Supplementary Materials for

The Occurrence and Diversity of Antibiotic Resistance and Virulence Factor Genes in Wastewater from Four North American Treatment Plants

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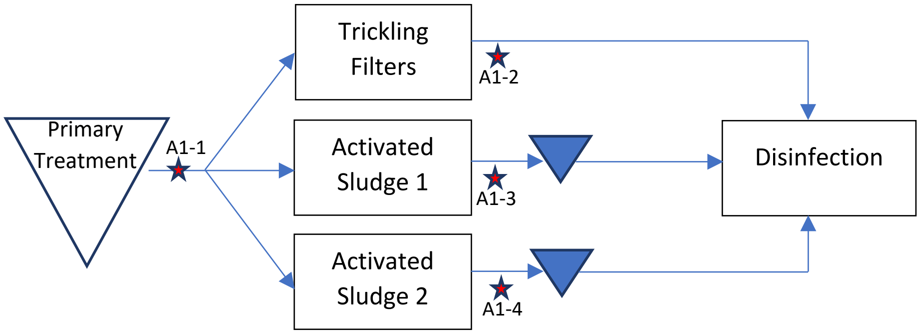
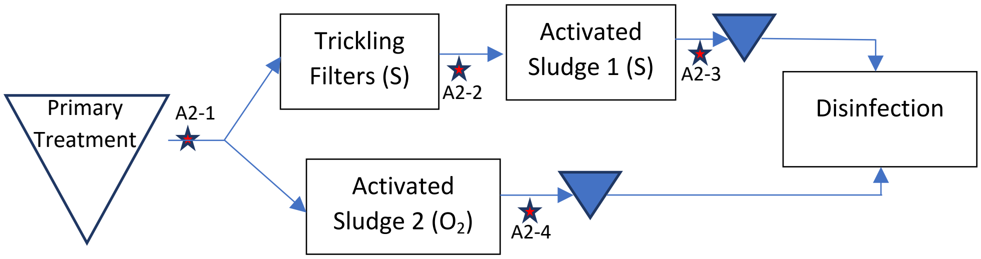
Plant A1



Plant A2



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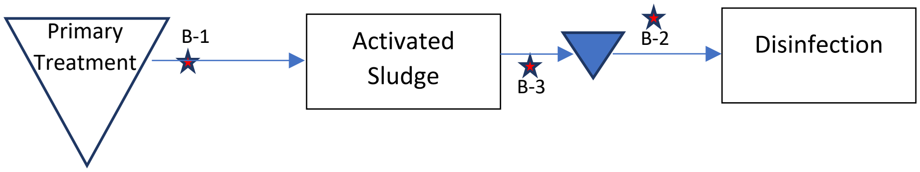

Plant C

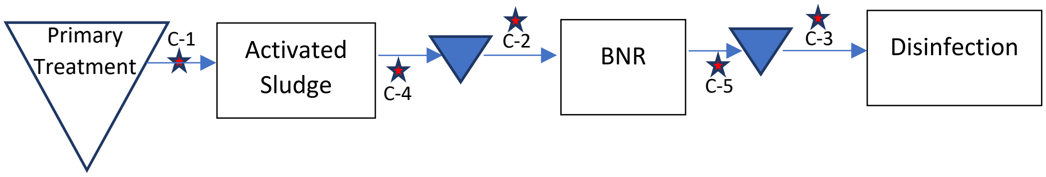

Fig. S1. Schematic illustration of sampling locations at four wastewater treatment plants.

Table S1. Descriptions of sewage samples used in this study

Sample Source & ID	Sample Type	Sampling Date
Plant A1, OC, CA		May 2018
A1-1	Primary effluent	
A1-2	Biofilm from trickling filters	
A1-3	MLSS from activated sludge train 1	
A1-4	MLSS from activated sludge train 2	
Plant A2, OC, CA		May 2018
A2-1	Primary effluent	
A2-2	Biofilm from trickling filters (Solids Contact)	
A2-3	MLSS from activated sludge train 1 (follows the trickling filters)	
A2-4	MLSS from O2 activated sludge train 2	
Plant B, LA, CA		May 2018
B-1	Primary effluent	
B-2	Activated sludge effluent (secondary effluent)	
B-3	MLSS from activated sludge	
Plant C, Washington DC		June 2018
C-1	Primary effluent	
C-2	Activated sludge effluent (secondary effluent)	
C-3	Effluent after biological nutrient removal (BNR)	
C-4	MLSS from before BNR	
C-5	MLSS after BNR	

OC: Orange County; LA: Los Angeles County

Table S2. Search criteria for antimicrobial classes and their corresponding KOs-based ARGs and ABSGs

Antimicrobial class/ Antibiotics	Encoded enzymes	Gene (KO)
Aminoglycosides	N-Acetyltransferases	*aac2-I* (K17840), *aac3-I* (K03395), *aac6-I/aacA7* (K18816), *aacC* (K00662)
	O-Nucleotidyltransferases	*aadD* (K17882), *aadK* (K05593)
	O-Phosphotransferases	*ant9* (K19279), *aph3-II* (K19300), *aph3-III* (K19299), *aphA* (K00897), *hph* (K18817)
	16S rRNA methyltransferases	*npmA* (K18846), *rmt/armA* (K18845)
β-Lactams	Class A β-lactamase	$bla_{CARB\text{-}1}$ (K18795), $bla_{CTX\text{-}M}$ (K18767), bla_{IMI} (K19316), bla_{KPC} (K18768), bla_{PER} (K18797), bla_{SHV} (K18699), bla_{TEM} (K18698), *penP* (K17836)
	Class B β-lactamase	bla_{IMP} (K18782), bla_{NDM} (K18780)
	Class C β-lactamase	*ampC* (K01467), bla_{PDC} (K20320)
	Class D β-lactamase	$bla_{OXA\text{-}1}$ (K18790), $bla_{OXA\text{-}2}$ (K18791), $bla_{OXA\text{-}10}$ (K18792), $bla_{OXA\text{-}23}$ (K18793), *oxa* (K17838)
	β-N-acetylhexosaminidase	*nagZ* (K01207)
	imipenem/basic amino acid-specific outer membrane pore	*oprD* (K18093)
	major outer membrane protein	*porB* (K18133)
	methicillin resistance regulatory proteins	*mecI/blaI* (K02546), *mecR1* (K02547)
	oligopeptide transport system	*oppA/mppA* (K15580), *oppB* (K15581), *oppC* (K15582), *oppD* (K15583), *oppF* (K10823)
	outer membrane pore proteins	*ompC* (K09475), *ompF* (K09476)
	penicillin-binding proteins	*ftsI* (K03587), *mecA1_2* (K16511), *mrcA* (K05366), *pbp2A* (K12555), *pbp2B/penA* (K00687), *pbp2X* (K12556)
CAMP (Cationic Antimicrobial Peptide)	4-amino-4-deoxy-L-arabinose transferase	*arnT/pmrK* (K07264)
	Kdo2-lipid ethanolaminephosphotransferase	*eptB* (K12975)
	lipid A ethanolaminephosphotransferase	*eptA/ pmrC* (K03760)
	lipid IVA palmitoyltransferase	*pagP/ crcA* (K12973)
	OmpR family, response regulator BasR	*basR* (K07771)
	OmpR family, sensor histidine kinase BasS	*basS* (K07643)
	OmpR family, response regulator protein GraR	*graR* (K19078)
	OmpR family, sensor histidine kinase GraS	*graS* (K19077)
	OmpR family, sensor histidine kinase PhoQ	*phoQ* (K07637)
	OmpR family, response regulator PhoP	*phoP* (K07660)
	phosphatidylglycerol lysyltransferase	*mprF/fmtC* (K14205)
	UDP-4-amino-4-deoxy-L-arabinose formyltransferase	*arnA/pmrI* (K10011)

	UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase	*arnB/pmrH* (K07806)
	UDP-N-acetylglucosamine acyltransferase	*lpxA* (K00677)
	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	*arnC/pmrF* (K10012)
FCA (fluoroquinolone, quinolone, florfenicol, chloramphenicol, and amphenicol)	chloramphenicol O-acetyltransferase	*catA* (K19271), *catB* (K00638), *cpt* (K18554)
	fluoroquinolone resistance protein	*qnr/mcbG* (K18555)
Fosfomycin	metallothiol transferase	*fosB* (K11210)
MLSB (macrolides, lincosamide, and streptogramin B)	23S rRNA methyltransferases	*ermC/ermA* (K00561), *rlmA2* (K14336)
	lincosamide nucleotidyltransferase	*lnuA_C_D_E/lin* (K19545)
	macrolide-specific efflux	*macA* (K13888), *macB* (K05685)
	chloramphenicol efflux transport protein	*mdfA/cmr* (K08160)
	virginiamycin A acetyltransferase	*vat* (K18234)
	virginiamycin B lyase	*vgb* (K18235)
Multidrug	AraC family transcriptional regulator	*marA* (K13632)
	efflux pump AbcA	*abcA/bmrA* (K18104), *norG* (K18907)
	efflux pump AcrEF-TolC	*acrE* (K18141), *acrF* (K18142), *tolC* (K12340)
	efflux pump MdtEF-TolC	*evgA/bvgA* (K07690), *mdtE* (K18898), *mdtF* (K18899)
	efflux pump MepA	*mepA* (K18908)
	efflux pump MexAB-OprM	*acrA/ mexA/adeI/smeD/mtrC/cmeA* (K03585), *acrB/mexB/adeJ/smeE/mtrD/cmeB* (K18138), *mexR* (K18131), *oprM/emhC/ttgC/cusC/adeK/smeF/mtrE/cmeC/gesC* (K18139)
	efflux pump MexCD-OprJ	*oprJ* (K08721)
	efflux pump MexPQ-OpmE	*lasR* (K18304)
	efflux pump NorB	*norB/norC* (K08170)
	efflux pump Tet38	*mgrA* (K18906)
	Electrochemical potential-driven transporters	*emrE/qac/mmr/smr* (K03297), *ykkD* (K18925)
	OmpR family, sensor histidine kinase CpxA	*cpxA* (K07640)
	OmpR family, response regulator CpxR	*cpxR* (K07662)
	MarR family transcriptional regulator	*marR* (K03712)
	MFS transporter, DHA1 family	*mdtH* (K08162), *mdtL* (K08163)
	MFS transporter, DHA2 family	*emrB* (K03446), *emrY* (K07786), *mdtD* (K18326), *smvA/qacA/lfrA* (K08167)
	Multidrug and Toxin Extrusion (MATE) family	*TC.MATE/SLC47A/norm/mdtK/dinF* (K03327)
	multidrug resistance protein K	*emrK* (K07797), *mdtO* (K15547)

