Supporting Information Appendix

Supplemental Table 1.
Antibiotic classes and drugs administered in this study.

Antibiotic Classes	Drug
Aminoglycosides	Tobramycin, Gentamicin, Amikacin
Carbapenems	Meropenem, Ertapenem, Imipenem, Doripenem
Cephalosporins	1st generation: Cephalexin, Cefazolin, Cefalexin, Cefadroxil,
	2nd generation: Ceftin, Cefuroxime, Cefoxitin
	3rd generation: Cefditoren, Cefixime, Cefpodoxime, Ceftriaxone, Cefdinir, Ceftazidime
	4th generation: Cefepime
Glycopeptides	Vancomycin
Lincosamides	Clindamycin
Macrolides	Azithromycin, Erythromycin, Clarithromycin
Nitrofurans	Nitrofurantoin
Nitroimidazoles	Metronidazole
Oxazolidinones	Linezolid
Penicillins	Ampicillin, Amoxicillin, Nafcillin, Piperacillin, Penicillin
Penicillin Combinations	Amoxicillin-Clavulanate, Ampicillin-Sulbactam, Piperacillin-Tazobactam
Quinolones	Liprofloxacin, Levofloxacin, Moxifloxacin, Ciprofloxacin
Sulfonamides	Trimethoprim-Sulfamethoxazole
Tetracyclines	Doxycycline, Tetracycline, Declomycin
Lipopeptide	Daptomycin
Triazoles	Fluconazole, Diflucan
Monobactams	Aztreonam
Rifampicin	Rifampin

Supplemental Table 2
a. Number of patients exposed to each antibiotic class in this study.

Number of participants	
Cephalosporins	124
Quinolones	120
Penicillin Combinations	56
Glycopeptides	56
Sulfonamides	41
Aminoglycosides	31
Penicillins	29
Nitroimidazoles	24
Nitrofurans	22
Macrolides	17
Tetracyclines	15
Carbapenems	15
Oxazolidinones	12
Lincosamides	9
Triazoles	7
Lipopeptide	3
Monobactams	2
Rifampicin	1

Supplemental Table 2
b. Spectrum of activity of each antibiotic class against MDRO of interest in this study. TRUE = effective; FALSE = ineffective due to intrinsic resistance.

* only effective against E. faecalis
** true for piperacillin/tazobactam
*** E. faecalis (not E. faecium) is susceptible to piperacillin/tazobactam, ampicillin/sulbactam, and amoxicillin/clavulanate but not ticarcillin/clavulanic acid.
**** Only ceftazidime, not cefotaxime, ceftriaxone, etc.

	Non-aminopenicillin penicillins	Amino-penicillins	Ureido-penicillin	Penicillin combinations
P. mirabilis	TRUE	TRUE	TRUE	TRUE
A. baumannii	FALSE	FALSE	FALSE	TRUE
P. aeruginosa	FALSE	FALSE	TRUE	TRUE**
VRE	TRUE *	TRUE	TRUE	TRUE***
E. coli	FALSE	TRUE	TRUE	TRUE
MRSA	FALSE	FALSE	FALSE	FALSE

	Cephalosporins			
	1st Gen	2nd Gen	3rd Gen	4th Gen
P. mirabilis	TRUE	TRUE	TRUE	TRUE
A. baumannii	FALSE	FALSE	TRUE	TRUE
P. aeruginosa	FALSE	FALSE	TRUE****	TRUE
VRE	FALSE	FALSE	FALSE	FALSE
E. coli	TRUE	TRUE	TRUE	TRUE
MRSA	FALSE	FALSE	FALSE	FALSE

	Macrolides	Meropenem/ Doripenem	Ertapenem	Imipenem
P. mirabilis	FALSE	TRUE	TRUE	FALSE
A. baumannii	FALSE	TRUE	FALSE	TRUE
P. aeruginosa	FALSE	TRUE	FALSE	TRUE
VRE	FALSE	FALSE	FALSE	TRUE *
E. coli	FALSE	TRUE	TRUE	TRUE
MRSA	TRUE	FALSE	FALSE	FALSE

	Nitrofurantoin	Glycopeptides	Aminoglycosides	Fluoroquinolones
P. mirabilis	FALSE	FALSE	TRUE	TRUE
A. baumannii	FALSE	FALSE	TRUE	TRUE
P. aeruginosa	FALSE	FALSE	TRUE	TRUE
VRE	TRUE	FALSE	TRUE	TRUE
E. coli	TRUE	FALSE	TRUE	TRUE
MRSA	TRUE	TRUE	TRUE	TRUE

	Sulfonamides	Lincosamides
P. mirabilis	TRUE	FALSE
A. baumannii	TRUE	FALSE
P. aeruginosa	FALSE	FALSE
VRE	FALSE	FALSE
E. coli	TRUE	FALSE
MRSA	TRUE	TRUE

Supplemental Table 3
The hazard ratio of acquiring a secondary resistant organism within 30 days when a primary resistant organism is present (row name: primary organism/secondary organism), unadjusted for resident-level covariates. Species pairs that have a hazard ratio > 2 and p value < 0.05 are highlighted.

