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Mark A. Schembri, Matthew A. Mulvey, Scott Corresponding author(s): A. Beatson

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Reporting Summary

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Statistics

all st	atistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
Сог	nfirmed
	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
	A description of all covariates tested
	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.
	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
	Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

Software and code

Policy information about availability of computer code							
Data collection	Provide a description of all commercial, open source and custom code used to collect the data in this study, specifying the version used OR state that no software was used.						
Data analysis	Provide a description of all commercial, open source and custom code used to analyse the data in this study, specifying the version used OR state that no software was used.						

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a <u>data availability statement</u>. This statement should provide the following information, where applicable: - Accession codes, unique identifiers, or web links for publicly available datasets

- A list of figures that have associated raw data
- A description of any restrictions on data availability

Genome data has been deposited to NCBI under the Bioprojects PRJNA516746 [https://www.ncbi.nlm.nih.gov//bioproject/516746], PRJNA516747 [https:// www.ncbi.nlm.nih.gov//bioproject/516747], PRJNA516748 [https://www.ncbi.nlm.nih.gov//bioproject/516748], PRJNA516749 [https://www.ncbi.nlm.nih.gov// bioproject/516749] and PRJNA520966 [https://www.ncbi.nlm.nih.gov//bioproject/520966]. Raw PacBio sequence read data for isolates U12A, U13A, U14A and U15A has been deposited to the Sequence Read Archive (SRA) under the accessions SRR8504955 [https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956], SRR8504956 [[https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956], SRR8504956 [[https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956], SRR8504974 [[https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956]], SRR8504956] [https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956]], SRR8504956] [https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956]], SRR8504956] [https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956]], SRR8504956] [https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8504956]], SRR8504956]], SRR850495

Field-specific reporting

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Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample sizes were determined based on availability on isolates for sequence analysis			
Data exclusions	No data were excluded from the analysis			
Replication	This study involved the collection and genome sequencing of E. coli isolates from urine and fecal samples from a single patient over a 5-year period. It is not possible to repeat these experiments using a controlled protocol.			
Randomization	Randomization was not relevant to this study.			
Blinding	Blinding was not relevant to this study.			

Reporting for specific materials, systems and methods

Methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

the study

Materials & experimental systems

n/a	Involved in the study	n/a	Involved in the study
\boxtimes	Antibodies	\boxtimes	ChIP-seq
\boxtimes	Eukaryotic cell lines	\boxtimes	Flow cytometry
\boxtimes	Palaeontology	\boxtimes	MRI-based neuroimaging
\boxtimes	Animals and other organisms		
	Human research participants		
\boxtimes	Clinical data		

Human research participants

Policy information about studies involving human research participants

Population characteristics	The patient examined is a Caucasian female who first presented to the Urology Clinic at the University of Utah Hospital in 2011 at 74 years old. She has a pertinent past medical history of lifelong irritable bowel symptoms and colonic diverticulosis, and has been taking amitriptyline for nausea since the early 1980s. The patient also uses the ACE inhibitor Lisinopril (20 mg daily), the beta blocker Atenolol (50 mg daily), and the diuretic Hydrochlorothiazide (25 mg daily) to control high blood pressure and the non-steroidal anti-inflammatory drug Meloxicam (15 mg as needed) for back pain. She regularly takes vitamin pills, including iron supplements. The patient experiences frequent UTIs, which began soon after a vaginal hysterectomy in 1971. Her UTIs are accompanied by symptoms of dysuria and urinary frequency/urgency, fatigue, and bladder pain, all of which usually resolve with administration of culture-specific antibiotic treatments. In 2010, outside hospital providers became concerned about a possible colovesical fistula based on the patient's history of recurrent UTIs and the close proximity of her colon to the bladder, as revealed by CT scan imaging. The patient subsequently underwent resection of 12 inches of colon, and a flap of omentum was placed between the colon and bladder wall. This intervention did not reduce her UTI frequency. Over the years, the patient has suffered frequent UTIs and has been seen by multiple healthcare providers who have prescribed a variety of antibiotics.
Recruitment	The study involved the characterization of E. coli isolates recovered from the urine and feces of a single individual over a 5-year period
Ethics oversight	The research described in this study was undertaken with approval from the University of Utah Institutional Review Board (IRB_00070563). The patient provided both written and oral consent to participate in the study and to have her details published.

Note that full information on the approval of the study protocol must also be provided in the manuscript.