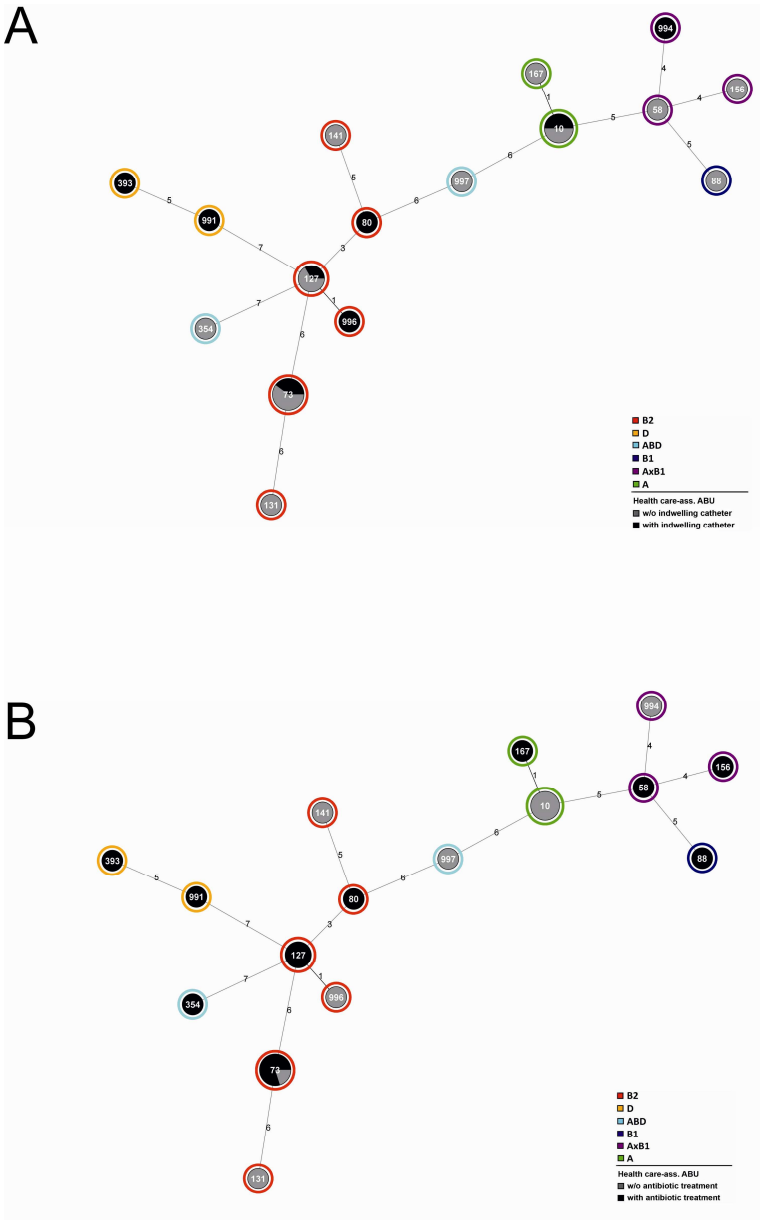

Figure S1: Phylogenetic background of health care-associated ABU *E. coli* isolates from patients with indwelling catheters or antibiotic treatment.

The minimum spanning tree of the concatenated MLST sequences as calculated by ClonalFrame has been depicted with Seqsphere (Ridom GmbH). The distribution of the ABU isolates with or without indwelling catheters A) (without indwelling catheter, dark grey; with indwelling catheter, black) or from patients with or without antibiotic treatment B) (without antibiotic treatment, dark grey; with antibiotic treatment, black) is indicated by pie charts. The size of the pie chart mirrors the number of strains allocated to the individual ST. Phylogenetic groups (A, B1, B2, D, AxB1, and ABD) as determined by STRUCTURE analysis of the MLST sequence data are indicated by the outmost ring of the tree.

