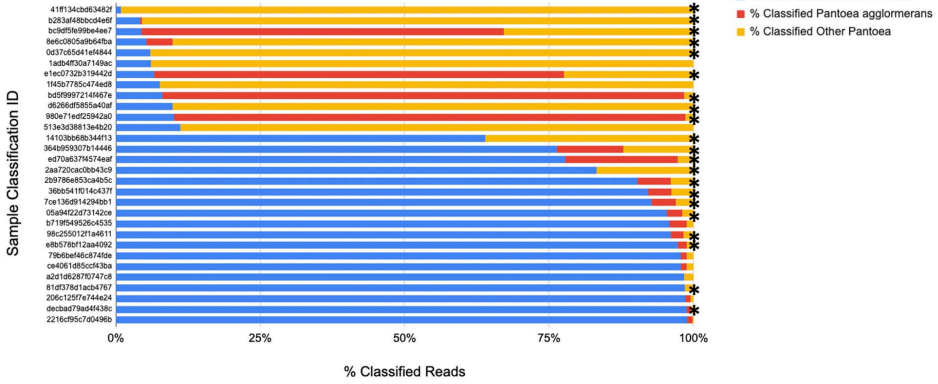
Yersinia enterocolitica Entero (blue) qPCR dilution series with SCCG (green) internal control



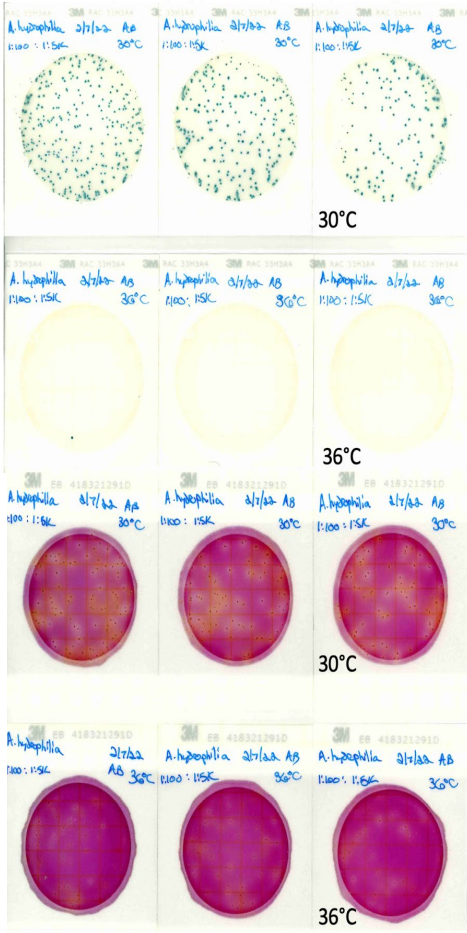
Aeromonas hydrophila Entero (blue) qPCR dilution series with SCCG (green) internal control



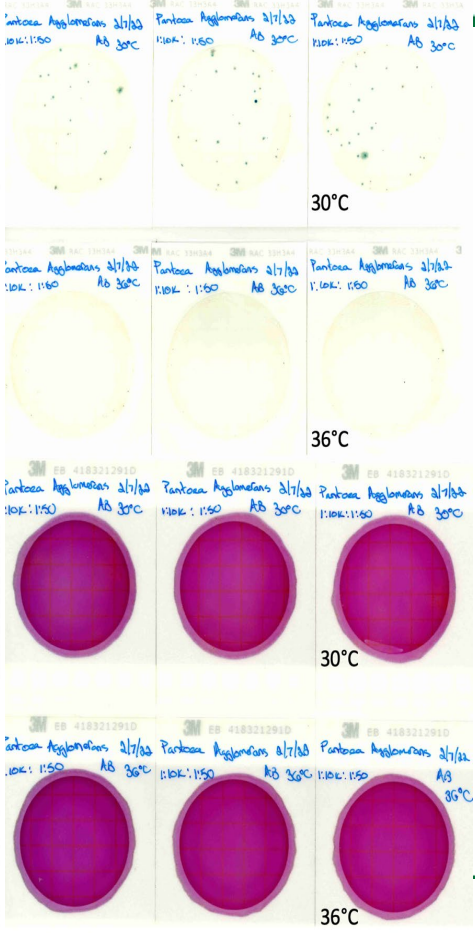
%Reads Classified as Pantoea in Samples >1% Pantoea



Aeromonas hydrophila ATCC 7966 @30°C vs 36°C
RAC plates (top) and EB plates (bottom)



Pantoea agglomerans: 30°C vs 36°C
RAC plates(top) and EB plates (bottom)



42 Cannabis Genomes

Cold Spring Harbor Laboratory

bioRxiv

THE PREPRINT SERVER FOR BIOLOGY

bioRxiv is receiving many new papers on coronavirus SARS-CoV-2. A reminder: these are preliminar
not be regarded as conclusive, guide clinical practice/health-related behavior, or be reported in news

New Results

Comments (2)

Sequence and annotation of 42 cannabis genomes reveals extensive copy number variation in cannabinoid synthesis and pathogen resistance genes

Kevin J. McKernan, Yvonne Helbert, Liam T. Kane, Heather Ebling, Lei Zhang, Biao Liu, Zachary Eaton, Stephen McLaughlin, Sarah Kingan, Primo Baybayan, Gregory Concepcion, Mark Jordan, Alberto Riva, William Barbazuk, Timothy Harkins

doi: https://doi.org/10.1101/2020.01.03.894428

This article is a preprint and has not been certified by peer review [what does this mean?].

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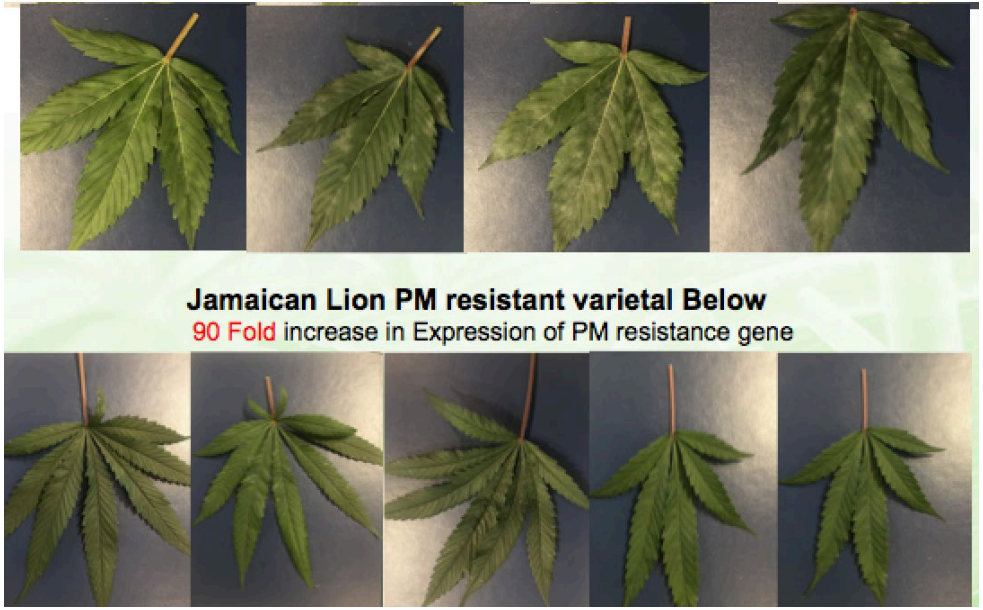
What Can We Learn from the Cannabis Genome?



PM susceptible

PM Resistant

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HiC + HiFi on a Cannabis Trio

Table 1A. Pacific Biosciences coverage and sequencing statistics of three Jamaican Lion cannabis genomes**.** Genomes were sequenced with continuous long read mode (CLR). F1 was female. BUSCO: benchmarking universal single-copy orthologs. Software and database versions: BUSCO.py 3.0.2, Augustus 3.3.21, Hmmer 3.2.1, Blast 2.7.1, eudicotyledons_odb10(Simao et al. 2015).

Coverage	**Mother**	**Father**	**Daughter (JL5)**
N50	3,283,100	1,668,042	3,491,975
Contig number (> 5 Kb)	481	1264	658
Genome size (bp)	875,793,298	1,009,156,132	999,122,115
Complete BUSCOs (%)	96.1	97.0	97.3
Single-copy BUSCOs (%)	83.5	63.3	63.5
Duplicated BUSCOs (%)	12.6	33.7	33.8
Sequencing statistics			
Unique molecular yield (Gb)	125	150	84.8
N50 RL (Kb)	34.6	35.6	50
N50 Subread (Kb)	20	24	19

The 33X coverage HiFi assembly delivered a higher
N50 (5.2Mb) assembly
BUSCO Primary (93.7%C, 82.8% single, 10.9% duplicate)
BUSCO Primary + Alts (**97.4%**, 41.2% single, 56.2% duplicate)

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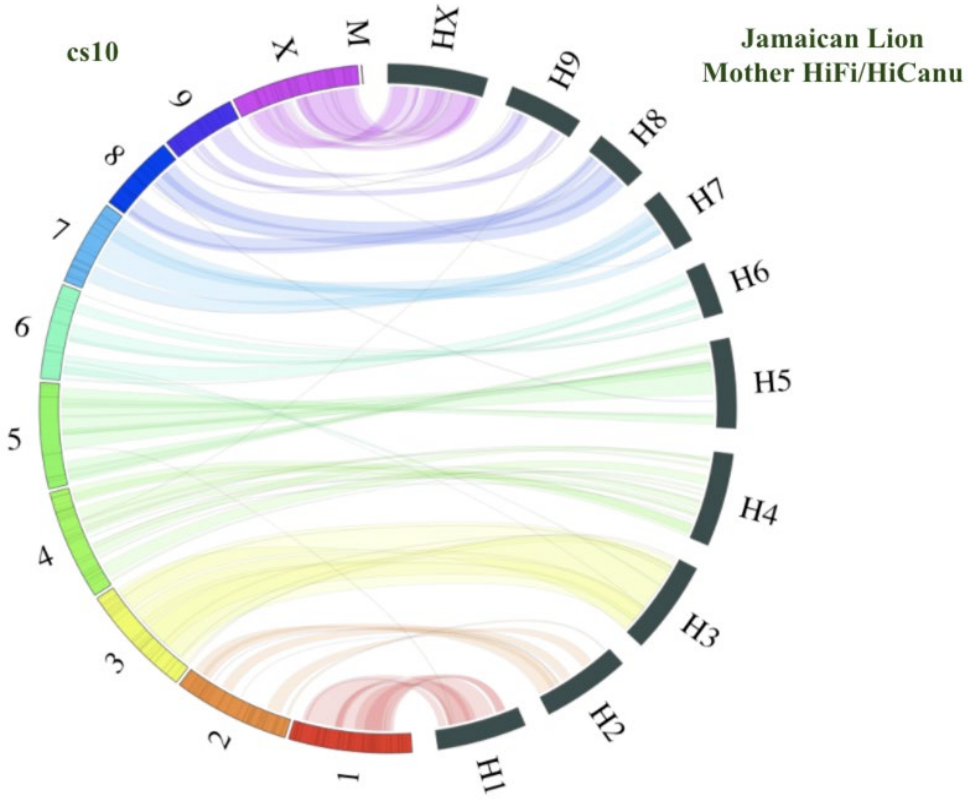
(NCBI accession number: JAATIP000000000)

