Organização e apresentação de arquivos e resultados

Drª Desirrê Petters-Vandresen

Princípios gerais

- Uma boa organização e apresentação das informações, anotações, predições, resultados e conclusões obtidos no estudo:
  - Compreensível para os leitores
  - Tem relação com as perguntas, hipóteses e objetivos do estudo
  - Facilita a percepção e observação de aspectos e tendências gerais
  - Destaca eventuais particularidades de interesse ao estudo
  - Permite que os dados (ou métodos) desenvolvidos possam ser utilizados em estudos futuros

Arquivos brutos ou de resultados (output de softwares)

- Devem ser disponibilizados sempre que possível

- Garantem a reprodutibilidade do estudo e servem de base para vários estudos futuros

- Exemplos:
  - Reads de sequenciamento de genoma e transcriptoma
  - Montagens de genomas e transcriptoma
  - Anotações de genes, TEs e anotações funcionais

Alguns exemplos

SRA | SRA | Advanced

Full

SRX9601541: Phyllosticta citricarpa CBS 111.20 Standard Draft
1 PACBIO_SMRT (PacBio RS II) run: 6.1M spots, 53.4G bases, 12.6Gb downloads

External Id: JGI-SRA-181144

Submitted by: DOE Joint Genome Institute (JGI)

Study: Phyllosticta citricarpa CBS 111.20 Standard Draft genome sequencing
PRJNA677129 • SRP294733 • All experiments • All runs
show Abstract

Sample: Phyllosticta citricarpa CBS 111.20 Standard Draft
SAMN16773214 • SRS7805318 • All experiments • All runs
Organism: Phyllosticta citricarpa

Library:
Name: GUZGO
Instrument: PacBio RS II
Strategy: WGS
Source: GENOMIC
Selection: RANDOM
Layout: SINGLE
Construction protocol: Regular (DNA)

Runs: 1 run, 6.1M spots, 53.4G bases, 12.6Gb

Run	# of Spots	# of Bases	Size	Published
SRR13162647	6,063,335	53.4G	12.6Gb	2020-11-29

ID: 12544978

ASM698474v1

Organism name: Phyllosticta citricarpa (ascomycetes)
Infraspecific name: Strain: LGMF06
BioSample: SAMN09869335
BioProject: PRJNA486917
Submitter: Instituto Agronomico
Date: 2019/07/15
Assembly level: Scaffold
Genome representation: full
GenBank assembly accession: GCA_006984745.1 (latest)
RefSeq assembly accession: n/a
RefSeq assembly and GenBank assembly identical: n/a
WGS Project: QXPX01
Assembly method: CLCGenomicsWorkbench v. 6.5.1
Expected final version: no
Genome coverage: 850x
Sequencing technology: Illumina HiSeq

IDs: 3822611 [UID] 12078858 [GenBank]

History (Show revision history)

Comment

Global statistics

Total sequence length	29,759,385
Total ungapped length	29,757,884
Gaps between scaffolds	0
Number of scaffolds	17,844
Scaffold N50	3,015
Scaffold L50	3,002
Number of contigs	17,900
Contig N50	3,008
Contig L50	3,015
Total number of chromosomes and plasmids	0
Number of component sequences (WGS or clone)	17,844

Alguns exemplos

JGI MycoCosm
THE FUNGAL GENOMICS RESOURCE

JGI HOME GENOME PORTAL MYCOCOSM

JGI MycoCosm
THE FUNGAL GENOMICS RESOURCE

JGI HOME GENOME PORTAL MYCOCOSM PHYCOCOSM LOGIN

We're soliciting feedback from JGI primary and data users on JGI Data Release and Utilization policies. Fill out our Request for Information by April 21.

Home • Colletotrichum nymphaeae SA-01

SEARCH BLAST BROWSE ANNOTATIONS MCL CLUSTERS SYNTENY DOWNLOAD INFO HOME HELP!

Colletotrichum on its hosts.
Image Credit: Riccardo Baroncelli

The genome sequence and gene models of *Colletotrichum nymphaeae* SA-01 were provided by Michael Thon at the University of Salamanca, Spain. In order to allow comparative analyses with other fungal genomes sequenced by the Joint Genome Institute, a copy of this genome is incorporated into Mycocosm.

The genus *Colletotrichum* (phylum Ascomycota, subphylum Sordariomycetes, order Glomerelalles) contains at least 150 species divided into ten major clades. One of the largest of these is the *Colletotrichum acutatum* species complex (CAsc), which includes fungal pathogens that infect a wide diversity of plants in natural and managed ecosystems. The species complex has a very wide host range, and strains have been associated with diseases of more than 90 genera of plants and at least three insect species. The complex taxonomy of CAsc reflects a complexity in evolutionary history, likely brought about by recent host jumps and/or changes in host range followed by adaptation. The CAsc also display great diversity of reproductive behaviors although most species seem to have lost their mating capability. Thus, the CAsc are excellent candidates for studying the process of speciation, host adaptation and the evolution of mating behavior.

Members of CAsc also show significant expansions in gene families associated carbohydrate metabolism, particularly in families of xyloglucanases and other plant cell wall degrading enzymes and possibly contain the largest diversity of carbohydrate active enzymes in the Ascomycetes. How this repertoire of enzymes has evolved, and why CAsc species maintain such diversity is unknown. Comparative analysis of these species will give us insight into the mode and tempo of gene duplications, selective pressures and other evolutionary processes that lead expansion of carbohydrate active enzymes.

Genome Reference(s)

Please cite the following publication(s) if you use the data from this genome in your research:

Baroncelli R, Amby DB, Zapparata A, Sarrocco S, Vannacci G, Le Floch G, Harrison RJ, Holub E, Sukno SA, Sreenivasaprasad S, Thon MR
Gene family expansions and contractions are associated with host range in plant pathogens of the genus Colletotrichum.
BMC Genomics. 2016 Aug 5;17():555. doi: 10.1186/s12864-016-2917-6

Alguns exemplos

May 12, 2020

Assemblies and annotations f "Genome compartmentalizati species divergence in the plan Zymoseptoria"

Feurtey, Alice; Lorrain, Cécile; Croll, Daniel; Eschenbrenner, Christoph; Freitag, Möller, Mareike; Schotanus, Klaas; Stukenbrock, Eva

These files are the assemblies and annotations produced and analyzed in the "Genome compartmentalization predates species divergence in the plant pat

Files (356.1 MB)

Name		
Annotations_2018_genomes_for_publication.tab md5:04b083a07d68729d551d5555c8e7e095		
Annotations_emapper_2018_genomes_for_publication.tab md5:c19bd5609fded06ca11cb22f6672d27c		
Expression_data_Ztritici_inplanta.xlsx md5:5db507efc693b329d23bec41b0e9c221		
Zpa63_softmasked_for_publication.fa md5:72c76aa814e2bf40d5e610aa9eaff398	41.8 MB	Download
Zt05_2019_for_publication.gff3 md5:5651e9c675691a5b2bd5bfd8c36651bf	9.4 MB	Download
Zt05_softmasked_for_publication.fa md5:32ab9ba9e846e3abf54dd5df1d9a8c34	41.7 MB	Download
Zt10_2019_for_publication.gff3 md5:e4f98fb346afea5f18ff243cfc6ff3db	9.1 MB	Download
Zt10_softmasked_for_publication.fa	39.6 MB	Download

Availability of data and materials

The datasets generated and analyzed during the current study are available in the NCBI Short Read Archive (https://www.ncbi.nlm.nih.gov/bioproject/?term=) under the BioProject accession numbers: PRJNA638605, PRJNA639021 (Zpa63), PRJNA638553 (Zb87), PRJNA638515 (Zp13), PRJNA638382 (Za17), PRJNA414407 (Zt05 and Zt10). All the data supporting the findings of this study are openly available at https://doi.org/10.5281/zenodo.3820378. The assembled genomes can be found at https://doi.org/10.5281/zenodo.3820378. The gene annotations are deposited at https://doi.org/10.5281/zenodo.3820378. The functional annotation pipeline, additional scripts and command lines used to create the results presented in this manuscript can be found at https://gitlab.gwdg.de/alice.feurtey/genome_architecture_zymoseptoria. In planta

Alguns exemplos

August 18, 2020

Dataset | Open Access

Mating-type locus rearrangements and shifts in thallism states in Citrus-associated Phyllosticta species

Desirrê A. L. Petters-Vandresen

Files related to the manuscript published in to Fungal Genetics and Biolo
with preprint available in bioRxiv (https://doi.org/10.1101/2020.04.14.04

Contains:

- 03 genome assemblies: Phyllosticta capitalensis LGMF01, Phyllosticta
LGMF06;

- 14 protein-coding gene annotation based in 14 Phyllosticta genomes;

- Mating-type locus annotation from the 14 Phyllosticta strains in GBK fo

Preview

FastQC v 0.11.8 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/) was employed to check the quality of reads after processing in Trimmomatic. *De novo* genome assemblies were generated with SPAdes v 3.13 (Bankevich et al., 2012), using default parameters. Contigs smaller than 500 bp were filtered and removed from the final assemblies, which were then evaluated with QUAST v 4.6.3 (Gurevich et al., 2013). Library and assembly statistics for the new assemblies are summarized in Table S1 and assemblies are available at Zenodo (https://doi.org/10.5281/zenodo.3750350).

with BLASTp. After confirmation, the gene annotations were further refined by comparison with the *MAT* loci from *Phyllosticta citricarpa* and some *Botryosphaeriaceae* species (Nagel et al., 2018). The sequences and annotations are deposited in Zenodo (https://doi.org/10.5281/zenodo.3750350). Functional domains in the annotated genes were determined using the Conserved Domain Search Service (CD-Search) from NCBI (Lu et al., 2020), using an e-value of 0.01 as threshold.

Códigos e scripts

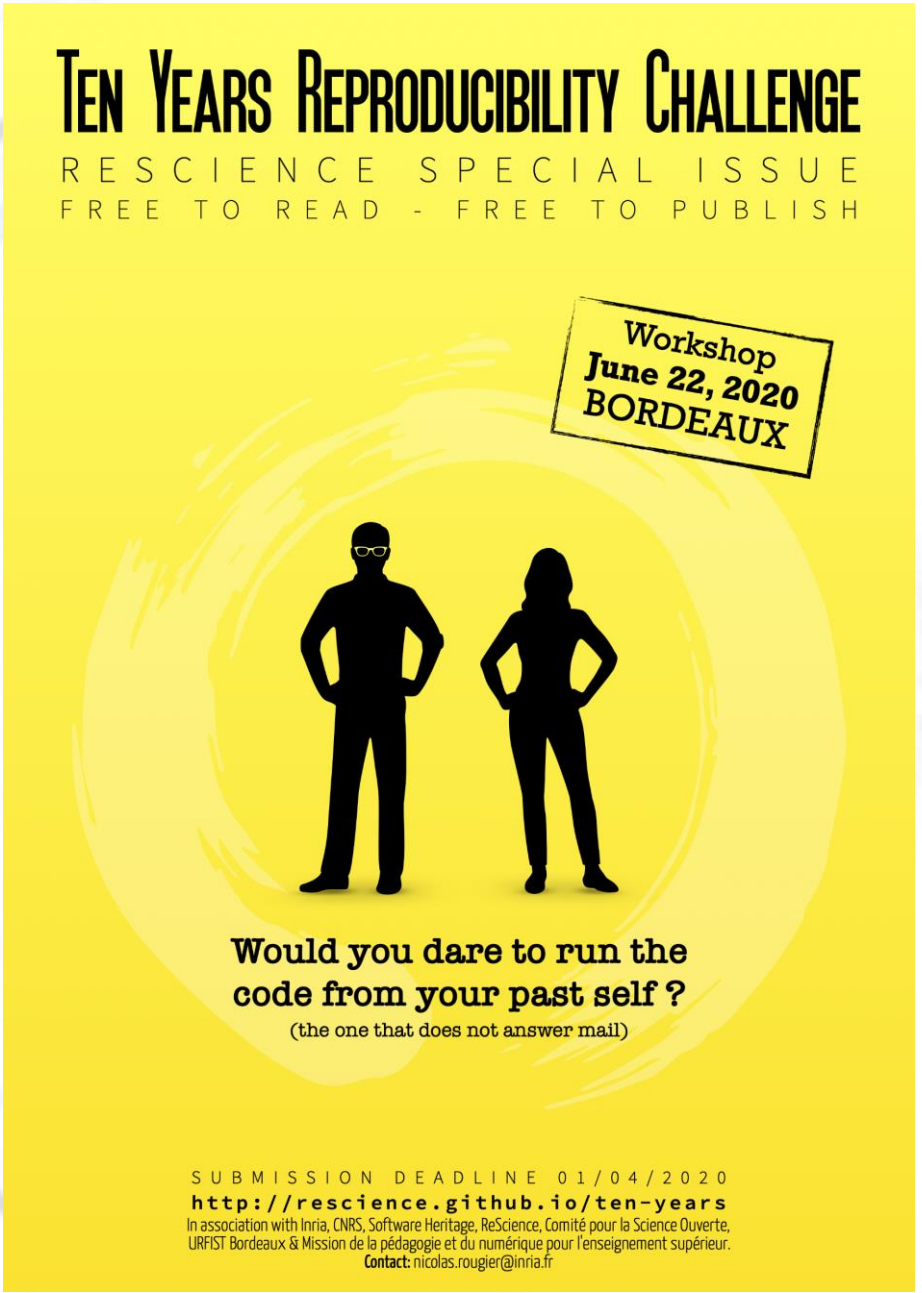
- Devem ser disponibilizados sempre que possível, devidamente comentados e de forma compreensível

- Garantem a reprodutibilidade do estudo e servem de base para vários estudos futuros

GitHub

SOURCEFORGE

GitLab



Alguns exemplos

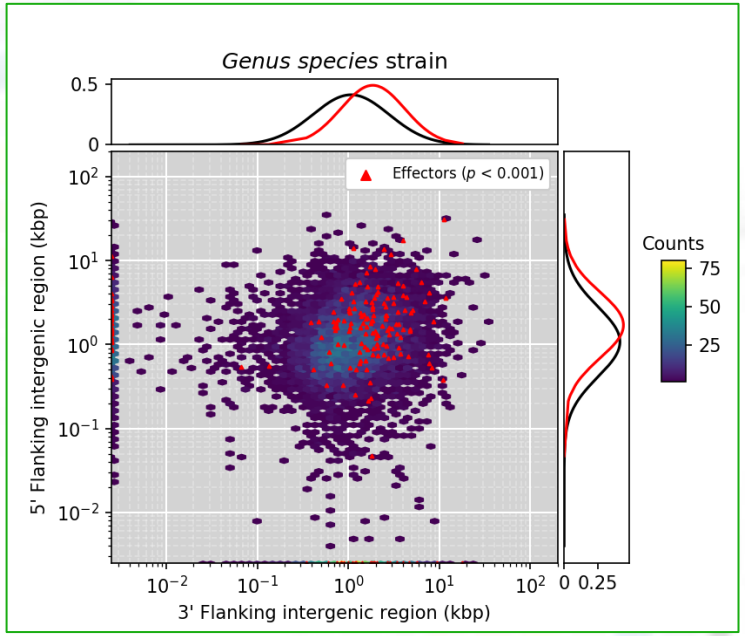
PlantDr430 / CSU_scripts

Code | Issues | Pull requests | Actions | Projects | Wiki | Security | Insights

master | 1 branch | 0 tags | Go to file | Add file | Code

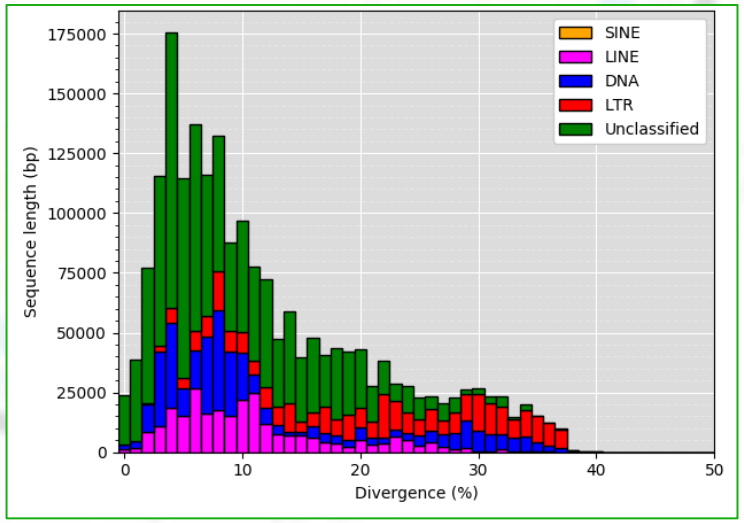
PlantDr430 Missed a line to comment out — 8ed9e1d on 7 Jun 2020 — 88 commits

