

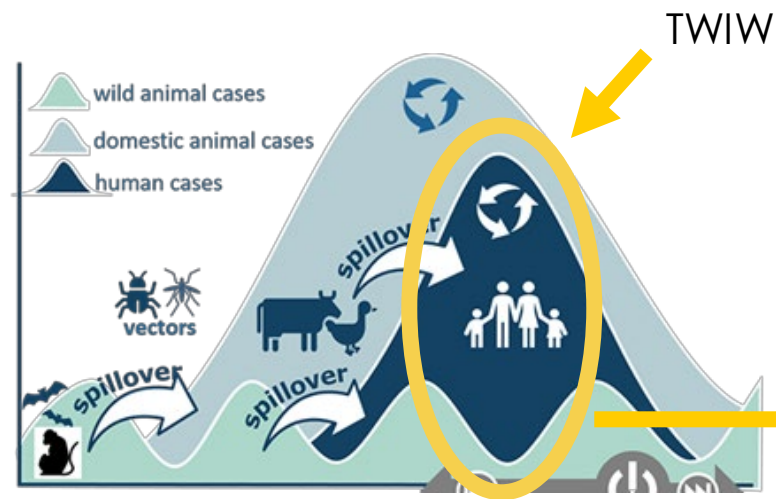


The Two Year Mark

TWIIW 2020

(TWIW: Two Weeks in the World)

“Frank’s Pyramids”



Gunhild



Laura



Judit



Máté

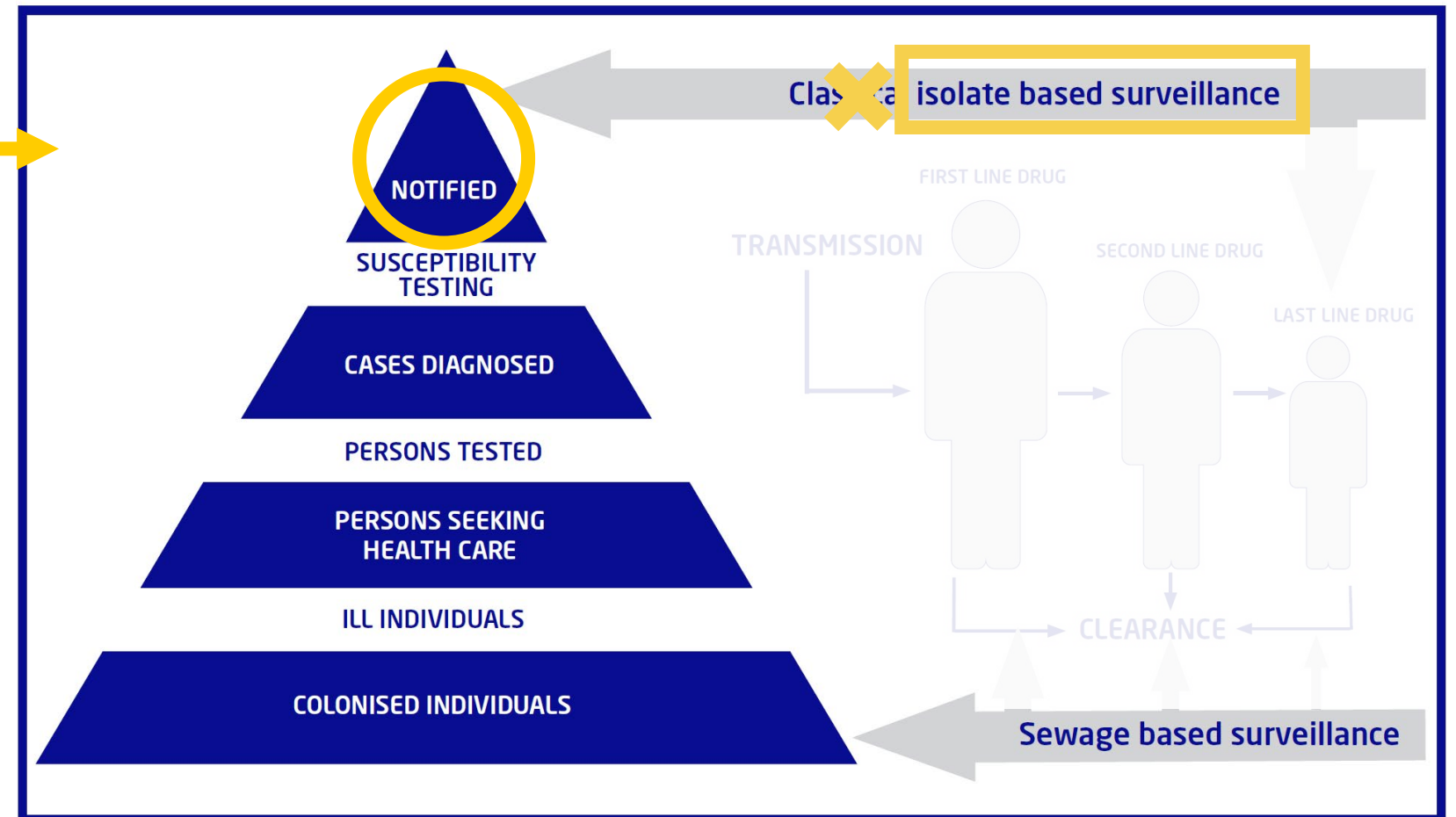


Wojciech



Derya

And Christina, Jacob, Birthe, Hanne, Hanne, Michella, Ditte... and Frank



TWIW – “untargeted” sampling

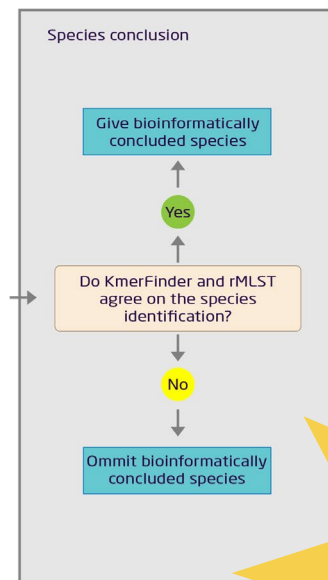
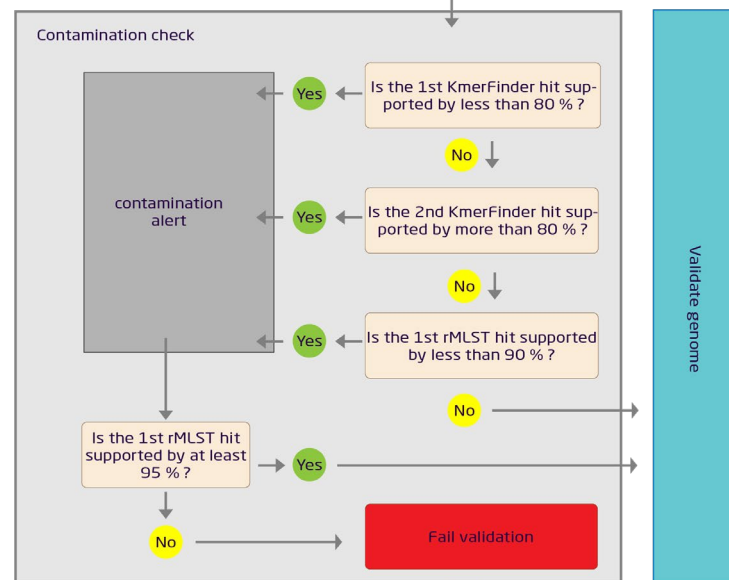
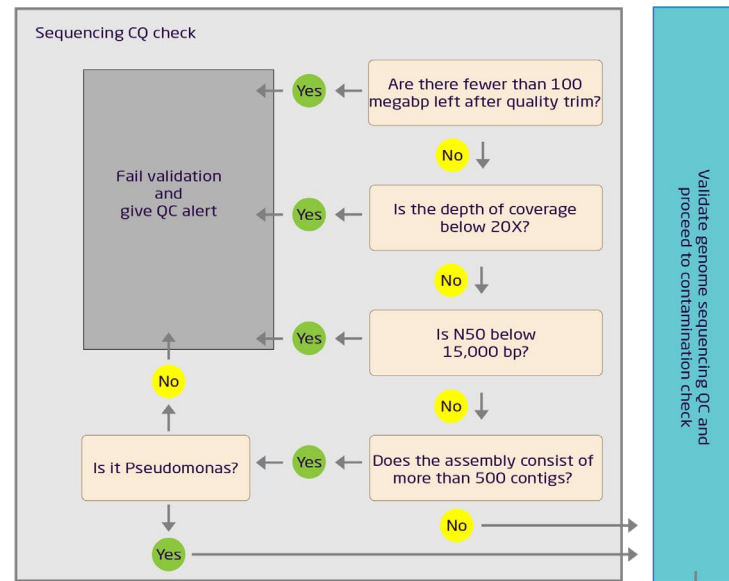
“Dear microbiological diagnostic unit”,

- Over the course of a week, collect every “ n^{th} ” sample until you reach approximately 60.
- Collect the samples from the entire body of samples that the unit processes.

