Centre for Genomic
Pathogen Surveillance

Herramientas para el uso de la secuenciación de genomas completos en salud pública

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29/11/2017

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wellcome trust sanger institute

WELLCOME GENOME CAMPUS

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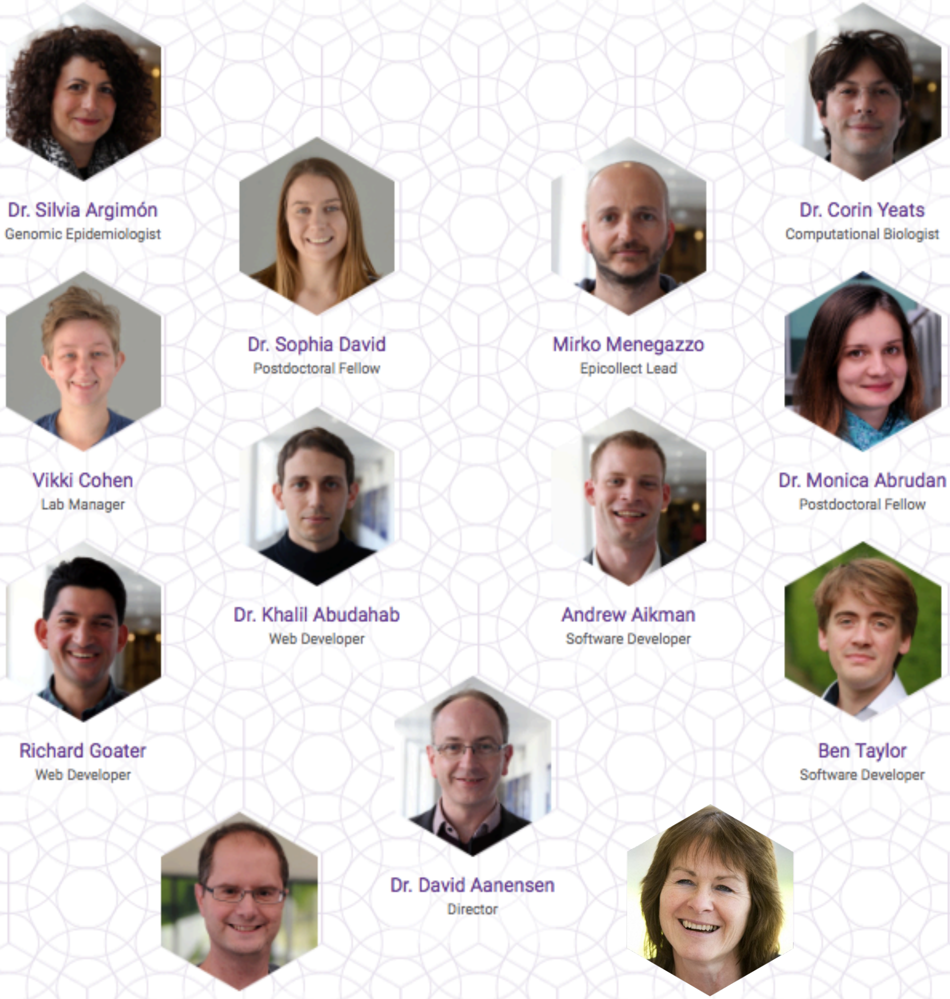

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Ben Taylor
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Director

Dr. Simon Harris
Associate Scientist

Carol Churcher
Project Manager

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APLICACIONES GRATUITAS

epicollect

http://www.epicollect.net

Phylocanvas

http://phylocanvas.org

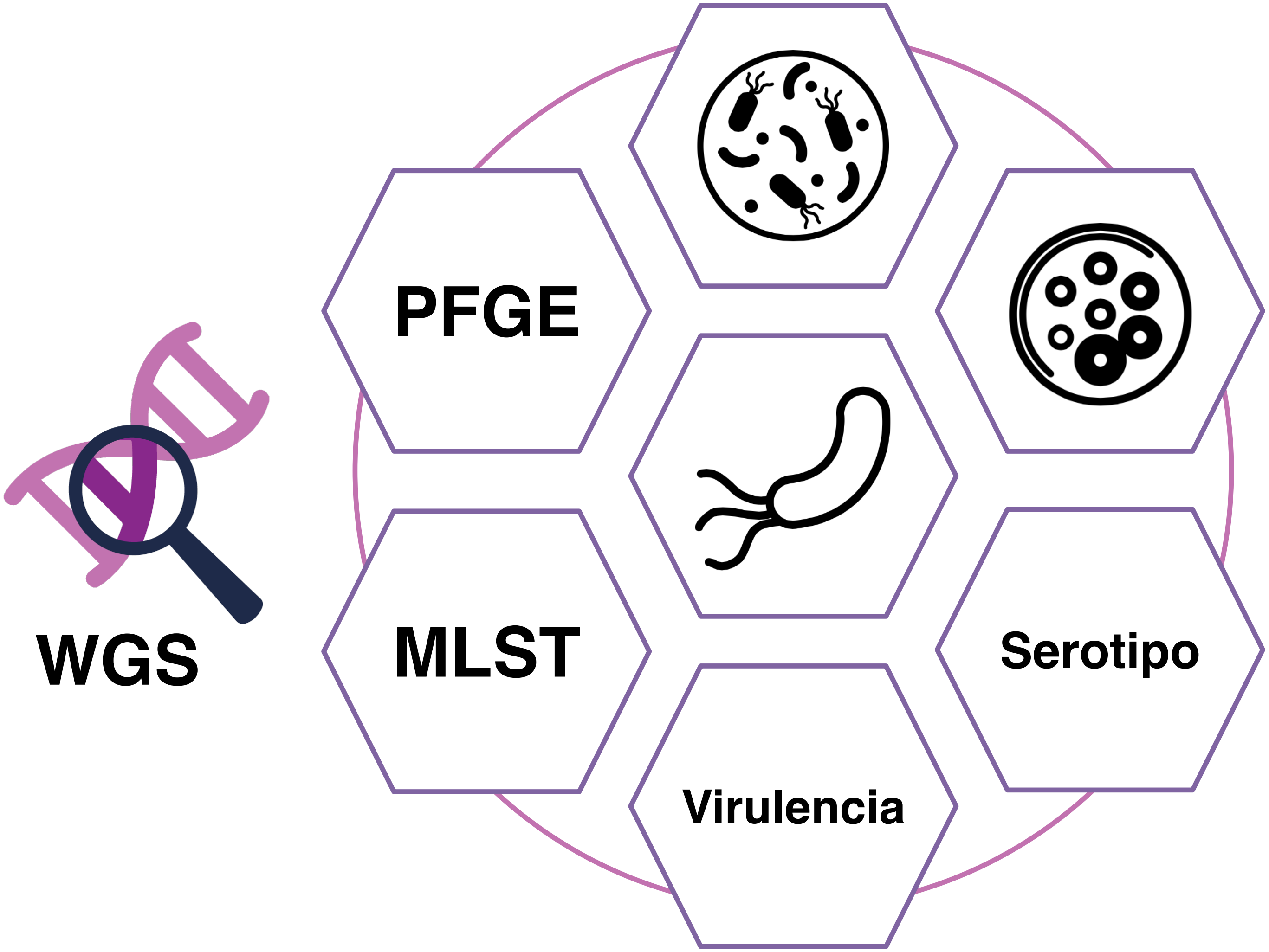
Microreact

http://microreact.org

WGSA

http://wgsa.net

VIGILANCIA DE ENFERMEDADES INFECCIOSAS



WGS

PFGE

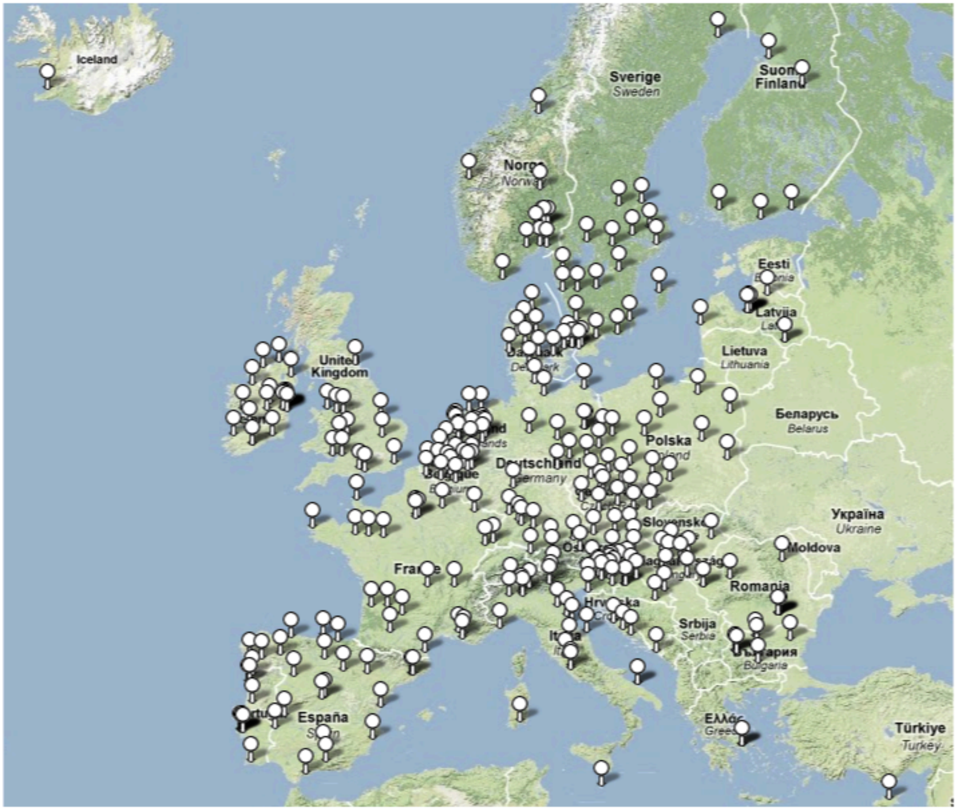
MLST

Serotipo

Virulencia

ESTUDIO ESTRUCTURADO DE *S. aureus*

- 26 países europeos
- 450 hospitales, 357 laboratorios
- Enviar los primeros 5 aislamientos MSSA y los primeros 5 MRSA de pacientes con efermedad invasiva
- Septiembre 2006 – Febrero 2007
- 3000 aislamientos
- 660 tipos *spa*



Ubicación de los hospitales participantes

Grundmann et al. 2010 *PLoS Med* 7(1): e1000215.

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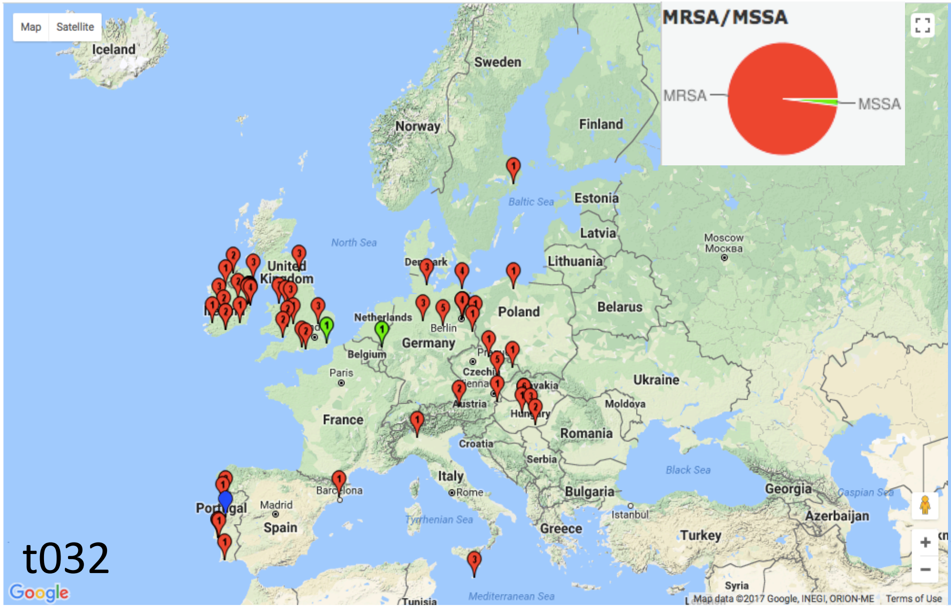
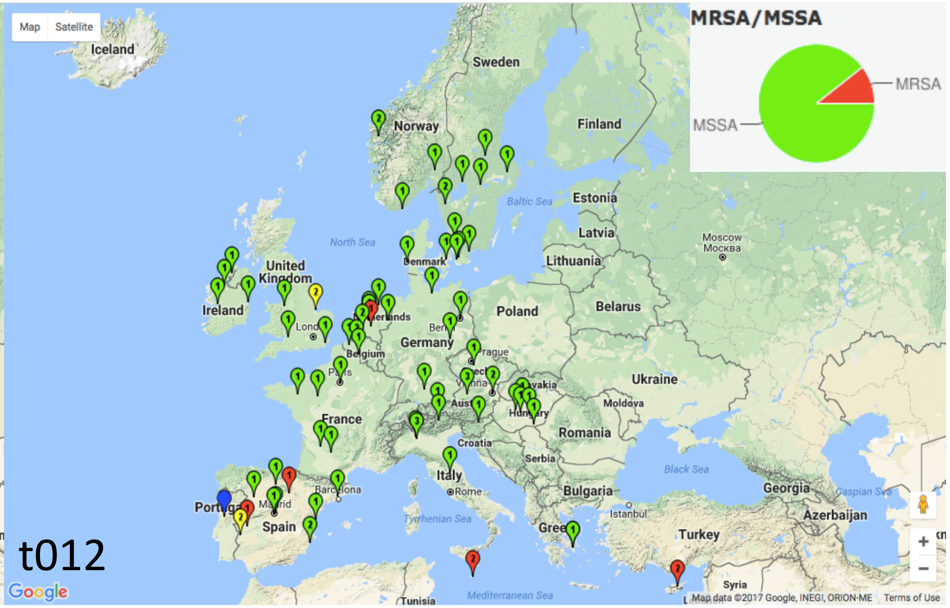
ESTUDIO ESTRUCTURADO DE *S. aureus*

Los principales tipos *spa* de los aislamientos SARM forman grupos geográficos.