HiC + HiFi



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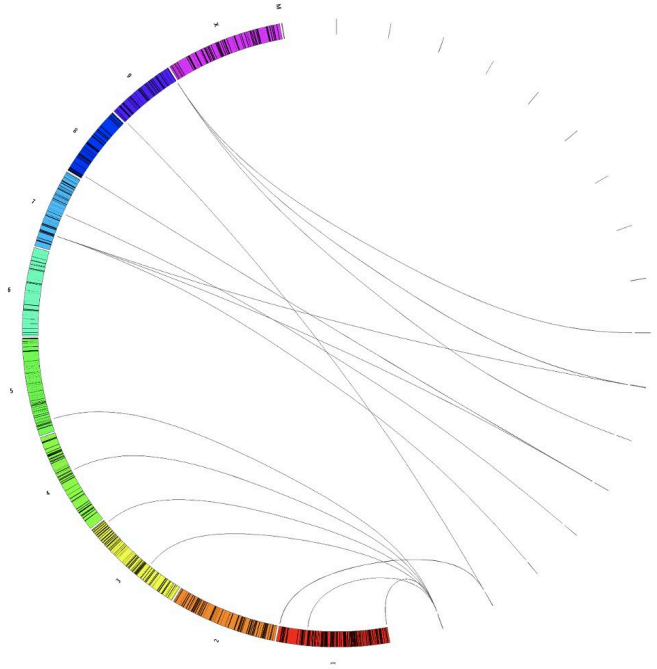
HiCanu Telomeres

Supplementary Table 1. Contigs in the Jamaican Lion HiFi-HiCanu assembly with terminal Telomeric sequences and their respective lengths.

Contig	Telomere Len (Kb)	Contig Length
tig00005375	25.7	250,103
tig00005432	2.9	230,364
tig00005460	23.8	142,906
tig00005486	7.7	167,894
tig00005511	1.8	170,382
tig00005736	16.6	102,145
tig00005782	35.2	85,691
tig00005821	26	67,613
tig00005878	26.9	107,231
tig00005912	22.4	27,710
tig00005913	17.8	27,527
tig00005915	23.1	44,441
tig00006147	13.2	32,702
tig00006532	5.3	35,243
tig00007704	18.9	26,164
tig00043130	4.2	401,659
tig00043131	42.9	45,132

Supplemental Figure 18. Jamaican Lion HiCanu telomeric contigs (right) mapped to the Cs10 assembly (Left) with minimap and displayed with Circos.



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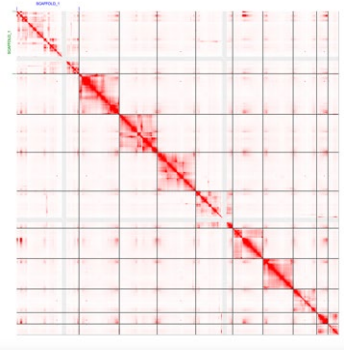
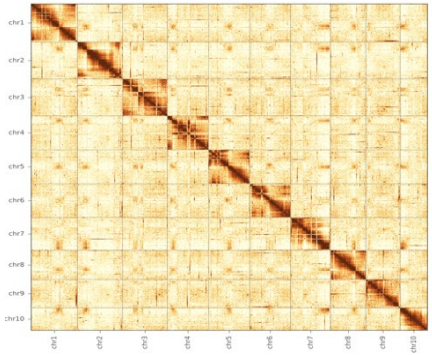
Genetic Map Concordance with HiC

63% AT rich
63% Long Terminal Repeats (LTR)
Lots of Simple Sequence Repeats (SSRs)

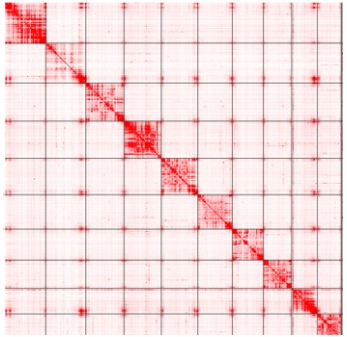
JL scaffolds organized according to BLAST to Cs10 Chromosomes



Gao et al JL-China



JL Hi-C mapped to Cs10 reference



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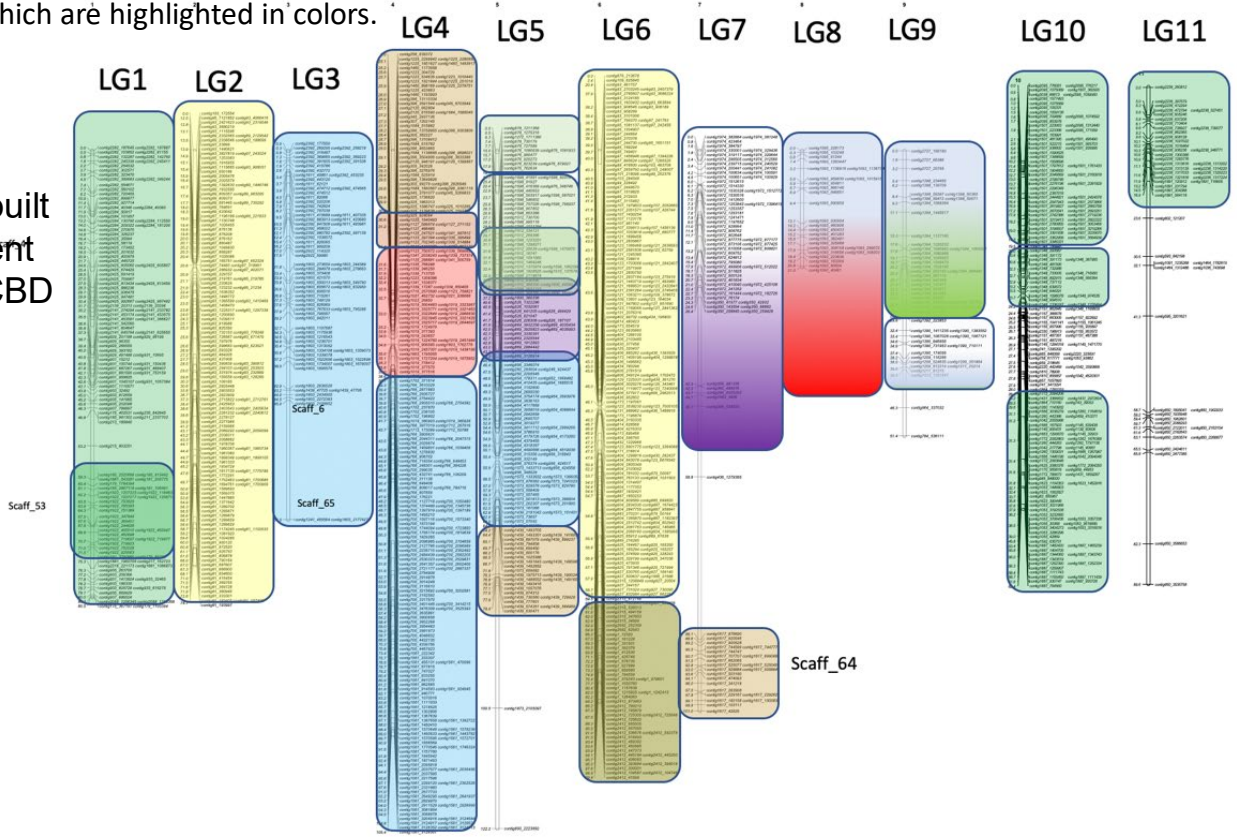
Genetic Map Concordance with HiC 85K SNP Chip - CannSNP90

The genetic map and physical map was compared and most of the marker position was confirmed which are highlighted in colors.

Genetic Map was built with F2 from different cultivars: Oregon CBD

Genetic Map from Jamaican Lion F1 underway



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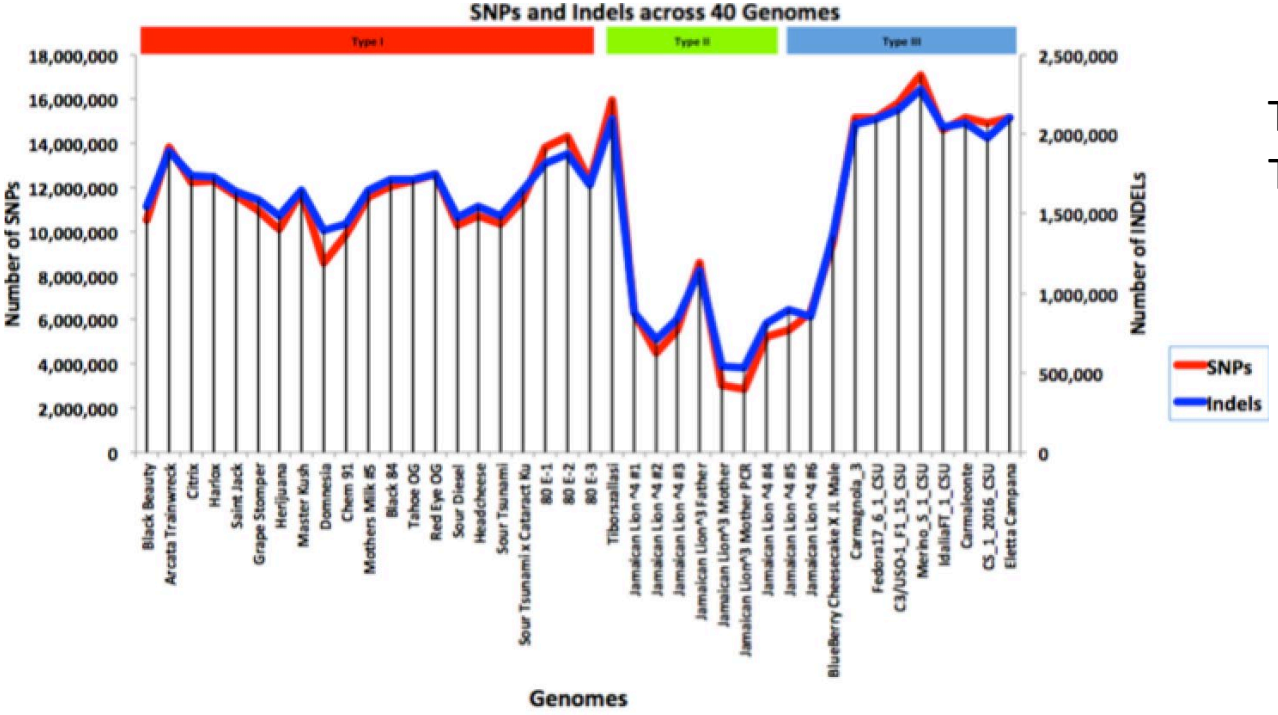
eurofins

40 WGS with ILMN NovaSeq
5 cycles of PCR with NEB UMIs

58,262,496 Unique SNPs across 40 Genomes.