	and MdtO	
	TetR/AcrR family transcriptional regulator	*acrR* (K18136), *qacR* (K18938)
Tetracycline	ribosomal protection tetracycline resistance protein	*tetM/tetO* (K18220)
Trimethoprim	dihydrofolate reductase (trimethoprim resistance protein)	*dfrA1/dhfr* (K18589), *dfrD/ dhfr* (K18591)
Glycopeptides (Vancomycin)	D-alanine---(R)-lactate ligase	*vanB/ vanA/ vanD* (K15739)
	D-alanine---D-serine ligase	*vanC/ vanE/ vanG* (K18856)
	NarL family	*vraS* (K07681), *vraR* (K07694),
	vancomycin resistance protein	*vanW* (K18346)
	zinc D-Ala-D-Ala carboxypeptidase	*vanY* (K07260)
	zinc D-Ala-D-Ala dipeptidase	*vanX* (K08641)
Novobiocin (**Aminocoumarins**)	novobiocin biosynthesis protein	*novH* (K12701), *novK* (K12704)
	8-demethylnovobiocic acid synthase	*novL/ cloL/ couL* (K12709)
	L-demethylnoviosyl transferase	*novM/ cloM/ couM* (K12711)
	decarbamoylnovobiocin carbamoyltransferas	*novN* (K12713)
	8-demethylnovobiocic acid C8-methyltransferase	*novO/ couO* (K12705)
	demethyldecarbamoylnovobiocin O-methyltransferase	*novP/ cloP/ couP* (K12712)
	4-hydroxyphenylpyruvate 3-dimethylallyltransferase	*novQ/ cloQ* (K12707)
	4-hydroxy-3-prenylbenzoate synthase	*novR/ cloR* (K12708)
Neomycin, kanamycin and gentamicin (**Aminoglycosides**)	2'-deamino-2'-hydroxyneamine 1-alpha-D-kanosaminyltransferase	*kanE/ kanM2* (K20573)
	2-deoxy-scyllo-inosose synthase	*btrC/ neoC/ kanC* (K13546)
	2-deoxystreptamine glucosyltransferase	*btrM/ neoD/ kanF* (K13550)
	2'-N-acetylparomamine deacetylase	*btrD* (K13551), *neoL* (K17078)
	5''-phosphoribostamycin phosphatase	*btrP* (K13555)
	6'''-hydroxyparomomycin oxidase	*livQ/ parQ* (K20584)
	butirosin acyl-carrier proteins	*btrJ* (K13559), *btrK* (K13560), *btrO* (K13561)
	gamma-L-glutamyl-butirosin B gamma-L-glutamyl cyclotransferase	*btrG* (K13564)
	inosamine dehydrogenase	*btrN* (K13549), *neoA* (K13548)
	kanamycin B dioxygenase	*kanJ/ kacB* (K20574)
	kanamycin reductase	*kanK/ kacC* (K20152)
	L-glutamine:2-deoxy-scyllo-inosose	*btrR/ neoB/ kanB* (K13547)
	neamine transaminase	*kacL* (K20568)
	nebramycin 5' synthase	*tobZ* (K20579)
	neomycin C epimerase	*neoN/ neoH* (K13557)
	paromamine 6'-oxidase	*neoG/ neoQ* (K20565)

Streptomycin (**Aminoglycosides**)	dTDP-4-dehydrorhamnose 3,5-epimerase	*rfbC/ rmlC* (K01790)
	dTDP-4-dehydrorhamnose reductase	*rfbD/ rmlD* (K00067)
	dTDP-glucose 4,6-dehydratase	*rfbB/ rmlB/ rffG* (K01710)
	glucose-1-phosphate thymidylyltransferase	*rfbA/ rmlA/ rffH* (K00973)
	myo-inositol 2-dehydrogenase	*iolG* (K00010)
Penicillin and cephalosporin (**β-Lactams**)	cephalosporin-C deacetylase	*cah* (K01060)
	deacetoxycephalosporin-C hydroxylase	*cefF* (K12745)
	glutaryl-7-aminocephalosporanic-acid acylase	*gca* (K12748)
	isopenicillin-N epimerase	*cefD* (K04127)
Carbapenem (**Carbapenems**)	carbapenem-3-carboxylate synthase	*cpmA/carA* (K18316)
Tetracycline, oxytetracycline and chlortetracycline (**Tetracyclines**)	ketoreductase	*actIII/ oxyJ/ snoaD/ aknA* (K12420)
	polyketide synthase- acyl carrier protein	*actI3/ oxyC/ tcmM/ snoa3/ aknD/ mtmS* (K05553)
	polyketide synthase chain-length factor	*actI2/ oxyB/ tcmL/ snoa2/ aknC/ mtmK* (K05552)
	polyketide synthase-ketosynthase	*actI1/ oxyA/ tcmK/ snoa1/ aknB/ mtmP* (K05551)
Vancomycin (**Glycopeptides**)	3,5-dihydroxyphenylacetyl-CoA synthase	*dpgA* (K16424)
	4-hydroxymandelate oxidase	*hmo* (K16422)
	4-hydroxymandelate synthase	*hmaS* (K16421)
	chloroorienticin B synthase	*gtfA* (K16440)
	dTDP-2,6-dideoxy-D-kanosamine transaminase	*evaB/ megDII/ angB/ staI* (K16436)
	glycosyltransferase	*gtfC* (K16442)
	vancomycin aglycone glucosyltransferase	*gtfB/ gtfE* (K16444)
	vancomycin vancosaminetransferase	*gtfD* (K16443)

Table S3. Summary of alpha diversity metrics

Sample label	Type	Location	Chao1	Shannon
A1-1	PE	A1	1464.987	7.491
A1-2	Biofilm	A1	1211.455	7.201
A1-3	MLSS	A1	642.904	4.569
A1-4	MLSS	A1	589.205	4.198
A2-1	PE	A2	1603.097	7.299
A2-2	Biofilm	A2	1404.754	7.217
A2-3	MLSS	A2	828.054	6.944
A2-4	MLSS	A2	1128.636	7.291
B-1	PE	B	1568.480	7.410
B-3	MLSS	B	516.771	4.991
C-1	PE	C	496.435	5.625
C-2	SE	C	776.188	6.697
C-3	SE	C	419.962	6.065
C-4	MLSS	C	876.000	6.645
C-5	MLSS	C	522.283	5.514

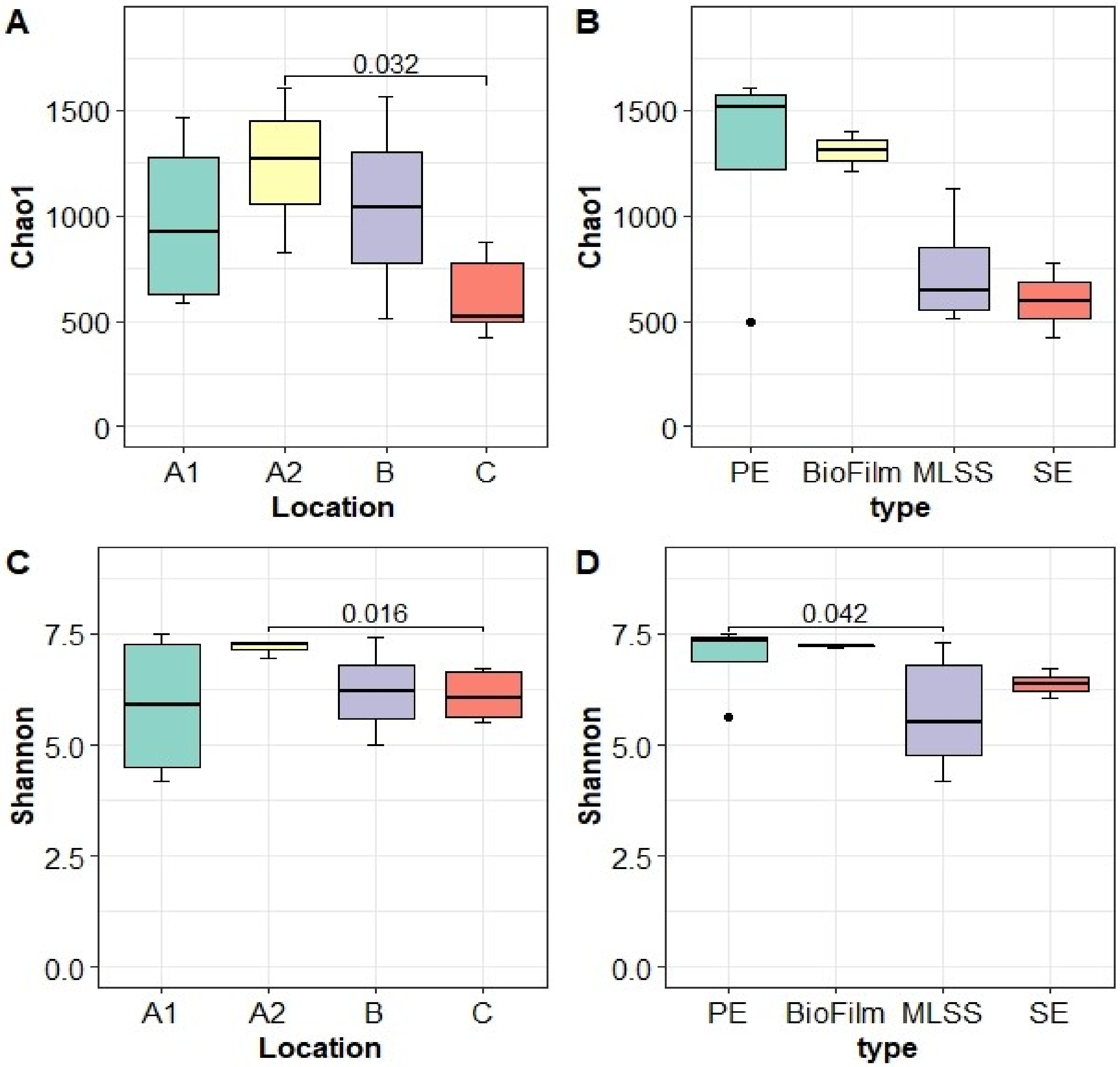

Fig. S2. Microbial richness (chao 1 index shows in **A** and **B**) and diversity (Shannon's index shows in **C** and **D**) of WTTP samples. Each boxplot shows the median (the middle bar) with the error bar indicating the mean ± SD, and the 25th and 75th percentiles (the upper and lower hinges of the box), the maximum and minimum points (end of whiskers), and outliers (dots). Shannon's indices of the Biofilm samples were tied, indicating less variation in the diversity of microbial community between these samples. Differences in the median values of chao1 and Shannon's indices between each sampling WWTP and treatment type were evaluated by Wilcoxon rank-sum test. Statistical significance was considered at a $p < 0.05$. Although the microbial richness according to the chao1 index did not differ significantly between the samples grouped by treatment type, the MLSS samples showed a significant reduction in the Shannon diversity compared to the primary effluents (p = 0.042). The primary effluent from Plant C (C-1) is presented as an outlier, suggesting the very different microbial community structure in the raw sewage from the east coast verse those from the west coast.

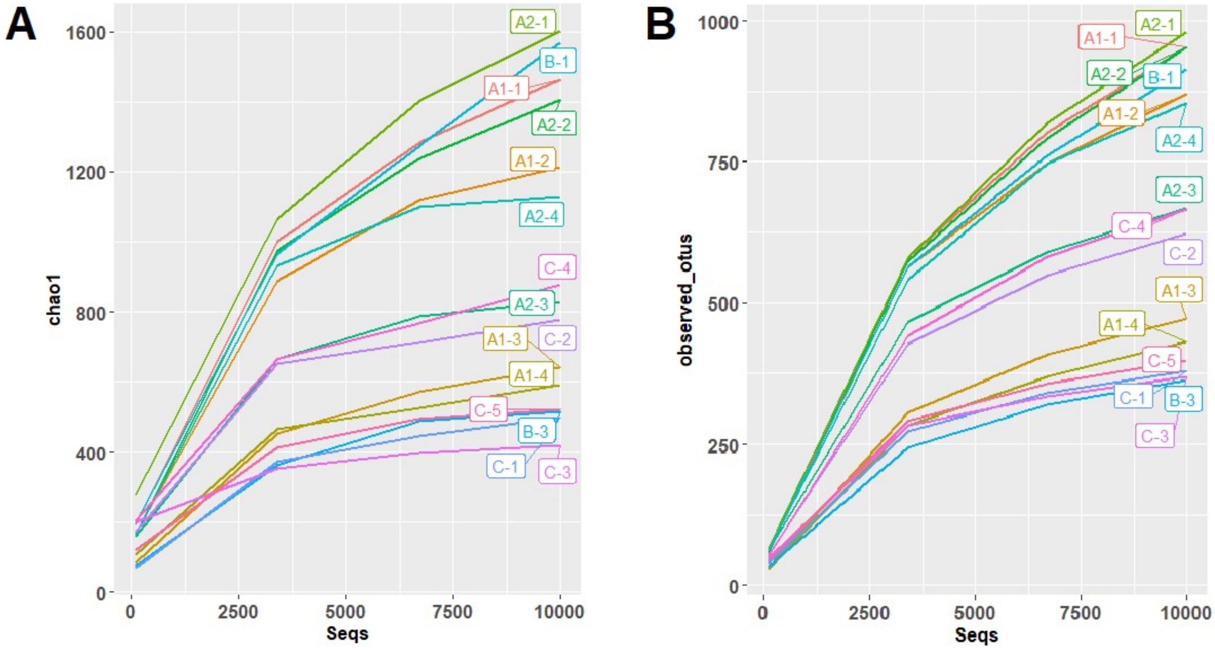

Fig. S3. Rarefaction curves showing the microbial richness and diversity of the fifteen sewage samples. Each color represents a sample. The x axis signifies the number of sequences per sample while the y axis represents a rarefaction measure of the species richness indicated by **(A)** chao1 index and **(B)** observed OTU counts. The sample labels are identical as Fig. 1 in the manuscript.

