

Table S1. Proportion of each predictor gene by *E. coli* pathotype.

<b>Proportion of isolates encoding gene</b>						
<b>Gene</b>	DEC	Animal commensal	Human commensal	APEC	NMEC	UPEC
	(n=29)	(n=32)	(n=67)	(n=30)	(n=30)	(n=293)
<i>vat</i>	0.00	0.09	0.33	0.50	0.57	0.58
<i>fyuA</i>	0.24	0.31	0.60	0.57	0.90	0.87
<i>chuA</i>	0.28	0.28	0.52	0.57	0.80	0.78
<i>yfcV</i>	0.00	0.19	0.48	0.23	0.83	0.69

Table S2. Proportion of each predictor gene in subdivisions of the pathotypes.

<b>Gene</b>	<b>DEC</b>			<b>APEC</b>			<b>UPEC</b>			
	<b>EPEC</b>	<b>ETEC</b>	<b>EHEC</b>	<b>APEC1</b>	<b>APEC2</b>	<b>APEC3</b>	<b>ABU</b>	<b>Cystitis</b>	<b>Comp. UTI</b>	<b>Pyelonephritis</b>
<i>vat</i>	0.00	0.00	0.00	0.30	0.60	0.60	0.6	0.55	0.49	0.68
<i>fyuA</i>	0.10	0.20	0.40	0.50	0.60	0.60	0.85	0.84	0.85	0.94
<i>chuA</i>	0.50	0.00	0.30	0.50	0.60	0.60	0.71	0.82	0.68	0.90
<i>yfcV</i>	0.00	0.00	0.00	0.10	0.30	0.30	0.66	0.71	0.62	0.77