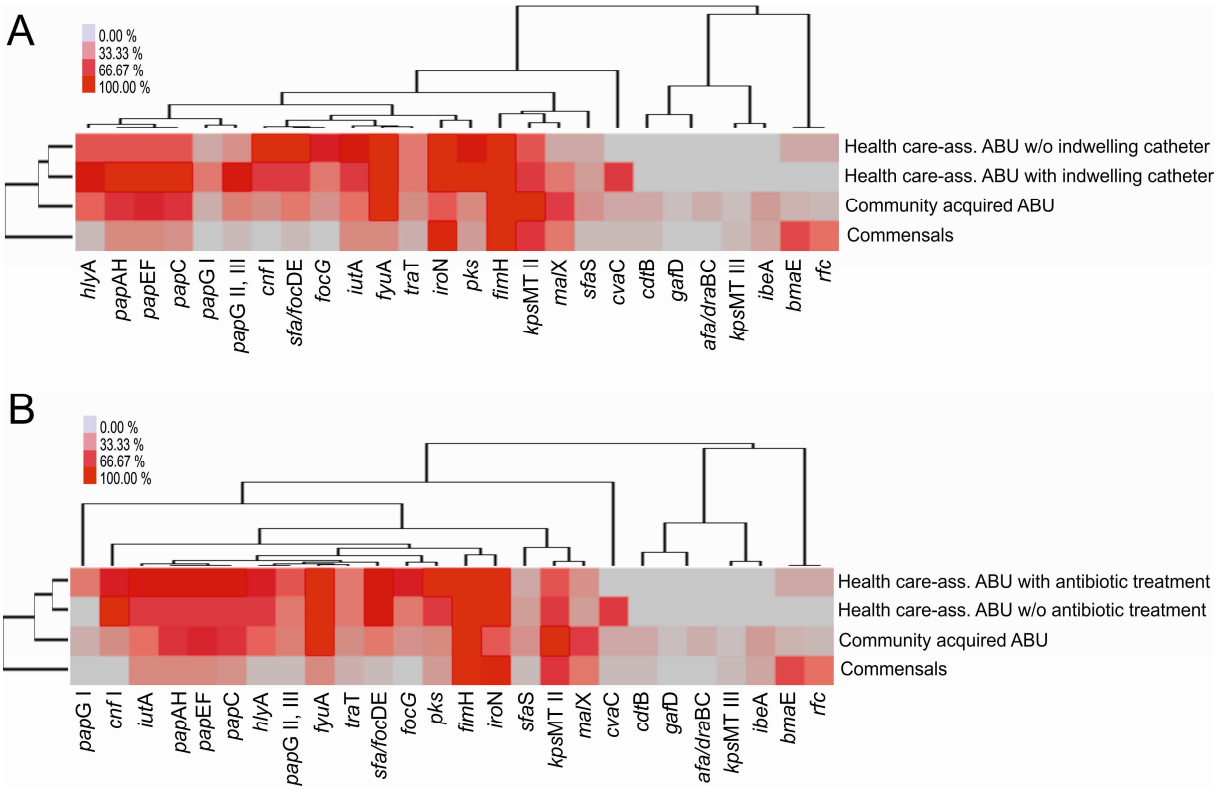

Figure S2: Virulence gene prevalences in health care-associated ABU *E. coli* isolates from patients with indwelling catheters or antibiotic treatment. Gene prevalence results of health care-associated ABU *E. coli* isolates dependent on long-term catheterization (A) or antibiotic treatment (B) were compared with that of community acquired ABU or commensal *E. coli* isolates by two-way clustering. A heat map was constructed based upon the percentage of each gene examined among each of the groups of isolates.

