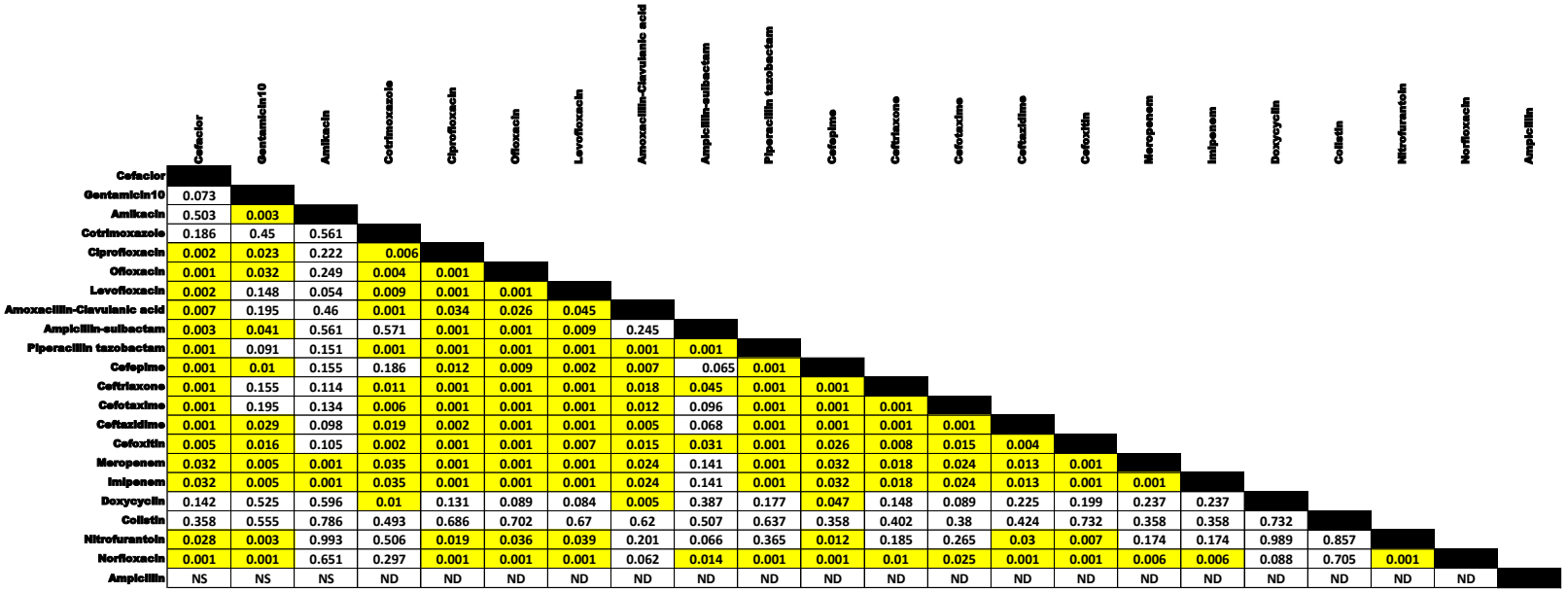
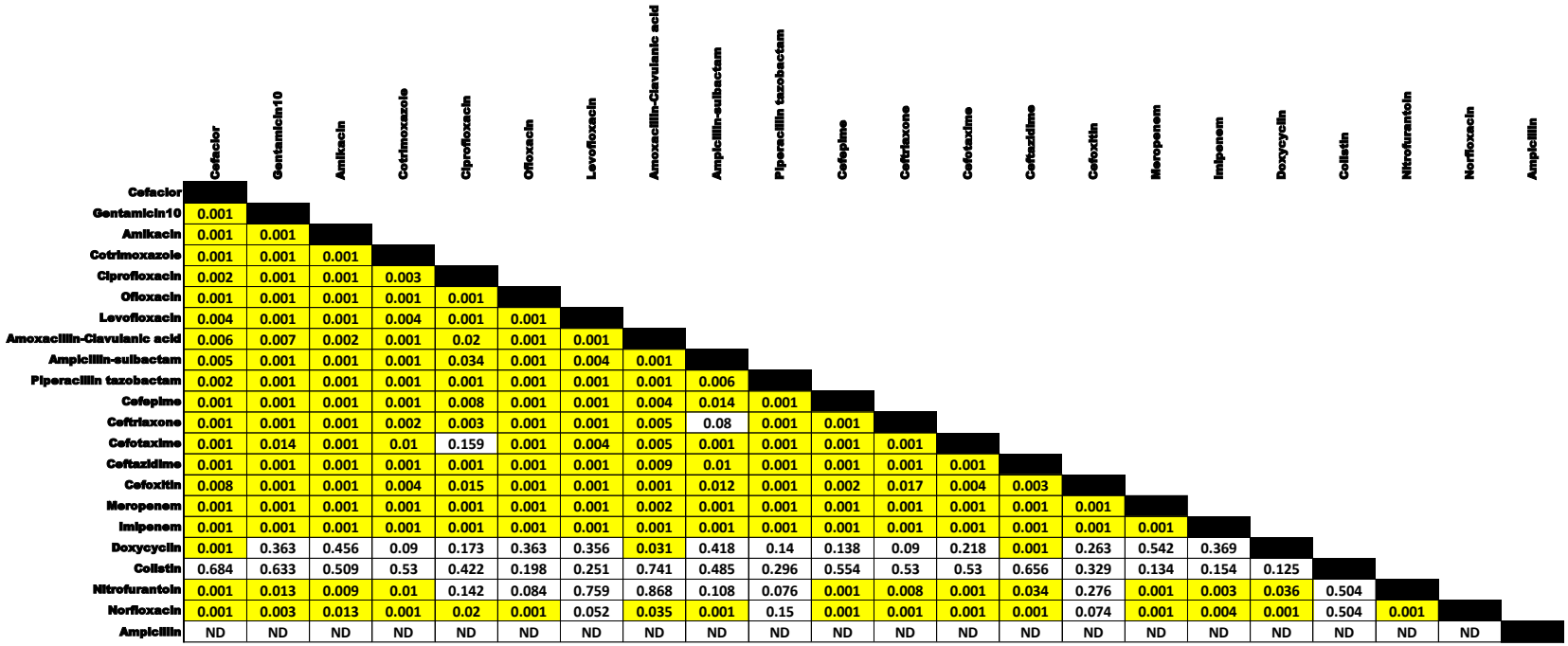
Supplementary Material