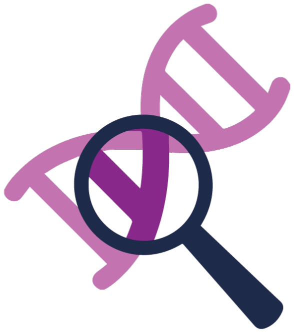




Rojo: MRSA. Verde: MSSA. Amarillo: MSSA+MRSA

Grundmann et al. 2010 *PLoS Med* 7(1): e1000215.

SECUENCIACIÓN DE GENOMAS COMPLETOS



308 aislamientos
21 países

análisis
bioinformático

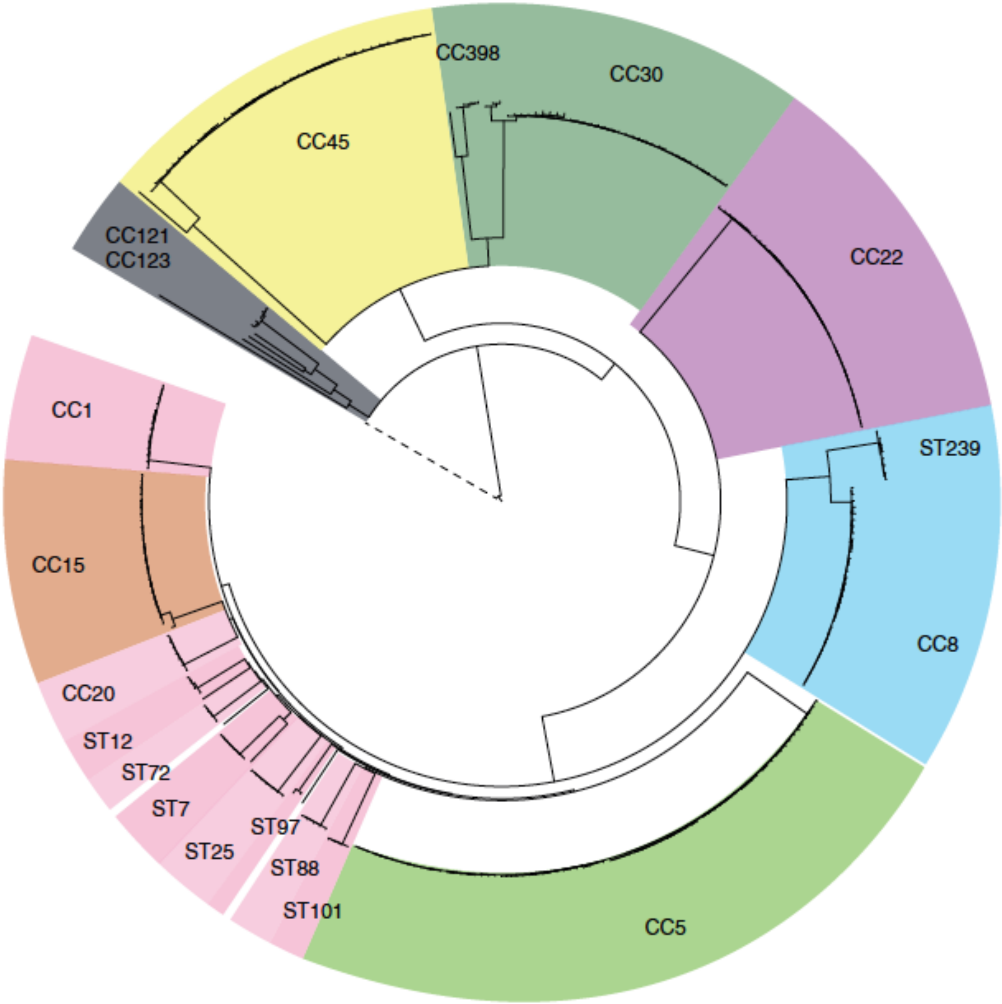


FIG 1 Phylogenetic relationship of the invasive *S. aureus* population circulating in Europe in 2006. A rooted neighbor-joining tree based on 235,226 genomewide core SNPs is shown. Lineages are highlighted and named according to the corresponding CC or ST.

Aanensen et al, 2016. *Mbio* 7(3):e00444-16

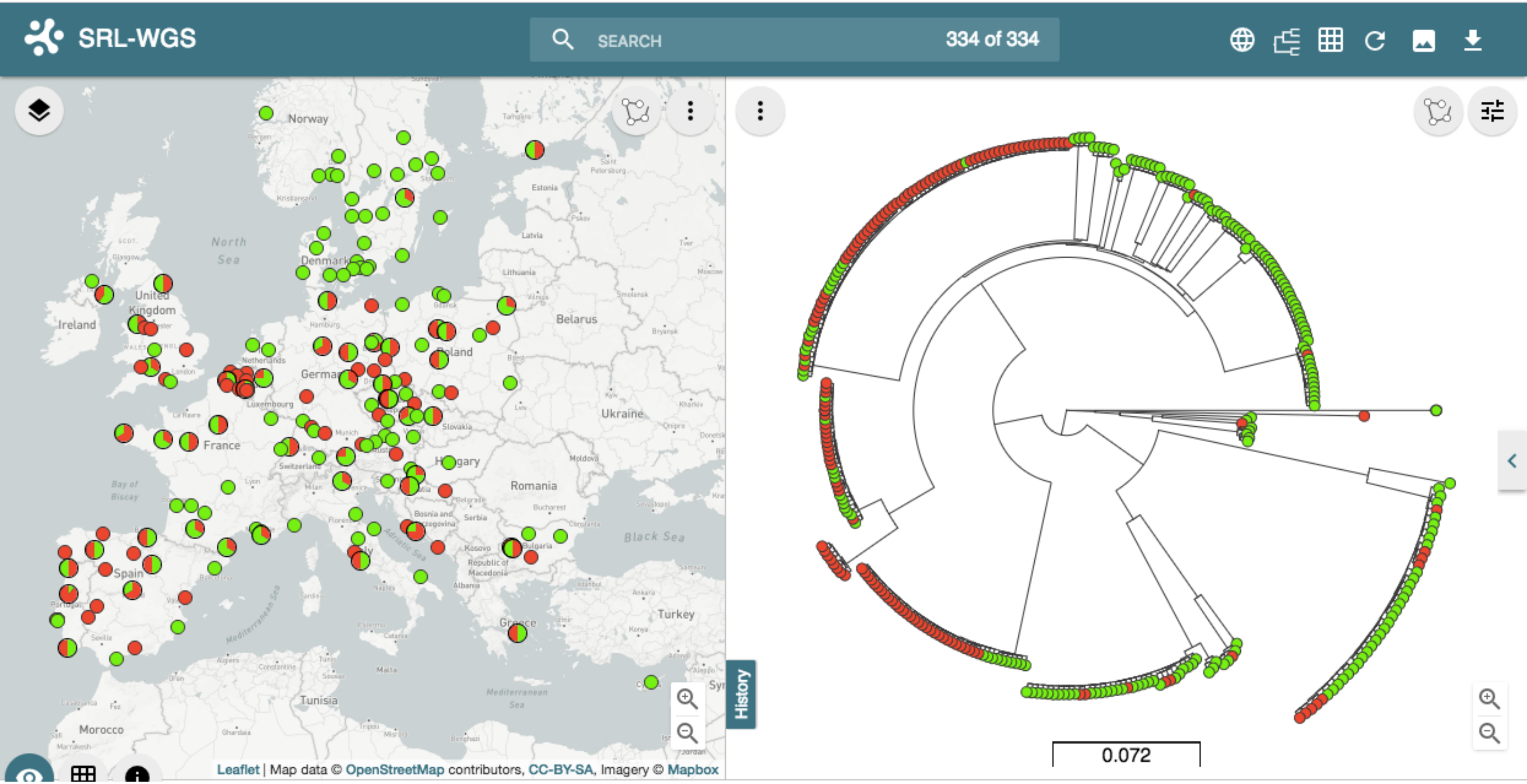
MICROREACT: VISUALIZACIÓN

Microreact

http://microreact.org

Argimón et al, 2016. *MGen* 2(11): doi:10.1099/mgen.0.000093

VISUALIZACiÓN EN MICROREACT



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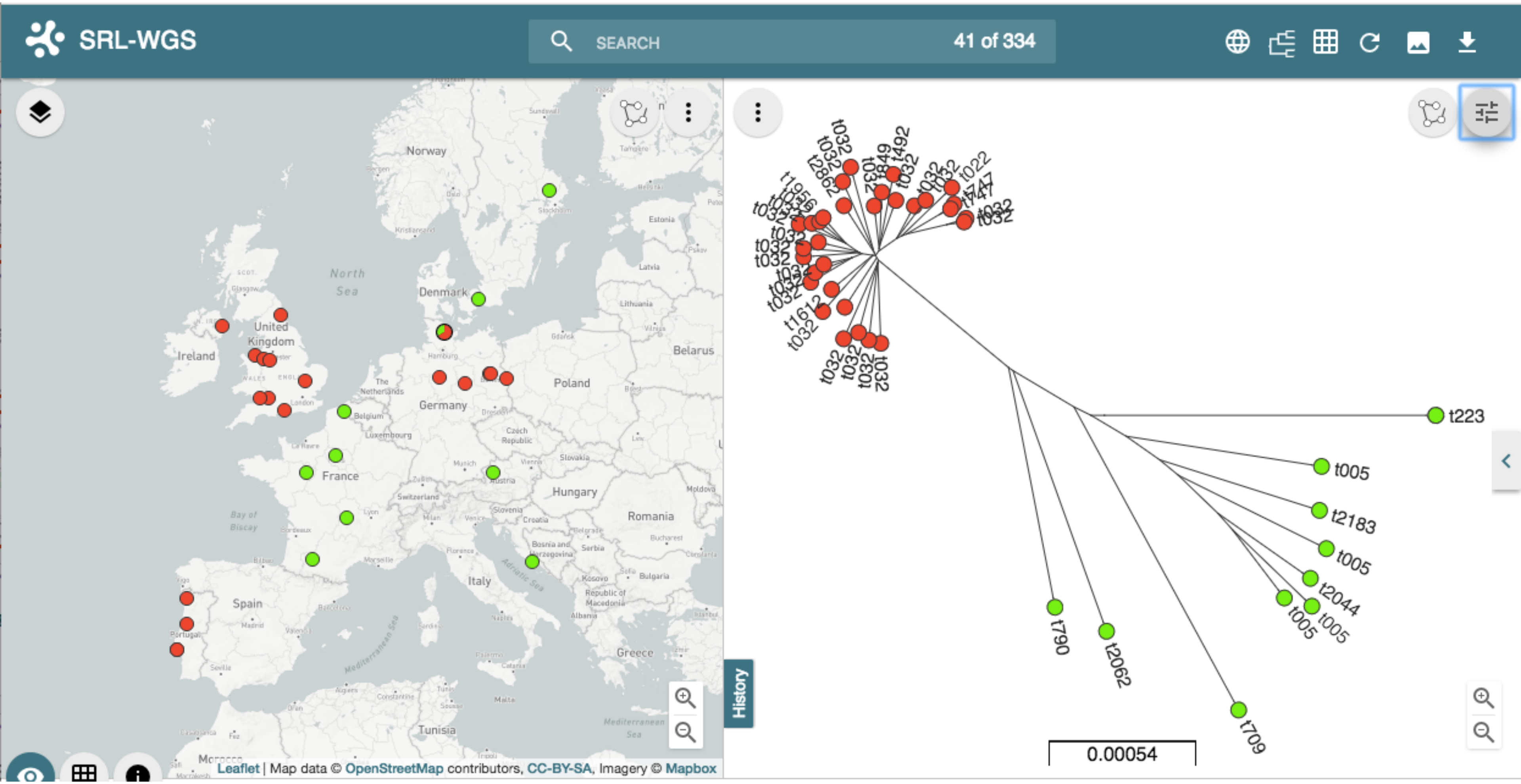
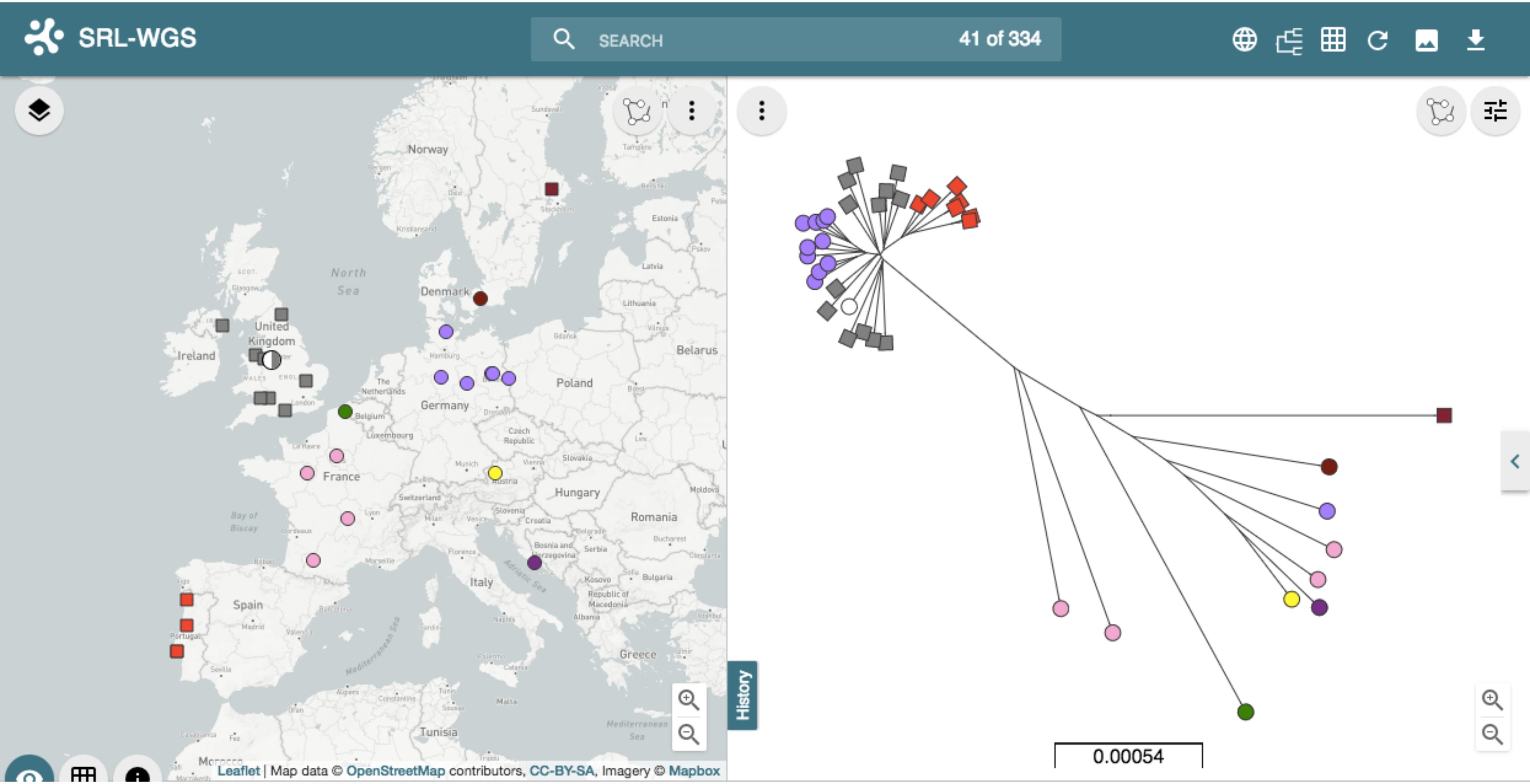
VISUALIZACiÓN EN MICROREACT