Primary/Secondary organism	Hazard ratio (confidence interval; p value)
VRE/MRSA	HR = 1.49 (CI = 0.65-3.44; p = 0.346)
VRE/Acinetobacter_baumanii	HR = 3.64 (CI = 1.21-10.92; p = 0.021)
VRE/Escherichia_coli	HR = 1.55 (CI = 0.51-4.67; p = 0.437)
VRE/Proteus_mirabilis	HR = 1.39 (CI = 0.47-4.16; p = 0.551)
VRE/Pseudomonas_aeruginosa	HR = 2.91 (CI = 0.88-9.65; p = 0.08)
MRSA/VRE	HR = 1.71 (CI = 0.57-5.09; p = 0.335)
MRSA/Acinetobacter_baumanii	HR = 0.67 (CI = 0.09-5.23; p = 0.706)
MRSA/Escherichia_coli	HR = 0.37 (CI = 0.05-2.75; p = 0.329)
MRSA/Proteus_mirabilis	HR = 1.76 (CI = 0.59-5.25; p = 0.307)
Acinetobacter_baumanii/VRE	HR = 2.57 (CI = 0.34-19.56; p = 0.361)
Acinetobacter_baumanii/MRSA	HR = 0.56 (CI = 0.07-4.11; p = 0.565)
Acinetobacter_baumanii/Escherichia_coli	HR = 1.65 (CI = 0.22-12.64; p = 0.627)
Acinetobacter_baumanii/Proteus_mirabilis	HR = 7.51 (CI = 2.51-22.44; p = 0.001)
Acinetobacter_baumanii/Pseudomonas_aeruginosa	HR = 1.67 (CI = 0.21-13.37; p = 0.627)
Escherichia_coli/VRE	HR = 1.4 (CI = 0.59-3.3; p = 0.447)
Escherichia_coli/MRSA	HR = 2.06 (CI = 1.08-3.92; p = 0.027)
Escherichia_coli/Acinetobacter_baumanii	HR = 2.43 (CI = 0.81-7.29; p = 0.115)
Escherichia_coli/Proteus_mirabilis	HR = 2.42 (CI = 1.07-5.46; p = 0.033)
Escherichia_coli/Pseudomonas_aeruginosa	HR = 2.15 (CI = 0.72-6.45; p = 0.173)
Proteus_mirabilis/VRE	HR = 2.32 (CI = 1-5.35; p = 0.049)
Proteus_mirabilis/MRSA	HR = 2.18 (CI = 1.13-4.2; p = 0.019)
Proteus_mirabilis/Acinetobacter_baumanii	HR = 3.58 (CI = 1.26-10.18; p = 0.017)
Proteus_mirabilis/Escherichia_coli	HR = 2.32 (CI = 0.94-5.71; p = 0.067)
Proteus_mirabilis/Pseudomonas_aeruginosa	HR = 1.68 (CI = 0.56-4.98; p = 0.353)
Pseudomonas_aeruginosa/VRE	HR = 2.32 (CI = 0.55-9.8; p = 0.253)
Pseudomonas_aeruginosa/MRSA	HR = 2.72 (CI = 0.96-7.67; p = 0.059)
Pseudomonas_aeruginosa/Acinetobacter_baumanii	HR = 2.01 (CI = 0.26-15.32; p = 0.499)
Pseudomonas_aeruginosa/Escherichia_coli	HR = 2.66 (CI = 0.61-11.55; p = 0.193)
Pseudomonas_aeruginosa/Proteus_mirabilis	HR = 4.13 (CI = 1.41-12.07; p = 0.01)

Supplemental Table 4
The hazard ratio of acquiring a resistant organism upon antibiotic exposure within 30 days (row name: acquired organism/antibiotic), unadjusted for resident-level covariates. Species/antibiotic pair that have a hazard ratio > 2 and p value < 0.05 are highlighted.

Organism/antibiotic exposed	Hazard ratio (confidence interval; p value)
VRE/Aminoglycosides	HR = 5.66 (CI = 2.28-14.03; p < 0.001)
VRE/Carbapenems	HR = 2.24 (CI = 0.3-16.75; p = 0.433)
VRE/Cephalosporins	HR = 2.4 (CI = 1.13-5.09; p = 0.022)
VRE/Glycopeptides	HR = 6.26 (CI = 2.98-13.14; p < 0.001)
VRE/Lincosamides	HR = 3.84 (CI = 0.5-29.73; p = 0.197)
VRE/Macrolides	HR = 1.46 (CI = 0.2-10.76; p = 0.712)
VRE/Nitrofurans	HR = 3.33 (CI = 1-11.15; p = 0.051)
VRE/Oxazolidinones	HR = 1.54 (CI = 0.21-11.5; p = 0.672)
VRE/Penicillins	HR = 0.66 (CI = 0.09-4.89; p = 0.683)
VRE/Penicillin Combinations	HR = 1.89 (CI = 0.66-5.41; p = 0.238)
VRE/Quinolones	HR = 1.83 (CI = 0.84-3.98; p = 0.127)
VRE/Sulfonamides	HR = 0.73 (CI = 0.17-3.06; p = 0.662)
VRE/Tetracyclines	HR = 2.83 (CI = 0.67-12.02; p = 0.158)
VRE/Echinocandin	HR = 1 (CI = 1-1; p = NaN)
VRE/Glycylcycline	HR = 1 (CI = 1-1; p = NaN)
VRE/Monobactams	HR = 1 (CI = 1-1; p = NaN)
MRSA/Aminoglycosides	HR = 0.46 (CI = 0.06-3.39; p = 0.45)
MRSA/Carbapenems	HR = 2.09 (CI = 0.5-8.77; p = 0.315)
MRSA/Cephalosporins	HR = 1.2 (CI = 0.55-2.6; p = 0.644)
MRSA/Glycopeptides	HR = 0.95 (CI = 0.37-2.42; p = 0.91)
MRSA/Nitrofurans	HR = 1.25 (CI = 0.3-5.21; p = 0.76)
MRSA/Nitroimidazoles	HR = 0.96 (CI = 0.23-3.98; p = 0.95)
MRSA/Penicillins	HR = 1.75 (CI = 0.54-5.73; p = 0.353)
MRSA/Penicillin Combinations	HR = 1.87 (CI = 0.78-4.45; p = 0.16)
MRSA/Quinolones	HR = 1.01 (CI = 0.47-2.17; p = 0.984)
MRSA/Sulfonamides	HR = 0.83 (CI = 0.26-2.69; p = 0.756)
MRSA/Tetracyclines	HR = 0.83 (CI = 0.11-6.04; p = 0.85)
MRSA/Echinocandin	HR = 1 (CI = 1-1; p = NaN)
MRSA/Glycylcycline	HR = 1 (CI = 1-1; p = NaN)
Acinetobacter_baumanii/Aminoglycosides	HR = 5.73 (CI = 1.62-20.24; p = 0.007)
Acinetobacter_baumanii/Carbapenems	HR = 4.84 (CI = 0.63-37.02; p = 0.128)
Acinetobacter_baumanii/Cephalosporins	HR = 2.06 (CI = 0.73-5.84; p = 0.175)
Acinetobacter_baumanii/Glycopeptides	HR = 3.43 (CI = 1.21-9.7; p = 0.02)
Acinetobacter_baumanii/Nitrofurans	HR = 1.63 (CI = 0.22-12.4; p = 0.635)