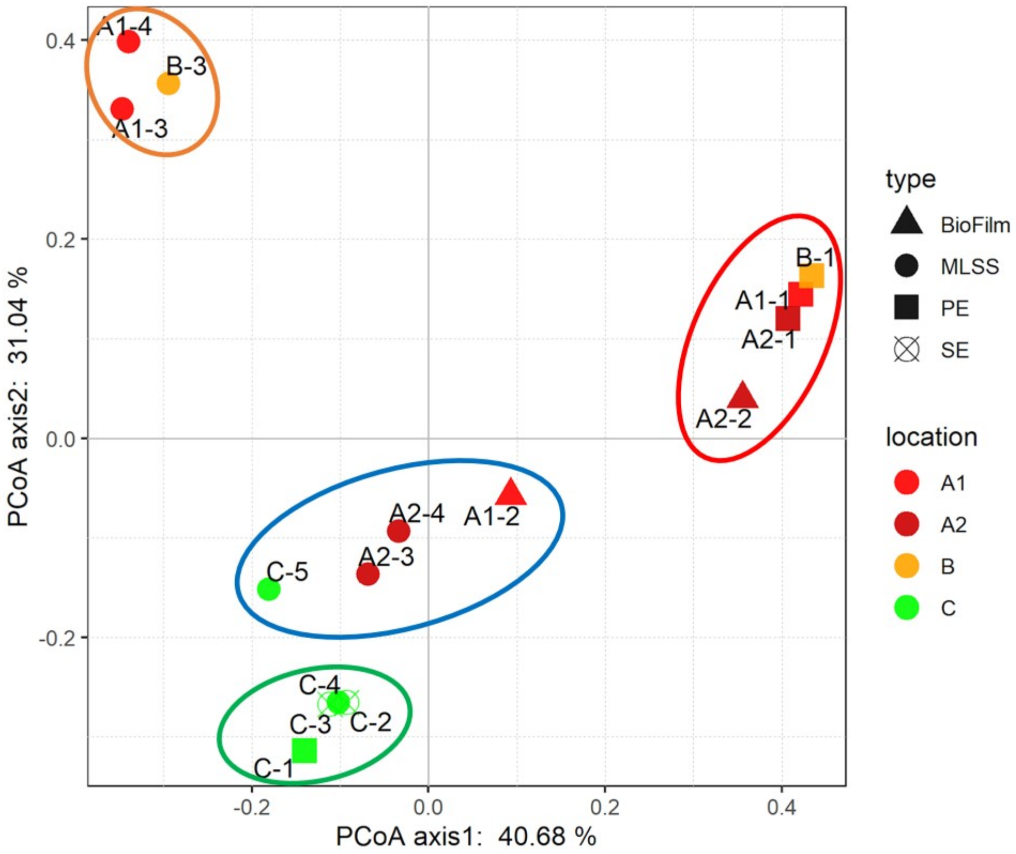

Fig. S4. Beta diversity represented by PCoA plot of the genus-level microbial communities of WWTP samples. Two primary axes represent 71.72 % of total variation (PC1=40.68%, PC2=31.04%). Each point on the graph represents the bacterial microbiome of each sample. The shape indicates the type of the treatment process, and color indicates the sample location. Sample labels are identical as Fig. 1 in the manuscript.

The primary effluents collected from all three Southern California plants (A1-1, A2-1 and B-1) and a biofilm sample (A2-2) collected from a short trickling filter (TF) from Plant A2 clustered into a group (red circle), signifying a similar structure of microbial community in those samples. This cluster characterizes the dominant microbial community in Southern California raw wastewater. The biofilm A2-2 was collected from a TF with half of the media depth of traditional TF that is used as a pretreatment step before the wastewater being further treated by ASP (Fig. S1). Therefore, the microbial community in the biofilm collected from this filter resembles primary effluent rather than the MLSS from ASP and biofilm from the convectional TF.

The second cluster (blue circle) included a mixture of the TF biofilm sample from Plant A1, ASP MLSS samples from A2 (A2-3 and A2-4), and from C-5. This cluster represents the microbial community that performs the major function of CBOD reduction and nitrification. It is interesting to observe that sample C-5, the MLSS collected after BNR at the Washington DC plant, is clustered with the MLSS and biofilm samples from Southern California. Yet, the microbial community of MLSS samples from plant A1 (A1-3 and A1-4) and sample B-3 formed a separate cluster (orange circle). The separation of MLSS samples in plant A1 from that of A2 suggests that treatment conditions shape the active microbial population since the primary effluent from A1 and A2 are very similar. It is also interesting to observe that the MLSS collected from the short ASP following the short TF (A2-3) grouped together with ASP train injected with pure oxygen (A2-4), suggesting pure oxygen did not have a dramatic impact on the active microbial composition.

In Plant C, the microbial communities in all samples, on the other hand, were closely related and self-contained (green circle), suggesting the importance of the source of raw wastewater on microbial community in WWTPs. As also illustrated in Fig. S4, although the primary effluents from Southern California plants (A1-1, A2-1, B-1) and Washington DC plant (C-1) were clustered apart from each other, the MLSS samples from these plants converge to be more similar (blue circle), showing that wastewater treatment processes converge the diverse microbial community into similar ones.

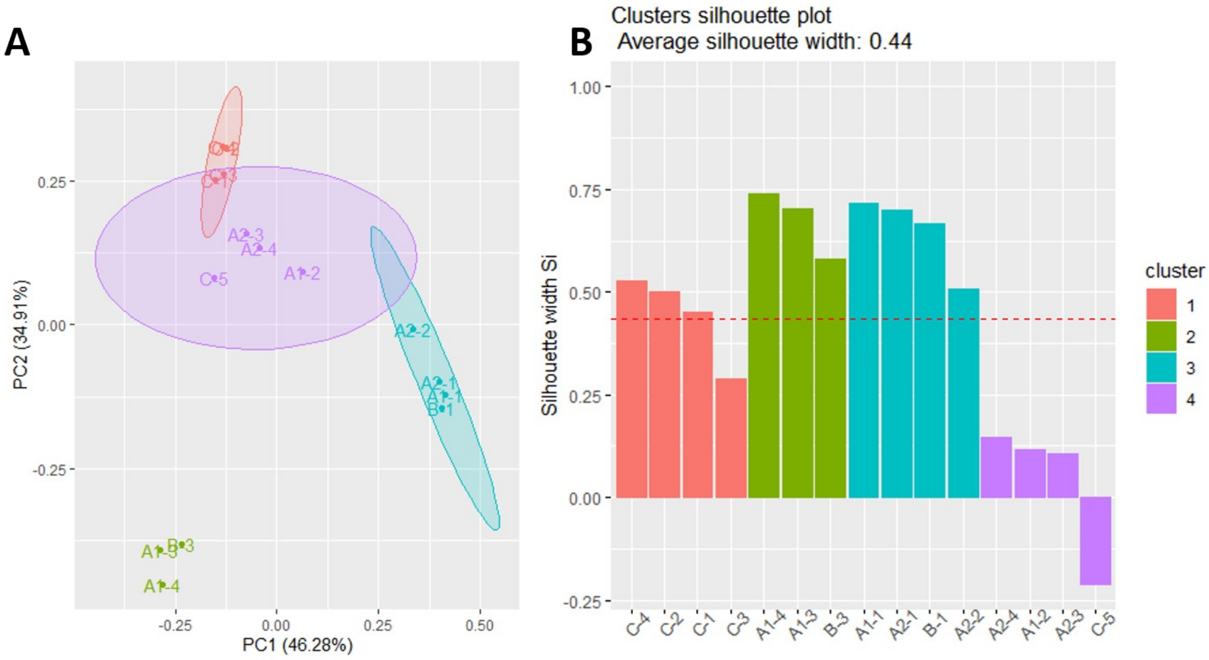

Fig. S5. Partitioning about medoids (PAM) analysis of genus-level microbial communities in WWTPs. **(A)** Bivariate plot (Clusplot) and **(B)** Silhouette plots showing PAM analysis results of k-means clustering of 4. Different colors indicate different clusters. Sample labels are identical as Fig. 1 in the manuscript.

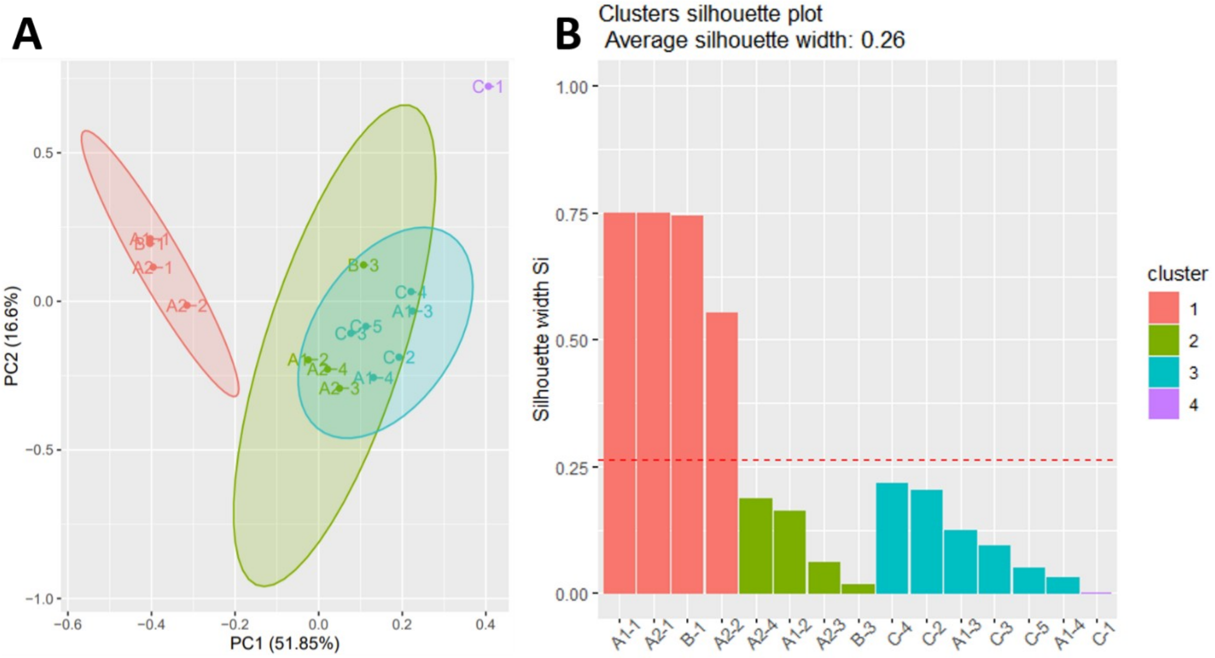

Fig. S6. Partitioning about medoids (PAM) analysis defined k =4 clusters of the ARGs profile in WWTPs. **(A)** Bivariate plot (Clusplot) and **(B)** Silhouette plots showing PAM analysis results of k-means clustering of 4. Different colors indicate different clusters. Sample labels are identical as Fig. 1 in the manuscript.