Adquisición de SCCmec

VISUALIZACiÓN EN MICROREACT



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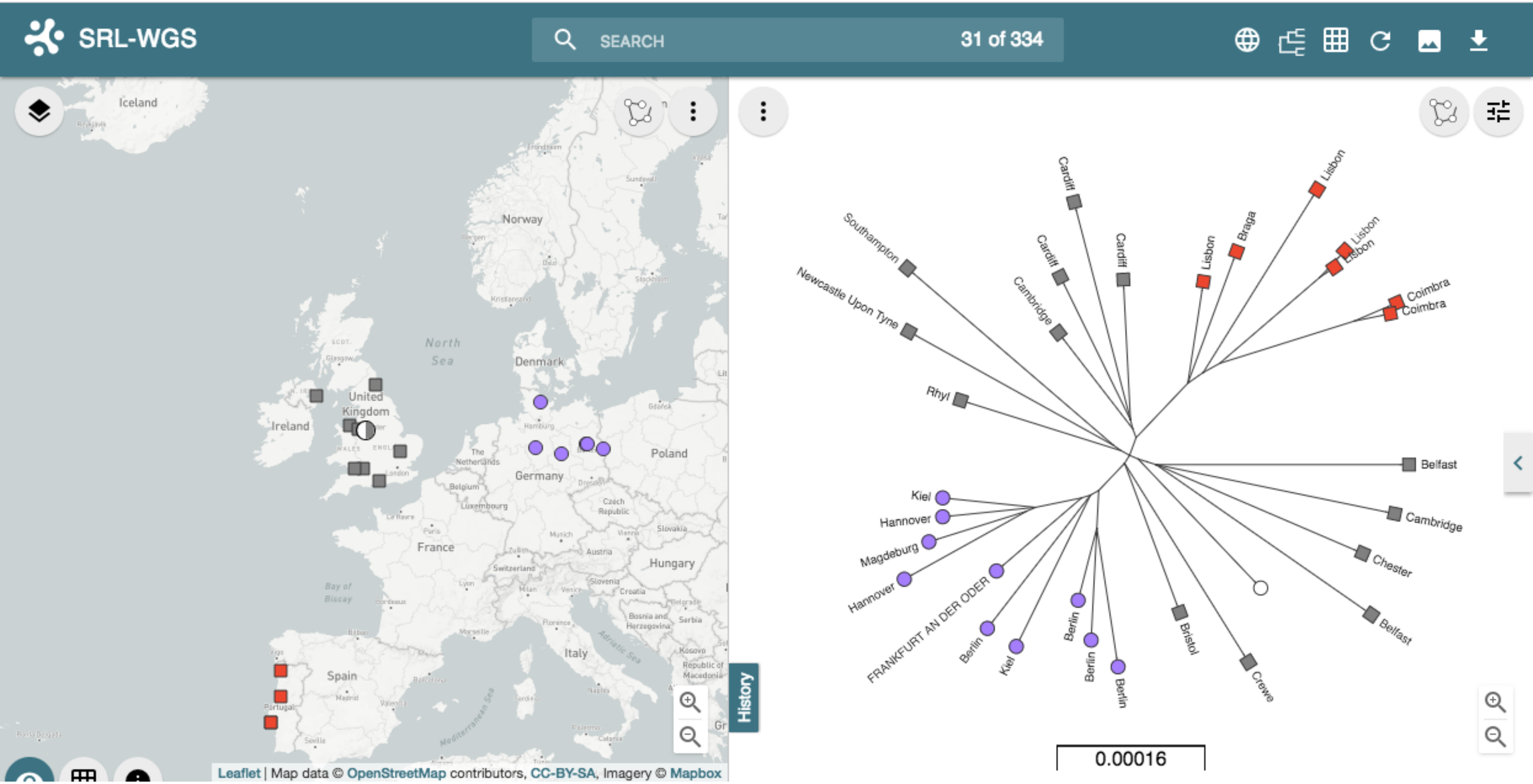
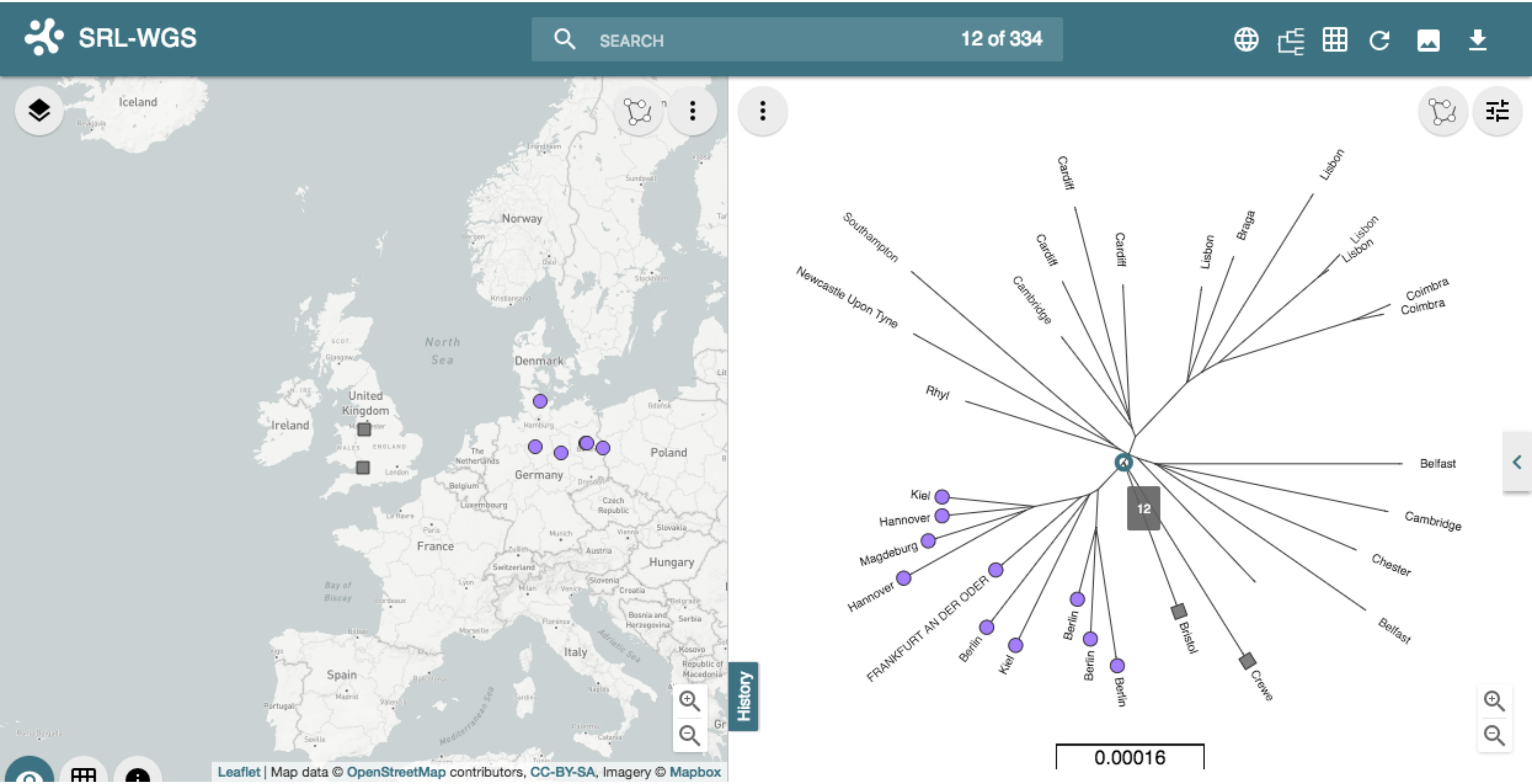
VISUALIZACiÓN EN MICROREACT



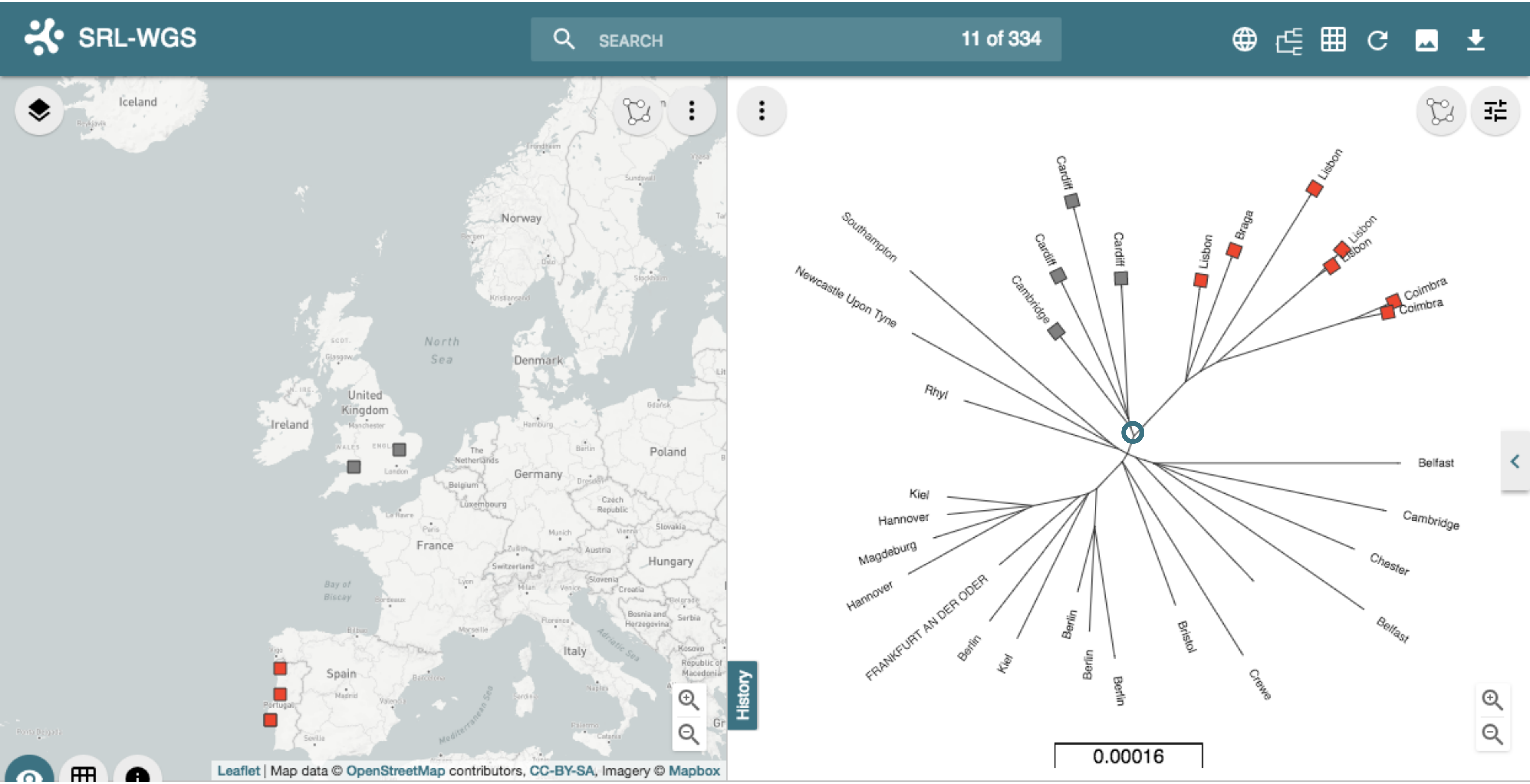
Identificación de transmisión intra-continental de MRSA