TypeI = 10-14 SNPs
TypeIII = 12-17M SNPs

Mapped with DRAGEN and ParaBricks

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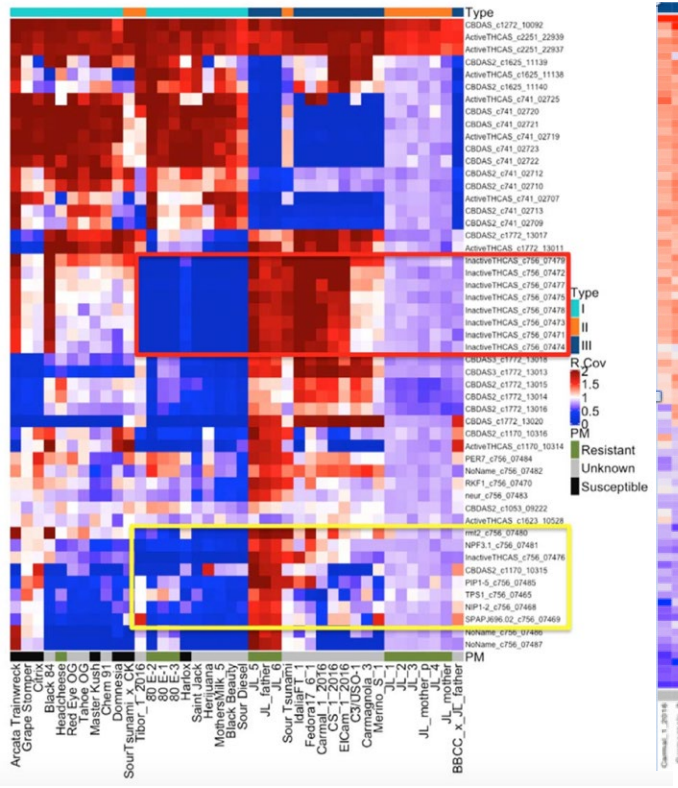
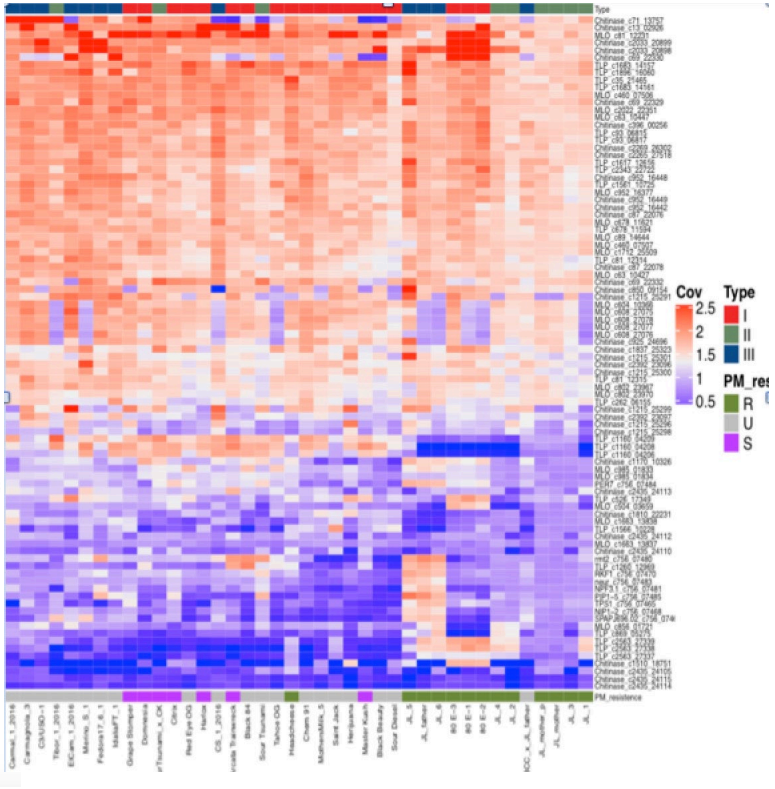
CNVs Galore (Copy Number Variation)





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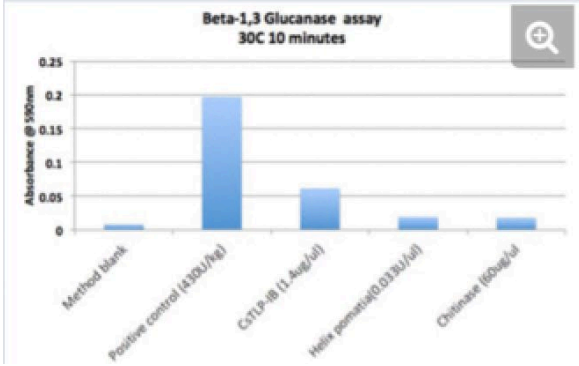
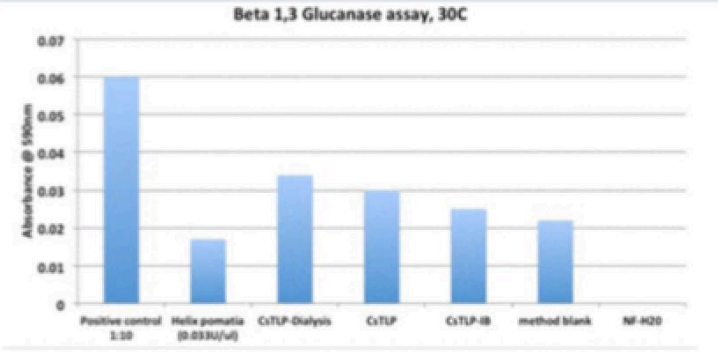
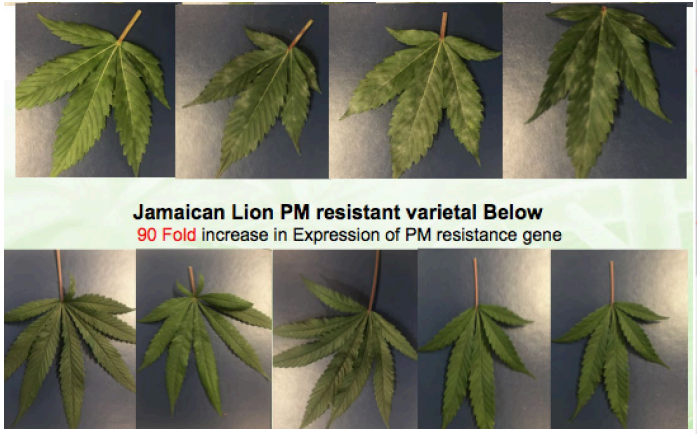
Cannabinoids Genes

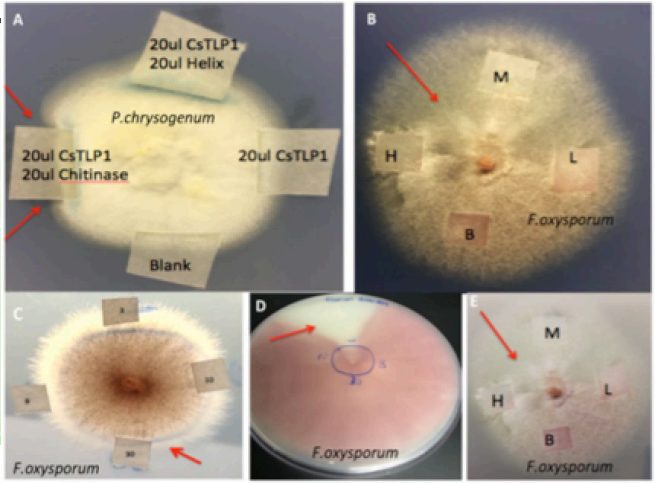
Pathogen Response Genes

Functional Validation of Cloned Cannabis Genes









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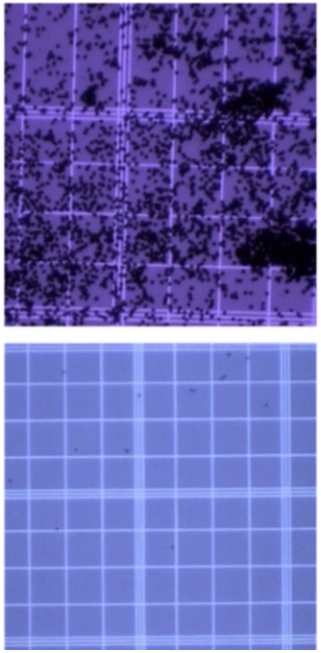
Aspergillus niger Growth in TSB

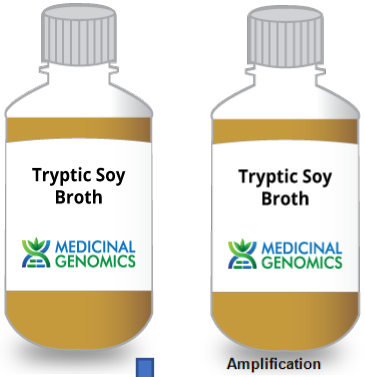
4X – 64X reduction with Cannabis Chitinase and Cannabis TLP