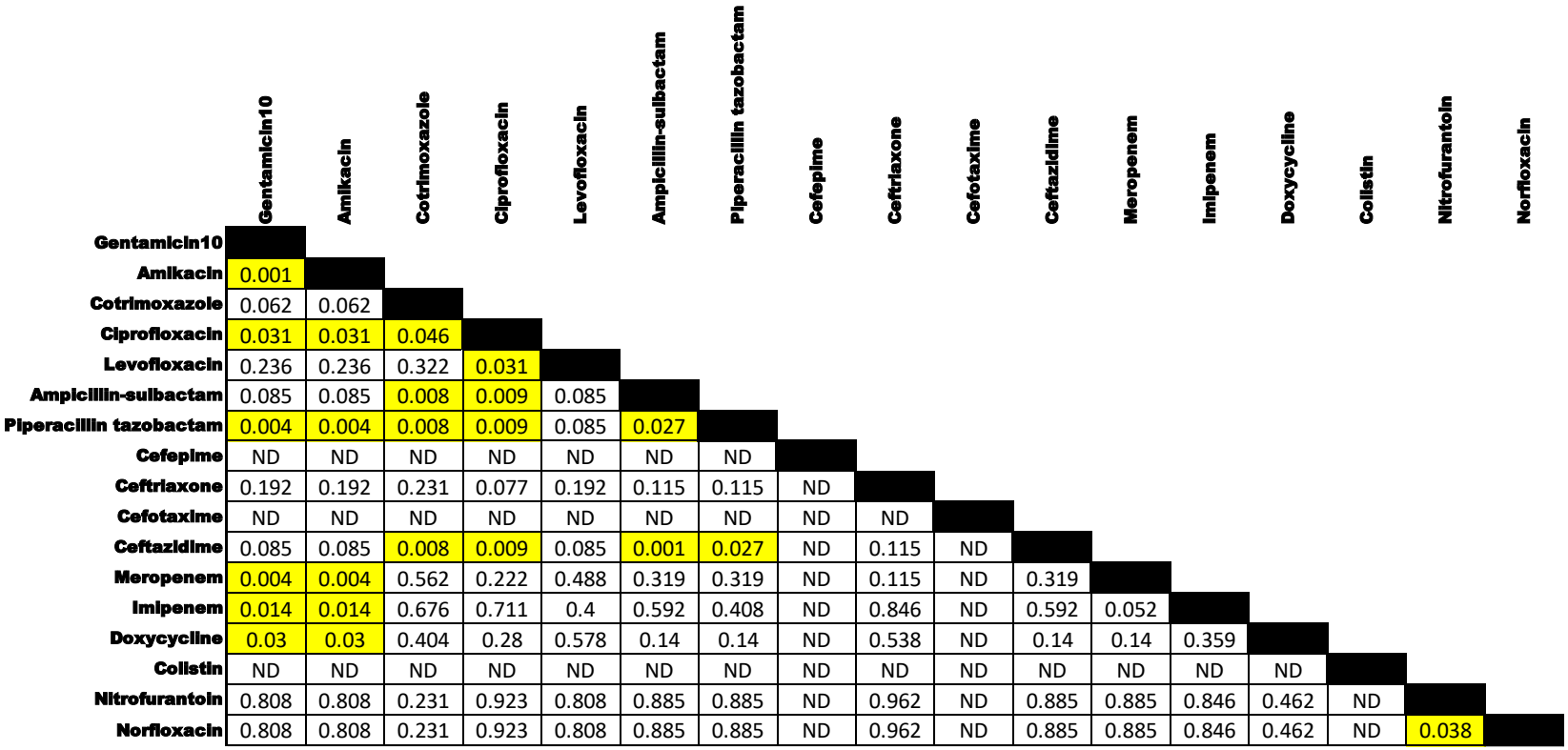
	Cefaclor	Gentamicin10	Amikacin	Cotrimoxazole	Ciprofloxacin	Ofloxacin	Levofloxacin	Amoxacillin-Clavulanic acid	Ampicillin-sulbactam	Piperacillin tazobactam	Cefepime	Ceftriaxone	Cefotaxime	Ceftazidime	Cefoxitin	Meropenem	Imipenem	Doxycycilin	Colistin	Nitrofurantoin	Norfloxacin	Ampicillin
Cefaclor																						
Gentamicin10	0.073																					
Amikacin	0.503	0.003																				
Cotrimoxazole	0.186	0.45	0.561																			
Ciprofloxacin	0.002	0.023	0.222	0.006																		
Ofloxacin	0.001	0.032	0.249	0.004	0.001																	
Levofloxacin	0.002	0.148	0.054	0.009	0.001	0.001																
Amoxacillin-Clavulanic acid	0.007	0.195	0.46	0.001	0.034	0.026	0.045															
Ampicillin-sulbactam	0.003	0.041	0.561	0.571	0.001	0.001	0.009	0.245														
Piperacillin tazobactam	0.001	0.091	0.151	0.001	0.001	0.001	0.001	0.001	0.001													
Cefepime	0.001	0.01	0.155	0.186	0.012	0.009	0.002	0.007	0.065	0.001												
Ceftriaxone	0.001	0.155	0.114	0.011	0.001	0.001	0.001	0.018	0.045	0.001	0.001											
Cefotaxime	0.001	0.195	0.134	0.006	0.001	0.001	0.001	0.012	0.096	0.001	0.001	0.001										
Ceftazidime	0.001	0.029	0.098	0.019	0.002	0.001	0.001	0.005	0.068	0.001	0.001	0.001	0.001									
Cefoxitin	0.005	0.016	0.105	0.002	0.001	0.001	0.007	0.015	0.031	0.001	0.026	0.008	0.015	0.004								
Meropenem	0.032	0.005	0.001	0.035	0.001	0.001	0.001	0.024	0.141	0.001	0.032	0.018	0.024	0.013	0.001							
Imipenem	0.032	0.005	0.001	0.035	0.001	0.001	0.001	0.024	0.141	0.001	0.032	0.018	0.024	0.013	0.001	0.001						
Doxycycilin	0.142	0.525	0.596	0.01	0.131	0.089	0.084	0.005	0.387	0.177	0.047	0.148	0.089	0.225	0.199	0.237	0.237					
Colistin	0.358	0.555	0.786	0.493	0.686	0.702	0.67	0.62	0.507	0.637	0.358	0.402	0.38	0.424	0.732	0.358	0.358	0.732				
Nitrofurantoin	0.028	0.003	0.993	0.506	0.019	0.036	0.039	0.201	0.066	0.365	0.012	0.185	0.265	0.03	0.007	0.174	0.174	0.989	0.857			
Norfloxacin	0.001	0.001	0.651	0.297	0.001	0.001	0.001	0.062	0.014	0.001	0.001	0.01	0.025	0.001	0.001	0.006	0.006	0.088	0.705	0.001		
Ampicillin	NS	NS	NS	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	