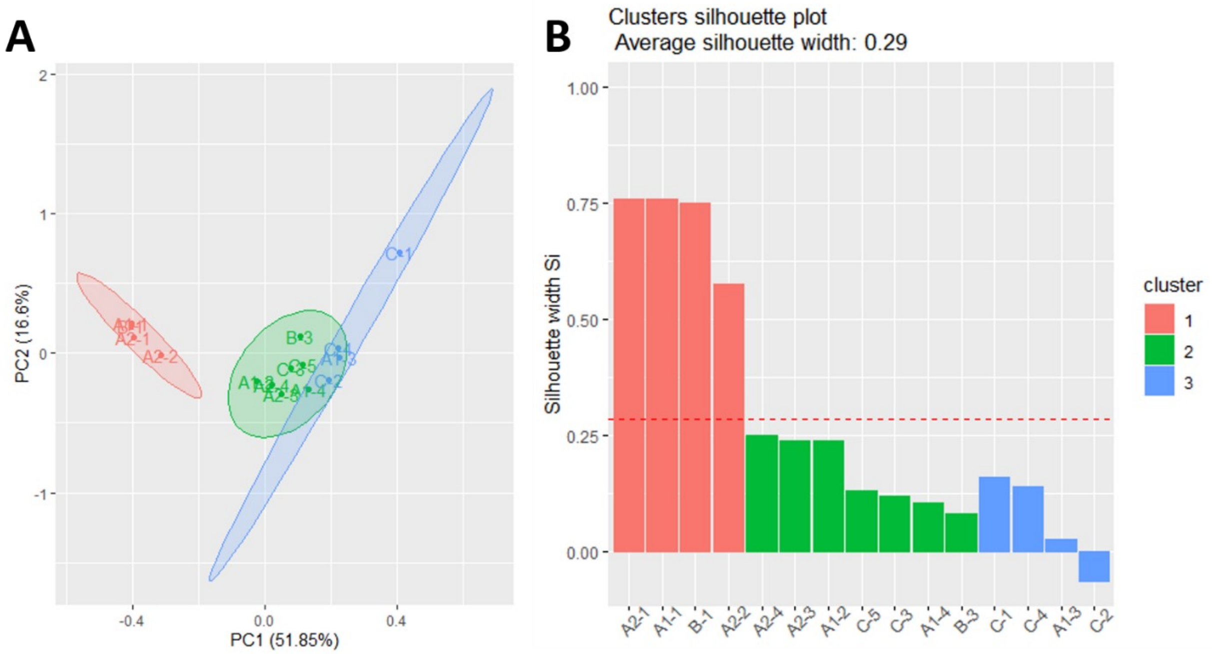

Fig. S7. Partitioning about medoids (PAM) analysis identified k = 3 clusters of the ARG profile in WWTPs. **(A)** Bivariate plot (Clusplot) and **(B)** Silhouette plots showing PAM analysis results of k-means clustering of 3. Different colors indicate different clusters. Sample labels are identical as Fig. 1 in the manuscript.

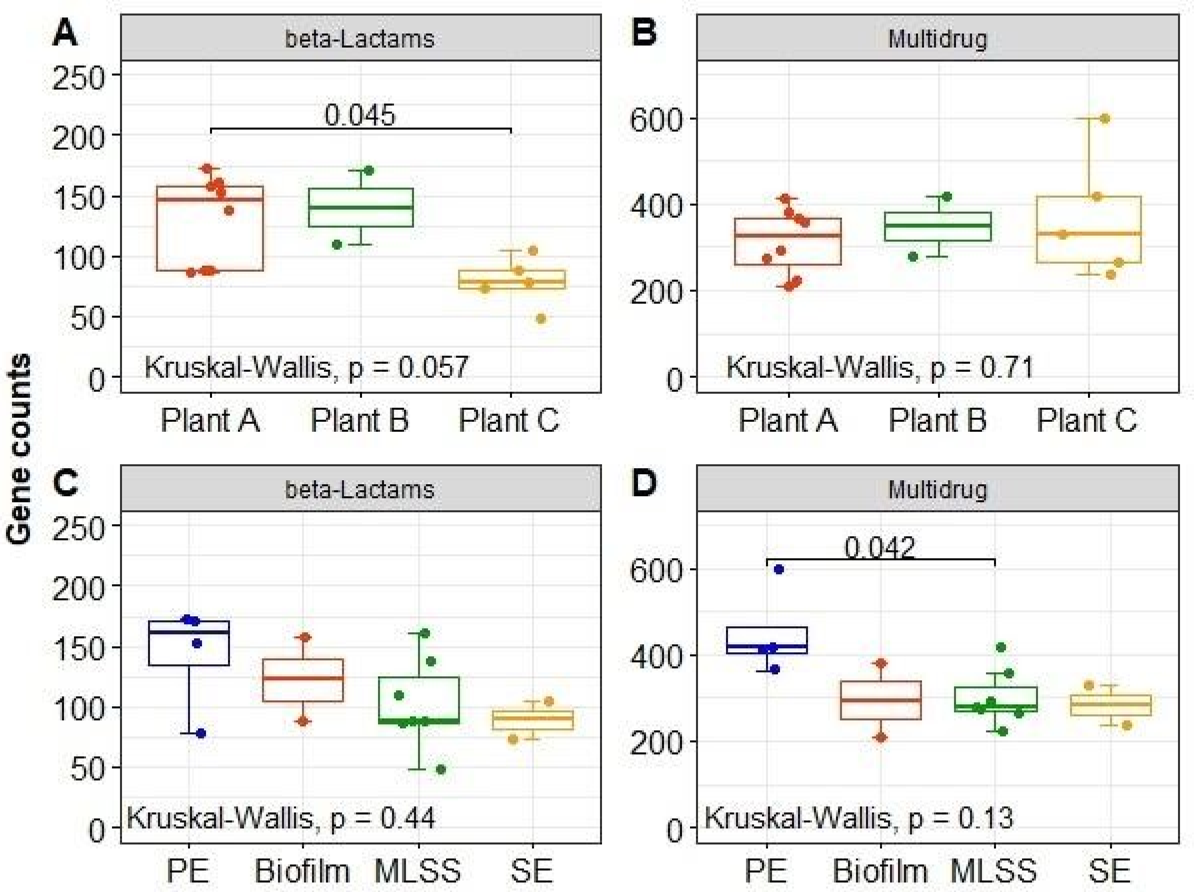

Fig. S8. The prevalence of beta-Lactams and multidrug ARGs detected in WWTP samples. Comparison of gene counts of beta-Lactam resistance genes **(A, C)** and multidrug resistance genes **(B, D)** among samples grouped by sampling location and treatment type. Statistical significance p-values evaluated by Kruskal-Wallis and post-hoc Wilcoxon rank-sum test are indicated in the boxplot ($p < 0.05$). Sample labels are identical as Fig. 3 in the manuscript.

Table S4. Median values for gene counts for each dominant ARG subtype.

Location/Type	beta-Lactam	Multidrug
Plant A	4,290	323
Plant B	5,019	348
Plant C	4,230	330
PE	5,389	416
Biofilm	4,090	295
MLSS	4,287	280
SE	4,014	284

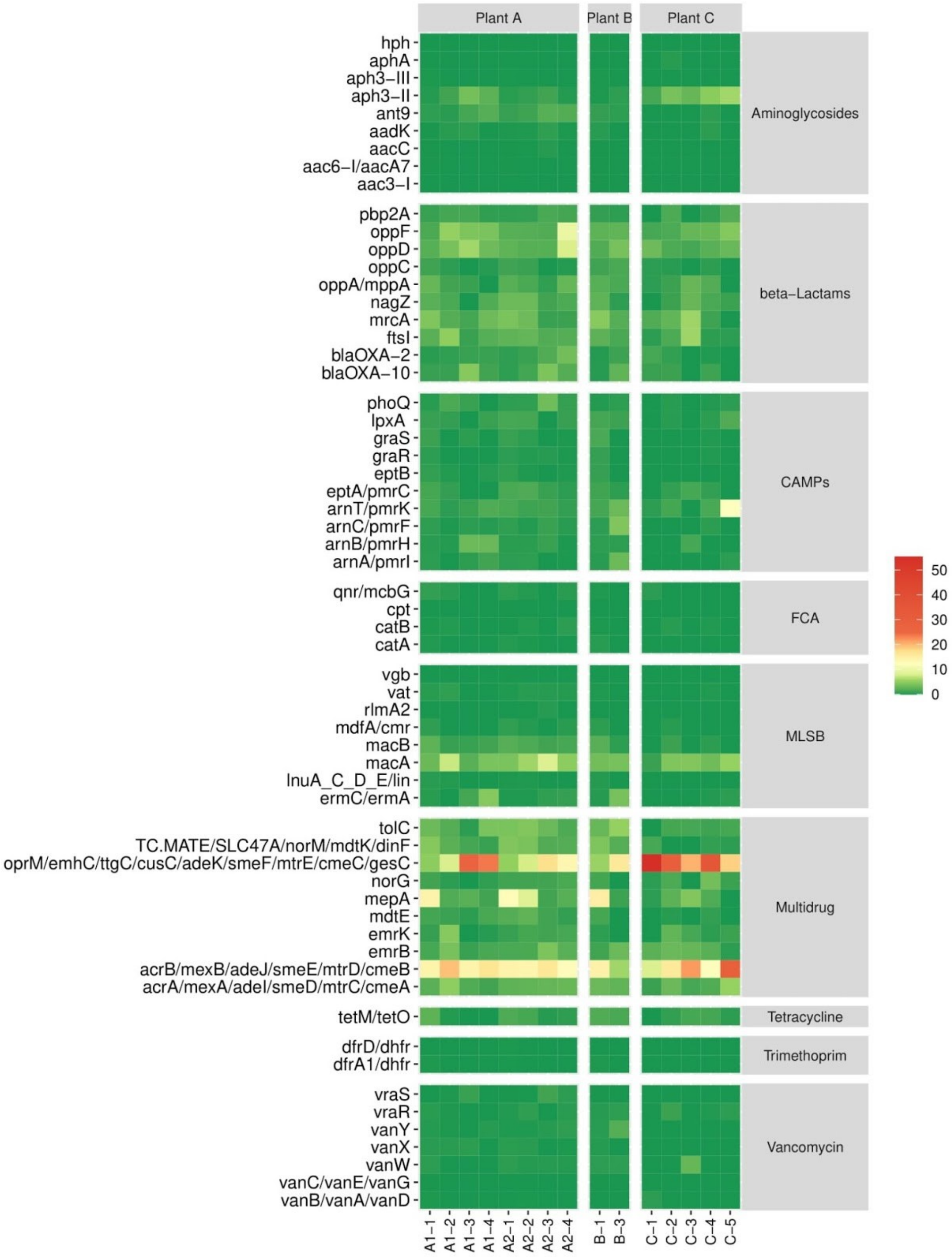

Fig. S9. Heatmap showing the relative abundances of all antimicrobial classes detected in WWTP samples. Colors reflect relative abundances (%) of top ten prevalent ARGs conferring for each antimicrobial class from lowest (green) to highest abundance (red).