Declump and count 15 Spores

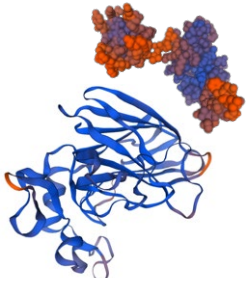


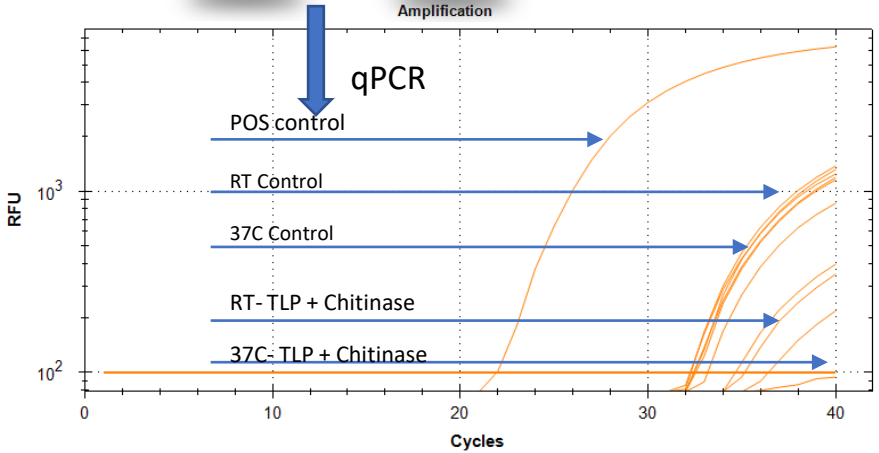
AOAC EUA TYM

Grow at RT and 37C for 22 hours



TLP & Chitinase





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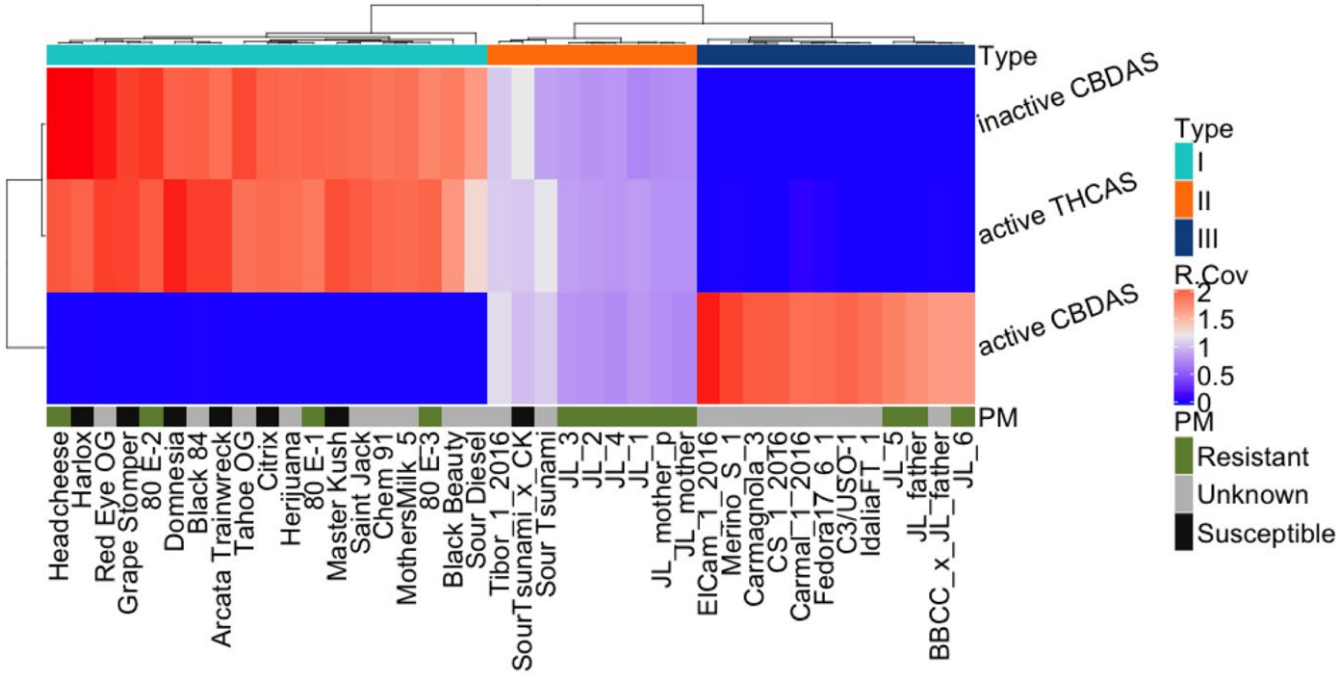
Copy Number of THCAS and CBDAS across 42 genomes



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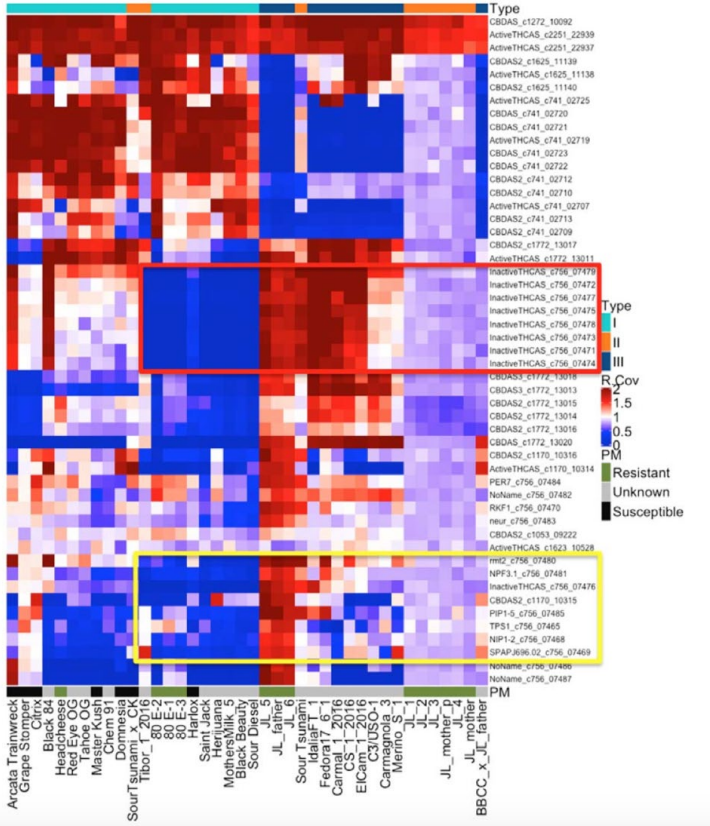
2Mb CBCA deletion
Often co-deleted with Pathogen Response genes

Same Contig



Gibberillin transporter –**NPF3**
Viral Defense -**RMT1**
PAMP-induced secreted peptides **-PIP1**
Aquaporin/H2O2 defense **-NIP1**

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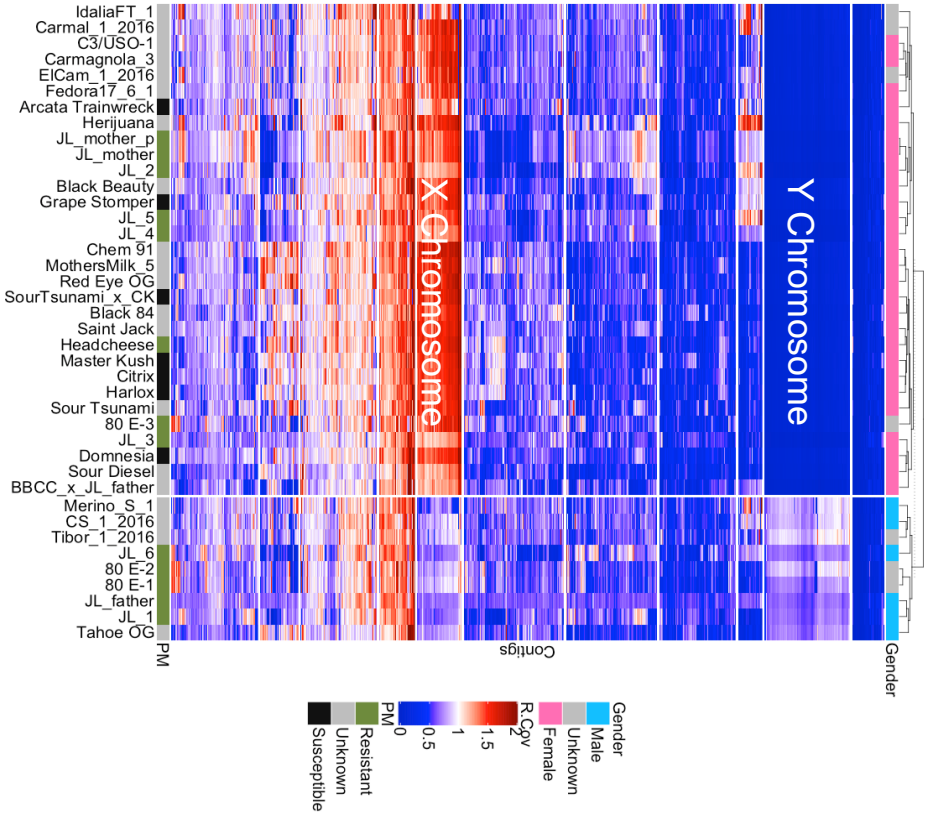
Differential WGS Coverage Validates Y chromosome



Female

Male

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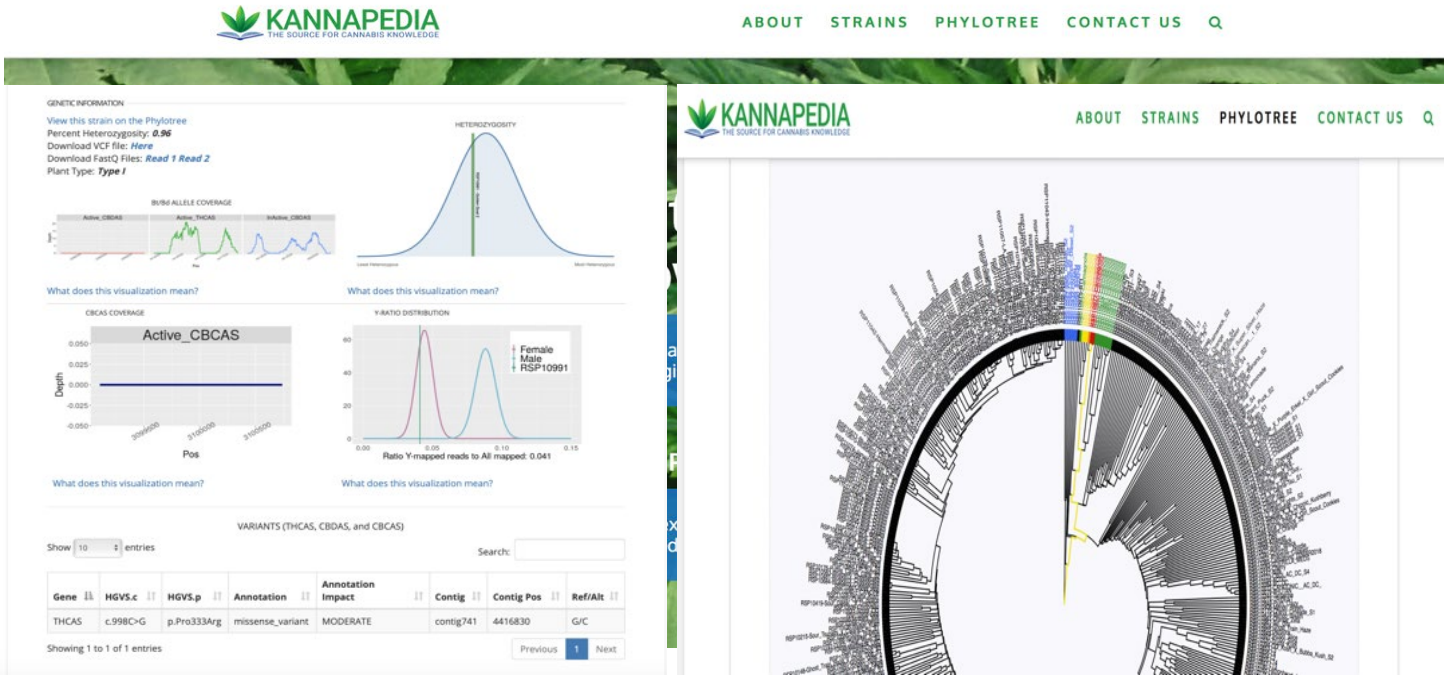
StrainSEEK: 3.2Mb &10Mb Agilent Panel WGS & CannSNP90K data input