VISUALIZACiÓN EN MICROREACT



Reino Unido - Alemania

VISUALIZACiÓN EN MICROREACT



Reino Unido - Portugal

PREDICCIONES DE RESISTENCIA A ANTIMICROBIANOS

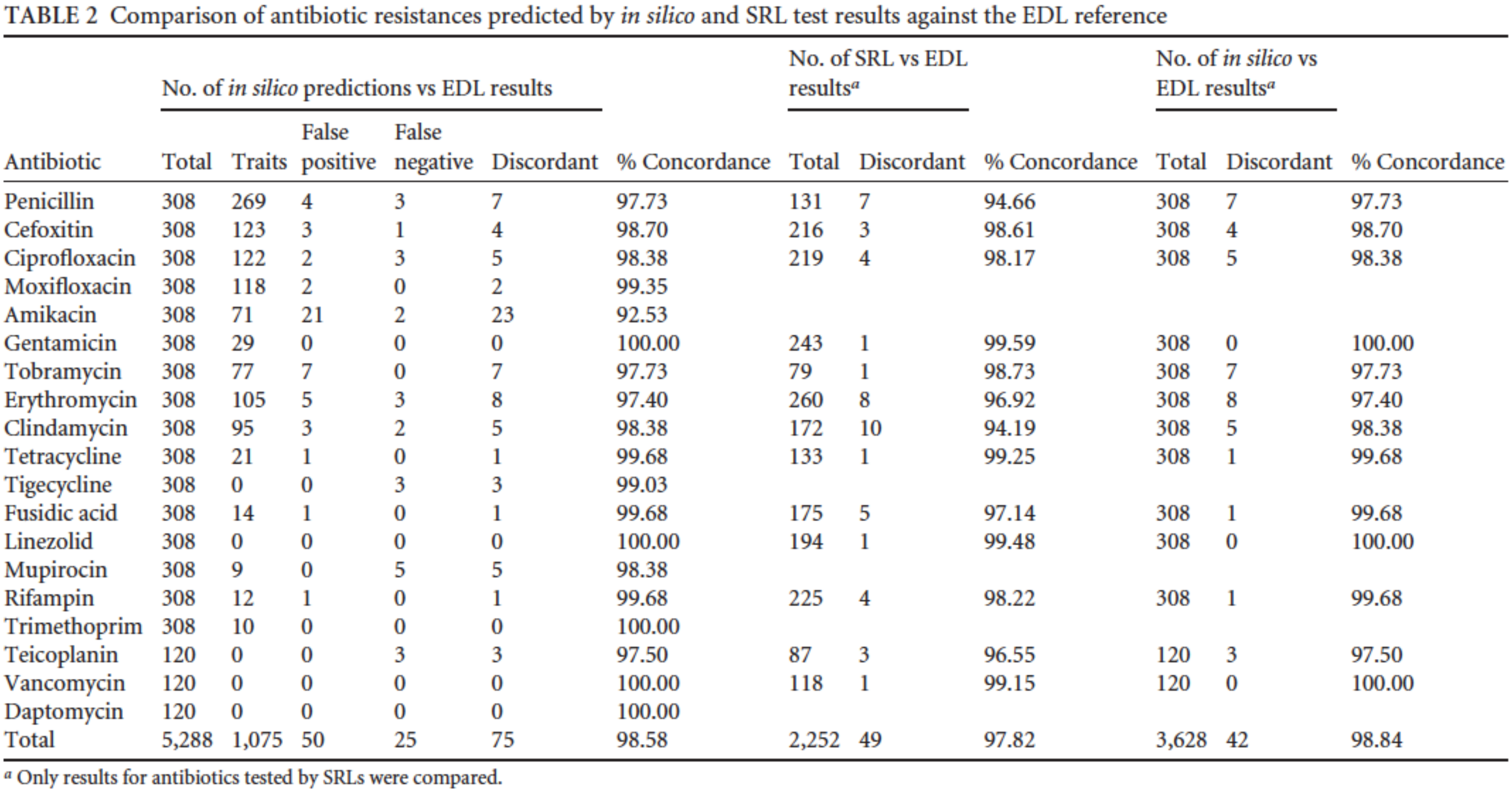


TABLE 2 Comparison of antibiotic resistances predicted by *in silico* and SRL test results against the EDL reference

	No. of *in silico* predictions vs EDL results						No. of SRL vs EDL results[a]			No. of *in silico* vs EDL results[a]		
Antibiotic	Total	Traits	False positive	False negative	Discordant	% Concordance	Total	Discordant	% Concordance	Total	Discordant	% Concordance
Penicillin	308	269	4	3	7	97.73	131	7	94.66	308	7	97.73
Cefoxitin	308	123	3	1	4	98.70	216	3	98.61	308	4	98.70
Ciprofloxacin	308	122	2	3	5	98.38	219	4	98.17	308	5	98.38
Moxifloxacin	308	118	2	0	2	99.35						
Amikacin	308	71	21	2	23	92.53						
Gentamicin	308	29	0	0	0	100.00	243	1	99.59	308	0	100.00
Tobramycin	308	77	7	0	7	97.73	79	1	98.73	308	7	97.73
Erythromycin	308	105	5	3	8	97.40	260	8	96.92	308	8	97.40
Clindamycin	308	95	3	2	5	98.38	172	10	94.19	308	5	98.38
Tetracycline	308	21	1	0	1	99.68	133	1	99.25	308	1	99.68
Tigecycline	308	0	0	3	3	99.03						
Fusidic acid	308	14	1	0	1	99.68	175	5	97.14	308	1	99.68
Linezolid	308	0	0	0	0	100.00	194	1	99.48	308	0	100.00
Mupirocin	308	9	0	5	5	98.38						
Rifampin	308	12	1	0	1	99.68	225	4	98.22	308	1	99.68
Trimethoprim	308	10	0	0	0	100.00						
Teicoplanin	120	0	0	3	3	97.50	87	3	96.55	120	3	97.50
Vancomycin	120	0	0	0	0	100.00	118	1	99.15	120	0	100.00
Daptomycin	120	0	0	0	0	100.00						
Total	5,288	1,075	50	25	75	98.58	2,252	49	97.82	3,628	42	98.84

[a] Only results for antibiotics tested by SRLs were compared.

Aanensen et al, 2016. *Mbio* 7(3):e00444-16

WGSA: ANÁLISIS

WGSA

http://wgsa.net

Yeats et al. In preparation
Argimón et al. In preparation

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ANÁLISIS DE GENOMAS COMPLETOS EN WGSA

Global Pathogen Surveillance through Whole Genome Sequencing

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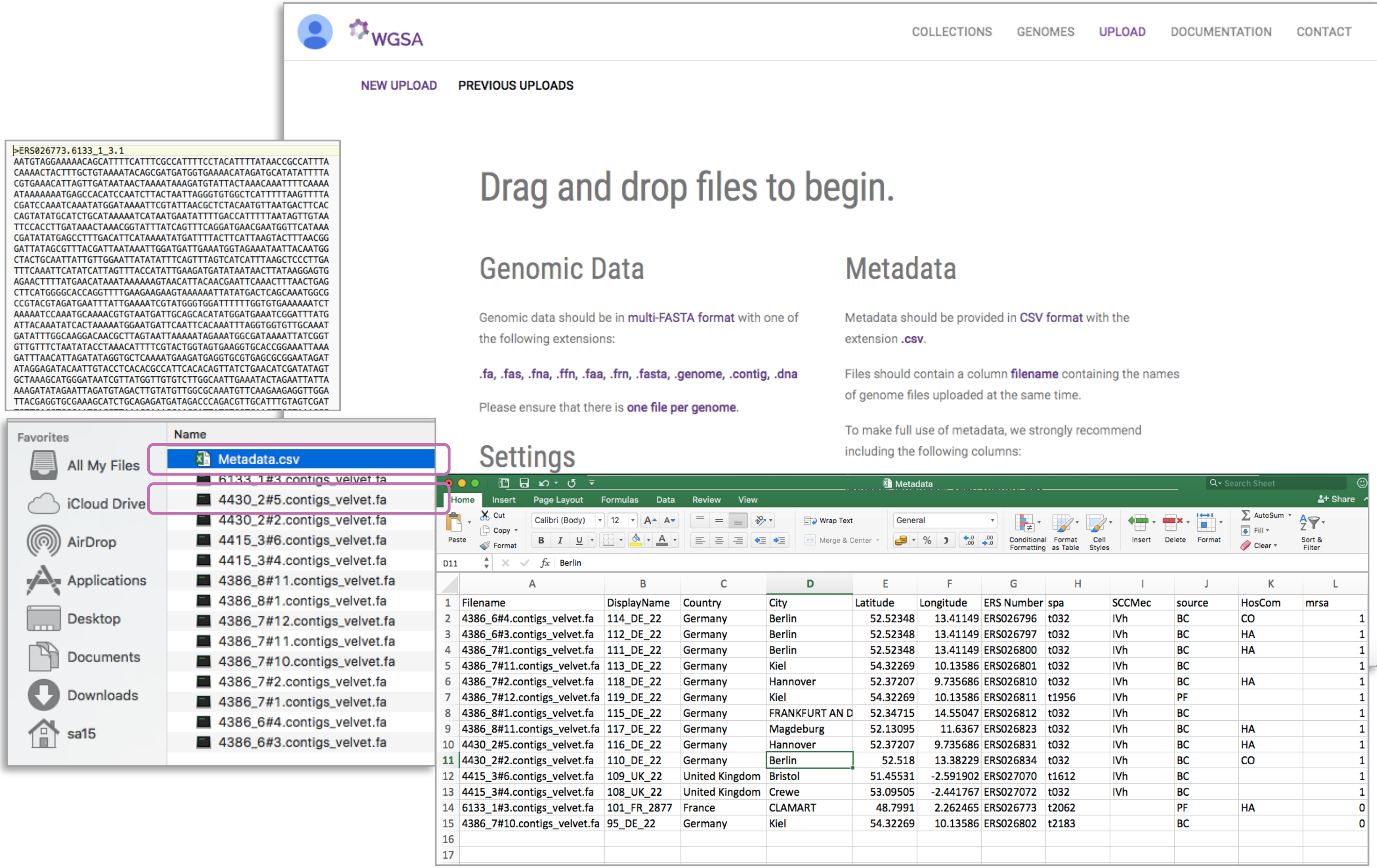
ANALISIS DE GENOMAS COMPLETOS EN WGSA



Drag and drop files to begin.

Genomic Data

Genomic data should be in **multi-FASTA format** with one of the following extensions:

.fa, .fas, .fna, .ffn, .faa, .frn, .fasta, .genome, .contig, .dna

Please ensure that there is **one file per genome**.

Metadata

Metadata should be provided in **CSV format** with the extension **.csv**.

Files should contain a column **filename** containing the names of genome files uploaded at the same time.

To make full use of metadata, we strongly recommend including the following columns:

Settings

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>ERS026773.6133_1_3.1
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- 4415_3#6.contigs_velvet.fa
- 4415_3#4.contigs_velvet.fa
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- 4386_8#1.contigs_velvet.fa
- 4386_7#12.contigs_velvet.fa
- 4386_7#11.contigs_velvet.fa
- 4386_7#10.contigs_velvet.fa
- 4386_7#2.contigs_velvet.fa
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- 4386_6#4.contigs_velvet.fa
- 4386_6#3.contigs_velvet.fa