Acinetobacter_baumanii/Nitroimidazoles	HR = 1.33 (CI = 0.18-10.15; p = 0.78)
Acinetobacter_baumanii/Oxazolidinones	HR = 2.54 (CI = 0.33-19.59; p = 0.37)
Acinetobacter_baumanii/Penicillins	HR = 1.08 (CI = 0.14-8.17; p = 0.94)
Acinetobacter_baumanii/Penicillin Combinations	HR = 0.8 (CI = 0.11-6.02; p = 0.825)
Acinetobacter_baumanii/Quinolones	HR = 0.84 (CI = 0.24-2.94; p = 0.789)
Acinetobacter_baumanii/Sulfonamides	HR = 0.62 (CI = 0.08-4.72; p = 0.649)
Acinetobacter_baumanii/Echinocandin	HR = 1 (CI = 1-1; p = NaN)
Acinetobacter_baumanii/Glycylcycline	HR = 1 (CI = 1-1; p = NaN)
Escherichia_coli/Aminoglycosides	HR = 3.79 (CI = 1.09-13.2; p = 0.036)
Escherichia_coli/Carbapenems	HR = 1.78 (CI = 0.24-13.29; p = 0.576)
Escherichia_coli/Cephalosporins	HR = 1.56 (CI = 0.58-4.24; p = 0.379)
Escherichia_coli/Glycopeptides	HR = 2.07 (CI = 0.76-5.63; p = 0.155)
Escherichia_coli/Nitroimidazoles	HR = 0.77 (CI = 0.1-5.77; p = 0.802)
Escherichia_coli/Oxazolidinones	HR = 3.71 (CI = 0.49-28.03; p = 0.203)
Escherichia_coli/Penicillins	HR = 3.1 (CI = 0.91-10.6; p = 0.072)
Escherichia_coli/Penicillin Combinations	HR = 1.18 (CI = 0.28-5.09; p = 0.82)
Escherichia_coli/Quinolones	HR = 1.8 (CI = 0.73-4.44; p = 0.2)
Escherichia_coli/Sulfonamides	HR = 0.47 (CI = 0.06-3.5; p = 0.461)
Escherichia_coli/Tetracyclines	HR = 1.59 (CI = 0.21-11.84; p = 0.652)
Escherichia_coli/Echinocandin	HR = 1 (CI = 1-1; p = NaN)
Escherichia_coli/Glycylcycline	HR = 1 (CI = 1-1; p = NaN)
Proteus_mirabilis/Aminoglycosides	HR = 3.54 (CI = 1.05-11.94; p = 0.041)
Proteus_mirabilis/Cephalosporins	HR = 2.35 (CI = 1.06-5.22; p = 0.036)
Proteus_mirabilis/Glycopeptides	HR = 1.11 (CI = 0.33-3.75; p = 0.861)
Proteus_mirabilis/Nitrofurans	HR = 8.95 (CI = 3.69-21.72; p < 0.001)
Proteus_mirabilis/Penicillins	HR = 1.95 (CI = 0.45-8.39; p = 0.369)
Proteus_mirabilis/Penicillin Combinations	HR = 0.46 (CI = 0.06-3.44; p = 0.452)
Proteus_mirabilis/Quinolones	HR = 1.06 (CI = 0.43-2.64; p = 0.902)
Proteus_mirabilis/Sulfonamides	HR = 1.26 (CI = 0.38-4.19; p = 0.711)
Proteus_mirabilis/Echinocandin	HR = 1 (CI = 1-1; p = NaN)
Proteus_mirabilis/Glycylcycline	HR = 1 (CI = 1-1; p = NaN)
Pseudomonas_aeruginosa/Aminoglycosides	HR = 7.17 (CI = 1.97-26.16; p = 0.003)
Pseudomonas_aeruginosa/Carbapenems	HR = 10.88 (CI = 3-39.49; p < 0.001)
Pseudomonas_aeruginosa/Cephalosporins	HR = 0.81 (CI = 0.18-3.63; p = 0.787)
Pseudomonas_aeruginosa/Glycopeptides	HR = 4.73 (CI = 1.58-14.19; p = 0.006)
Pseudomonas_aeruginosa/Nitrofurans	HR = 1.3 (CI = 0.17-10.11; p = 0.804)
Pseudomonas_aeruginosa/Oxazolidinones	HR = 7.62 (CI = 1.66-35.11; p = 0.009)
Pseudomonas_aeruginosa/Penicillin	HR = 0.87 (CI = 0.11-6.69; p = 0.897)

Combinations	
Pseudomonas_aeruginosa/Quinolones	HR = 1.23 (CI = 0.34-4.41; p = 0.756)
Pseudomonas_aeruginosa/Sulfonamides	HR = 0.8 (CI = 0.1-6.13; p = 0.83)
Pseudomonas_aeruginosa/Echinocandin	HR = 1 (CI = 1-1; p = NaN)
Pseudomonas_aeruginosa/Glycylcycline	HR = 1 (CI = 1-1; p = NaN)

Supplemental Table 5

Hazard ratios used for constructing interaction network showing association between risk factors and colonization (Figure 2). ** $p < 0.05$.

