

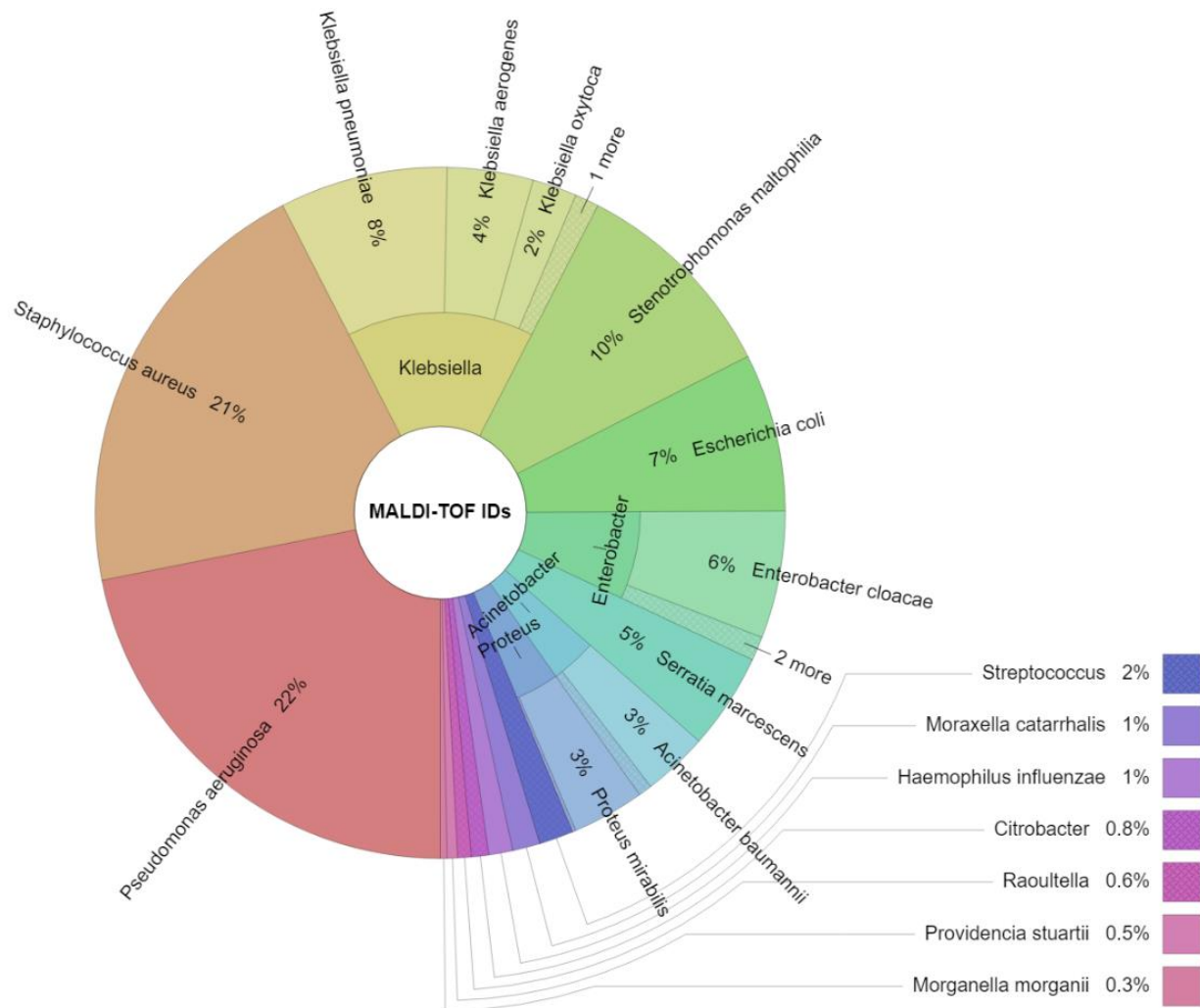
SUPPLEMENTARY FIGURES AND TABLES

Sample	Isolate	MALDI-TOF	WGS-taxonomy
1	AS012628	<i>Pseudomonas</i>	<i>Stenotrophomonas</i>
	AS012871	<i>Staphylococcus</i>	<i>Staphylococcus</i>
2	AS012643	<i>Stenotrophomonas</i>	<i>Pseudomonas</i>
	AS012644	<i>Stenotrophomonas</i>	<i>Stenotrophomonas</i>
3	AS012483	<i>Klebsiella</i>	<i>Providencia</i>
4	AS012728	<i>Stenotrophomonas</i>	<i>Pseudomonas</i>
	AS012789	<i>Stenotrophomonas</i>	<i>Stenotrophomonas</i>

Supplementary Table 1: Taxonomic identifications obtained with matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) and whole genome sequencing (WGS) for the 4 isolates (bolded) discrepant at the genus level. Additional isolates that resulted from the same original patient samples are listed underneath each discrepant isolate.

Strain ID	Identified By
<i>Acinetobacter baumannii</i>	WGS & MALDI-TOF
<i>Acinetobacter lactucaae</i>	WGS
<i>Acinetobacter nosocomialis</i>	WGS & MALDI-TOF
<i>Acinetobacter pittii</i>	WGS & MALDI-TOF
<i>Citrobacter freundii</i>	WGS & MALDI-TOF
<i>Citrobacter koseri</i>	WGS & MALDI-TOF
<i>Citrobacter</i> species FDAARGOS 156	WGS
<i>Enterobacter asburiae</i>	WGS & MALDI-TOF
<i>Enterobacter cloacae</i>	WGS & MALDI-TOF
<i>Enterobacter hormaechei</i>	WGS
<i>Enterobacter kobei</i>	MALDI-TOF
<i>Enterobacter xiangfangensis</i>	WGS
<i>Escherichia coli</i>	WGS & MALDI-TOF
<i>Haemophilus influenzae</i>	WGS & MALDI-TOF
<i>Klebsiella aerogenes</i>	WGS & MALDI-TOF
<i>Klebsiella michiganensis</i>	WGS
<i>Klebsiella oxytoca</i>	WGS & MALDI-TOF
<i>Klebsiella pneumoniae</i>	WGS & MALDI-TOF
<i>Klebsiella variicola</i>	WGS & MALDI-TOF