.gitignore	Initial commit	2 years ago
Domain_enrichment.py	Utilized two multi-correction tests	12 months ago
Fungal_recombination.py	Missed a line to comment out	11 months ago
LICENSE	Initial commit	2 years ago
README.md	Updated genome_speed_hexbin image example	2 years ago
RIP_blast_analysis.py	Added gene counts function	15 months ago



Gene Density Compartmentalization

A custom script (https://github.com/PlantDr430/CSU_scripts/blob/master/genome_speed_hexbins.py) was used to calculate local gene density measured as 5′ and 3′ flanking distances between neighboring genes (intergenic regions). To statistically



Alguns exemplos

G

Genome_architecture_Zymoseptoria

Project ID: 8197

Star 0

26 Commits **1** Branch **0** Tags **1.9 MB** Files **1.9 MB** Storage

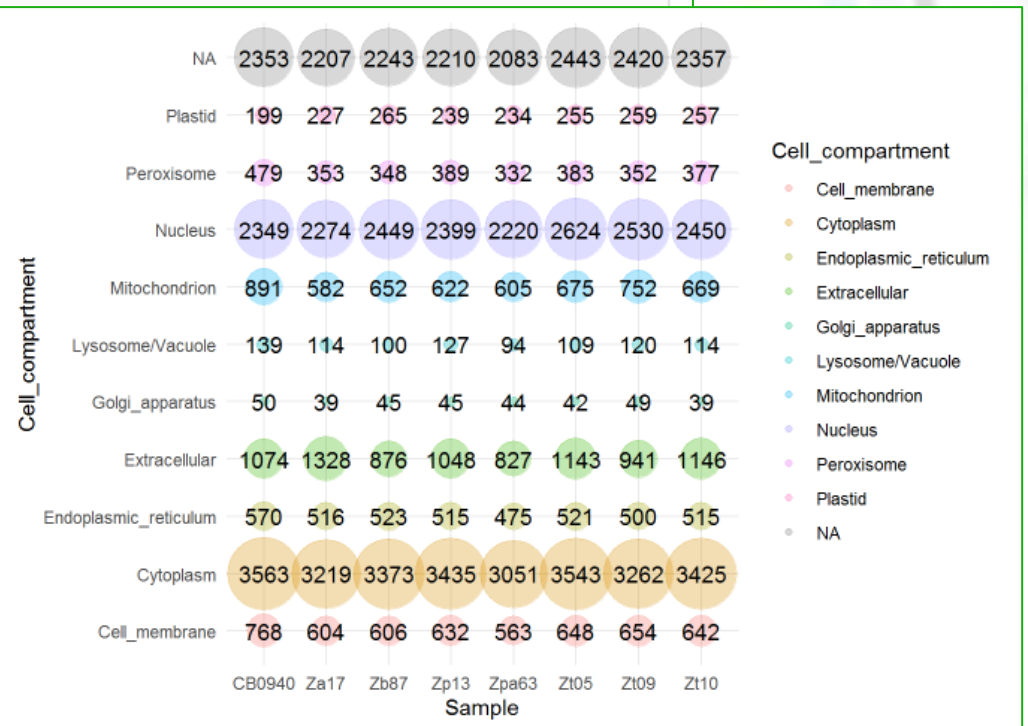
master genome_architecture_zymoseptoria History Find file Clone

Second trial at clean up

alice.feurtey authored 8 months ago

README No license. All rights reserved

Name	Last commit
0_Assemblies	Second trial at clean up
1_Gene_prediction	Add schematic pipeline
2_Functional_predictions	Delete Parsing_functions_V1_0.py



https://doi.org/10.5281/zenodo.3820378. The functional annotation pipeline, additional scripts and command lines used to create the results presented in this manuscript can be found at https://gitlab.gwdg.de/alice.feurtey/genome_architecture_zymoseptoria. In planta

Tabelas

- Armazenam grandes quantidades de informação com alto nível de detalhamento
- Úteis para leitores mais especializados e que precisem consultar detalhes específicos do estudo
- Auxiliam na seleção de genes candidatos para estudos funcionais
- Tabelas maiores geralmente incluídas como material suplementar

Alguns exemplos

Adaptado de:
PETTERS-VANDRESEN et al. 2020. **Fungal Genetics and Biology.** DOI: 10.1016\j.fgb.2020.103444

Table 1
Genome and strain information of *Phyllosticta* spp. evaluated in this study.

Species	Strain[a]	Host	Origin	Thallism	Mating-type	Mating-locus location	Genome size (bp)	Contigs	N50	L50	GC content	Repeat content	Predicted genes	BUSCO[b]	Assembly
P. capitalensis	**CBS 128856**	*Stanhopea* sp.	Brazil	Homothallic	Both	Scaffold 10	32,461,131	14	2,860,346	5	54.58%	1.54%	9977	97.9%	(Guarnaccia et al., 2019)
	Gm33	*Citrus sinensis*	USA	Homothallic	Both	Contigs 513 and 1011	32,454,403	1341	51,729	184	54.56%	0.49%	10,183	94.4%	(Wang et al., 2016)
	LGMF 01	*Citrus latifolia* (leaf)	Brazil	Homothallic	Both	Contig 24	32,606,250	231	1,366,738	9	54.48%	0.15%	9953	98%	This study
P. citriasiana	**CBS 120486**	*Citrus maxima* (fruit)	Thailand	Heterothallic	*MAT1-1*	Scaffold 34	32,696,106	133	807,147	14	51.56%	8.32%	9282	98.1%	(Guarnaccia et al., 2019)
	CGMCC 3.14344	*Citrus* sp.	China	Heterothallic	*MAT1-2*	Unitig 22	34,225,214	92	968,885	10	51.42%	14.50%	9291	97.9%	(Wang et al., 2020)
P. citribraziliensis	**CBS 100098**	*Citrus* sp. (leaf)	Brazil	Heterothallic	*MAT1-1*	Scaffold 7	31,670,975	32	1,720,616	7	54.17%	6%	9574	98%	(Guarnaccia et al., 2019)
	LGMF 08	*Citrus* sp. (leaf)	Brazil	Heterothallic	*MAT1-1*	Contig 61	31,002,620	563	263,424	40	54.34%	4.83%	9941	97.9%	This study
P. citricarpa	**CBS 127454**	*Citrus limon*	Australia	Heterothallic	*MAT1-2*	Scaffold 46	28,952,665	152	440,231	23	54.60%	1.30%	9108	96.1%	(Guarnaccia et al., 2019)
	CPC 27913	*Citrus sinensis* (leaf litter)	Malta	Heterothallic	*MAT1-2*	Scaffold 20	32,267,666	82	900,945	13	52.56%	8.07%	9352	97.6%	(Guarnaccia et al., 2019)
	Gc 12	*Citrus sinensis*	USA	Heterothallic	*MAT1-2*	Contigs 1345, 2477, 3787	31,127,197	5748	21,637	411	53.05%	5.93%	9472	94.5%	(Wang et al., 2016)
	CGMCC 3.14348	N/A	China	Heterothallic	*MAT1-1*	Contigs 4070 and 4071	32,007,210	6716	11,522	811	52.57%	7.94%	9768	87.5%	GenBank Assembly: GCA_000382785.1
	LGMF 06	*Citrus sinensis*	Brazil	Heterothallic	*MAT1-2*	Contig 51	32,021,677	354	421,474	28	52.68%	0.64%	11,217	97.8%	This study
P. citrichinaensis	**CBS 130529**	*Citrus maxima* (leaf)	China	Homothallic	Both	Scaffolds 6 and 9	29,162,704	25	2,710,567	4	55.07%	2.99%	9131	97.5%	(Guarnaccia et al., 2019)
P. paracitricarpa	**CBS 141357**	*Citrus limon* (leaf litter)	Greece	Heterothallic	*MAT1-2*	Scaffold 48	29,529,839	134	510,184	23	54.35%	2.45%	9083	96.2%	(Guarnaccia et al., 2019)

N/A: not available or not applicable to the present study.

[a] Type strains included in the analysis are indicated in **bold**. Culture collection abbreviations: CBS = Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands; CPC = Collection of Pedro W. Crous, held at the Westerdijk Fungal Biodiversity Institute; CGMCC = China General Microbiological Culture Collection Center, Chinese Academy of Sciences, Beijing, China; LGMF = Laboratório de Bioprospecção e Genética Molecular de Microrganismos, Universidade Federal do Paraná, Paraná, Brazil.

[b] BUSCO completeness assessed with the Pezizomycotina dataset.

Alguns exemplos

Species	*Zymoseptoria tritici*		*Zymoseptoria pseudotritici*	*Zymoseptoria brevis*	*Zymoseptoria ardabiliae*	*Zymoseptoria passerinii*
Isolate	Zt05	Zt10	Zp13	Zb87	Za17	Zpa63
Origin	Denmark	Iran, Ilam province	Iran, Ardabil province	Iran	Iran, Ardabil province	USA
Host	*Triticum aestivum*	*Triticum aestivum*	*Dactylis glomerata*	*Phalaris paradoxa*	*Lolium perenne*	*Hordeum vulgare*
Year (of isolation)	2004	2001	2004		2004	
Contig number	30	19	42	29	50	103
Total length (bp)	41,240,984	39,248,105	40,312,446	41,586,671	38,100,668	41,398,787
Mean contig size (bp)	1,374,699	2,065,690	59,820	1,434,023	762,013	401,930
N50	2,454,671	2,925,395	2,115,121	2,744,794	1,156,695	737,698
L50	6	5	7	7	11	18
Contigs with telomeric repeats on both ends	12	19	5	9	0	0
Complete BUSCO genes (%)	98.4	98.7	98.5	97.0	98.2	97.5
Number of genes	12,386	11,991	11,661	11,480	11,463	10,528
Repeat content (%)	19.9	16.5	20.8	29.2	18.2	31.4
Percentage of non-core sequences compared to the IPO323 reference	12.49	8.69	4.27	4.6	3.45	6.85
NCBI Biosample	SAMN04494882	SAMN02981321	SAMN02981322	SAMN03294124	SAMN02981326	SAMN02981330

Adaptado de:
FEURTEY et al. 2020. **BMC Genomics.** DOI: 10.1186/s12864-020-06871-w

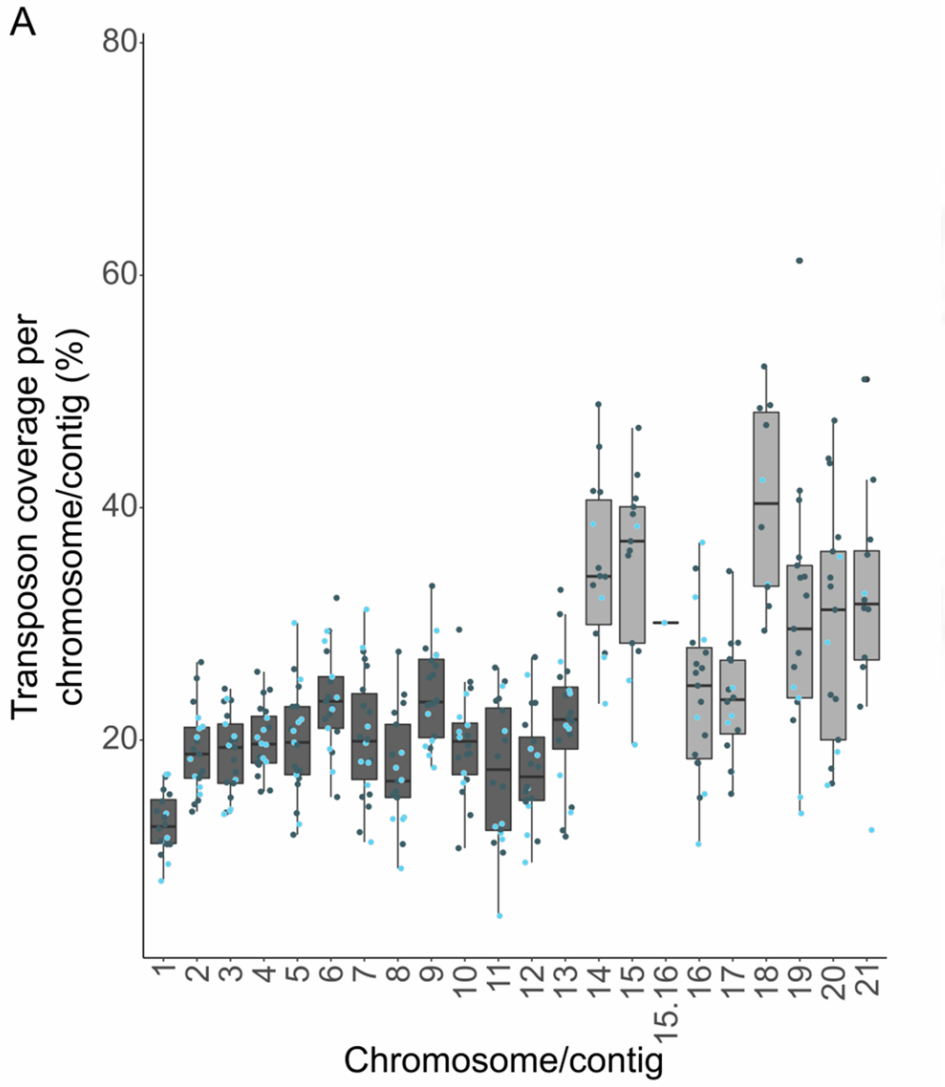
Figuras

- Úteis para todos os tipos de leitores do trabalho: entendimento de tendências gerais e dos principais resultados de um estudo

- Presentes no texto principal e material suplementar

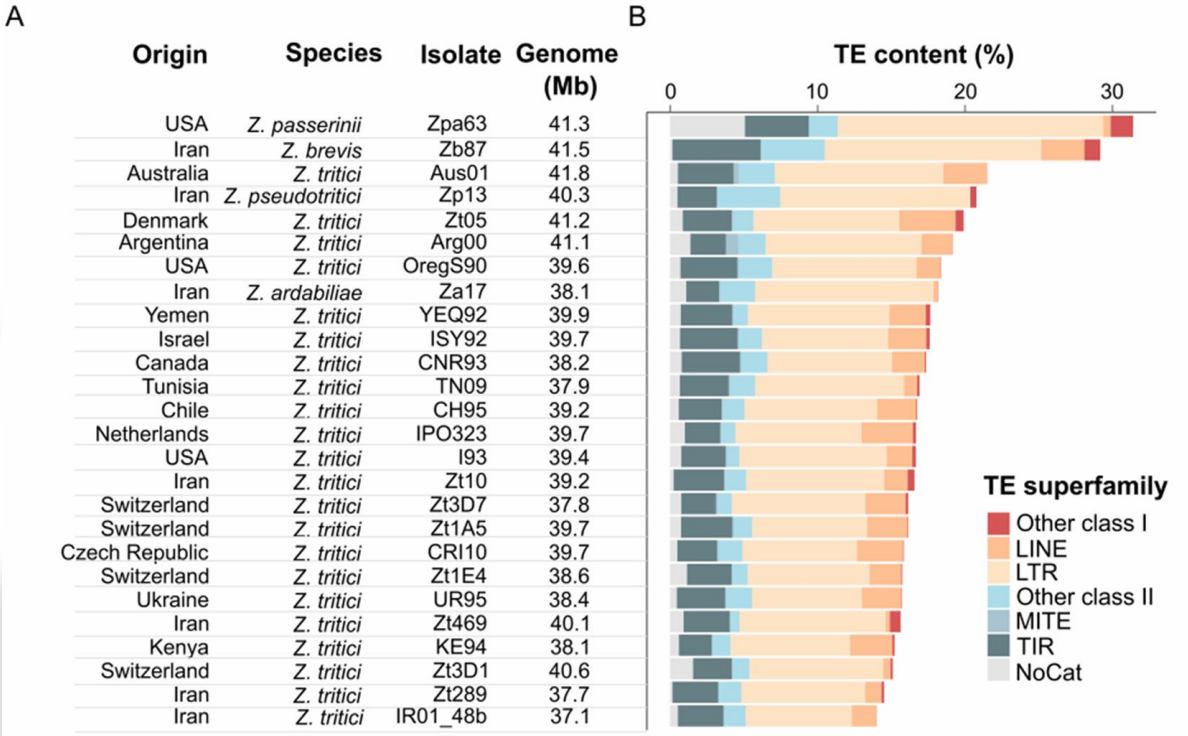
- **Cenário ideal:** figuras que reúnam e apresentem os diversos resultados e aspectos importantes de um estudo