Figure S1: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Escherichia coli*. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *p*-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).



	Cefaclor	Gentamicin10	Amikacin	Cotrimoxazole	Ciprofloxacin	Ofloxacin	Levofloxacin	Amoxacillin-Clavulanic acid	Ampicillin-sulbactam	Piperacillin tazobactam	Cefepime	Ceftriaxone	Cefotaxime	Ceftazidime	Cefoxitin	Meropenem	Imipenem	Doxycyclin	Colistin	Nitrofurantoin	Norfloxacin	Ampicillin
Cefaclor																						
Gentamicin10	0.001																					
Amikacin	0.001	0.001																				
Cotrimoxazole	0.001	0.001	0.001																			
Ciprofloxacin	0.002	0.001	0.001	0.003																		
Ofloxacin	0.001	0.001	0.001	0.001	0.001																	
Levofloxacin	0.004	0.001	0.001	0.004	0.001	0.001																
Amoxacillin-Clavulanic acid	0.006	0.007	0.002	0.001	0.02	0.001	0.001															
Ampicillin-sulbactam	0.005	0.001	0.001	0.001	0.034	0.001	0.004	0.001														
Piperacillin tazobactam	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.006													
Cefepime	0.001	0.001	0.001	0.001	0.008	0.001	0.001	0.004	0.014	0.001												
Ceftriaxone	0.001	0.001	0.001	0.002	0.003	0.001	0.001	0.005	0.08	0.001	0.001											
Cefotaxime	0.001	0.014	0.001	0.01	0.159	0.001	0.004	0.005	0.001	0.001	0.001	0.001										
Ceftazidime	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.009	0.01	0.001	0.001	0.001	0.001									
Cefoxitin	0.008	0.001	0.001	0.004	0.015	0.001	0.001	0.001	0.012	0.001	0.002	0.017	0.004	0.003								
Meropenem	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001							
Imipenem	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001						
Doxycyclin	0.001	0.363	0.456	0.09	0.173	0.363	0.356	0.031	0.418	0.14	0.138	0.09	0.218	0.001	0.263	0.542	0.369					
Colistin	0.684	0.633	0.509	0.53	0.422	0.198	0.251	0.741	0.485	0.296	0.554	0.53	0.53	0.656	0.329	0.134	0.154	0.125				
Nitrofurantoin	0.001	0.013	0.009	0.01	0.142	0.084	0.759	0.868	0.108	0.076	0.001	0.008	0.001	0.034	0.276	0.001	0.003	0.036	0.504			
Norfloxacin	0.001	0.003	0.013	0.001	0.02	0.001	0.052	0.035	0.001	0.15	0.001	0.001	0.001	0.001	0.074	0.001	0.004	0.001	0.504	0.001		
Ampicillin	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	

Figure S2: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Klebsiella pneumoniae*. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *p*-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).