Blockchain based Genetic registry: The timestamps on your data are immutable



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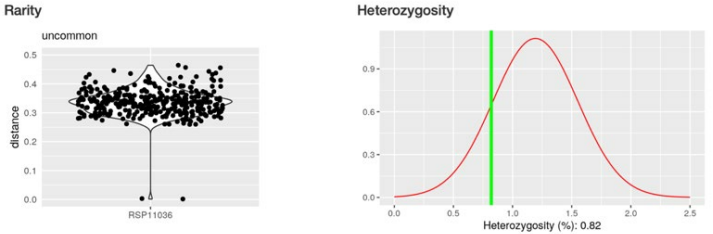
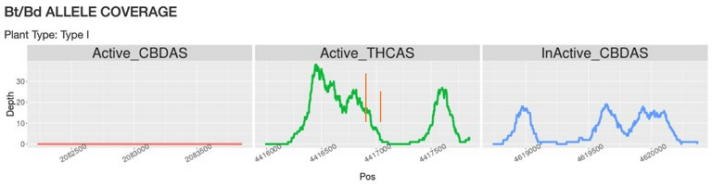
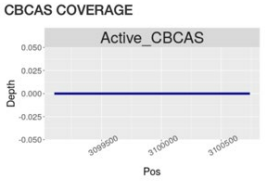
Differential WGS Coverage Validates Y chromosome







Type IV

Variants in Select Genes

CBDAS, THCAS

Show 10 entries Search:

	Gene	HGVS.c	HGVS.p	Annotation	Annotation Impact	Contig	Contig Pos	Ref/Alt
1	THCAS	c.998C>G	p.Pro333Arg	missense_variant	MODERATE	contig741	4416830	G/C

Showing 1 to 1 of 1 entries Previous 1 Next

CBDA in yeast makes ~20:1 CBDA:THCA

Type IV plant

1. No CBDAS gene.
2. Two Amino Acid Changing Mutations in THCAS
3. No CBCAS gene.
4. Zero THCA detected in 10%+ CBGA cultivar

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Kannapedia.net reports

NEAREST GENETIC RELATIVES IN PHYLOS DATASET:

Nearest Phylos Strain	Number of Overlapping SNPs	Concordar
SRR4448183	78	75

NEAREST GENETIC RELATIVES IN LYNCH DATASET:

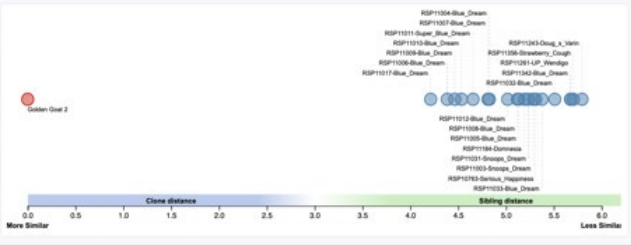
Nearest Lynch Strain	Number of Overlapping SNPs	Concordar
SRR3495217	7	7

BLOCKCHAIN REGISTRATION INFORMATION:

Transaction ID: fc01b0724f1cf53add58c49494dbcb7d901e28f2c945706d52714e87d82b73c9
Stamping Certificate: PDF
SHASUM Hash: ***b21a1f370d90ff4a0423cffedaa12b6e4091f0a46a1e0674b25823fff7197f1f***

Comparison to other public datasets and blockchain time stamps

NEAREST GENETIC RELATIVES TO Golden Goat 2:



#	Relative	Genetic Distance
1	RSP11017-Blue Dream	4.21
2	RSP11006-Blue Dream	4.39
3	RSP11009-Blue Dream	4.46
4	RSP11010-Blue Dream	4.53
5	RSP11011-Super Blue Dream	4.66
6	RSP11007-Blue Dream	4.81
7	RSP11004-Blue Dream	4.83
8	RSP11012-Blue Dream	5.02
9	RSP11008-Blue Dream	5.12
10	RSP11005-Blue Dream	5.13

Relationships

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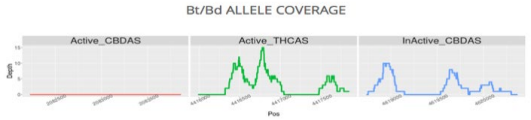
StrainSEEK Sequence Coverage of the Bt:Bd allele predicts chemotype

Sequencing Coverage

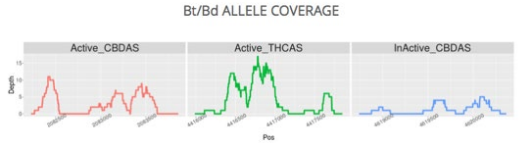
Active CBDAS Active THCAS Inactive CBDAS

Plant Type: ***Type I***



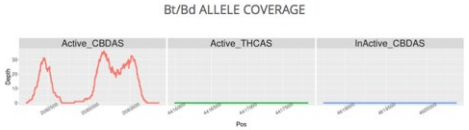
Type I
No Coverage on CBDAS

Plant Type: ***Type II***



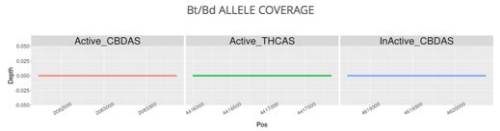
Type II
Good Coverage on CBDAS

Plant Type: ***Type III***



Type III
Good Coverage on CBDAS
No Coverage on THCA

Plant Type: ***Type IV***



Type IV
No Coverage on THCAS
No Coverage on CBDAS.

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January 25, 2022

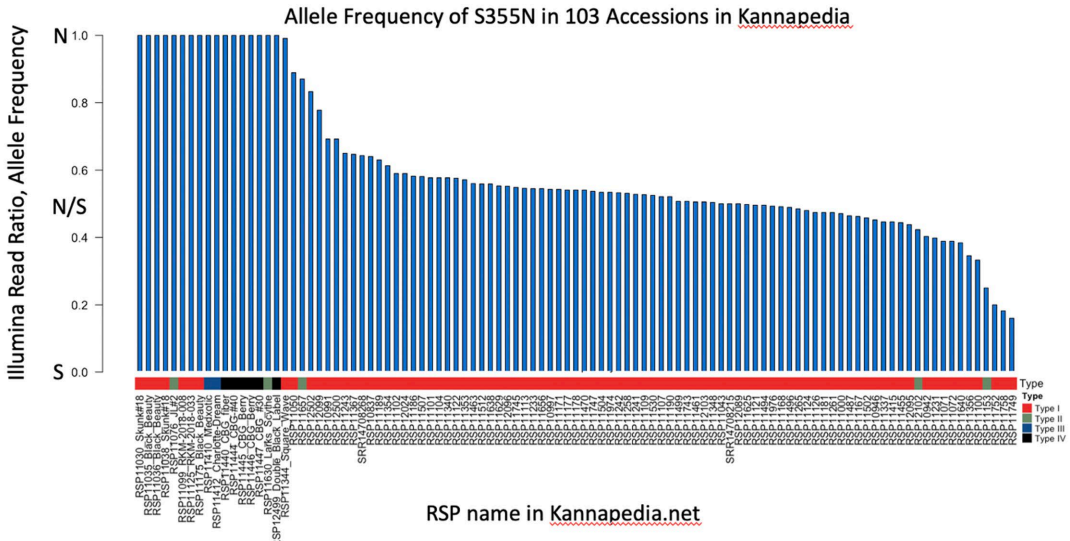
Preprint Open Access

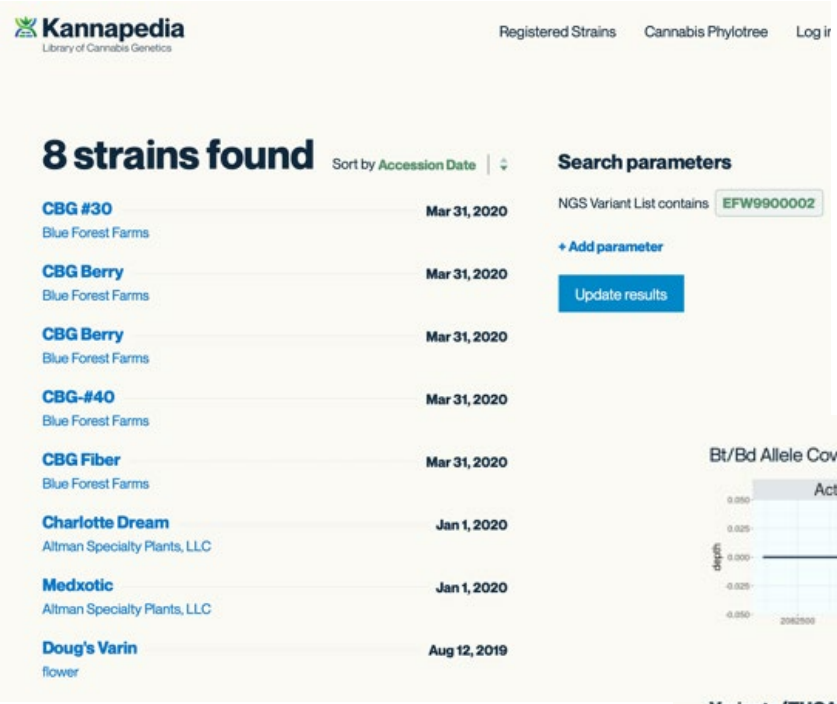
Missense mutations in THCAS are associated with Cannabigerolic Acid expression in Cannabis sativa L.