<i>Moraxella catarrhalis</i>	WGS & MALDI-TOF
<i>Morganella morganii</i>	WGS & MALDI-TOF
<i>Proteus mirabilis</i>	WGS & MALDI-TOF
<i>Proteus vulgaris</i>	MALDI-TOF
<i>Providencia stuartii</i>	WGS & MALDI-TOF
<i>Pseudomonas aeruginosa</i>	WGS & MALDI-TOF
<i>Raoultella ornithinolytica</i>	WGS & MALDI-TOF
<i>Raoultella planticola</i>	MALDI-TOF
<i>Serratia marcescens</i>	WGS & MALDI-TOF
<i>Staphylococcus aureus</i>	WGS & MALDI-TOF
<i>Stenotrophomonas maltophilia</i>	WGS & MALDI-TOF
<i>Streptococcus mitis</i>	WGS
<i>Streptococcus pneumoniae</i>	WGS & MALDI-TOF
<i>Streptococcus salivarius</i>	WGS & MALDI-TOF
<i>Streptococcus vestibularis</i>	MALDI-TOF

Supplementary Table 2: Species identified by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) or whole genome sequencing (WGS)-based identification or both. If only one method is listed, the other method did not identify the species in any of the isolates.



Supplementary Figure 1: Overview of pathogen identification as determined by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF). The pathogen distribution is only reflective of the analyzed data set and not lower respiratory tract infection in general. Grouped species ('2 more') under the genus Enterobacter include Enterobacter kobei and Enterobacter asburiae; grouped species under the genus Acinetobacter include Acinetobacter pittii and Acinetobacter nosocomialis; grouped species under the genus Streptococcus include Streptococcus salivarius, Streptococcus cristatus, Streptococcus species and Streptococcus vestibularis. Collapsed species represent less than 2% of the identifications.

