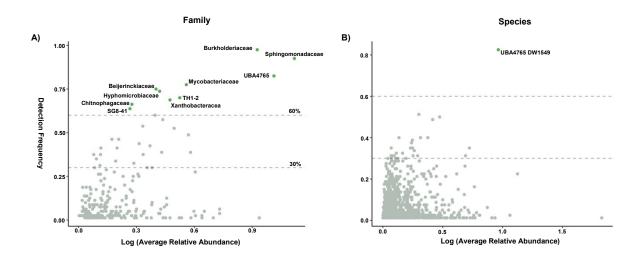
1 2	SUPPORTING INFORMATION				
2 3	New drinking water genome catalog identifies a globally distributed bacterial genus				
4	adapted to disinfected drinking water systems				
5	Ashwin S Sudarshan ¹ , Zihan Dai ¹ , Marco Gabrielli ² , Solize Oosthuizen-Vosloo ³ , Konstantinos				
6	T. Konstantinidis ¹ , Ameet J Pinto ^{1,4*}				
7					
8	¹ School of Civil and Environmental Engineering, Georgia Institute of Technology, Atlanta,				
9	USA				
10	² Department of Environmental Microbiology, Eawag, Swiss Federal Institute of Aquatic				
11	Science and Technology, Dubendorf, Switzerland,				
12	³ Institute for Cellular and Molecular Medicine, Department of Immunology, Faculty of Health				
13	Sciences, University of Pretoria, Pretoria, South Africa				
14	⁴ School of Earth and Atmospheric Sciences, Georgia Institute of Technology, Atlanta, USA				
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16	*Corresponding authors: ameet.pinto@ce.gatech.edu				
17					
18	Supporting information: Four pages, eight tables, and two figures.				
19					
20 21 22 23 24 25 26 27 28 29					

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33	Supplementary Table S1: (A) Details of metagenomes used to construct the DWGC. (B)
34 35	Accession numbers for isolate genomes obtained from NCBI and their isolation sources (see Excel spreadsheet).
36 37	Supplementary Table S2: SILVA v138.1 Phreatobacter sequences used for comparative
38 39	analysis (see Excel spreadsheet).
40 41 42	Supplementary Table S3: Summary of metagenome assembly and bins across different distribution systems (see Excel spreadsheet).
43 44	Supplementary Table S4 : Detailed taxonomy and genomic information for 1141 MAGs within the DWGC. Taxonomy was estimated using GTRDB (release 207 v2),
45 46	completeness/redundancy were estimated using CheckM2, while presence/absence of tRNAs/rRNA genes was determined using Prokka v1.14.6 (see Excel spreadsheet).
47	
48 49 50	Supplementary Table S5 : Relative Abundance of Species across the 80 distribution systems used to determine the core microbiome (see Excel spreadsheet).
51	Supplementary Table S6: Detection frequency and average relative abundance of genera in the
52 53	DWGC (see Excel spreadsheet).
54 55	Supplementary Table S7 : Metabolism annotation results for Lineage 1 (L1) and Lineage 2 (L2) MAGs (see Excel spreadsheet).
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Proposed Taxon	Etymology	Description	Parent Taxon	Туре	Registry URL
Genus Raskinella	[Ras.ki.ne'lla] N.L. fem. n. Raskin, Derived from Dr. Lutgarde Raskin; N.L. fem. dim. n. Raskinella, Named after Dr. Lutgarde Raskin	Raskinella is a novel genus under the family Phreatobacterac eae and order Rhizobiales. Organisms within this genus were identified in disinfected drinking water distribution systems.	Phreatobactera ceae	Raskinella chloraquaticus ^{Ts}	seqco.de/i:46 679
Species Raskinella chloraquatic us ^{Ts}	[chlor.a.qua'ti. cus] N.L. neut. n. chlorum, chlorine; L. masc. adj. aquaticus, of or from water; N.L. masc. n. chloraquaticus , relating to chlorinated water	Raskinella Chlorumaquati cus is a globally prevalent and abundant species that has been identified within disinfected drinking water systems. It is part of a unclassified genus "Raskinella" under the family Phreatobacterac eae.	Raskinella	NCBI Assembly: GCA_00236517 5.1 ^{Ts}	seqco.de/i:46 680

Supplementary Table S8: Complete list of names proposed in the current register SeqCode list.

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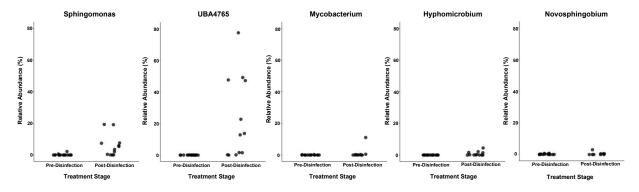
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89 Supplementary Figure S1: A) Detection Frequency Vs Log of Average Relative abundance of

90 the DWGC genomes at Family level. B) Detection Frequency Vs Log of Average Relative

abundance of the DWGC genomes at Species level.





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Supplementary Figure 2: Relative abundance of MAGs from five genera observed in more than

60% of the systems Pre- and Post-disinfection in studies where Pre-disinfection metagenomeswere available.

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