



Pathogens	RESULTS:							RANGE:
			04	58	9 12	13 16	17 20	
Citrobacter freundii	6.0	HIGH	0 4	58	9 12	13 16	17 20	<dl< td=""></dl<>
Enterococcus faecalis	10.8	HIGH	0 4	58	9 12	13 16	17 20	<dl< td=""></dl<>
Klebsiella pneumoniae	16.4	HIGH	0 4	58	9 12	13 16	17 20	<dl< td=""></dl<>
Proteus mirabilis	18.9	HIGH	0 4	58	9 12	13 16	17 20	<dl< td=""></dl<>
Pseudomonas aeruginosa	0.7	HIGH	0 4	58	9 12	13 16	17 20	<dl< td=""></dl<>
Serratia marcescens	4.0	HIGH	0 4	5 8	9 12	13 16	17 20	<dl< td=""></dl<>
Uropathogenic E. coli (UPEC)	1.3	HIGH		5 0	912	10 10	17 20	<dl< td=""></dl<>

The Urinary EcologiX[™] profile utilises the highly sensitive quantitative PCR (qPCR) TaqMan technology for analysis of the Urinary Tract microbiota Microbial genes of interest are quantified within a sample and their abundances are normalised to an endogenous and highly conserved gene The qPCR results are therefore reported as the relative abundance of a microorganism as proportional to the whole microbial community