Kevin McKernan; Lei Zhang; Yvonne Helbert; Liam T Kane; McLaughlin, Stephen

The chemical expression of THCA and CBDA has been previously attributed to copy number gains and losses in THCAS and CBDAS. Here we describe an alternative mechanism to ablate THCAS activity in 5 CBGA dominant cannabis varietals. Five cannabis cultivars from three unique cultivators surprisingly contain a THCAS gene but also share homozygous Pro333Arg and Ser355Asn mutations in THCAS. Pro333Arg is commonly found in THCAS dominant varietals but is uniquely found in a homozygous state in CBGA varietals in conjunction with homozygous Ser355Asn missense mutations. These results hint at convergent evolution in cannabinoid synthesis where selection for and against THCA synthesis has been applied.

Figure 4. Allele frequency (Illumina read count ratio) in 103 samples with P333R mutations in THCAS. The samples with Allele ratio of 1 have their cultivar name added. Two samples are SRR#s NCBI.





Type IV (CBGA) that contain a THCA gene

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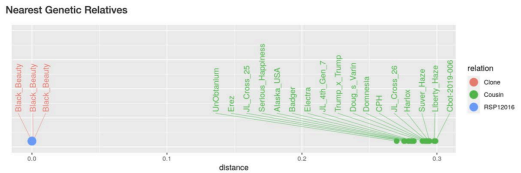
Many different tools

SS2 vs SS3, same samples: RSP12016



	MGC_ID	Strain Name	Genetic Distance	Relationship
1	RSP11035	Black_Beauty	0.00%	Clone
2	RSP11175	Black_Beauty	0.08%	Clone
3	RSP11036	Black_Beauty	0.08%	Clone

SS1	Edit	RSP10697	10509 Medicinal Genomics Customer	Complete	3/1/2017 3:31 pm	Black Beauty
SS2	Edit	RSP11035	10509 Medicinal Genomics Customer	Complete	11/20/2017 4:55 pm	Black Beauty
SS2	Edit	RSP11036	10509 Medicinal Genomics Customer	Complete	11/20/2017 4:56 pm	Black Beauty
WGS	Edit	RSP11175	10509 Medicinal Genomics Customer	Complete	6/26/2019 3:51 pm	Black Beauty
SS3	Edit	RSP12016	9650 Medicinal Genomics	In Process	6/4/2021 10:24 am	Black Beauty

Confidential

GOOD

CannSNP90 CHIP

FOR GENOTYPING PLANTS

view the technical sheet

SNP CHIP GENOTYPING (PROBE SINGLE LOCATIONS)

- 89K+ SNPS
- GENDER DETERMINATION
- CHEMOTYPE DETERMINATION
- SNP LOCI FOR:
  - CANNABINOID SYNTHASE GENES (THCA, CBDA, CBCA)
  - DISEASE RESISTANCE
  - TERPENES
  - GENOME-WIDE TAG DISTRIBUTION
  - StrainSEEK OVERLAP TAGS
- DOWNLOADABLE VARIANT DATA
- KANNAPEDIA REPORT INCLUDED

BETTER

StrainSEEK®

FOR FINDING NOVEL VARIANTS IN KEY GENOMIC AREAS

DNA SEQUENCING PANEL (SEQUENCE AREAS OF INTEREST)

- 10M+ BASES SEQUENCED
- 300K-500K SNPS
- TAGS IN 7,500+ GENES
- GENDER DETERMINATION
- CHEMOTYPE DETERMINATION
- FULL/PARTIAL COVERAGE FOR:
  - CANNABINOID SYNTHASE GENES (THCA, CBDA, CBCA)
  - DISEASE RESISTANCE
  - TERPENES
  - FLAVINOIDS
  - FLOWERING
  - SEEDING
  - OTHERS
- DOWNLOADABLE VARIANT, MAPPING, & SEQUENCE DATA
- KANNAPEDIA REPORT INCLUDED

BEST

WHOLE GENOME

FOR THE MOST COMPLETE, FUTURE-PROOF GENOMIC PROFILE

SHOTGUN DNA SEQUENCING (SEQUENCE ENTIRE GENOME)

- 876M BASES SEQUENCED
- 3M-15M SNPS
- 27K+ GENES
- GENDER DETERMINATION
- CHEMOTYPE DETERMINATION
- FULL COVERAGE FOR:
  - CANNABINOID SYNTHASE GENES (THCA, CBDA, CBCA)
  - DISEASE RESISTANCE
  - TERPENES
  - FLAVINOIDS
  - FLOWERING
  - SEEDING
  - MANY, MANY OTHERS
- DOWNLOADABLE VARIANT, MAPPING, & SEQUENCE DATA
- KANNAPEDIA REPORT INCLUDED

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Genes of Interest - compare coverage 10Mb vs 3.2Mb panel

- Genes of interest have been divided into 9 distinct categories (complete genes lists are here)

1. Flowering genes - 23 genes that were pulled out of the annotation for Jamaican Lion Female matching the term “flower”
2. TLP1 genes - 6 genes that were included in *Fig 6B* of MGC’s 40-genome pre-print implicated in Powdery Mildew Resistance
3. TLP genes - The 23 TLP genes included in Fig6A
4. Known Disease Associated - 280 genes pulled out of JL annotation matching term “disease”
5. Kannapedia select genes of interest - 27 genes manually curated by MGC scientists for which MGC report variants on in Kannapedia (there are also flowering genes on this list, but these have been pulled out into the *Flowering Genes* group for this analysis
6. Chitinase - 35 Chitinase genes included in Fig6A
7. MLO - 23 genes included in Fig6A
8. CBCA “Pathogen Response” genes - 35 genes on contig756 of the JL Female reference also included in Fig6A
9. Fig 6A - all 90 genes included in Fig6A (includes TLP, Chitinase, MLO, and CBCA Pathogen response from above)

Breeding Using CannSNP90 Bead Chip

CannSNP90 bead chip

- Content
- Validation
- Applications

Molecular Breeding

- Evolution of Molecular Markers
- Applications of Genotyping
- Construction of Hemp Genetic Map

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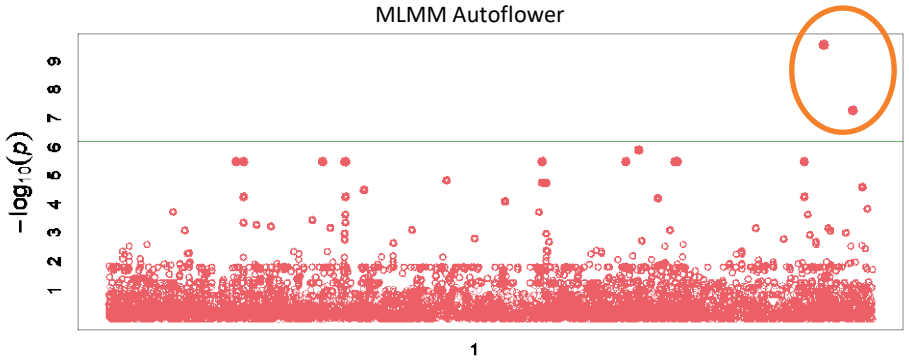
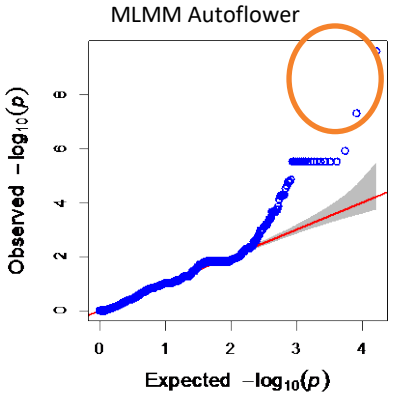
CannSNP90 Case Study by Oregon CBD

Multiple Locus Mixed Linear Model (MLMM)

Dr. Hsuan Chen





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CannSNP90 Case Study by Oregon CBD

vs.

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Background in Open Source Fungal Genomics

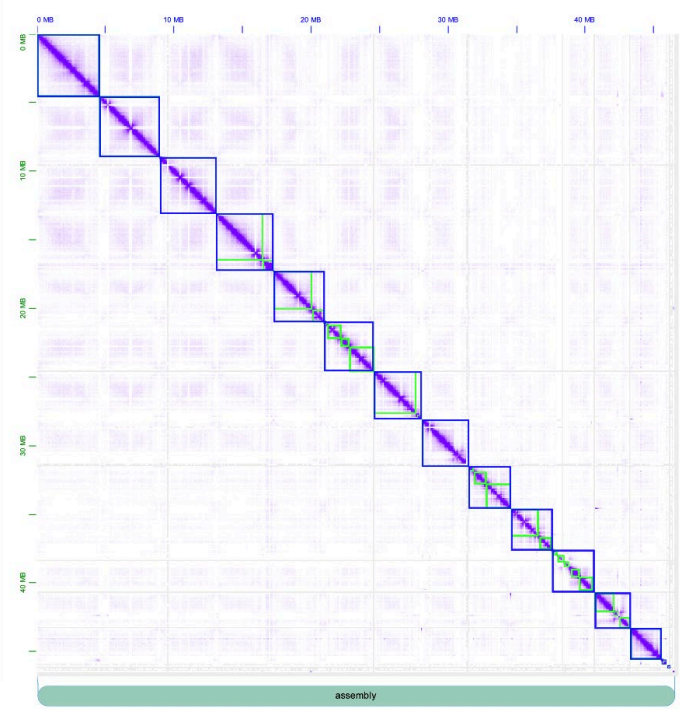

Figure 1. HiC contact map displayed in Juicebox. 13 large scaffolds emerge with total of 26 scaffolds. Mitochondria is on scaffold 20