VRE	Hazard ratio	p-value
Aminoglycosides	2.30e+00	1.59e-01
Cephalosporins	1.31e+00	5.90e-01
Glycopeptides**	5.94e+00	9.00e-04
Nitrofurans	2.38e+00	2.66e-01
Proteus mirabilis**	5.79e+00	1.00e-04
Sex	1.07e+00	8.78e-01

Acinetobacter baumannii	Hazard ratio	p-value
Aminoglycosides **	6.43e+00	1.45e-02
Glycopeptides	2.64e+00	1.30e-01
VRE**	5.50e+00	1.90e-03
Proteus mirabilis**	5.03e+00	3.70e-03
Sex	1.14e+00	8.20e-01

Escherichia coli	Hazard ratio	p-value
Aminoglycosides	3.15e+00	8.12e-02
Penicillins**	4.52e+00	2.54e-02
Proteus mirabilis	2.17e+00	8.61e-02
Sex	7.21e-01	4.41e-01

Proteus mirabilis	Hazard ratio	p-value
Aminoglycosides	1.72e+00	4.17e-01
Cephalosporins	1.31e+00	5.37e-01
Nitrofurans**	8.98e+00	0.00e+00
Acinetobacter baumanii**	1.13e+01	0.00e+00
Escherichia coli	1.82e+00	1.47e-01
Pseudomonas aeruginosa**	3.25e+00	4.69e-02
Sex	1.46e+00	3.51e-01

Pseudomonas aeruginosa	Hazard ratio	p-value
Aminoglycosides **	5.68e+00	1.25e-02
Carbapenems**	7.33e+00	3.04e-02
Glycopeptides	1.16e+00	8.52e-01
Oxazolidinones	2.49e+00	3.43e-01
VRE**	3.79e+00	2.21e-02
Sex	1.12e+00	8.42e-01

MRSA	Hazard ratio	p-value
Escherichia coli**	2.33e+00	3.29e-02
Proteus mirabilis**	3.32e+00	1.80e-03
Pseudomonas aeruginosa**	3.42e+00	4.71e-02
Sex	2.54e+00	2.30e-02

Supplemental Table 6
Risk of having positive urine culture when mono-colonized and co-colonized (Figure 3). * $p <$ 0.1.

MRSA in urine	Hazard ratio	p-value
MRSA colonization alone	2.70e+00	2.33e-01
Any other MDROs	2.08e-01	1.39e-01
Both	1.75e+00	4.89e-01
Functional status	1.07e+00	3.65e-01
Sex	1.98e+00	2.72e-01

MRSA in urine	Hazard ratio	p-value
MRSA colonization	2.63e+00	1.73e-01
Escherichia coli colonization	7.04e-01	7.46e-01
Both	3.94e+00	2.34e-01
Functional status	1.08e+00	3.39e-01
Sex	2.00e+00	2.78e-01

MRSA in urine	Hazard ratio	p-value
MRSA colonization	2.05e+00	3.78e-01
Proteus mirabilis colonization	7.32e-01	7.75e-01
Both*	4.84e+00	6.60e-02
Functional status	1.07e+00	3.79e-01
Sex	1.94e+00	2.96e-01

***E. coli* in urine**	Hazard ratio	p-value
Escherichia coli colonization alone	6.12e-01	6.50e-01
Any other MDROs	1.01e+00	9.86e-01
Both	2.53e+00	1.24e-01
Functional status	1.05e+00	4.67e-01
Sex	6.75e-01	4.55e-01

***E. coli* in urine**	Hazard ratio	p-value
MRSA colonization	9.36e-01	9.51e-01
Escherichia coli colonization	1.73e+00	3.18e-01
Both	9.78e-01	9.84e-01
Functional status	1.06e+00	3.95e-01

Sex	6.77e-01	4.71e-01

***E. coli* in urine**	Hazard ratio	p-value
Escherichia coli colonization	1.32e+00	7.05e-01
Proteus mirabilis colonization	1.92e+00	3.18e-01
Both*	3.11e+00	9.81e-02
Functional status	1.05e+00	4.42e-01
Sex	7.06e-01	5.08e-01

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VRE in urine	Hazard ratio	p-value
VRE colonization alone	6.40e-01	7.05e-01
Any other MDROs	3.94e-01	1.59e-01
Both	1.06e+00	9.31e-01
Functional status	1.13e+00	1.20e-01
Sex	1.49e+00	5.44e-01

VRE in urine	Hazard ratio	p-value
Escherichia coli colonization	3.90e-01	2.68e-01
VRE colonization	3.38e-01	3.21e-01
Both*	4.04e+00	6.23e-02
Functional status	1.12e+00	1.12e-01
Sex	1.43e+00	5.44e-01

VRE in urine	Hazard ratio	p-value
VRE colonization	1.38e+00	6.51e-01
Proteus mirabilis colonization	9.12e-02	5.12e-02
Both	4.28e-01	4.86e-01
Functional status	1.16e+00	7.07e-02
Sex	1.49e+00	5.46e-01