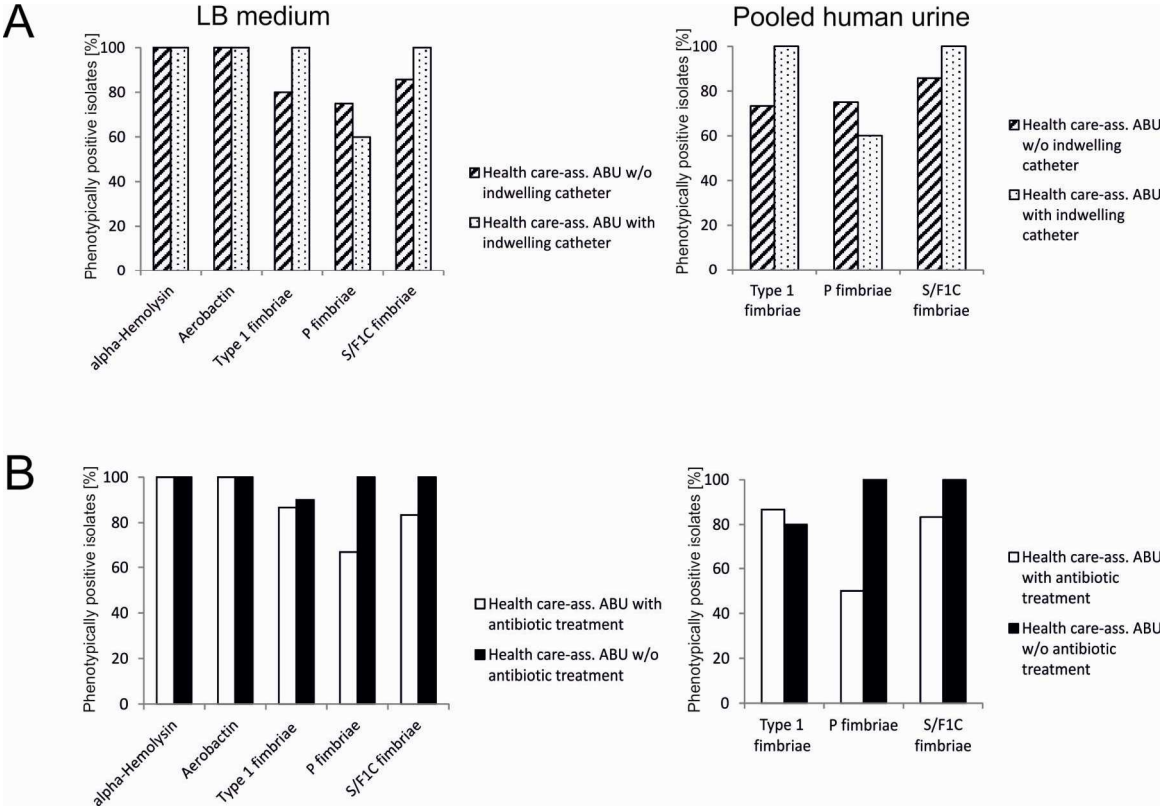

Figure S3: Phenotypic expression of selected virulence factors dependent on long-term catheterization (A) or antibiotic treatment (B) was analyzed upon in vitro cultivation of the isolates in LB or pooled human urine. The percentages of phenotypically positive isolates per group are indicated.