Definition: “dataset” VS “final dataset”

“**dataset**”: Received samples + metadata

“**final dataset**”: samples in dataset where sequenced genome has been validated by internal bioinformatic assessment → applicable for downstream analysis



Examples of differences:

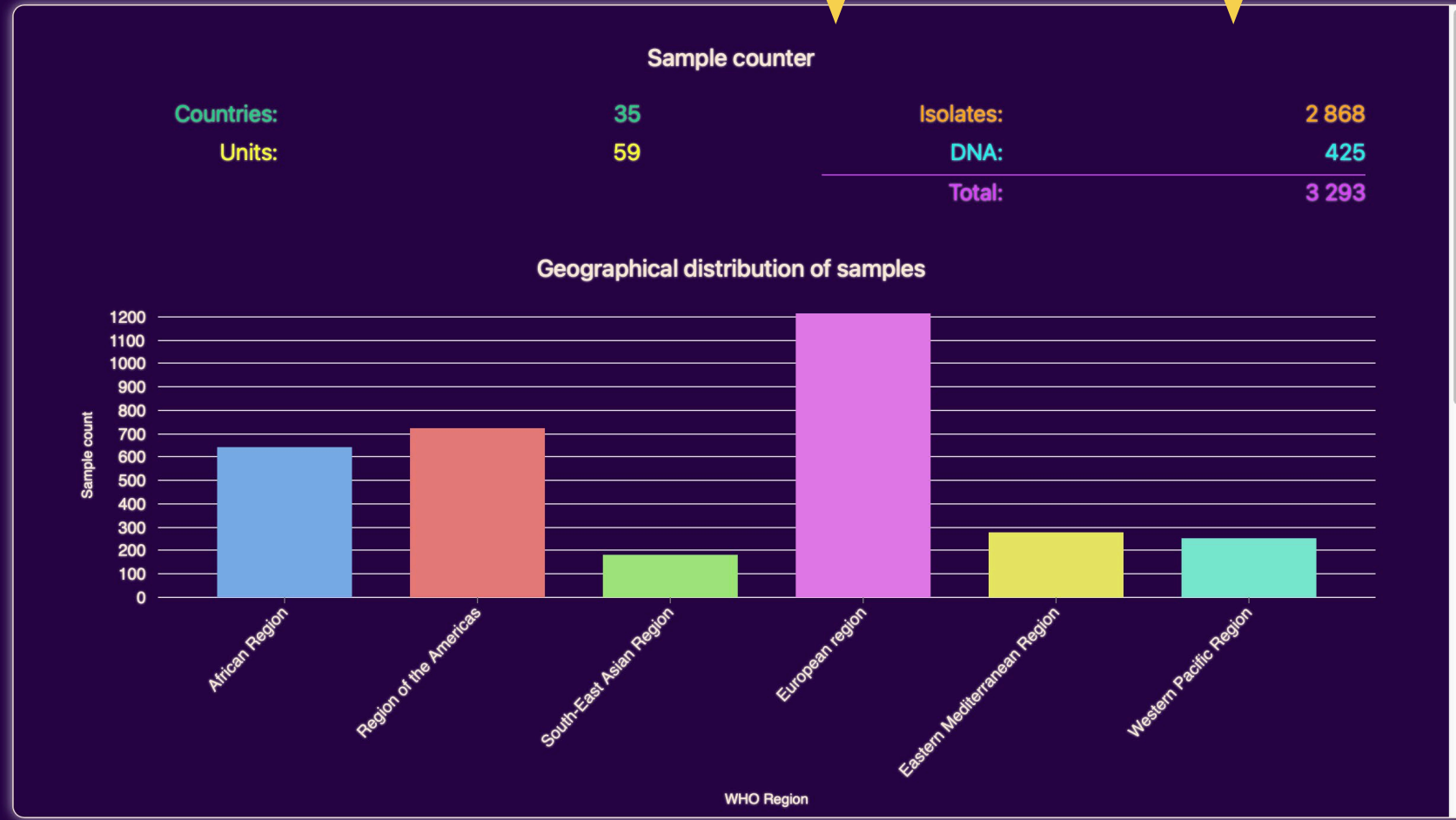
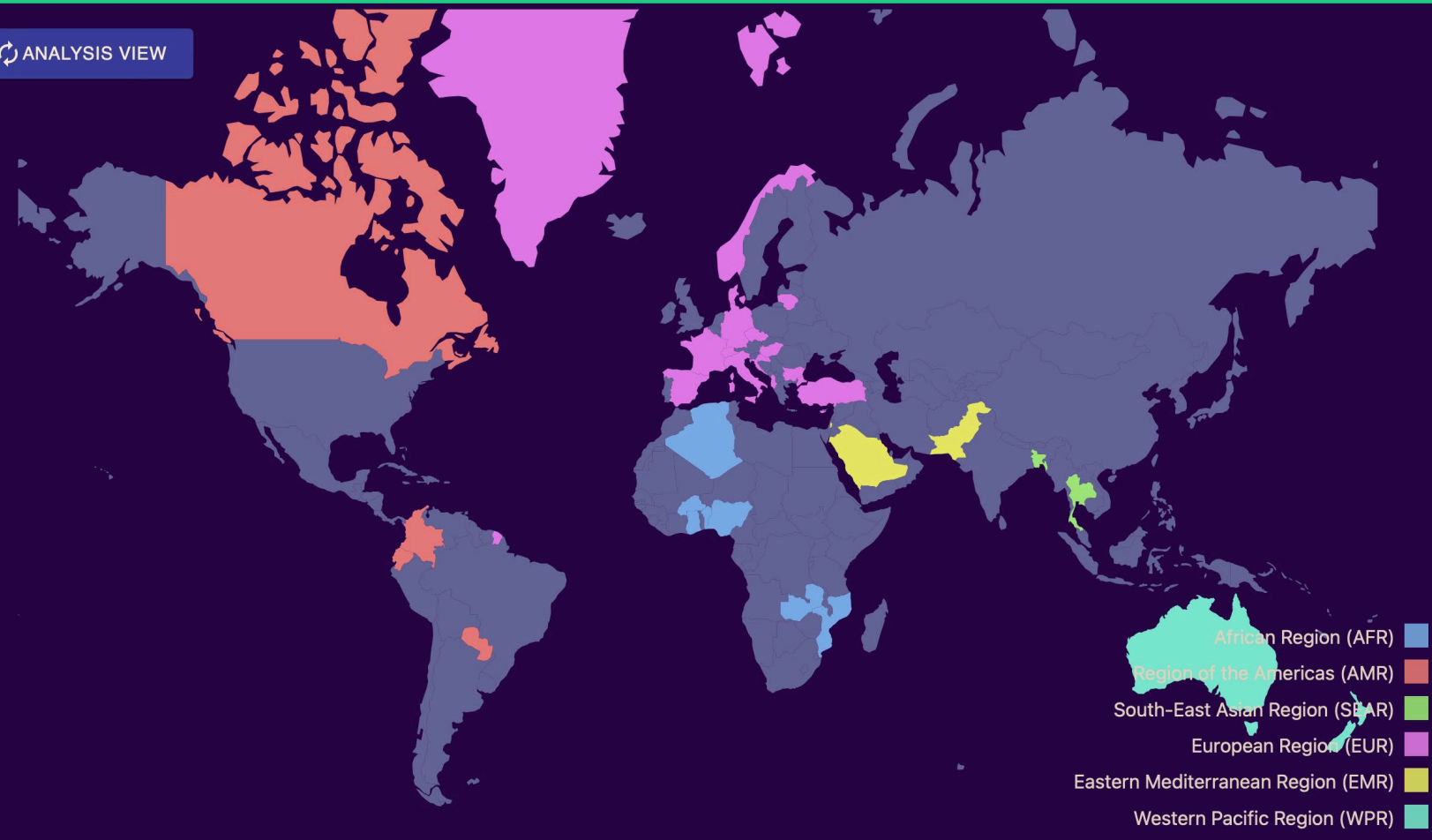
Unviable samples: Helicobacter, Corynebacterium, Neisseria, Haemophilus...

Contaminations: fungal, Proteus, bacterial in pre-extracted DNA (cannot be regrown and re-isolated in-house)