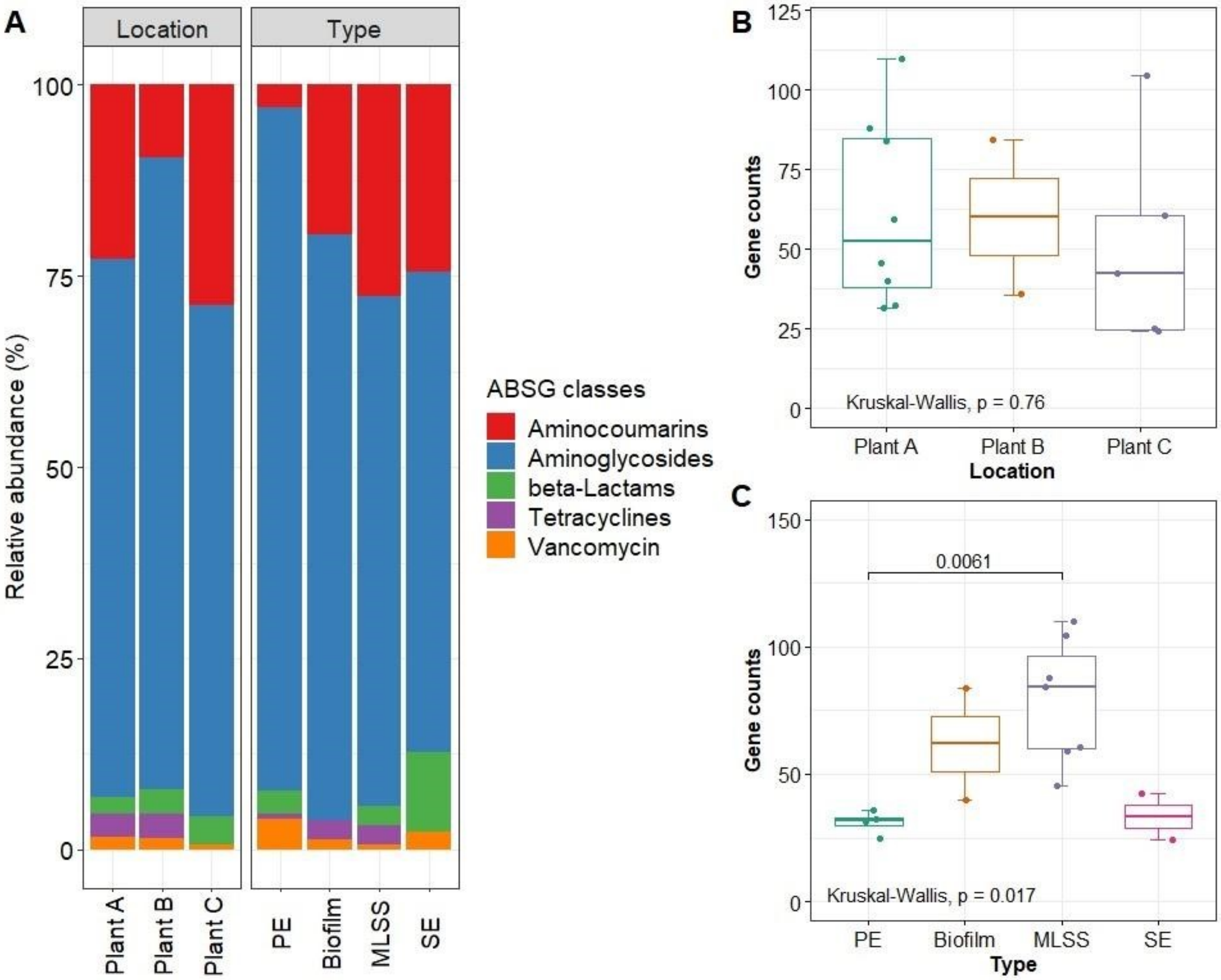

Fig. S10. The occurrence and abundance of all antibiotic biosynthetic gene (ABSG) types detected in WWTP samples. **(A)** Relative abundance is represented as the percentage of each antimicrobial class among total ABSGs in a sample. The identified ABSG types are aminocoumarin, aminoglycosides, beta-Lactams, tetracyclines, and vancomycin. Samples were grouped by sampling location and treatment type. **(B)** and **(C)** Changes in the normalized gene counts of total ABSGs between sampling site and treatment type evaluated by Kruskal-Wallis with post-hoc Wilcoxon rank sum test. Outliers are points beyond the maximum-minimum range (end of whiskers). Statistical significance was considered at $p < 0.05$. Sample labels are identical as Fig. 3 in the manuscript.

Table S5. Median values for total ARG, ABSG, VFG counts in each location and treatment group.

Location/Type	Median of total ARGs	Median of total ABSGs	Median of total VFGs
Plant A	565	52	4,290
Plant B	661	60	5,019
Plant C	477	42	4,230
PE	731	32	5,389
Biofilm	534	62	4,090
MLSS	510	84	4,287
SE	440	33	4,014

Table S6. Descriptions of the KOs-associated virulence factor genes (VFGs) detected in the samples.

#KO	Gene name	Descriptions
K11029	cyaA	anthrax edema toxin adenylate cyclase [EC:4.6.1.1]
K00681	ggt	gamma-glutamyltranspeptidase / glutathione hydrolase [EC:2.3.2.2 3.4.19.13]
K07282	capA, pgsA	gamma-polyglutamate biosynthesis protein CapA
K11031	slo	thiol-activated cytolysin
K15125	fhaB	filamentous hemagglutinin
K12681	prn	pertactin
K07345	fimA	major type 1 subunit fimbrin (pilin)
K07347	fimD, fimC, mrkC, htrE, cssD	outer membrane usher protein
K12081	ptlE	type IV secretion system protein PtlE
K12085	ptlF	type IV secretion system protein PtlF
K12082	ptlG	type IV secretion system protein PtlG
K12083	ptlH	type IV secretion system protein PtlH [EC:7.4.2.8]
K12683	brkA	serum resistance protein
K07058	K07058	membrane protein
K13019	wbpI, wlbD	UDP-GlcNAc3NAcA epimerase [EC:5.1.3.23]
K13017	wbpE, wlbC	UDP-2-acetamido-2-deoxy-ribo-hexuluronate aminotransferase [EC:2.6.1.98]
K13018	wbpD, wlbB	UDP-2-acetamido-3-amino-2,3-dideoxy-glucuronate N-acetyltransferase [EC:2.3.1.201]
K03219	yscC, sctC, ssaC	type III secretion protein C
K03229	yscU, sctU, hrcU, ssaU	type III secretion protein U
K03225	yscQ, sctQ, hrcQ, ssaQ, spaO	type III secretion protein Q
K03224	yscN, sctN, hrcN, ssaN	ATP synthase in type III secretion protein N [EC:7.4.2.8]
K03223	yscL, sctL	type III secretion protein L
K03222	yscJ, sctJ, hrcJ, ssaJ	type III secretion protein J
K03230	yscV, sctV, hrcV, ssaV, invA	type III secretion protein V
K12340	tolC, bepC, cyaE, raxC, sapF, rsaF, hasF	outer membrane protein
K07326	fhaC	hemolysin activation/secretion protein
K03199	virB4, lvhB4	type IV secretion system protein VirB4 [EC:7.4.2.8]
K03200	virB5, lvhB5	type IV secretion system protein VirB5
K03201	virB6, lvhB6	type IV secretion system protein VirB6
K00971	manC, cpsB	mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
K13010	per, rfbE	perosamine synthetase [EC:2.6.1.102]
K02650	pilA	type IV pilus assembly protein PilA
K02654	pilD, pppA	leader peptidase (prepilin peptidase) / N-methyltransferase [EC:3.4.23.43 2.1.1.-]
K02669	pilT	twitching motility protein PilT

K13287	sipD, ipaD, bipD	invasin D
K03746	hns	DNA-binding protein H-NS
K13285	sipB, ipaB, bipB	invasin B
K11903	hcp	type VI secretion system secreted protein Hcp
K11904	vgrG	type VI secretion system secreted protein VgrG
K02415	fliL	flagellar protein FliL
K02416	fliM	flagellar motor switch protein FliM
K02417	fliN	flagellar motor switch protein FliN
K02419	fliP	flagellar biosynthesis protein FliP
K02414	fliK	flagellar hook-length control protein FliK
K02413	fliJ	flagellar protein FliJ
K02412	fliI	flagellum-specific ATP synthase [EC:7.4.2.8]
K02411	fliH	flagellar assembly protein FliH
K02410	fliG	flagellar motor switch protein FliG
K02409	fliF	flagellar M-ring protein FliF
K02408	fliE	flagellar hook-basal body complex protein FliE
K02422	fliS	flagellar secretion chaperone FliS
K02399	flgN	flagellar biosynthesis protein FlgN
K02398	flgM	negative regulator of flagellin synthesis FlgM
K02387	flgB	flagellar basal-body rod protein FlgB
K02388	flgC	flagellar basal-body rod protein FlgC
K02390	flgE	flagellar hook protein FlgE
K02391	flgF	flagellar basal-body rod protein FlgF
K02392	flgG	flagellar basal-body rod protein FlgG
K02395	flgJ	peptidoglycan hydrolase FlgJ
K02396	flgK	flagellar hook-associated protein 1
K02397	flgL	flagellar hook-associated protein 3 FlgL
K02405	fliA, whiG	RNA polymerase sigma factor FliA
K04562	flhG, fleN	flagellar biosynthesis protein FlhG
K02404	flhF	flagellar biosynthesis protein FlhF
K02400	flhA	flagellar biosynthesis protein FlhA
K02401	flhB	flagellar biosynthesis protein FlhB
K03413	cheY	two-component system, chemotaxis family, chemotaxis protein CheY
K03412	cheB	two-component system, chemotaxis family, protein-glutamate methylesterase/glutaminase [EC:3.1.1.61 3.5.1.44]
K03411	cheD	chemotaxis protein CheD [EC:3.5.1.44]
K00575	cheR	chemotaxis protein methyltransferase CheR [EC:2.1.1.80]
K05874	tsr	methyl-accepting chemotaxis protein I, serine sensor receptor
K03408	cheW	purine-binding chemotaxis protein CheW
K03407	cheA	two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3]