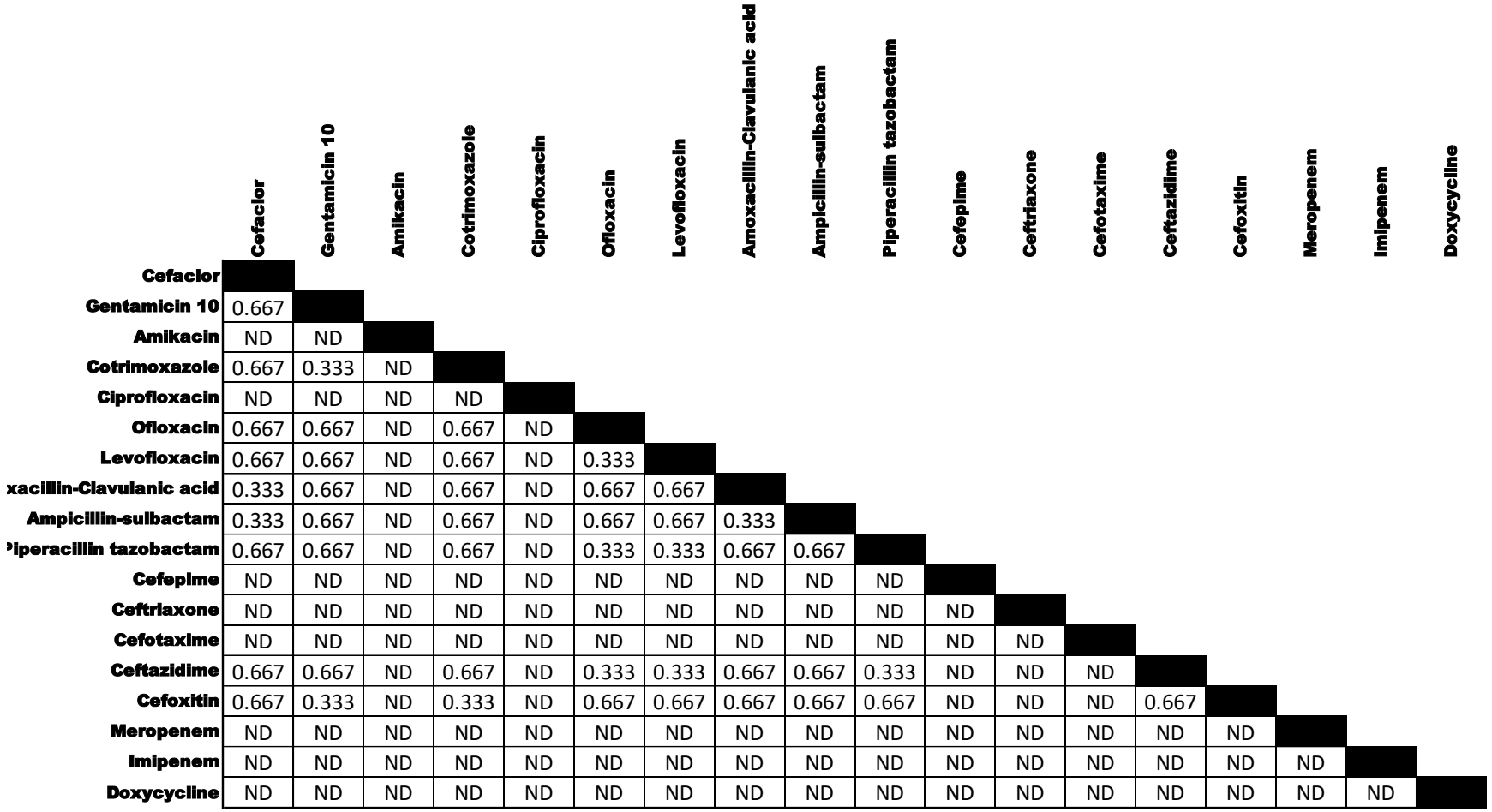


	Gentamicin10	Amikacin	Cotrimoxazole	Ciprofloxacin	Levofloxacin	Ampicillin-sulbactam	Piperacillin tazobactam	Cefepime	Ceftriaxone	Cefotaxime	Ceftazidime	Meropenem	Imipenem	Doxycycline	Colistin	Nitrofurantoin	Norfloxacin
Gentamicin10																	
Amikacin	0.001																
Cotrimoxazole	0.062	0.062															
Ciprofloxacin	0.031	0.031	0.046														
Levofloxacin	0.236	0.236	0.322	0.031													
Ampicillin-sulbactam	0.085	0.085	0.008	0.009	0.085												
Piperacillin tazobactam	0.004	0.004	0.008	0.009	0.085	0.027											
Cefepime	ND	ND	ND	ND	ND	ND	ND										
Ceftriaxone	0.192	0.192	0.231	0.077	0.192	0.115	0.115	ND									
Cefotaxime	ND	ND	ND	ND	ND	ND	ND	ND	ND								
Ceftazidime	0.085	0.085	0.008	0.009	0.085	0.001	0.027	ND	0.115	ND							
Meropenem	0.004	0.004	0.562	0.222	0.488	0.319	0.319	ND	0.115	ND	0.319						
Imipenem	0.014	0.014	0.676	0.711	0.4	0.592	0.408	ND	0.846	ND	0.592	0.052					
Doxycycline	0.03	0.03	0.404	0.28	0.578	0.14	0.14	ND	0.538	ND	0.14	0.14	0.359				
Colistin	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND			
Nitrofurantoin	0.808	0.808	0.231	0.923	0.808	0.885	0.885	ND	0.962	ND	0.885	0.885	0.846	0.462	ND		
Norfloxacin	0.808	0.808	0.231	0.923	0.808	0.885	0.885	ND	0.962	ND	0.885	0.885	0.846	0.462	ND	0.038	

Figure S3: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Acinetobacter baumannii*. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *p*-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).