Compound	<u>Aminoglycosides</u>																										
	Amikacin	66.7	IR	0.0	ND	ND	ND	ND	ND	18.2	ND	ND	ND														
	Gentamicin	23.5	IR	0.0	0.0	33.3	X	ND	0.0	7.7	0.0	X	0.0														
	Tobramycin	29.4	IR	0.0	0.0	ND	0.0	ND	33.3	15.4	ND	X	ND														
	<u>Penicillins</u>																										
	Amoxicillin-clavulanic acid	IR	IR	43.8	66.7	IR	ND	IR	ND	IR	40.0	IR	IR														
	Ampicillin	IR	IR	IR	8.8	IR	ND	IR	0.0	IR	IR	IR	IR														
	Piperacillin-tazobactam	34.4	IR	X	X	X	X	X	ND	0.0	X	X	ND														
	<u>Cephalosporins</u>																										
	Cefuroxime	IR	IR	0.0	11.1	0.0	ND	26.7	25.0	IR	50.0	IR	IR														
	Ceftazidime	51.6	13.2	0.0	14.3	40.0	100.0	12.5	ND	0.0	X	50.0	0.0														
	Ceftriaxone	IR	IR	0.0	0.0	31.2	16.7	22.2	0.0	ND	20.0	100.0	100.0														
	Cefepime	61.9	9.1	0.0	0.0	0.0	0.0	ND	0.0	0.0	ND	ND	ND														
	<u>Fluoroquinolones</u>																										
	Ciprofloxacin	10.0	ND	10.0	0.0	40.0	0.0	50.0	0.0	0.0	50.0	X	0.0														
	Levofloxacin	21.6	66.7	22.2	6.2	50.0	0.0	100.0	0.0	0.0	0.0	X	0.0														
	<u>Carbapenems</u>																										
	Ertapenem	IR	IR	0.0	100.0	80.0	100.0	50.0	ND	IR	ND	IR	ND														
	Imipenem	22.7	IR	0.0	X	ND	50.0	0.0	50.0	0.0	ND	ND	100.0														
Meropenem	21.1	IR	0.0	X	ND	X	ND	ND	0.0	ND	ND	ND															
<u>Folate pathway inhibitor</u>																											
Trimethoprim-sulfamethoxazole	ND	94.4	18.8	33.3	16.7	75.0	66.7	14.3	0.0	X	100.0	0.0															
		<i>Pseudomonas aeruginosa</i> (135)		<i>Stenotrophomonas maltophilia</i> (60)		<i>Klebsiella pneumoniae</i> (48)		<i>Escherichia coli</i> (46)		<i>Eiterobacter cloacae</i> (37)		<i>Serratia marcescens</i> (28)		<i>Klebsiella aerogenes</i> (25)		<i>Proteus mirabilis</i> (21)		<i>Acinetobacter baumannii</i> (19)		<i>Klebsiella oxytoca</i> (13)		<i>Citrobacter freundii</i> (4)		<i>Morganella morganii</i> (2)			
		Pathogen																									
Pathogen	<i>Staphylococcus aureus</i> (128)																										
		50.0	3.3	0.0	0.0	0.0	37.7	40.0	11.1	50.0																	
		Gentamicin																									
		Benzympenicillin																									
		Ciprofloxacin																									
		Levofloxacin																									
		Moxifloxacin																									
		Erythromycin																									
		Tetracycline																									
		Trimethoprim																									
	Trimethoprim-sulfamethoxazole																										
		Compound																									

Supplementary figure 2: Very major errors (VME) per species-compound pair, with results for Gram-negative bacteria shown on the top and *Staphylococcus aureus* on the bottom. Pairs where species are considered intrinsically resistant to the compound are labelled as “IR”. Species-compound pairs not tested by phenotypic susceptibility testing or without genotypic susceptibility prediction are labelled with “ND”. Species-compound pairs without resistant samples, for which VMEs cannot be calculated are labelled with “X”. Sample counts per species are listed in parentheses. VMEs below 1.5% are bolded.