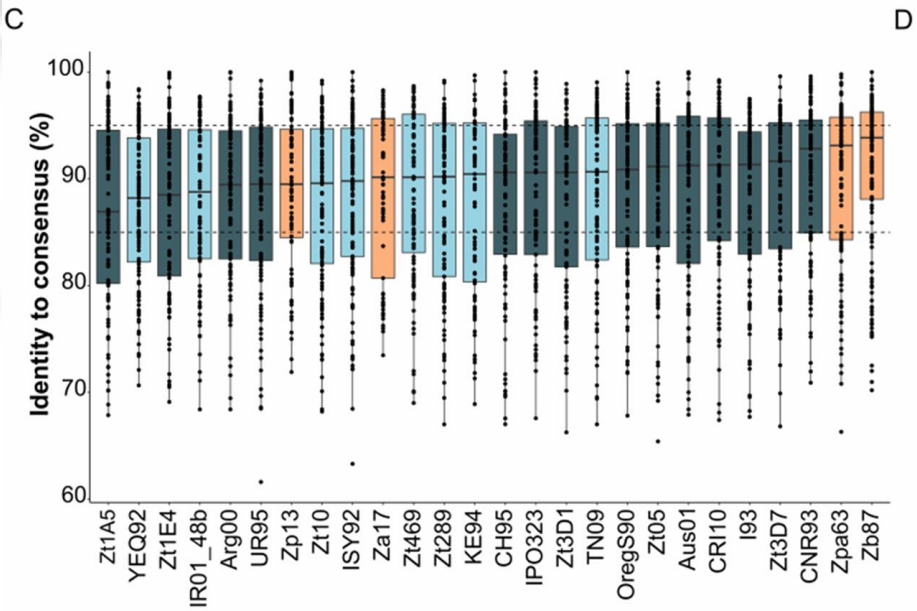
Gráfico de barras e box-plot

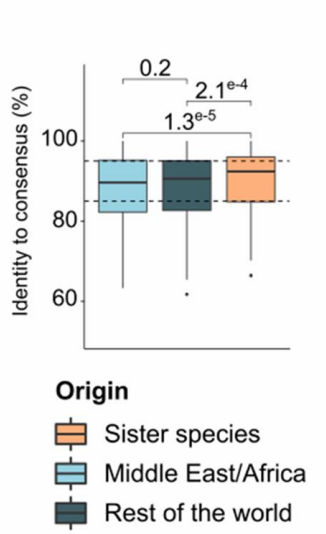


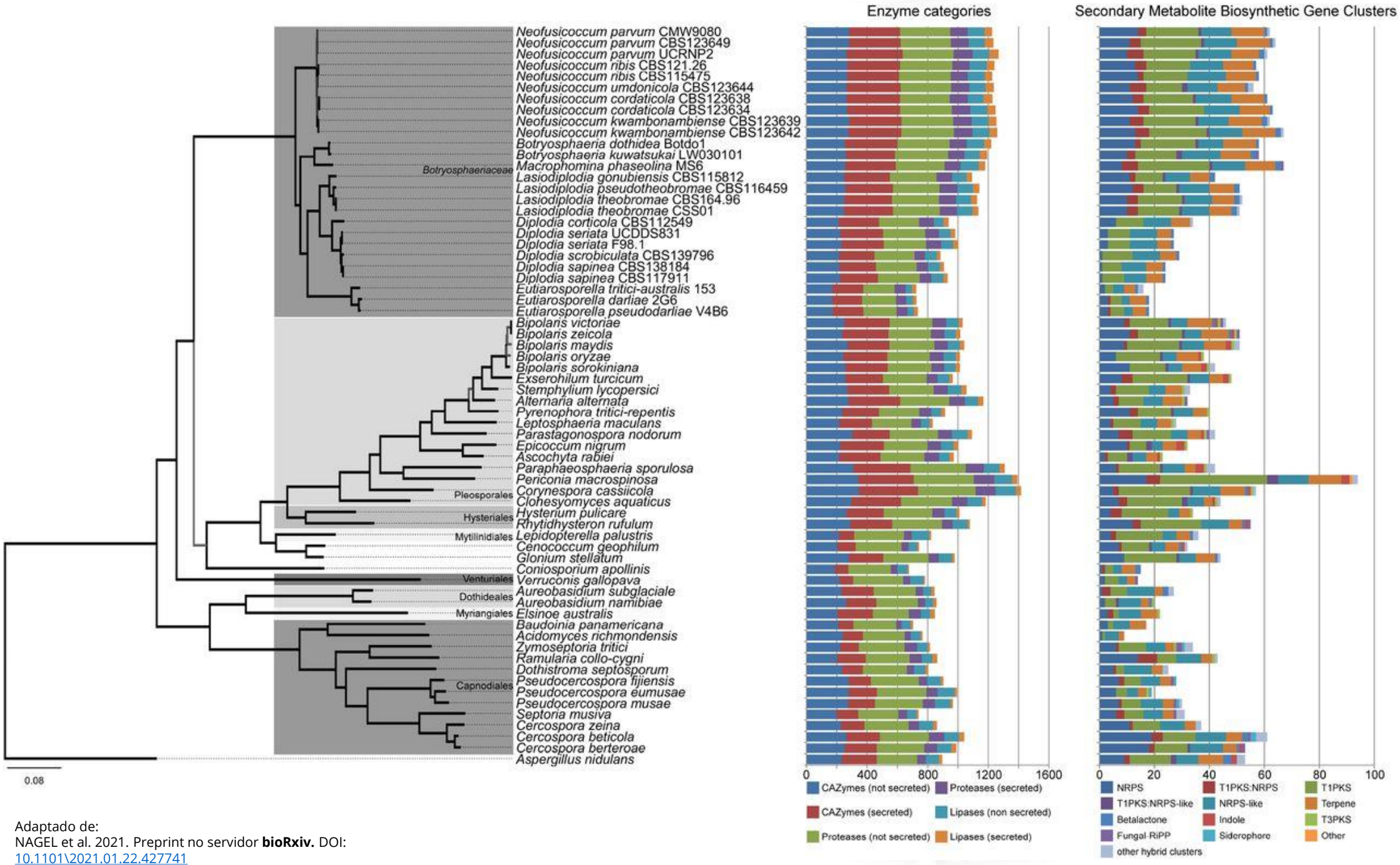
A

Origin	Species	Isolate	Genome (Mb)
USA	*Z. passerinii*	Zpa63	41.3
Iran	*Z. brevis*	Zb87	41.5
Australia	*Z. tritici*	Aus01	41.8
Iran	*Z. pseudotritici*	Zp13	40.3
Denmark	*Z. tritici*	Zt05	41.2
Argentina	*Z. tritici*	Arg00	41.1
USA	*Z. tritici*	OregS90	39.6
Iran	*Z. ardabiliae*	Za17	38.1
Yemen	*Z. tritici*	YEQ92	39.9
Israel	*Z. tritici*	ISY92	39.7
Canada	*Z. tritici*	CNR93	38.2
Tunisia	*Z. tritici*	TN09	37.9
Chile	*Z. tritici*	CH95	39.2
Netherlands	*Z. tritici*	IPO323	39.7
USA	*Z. tritici*	I93	39.4
Iran	*Z. tritici*	Zt10	39.2
Switzerland	*Z. tritici*	Zt3D7	37.8
Switzerland	*Z. tritici*	Zt1A5	39.7
Czech Republic	*Z. tritici*	CRI10	39.7
Switzerland	*Z. tritici*	Zt1E4	38.6
Ukraine	*Z. tritici*	UR95	38.4
Iran	*Z. tritici*	Zt469	40.1
Kenya	*Z. tritici*	KE94	38.1
Switzerland	*Z. tritici*	Zt3D1	40.6
Iran	*Z. tritici*	Zt289	37.7
Iran	*Z. tritici*	IR01_48b	37.1



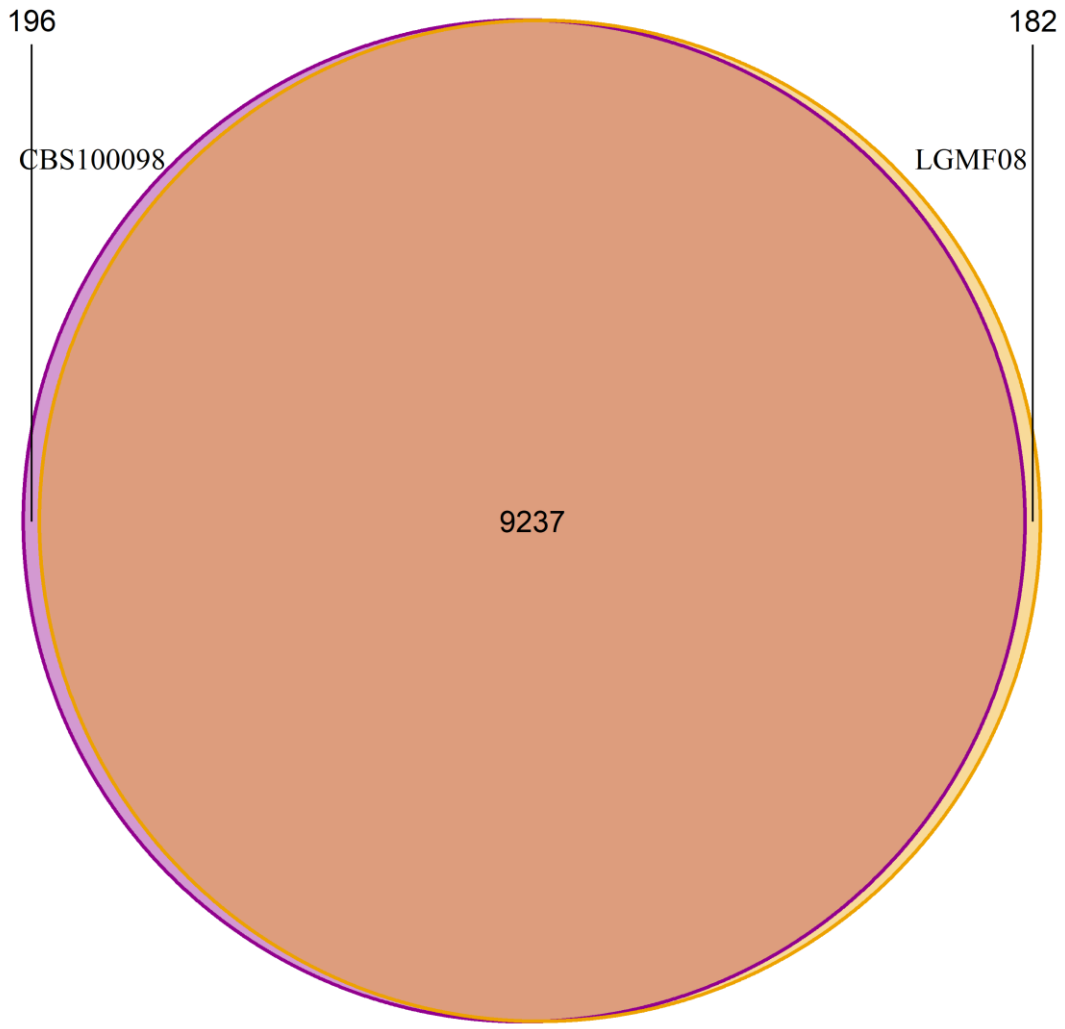






Adaptado de:
NAGEL et al. 2021. Preprint no servidor **bioRxiv.** DOI: 10.1101\2021.01.22.427741

Diagrama de Venn



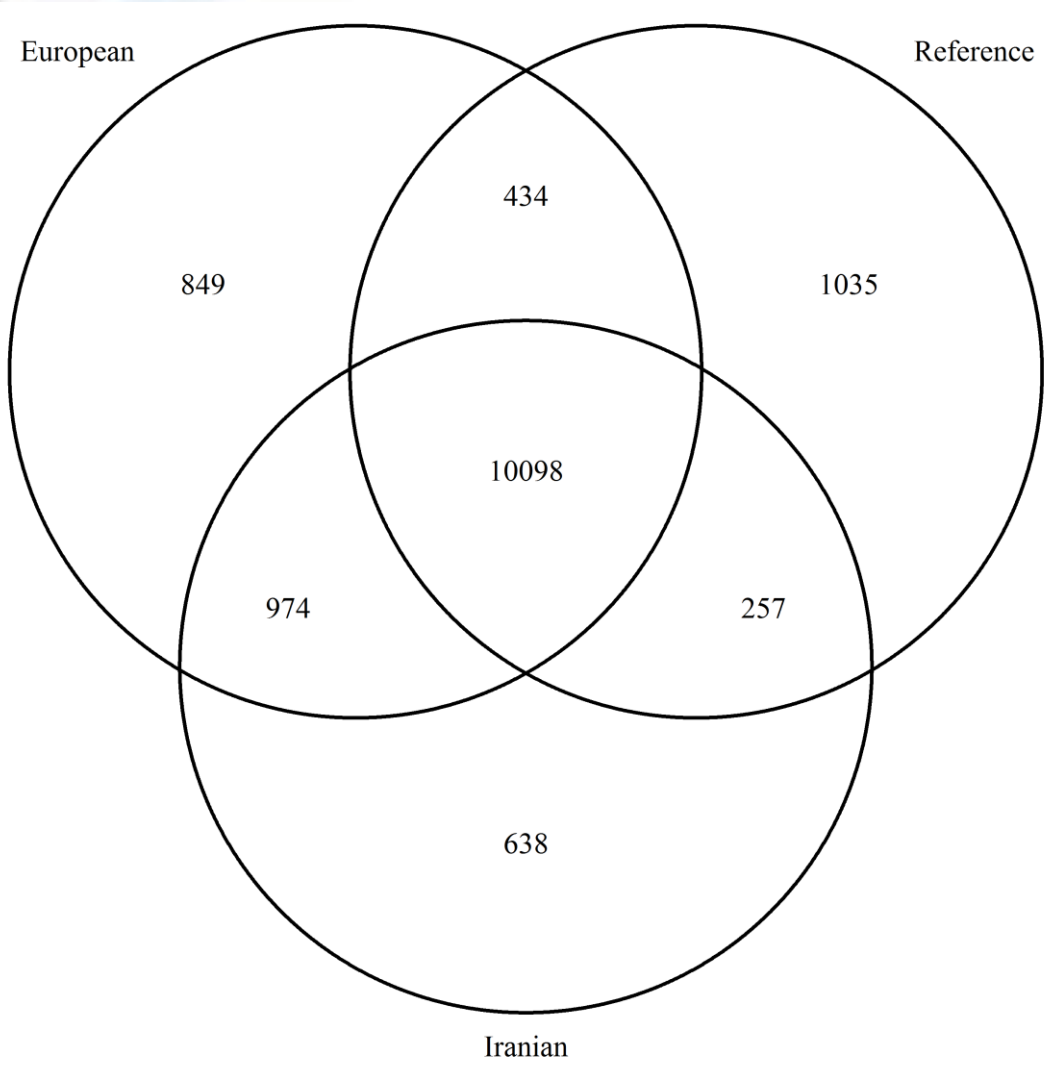
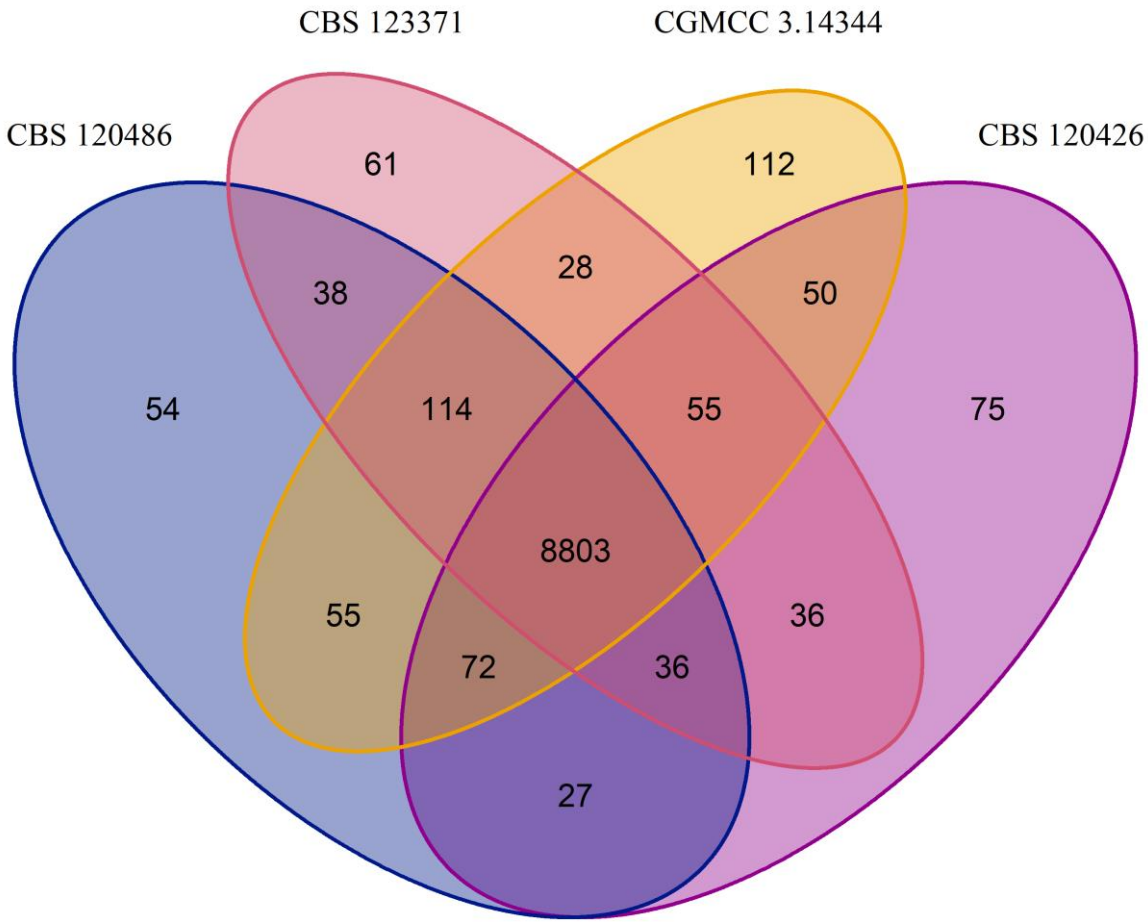