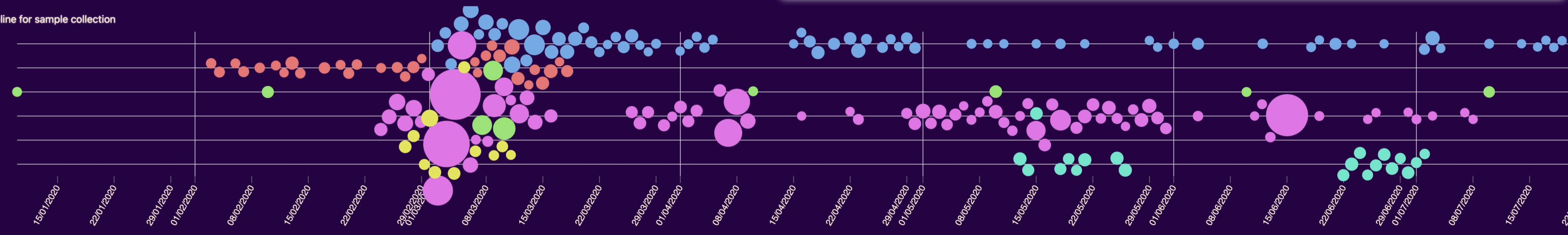




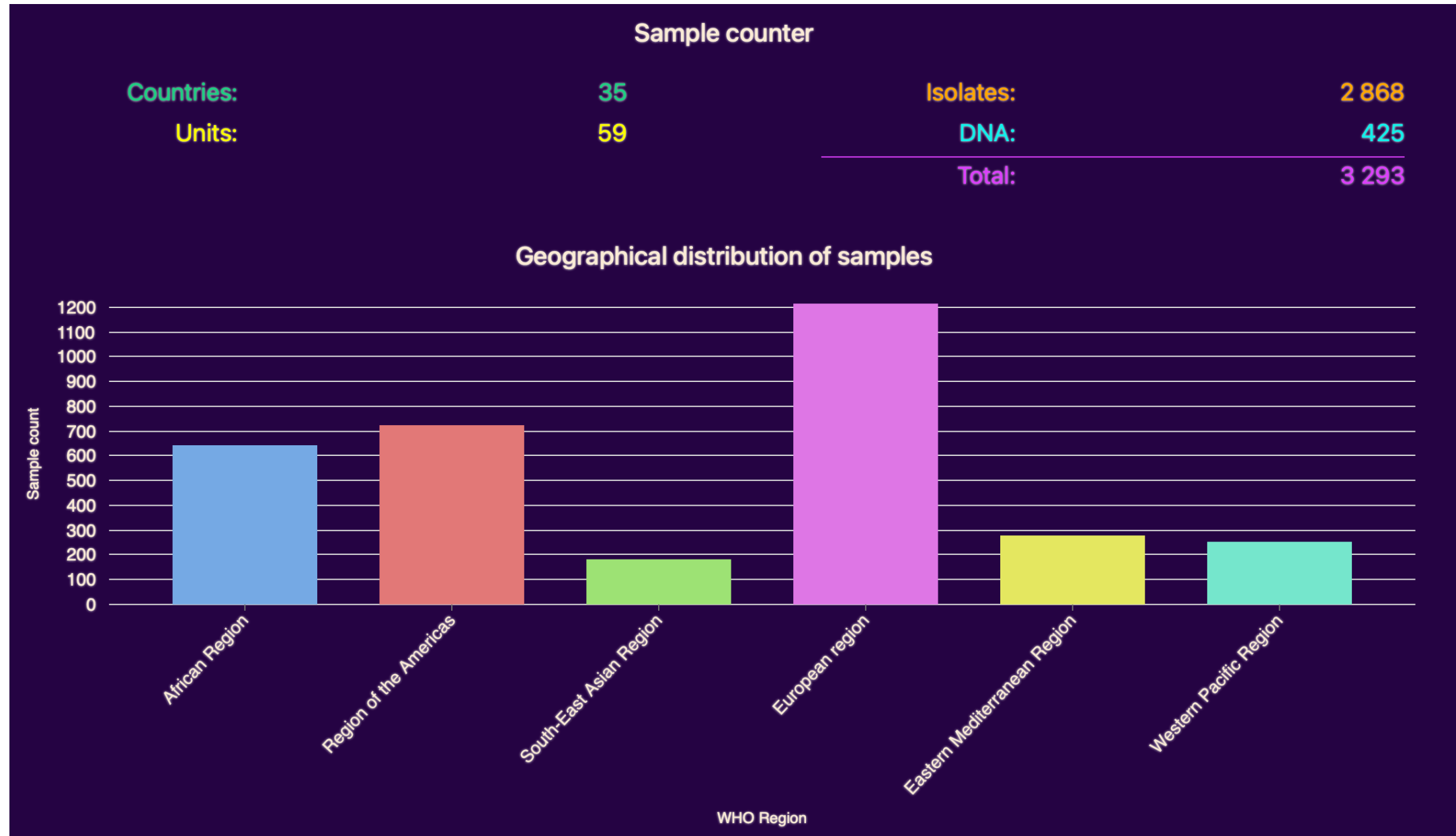
ANALYSIS VIEW



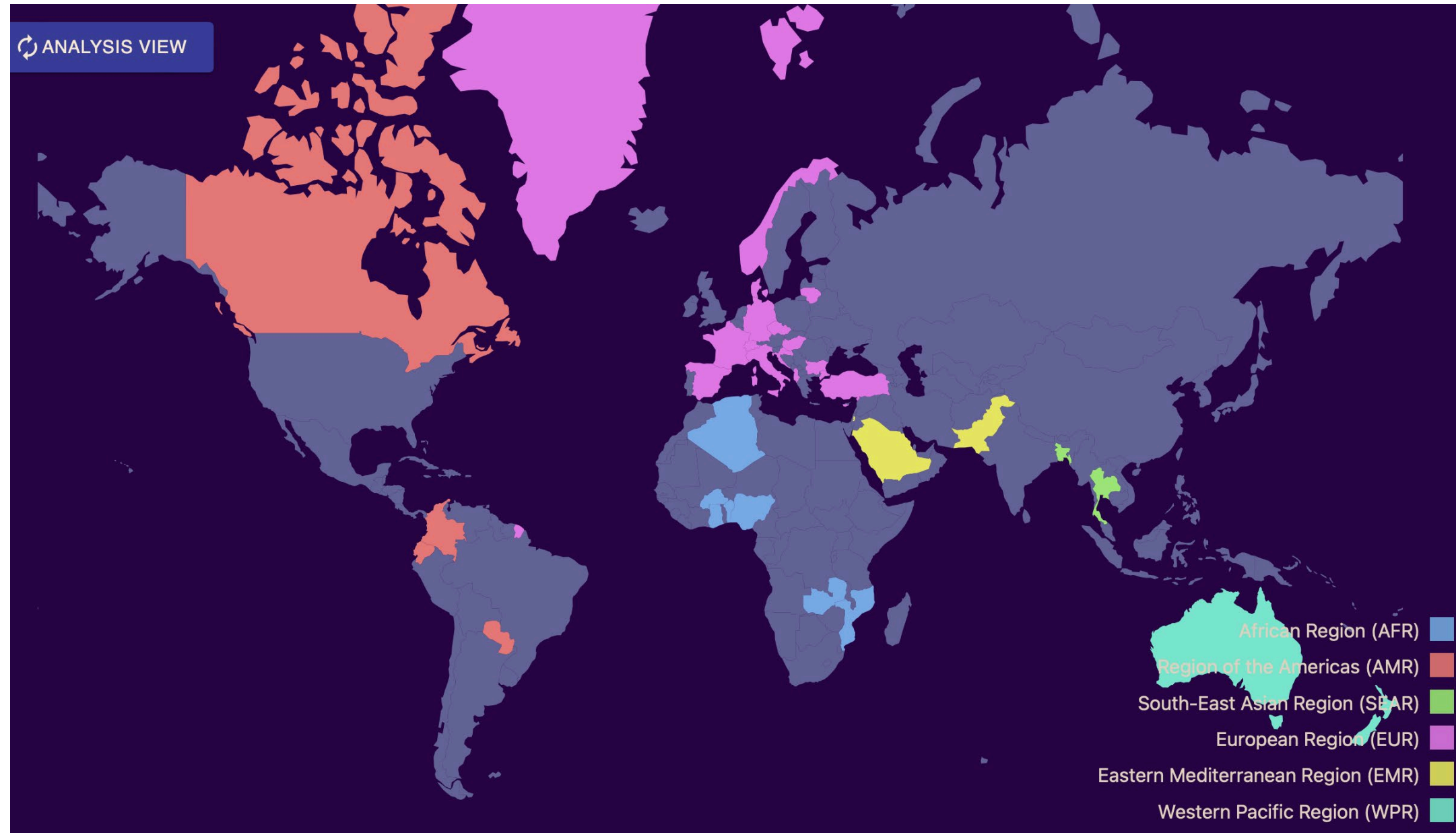
Timeline for sample collection



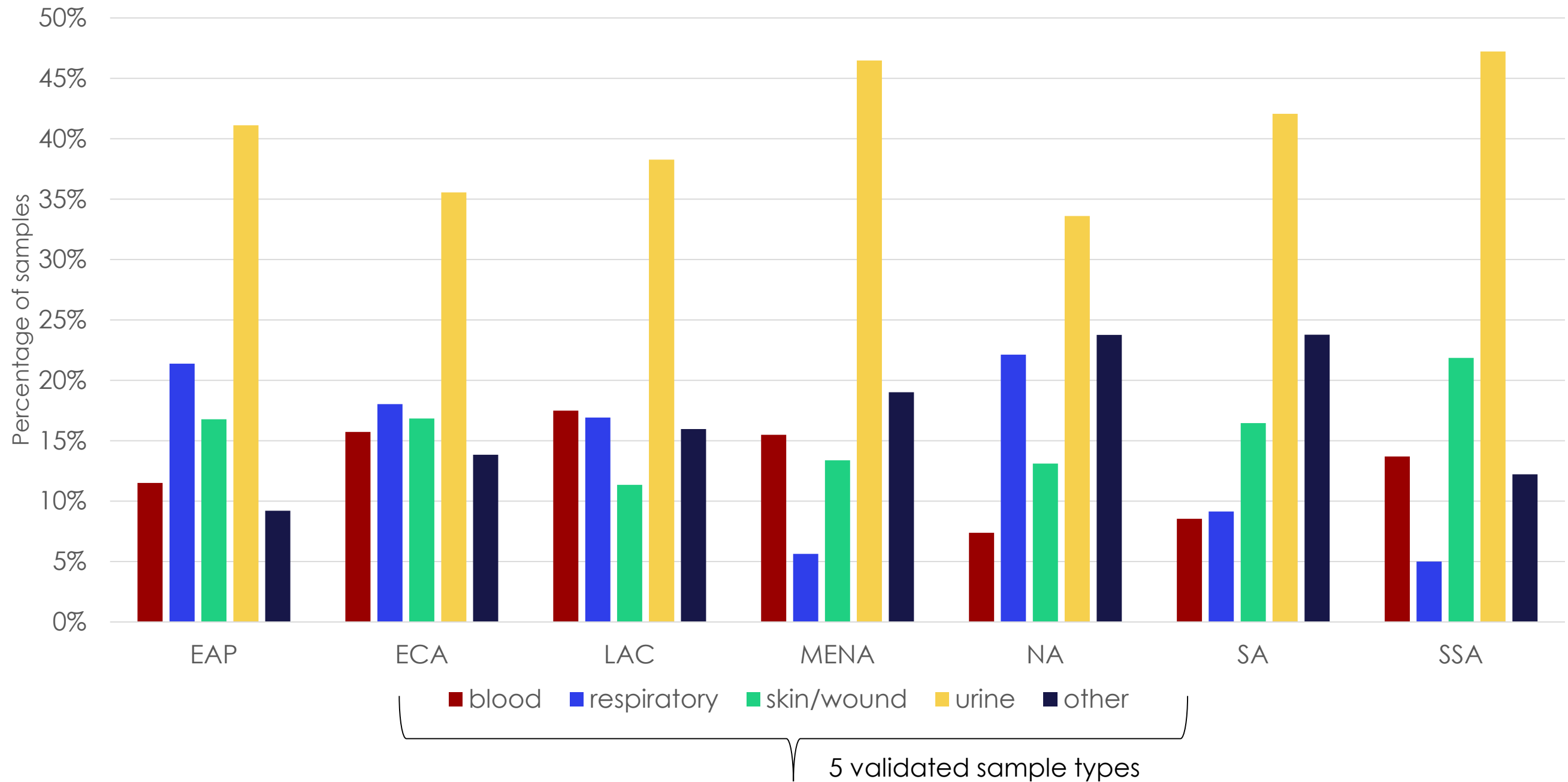
Status



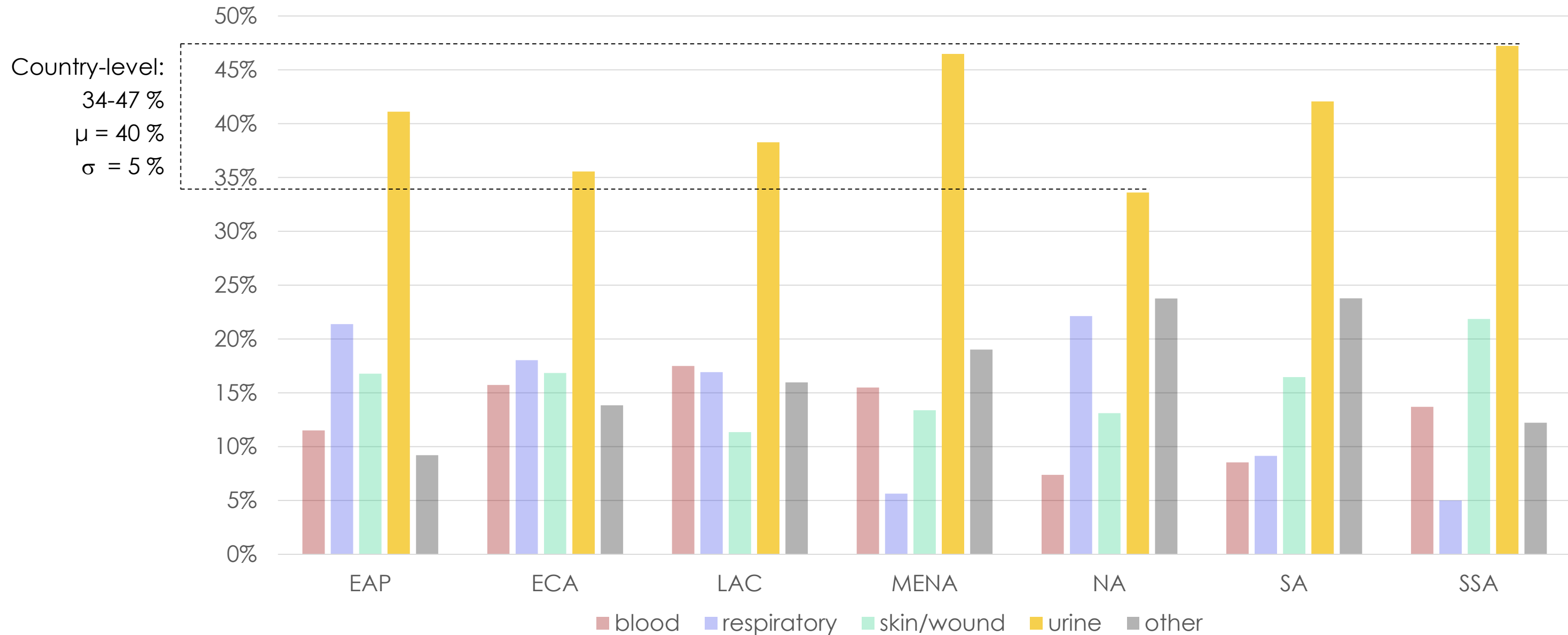
Status



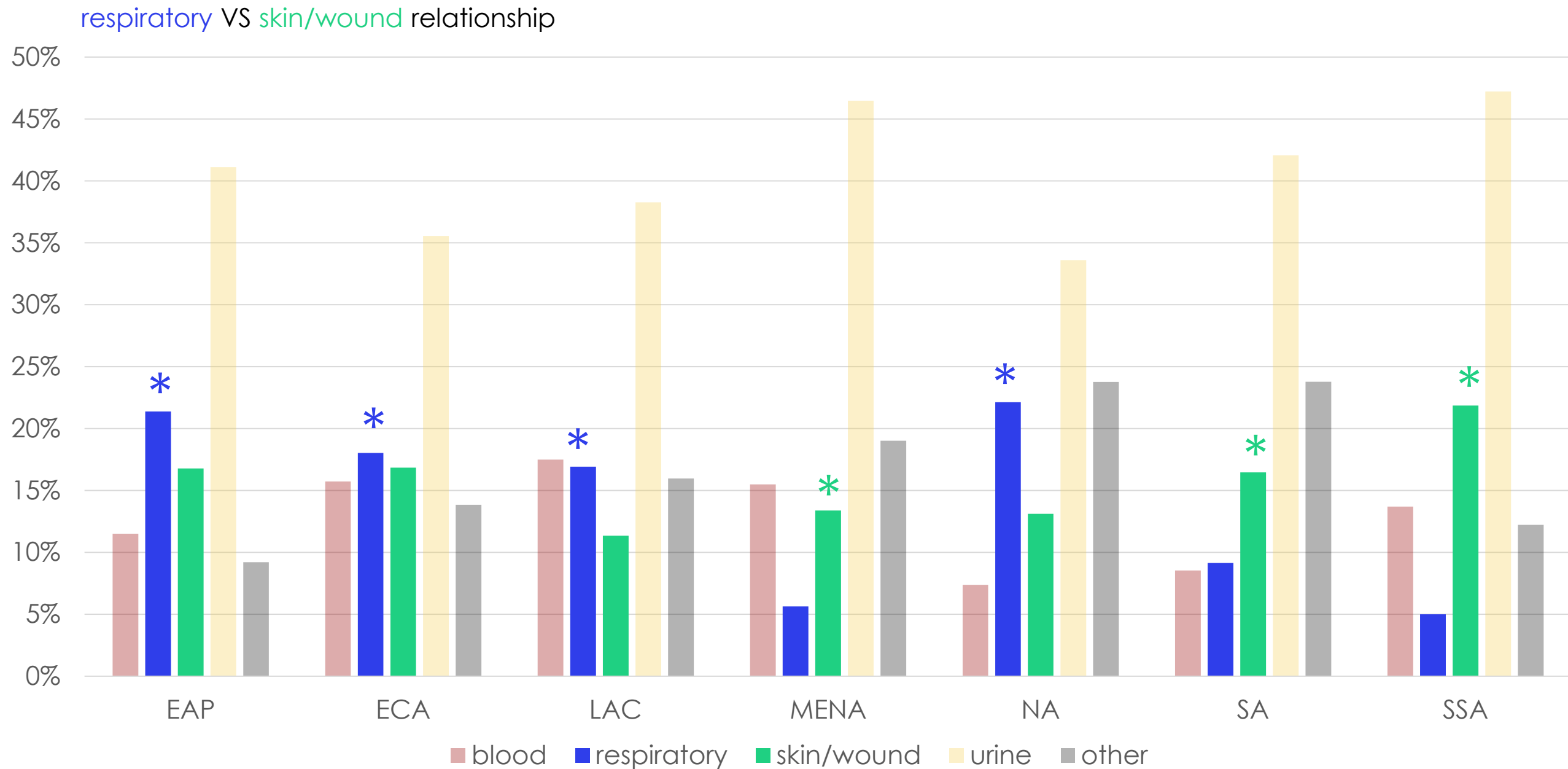