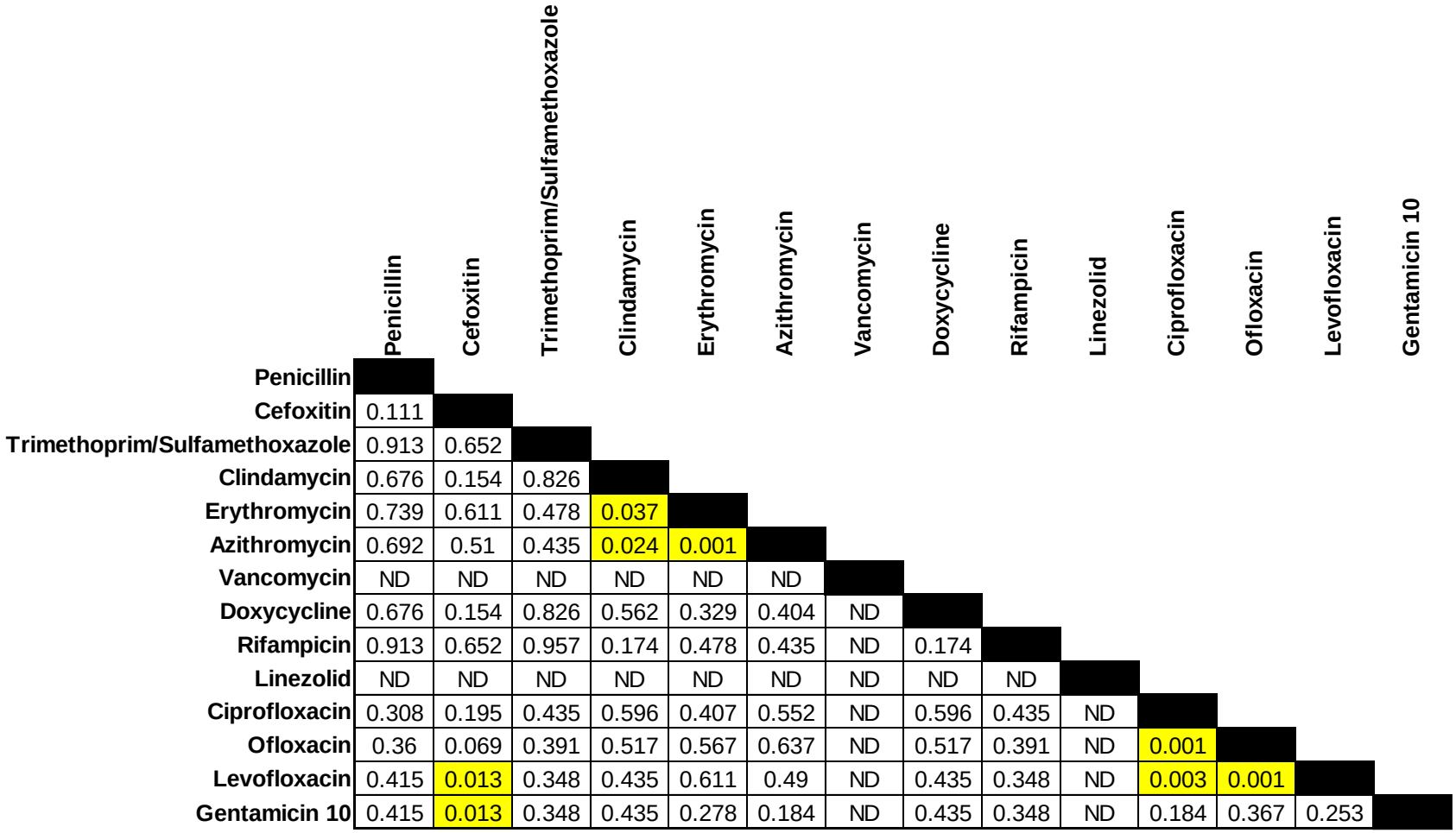
	Gentamicin 10	Amikacin	Ciprofloxacin	Ofloxacin	Levofloxacin	Piperacillin tazobactam	Cefepime	Ceftazidime	Meropenem	Imipenem	Colistin
Gentamicin 10											
Amikacin	0.002										
Ciprofloxacin	0.051	0.015									
Ofloxacin	0.529	0.296	0.051								
Levofloxacin	0.051	0.015	0.001	0.051							
Piperacillin tazobactam	0.7	0.035	0.035	0.7	0.035						
Cefepime	0.385	0.5	0.5	0.385	0.5	0.33					
Ceftazidime	0.175	0.035	0.035	0.594	0.035	0.21	0.67				
Meropenem	0.7	0.035	0.035	0.07	0.035	0.001	0.33	0.21			
Imipenem	0.028	0.133	0.133	0.238	0.133	0.005	0.231	0.545	0.005		
Colistin	0.571	0.5	0.5	0.429	0.5	0.714	0.786	0.286	0.714	0.357	

Figure S4: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Pseudomonas aeruginosa*. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *p*-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).