Diagrama de Venn



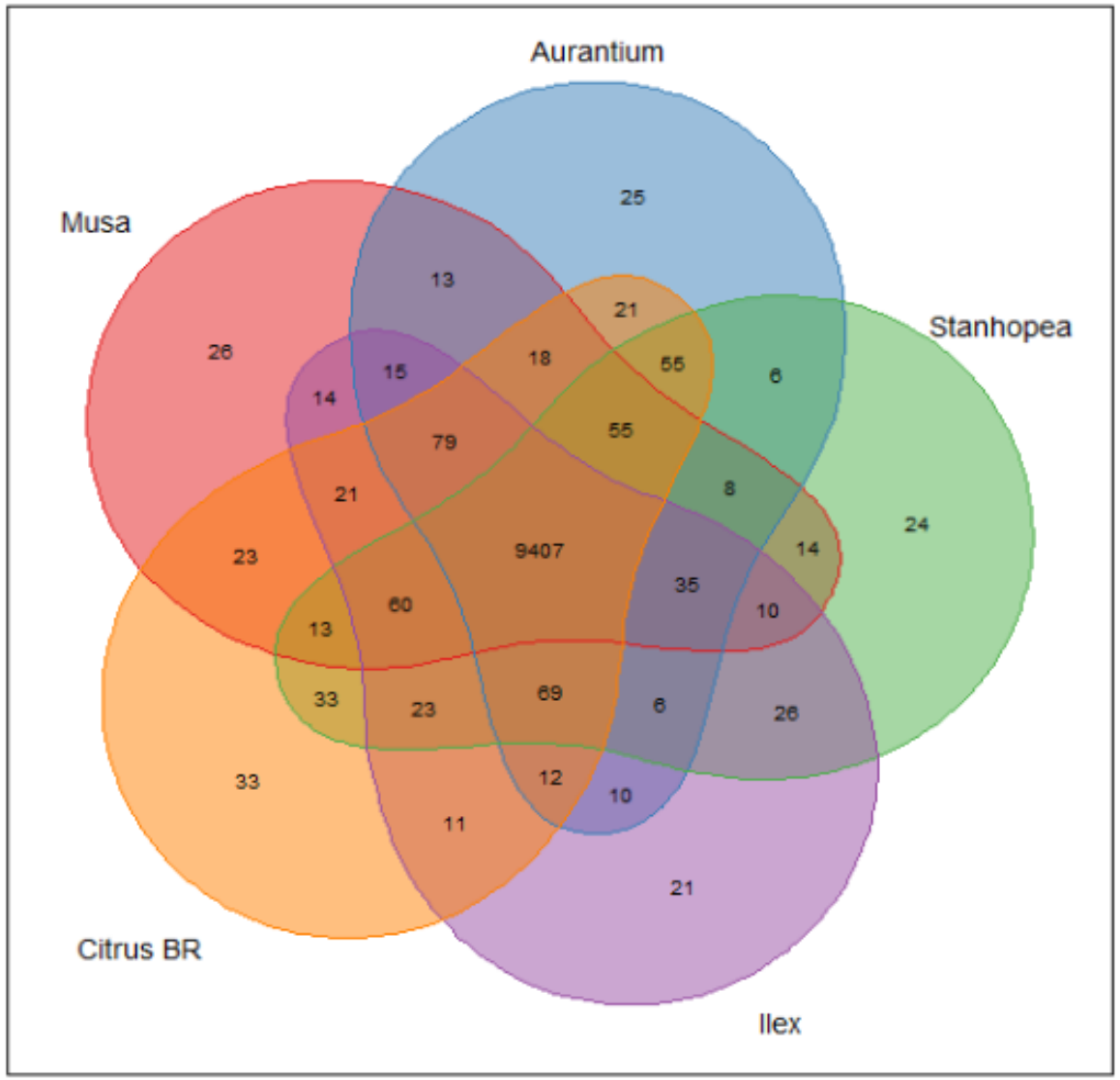
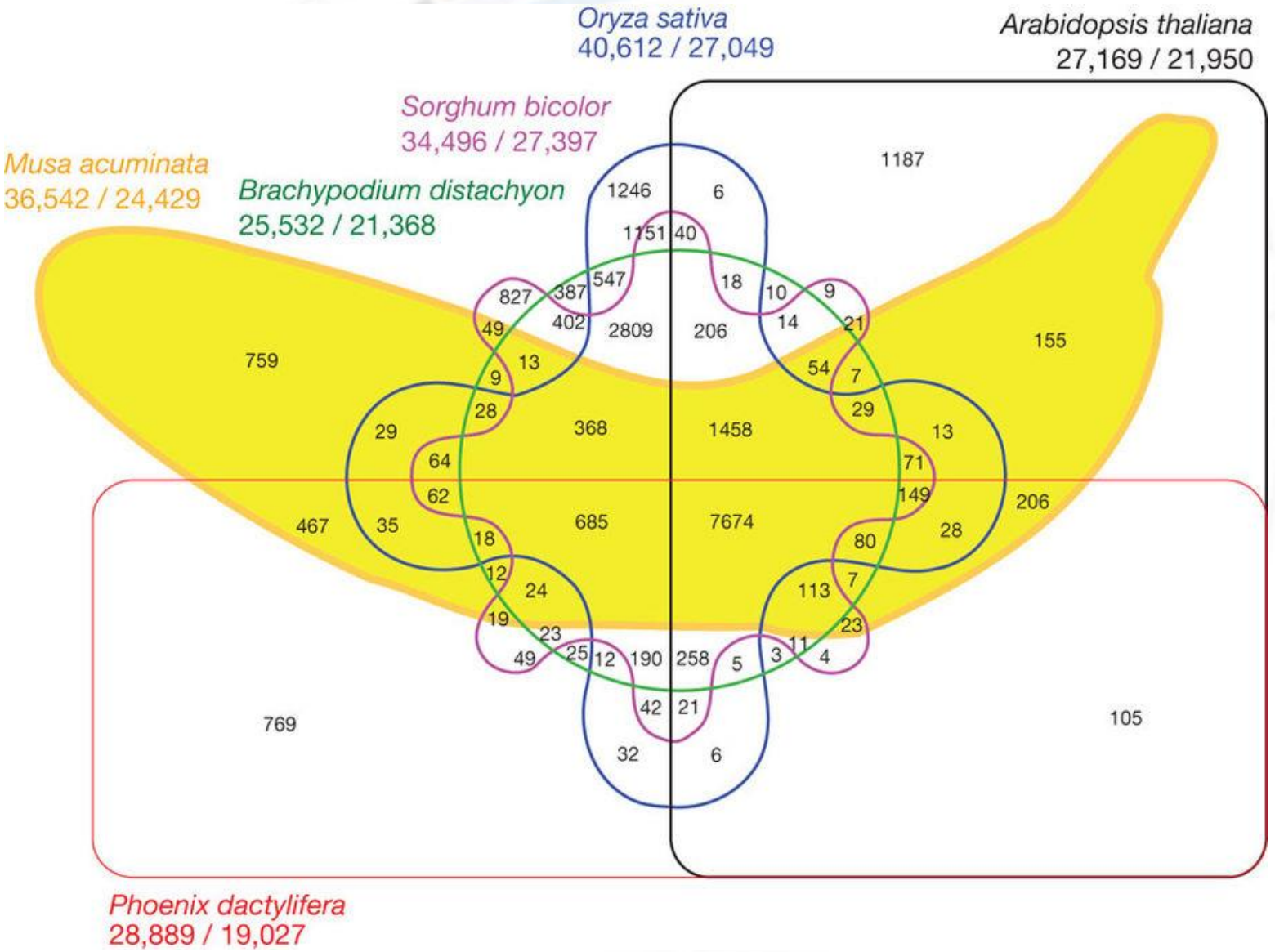
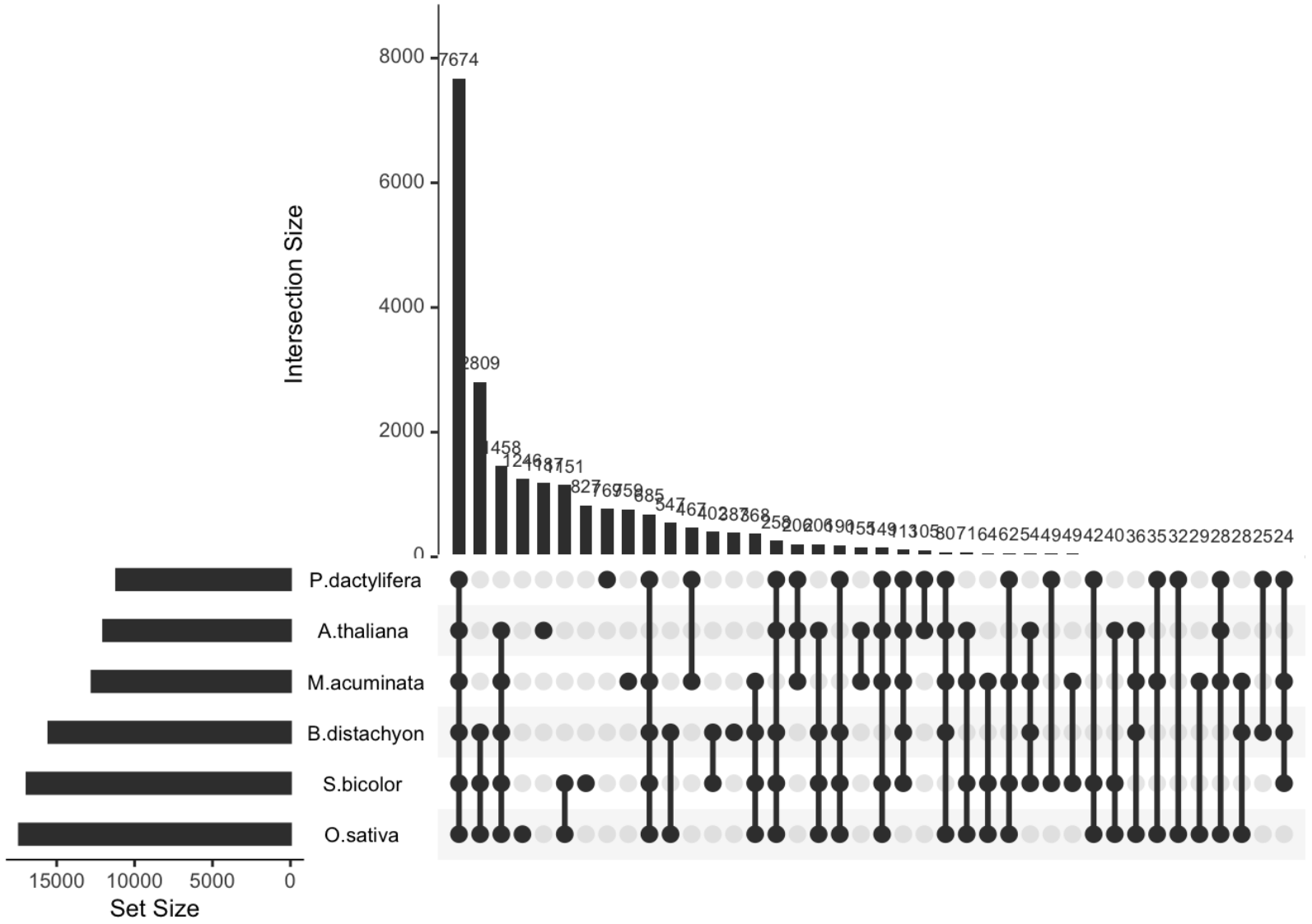