Sample types represented in dataset



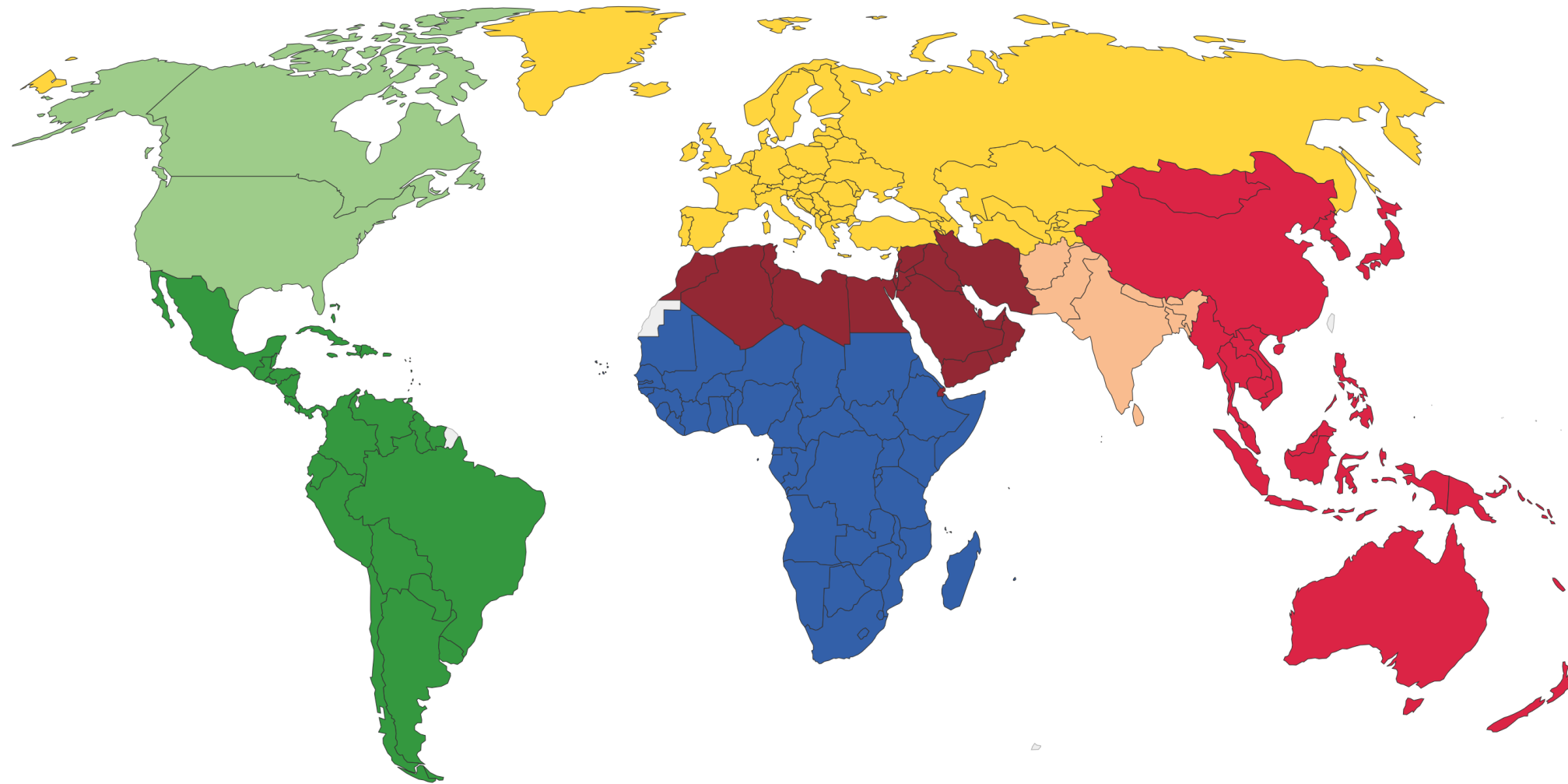
Isolates from urine samples dominate the dataset



Isolates from urine samples dominate the dataset

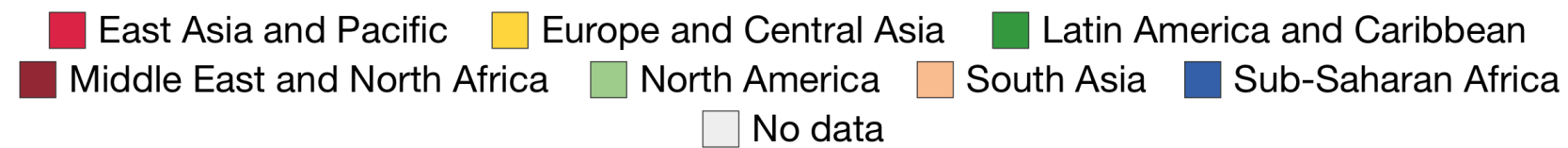


World regions according to the World Bank



Abbreviations:

