**Supplementary Information for**

**Occurrence and fate of ultramicrobacteria in a full-scale drinking water treatment plant**

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**Figure S4** Changes in total relative abundance of LB and UMB indicator taxa OTUs in different treatment units of the DWTP.

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**Figure S5** Procrustes analysis of functional and metabolic capabilities between UMB and LB microbial communities.

**Table S1** KEGG orthologue (KO) reference profiles used to calculate the predicted relative abundance of genes within functional or metabolic type. All data were extracted from the KEGG database www.genome.jp/kegg/.

| **Type** | **Subtype** | **KO** | **Functional or metabolic capabilities** |
| --- | --- | --- | --- |
| Energy/C/N associated metabolism | Amino acid metabolism | K00491 | nitric-oxide synthase, bacterial [EC:1.14.13.39] |
| Carbohydrate metabolism | K00929 | butyrate kinase [EC:2.7.2.7] |
| K01200 | pullulanase [EC:3.2.1.41] |
| Energy metabolism | K00260 | glutamate dehydrogenase [EC:1.4.1.2] |
| K02826 | cytochrome aa3-600 menaquinol oxidase subunit II [EC:1.10.3.12] |
| K02827 | cytochrome aa3-600 menaquinol oxidase subunit I [EC:1.10.3.12] |
| K02828 | cytochrome aa3-600 menaquinol oxidase subunit III [EC:1.10.3.12] |
| K02829 | cytochrome aa3-600 menaquinol oxidase subunit IV [EC:1.10.3.12] |
| Glycan biosynthesis and metabolism | K01227 | mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [EC:3.2.1.96] |
| Nucleotide and amino acid metabolism | K05822 | tetrahydrodipicolinate N-acetyltransferase [EC:2.3.1.89] |
| K05823 | N-acetyldiaminopimelate deacetylase [EC:3.5.1.47] |
| K06209 | chorismate mutase [EC:5.4.99.5] |
| K13853 | 3-deoxy-7-phosphoheptulonate synthase / chorismate mutase [EC:2.5.1.54 5.4.99.5] |
| Nucleotide metabolism | K03816 | xanthine phosphoribosyltransferase [EC:2.4.2.22] |
| K07816 | putative GTP pyrophosphokinase [EC:2.7.6.5] |
| K15518 | deoxyguanosine kinase [EC:2.7.1.113] |
| K15519 | deoxyadenosine/deoxycytidine kinase [EC:2.7.1.76 2.7.1.74] |
| Environmental Information Processing | Competence related DNA transformation transporter | K02236 | leader peptidase (prepilin peptidase) / N-methyltransferase [EC:3.4.23.43 2.1.1.-] |
| K02240 | competence protein ComFA |
| K02243 | competence protein ComGA |
| K02244 | competence protein ComGB |
| K02245 | competence protein ComGC |
| K02246 | competence protein ComGD |
| K02248 | competence protein ComGF |
| K02250 | competence protein ComK |
| Drug resistance | K02547 | methicillin resistance protein |
| K03740 | D-alanine transfer protein |
| K12553 | penicillin-binding protein 3 [EC:3.4.-.-] |
| Two component regulatory system | K02490 | two-component system, response regulator, stage 0 sporulation protein F |
| K07704 | two-component system, LytT family, sensor histidine kinase LytS [EC:2.7.13.3] |
| K07775 | two-component system, OmpR family, response regulator ResD |
| K11617 | two-component system, NarL family, sensor histidine kinase LiaS [EC:2.7.13.3] |
| K11629 | two-component system, OmpR family, bacitracin resistance sensor histidine kinase BceS [EC:2.7.13.3] |
| K11630 | two-component system, OmpR family, bacitracin resistance response regulator BceR |
| K14988 | two-component system, NarL family, secretion system sensor histidine kinase SalK |
| K14989 | two-component system, NarL family, secretion system response regulator SalR |
| ABC 2 type and other transporters | K09692 | teichoic acid transport system permease protein |
| K09693 | teichoic acid transport system ATP-binding protein [EC:3.6.3.40] |
| K11631 | bacitracin transport system ATP-binding protein |
| K11632 | bacitracin transport system permease protein |
| Drug efflux transporter pump | K08153 | MFS transporter, DHA1 family, multidrug resistance protein |
| Phosphate and amino acid transporters | K10039 | putative glutamine transport system substrate-binding protein |
| K10040 | putative glutamine transport system permease protein |
| K10041 | putative glutamine transport system ATP-binding protein [EC:3.6.3.-] |
| Environmental stress resistance | Environmental stress resistance | K04565 | Cu/Zn superoxide dismutase [EC:1.15.1.1] |
| K07233 | copper resistance protein B |
| K07570 | general stress protein 13 |
| K09825 | Fur family transcriptional regulator, peroxide stress response regulator |
| K13281 | UV DNA damage endonuclease [EC:3.-.-.-] |
| K13955 | zinc-binding alcohol dehydrogenase/oxidoreductase |
| DNA replication and repair | DNA replication and repair | K02086 | DNA replication protein |
| K03346 | replication initiation and membrane attachment protein |
| K03700 | recombination protein U |
| K03763 | DNA polymerase III subunit alpha, Gram-positive type [EC:2.7.7.7] |
| K11144 | primosomal protein DnaI |
| K13531 | methylated-DNA-[protein]-cysteine S-methyltransferase [EC:2.1.1.63] |
| K03630 | DNA repair protein RadC |
| K04483 | DNA repair protein RadA |
| K04484 | DNA repair protein RadB |