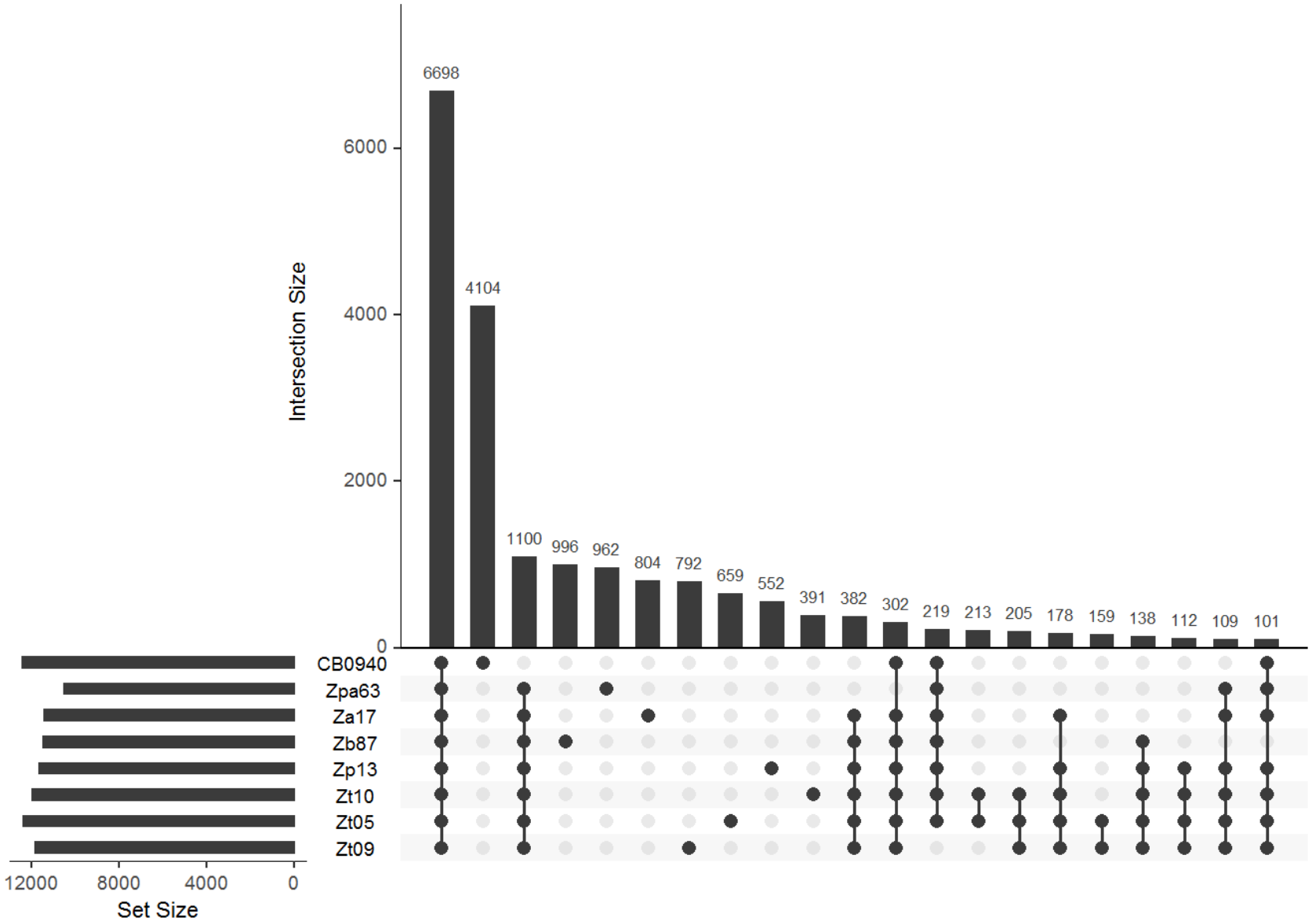
Diagrama de Venn



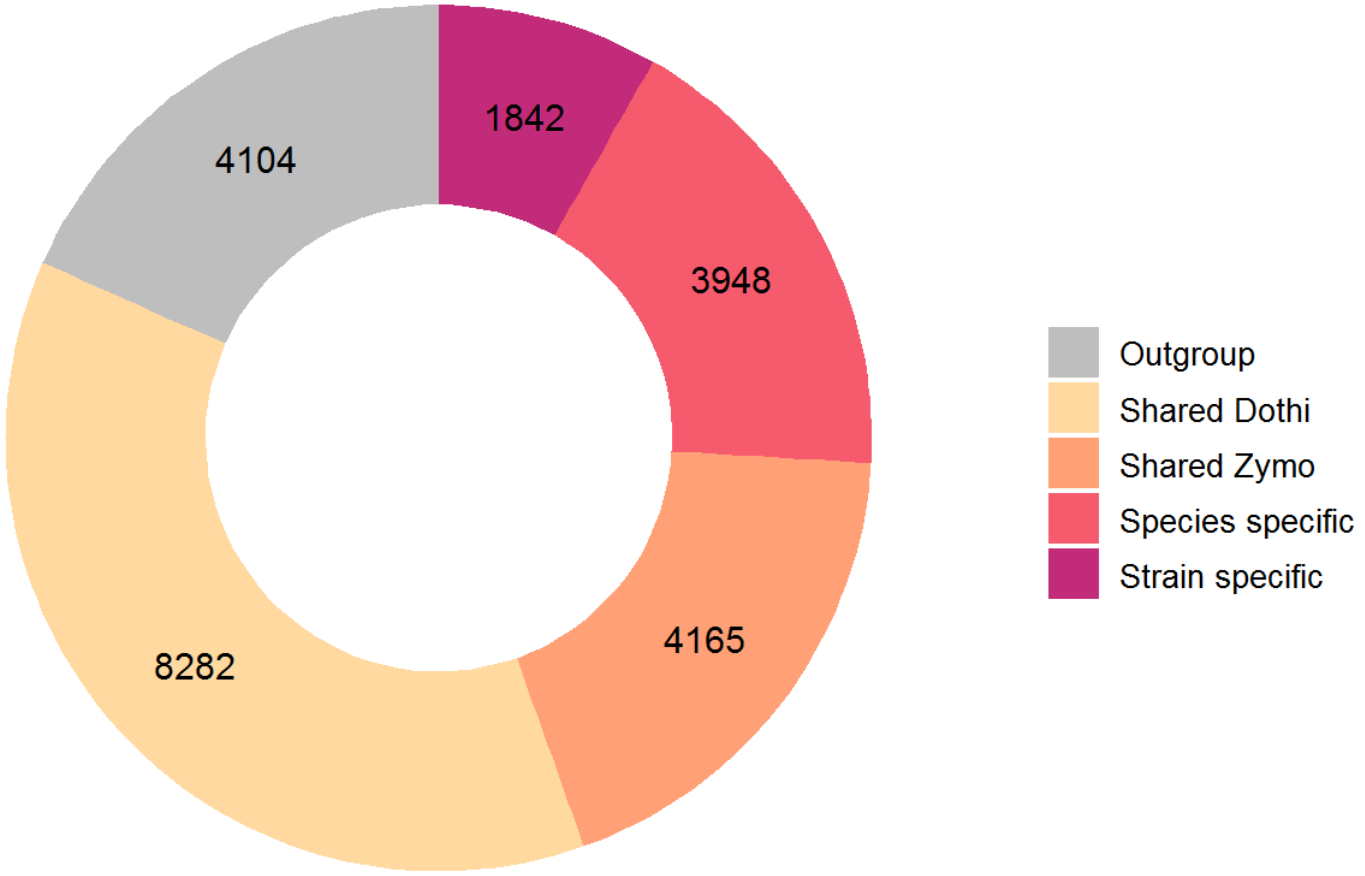
Upset plot


Intersection Size
8000
6000
4000
2000
0
7674
2809
P.dactylifera
A.thaliana
M.acuminata
B.distachyon
S.bicolor
O.sativa
15000
10000
5000
0
Set Size

UpSet plot


Intersection Size
6698
4104
1100
996
962
804
792
659
552
391
382
302
219
213
205
178
159
138
112
109
101
6000
4000
2000
0
CB0940
Zpa63
Za17
Zb87
Zp13
Zt10
Zt05
Zt09
12000
8000
4000
0
Set Size

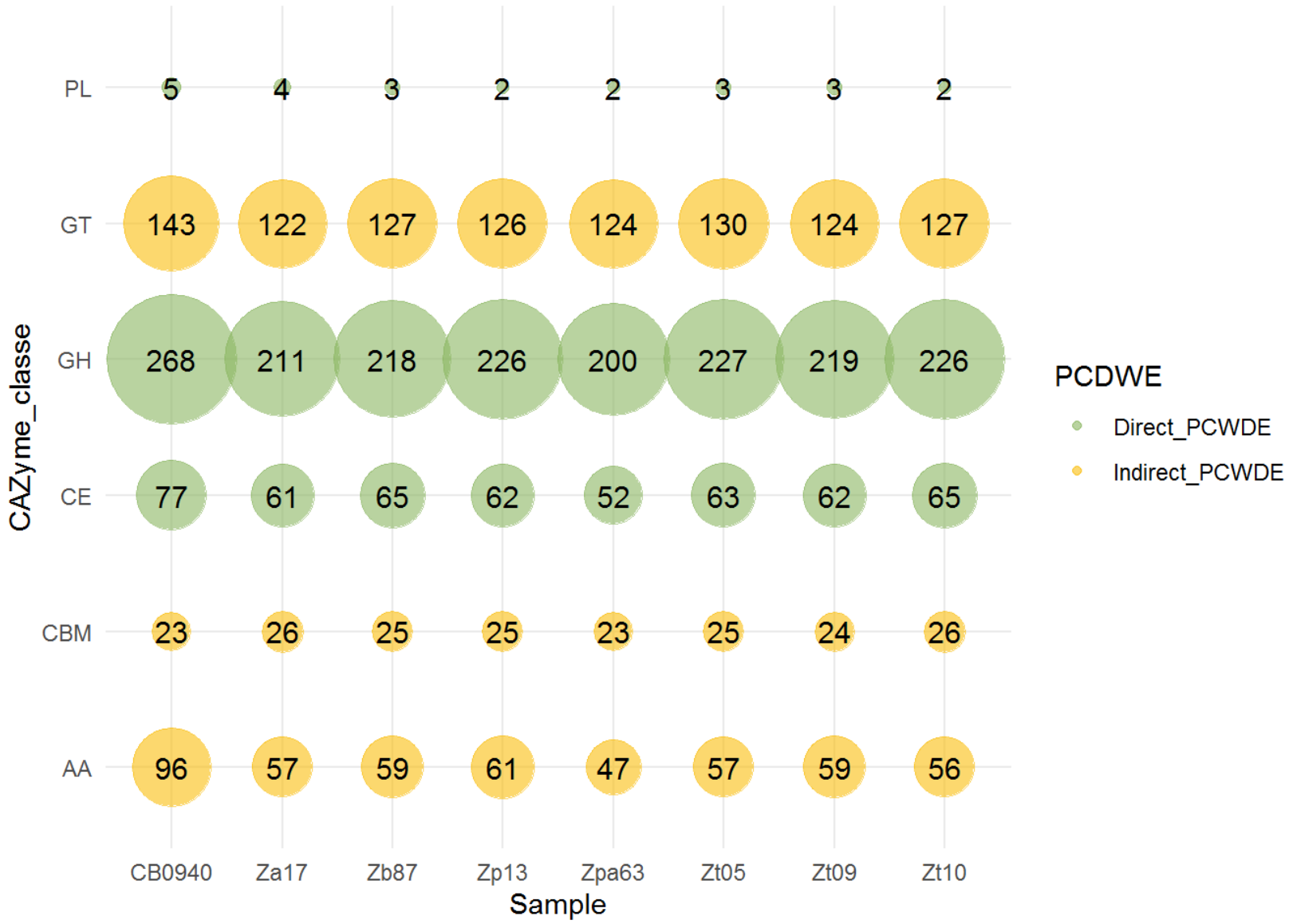
Donut plot


4104
1842
3948
8282
4165
Outgroup
Shared Dothi
Shared Zymo
Species specific
Strain specific

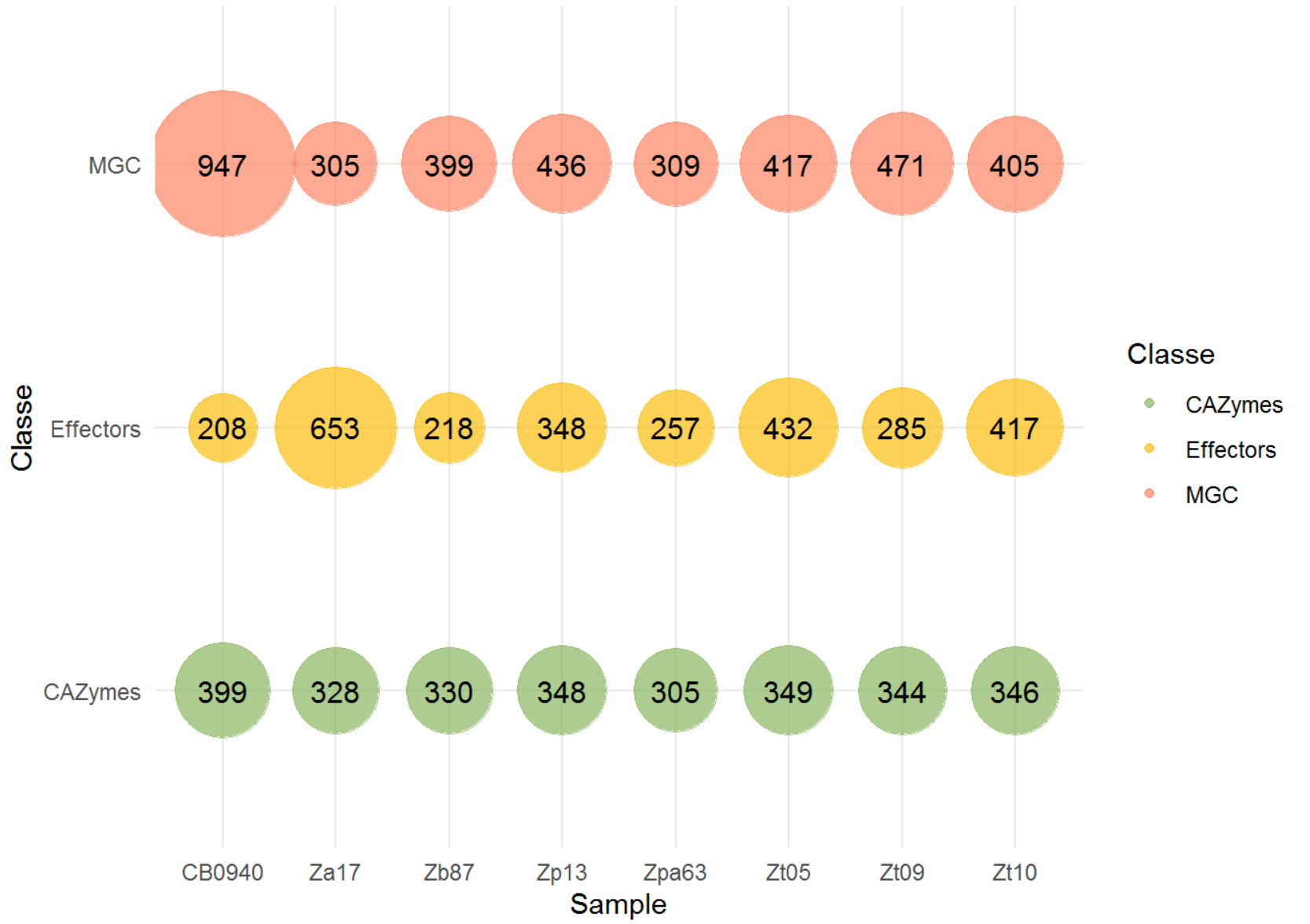
Bubble plot


NA 2353 2207 2243 2210 2083 2443 2420 2357
Plastid 199 227 265 239 234 255 259 257
Peroxisome 479 353 348 389 332 383 352 377
Nucleus 2349 2274 2449 2399 2220 2624 2530 2450
Mitochondrion 891 582 652 622 605 675 752 669
Lysosome/Vacuole 139 114 100 127 94 109 120 114
Golgi_apparatus 50 39 45 45 44 42 49 39
Extracellular 1074 1328 876 1048 827 1143 941 1146
Endoplasmic_reticulum 570 516 523 515 475 521 500 515
Cytoplasm 3563 3219 3373 3435 3051 3543 3262 3425
Cell_membrane 768 604 606 632 563 648 654 642
Cell_compartment
CB0940 Za17 Zb87 Zp13 Zpa63 Zt05 Zt09 Zt10
Sample
Cell_compartment
Cell_membrane
Cytoplasm
Endoplasmic_reticulum
Extracellular
Golgi_apparatus
Lysosome/Vacuole
Mitochondrion
Nucleus
Peroxisome
Plastid
NA