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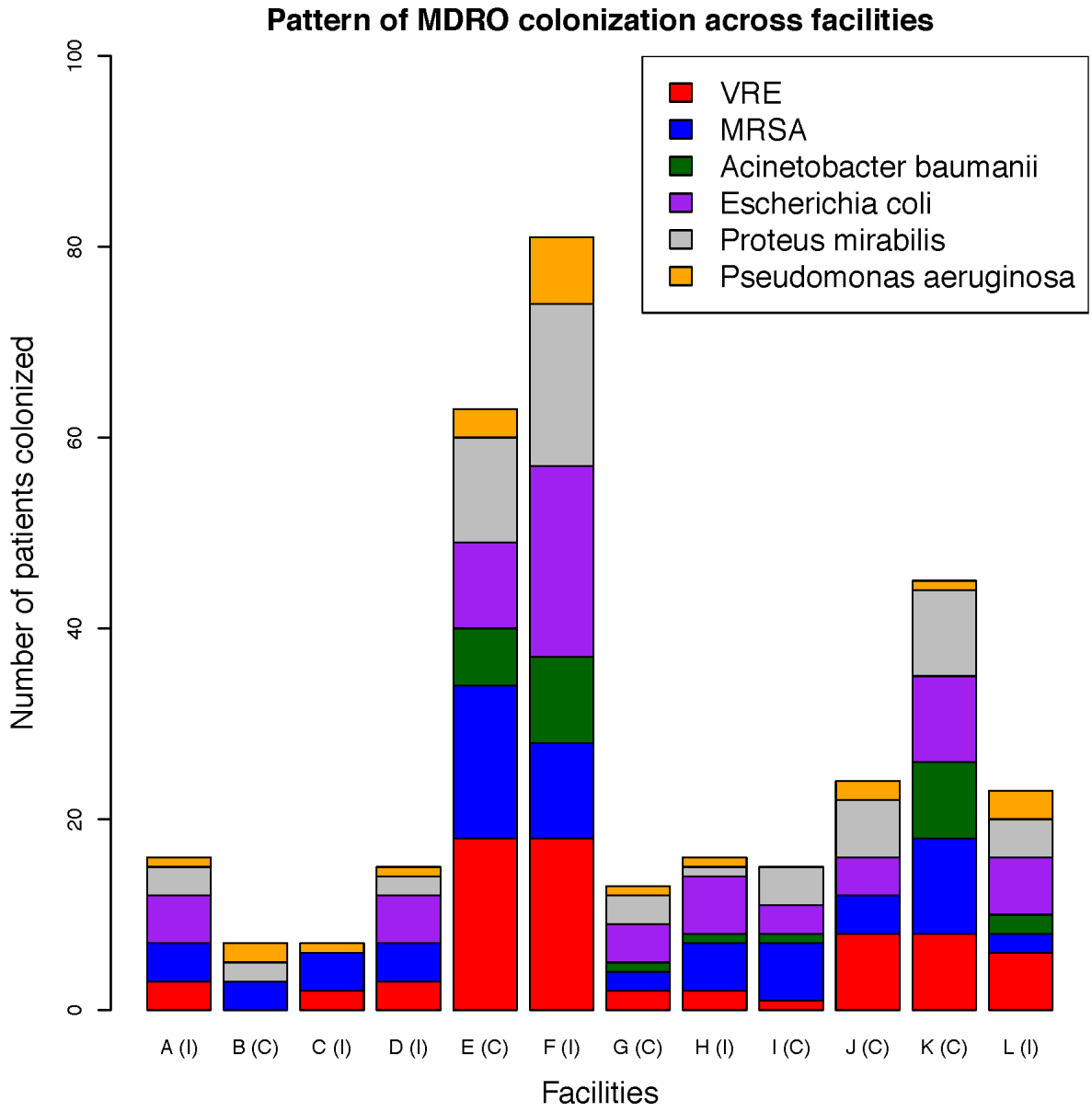
***P. mirabilis* in urine**	Hazard ratio	p-value
Proteus mirabilis colonization alone	1.22e+00	7.42e-01
Any other MDROs	6.49e-01	3.54e-01
Both	1.72e+00	2.39e-01
Functional status	1.00e+00	9.47e-01
Sex	2.26e+00	5.34e-02

