

**Supplemental Table S1.** Multivariate Analysis on risk factors associated to total antimicrobial use.

	Unstandardized coefficient		Standardized coefficient	P value
	B	Std Error	Beta	
<b>Constant</b>	15.549	5.907		0.010
<b>SAPS II (value)</b>	-0.190	0.094	-0.203	0.047
<b>Heart Disease (yes)</b>	-1.528	2.770	-0.048	0.583
<b>Pneumopathy (yes)</b>	1.644	3.223	0.046	0.612
<b>DM (yes)</b>	-0.943	3.074	-0.026	0.760
<b>CKD (yes)</b>	5.558	3.986	0.139	0.167
<b>Year of admission (PP)</b>	8.868	2.851	0.280	0.003
<b>ICU stay (days)</b>	1.239	0.355	0.551	0.001
<b>IMV duration (days)</b>	-0.047	0.511	-0.015	0.927
<b>Acute respiratory failure after surgery (yes)</b>	-8.108	3.072	-0.256	0.010

Reference in parenthesis; PP=pre-Pandemic; SAPS II, Simplified Acute Physiology Score II; DM, diabetes mellitus; CKD, chronic kidney disease; Intra-Pandemic (2020); ICU, intensive care unit; IMV, invasive mechanical ventilation.

**Supplemental Table S2:** Microbial isolations in blood, respiratory tract and urinary tract samples, divided in families in the two years.

PP: Pre-Pandemic		IP: Intra-Pandemic	
FAMILIES	n. (%)	n. (%)	FAMILIES
<i>Staphylococcus</i> spp.	23 (35.4)	18 (28.1)	<i>Candida</i> spp. §
<i>Enterobacteriaceae</i>	11 (16.9)	13 (20.3)	<i>Staphylococcus</i> spp.
<i>Pseudomonas aeruginosa</i>	10 (15.4)	9 (14.1)	<i>Others*</i>
<i>Others*</i>	6 (9.2)	8 (12.5)	<i>Pseudomonas aeruginosa</i>
<i>Acinetobacter baumannii</i>	3 (4.6)	5 (7.8)	<i>Enterobacteriaceae</i>
<i>Morganella morganii</i>	3 (4.6)	5 (7.8)	<i>Stenotrophomonas maltophilia</i>
<i>Streptococcus</i> spp.	2 (3.1)	2 (3.1)	<i>Streptococcus</i> spp.
<i>Candida</i> spp.	2 (3.1)	2 (3.1)	<i>Enterococcus faecalis</i>
<i>Stenotrophomonas maltophilia</i>	2 (3.1)	1 (1.6)	<i>Klebsiella</i> spp.
<i>Enterococcus faecalis</i>	1 (1.5)	1 (1.6)	<i>Haemophilus influenzae</i>
<i>Klebsiella</i> spp.	1 (1.5)	0 (0)	<i>Acinetobacter baumannii</i>
<i>Haemophilus influenzae</i>	1 (1.5)	0 (0)	<i>Morganella morganii</i>
<b>Total number of isolated microorganisms</b>	<b>65</b>	<b>64</b>	<b>Total number of isolated microorganisms</b>

*Legionella pneumophila*, *Proteus mirabilis*, *Corynebacterium* spp., *Serratia marcescens*, *Actinomyces*, *Lactobacillus casei*, *Citrobacter freundii*, *Alcaligenes xylosoxidans*, *Propionibacterium acnes*. § Chi-square test with p<0.05 comparing the relative percentage in the two groups.

**Figure S1:** Relative percentage of isolated microorganisms' classes in the cumulative positive cultures, bloodstream cultures, respiratory tract cultures and urinary tract cultures in the two years of analysis. PP, pre-pandemic; IP, intra-pandemic.