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4386_8#1.contigs_velvet.fa	115_DE_22	Germany	FRANKFURT AN D	52.34715	14.55047	ERS026812	t032	IVh	BC		1
4386_8#11.contigs_velvet.fa	117_DE_22	Germany	Magdeburg	52.13095	11.6367	ERS026823	t032	IVh	BC	HA	1
4430_2#5.contigs_velvet.fa	116_DE_22	Germany	Hannover	52.37207	9.735686	ERS026831	t032	IVh	BC	HA	1
4430_2#2.contigs_velvet.fa	110_DE_22	Germany	Berlin	52.518	13.38229	ERS026834	t032	IVh	BC	CO	1
4415_3#6.contigs_velvet.fa	109_UK_22	United Kingdom	Bristol	51.45531	-2.591902	ERS027070	t1612	IVh	BC		1
4415_3#4.contigs_velvet.fa	108_UK_22	United Kingdom	Crewe	53.09505	-2.441767	ERS027072	t032	IVh	BC		1
6133_1#3.contigs_velvet.fa	101_FR_2877	France	CLAMART	48.7991	2.262465	ERS026773	t2062		PF	HA	0
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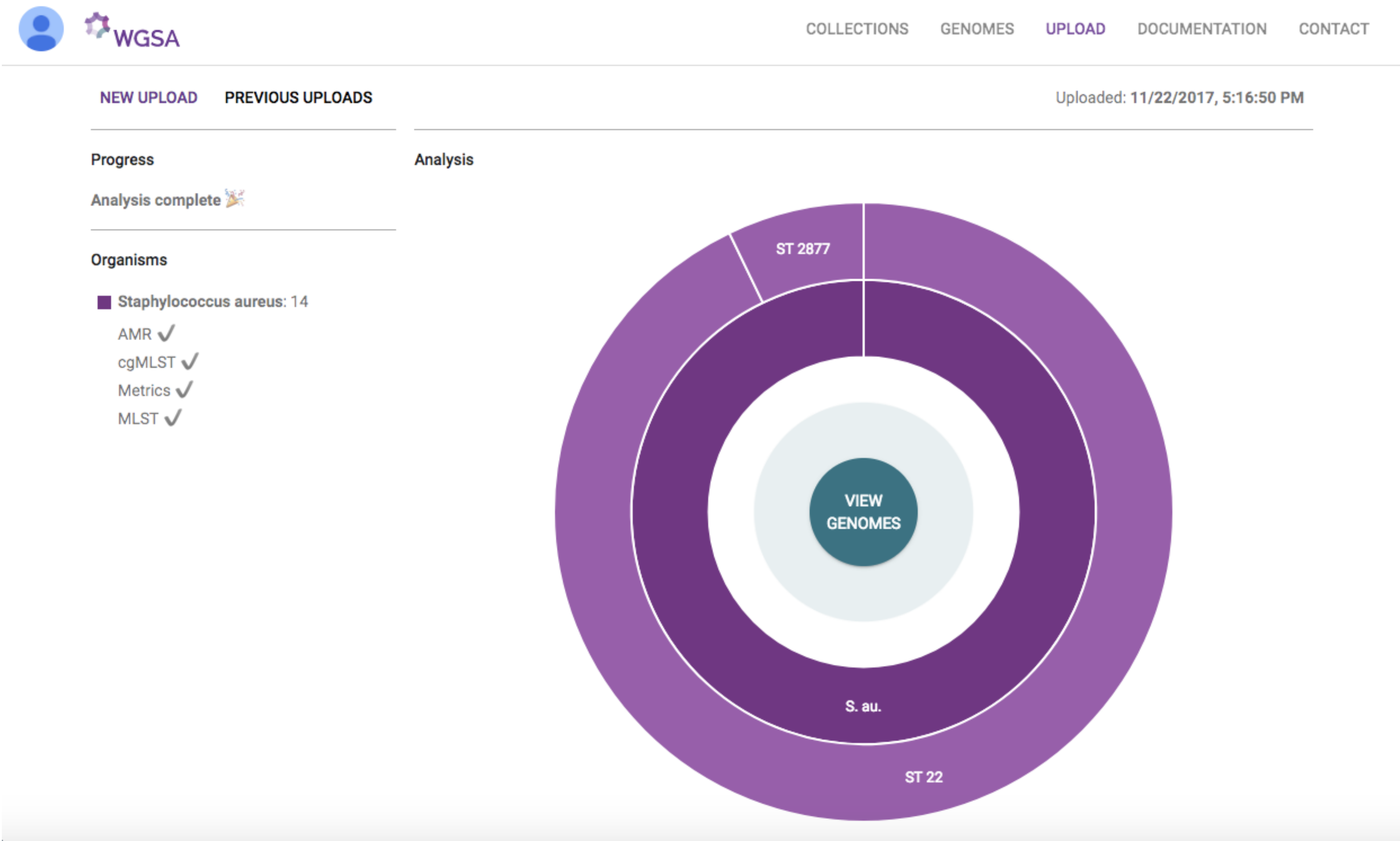
ANALISIS DE GENOMAS COMPLETOS EN WGSA



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Progress

Analysis complete

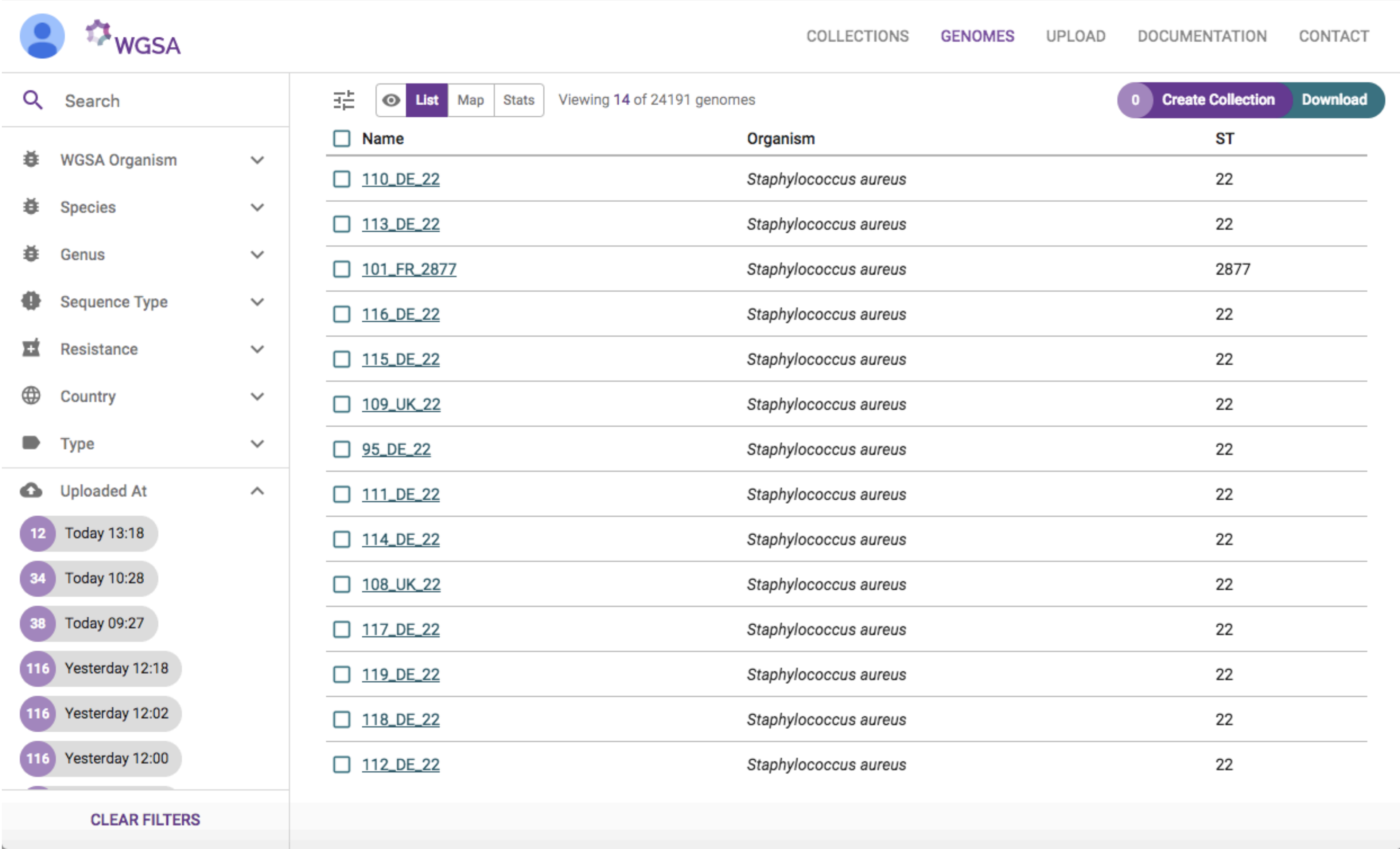
Organisms

■ **Staphylococcus aureus:** 14
- AMR ✓
- cgMLST ✓
- Metrics ✓
- MLST ✓

Analysis

CGPS

ANALISIS DE GENOMAS COMPLETOS EN WGSA

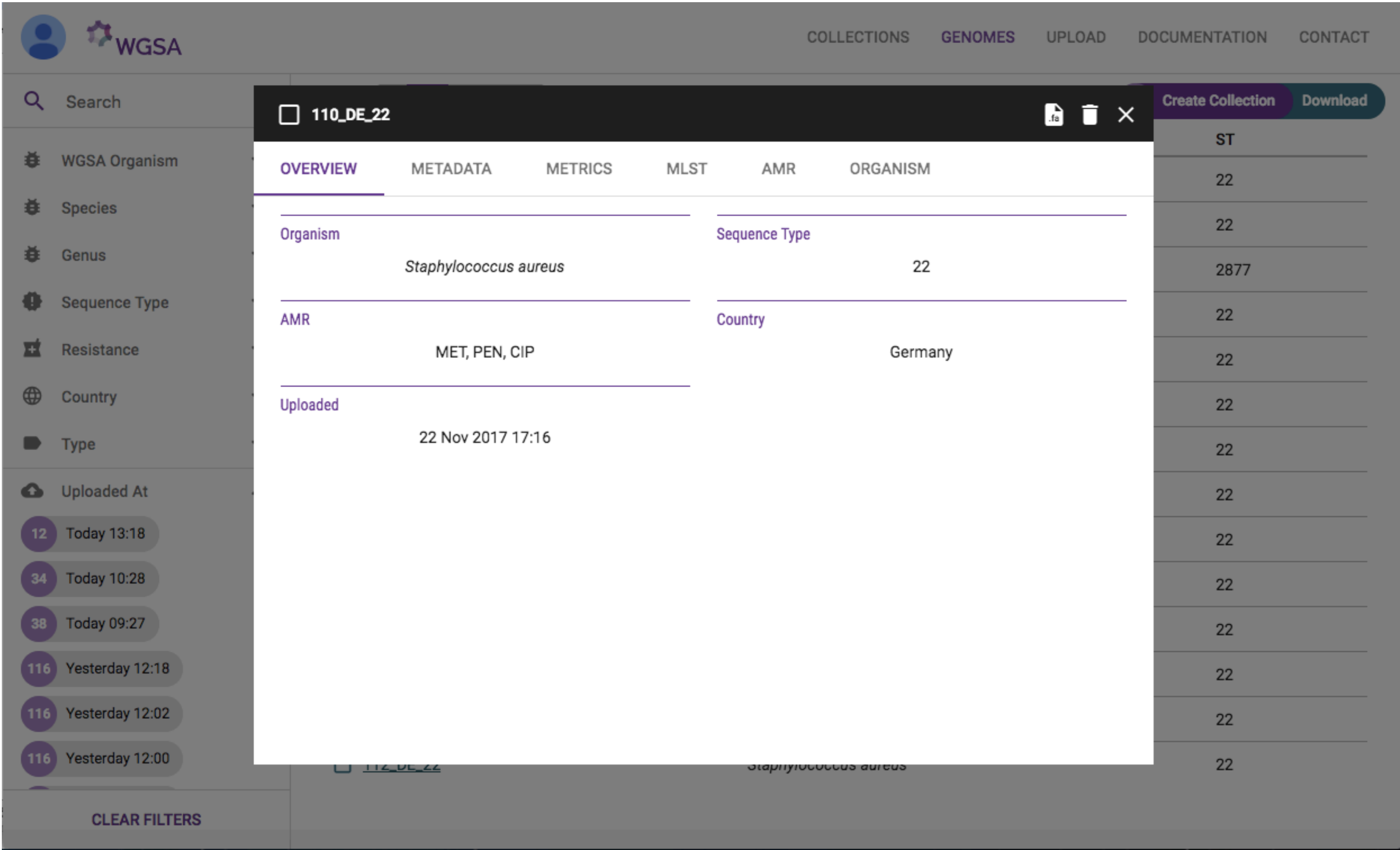


12 Today 13:18
34 Today 10:28
38 Today 09:27
116 Yesterday 12:18
116 Yesterday 12:02
116 Yesterday 12:00

Viewing 14 of 24191 genomes

☐ Name	Organism	ST
☐ 110_DE_22	*Staphylococcus aureus*	22
☐ 113_DE_22	*Staphylococcus aureus*	22
☐ 101_FR_2877	*Staphylococcus aureus*	2877
☐ 116_DE_22	*Staphylococcus aureus*	22
☐ 115_DE_22	*Staphylococcus aureus*	22
☐ 109_UK_22	*Staphylococcus aureus*	22
☐ 95_DE_22	*Staphylococcus aureus*	22
☐ 111_DE_22	*Staphylococcus aureus*	22
☐ 114_DE_22	*Staphylococcus aureus*	22
☐ 108_UK_22	*Staphylococcus aureus*	22
☐ 117_DE_22	*Staphylococcus aureus*	22
☐ 119_DE_22	*Staphylococcus aureus*	22
☐ 118_DE_22	*Staphylococcus aureus*	22
☐ 112_DE_22	*Staphylococcus aureus*	22