K02557	motB	chemotaxis protein MotB
K02556	motA	chemotaxis protein MotA
K02406	fliC, hag	flagellin
K02407	fliD	flagellar hook-associated protein 2
K02535	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [EC:3.5.1.108]
K03273	gmhB	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.82 3.1.3.83]
K15669	hddC	D-glycero-alpha-D-manno-heptose 1-phosphate guanylyltransferase [EC:2.7.7.71]
K03271	gmhA, lpcA	D-sedoheptulose 7-phosphate isomerase [EC:5.3.1.28]
K07031	hddA	D-glycero-alpha-D-manno-heptose-7-phosphate kinase [EC:2.7.1.168]
K01711	gmd, GMDS	GDPmannose 4,6-dehydratase [EC:4.2.1.47]
K16011	algA, xanB, rfbA, wbpW, pslB	mannose-1-phosphate guanylyltransferase / mannose-6-phosphate isomerase [EC:2.7.7.13 5.3.1.8]
K03196	virB11, lvhB11	type IV secretion system protein VirB11 [EC:7.4.2.8]
K03760	eptA, pmrC	lipid A ethanolaminephosphotransferase [EC:2.7.8.43]
K03415	cheV	two-component system, chemotaxis family, chemotaxis protein CheV
K03092	rpoN	RNA polymerase sigma-54 factor
K02386	flgA	flagellar basal body P-ring formation protein FlgA
K13626	fliW	flagellar assembly factor FliW
K01387	colA	microbial collagenase [EC:3.4.24.3]
K01197	hya	hyaluronoglucosaminidase [EC:3.2.1.35]
K01186	NEU1	sialidase-1 [EC:3.2.1.18]
K20382	asa1	aggregation substance
K19975	mntC	manganese transport system substrate-binding protein
K09692	tagG	teichoic acid transport system permease protein
K09693	tagH	teichoic acid transport system ATP-binding protein [EC:7.5.2.4]
K01854	glf	UDP-galactopyranose mutase [EC:5.4.99.9]
K00075	murB	UDP-N-acetylmuramate dehydrogenase [EC:1.3.1.98]
K09809	tagF	CDP-glycerol glycerophosphotransferase [EC:2.7.8.12]
K00981	E2.7.7.41, CDS1, CDS2, cdsA	phosphatidate cytidylyltransferase [EC:2.7.7.41]
K00806	uppS	undecaprenyl diphosphate synthase [EC:2.5.1.31]
K07707	agrA, blpR, fsrA	two-component system, LytTR family, response regulator AgrA
K02529	lacI, galR	LacI family transcriptional regulator
K12684	esp, sigA, sepA	serine protease autotransporter [EC:3.4.21.-]
K02527	kdtA, waaA	3-deoxy-D-manno-octulosonic-acid transferase [EC:2.4.99.12 2.4.99.13 2.4.99.14 2.4.99.15]
K03272	gmhC, hldE, waaE, rfaE	D-beta-D-heptose 7-phosphate kinase / D-beta-D-heptose 1-phosphate adenosyltransferase [EC:2.7.1.167 2.7.7.70]
K03274	gmhD, rfaD	ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]
K07270	K07270	glycosyl transferase, family 25
K03286	TC.OOP	OmpA-OmpF porin, OOP family
K01347	iga	IgA-specific serine endopeptidase [EC:3.4.21.72]

K16087	TC.FEV.OM3, tbpA, hemR, lbpA, hpuB, bhuR, hugA, hmbR	hemoglobin/transferrin/lactoferrin receptor protein
K02010	afuC, fbpC	iron(III) transport system ATP-binding protein [EC:7.2.2.7]
K00979	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase (CMP-KDO synthetase) [EC:2.7.7.38]
K00912	lpxK	tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]
K11085	msbA	ATP-binding cassette, subfamily B, bacterial MsbA [EC:7.5.2.6]
K02560	lpxM, msbB	lauroyl-Kdo2-lipid IVA myristoyltransferase [EC:2.3.1.243]
K02428	rdgB	XTP/dITP diphosphohydrolase [EC:3.6.1.66]
K11211	kdkA	3-deoxy-D-manno-octulosonic acid kinase [EC:2.7.1.166]
K01784	galE, GALE	UDP-glucose 4-epimerase [EC:5.1.3.2]
K03269	lpxH	UDP-2,3-diacylglucosamine hydrolase [EC:3.6.1.54]
K01840	manB	phosphomannomutase [EC:5.4.2.8]
K00963	UGP2, galU, galF	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]
K01710	rfbB, rmlB, rffG	dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]
K02536	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [EC:2.3.1.191]
K00748	lpxB	lipid-A-disaccharide synthase [EC:2.4.1.182]
K00677	lpxA	UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]
K02843	waaF, rfaF	heptosyltransferase II [EC:2.4.-.-]
K00983	neuA, nnaC	N-acylneuraminate cytidylyltransferase [EC:2.7.7.43]
K02517	lpxL, htrB	Kdo2-lipid IVA lauroyltransferase/acyltransferase [EC:2.3.1.241 2.3.1.-]
K01627	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase) [EC:2.5.1.55]
K00785	lst	N-acetyllactosaminide alpha-2,3-sialyltransferase [EC:2.4.99.6]
K02851	wecA, tagO, rfe	UDP-GlcNAc:undecaprenyl-phosphate/decaprenyl-phosphate GlcNAc-1-phosphate transferase [EC:2.7.8.33 2.7.8.35]
K14048	ureAB	urease subunit gamma/beta [EC:3.5.1.5]
K01428	ureC	urease subunit alpha [EC:3.5.1.5]
K03191	ureI	acid-activated urea channel
K03187	ureE	urease accessory protein
K03188	ureF	urease accessory protein
K03189	ureG	urease accessory protein
K03190	ureD, ureH	urease accessory protein
K04047	dps	starvation-inducible DNA-binding protein
K15897	pseG	UDP-2,4-diacetamido-2,4,6-trideoxy-beta-L-altropyranose hydrolase [EC:3.6.1.57]
K02429	fucP	MFS transporter, FHS family, L-fucose permease
K02841	waaC, rfaC	heptosyltransferase I [EC:2.4.-.-]
K00954	E2.7.7.3A, coaD, kdtB	pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]
K02377	TSTA3, fcl	GDP-L-fucose synthase [EC:1.1.1.271]
K02389	flgD	flagellar basal-body rod modification protein FlgD
K03406	mcp	methyl-accepting chemotaxis protein

K15895	pseC	UDP-4-amino-4,6-dideoxy-L-N-acetyl-beta-L-altrosamine transaminase [EC:2.6.1.92]
K15894	pseB, wbjB	UDP-N-acetylglucosamine 4,6-dehydratase/5-epimerase [EC:4.2.1.115 5.1.3.-]
K03474	pdxJ	pyridoxine 5-phosphate synthase [EC:2.6.99.2]
K00097	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase [EC:1.1.1.262]
K04077	groEL, HSPD1	chaperonin GroEL
K02195	ccmC	heme exporter protein C
K03305	TC.POT	proton-dependent oligopeptide transporter, POT family
K04758	feoA	ferrous iron transport protein A
K04759	feoB	ferrous iron transport protein B
K03782	katG	catalase-peroxidase [EC:1.11.1.21]
K03773	fklB	FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8]
K04564	SOD2	superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
K04565	SOD1	superoxide dismutase, Cu-Zn family [EC:1.15.1.1]
K02455	gspF	general secretion pathway protein F
K02456	gspG	general secretion pathway protein G
K02457	gspH	general secretion pathway protein H
K02458	gspI	general secretion pathway protein I
K02459	gspJ	general secretion pathway protein J
K02460	gspK	general secretion pathway protein K
K02454	gspE	general secretion pathway protein E [EC:7.4.2.8]
K02453	gspD	general secretion pathway protein D
K02461	gspL	general secretion pathway protein L
K02462	gspM	general secretion pathway protein M
K02666	pilQ	type IV pilus assembly protein PilQ
K07126	K07126	uncharacterized protein
K02452	gspC	general secretion pathway protein C
K02193	ccmA	heme exporter protein A [EC:7.6.2.5]
K02194	ccmB	heme exporter protein B
K02196	ccmD	heme exporter protein D
K02197	ccmE	cytochrome c-type biogenesis protein CcmE
K02198	ccmF	cytochrome c-type biogenesis protein CcmF
K07001	K07001	NTE family protein
K03767	PPIA	peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]
K16239	bsdC	4-hydroxybenzoate decarboxylase subunit C [EC:4.1.1.61]
K02674	pilY1	type IV pilus assembly protein PilY1
K06131	clsA_B	cardiolipin synthase A/B [EC:2.7.8.-]
K07154	hipA	serine/threonine-protein kinase HipA [EC:2.7.11.1]
K09761	rsmE	16S rRNA (uracil1498-N3)-methyltransferase [EC:2.1.1.193]
K01114	plc	phospholipase C [EC:3.1.4.3]

K01771	plc	1-phosphatidylinositol phosphodiesterase [EC:4.6.1.13]
K13730	inlA	internalin A
K13731	inlB	internalin B
K01358	clpP, CLPP	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
K01447	xlyAB	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]
K03696	clpC	ATP-dependent Clp protease ATP-binding subunit ClpC
K03697	clpE	ATP-dependent Clp protease ATP-binding subunit ClpE
K07784	uhpT	MFS transporter, OPA family, hexose phosphate transport protein UhpT
K03800	lplA, lplJ, lipL1	lipoate---protein ligase [EC:6.3.1.20]
K03101	lspA	signal peptidase II [EC:3.4.23.36]
K01442	cbh	choloylglycine hydrolase [EC:3.5.1.24]
K04072	adhE	acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]
K07533	prsA	foldase protein PrsA [EC:5.2.1.8]
K01637	E4.1.3.1, aceA	isocitrate lyase [EC:4.1.3.1]
K16645	hbhA	heparin binding hemagglutinin HbhA
K02483	K02483	two-component system, OmpR family, response regulator
K01909	mbtM	long-chain-fatty-acid--[acyl-carrier-protein] ligase [EC:6.2.1.20]
K04788	mbtB	mycobactin phenyloxazoline synthetase
K03709	troR	DtxR family transcriptional regulator, Mn-dependent transcriptional regulator
K18851	fbp	diacylglycerol O-acyltransferase / trehalose O-mycolyltransferase [EC:2.3.1.20 2.3.1.122]
K04793	mbtG	mycobactin lysine-N-oxygenase
K00951	relA	GTP pyrophosphokinase [EC:2.7.6.5]
K14743	mycP	membrane-anchored mycosin MYCP [EC:3.4.21.-]
K04781	mbtI, irp9, ybtS	salicylate synthetase [EC:5.4.4.2 4.2.99.21]
K14698	irtA, ybtP	ATP-binding cassette, subfamily B, bacterial IrtA/YbtP [EC:7.-.-.-]
K14699	irtB, ybtQ	ATP-binding cassette, subfamily B, bacterial IrtB/YbtQ [EC:7.-.-.-]
K02484	K02484	two-component system, OmpR family, sensor kinase [EC:2.7.13.3]
K02078	acpP	acyl carrier protein
K00257	mbtN, fadE14	acyl-ACP dehydrogenase [EC:1.3.99.-]
K18133	K18133, porB	major outer membrane protein P.IB
K02012	afuA, fbpA	iron(III) transport system substrate-binding protein
K03543	emrA	membrane fusion protein, multidrug efflux system
K03446	emrB	MFS transporter, DHA2 family, multidrug resistance protein
K03585	acrA, mexA, adeI, smeD, mtrC, cmeA	membrane fusion protein, multidrug efflux system
K18138	acrB, mexB, adeJ, smeE, mtrD, cmeB	multidrug efflux pump
K18139	oprM, emhC, ttgC, cusC, adeK, smeF, mtrE, cmeC, gesC	outer membrane protein, multidrug efflux system
K03781	katE, CAT, catB,	catalase [EC:1.11.1.6]