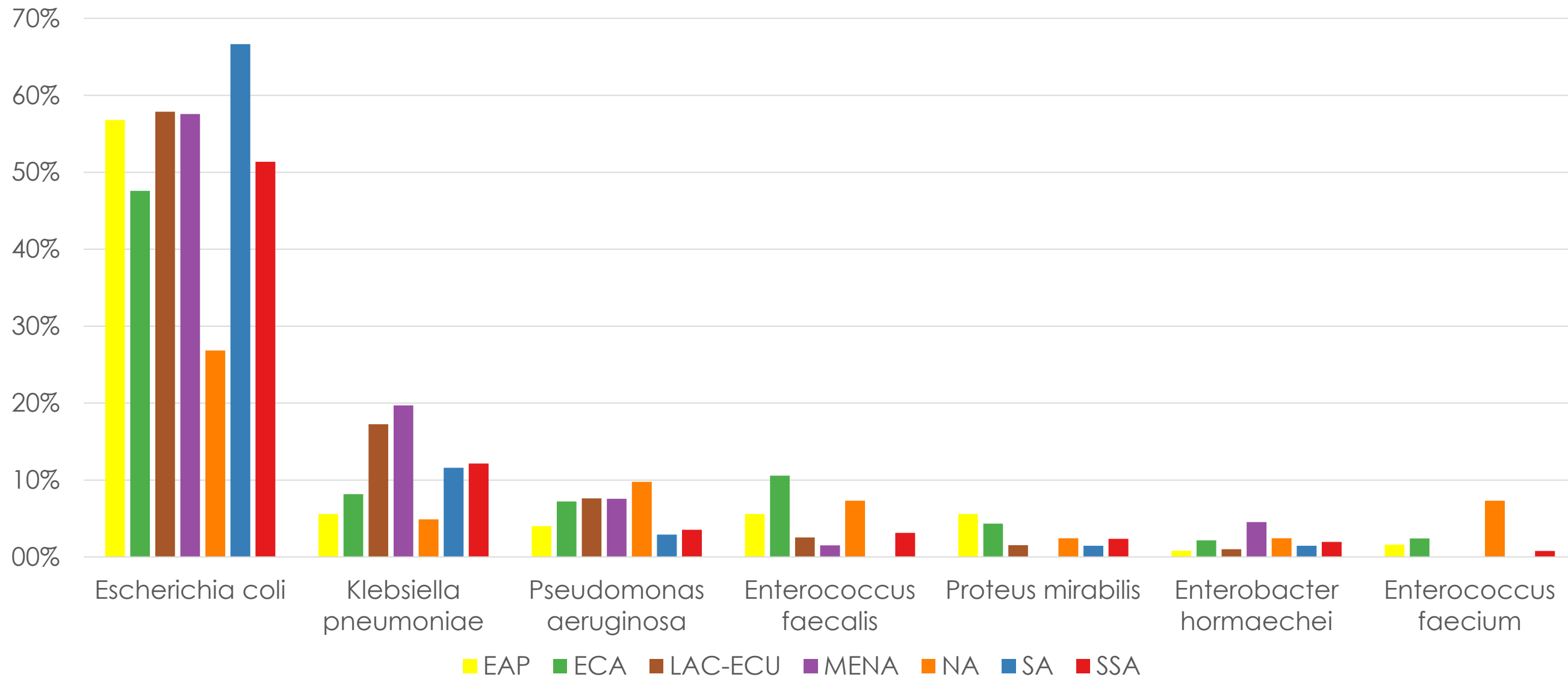
- EAP:** East Asia and Pacific
- ECA:** Europe and Central Asia
- LAC:** Latin America and Caribbean
- MENA:** Middle East and North Africa
- NA:** North America
- SA:** South Asia
- SSA:** Sub-Saharan Africa