ANALISIS DE GENOMAS COMPLETOS EN WGSA



☐ **110_DE_22**

Organism
Staphylococcus aureus

Sequence Type
22

AMR
MET, PEN, CIP

Country
Germany

Uploaded
22 Nov 2017 17:16

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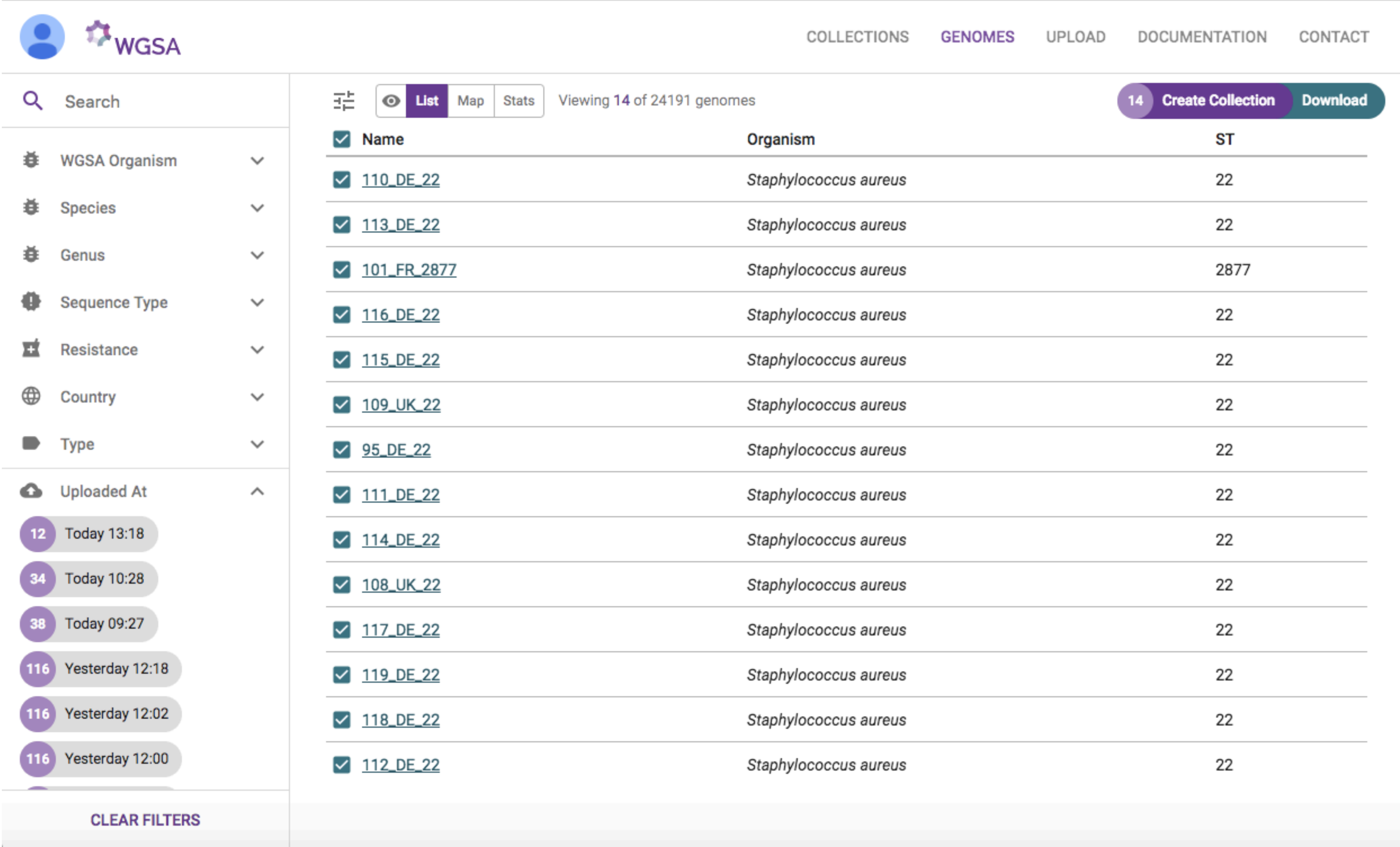
ANALISIS DE GENOMAS COMPLETOS EN WGSA



Viewing 14 of 24191 genomes

☑	Name	Organism	ST
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☑	113_DE_22	*Staphylococcus aureus*	22
☑	101_FR_2877	*Staphylococcus aureus*	2877
☑	116_DE_22	*Staphylococcus aureus*	22
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☑	111_DE_22	*Staphylococcus aureus*	22
☑	114_DE_22	*Staphylococcus aureus*	22
☑	108_UK_22	*Staphylococcus aureus*	22
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☑	119_DE_22	*Staphylococcus aureus*	22
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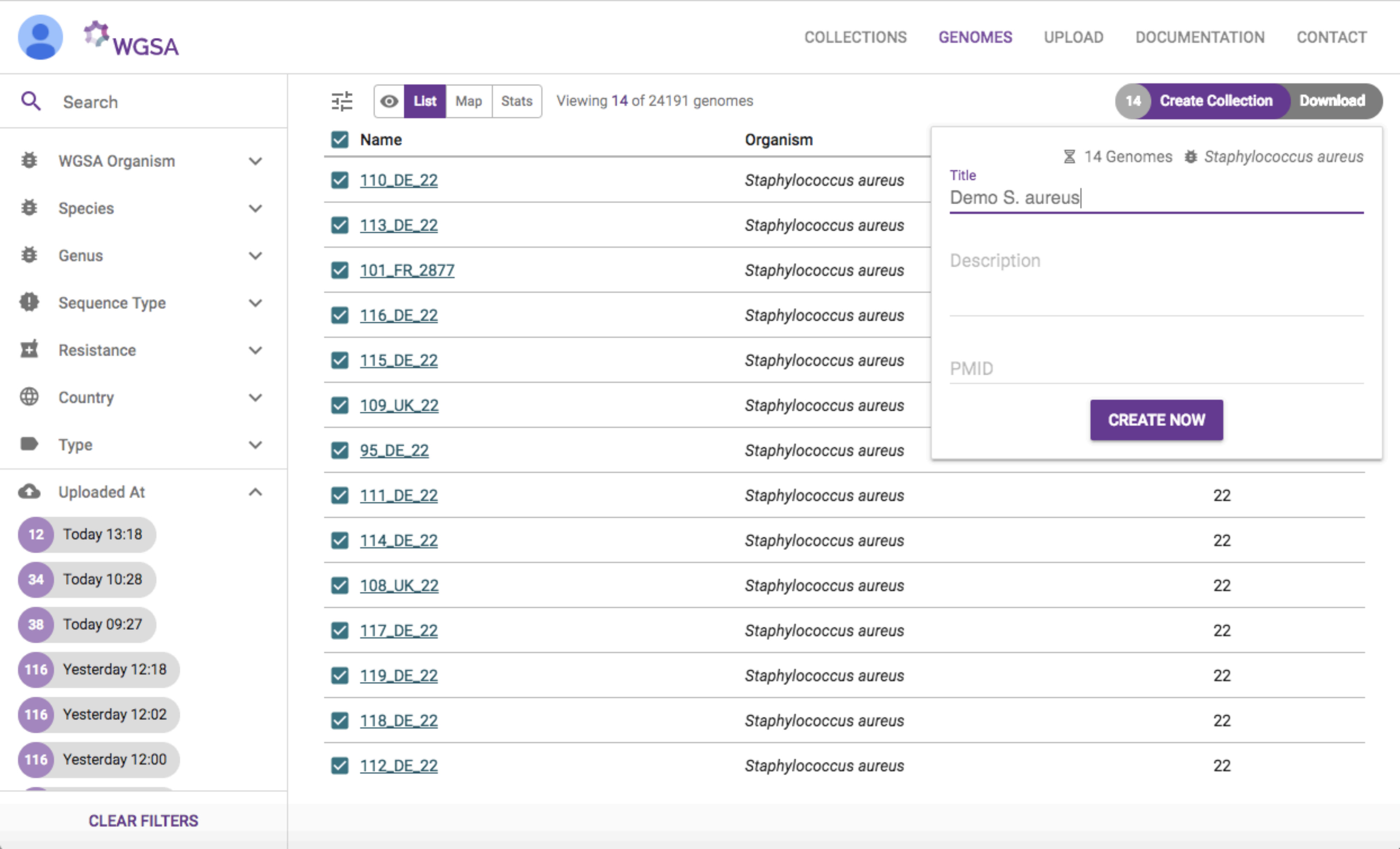
☑	112_DE_22	*Staphylococcus aureus*	22

ANALISIS DE GENOMAS COMPLETOS EN WGSA



Viewing 14 of 24191 genomes

☑ Name	Organism	
☑ 110_DE_22	*Staphylococcus aureus*	
☑ 113_DE_22	*Staphylococcus aureus*	
☑ 101_FR_2877	*Staphylococcus aureus*	
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☑ 119_DE_22	*Staphylococcus aureus*	22
☑ 118_DE_22	*Staphylococcus aureus*	22
☑ 112_DE_22	*Staphylococcus aureus*	22

14 Genomes *Staphylococcus aureus*

Title: Demo S. aureus

Description

PMID

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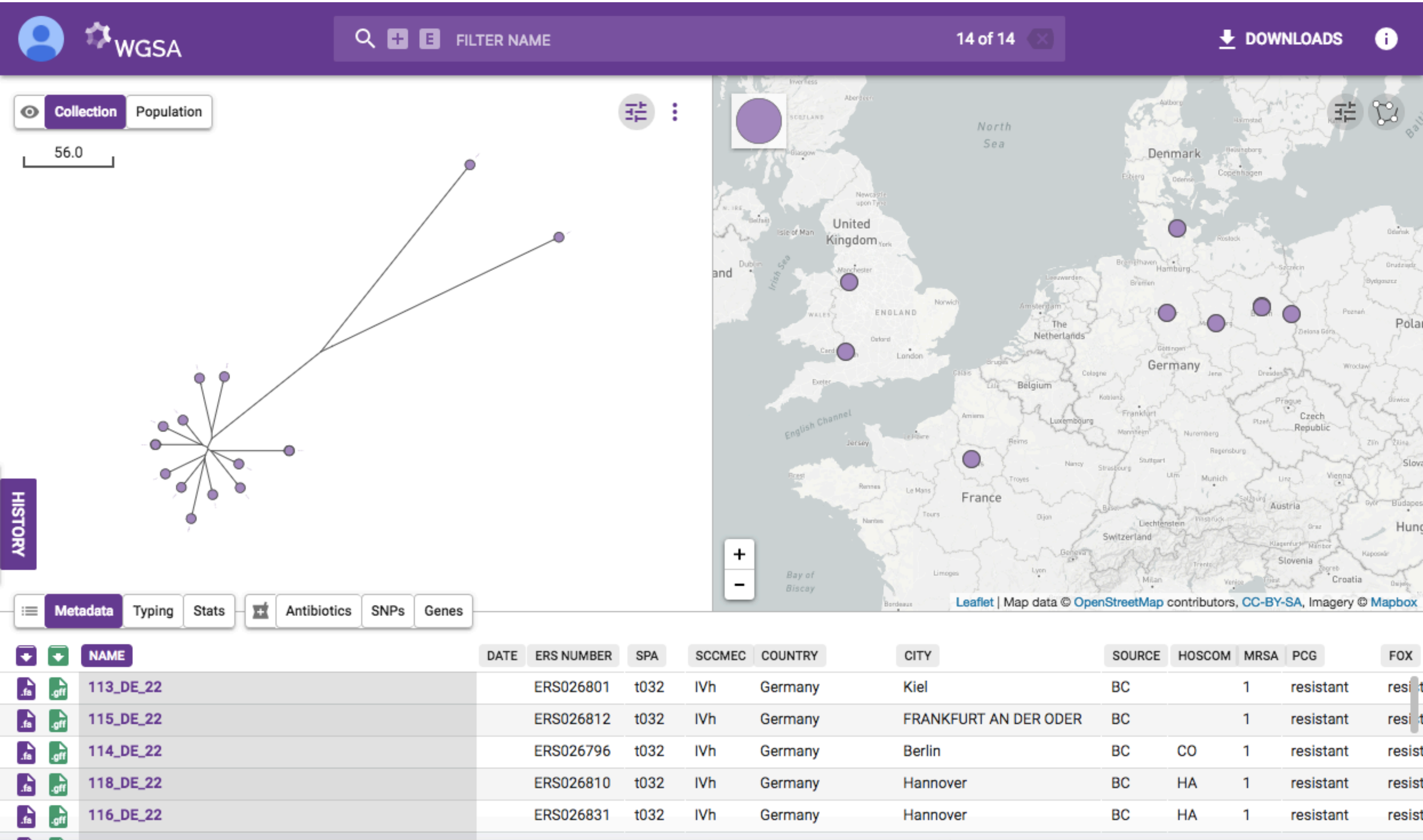
ANALISIS DE GENOMAS COMPLETOS EN WGSA



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NAME	DATE	ERS NUMBER	SPA	SCCMEC	COUNTRY	CITY	SOURCE	HOSCOM	MRSA	PCG	FOX
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115_DE_22		ERS026812	t032	IVh	Germany	FRANKFURT AN DER ODER	BC		1	resistant	resi
114_DE_22		ERS026796	t032	IVh	Germany	Berlin	BC	CO	1	resistant	resist
118_DE_22		ERS026810	t032	IVh	Germany	Hannover	BC	HA	1	resistant	resist
116_DE_22		ERS026831	t032	IVh	Germany	Hannover	BC	HA	1	resistant	resist