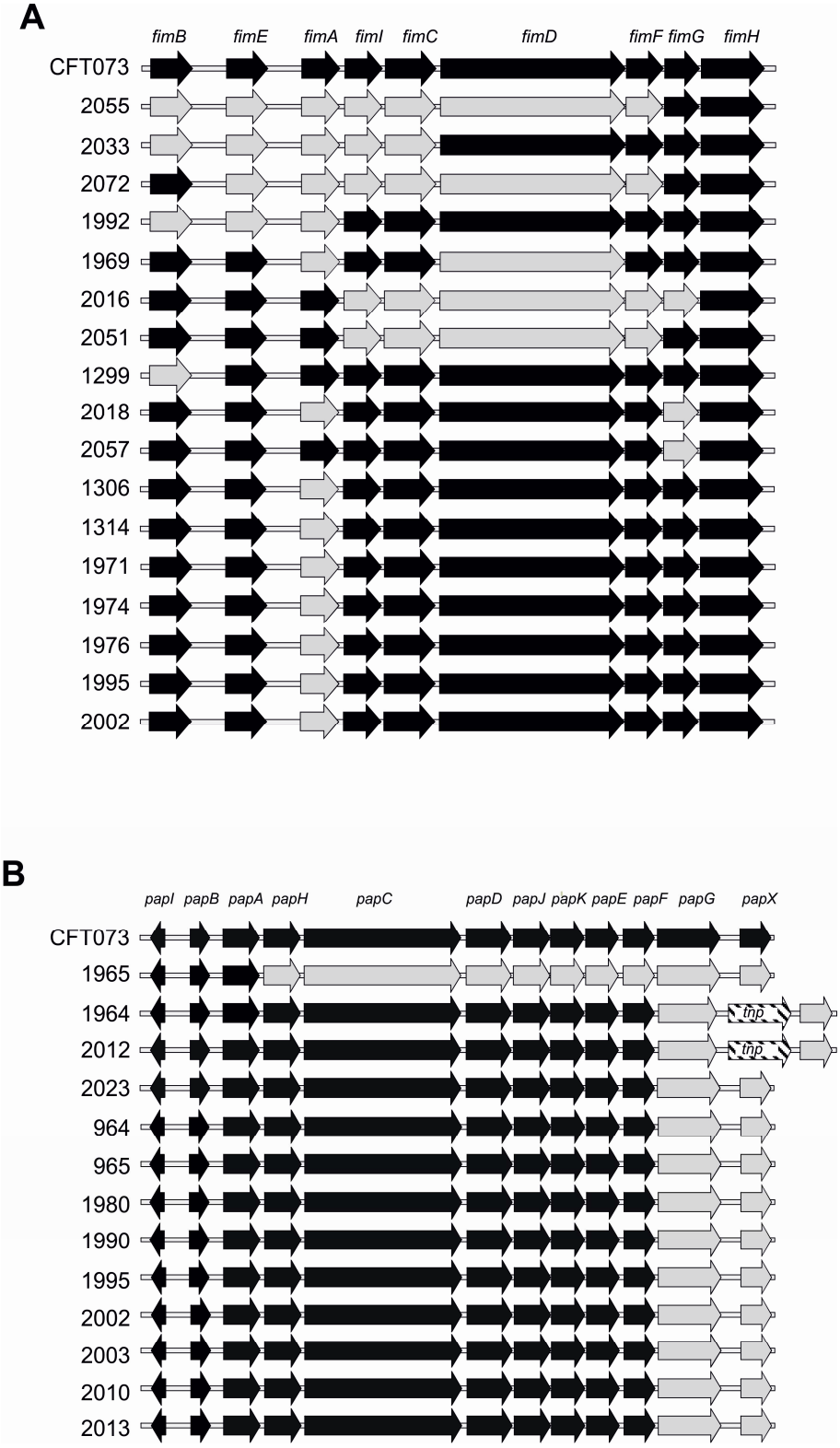

Figure S4: Genetic structures of the *fim* determinant A) and the *pap* determinant B) in ABU *E. coli* isolates. The scheme is based on the uropathogenic *E. coli* CFT073 chromosome. Arrows denote genes of the fim or pap determinant. Black arrows denote detectable ORFs, grey arrows denote ORFs which could not be amplified by PCR. The IS*3*-related, non-functional transposase-encoding gene is indicated by a hatched arrow.

Table S1: Genotypic characterization of *E. coli* from community acquired ABU or health care-associated patients

	% of prevalence relative to the total no. of isolates			Statistical significance of prevalence		
	Community acquired ABU (n=87)	Health care-associated ABU (n=25)	Commensal (n=39)	Community acquired ABU vs. Health care-associated ABU	Community acquired ABU vs. Commensal	Health care-associated ABU vs. Commensal
hlyA	25.29	32.00	2.56	-	** (*P*=0.002)	*** (*P*<0.0001)
*cnf*1	13.79	40.00	0.00	** (*P*=0.0081)	* (*P*=0.0174)	*** (*P*<0.0001)
cdtB	6.90	0.00	2.56	-	-	-
iutA	22.99	36.00	15.38	-	-	-
fyuA	45.98	68.00	15.38	-	** (*P*=0.0012)	*** (*P*<0.0001)
fimH	91.95	100.00	92.31	-	-	-
papAH	31.03	36.00	10.26	-	* (*P*=0.0136)	* (*P*=0.0234)
papEF	32.18	36.00	10.26	-	** (*P*=0.0084)	* (*P*=0.0234)
papC	31.03	36.00	10.26	-	* (*P*=0.0136)	* (*P*=0.0234)
papG allele I	5.75	12.00	0.00	-	-	-
papG alleles II, III	18.39	24.00	2.56	-	* (*P*=0.0213)	* (*P*=0.019)
sfa/focDE	20.69	40.00	2.56	-	** (*P*=0.0069)	*** (*P*=0.0002)
sfaS	12.64	8.00	2.56	-	-	-
focG	12.64	28.00	0.00	-	* (*P*=0.0174)	*** (*P*=0.0008)
kpsMT II	49.43	28.00	30.77	-	-	-
kpsMT III	2.30	0.00	2.56	-	-	-
PAI (*malX*)	29.89	12.00	20.51	-	-	-
cvaC	6.90	12.00	2.56	-	-	-
ibeA	10.34	0.00	7.69	-	-	-
bmaE	4.60	4.00	28.21	-	*** (*P*<0.0001)	* (*P*=0.0204)
rfc	3.45	4.00	23.08	-	** (*P*=0.0013)	-
traT	13.79	20.00	5.13	-	-	-
gafD	2.30	0.00	0.00	-	-	-
afa/draBC	5.75	0.00	0.00	-	-	-
iroN	26.44	72.00	43.59	*** (*P*<0.0001)	-	-
pks	14.94	44.00	10.26	** (*P*=0.0043)	-	** (*P*=0.0028)