Source: World Bank

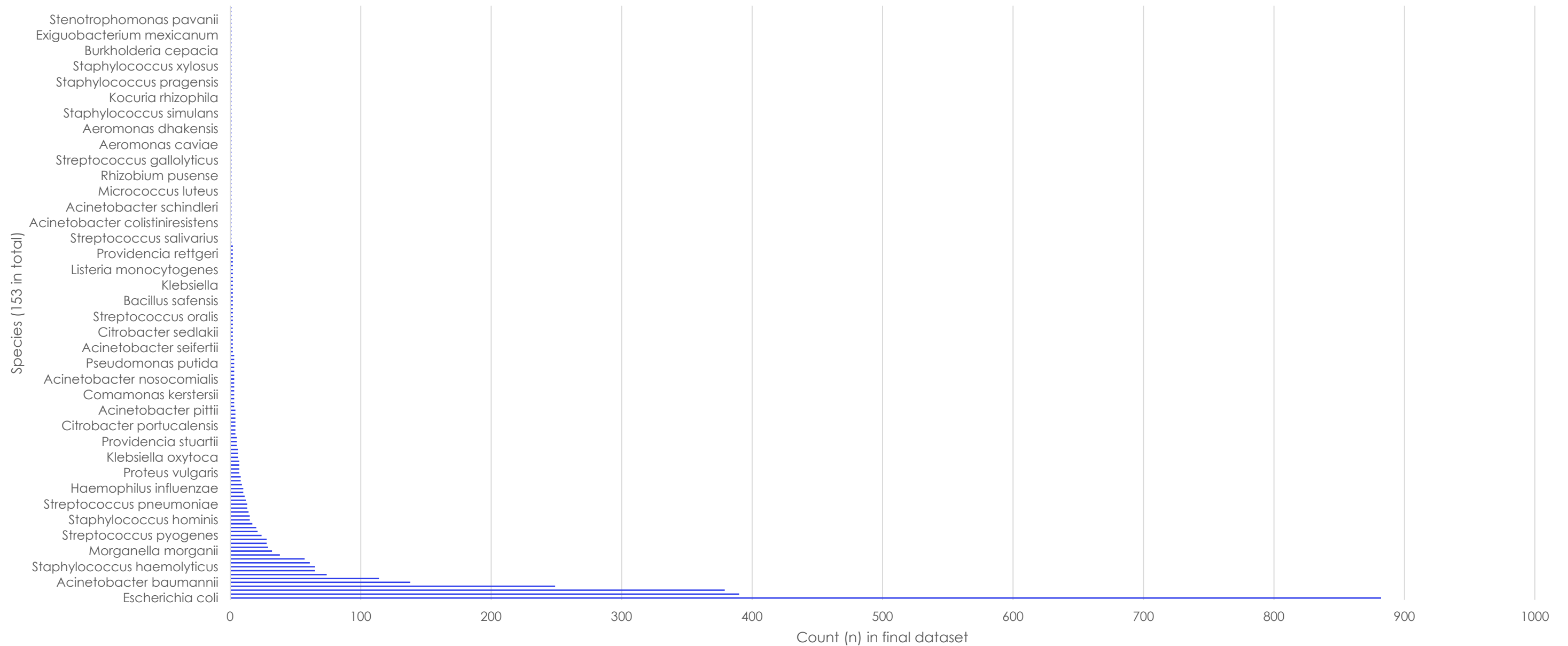
CC BY

Escherichia coli dominate the urine samples



153 species, 46 genera in final dataset

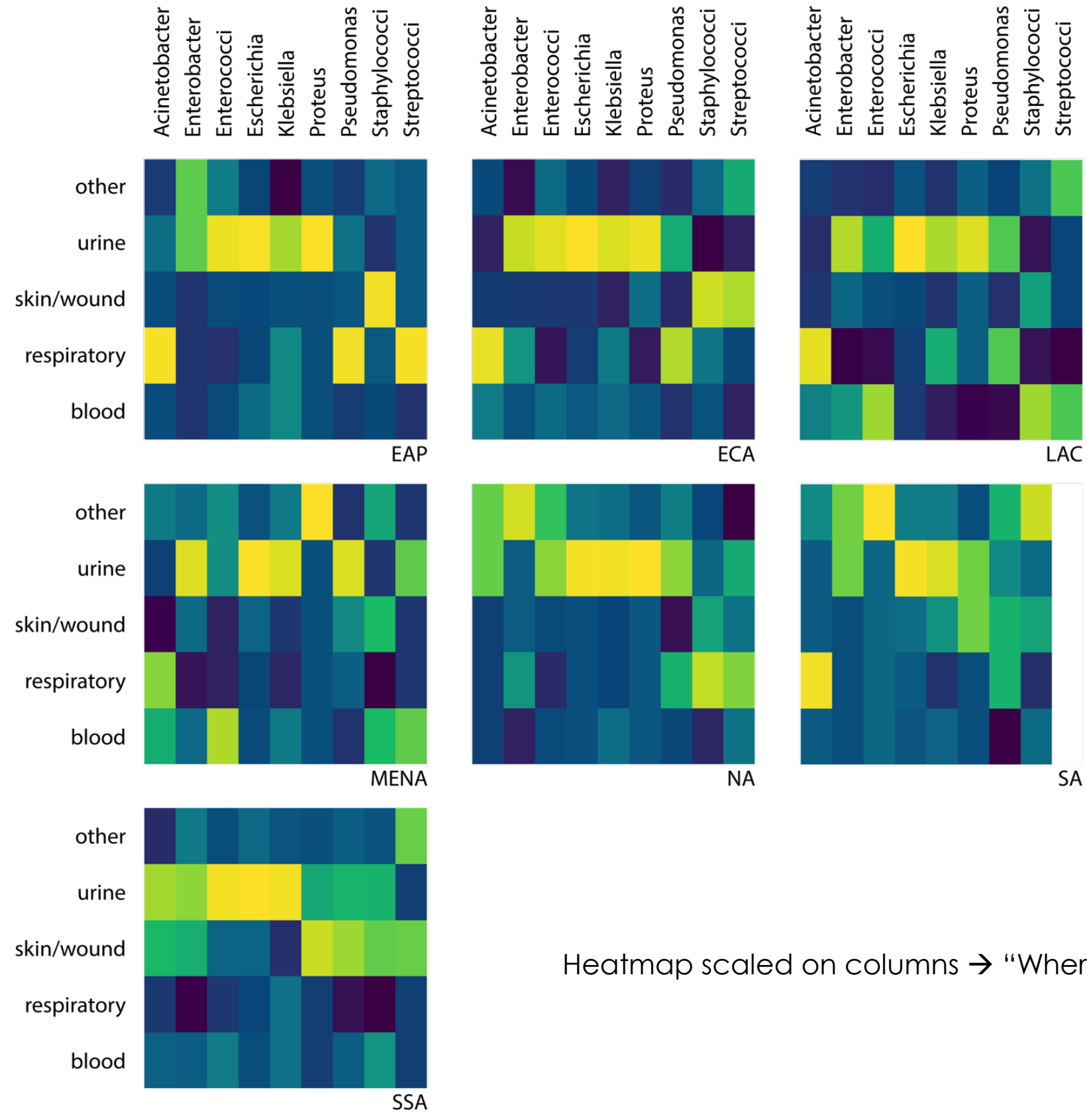
Species distribution



Main TWIW pathogen groups VS GLASS pathogens

Group	Nine main TWIW genera	Twenty-seven main TWIW species	GLASS-targeted pathogens
Definition level	Genus	Species	Genus and species
Percentage of isolates	91 %	90 %	59 %
Percentage of AMR gene hits	94 %	95 %	62 %
Number of genera included	9/46 (20 %)	14/46 (30 %)	9/46 (20 %)
Number of species included	85/153 (46 %)	27/153 (15 %)	23/153 (13 %)
Content	<p>Acinetobacter spp. (ONS = 15), Enterobacter spp. (ONS = 7), Enterococci spp. (ONS = 6), Escherichia spp. (ONS = 2), Klebsiella spp. (ONS = 9), Proteus spp. (ONS = 3), Pseudomonas spp. (ONS = 5), Staphylococci spp. (ONS = 17) and Streptococci spp. (ONS = 15) (All genera except Escherichia include a few isolates only identified at genus level)</p>	<p>Acinetobacter baumannii, Citrobacter koseri, Enterobacter cloacae, Enterobacter hormaechei, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Klebsiella aerogenes, Klebsiella pneumoniae, Klebsiella quasipneumoniae, Klebsiella variicola, Morganella morganii, Proteus mirabilis, Pseudomonas aeruginosa, Salmonella enterica, Serratia marcescens, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Staphylococcus hominis, Staphylococcus lugdunensis, Staphylococcus saprophyticus, Stenotrophomonas maltophilia, Streptococcus agalactiae, Streptococcus dysgalactiae, Streptococcus pyogenes, Streptococcus pneumoniae</p>	<p>Acinetobacter spp. (ONS. = 15), Escherichia coli, Klebsiella pneumoniae, Neisseria gonorrhoeae, Salmonella spp. (ONS. 1), Shigella spp. (ONS = 2), Staphylococcus aureus, and Streptococcus pneumoniae</p>

Source-pathogen correlations

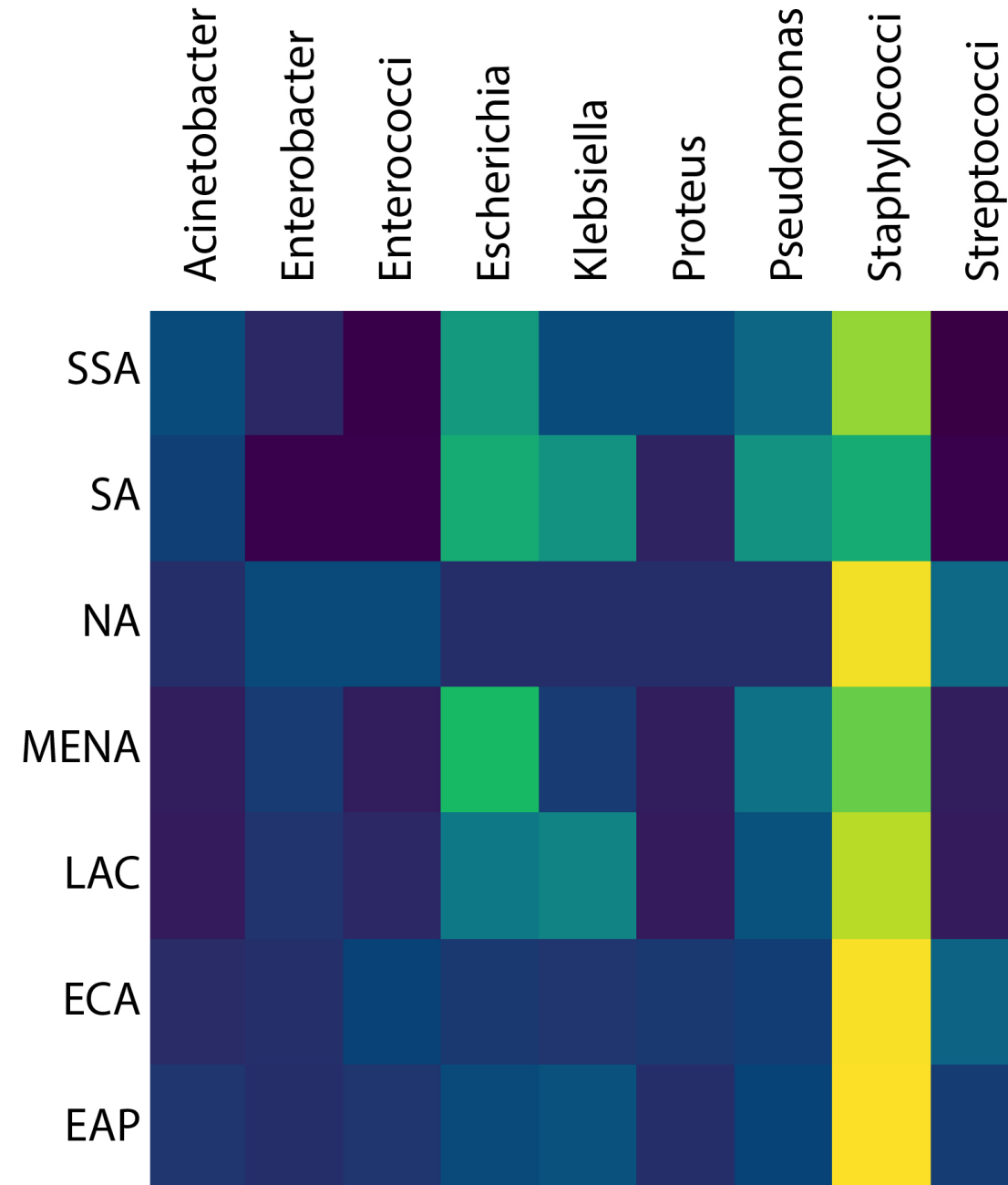


Heatmap scaled on columns → “Where do we find genus X”

Skin/wound

Source-pathogen correlations

2nd largest source-pathogen group (in numbers) = Staphylococci from skin/wound samples (36 % of all Staphylococci fall in this group)



Heatmap scaled on rows
 → “Which genera stand out for region X”

AMR genes identified – ResFinder 4.0 (assemblies)

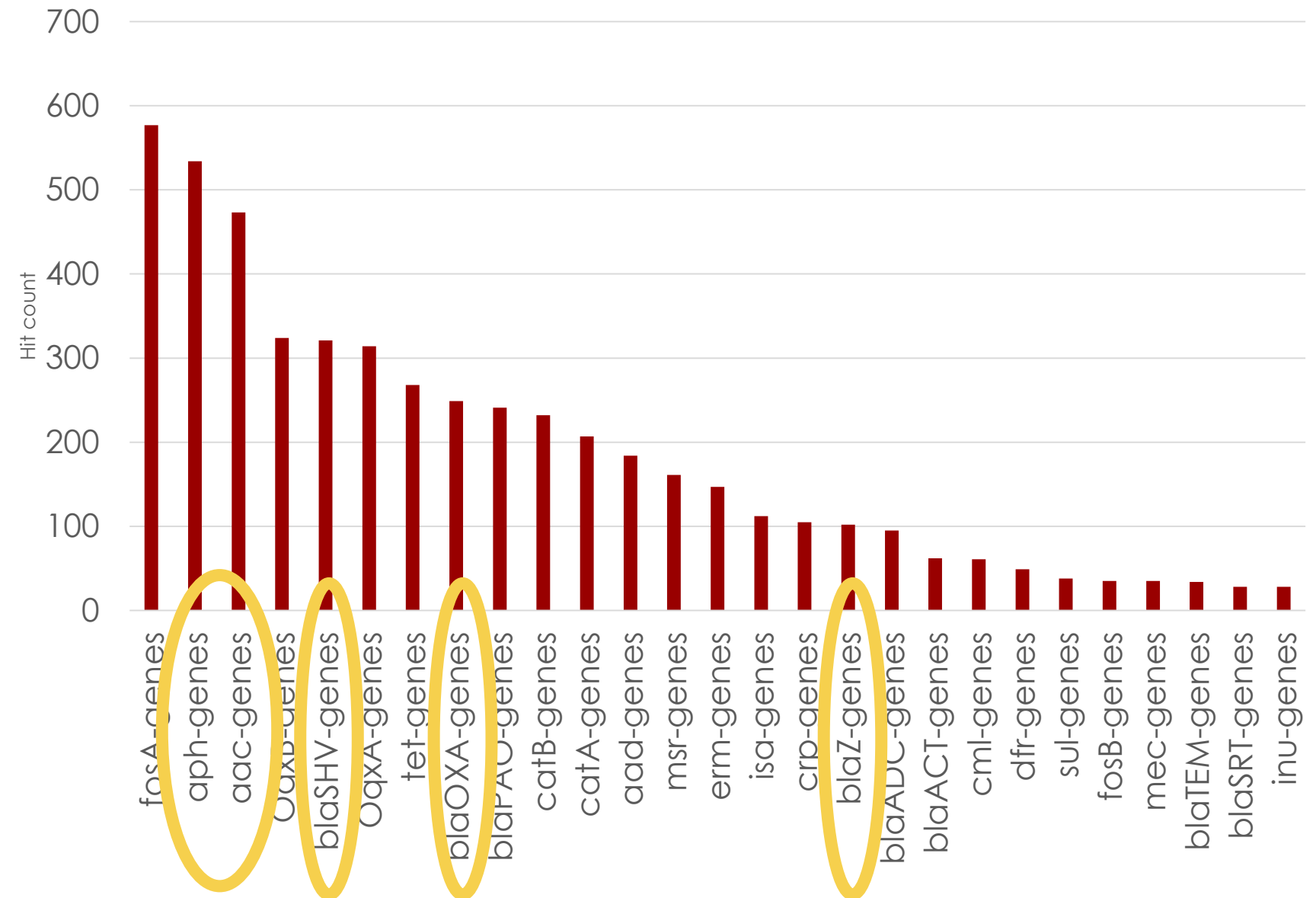
Hits across dataset with > 80 % query coverage and > 80 % identity percentage: 17,396

	Identity percentage				
Query coverage	100%	95% - 100%	90% - 95%	85% - 90%	80% - 85%
100%	58.65%	30.52%	0.83%	0.31%	0.07%
95% - 100%	1.86%	2.67%	0.29%	1.83%	0.51%
90% - 95%	0.22%	0.14%	0.00%	0.11%	0.02%
85% - 90%	0.24%	0.15%	0.00%	0.02%	0.02%
80% - 85%	0.10%	0.10%	0.00%	0.01%	0.00%