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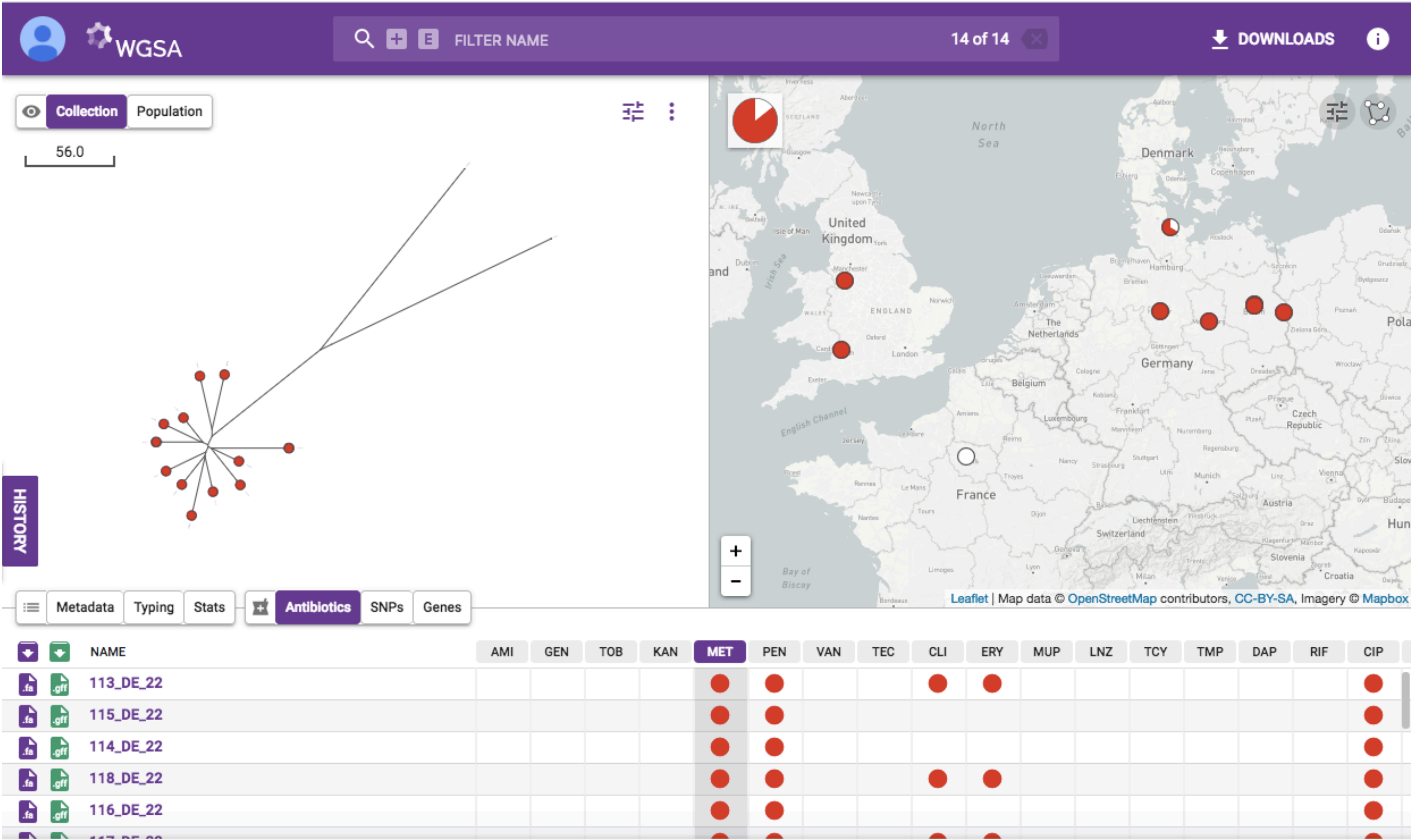
ANALISIS DE GENOMAS COMPLETOS EN WGSA



NAME	AMI	GEN	TOB	KAN	MET	PEN	VAN	TEC	CLI	ERY	MUP	LNZ	TCY	TMP	DAP	RIF	CIP
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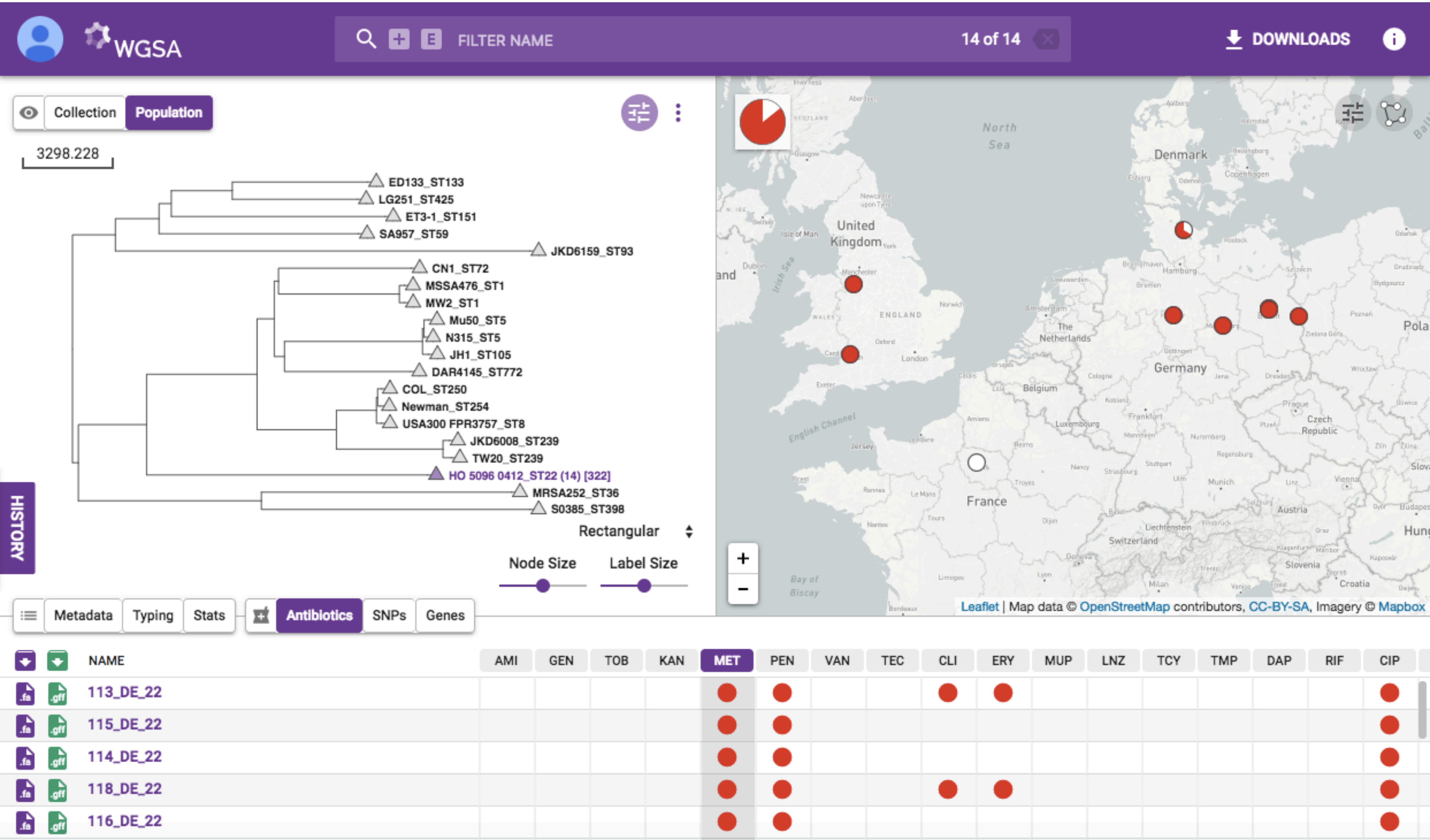
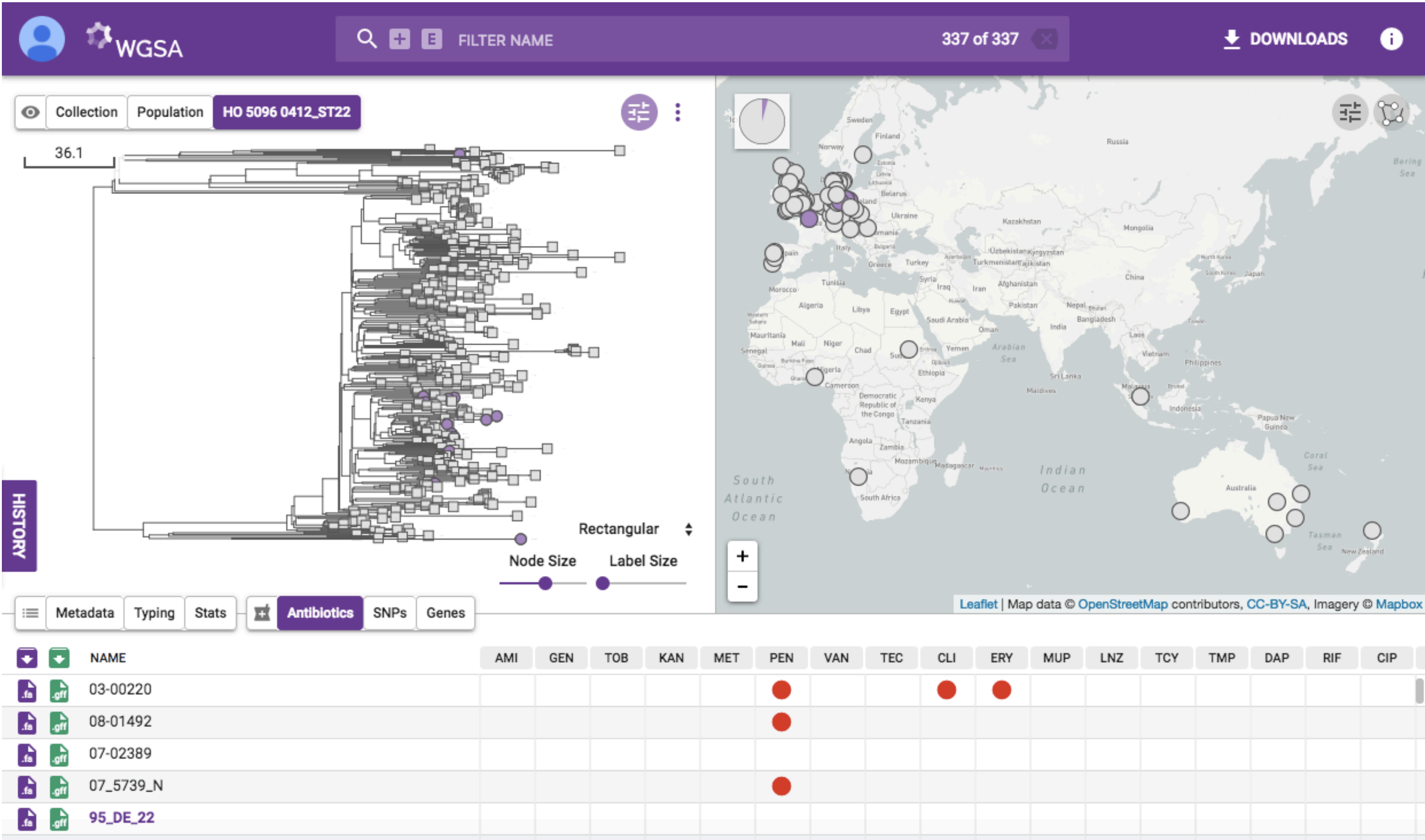
115_DE_22					●	●											●
114_DE_22					●	●											●
118_DE_22					●	●			●	●							●
116_DE_22					●	●											●

ANALISIS DE GENOMAS COMPLETOS EN WGSA



NAME	AMI	GEN	TOB	KAN	MET	PEN	VAN	TEC	CLI	ERY	MUP	LNZ	TCY	TMP	DAP	RIF	CIP
113_DE_22					●	●			●	●							●
115_DE_22					●	●											●
114_DE_22					●	●											●
118_DE_22					●	●			●	●							●
116_DE_22					●	●											●

ANALISIS DE GENOMAS COMPLETOS EN WGSA



NAME	AMI	GEN	TOB	KAN	MET	PEN	VAN	TEC	CLI	ERY	MUP	LNZ	TCY	TMP	DAP	RIF	CIP
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08-01492						●											
07-02389																	
07_5739_N						●											
95_DE_22																	

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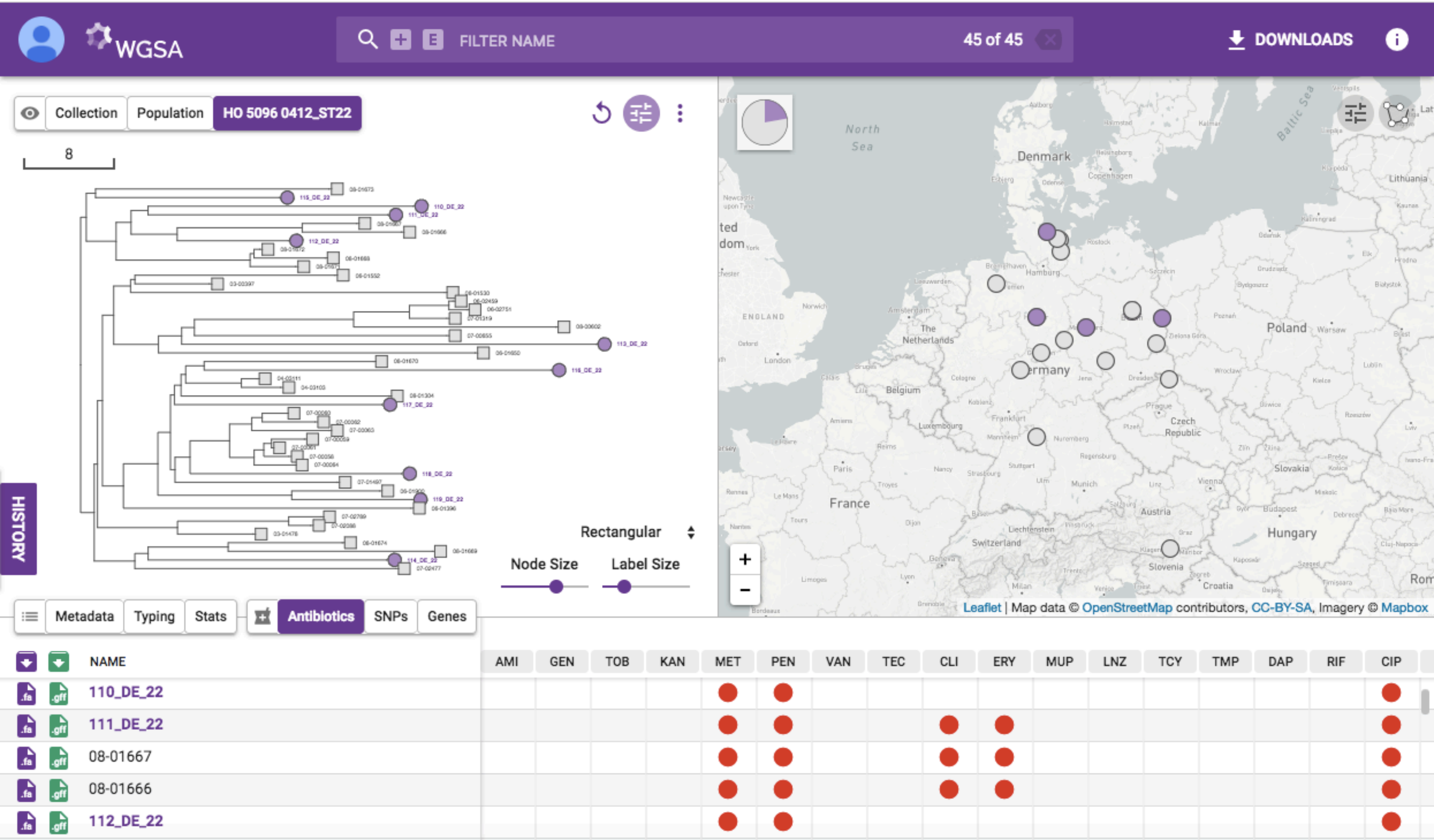
ANALISIS DE GENOMAS COMPLETOS EN WGSA