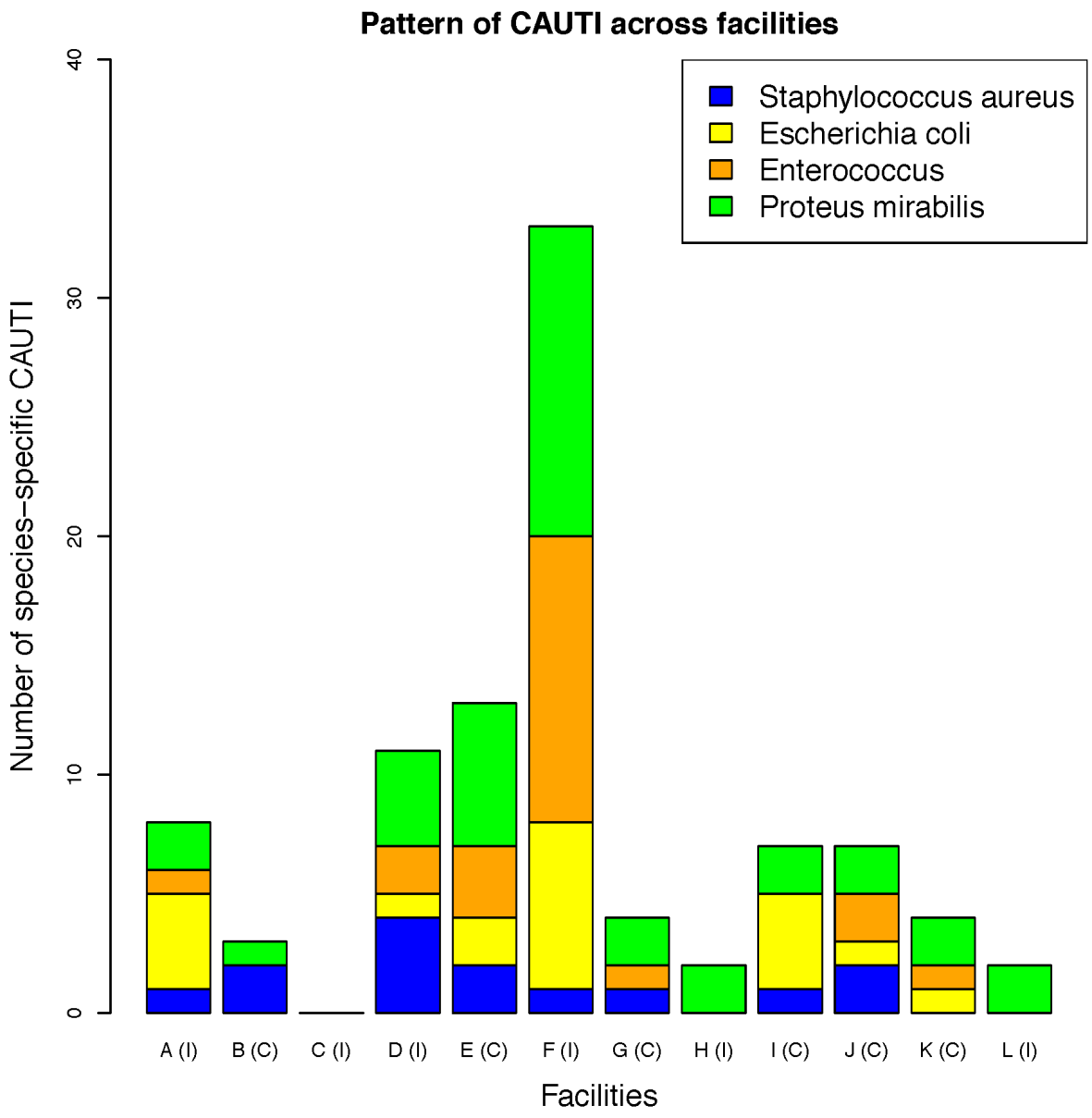
***P. mirabilis* in urine**	Hazard ratio	p-value
MRSA colonization	1.09e+00	8.90e-01
Proteus mirabilis colonization	1.52e+00	3.35e-01
Both	2.68e+00	1.10e-01
Functional status	1.01e+00	8.63e-01
Sex	2.07e+00	8.50e-02

***P. mirabilis* in urine**	Hazard ratio	p-value
Escherichia coli colonization	8.15e-01	7.28e-01
Proteus mirabilis colonizatoin	2.05e+00	9.45e-02
Both	9.51e-01	9.42e-01
Functional status	1.01e+00	9.23e-01
Sex	2.07e+00	8.62e-02

***P. mirabilis* in urine**	Hazard ratio	p-value
VRE colonization	3.05e-01	2.55e-01
Proteus mirabilis colonization	1.36e+00	4.96e-01
Both	2.30e+00	1.41e-01
Functional status	1.00e+00	9.36e-01
Sex	2.23e+00	5.61e-02

Supplemental Figure 1
Distribution of MDRO colonization and species-specific CAUTI across different facilities in this study. Control facilities are indicated as "C" and intervention facilities are indicated as "I" in brackets.




Pattern of CAUTI across facilities
Staphylococcus aureus
Escherichia coli
Enterococcus
Proteus mirabilis
Number of species−specific CAUTI
0
10
20
30
40
A (I)
B (C)
C (I)
D (I)
E (C)
F (I)
G (C)
H (I)
I (C)
J (C)
K (C)
L (I)
Facilities