Pacific Biosciences HiFi assembly
N50 3.3Mb, 97.6% BUSCO complete

Phase Genomics Hi-C Chromatin Capture map of Psilocybe cubensis

Psilocybe cubensis is now in 13 chromosomes

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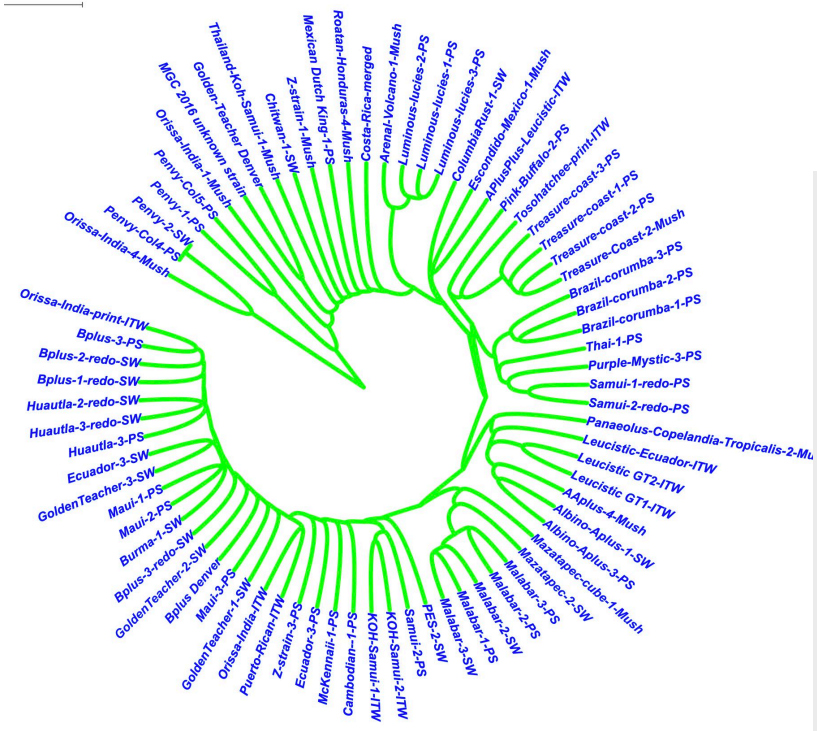
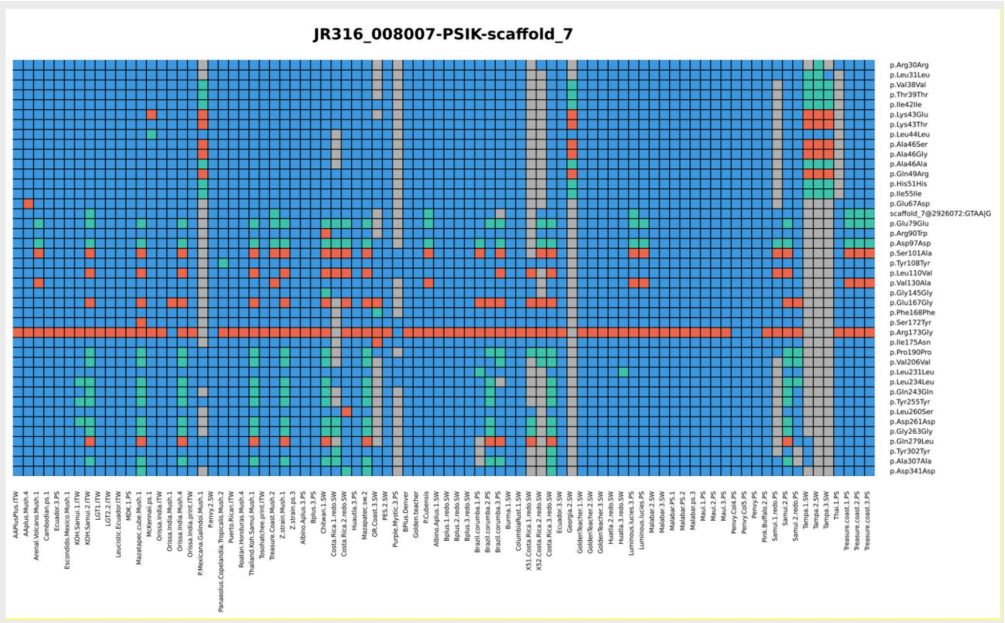
Kannapedia.net: Open Source Fungal Genomics



81 Whole genome assemblies of Psilocybe

Damaging variants in the Pathway identified



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Psilocybe Mating Type Loci identified on Chr. 1

Psilocybe has at least 4 genders
Mating Type Loci can guide which strains will make compatible crosses

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Psilocydia- The Kannapedia fork for Psilocybe

Penvy-2-SW

PSP 10075 · Grower: Medicinal Genomics

General Information

Accession Date
June 13, 2021

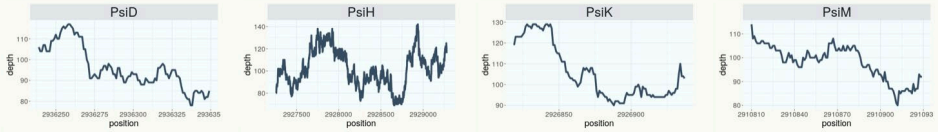
Report Type
Whole-Genome Sequencing

Genetic Information

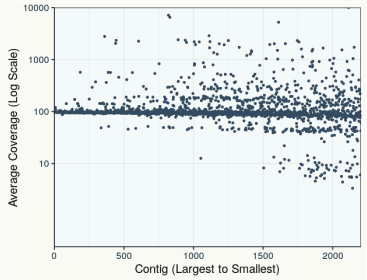
FILE DOWNLOADS

- Annotated VCF
- Annotated VCF Index
- BAM
- BAM Index
- BAM (Mapped to Assembly)
- BAM (Mapped to Assembly) Index
- FASTQ Read 1
- FASTQ Read 2
- Assembled Genome, FASTA
- Assembled Genome, FASTA Index

Psilocybin Synthase Gene Coverage



Coverage vs. Contig Size



No. of Contigs (>= 25K bp) 414	**Total Length (>= 50K bp)** 21,463,896	**Total Length** 42,071,211
No. of Contigs (>= 50K bp) 198	**Total Contigs** 5,188	**GC (%)** 46.06
Total Length (>= 25K bp) 29,251,567	**Largest Contig** 432,312	**N50** 51,488

Variants

search variants

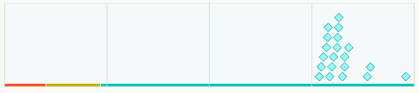
GENE	HGVS.C	ANNOTATION	ANNOTATION IMPACT	CONTIG	CONTIG POS	REF/ALT
PsiD	c.*1447A>G	downstream gene variant	modifier	scaffold_7	2934482 IGV: Start, Jump	T/C

NEAREST GENETIC RELATIVES (ALL SAMPLES)

clone distance · sibling distance · more distant

- 0.007 Penvy-Col5-PS (PSP10044)
- 0.007 Penvy-1-PS (PSP10045)
- 0.008 Penvy-Col4-PS (PSP10043)
- 0.240 Tampa-1-SW (PSP10050)
- 0.246 Tampa-2-SW (PSP10051)

MOST GENETICALLY DISTANT STRAINS (ALL SAMPLES)



clone distance · sibling distance · more distant

- 0.979 Bplus-3-PS (PSP10001)
- 0.893 Huautla-3-PS (PSP10005)
- 0.885 Huautla-3-redo-SW (PSP10031)
- 0.840 Maui-2-PS (PSP10041)
- 0.830 Bplus-2-redo-SW (PSP10015)

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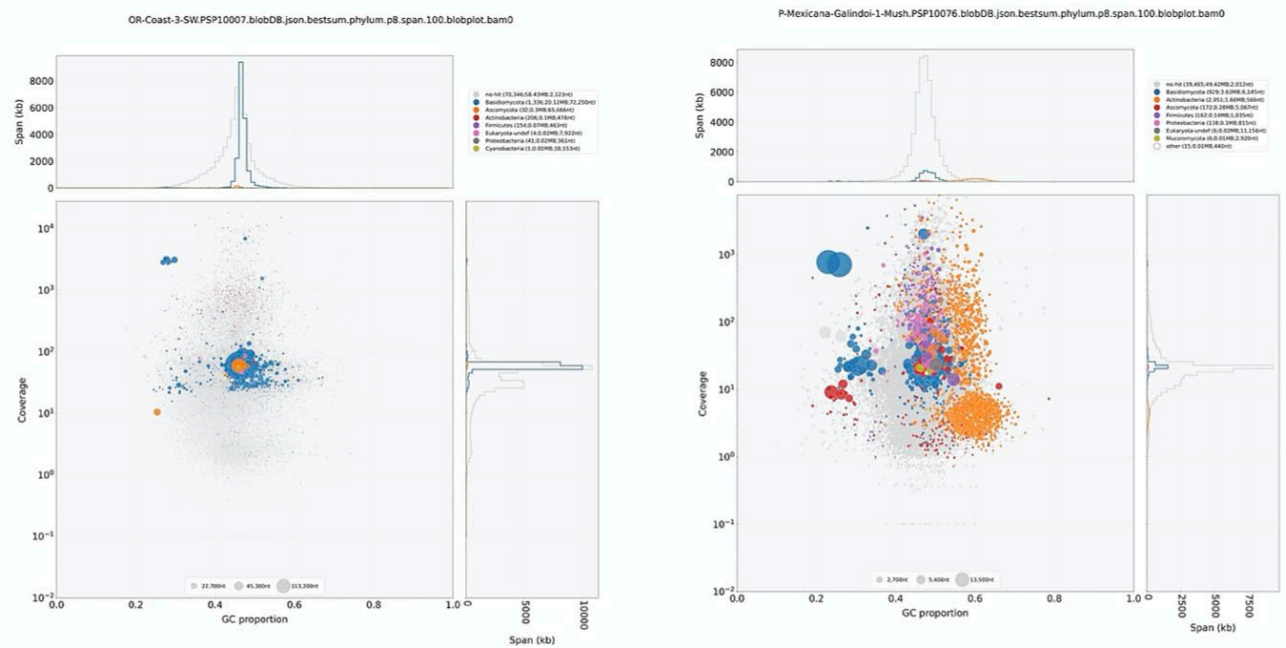
Psilocybe microbomes



Supplementary Figure 2. Taxon annotated GC-Plot of *P.azurescens* (OR-Coast Left) and *P.galindoi* (Right) demonstrate some metagenomic bacterial contamination in the *P.galindoi* library. Contigs with Psilocybin producing genes in *P.galindoi* have been identified using tBLASTn.

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McKernan et al

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14 Viruses/Viroid assays

Released

1. Hop Latent Viroid
2. Lettuce Chlorosis Virus
3. Cannabis Cryptic Virus
4. Beat Curly Top Virus
5. Tobacco Mosaic Virus

Pipeline

1. Tobacco Streak Virus
2. Tobacco Ring Spot Virus
3. Arabis Mosaic Virus
4. Cucumber Mosaic Virus
5. Hop Mosaic Virus
6. Alfalfa Mosaic Virus
7. Tomato Ring Spot Virus
8. Rasberry Dwarf Virus
9. Hop Stunt Viroid

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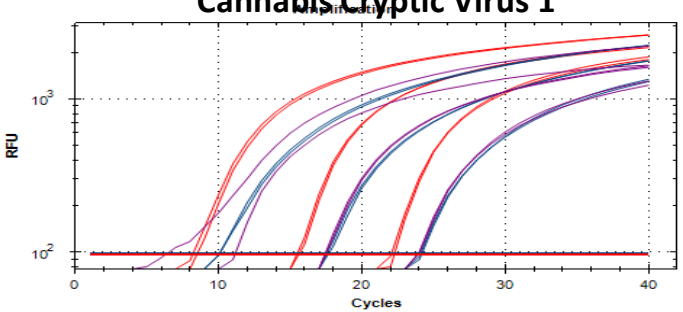
qPCR enables the detection of pathogens that don't culture.