NAME	AMI	GEN	TOB	KAN	MET	PEN	VAN	TEC	CLI	ERY	MUP	LNZ	TCY	TMP	DAP	RIF	CIP
110_DE_22					●	●											●
111_DE_22					●	●			●	●							●
08-01667					●	●			●	●							●
08-01666					●	●			●	●							●
112_DE_22					●	●											●

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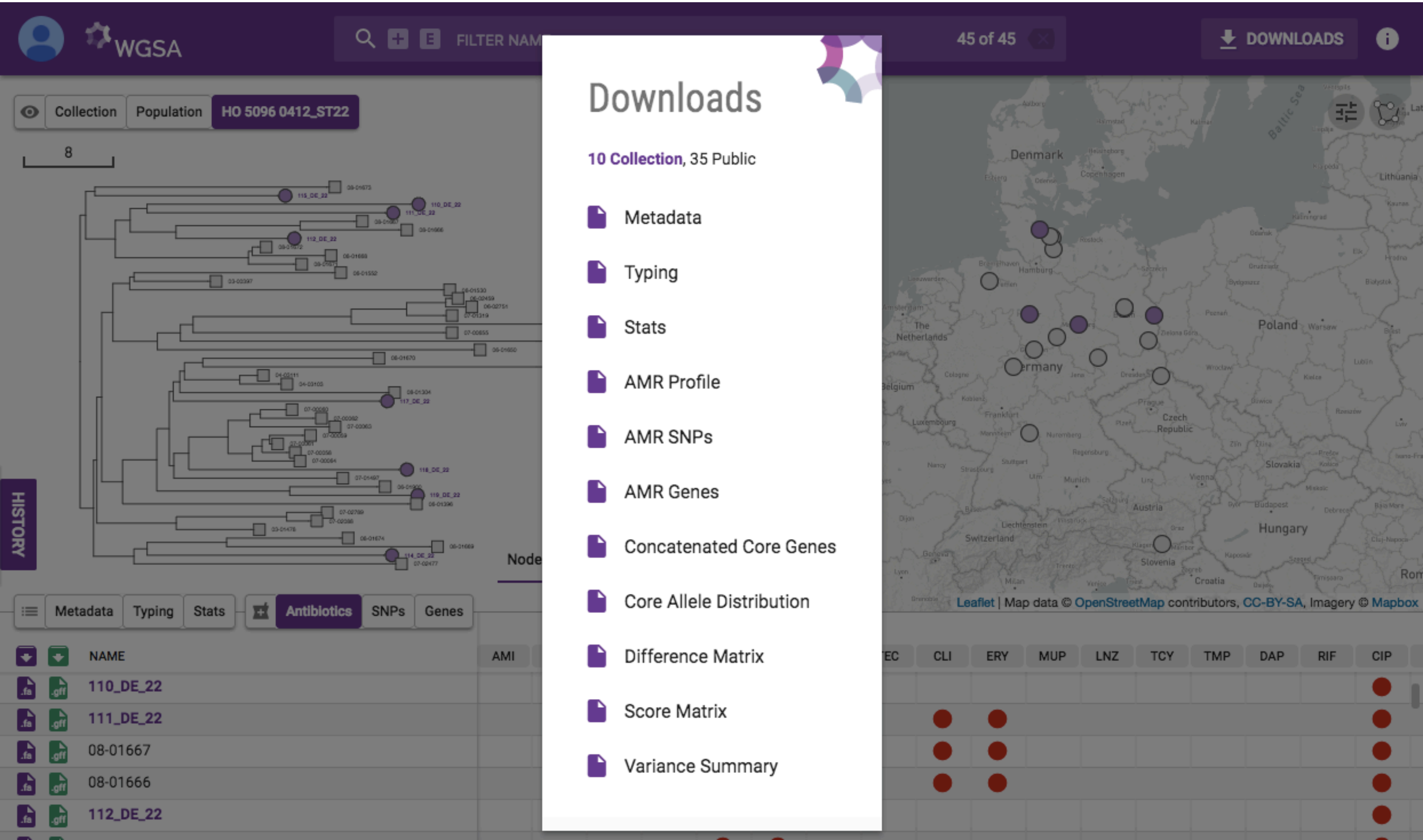

Downloads

10 Collection, 35 Public

- Metadata
- Typing
- Stats
- AMR Profile
- AMR SNPs
- AMR Genes
- Concatenated Core Genes
- Core Allele Distribution
- Difference Matrix
- Score Matrix
- Variance Summary

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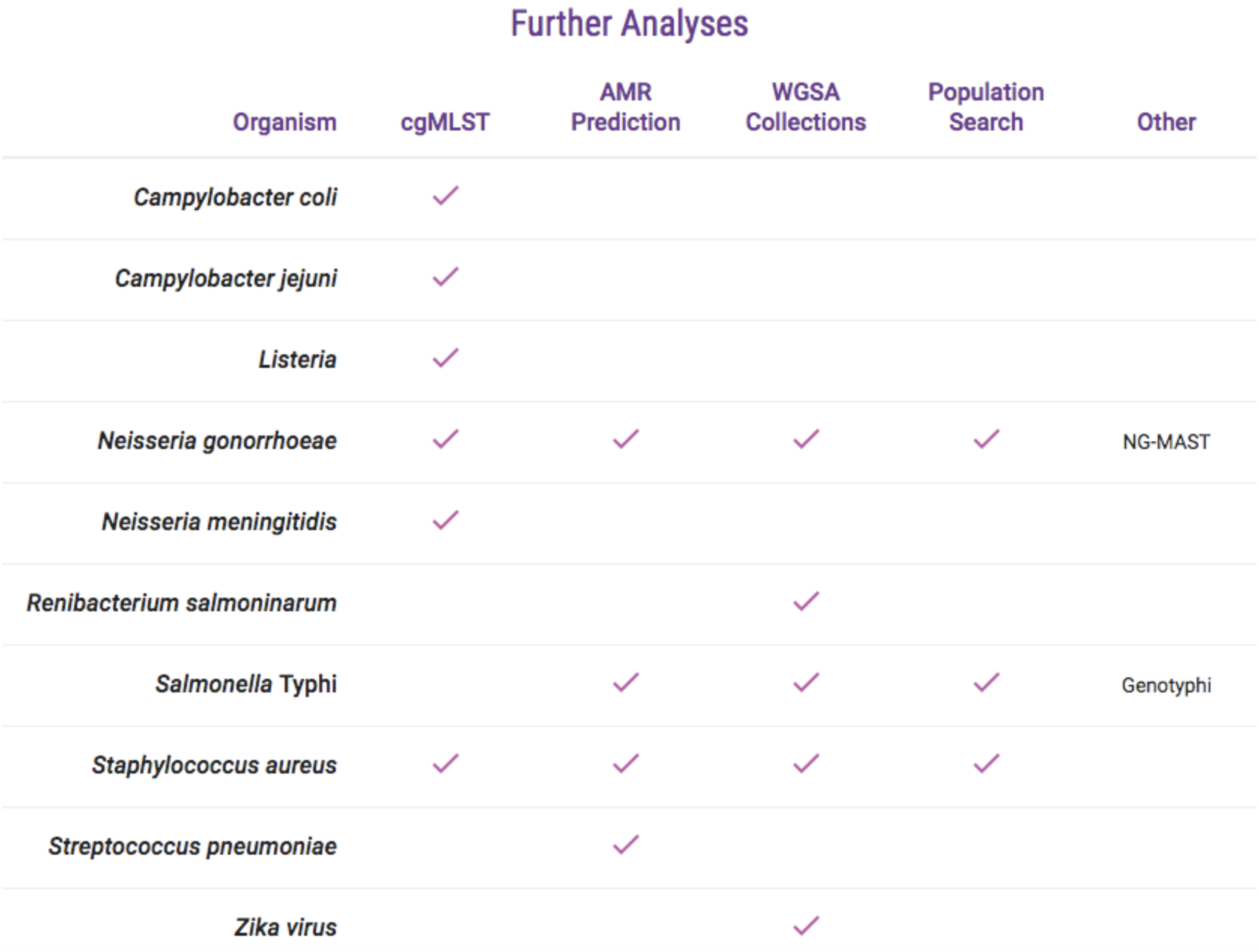

Further Analyses

Organism	cgMLST	AMR Prediction	WGSA Collections	Population Search	Other
Campylobacter coli	✓				
Campylobacter jejuni	✓				
Listeria	✓				
Neisseria gonorrhoeae	✓	✓	✓	✓	NG-MAST
Neisseria meningitidis	✓				
Renibacterium salmoninarum			✓		
Salmonella Typhi		✓	✓	✓	Genotyphi
Staphylococcus aureus	✓	✓	✓	✓	
Streptococcus pneumoniae		✓			
Zika virus			✓		

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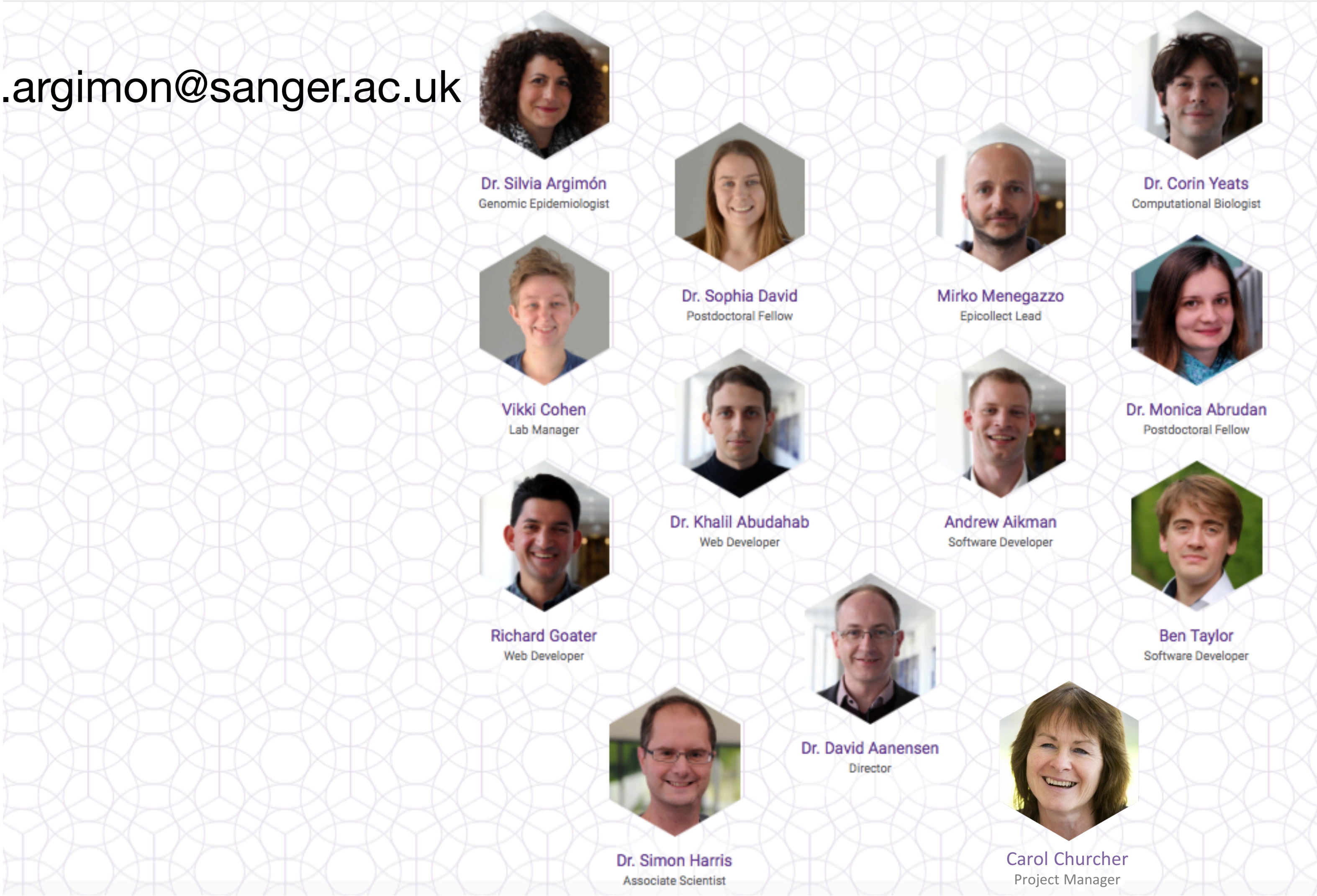

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