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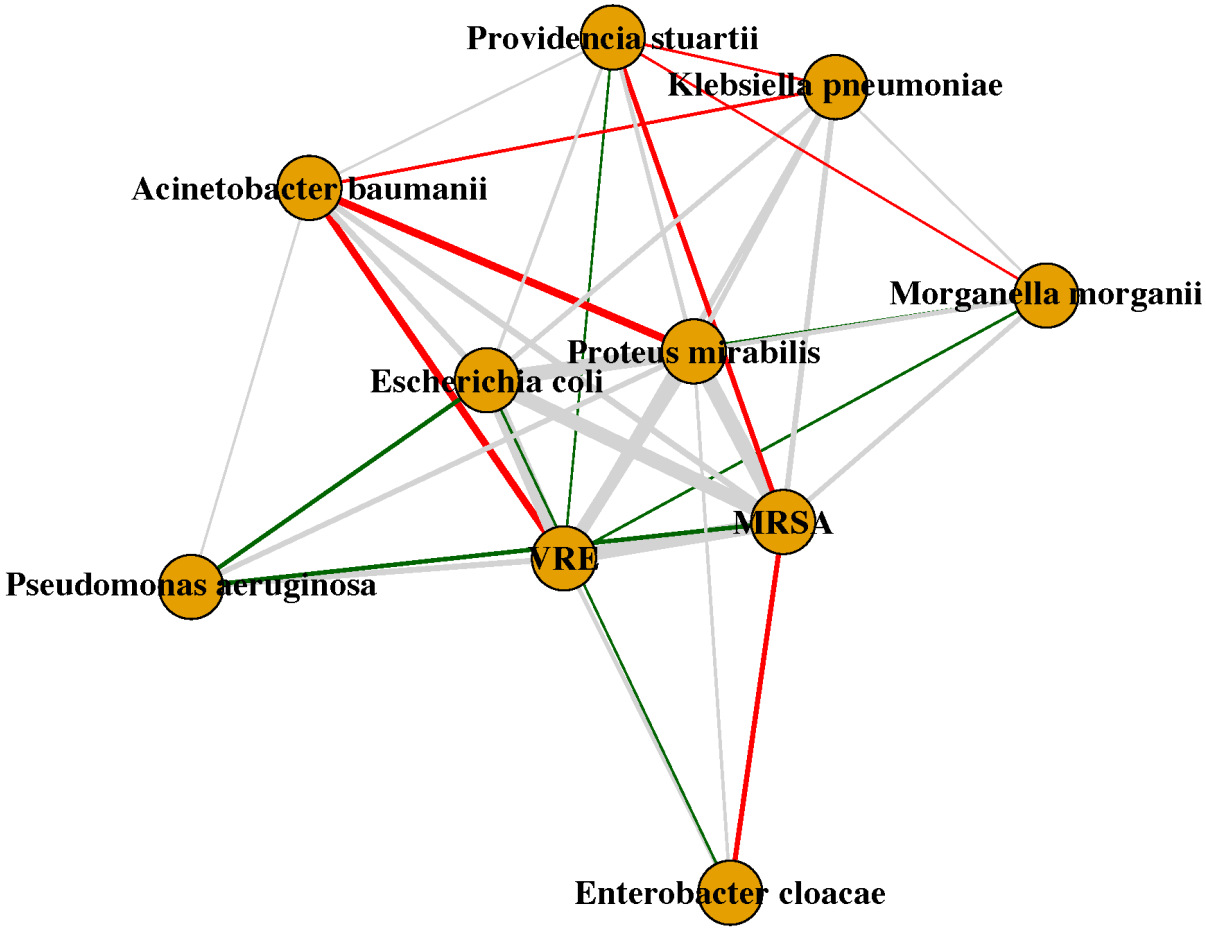
20

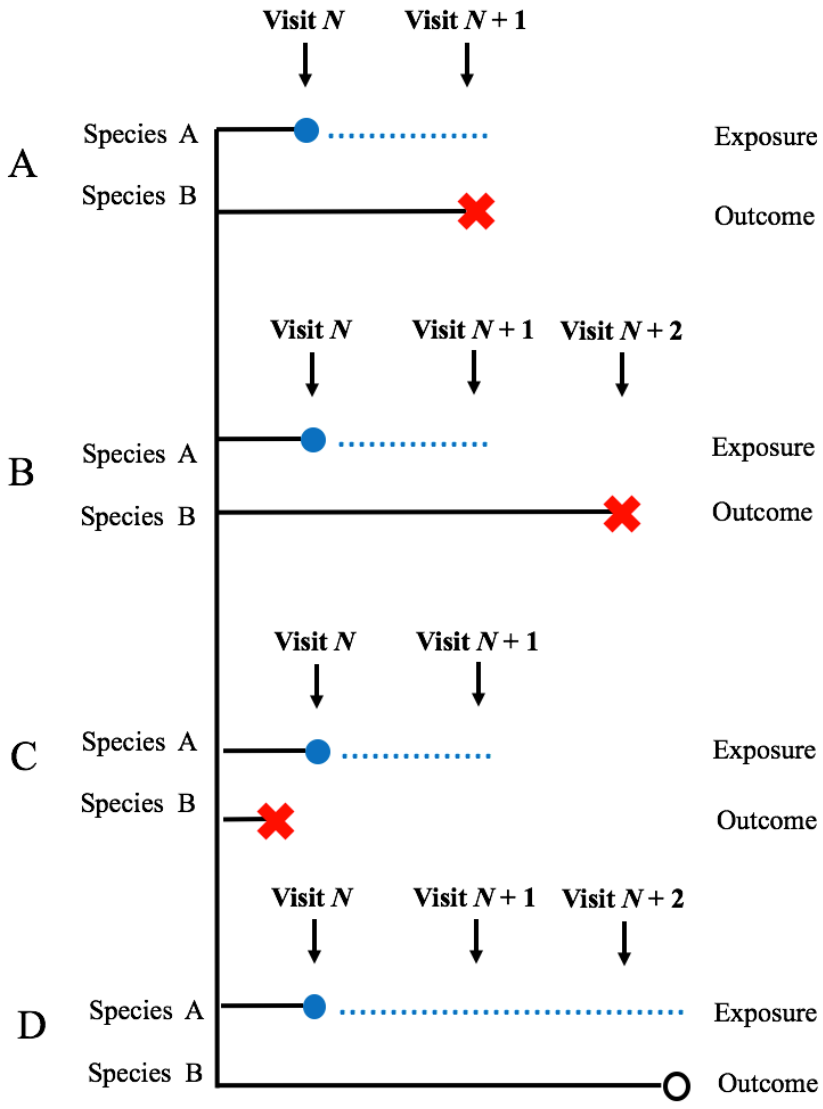
Supplemental Figure 2

Co-occurrence network constructed using EcoSimR. The number of occurrences of particular species pairs colonizing the same patient (rectal and groin areas) was compared to 1000 randomized matrices where the presence of each species is shuffled across patients and the number of bacteria in each patient harbors is fixed ("sim9" algorithm). Circles represent bacterial species and lines between two circles indicate that these species are found to co-colonize in more than five patients. Red lines indicate aggregation, green lines indicate segregation, grey lines indicate random co-occurrence. The thickness of the lines corresponds to the number of patients in which species pairs are found. All interactions shown have $p < 0.1$.