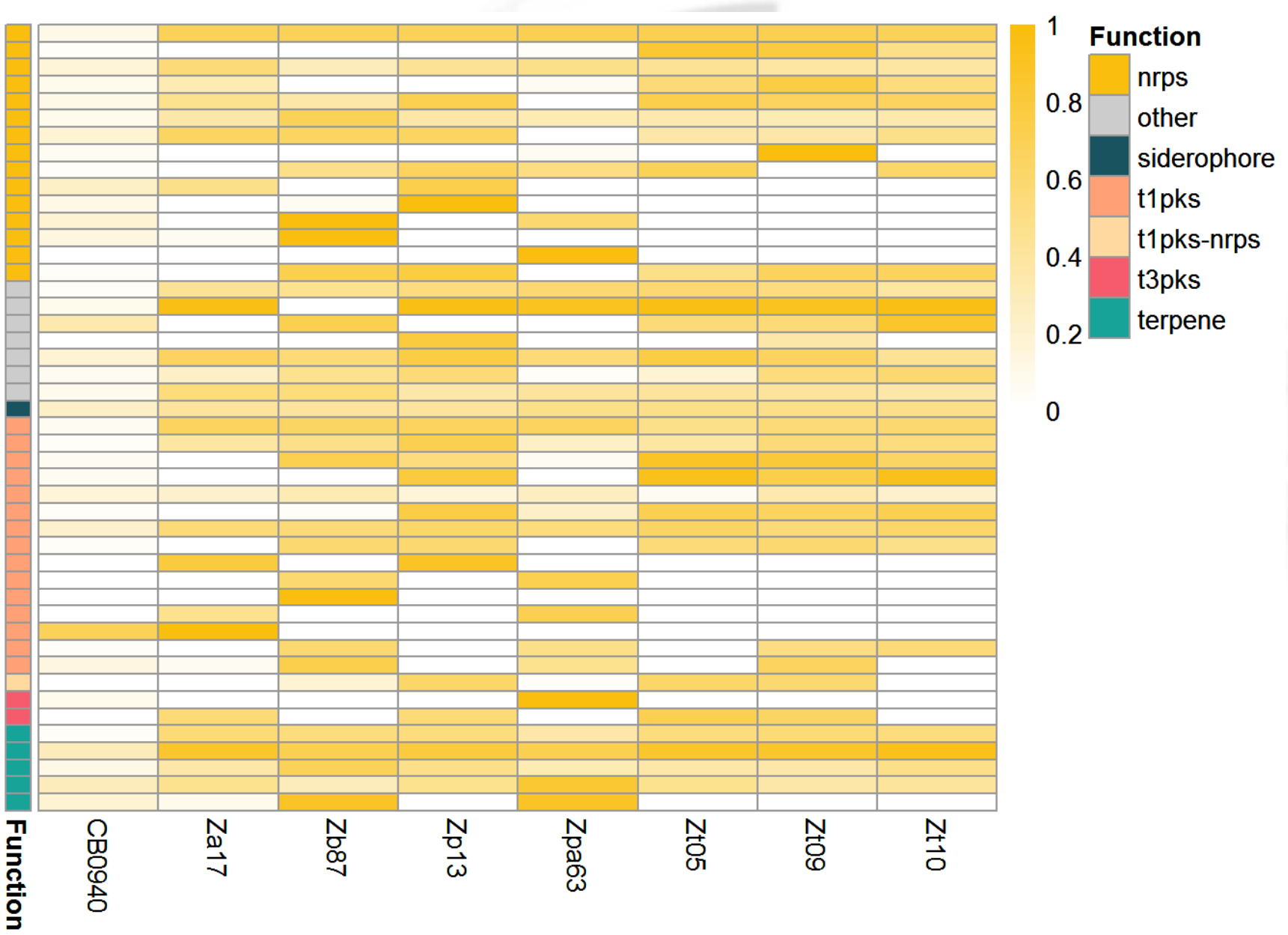
Bubble plot

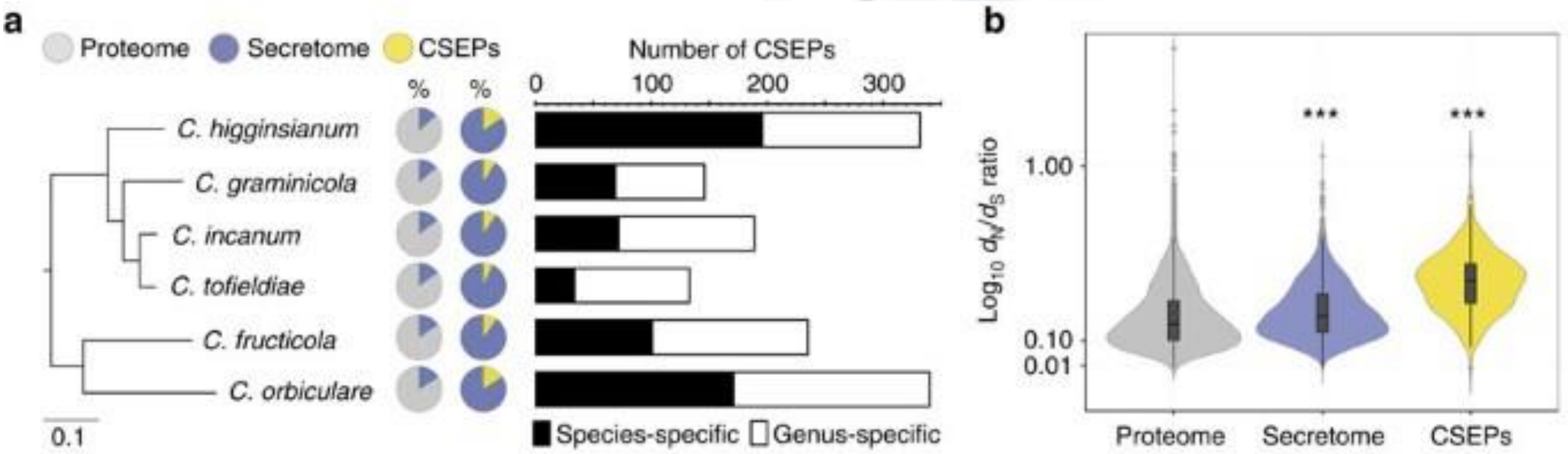

PL
GT
GH
CE
CBM
AA
CAZyme_classe
5 4 3 2 2 3 3 2
143 122 127 126 124 130 124 127
268 211 218 226 200 227 219 226
77 61 65 62 52 63 62 65
23 26 25 25 23 25 24 26
96 57 59 61 47 57 59 56
CB0940 Za17 Zb87 Zp13 Zpa63 Zt05 Zt09 Zt10
Sample
PCDWE
Direct_PCWDE
Indirect_PCWDE

Bubble plot


MGC
947
305
399
436
309
417
471
405
Effectors
208
653
218
348
257
432
285
417
CAZymes
399
328
330
348
305
349
344
346
Classe
CB0940
Za17
Zb87
Zp13
Zpa63
Zt05
Zt09
Zt10
Sample
Classe
CAZymes
Effectors
MGC

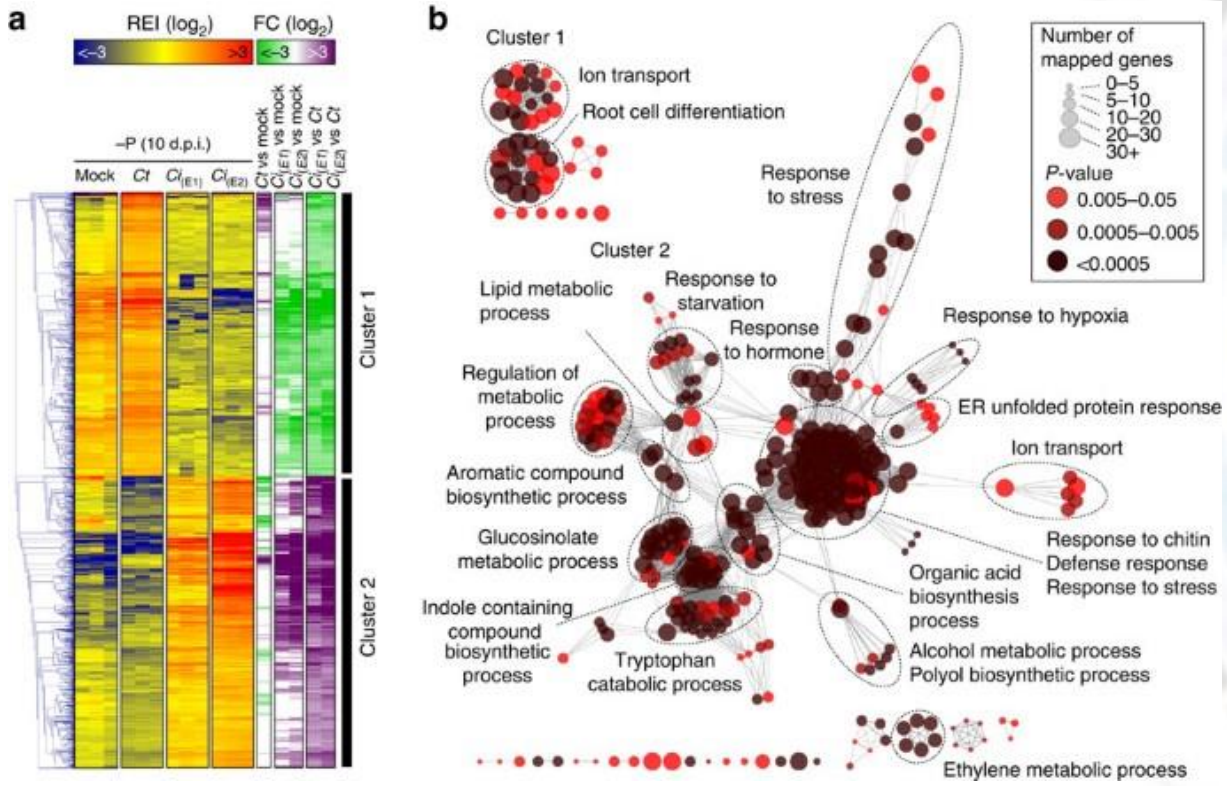
Heatmap


Function
CB0940
Za17
Zb87
Zp13
Zpa63
Zt05
Zt09
Zt10
1
0.8
0.6
0.4
0.2
0
Function
nrps
other
siderophore
t1pks
t1pks-nrps
t3pks
terpene

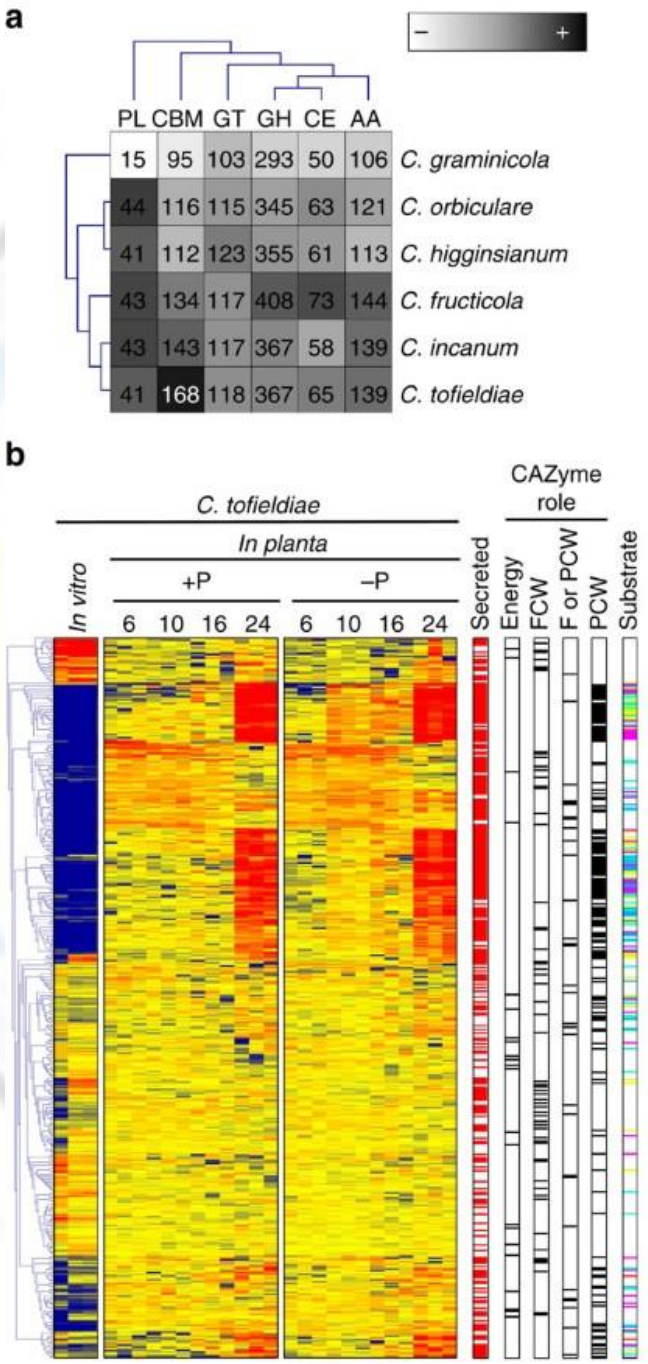


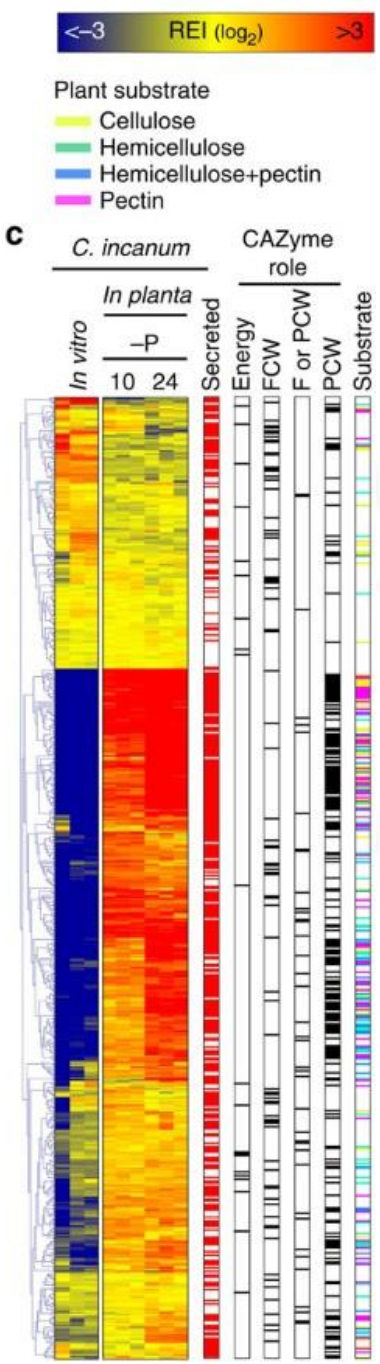
Adaptado de:
HACQUARD et al. 2016. **Nature Communications.** DOI: 10.1038/ncomms11362

Combinando dados de expressão gênica

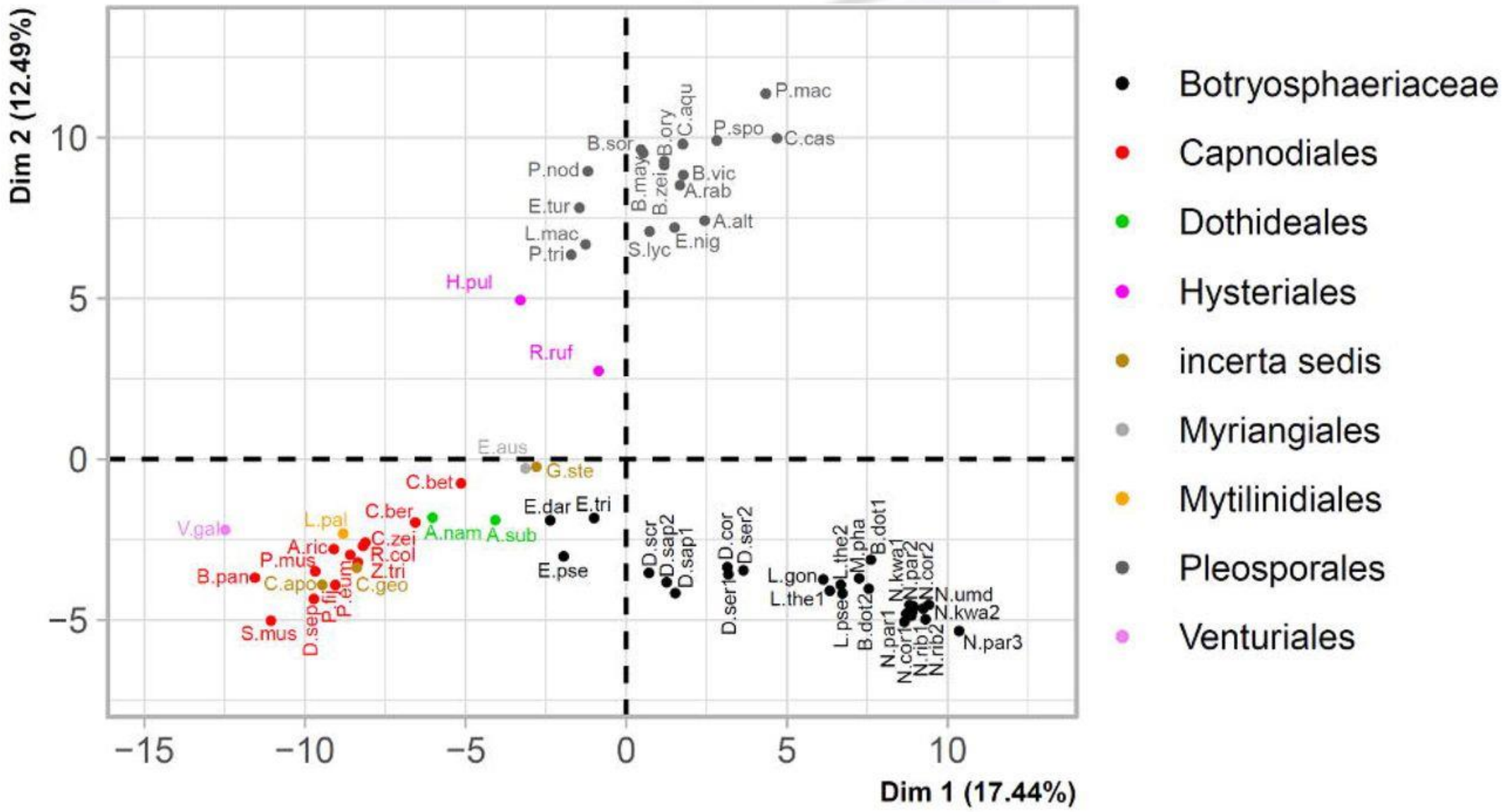


Adaptado de:
HACQUARD et al. 2016. **Nature Communications.** DOI: 10.1038/ncomms11362