	srpA	
K12267	msrAB	peptide methionine sulfoxide reductase msrA/msrB [EC:1.8.4.11 1.8.4.12]
K03631	recN	DNA repair protein RecN (Recombination protein N)
K11384	algB	two-component system, NtrC family, response regulator AlgB
K07740	rsd	regulator of sigma D
K03088	rpoE	RNA polymerase sigma-70 factor, ECF subfamily
K00066	algD	GDP-mannose 6-dehydrogenase [EC:1.1.1.132]
K19290	alg8	mannuronan synthase [EC:2.4.1.33]
K19291	alg44	mannuronan synthase [EC:2.4.1.33]
K19292	algK	alginate biosynthesis protein AlgK
K16081	algE	alginate production protein
K01795	algG	mannuronan 5-epimerase [EC:5.1.3.37]
K19293	algX	alginate biosynthesis protein AlgX
K01729	algL	poly(beta-D-mannuronate) lyase [EC:4.2.2.3]
K19295	algJ	alginate O-acetyltransferase complex protein AlgJ
K03597	rseA	sigma-E factor negative regulatory protein RseA
K03598	rseB	sigma-E factor negative regulatory protein RseB
K05789	wzzB	chain length determinant protein (polysaccharide antigen chain regulator)
K02844	waaG, rfaG	UDP-glucose:(heptosyl)LPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]
K02848	waaP, rfaP	heptose I phosphotransferase [EC:2.7.1.-]
K01406	prtC	serralysin [EC:3.4.24.40]
K08642	lasA	LasA protease [EC:3.4.24.-]
K13060	lasI	acyl homoserine lactone synthase [EC:2.3.1.184]
K18100	rhlA	rhamnosyltransferase subunit A [EC:2.4.1.-]
K10531	pvdA, SIDA	L-ornithine N5-monooxygenase [EC:1.14.13.195 1.14.13.196]
K16088	TC.FEV.OM1, fhuE, fpvA, fptA	outer-membrane receptor for ferric coprogen and ferric-rhodotorulic acid
K12243	pchR	AraC family transcriptional regulator, transcriptional activator of the genes for pyochelin and ferripyochelin receptors
K04782	pchB	isochorismate pyruvate lyase [EC:4.2.99.21]
K01851	pchA	salicylate biosynthesis isochorismate synthase [EC:5.4.4.2]
K20968	exsA	AraC family transcriptional regulator, exoenzyme S synthesis regulatory protein ExsA
K06147	ABCB-BAC	ATP-binding cassette, subfamily B, bacterial
K06148	ABCC-BAC	ATP-binding cassette, subfamily C, bacterial
K02004	ABC.CD.P	putative ABC transport system permease protein
K02003	ABC.CD.A	putative ABC transport system ATP-binding protein
K04771	degP, htrA	serine protease Do [EC:3.4.21.107]
K04691	hhoB, degS	serine protease DegS [EC:3.4.21.-]
K11749	rseP	regulator of sigma E protease [EC:3.4.24.-]
K01626	E2.5.1.54, aroF, aroG, aroH	3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]

K06998	phzF	trans-2,3-dihydro-3-hydroxyanthranilate isomerase [EC:5.3.3.17]
K01953	asnB, ASNS	asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]
K07116	pvdQ, quiP	acyl-homoserine-lactone acylase [EC:3.5.1.97]
K00836	ectB, dat	diaminobutyrate-2-oxoglutarate transaminase [EC:2.6.1.76]
K07346	fimC	fimbrial chaperone protein
K04335	csgB	minor curlin subunit
K04334	csgA	major curlin subunit
K04336	csgC	curli production protein
K04337	csgE	curli production assembly/transport component CsgE
K06214	csgG	curli production assembly/transport component CsgG
K15353	sspH2	E3 ubiquitin-protein ligase SspH2
K15345	sseC	secreted effector protein SseC
K01531	mgtA, mgtB	P-type Mg2+ transporter [EC:7.2.2.14]
K18015	elaD, sseL	deubiquitinase [EC:3.4.22.-]
K15352	pipB2	secreted effector protein PipB2
K04333	csgD	LuxR family transcriptional regulator, csgAB operon transcriptional regulatory protein
K03894	iucA	N2-citryl-N6-acetyl-N6-hydroxylysine synthase [EC:6.3.2.38]
K03896	iucB	acetyl CoA:N6-hydroxylysine acetyl transferase [EC:2.3.1.102]
K03895	iucC	aerobactin synthase [EC:6.3.2.39]
K03897	iucD	lysine N6-hydroxylase [EC:1.14.13.59]
K02014	TC.FEV.OM	iron complex outermembrane recepter protein
K12679	icsA, virG	outer membrane protein IcsA
K20534	gtrB, csbB	polyisoprenyl-phosphate glycosyltransferase [EC:2.4.-.-]
K02016	ABC.FEV.S	iron complex transport system substrate-binding protein
K02015	ABC.FEV.P	iron complex transport system permease protein
K02013	ABC.FEV.A	iron complex transport system ATP-binding protein [EC:7.2.2.-]
K14194	sdrC_D_E	serine-aspartate repeat-containing protein C/D/E
K11936	pgaC, icaA	poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
K01791	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14]
K02472	wecC	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase [EC:1.1.1.336]
K01046	lip, TGL2	triacylglycerol lipase [EC:3.1.1.3]
K03466	ftsK, spoIIIE	DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family
K14197	sbi	immunoglobulin G-binding protein Sbi
K00012	UGDH, ugd	UDPglucose 6-dehydrogenase [EC:1.1.1.22]
K15051	endA	DNA-entry nuclease
K01364	speB	streptopain [EC:3.4.22.10]
K09815	znuA	zinc transport system substrate-binding protein
K01104	E3.1.3.48	protein-tyrosine phosphatase [EC:3.1.3.48]
K01227	ENGASE	mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [EC:3.2.1.96]

K19971	psaA, scaA, sloC	manganese/zinc transport system substrate-binding protein
K17716	capD	UDP-glucose 4-epimerase [EC:5.1.3.2]
K19068	wbjC	UDP-2-acetamido-2,6-beta-L-arabino-hexul-4-ose reductase [EC:1.1.1.367]
K01185	E3.2.1.17	lysozyme [EC:3.2.1.17]
K02372	fabZ	3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]
K13925	pfbA	plasmin and fibronectin-binding protein A
K10965	tcpT	toxin coregulated pilus biosynthesis protein T
K10934	tcpE	toxin coregulated pilus biosynthesis protein E
K10954	zot	zona occludens toxin
K10953	rtxA	RTX toxin RtxA
K11018	tlh	thermolabile hemolysin
K10948	hlyA	hemolysin
K07173	luxS	S-ribosylhomocysteine lyase [EC:4.4.1.21]
K02073	metQ	D-methionine transport system substrate-binding protein
K08566	pla	plasminogen activator [EC:3.4.23.48]
K02425	fliZ	regulator of sigma S factor FliZ
K02423	fliT	flagellar protein FliT
K03516	flhE	flagellar protein FlhE
K02402	flhC	flagellar transcriptional activator FlhC
K02403	flhD	flagellar transcriptional activator FlhD
K13005	rfbV, wbaV	O-antigen biosynthesis alpha-1,3-abequosyltransferase [EC:2.4.1.60]
K01790	rfbC, rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13]
K01709	rfbG	CDP-glucose 4,6-dehydratase [EC:4.2.1.45]
K00978	rfbF	glucose-1-phosphate cytidylyltransferase [EC:2.7.7.33]
K06132	clsC	cardiolipin synthase C [EC:2.7.8.-]
K02361	entC	isochorismate synthase [EC:5.4.4.2]
K01590	hdc, HDC	histidine decarboxylase [EC:4.1.1.22]
K01252	entB, dhbB, vibB, mxcF	bifunctional isochorismate lyase / aryl carrier protein [EC:3.3.2.1 6.3.2.14]
K02363	entE, dhbE, vibE, mxcE	2,3-dihydroxybenzoate---[aryl-carrier protein] ligase [EC:6.3.2.14 6.2.1.71]
K09790	K09790	uncharacterized protein
K11935	pgaA	biofilm PGA synthesis protein PgaA
K11931	pgaB	poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase [EC:3.5.1.-]
K11937	pgaD	biofilm PGA synthesis protein PgaD
K16692	etk-wzc	tyrosine-protein kinase Etk/Wzc [EC:2.7.10.-]
K01810	GPI, pgi	glucose-6-phosphate isomerase [EC:5.3.1.9]
K07782	sdiA	LuxR family transcriptional regulator, quorum-sensing system regulator SdiA
K07661	rstA	two-component system, OmpR family, response regulator RstA
K07639	rstB	two-component system, OmpR family, sensor histidine kinase RstB [EC:2.7.13.3]

K07262	pbpG	serine-type D-Ala-D-Ala endopeptidase (penicillin-binding protein 7) [EC:3.4.21.-]
K02450	gspA	general secretion pathway protein A
K02451	gspB	general secretion pathway protein B
K02463	gspN	general secretion pathway protein N
K02283	cpaF, tadA	pilus assembly protein CpaF [EC:7.4.2.8]
K03496	parA, soj	chromosome partitioning protein
K00059	fabG, OAR1	3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]
K03194	virB1	type IV secretion system protein VirB1
K03197	virB2, lvhB2	type IV secretion system protein VirB2
K03198	virB3, lvhB3	type IV secretion system protein VirB3
K03203	virB8, lvhB8	type IV secretion system protein VirB8
K03204	virB9, lvhB9	type IV secretion system protein VirB9
K03195	virB10, lvhB10	type IV secretion system protein VirB10
K18434	virD2	type IV secretion system T-DNA border endonuclease VirD2
K03640	pal	peptidoglycan-associated lipoprotein
K16698	tuaG	teichuronic acid biosynthesis glycosyltransferase TuaG [EC:2.4.-.-]
K00640	cysE	serine O-acetyltransferase [EC:2.3.1.30]
K03980	murJ, mviN	putative peptidoglycan lipid II flippase
K01809	manA, MPI	mannose-6-phosphate isomerase [EC:5.3.1.8]
K03328	TC.PST	polysaccharide transporter, PST family
K00666	K00666	fatty-acyl-CoA synthase [EC:6.2.1.-]
K15652	asbF	3-dehydroshikimate dehydratase [EC:4.2.1.118]
K07145	isdG, isdI	heme oxygenase (staphylobilin-producing) [EC:1.14.99.48]
K07277	SAM50, TOB55, bamA	outer membrane protein insertion porin family
K04095	fic	cell filamentation protein
K07690	evgA, bvgA	two-component system, NarL family, response regulator EvgA
K07679	evgS, bvgS	two-component system, NarL family, sensor histidine kinase EvgS [EC:2.7.13.3]
K10011	arnA, pmrI	UDP-4-amino-4-deoxy-L-arabinose formyltransferase / UDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating) [EC:2.1.2.13 1.1.1.305]
K12973	pagP, crcA	lipid IVA palmitoyltransferase [EC:2.3.1.251]
K07315	rsbU_P	phosphoserine phosphatase RsbU/P [EC:3.1.3.3]
K07552	bcr, tcaB	MFS transporter, DHA1 family, multidrug resistance protein
K01835	pgm	phosphoglucomutase [EC:5.4.2.2]
K02364	entF	L-serine---[L-seryl-carrier protein] ligase [EC:6.3.2.14 6.2.1.72]
K00216	entA	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [EC:1.3.1.28]
K02362	entD	enterobactin synthetase component D [EC:6.3.2.14 2.7.8.-]
K05813	ugpB	sn-glycerol 3-phosphate transport system substrate-binding protein
K00652	bioF	8-amino-7-oxononanoate synthase [EC:2.3.1.47]
K01495	GCH1, folE	GTP cyclohydrolase IA [EC:3.5.4.16]