AMR genes identified – ResFinder 4.0 (assemblies)

Query coverage	Identity percentage				
	100%	95% - 100%	90% - 95%	85% - 90%	80% - 85%
100%	58.65%	30.52%	0.83%	0.31%	0.07%
95% - 100%	1.86%	2.67%	0.29%	1.83%	0.51%
90% - 95%	0.22%	0.14%	0.00%	0.11%	0.02%
85% - 90%	0.24%	0.15%	0.00%	0.02%	0.02%
80% - 85%	0.10%	0.10%	0.00%	0.01%	0.00%

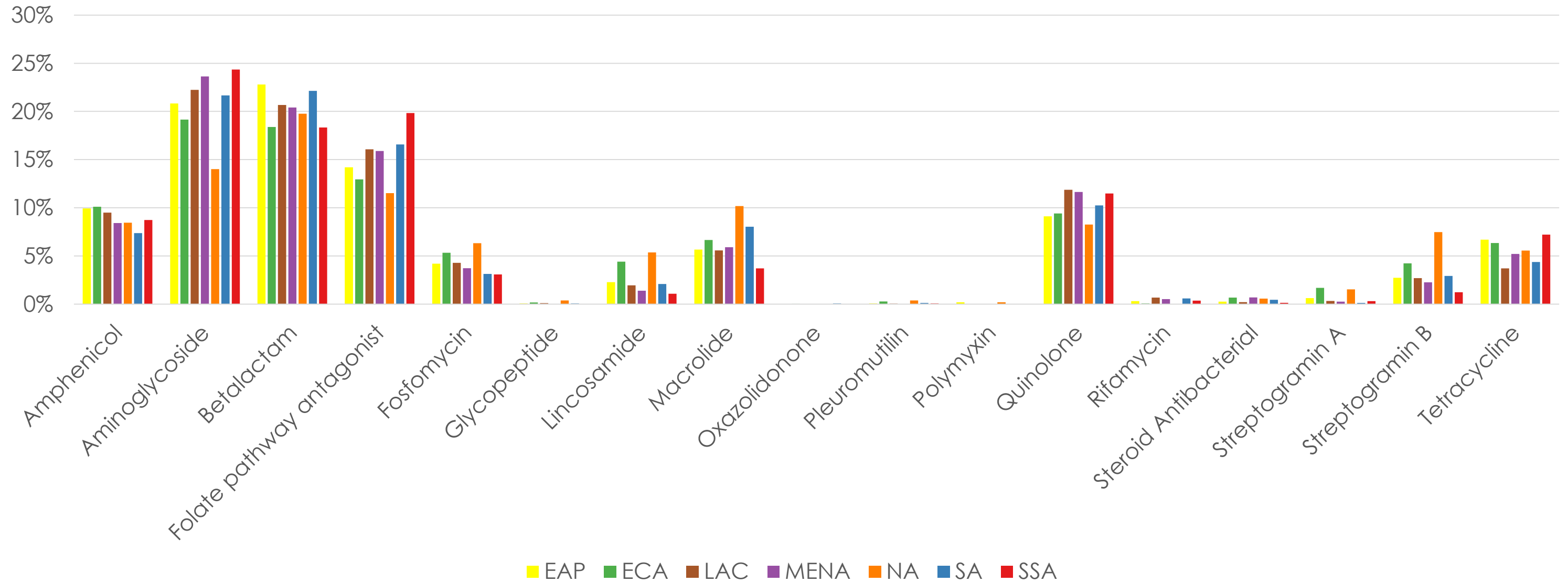
Majority (93 %) of hits with 100 % query coverage and 95-100 % identity coverage



← New variants ← Gene diversity

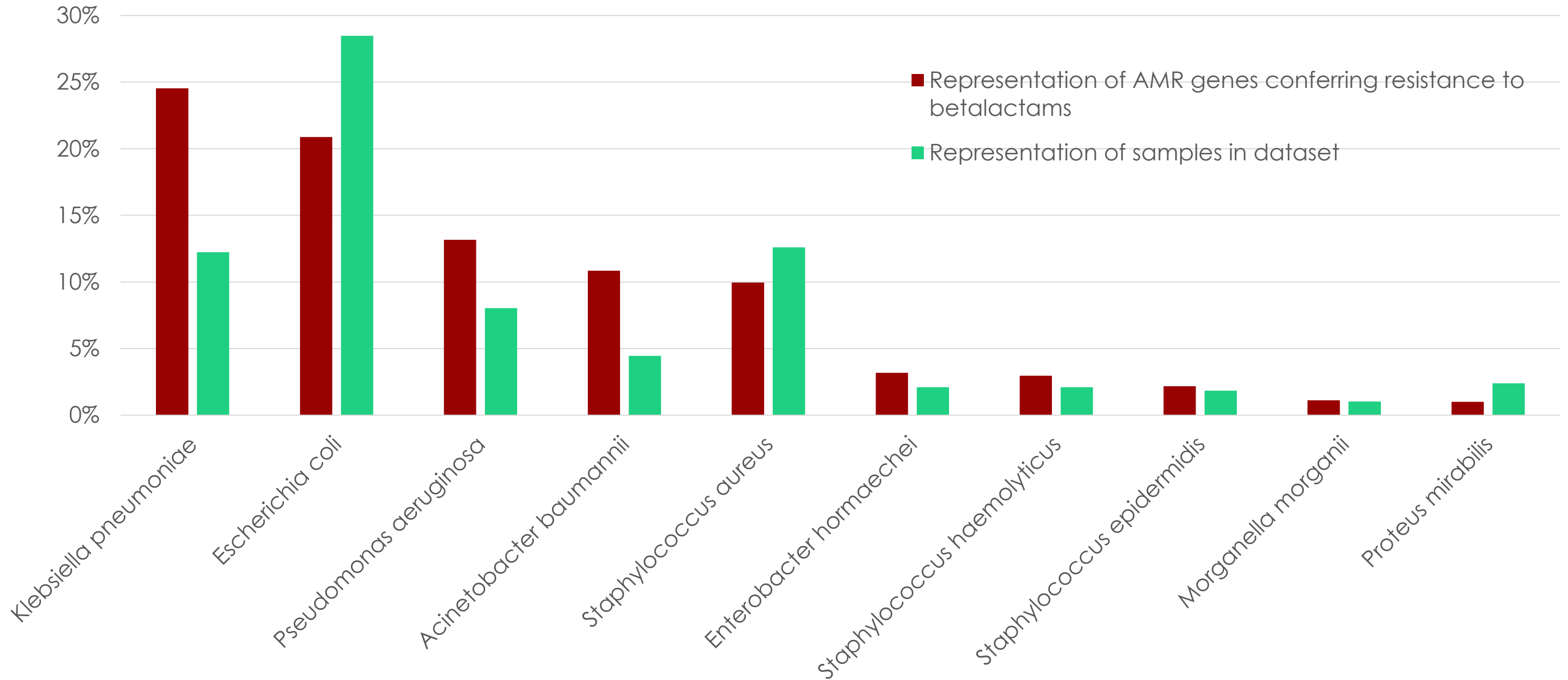
AMR genes identified – class level grouping

Percentage of AMR gene hits – within region – conferring resistance to antimicrobial class



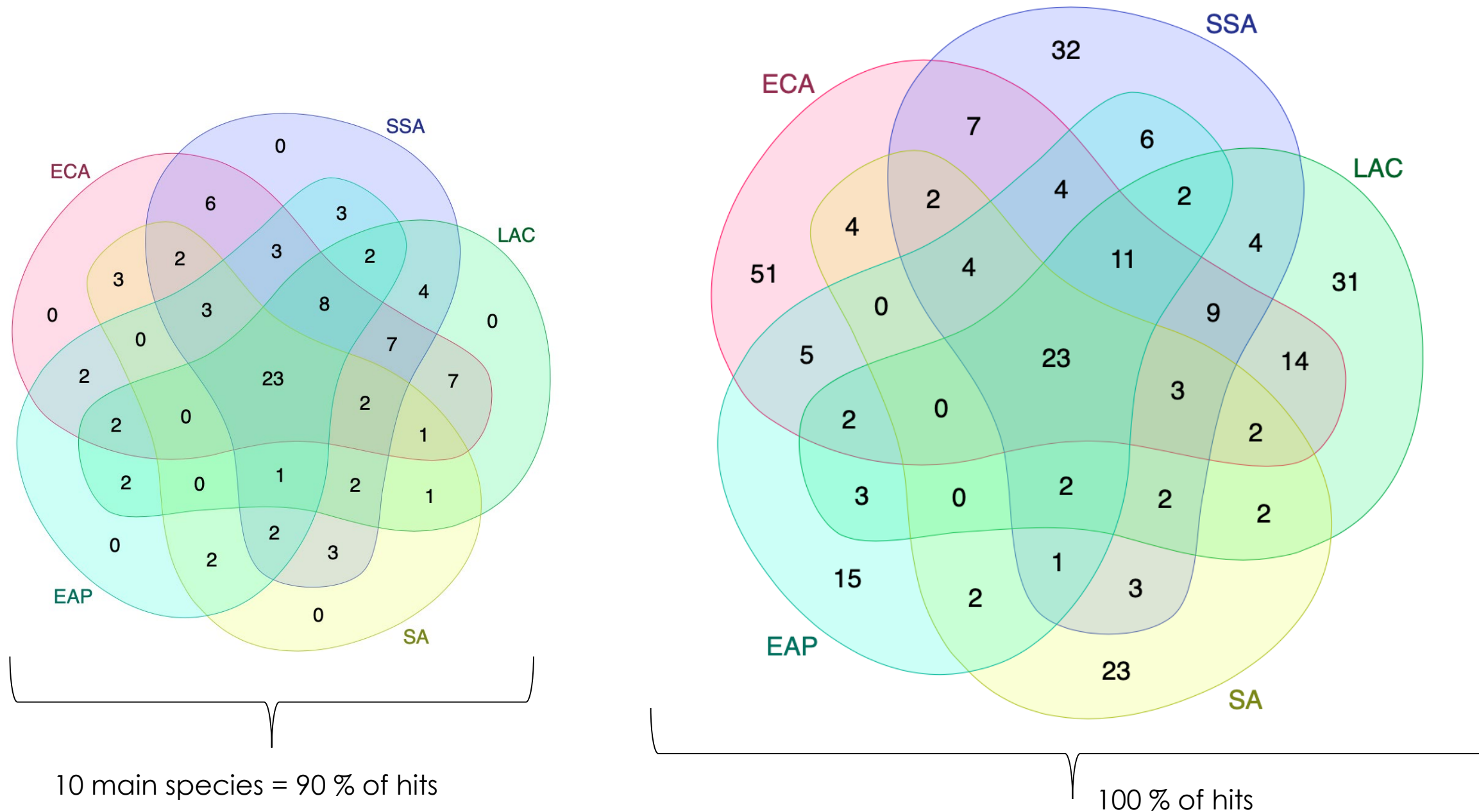
AMR genes identified – (conferring resistance against) **Betalactams**