Compound	Pathogen	Major error (ME) rates per species-compound pair												
		0.8	IR	0.0	ND	ND	ND	ND	0.0	ND	ND	ND		
Aminoglycosides	Amikacin	0.8	IR	0.0	ND	ND	ND	ND	0.0	ND	ND	ND		
	Gentamicin	5.1	IR	0.0	0.0	0.0	7.1	ND	5.6	16.7	0.0	0.0		
	Tobramycin	4.2	IR	2.5	7.0	ND	3.8	ND	0.0	0.0	ND	25.0		
Penicillins	Amoxicillin-clavulanic acid	IR	IR	3.1	0.0	IR	ND	IR	ND	IR	0.0	IR		
	Ampicillin	IR	IR	IR	8.3	IR	ND	IR	0.0	IR	IR	IR		
Cephalosporins	Piperacillin-tazobactam	20.4	IR	16.7	0.0	21.6	3.6	12.0	ND	0.0	38.5	25.0		
	Cefuroxime	IR	IR	15.8	0.0	76.9	ND	60.0	11.8	IR	14.3	IR		
Fluoroquinolones	Ceftazidime	10.6	22.7	0.0	5.1	22.7	0.0	47.1	ND	0.0	7.7	0.0		
	Ceftriaxone	IR	IR	0.0	0.0	33.3	0.0	50.0	5.6	ND	0.0	0.0		
	Cefepime	14.0	40.0	2.5	2.4	5.6	0.0	ND	10.5	37.5	ND	ND		
Carbapenems	Ciprofloxacin	9.5	ND	5.3	0.0	0.0	16.0	4.3	0.0	0.0	0.0	X		
	Levofloxacin	10.7	8.3	0.0	0.0	6.1	7.7	8.3	0.0	0.0	0.0	X		
Folate pathway inhibitor	Ertapenem	IR	IR	8.7	2.3	6.2	0.0	47.6	ND	IR	ND	IR		
	Imipenem	15.4	IR	0.0	0.0	ND	3.8	0.0	41.2	0.0	ND	ND		
	Meropenem	21.6	IR	15.2	4.3	ND	0.0	ND	ND	0.0	ND	ND		
Trimethoprim-sulfamethoxazole	ND	2.4	0.0	3.6	0.0	0.0	4.5	0.0	20.0	15.4	0.0	X		
			<i>Pseudomonas aeruginosa</i> (135)	<i>Stenotrophomonas maltophilia</i> (60)	<i>Klebsiella pneumoniae</i> (48)	<i>Escherichia coli</i> (46)	<i>Enterobacter cloacae</i> (37)	<i>Serratia marcescens</i> (28)	<i>Klebsiella aerogenes</i> (25)	<i>Proteus mirabilis</i> (21)	<i>Acinetobacter baumannii</i> (19)	<i>Klebsiella oxytoca</i> (13)	<i>Citrobacter freundii</i> (4)	<i>Morganella morganii</i> (2)
			Pathogen											
	<i>Staphylococcus aureus</i> (128)	0.0	11.8	1.8	5.3	5.2	10.0	8.1	0.8	22.5				
			Gentamicin	Benzylpenicillin	Ciprofloxacin	Levofloxacin	Moxifloxacin	Erythromycin	Tetracycline	Trimethoprim	Trimethoprim-sulfamethoxazole			
			Compound											

Supplementary figure 3: Major error (ME) rates per species-compound pair, with results for Gram-negative bacteria shown on the top and those for *Staphylococcus aureus* on the bottom. Pairs where species are considered intrinsically resistant to the compound are labelled as “IR”. Species-compound pairs not tested by phenotypic susceptibility testing or without genotypic susceptibility prediction are labelled with “ND”. Species-compound pairs without susceptible samples for which MEs cannot be calculated are labelled with “X”. Sample counts per species are listed in parentheses. MEs below 3.5% are bolded.