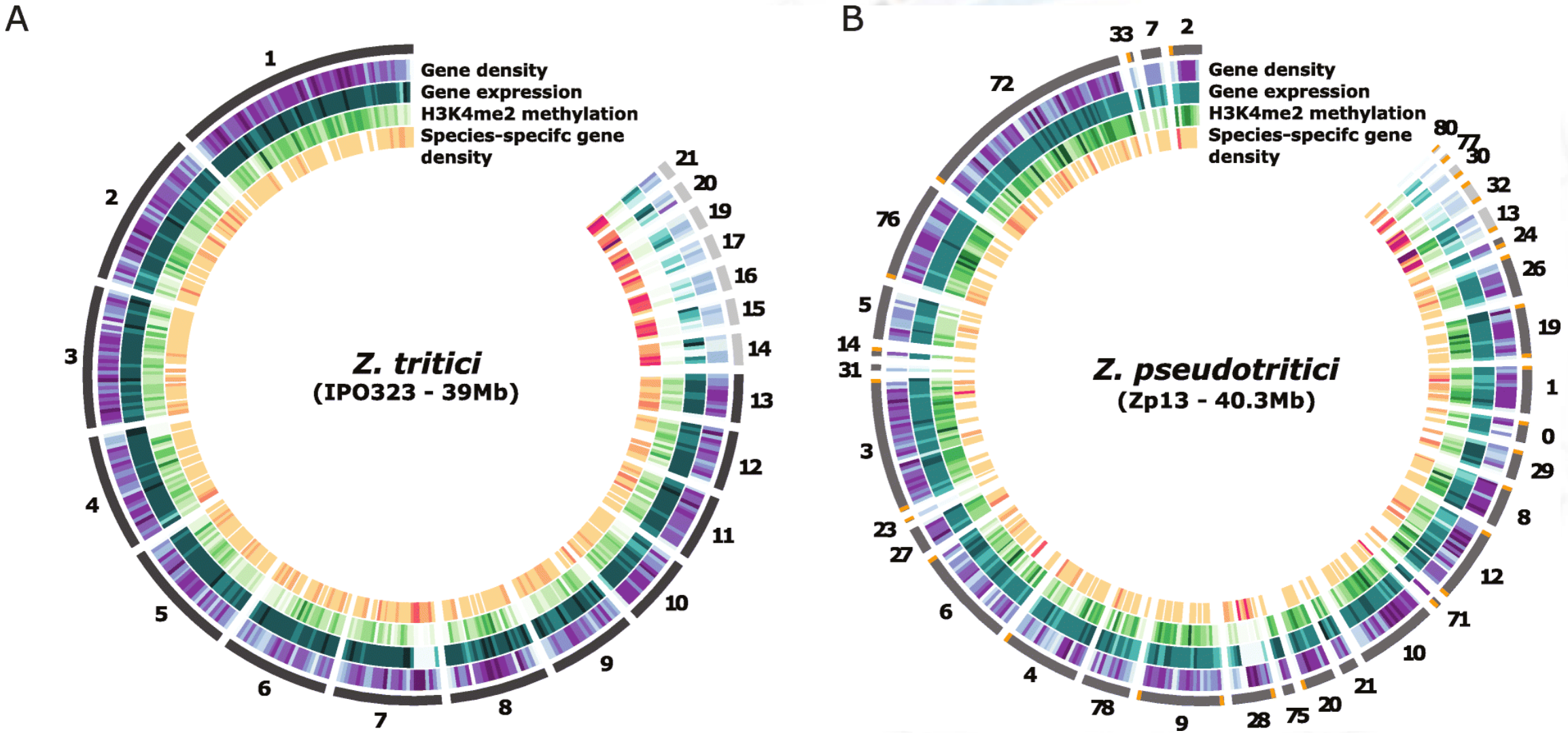


PCA



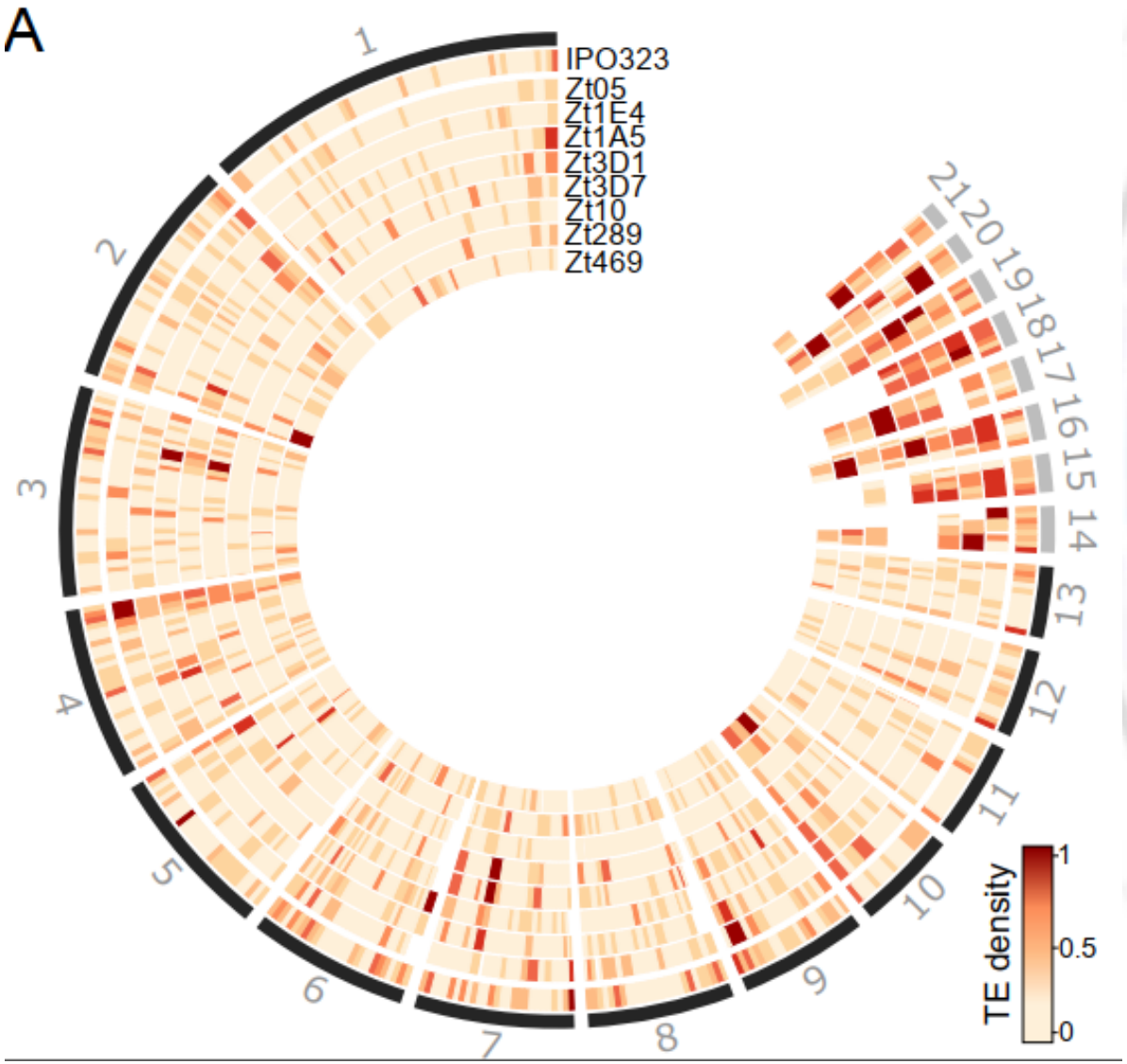
Adaptado de:
NAGEL et al. 2021. Preprint no servidor **bioRxiv.** DOI: 10.1101\2021.01.22.427741

Circos plot (heatmap, diferentes características)

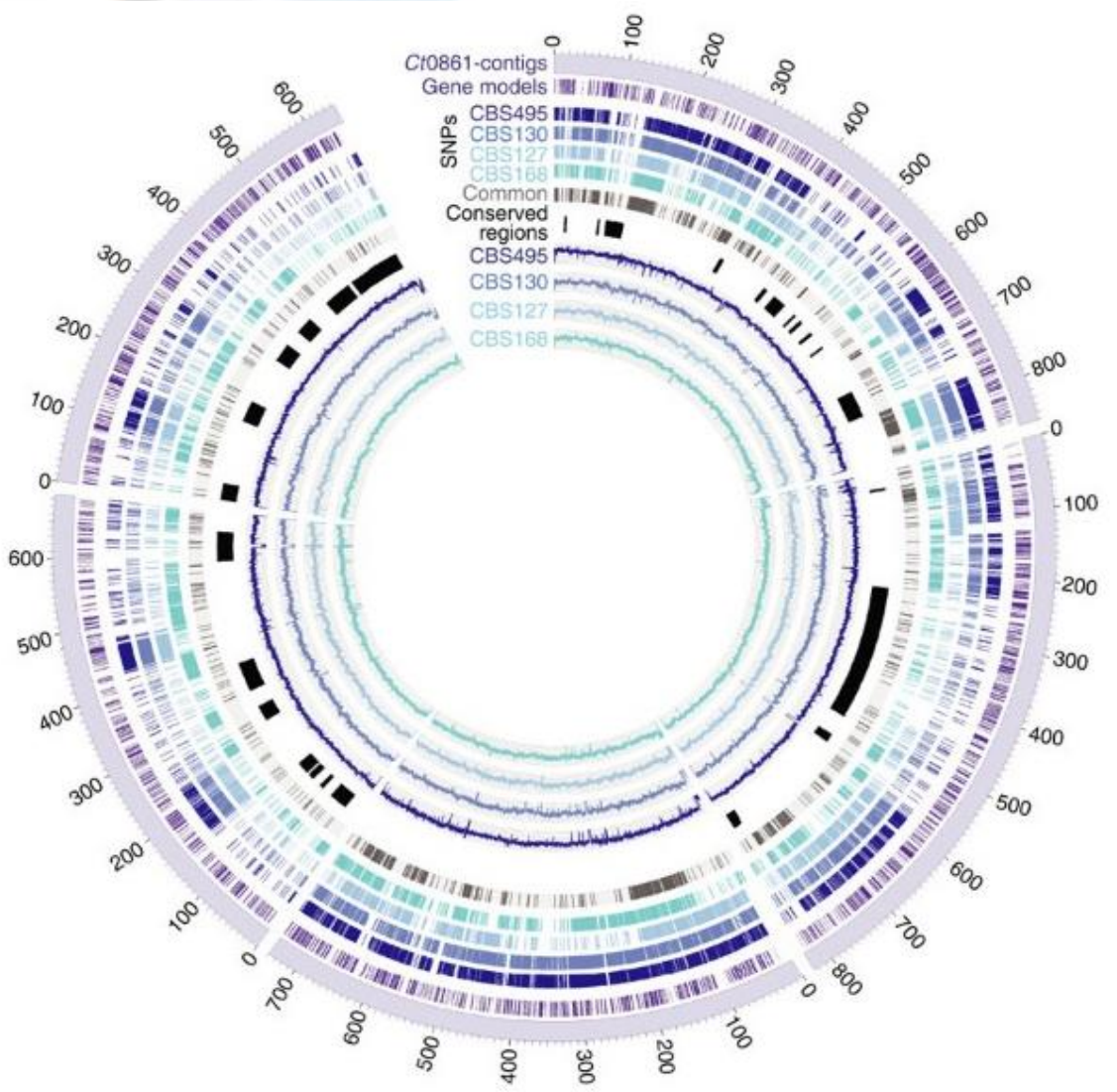


Adaptado de:
FEURTEY et al. 2020. **BMC Genomics.** DOI: 10.1186/s12864-020-06871-w

Circos plot (heatmap, diferentes indivíduos)



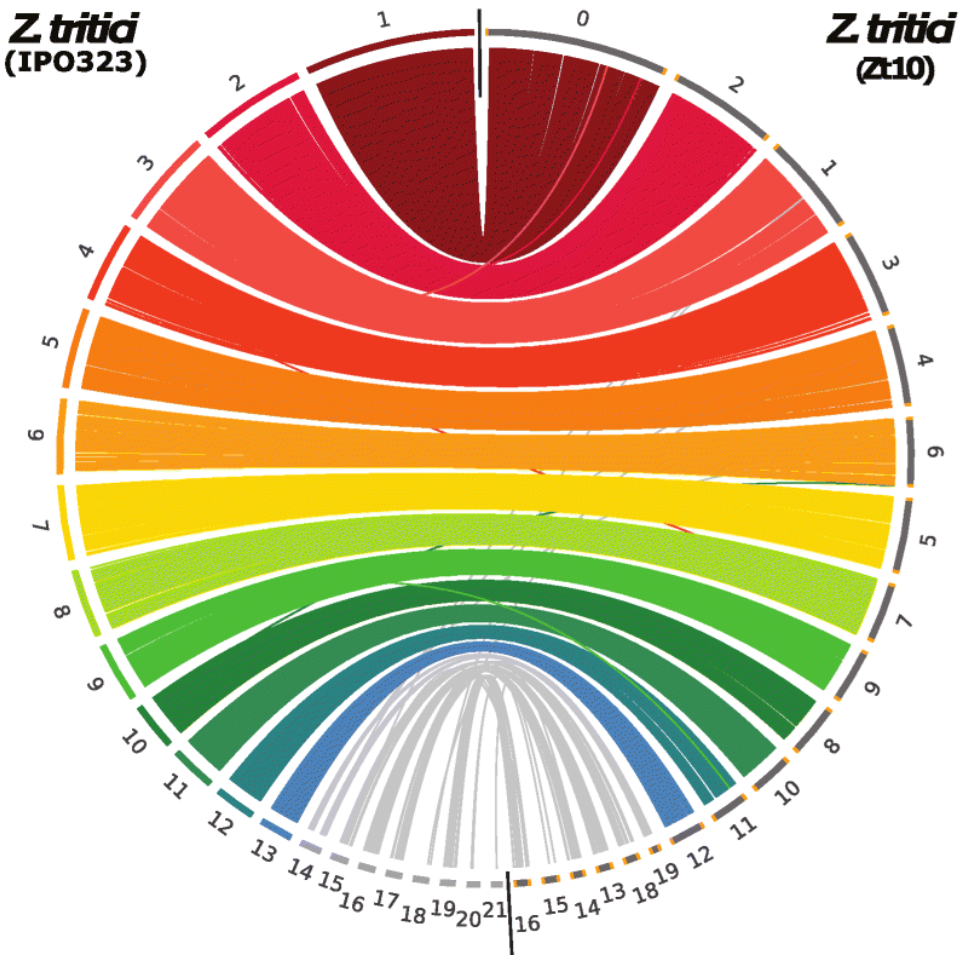
Adaptado de:
LORRAIN et al. 2020. Preprint no servidor **bioRxiv.** DOI: 10.1101\2020.05.13.092635