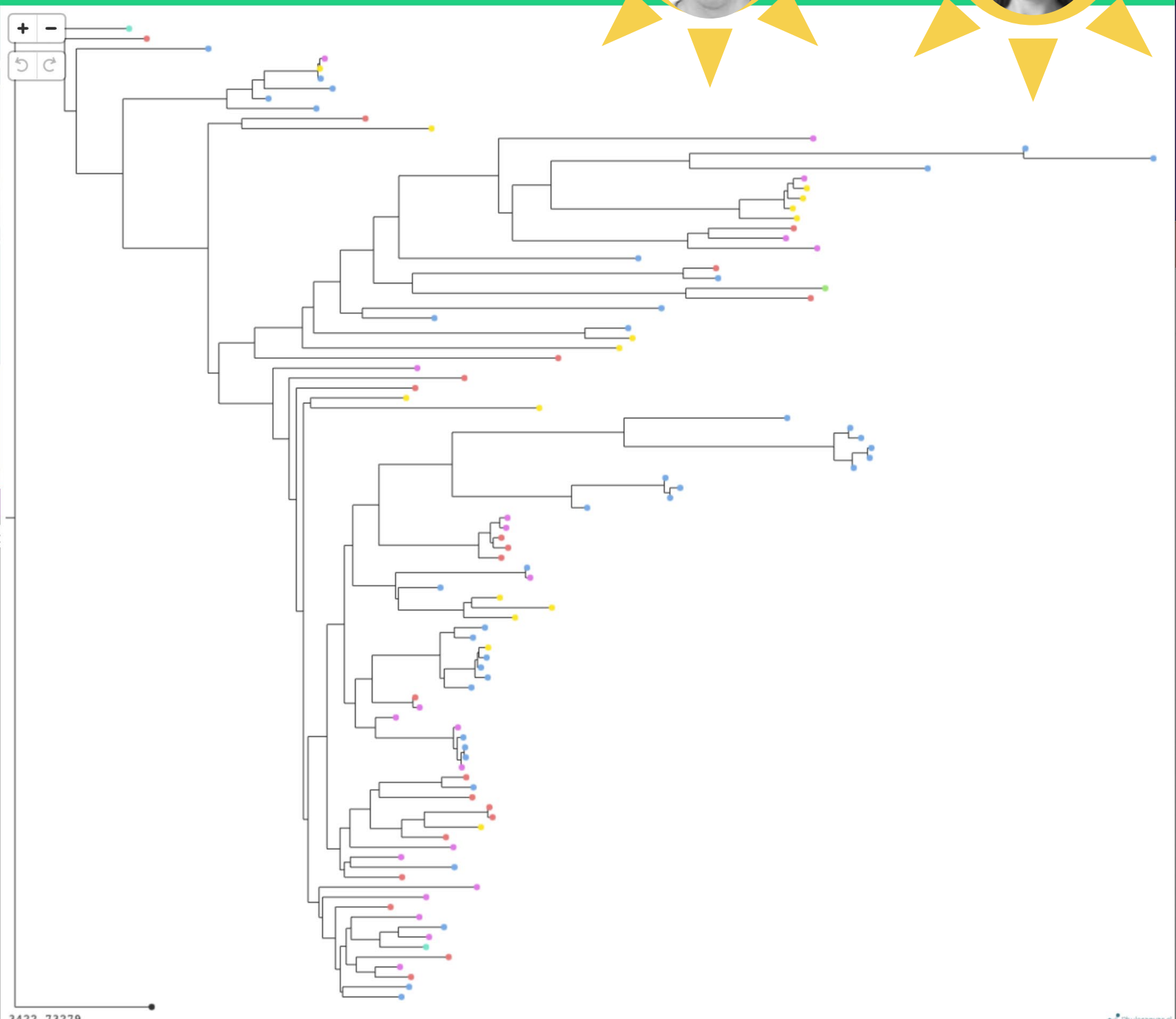
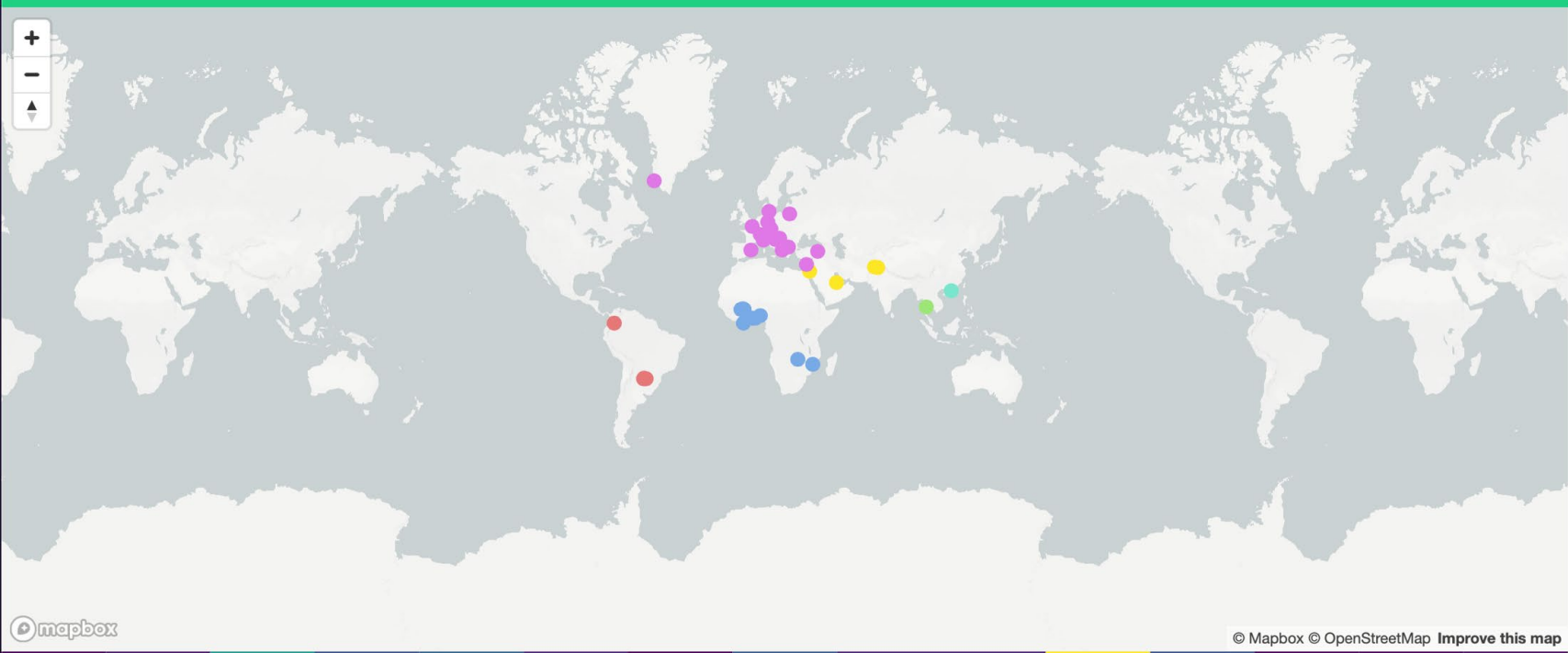
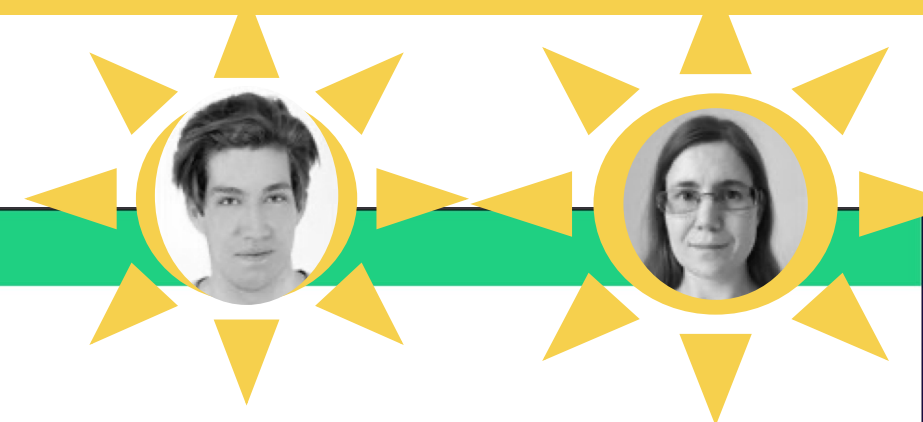
10 species account for 90 % of all AMR gene hits conferring resistance towards betalactams



AMR genes identified – (conferring resistance against) **Betalactams**

- blaACT-7** (Global)
- blaADC-25** (Global)
- blaCTX-M-15** (Global)
- blaCTX-M-27**
- blaNDM-1**
- blaOXA-1** (Global)
- blaOXA-23**
- blaOXA-395** (Global)
- blaOXA-486**
- blaOXA-488** (Global)
- blaOXA-494** (Global)
- blaOXA-50** (Global)
- blaPAO** (Global)
- blaSHV-106** (Global)
- blaSHV-11**
- blaSHV-172**
- blaSHV-199**
- blaSHV-27**
- blaSHV-89** (Global)
- blaTEM-1B** (Global)
- blaTEM-216**
- blaZ** (Global)
- mecA** (Global)





0 row selected [Deselect all](#) [Reset Filters](#) [Show sample context](#)

Select all	id	description	date from	to	country	region
<input type="checkbox"/>	Select ID(s)	search	YYYY-M-D	YYYY-M-D	Select one/multiple	search
<input type="checkbox"/>	1000026	DTU_2020_TWIW_01_HRV_ZAG_027	2020-02-24		Croatia	EUR
<input type="checkbox"/>	1000097	DTU_2020_TWIW_01_FRA_LIL_038	2020-03-02		France	EUR
<input type="checkbox"/>	1000152	DTU_2020_TWIW_01_ESP_BAR_028	2020-03-03		Spain	EUR

Visualised Tree: *Escherichia_coli_ETEC_H10407_NC_017633_1* Colour column: region Show help