Triplex Virus/Viroid test
Hops Latent Viroid,
Lettuce Chlorosis Virus,
Cannabis Cryptic Virus 1



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LCV Virus Phenotype More Pronounced in Flowering

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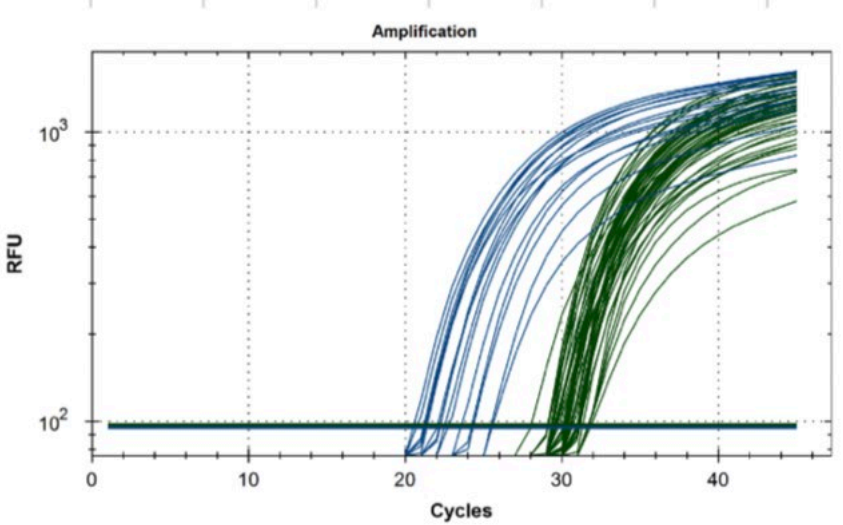
Hop Latent Viroid is in the Roots, Stems and leaves

Sample Number	Sample Name	Target (FAM)	Ct (FAM)	Target (HEX)	Ct (HEX)
10.1	Chem 4 Mom	HLVd	ND	SCCG	29.73
10.1	Chem 4 Mom	HLVd	ND	SCCG	30.25
10.2	Chem 4 Clone 1	HLVd	ND	SCCG	30.60
10.2	Chem 4 Clone 1	HLVd	ND	SCCG	30.67
10.3	Chem 4 Clone 2	HLVd	ND	SCCG	31.83
10.3	Chem 4 Clone 2	HLVd	ND	SCCG	30.81
11.1	Motorbreath Clone 1	HLVd	ND	SCCG	31.10
11.1	Motorbreath Clone 1	HLVd	ND	SCCG	31.28
11.2	Motorbreath Clone 2	HLVd	ND	SCCG	30.22
11.2	Motorbreath Clone 2	HLVd	ND	SCCG	29.09
12.1	Old Family Purp Rooted, Leaf	HLVd	22.14	SCCG	31.07
12.1	Old Family Purp Rooted, Leaf	HLVd	20.78	SCCG	29.61
12.1	Old Family Purp Rooted, Root	HLVd	23.59	SCCG	29.59
12.1	Old Family Purp Rooted, Root	HLVd	22.59	SCCG	29.57
13.1	Sour Diesel Mom	HLVd	ND	SCCG	30.13
13.1	Sour Diesel Mom	HLVd	ND	SCCG	30.27
13.2	Sour Diesel Clone 1	HLVd	ND	SCCG	30.24
13.2	Sour Diesel Clone 1	HLVd	ND	SCCG	30.18
13.3	Sour Diesel Clone 2	HLVd	ND	SCCG	31.13
13.3	Sour Diesel Clone 2	HLVd	ND	SCCG	31.80
13.4	Sour Diesel Clone 3	HLVd	ND	SCCG	31.07
13.4	Sour Diesel Clone 3	HLVd	ND	SCCG	30.28
13.5	Sour Diesel Rooted, Leaf	HLVd	ND	SCCG	30.07
13.5	Sour Diesel Rooted, Leaf	HLVd	ND	SCCG	30.68
13.5	Sour Diesel Rooted, Root	HLVd	ND	SCCG	37.71
13.5	Sour Diesel Rooted, Root	HLVd	ND	SCCG	31.02
14.1	GMO Mom	HLVd	ND	SCCG	30.59
14.1	GMO Mom	HLVd	ND	SCCG	30.10
15.1	Strawberry Rooted, Leaf	HLVd	21.18	SCCG	28.04
15.1	Strawberry Rooted, Leaf	HLVd	21.31	SCCG	29.88
15.1	Strawberry Rooted, Root	HLVd	24.18	SCCG	30.05
15.1	Strawberry Rooted, Root	HLVd	25.44	SCCG	30.36
15.2	Strawberry Alive	HLVd	24.27	SCCG	31.74
15.2	Strawberry Alive	HLVd	25.56	SCCG	31.90
16.1	Strawnana Rooted, Leaf	HLVd	20.52	SCCG	29.52
16.1	Strawnana Rooted, Leaf	HLVd	21.21	SCCG	29.80
16.1	Strawnana Rooted, Root	HLVd	21.12	SCCG	29.12
16.1	Strawnana Rooted, Root	HLVd	22.16	SCCG	29.33
16.2	Strawnana Alive	HLVd	22.81	SCCG	30.74
16.2	Strawnana Alive	HLVd	22.02	SCCG	29.62
17.1	Triangle Wave Backup 2	HLVd	38.29	SCCG	33.04
17.1	Triangle Wave Backup 2	HLVd	37.78	SCCG	30.38
17.2	Triangle Wave Mom 2	HLVd	ND	SCCG	30.21
17.2	Triangle Wave Mom 2	HLVd	ND	SCCG	31.79
17.3	Triangle Wave Mom 3	HLVd	ND	SCCG	30.99
17.3	Triangle Wave Mom 3	HLVd	ND	SCCG	29.30
18.1	Trop Cookies Clone 1	HLVd	ND	SCCG	29.75
18.1	Trop Cookies Clone 1	HLVd	ND	SCCG	29.44
18.2	Trop Cookies Clone 2	HLVd	ND	SCCG	30.20
18.2	Trop Cookies Clone 2	HLVd	ND	SCCG	29.08
18.3	Trop Cookies Clone 3	HLVd	ND	SCCG	30.42
18.3	Trop Cookies Clone 3	HLVd	ND	SCCG	29.25
	Positive Control	HLVd	15.54	SCCG	39.26
	NTC	HLVd	ND	SCCG	37.64



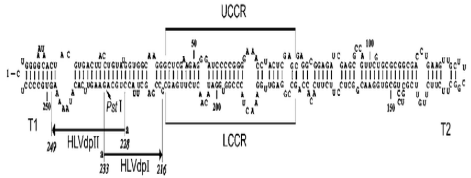
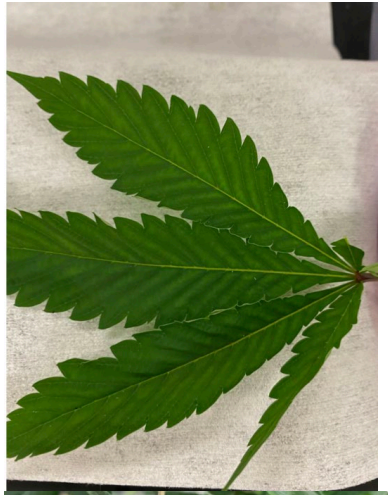


Figure 4 Secondary structure (Puchta et al., 1988) of HLVd and localization of primers for RT-PCR analysis of viroid infection in pollen.
UCCR, upper part of the central conserved region; LCCR, lower part of the central conserved region; T1 and T2, left and right terminal domains. Primer binding sites are localized in the lower part of the viroid structure and cover a unique PstI restriction site. Primers are represented by arrows and positions are designated by numbers; a, position of a non-specific nucleotide.



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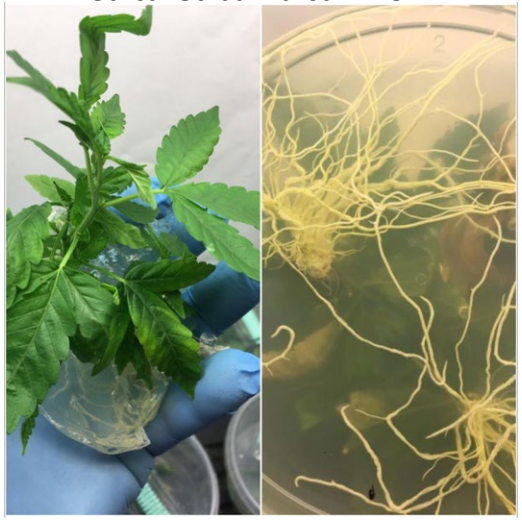
Jamaican Lion Becoming A Reference Standard

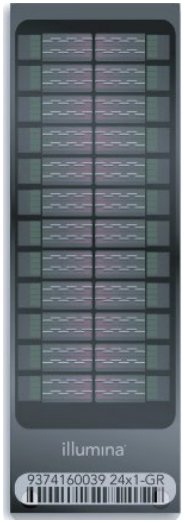
Vendors are consolidating on the Jamaican Lion references
Tissue Culture has been optimized for JL.
SNP Chips are Validated on JL. August 2020 Launch.
Mini-Exomes are available targeting Cannabinoid, Terpene, Chitinase, Y-chromosome, TLP, Flowering, CannFlavin, Edestin related genes.

Doug Klier (IGBR)- Tissue Cultured Jamaican Lion



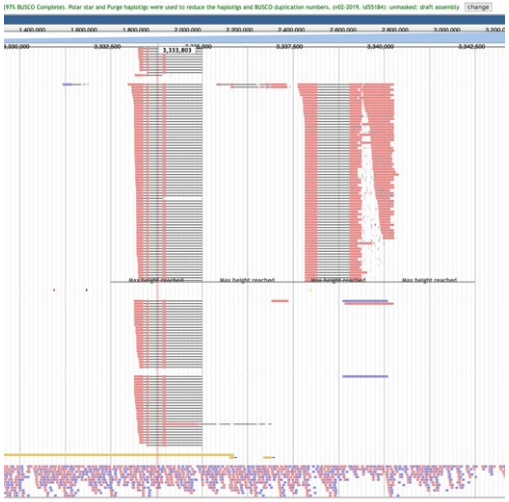
eurofins

85K SNP array



Agilent

Mini-Exomes (5-10Mb Seq panels)



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