Results of genotyping are given in percentages. Two-way comparisons were performed for each gene between the different groups examined using Fisher's exact test. For each comparison, a *P* value of <0.05 (*), a *P* value of <0.005 (**), and a *P* value of <0.001 (***) were considered statistically significant, while a *P* value of >0.05 (-) was not considered statistically significant.

Table S2: Primers used in this study for detection of the *fim* or *pap* determinant

Primer	Sequence (5'-> 3')	PCR product [bp]
papI-for	gtg aag cat gcc cac aaa ctg	232
papI-rev	ctg gaa ttt ctg aac agg cat aat g	
papB-for	ggc gca tca tga agt cat cag	309
papB-rev	gtc aaa tgc cga cga ctc atc	
papA-for	agc ttc ctt gag gca gga g	362
papA-rev	agt cag gtt gaa att cgc aac tg	
papH-for	gca tgt ccc ttc ctg aat act	331
papH-for	ctg cag att aat gcc ttt tgc ct	
papC-for	tta taa cgg gac tgt ggg gg	401
papC-rev	cga act gaa ctg tcc agg tc	
papD-for	atg gct gcc atc ccc ctg	414
papD-rev	ttg gtc tgg ttt taa ttg ctg cc	
papJ-for	tat ggt tgt gaa taa aac aac agc ag	403
papJ-rev	gat ggt cac agc cgg ata g	
papK-for	gat gat aaa aag cac agg cgc t	408
papK-rev	ctt ttc ccc ctg gcc ttt g	
papE-for	gtg aag cat gcc cac aaa ctg	232
papE-rev	ctg gaa ttt ctg aac agg cat aat g	
papF-for	cag att aac atc agg ggg aat g	396
papF-rev	cgc cat tca gta tcc cgc t	
papG-for	ccc caa ggg aca tta taa ttt tcc t	402
papG-rev	cca gcg taa tat ttc ctc act c	
papX-for	tga tgc aac tct gta tcc gtg t	329
papX-rev	gtt ctt tca gat atg tgt tct gcg	
fimB-for	aat acc ggg cct cat gct g	339
fimB-rev	gaa tct cca gtg aca acc cg	
fimE-for	atg cag gcg gtg tgt tac g	390
fimE-rev	gtt cat aac cac aag cat gcc t	
fimA-for	ggc tct ggc tga tac tac ac	437
fimA-rev	ccg gtt gca aaa taa cgc gc	
fimI-for	caa tgt ttg ctc tgg ccg g	386
fimI-rev	gcc gtt tcc agt ttg ctg g	
fimC-for	aat ggt ggt tgc cgg acg	445
fimC-rev	gag aat tcg cgc tac gac g	
fimD-for	gaa tct gct ggc gga tga tg	442
fimD-rev	cat cga aaa tat cgc cct gag	
fimF-for	gca cga tta cta tcc gcg g	397
fimF-rev	ctg tgt cgc cat tag ccg	
fimG-for	atg aaa tgg tgc aaa cgt ggg	434
fimG-rev	caa tgc tct gac ctg taa cgg	
fimH-for	ggg ctg gtc ggt aaa tgc	445
fimH-rev	cat cgc tgt tat agt tgt tgg tc	