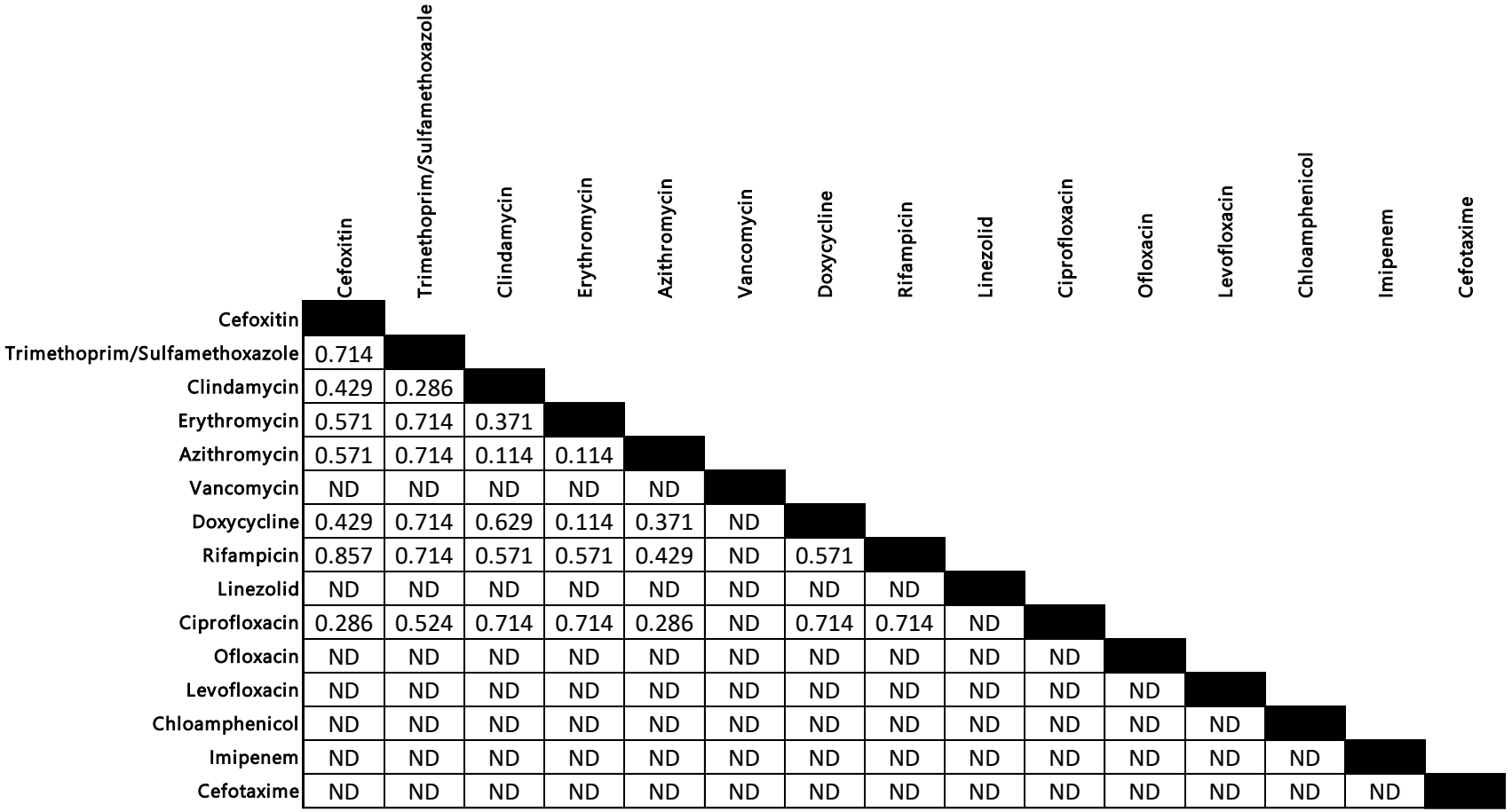
	Cefaclor	Gentamicin 10	Amikacin	Cotrimoxazole	Ciprofloxacin	Ofloxacin	Levofloxacin	Amoxacillin-Clavulanic acid	Ampicillin-sulbactam	Piperacillin tazobactam	Cefepime	Ceftriaxone	Cefotaxime	Ceftazidime	Cefoxitin	Meropenem	Imipenem	Doxycycline
Cefaclor																		
Gentamicin 10	0.667																	
Amikacin	ND	ND																
Cotrimoxazole	0.667	0.333	ND															
Ciprofloxacin	ND	ND	ND	ND														
Ofloxacin	0.667	0.667	ND	0.667	ND													
Levofloxacin	0.667	0.667	ND	0.667	ND	0.333												
xacillin-Clavulanic acid	0.333	0.667	ND	0.667	ND	0.667	0.667											
Ampicillin-sulbactam	0.333	0.667	ND	0.667	ND	0.667	0.667	0.333										
Piperacillin tazobactam	0.667	0.667	ND	0.667	ND	0.333	0.333	0.667	0.667									
Cefepime	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND								
Ceftriaxone	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND							
Cefotaxime	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND						
Ceftazidime	0.667	0.667	ND	0.667	ND	0.333	0.333	0.667	0.667	0.333	ND	ND	ND					
Cefoxitin	0.667	0.333	ND	0.333	ND	0.667	0.667	0.667	0.667	0.667	ND	ND	ND	0.667				
Meropenem	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND			
Imipenem	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND		
Doxycycline	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	

Figure S5: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Proteus* sp. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *p*-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).



	Penicillin	Cefoxitin	Trimethoprim/Sulfamethoxazole	Clindamycin	Erythromycin	Azithromycin	Vancomycin	Doxycycline	Rifampicin	Linezolid	Ciprofloxacin	Ofloxacin	Levofloxacin	Gentamicin 10
Penicillin														
Cefoxitin	0.111													
Trimethoprim/Sulfamethoxazole	0.913	0.652												
Clindamycin	0.676	0.154	0.826											
Erythromycin	0.739	0.611	0.478	0.037										
Azithromycin	0.692	0.51	0.435	0.024	0.001									
Vancomycin	ND	ND	ND	ND	ND	ND								
Doxycycline	0.676	0.154	0.826	0.562	0.329	0.404	ND							
Rifampicin	0.913	0.652	0.957	0.174	0.478	0.435	ND	0.174						
Linezolid	ND	ND	ND	ND	ND	ND	ND	ND	ND					
Ciprofloxacin	0.308	0.195	0.435	0.596	0.407	0.552	ND	0.596	0.435	ND				
Ofloxacin	0.36	0.069	0.391	0.517	0.567	0.637	ND	0.517	0.391	ND	0.001			
Levofloxacin	0.415	0.013	0.348	0.435	0.611	0.49	ND	0.435	0.348	ND	0.003	0.001		
Gentamicin 10	0.415	0.013	0.348	0.435	0.278	0.184	ND	0.435	0.348	ND	0.184	0.367	0.253	

Figure S6: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Staphylococcus aureus*. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *p*-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).



	Cefoxitin	Trimethoprim/Sulfamethoxazole	Clindamycin	Erythromycin	Azithromycin	Vancomycin	Doxycycline	Rifampicin	Linezolid	Ciprofloxacin	Ofloxacin	Levofloxacin	Chloamphenicol	Imipenem	Cefotaxime
Cefoxitin															
Trimethoprim/Sulfamethoxazole	0.714														
Clindamycin	0.429	0.286													
Erythromycin	0.571	0.714	0.371												
Azithromycin	0.571	0.714	0.114	0.114											
Vancomycin	ND	ND	ND	ND	ND										
Doxycycline	0.429	0.714	0.629	0.114	0.371	ND									
Rifampicin	0.857	0.714	0.571	0.571	0.429	ND	0.571								
Linezolid	ND	ND	ND	ND	ND	ND	ND	ND							
Ciprofloxacin	0.286	0.524	0.714	0.714	0.286	ND	0.714	0.714	ND						
Ofloxacin	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND					
Levofloxacin	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND				
Chloamphenicol	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND			
Imipenem	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND		
Cefotaxime	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	

Figure S7: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Streptococcus pneumoniae*. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *p*-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).