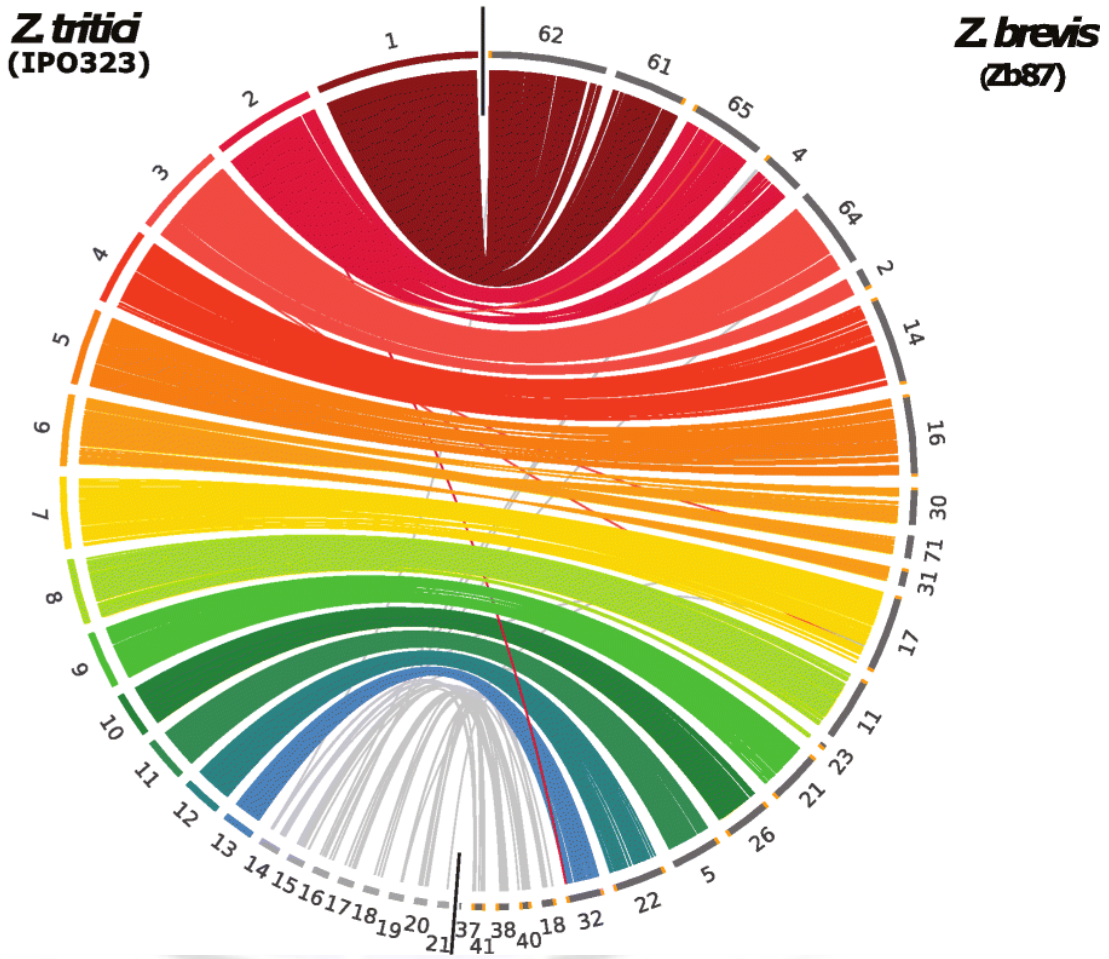
Adaptado de:
HACQUARD et al. 2016. **Nature Communications.** DOI: 10.1038/ncomms11362

Circos plot (sintenia)

A



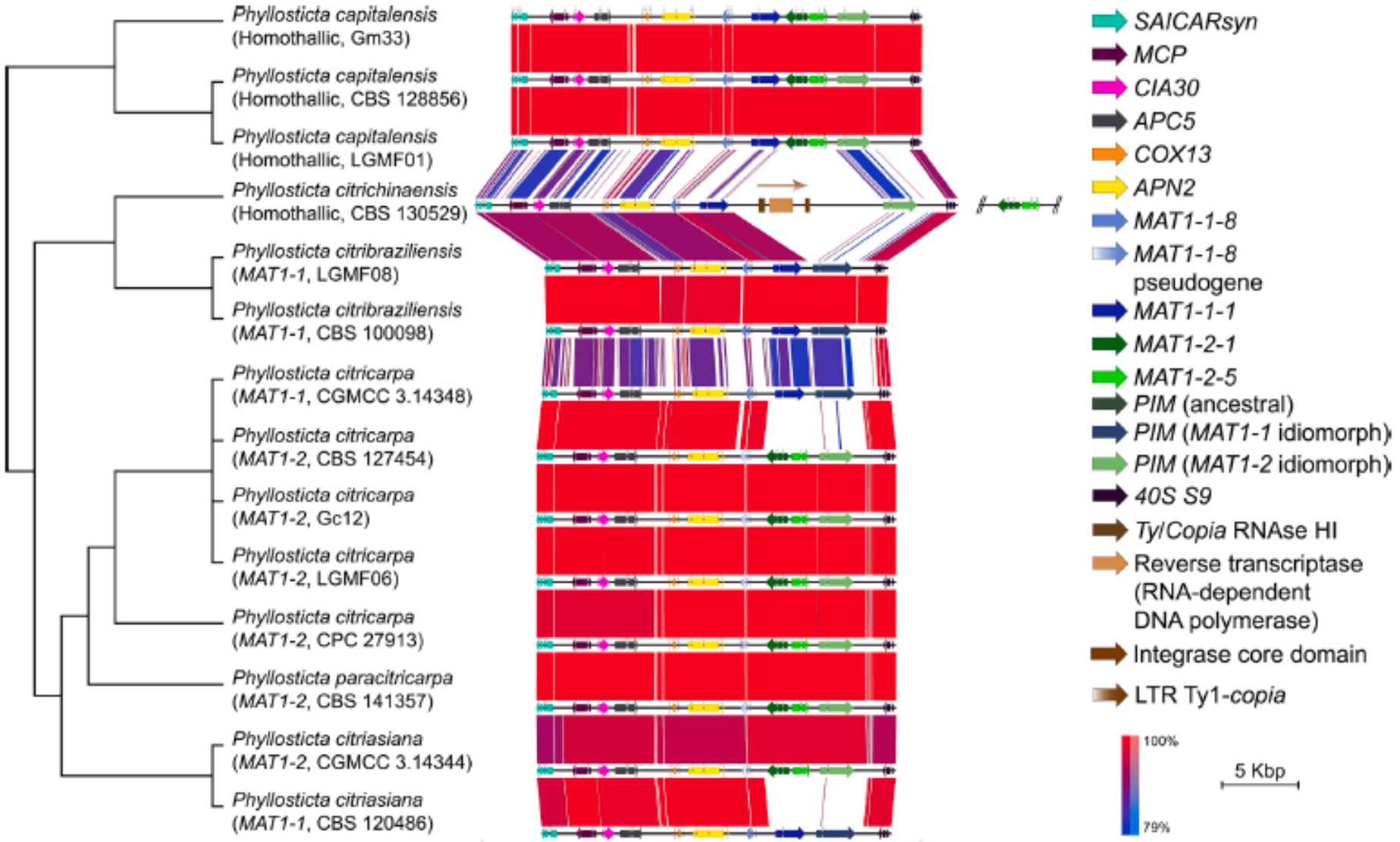
B



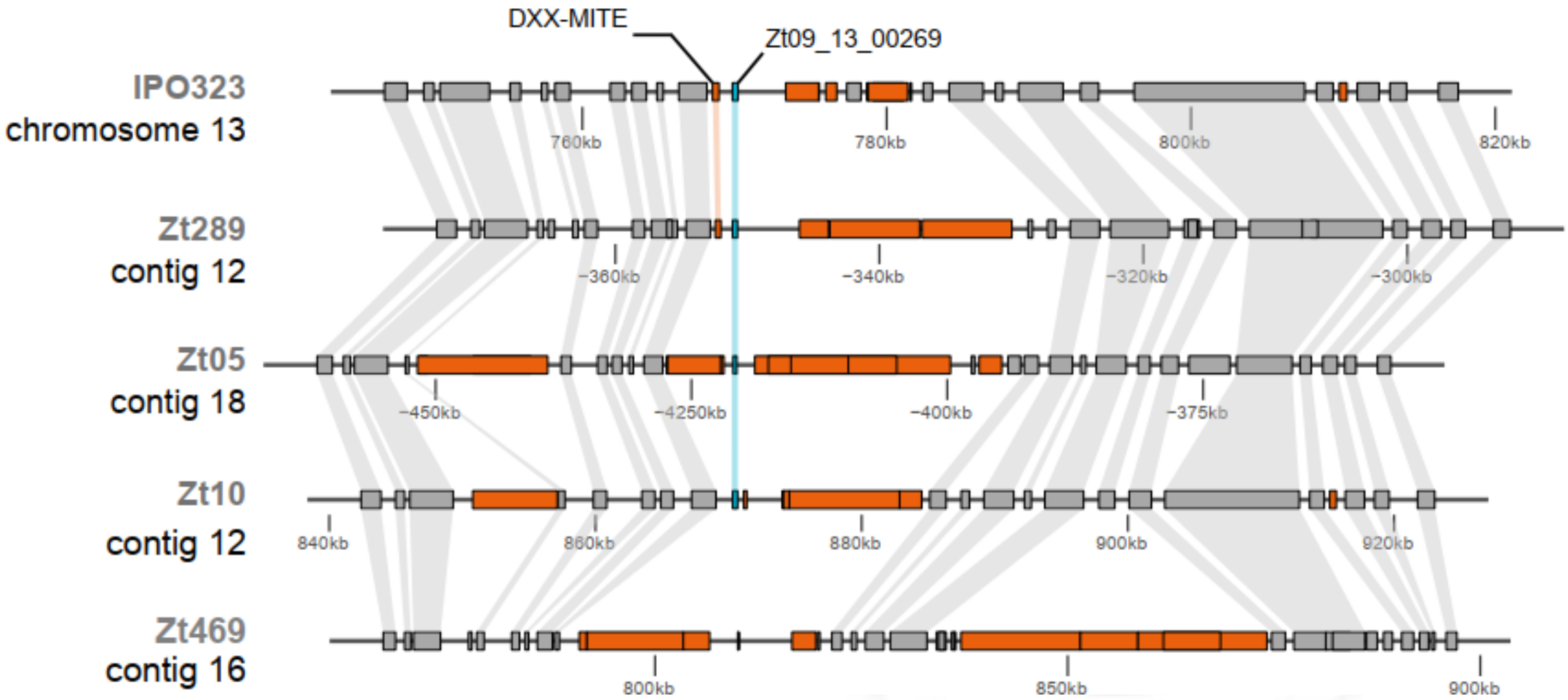
Adaptado de:
FEURTEY et al. 2020. **BMC Genomics.** DOI: 10.1186/s12864-020-06871-w

Sintenia (regiões específicas)

Adaptado de:
PETTERS-VANDRESEN et al. 2020. **Fungal Genetics and Biology.** DOI: 10.1016\j.fgb.2020.103444

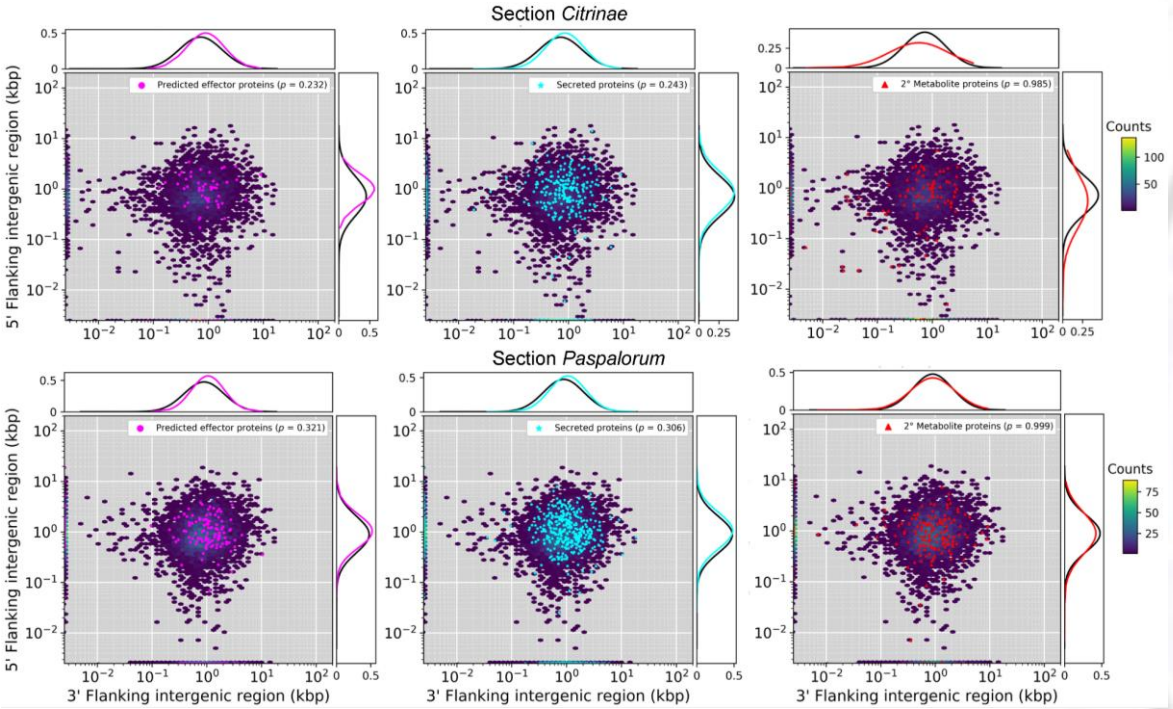


Sintenia (regiões específicas)

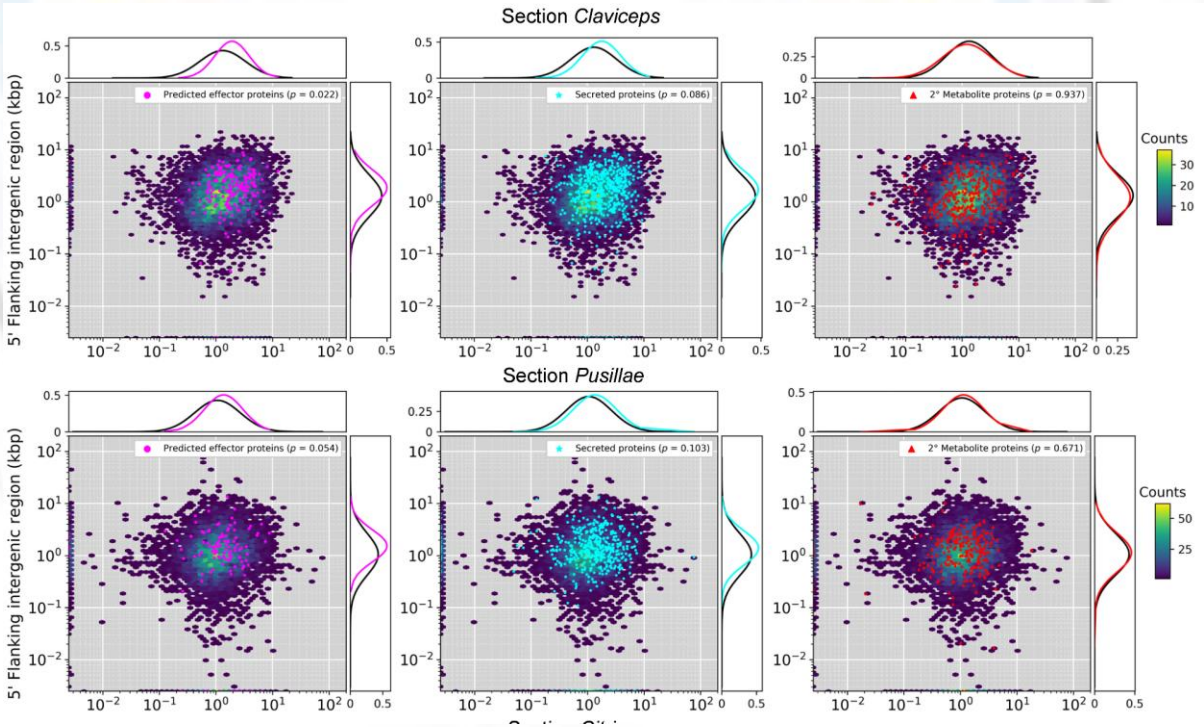


Adaptado de:
LORRAIN et al. 2020. Preprint no servidor **bioRxiv.** DOI: 10.1101\2020.05.13.092635

Hexbin plot



Adaptado de:
WYKA et al. 2021. **Genome Biology and Evolution.** DOI: 10.1093\gbe\evaa267



Como escolher o formato (ou combinação ideal)?

- Tentativa e erro
- Inspirações em artigos similares
- Consultando material especializado para compreender aplicações, vantagens e desvantagens

from Data to Viz

The R Graph Gallery

information is beautiful

storytelling with data

Checklist de submissão de um artigo

- Os dados brutos de sequenciamento estão disponíveis em uma base de dados pública?
- As montagens de genoma/transcriptoma e anotações estão disponíveis em uma base de dados pública?
- Arquivos de código utilizados para processamento dos dados ou produção de tabelas/figuras estão disponíveis em um repositório público?
- As informações de acesso a todos esses dados estão claras e disponíveis no artigo?