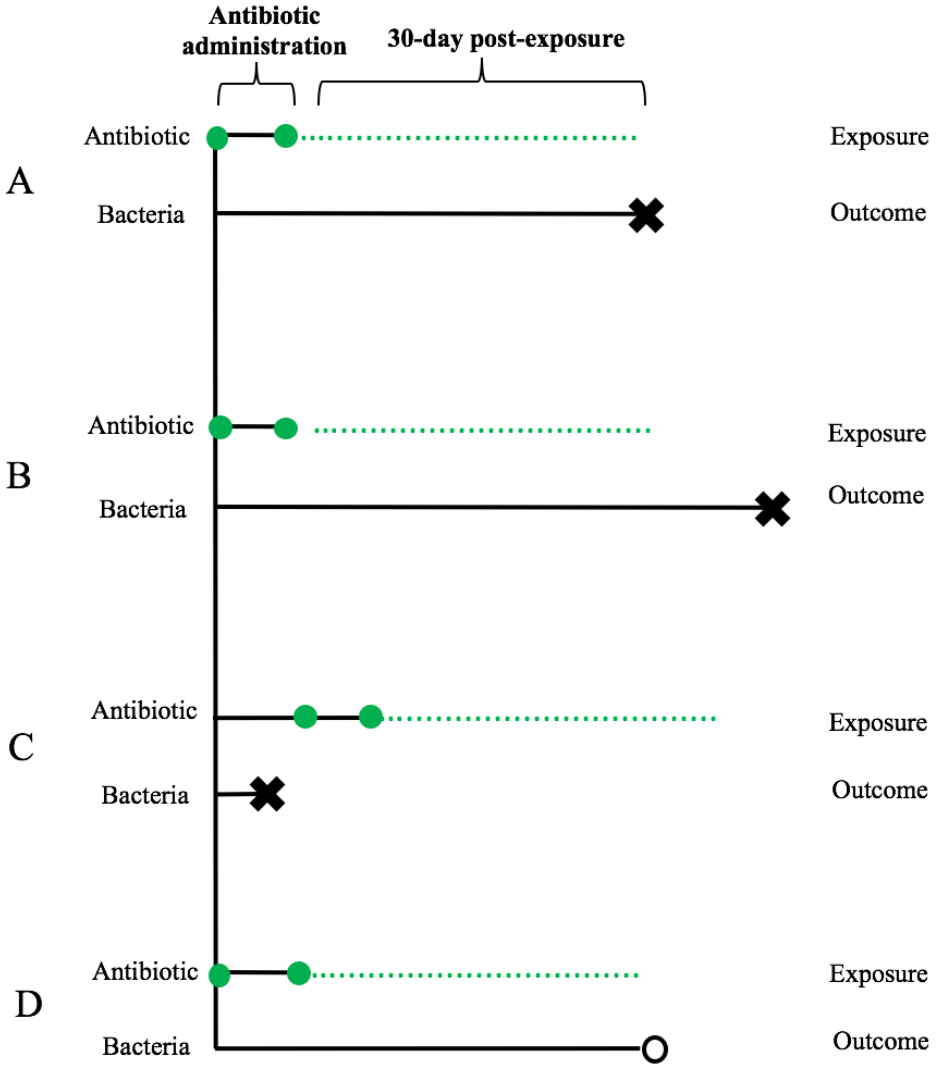
Supplemental Figure 3

Four possible scenarios of treating colonization as a time-varying variable. Blue: Species A; red: Species B; filled circle: primary colonization; X: secondary colonization; open circle: no secondary colonization; dashed line: assumed duration of colonization. A) Species A is detected at Visit N, and is assumed to persist until Visit N + 1. Species B is detected at Visit N + 1. Species A may be a risk factor for Species B colonization. B) Species A is detected at Visit N, and is assumed to persist until Visit N + 1. Species A is absent at Visit N + 1, and is assumed to be absent until Visit N + 2. Species B is found at Visit N + 2. Species A does not predict Species B colonization. C) Species A is detected at Visit N and is assumed to persist until Visit N + 1. Species B is detected prior to Visit N. Species A does not predict Species B colonization. D) Species A is detected at Visits N, N + 1, and N + 2, and is assumed to persist until the next visit. Species B is not detected before the end of the study. Species A does not predict Species B colonization.



Supplemental Figure 4

Four possible scenarios of treating antibiotic exposure as a time-varying variable. Green filled circle: start and end of antibiotic administration; black X: bacterial colonization; open circle: no colonization; dashed line: assumed prolonged effects after antibiotic exposure. A) Antibiotic is administered and the perturbation (on host microbiota, selective pressure, etc.) lasts for 30 days. ARO is detected at the end of the 30 days. The antibiotic is a risk factor for ARO colonization. B) Antibiotic is administered and the perturbation lasts for 30 days. ARO is detected after the 30 day period. The antibiotic does not predict ARO colonization. C) ARO colonization occurs before antibiotic administration. The antibiotic does not predict ARO colonization. D) Antibiotic is administered and the perturbation lasts for 30 days. No ARO colonization is detected before the end of the study. The antibiotic does not predict ARO colonization.



Supplemental Figure 5

Fractions of cases where colonizing MDROs were found to be associated with species-specific CAUTI. Body sites consist of the groin and peri-rectum. *x*-axis labels indicate the fraction of cases where the organism causing the CAUTI was present alone (mono), or occurring with other organisms. We observed higher co-occurrence frequency in organisms that were found to have interactions in our Cox regression model. We hypothesize that the absence of the potentially CAUTI-causing organisms was due to: 1. colonization abundance below the level of detection; 2. colonization by susceptible strains; 3. undetected transmission between visits.