	Penicillin	Erythromycin	Azithromycin	Vancomycin	Doxycycline	Rifampicin	Linezolid	Ciprofloxacin	Ofloxacin	Levofloxacin	Gentamicin 120	Chloamphenicol	Ampicillin
Penicillin													
Erythromycin	0.116												
Azithromycin	0.116	0.001											
Vancomycin	ND	ND	ND										
Doxycycline	0.286	0.45	0.45	ND									
Rifampicin	0.613	0.55	0.55	ND	0.418								
Linezolid	ND	ND	ND	ND	ND	ND							
Ciprofloxacin	0.618	0.307	0.307	ND	0.328	0.672	ND						
Ofloxacin	0.525	0.564	0.564	ND	0.541	0.459	ND	0.016					
Levofloxacin	0.475	0.564	0.564	ND	0.186	0.459	ND	0.016	0.002				
Gentamicin 120	0.387	0.223	0.223	ND	0.157	0.418	ND	0.265	0.015	0.015			
Chloamphenicol	0.496	0.649	0.649	ND	0.163	0.57	ND	0.396	0.038	0.038	0.011		
Ampicillin	0.022	0.601	0.601	ND	0.284	0.052	ND	0.468	0.699	0.313	0.144	0.231	

Figure S8: Matrix showing the association between antimicrobial resistance phenotypes and the tested antimicrobial in *Enterococci*. Where appropriate, the *P*-values were calculated using the Chi-Square or Fisher's exact tests. Significant associations with p-values ≤ 0.05 are highlighted with a yellow color. ND, p-values could not be determined as all isolates showed the same phenotype (resistant or susceptible).

Table S1: The MICs of the tested antimicrobial agents, phenotypic and molecular analysis of Carbapenemase-encoding genes, ESBLs, and *aac(6')Ib* of the tested isolates (*n* = 103):

Bacterial species	Resistance genes			No. of isolates	MIC range			
	ESBLs	CPases	*aac(6')-Ib*		IMP	CTX	FEP	CIP
E. coli	*bla*CTX-M, *bla*TEM	*bla*OXA-48	+	15	16–265	24–512	24–512	32–256
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48	+	7	16–128	32–512	256	32–128
	*bla*CTX-M, *bla*TEM	____	+	2	ND	32	256	32
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*IMP	+	1	ND	32	32	32
	*bla*CTX-M, *bla*TEM	*bla*VIM	+	1	ND	512	256	128
K. pneumoniae	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48	-	3	32	32–512	48–256	32–128
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48	+	24	12–255	32–512	48–256	32–127
	*bla*CTX-M, *bla*TEM	*bla*OXA-48	-	5	32–64	512	64–256	128
	*bla*CTX-M, *bla*TEM	*bla*OXA-48	+	5	64–128	24–512	32–256	32–256
	*bla*CTX-M, *bla*TEM	*bla*OXA-48, *bla*VIM, *bla*IMP	-	1	ND	32	256	6
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48, *bla*IMP	+	6	64–256	256–512	128–256	64–128
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48, *bla*IMP	-	1	16	24	256	32
	*bla*CTX-M, *bla*TEM	*bla*OXA-48, *bla*IMP	+	2	32	32–512	64–256	8_16
	*bla*CTX-M, *bla*TEM	___	+	1	ND	512	128	256
	*bla*CTX-M, *bla*TEM, *bla*SHV	___	-	2	ND	32	256	32
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48, *bla*VIM, *bla*IMP	+	1	ND	512	256	128
	*bla*CTX-M, *bla*TEM, *bla*SHV	____	+	1	64	512	128	128
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48	+	1	ND	256	64	64
A. baumannii	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48	+	2	32–128	32–512	256	32–128
	*bla*CTX-M, *bla*TEM	___	+	3	16–32	512	256–512	8–128
	*bla*CTX-M, *bla*TEM	*bla*OXA-48	+	2	32–256	512	256	64–512
	*bla*TEM	*bla*OXA-48	+	3	32–128	512	256	32–128
	*bla*CTX-M, *bla*TEM	*bla*VIM	-	1	ND	32	64	24

	*bla*CTX-M, *bla*TEM	*bla*OXA-48, *bla*VIM,	+	1	32	32	256	32
	*bla*TEM	*bla*OXA-48	-	1	32	32	256	32
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*VIM	+	1	32	32	256	32
	*bla*CTX-M, *bla*TEM	*bla*OXA-48	-	1	256	512	512	32
	*bla*CTX-M	*bla*OXA-48	+	1	256	512	256	64
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*OXA-48, *bla*NDM	+	1	32	32	256	32
	*bla*CTX-M	*bla*OXA-48	+	1	256	512	256	64
	*bla*TEM	*bla*OXA-48, *bla*VIM, *bla*KPC	+	1	256	512	256	64
	*bla*TEM	*bla*OXA-48, *bla*VIM	+	1	32	32	256	32
P. aeruginosa	*bla*CTX-M, *bla*TEM	———	+	2	128–256	512	512	64–128
	*bla*CTX-M, *bla*TEM, *bla*SHV	*bla*VIM	+	1	512	512	512	256
	*bla*CTX-M, *bla*TEM	*bla*OXA-48	+	1	16	512	512	8

Table S2. P-values of the association between CR genes and the resistance to carbapenems in various species

Bacterial Species	*Genes*	Meropenem	Imipenem
	bla$_{KPC}$	ND	ND
	bla$_{VIM}$	1	1
E. coli	*bla*$_{NDM}$	ND	ND
	bla$_{OXA-48}$	0.614	0.136
	bla$_{IMP}$	1	1
	bla$_{KPC}$	ND	ND
	bla$_{VIM}$	0.026	0.011
K. pneumoniae	*bla*$_{NDM}$	ND	ND
	bla$_{OXA-48}$	0.071	0.308
	bla$_{IMP}$	1	0.592
	bla$_{KPC}$	ND	1
	bla$_{VIM}$	ND	0.25
A. baumannii	*bla*$_{NDM}$	ND	1
	bla$_{OXA-48}$	ND	0.3
	bla$_{IMP}$	ND	ND
	bla$_{KPC}$	ND	ND
	bla$_{VIM}$	ND	ND
P. aeruginosa	*bla*$_{NDM}$	ND	ND
	bla$_{OXA-48}$	ND	ND
	bla$_{IMP}$	ND	ND

P-values were calculated by Chi-Square or Fisher's exact tests where appropriate. Significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *P*-values could not be calculated as all isolates showed the same resistance phenotype (resistant or sensitive) or all isolates had the same genotype (the gene was present or absent in all).

Table S3. P-values of the association between ESBL genes and the resistance to β-lactams in various species

Bacterial Species	*Gene*	CEC	AMP	FOX	AMC	SAM	TPZ	FEP	CRO	CTX	CAZ
E. coli	***bla*SHV**	**ND**	**1**	**1**	**1**	**0.529**	**0.628**	**ND**	**ND**	**ND**	**ND**
	***bla*CTX-M**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
	***bla*TEM**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
K. pneumoniae	***bla*SHV**	**ND**	**ND**	**0.567**	**ND**	**0.145**	**1**	**ND**	**ND**	**ND**	**ND**
	***bla*CTX-M**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
	***bla*TEM**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
A. baumannii	***bla*SHV**					**ND**	**1**	**ND**	**ND**	**ND**	**ND**
	***bla*CTX-M**					**ND**	**1**	**ND**	**ND**	**ND**	**ND**
	***bla*TEM**					**ND**	**ND**	**ND**	**ND**	**ND**	**ND**
P. aeruginosa	***bla*SHV**						**ND**	**ND**			**ND**
	***bla*CTX-M**						**ND**	**ND**			**ND**
	***bla*TEM**						**ND**	**ND**			**ND**

P-values were calculated by Chi-Square or Fisher's exact tests where appropriate. Black cells correspond to untested antimicrobial agents. ND, *P*-values could not be calculated as all isolates showed the same resistance phenotype (resistant or sensitive) or all isolates had the same genotype (the gene was present or absent in all). AMP, ampicillin; AMC, amoxacillin/clavulanic acid; CAZ, ceftazidime; CEC, cefaclor; CRO, ceftriaxone; CTX, cefotaxime; FEP, Cefepime; FOX, cefoxitin; SAM, ampicillin/sulbactam; TPZ, piperacillin/tazobactam.

Table S4. P-values of the association between the *aac(6′)-Ib* gene and the resistance to aminoglycosides and fluoroquinolones in various species

Bacterial species	Gentamicin 10	Amikacin	Ciprofloxacin	Ofloxacin	Levofloxacin
E. coli	ND	ND	ND	ND	ND
K. pneumoniae	0.677	0.244	1	0.07	0.07
A. baumannii	0.046	0.15	ND		0.404
P. aeruginosa	ND	ND	ND	ND	ND

P-values were calculated by Chi-Square or Fisher's exact tests where appropriate. Black cells correspond to untested antimicrobial agents, while significant associations with *p*-values ≤ 0.05 are highlighted with a yellow color. ND, *P*-values could not be calculated as all isolates showed the same resistance phenotype (resistant or sensitive) or all isolates had the same genotype (the gene was present or absent in all).

Table S5: Primers used in this study, expected PCR product sizes, and annealing temperatures (Ta)

PCR reaction	Gene	Primer	Primer sequence (5′ → 3′)	Expected PCR product size (bp)	T_a (°C)	References
Multiplex	*bla*KPC	P_f	TGTCACTGTATCGCCGTC	1011	50	[1]
		P_r	CTCAGTGCTCTACAGAAAACC			
	*bla*NDM	P_f	GGTTTGGCGATCTGGTTTTC	621		[2]
		P_r	CGGAATGGCTCATCACGAT			
Multiplex	*bla*VIM	P_f	TCTACATGACCGCGTCTGTC	748	50	[3]
		P_r	TGTGCTTTGACAACGTTCGC			
	*bla*OXA-48	P_f	GCGTGGTTAAGGATGAACAC	438		[1]
		P_r	CATCAAGTTCAACCCAACCG			
Monoplex	*bla*IMP	P_f	CTACCGCAGCAGAGTCTTTG	587	50	[4]
		P_r	AACCAGTTTTGCCTTACCAT			
Multiplex	*aac(6′)-Ib*	P_f	TTGCGATGCTCTATGAGTGG	358	49	[5]
		P_r	CGTTTGGATCTTGGTGACCT			
	*bla*SHV	P_f	GGTTATGCGTTATATTCGCC	867		[6]
		P_r	TTAGCGTTGCCAGTGCTC			
Multiplex	*bla*CTX-M	P_f	CGCTTTGCGATGTGCAG	550	51	[7]
		P_r	ACCGCGATATCGTTGGT			
	*bla*TEM	P_f	ATGAGTATTCAACATTTCCG	867		[6]
		P_r	CTGACAGTTACCAATGCTTA			

Abbreviations: P_f, forward primer; P_r, reverse primer; T_a, annealing temperature.