K02424	fliY, tcyA	L-cystine transport system substrate-binding protein
K17733	cwlK	peptidoglycan LD-endopeptidase CwlK [EC:3.4.-.-]
K13255	fhuF	ferric iron reductase protein FhuF
K10039	peb1A, glnH	aspartate/glutamate/glutamine transport system substrate-binding protein
K00860	cysC	adenylylsulfate kinase [EC:2.7.1.25]
K07010	K07010	putative glutamine amidotransferase
K06041	kdsD, kpsF	arabinose-5-phosphate isomerase [EC:5.3.1.13]
K01779	racD	aspartate racemase [EC:5.1.1.13]
K15898	pseI, neuB3	pseudaminic acid synthase [EC:2.5.1.97]
K18430	legI, neuB2	N,N'-diacetyllegionaminate synthase [EC:2.5.1.101]
K18429	legG, neuC2	GDP/UDP-N,N'-diacetylbacillosamine 2-epimerase (hydrolysing) [EC:3.2.1.184]
K15912	pglF	UDP-N-acetylglucosamine 4,6-dehydratase [EC:4.2.1.135]
K15913	pglD	UDP-N-acetylbacillosamine N-acetyltransferase [EC:2.3.1.203]
K15915	pglC	undecaprenyl phosphate N,N'-diacetylbacillosamine 1-phosphate transferase [EC:2.7.8.36]
K15914	pglA	N,N'-diacetylbacillosaminyl-diphospho-undecaprenol alpha-1,3-N-acetylgalactosaminyltransferase [EC:2.4.1.290]
K17251	pglB	undecaprenyl-diphosphooligosaccharide---protein glycotransferase [EC:2.4.99.19]
K17248	pglJ	N-acetylgalactosamine-N,N'-diacetylbacillosaminyl-diphospho-undecaprenol 4-alpha-N-acetylgalactosaminyltransferase [EC:2.4.1.291]
K17250	pglI	GalNAc5-diNAcBac-PP-undecaprenol beta-1,3-glucosyltransferase [EC:2.4.1.293]
K17249	pglH	GalNAc-alpha-(1->4)-GalNAc-alpha-(1->3)-diNAcBac-PP-undecaprenol alpha-1,4-N-acetyl-D-galactosaminyltransferase [EC:2.4.1.292]
K18431	legF, ptmB	CMP-N,N'-diacetyllegionaminic acid synthase [EC:2.7.7.82]
K06137	pqqC	pyrroloquinoline-quinone synthase [EC:1.3.3.11]
K04043	dnaK, HSPA9	molecular chaperone DnaK
K08587	cloSI	clostripain [EC:3.4.22.8]
K06442	tlyA	23S rRNA (cytidine1920-2'-O)/16S rRNA (cytidine1409-2'-O)-methyltransferase [EC:2.1.1.226 2.1.1.227]
K00343	nuoN	NADH-quinone oxidoreductase subunit N [EC:7.1.1.2]
K00209	fabV, ter	enoyl-[acyl-carrier protein] reductase / trans-2-enoyl-CoA reductase (NAD+) [EC:1.3.1.9 1.3.1.44]
K15778	pmm-pgm	phosphomannomutase / phosphoglucomutase [EC:5.4.2.8 5.4.2.2]
K01622	K01622	fructose 1,6-bisphosphate aldolase/phosphatase [EC:4.1.2.13 3.1.3.11]
K03789	rimI	[ribosomal protein S18]-alanine N-acetyltransferase [EC:2.3.1.266]
K00074	paaH, hbd, fadB, mmgB	3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]
K09748	rimP	ribosome maturation factor RimP
K01992	ABC-2.P	ABC-2 type transport system permease protein
K00937	ppk1	polyphosphate kinase [EC:2.7.4.1]
K01586	lysA	diaminopimelate decarboxylase [EC:4.1.1.20]
K02510	hpaI, hpcH	4-hydroxy-2-oxoheptanedioate aldolase [EC:4.1.2.52]
K13745	ddc	L-2,4-diaminobutyrate decarboxylase [EC:4.1.1.86]
K07796	cusC, silC	outer membrane protein, copper/silver efflux system

K16089	TC.FEV.OM2, cirA, cfrA, hmuR	outer membrane receptor for ferrienterochelin and colicins
K12687	flu	antigen 43
K19611	fepA, pfeA, iroN, pirA	ferric enterobactin receptor
K07017	K07017	uncharacterized protein
K15721	fyuA	pesticin/yersiniabactin receptor
K19353	eptC	heptose-I-phosphate ethanolaminephosphotransferase [EC:2.7.8.-]
K11139	hlyE, clyA, sheA	hemolysin E
K02464	gspO	general secretion pathway protein O [EC:3.4.23.43 2.1.1.-]
K05875	tar	methyl-accepting chemotaxis protein II, aspartate sensor receptor
K05803	nlpI	lipoprotein NlpI
K03431	glmM	phosphoglucosamine mutase [EC:5.4.2.10]
K02492	hemA	glutamyl-tRNA reductase [EC:1.2.1.70]
K01698	hemB, ALAD	porphobilinogen synthase [EC:4.2.1.24]
K01749	hemC, HMBS	hydroxymethylbilane synthase [EC:2.5.1.61]
K01719	hemD, UROS	uroporphyrinogen-III synthase [EC:4.2.1.75]
K01599	hemE, UROD	uroporphyrinogen decarboxylase [EC:4.1.1.37]
K00230	hemG	menaquinone-dependent protoporphyrinogen oxidase [EC:1.3.5.3]
K01772	hemH, FECH	protoporphyrin/coproporphyrin ferrochelatase [EC:4.99.1.1 4.99.1.9]
K01845	hemL	glutamate-1-semialdehyde 2,1-aminomutase [EC:5.4.3.8]
K02494	lolB	outer membrane lipoprotein LolB
K02495	hemN, hemZ	oxygen-independent coproporphyrinogen III oxidase [EC:1.3.98.3]
K02496	hemX	uroporphyrin-III C-methyltransferase [EC:2.1.1.107]
K03087	rpoS	RNA polymerase nonessential primary-like sigma factor
K07678	barA, gacS, varS	two-component system, NarL family, sensor histidine kinase BarA [EC:2.7.13.3]
K03563	csrA	carbon storage regulator
K02500	hisF	imidazole glycerol-phosphate synthase subunit HisF [EC:4.3.2.10]
K02501	hisH	imidazole glycerol-phosphate synthase subunit HisH [EC:4.3.2.10]
K00067	rfbD, rmlD	dTDP-4-dehydrorhamnose reductase [EC:1.1.1.133]
K00973	rfbA, rmlA, rffH	glucose-1-phosphate thymidylyltransferase [EC:2.7.7.24]
K04080	ibpA	molecular chaperone IbpA
K01972	E6.5.1.2, ligA, ligB	DNA ligase (NAD+) [EC:6.5.1.2]
K15580	oppA, mppA	oligopeptide transport system substrate-binding protein
K20074	prpC, phpP	PPM family protein phosphatase [EC:3.1.3.16]
K13292	lgt, umpA	phosphatidylglycerol---prolipoprotein diacylglyceryl transferase [EC:2.5.1.145]
K03367	dltA	D-alanine--poly(phosphoribitol) ligase subunit 1 [EC:6.1.1.13]
K12686	apeE, estA, lip-1	outer membrane lipase/esterase
K13640	hspR	MerR family transcriptional regulator, heat shock protein HspR
K00574	cfa	cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]

K00286	proC	pyrroline-5-carboxylate reductase [EC:1.5.1.2]
K16191	K16191, arfA	peptidoglycan-binding protein ArfA
K07671	prrA	two-component system, OmpR family, response regulator PrrA
K07669	mprA	two-component system, OmpR family, response regulator MprA
K00370	narG, narZ, nxrA	nitrate reductase / nitrite oxidoreductase, alpha subunit [EC:1.7.5.1 1.7.99.-]
K00766	trpD	anthranilate phosphoribosyltransferase [EC:2.4.2.18]
K01915	glnA, GLUL	glutamine synthetase [EC:6.3.1.2]
K03386	PRDX2_4, ahpC	peroxiredoxin 2/4 [EC:1.11.1.24]
K03086	rpoD	RNA polymerase primary sigma factor
K12426	fadD26	long-chain fatty acid adenylase/transferase FadD26 [EC:6.2.1.59]
K11628	mas	mycocerosic acid synthase [EC:2.3.1.111]
K06994	K06994	putative drug exporter of the RND superfamily
K01704	leuD, IPMI-S	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]
K03090	sigB	RNA polymerase sigma-B factor
K18955	whiB1_2_3_4	WhiB family transcriptional regulator, redox-sensing transcriptional regulator
K14953	lpqH	ipoprotein LpqH
K00371	narH, narY, nxrB	nitrate reductase / nitrite oxidoreductase, beta subunit [EC:1.7.5.1 1.7.99.-]
K00373	narJ, narW	nitrate reductase molybdenum cofactor assembly chaperone NarJ/NarW
K00374	narI, narV	nitrate reductase gamma subunit [EC:1.7.5.1 1.7.99.-]
K07695	devR	two-component system, NarL family, response regulator DevR
K07682	devS	two-component system, NarL family, sensor histidine kinase DevS [EC:2.7.13.3]
K01579	panD	aspartate 1-decarboxylase [EC:4.1.1.11]
K01923	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]
K12440	ppsA	phthiocerol/phenolphthiocerol synthesis type-I polyketide synthase A [EC:2.3.1.292]
K12441	ppsB	phthiocerol/phenolphthiocerol synthesis type-I polyketide synthase B [EC:2.3.1.292]
K12442	ppsC	phthiocerol/phenolphthiocerol synthesis type-I polyketide synthase C [EC:2.3.1.292]
K12443	ppsD	phthiocerol/phenolphthiocerol synthesis type-I polyketide synthase D [EC:2.3.1.292]
K12444	ppsE	phthiocerol/phenolphthiocerol synthesis type-I polyketide synthase E [EC:2.3.1.292]
K01990	ABC-2.A	ABC-2 type transport system ATP-binding protein
K01918	panC	pantoate--beta-alanine ligase [EC:6.3.2.1]
K12433	pks5	polyketide synthase 5
K14949	pknG	serine/threonine-protein kinase PknG [EC:2.7.11.1]
K08884	K08884	serine/threonine protein kinase, bacterial [EC:2.7.11.1]
K11609	kasAB	beta-ketoacyl ACP synthase [EC:2.3.1.293 2.3.1.294]
K01078	PHO	acid phosphatase [EC:3.1.3.2]
K02575	NRT, narK, nrtP, nasA	MFS transporter, NNP family, nitrate/nitrite transporter
K07655	prrB	two-component system, OmpR family, sensor histidine kinase PrrB [EC:2.7.13.3]
K07653	mprB	two-component system, OmpR family, sensor histidine kinase MprB [EC:2.7.13.3]
K02067	mlaD, linM	phospholipid/cholesterol/gamma-HCH transport system substrate-binding protein

K00336	nuoG	NADH-quinone oxidoreductase subunit G [EC:7.1.1.2]
K00604	MTFMT, fmt	methionyl-tRNA formyltransferase [EC:2.1.2.9]
K13993	HSP20	HSP20 family protein
K12430	pks1_15	4-hydroxyphenylalkanoate synthase [EC:2.3.1.261]
K14728	K14728	phthiodiolone/phenolphthiodiolone dimycocerosates ketoreductase [EC:1.2.-.-]
K01657	trpE	anthranilate synthase component I [EC:4.1.3.27]
K17947	wbiB	dTDP-L-rhamnose 4-epimerase [EC:5.1.3.25]
K12421	fadD9	fatty acid CoA ligase FadD9
K12423	fadD21	fatty acid CoA ligase FadD21
K03455	TC.KEF	monovalent cation:H+ antiporter-2, CPA2 family
K00121	frmA, ADH5, adhC	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]
K02027	ABC.MS.S	multiple sugar transport system substrate-binding protein
K02025	ABC.MS.P	multiple sugar transport system permease protein
K02026	ABC.MS.P1	multiple sugar transport system permease protein
K10112	msmX, msmK, malK, sugC, ggtA, msiK	multiple sugar transport system ATP-binding protein [EC:7.5.2.-]
K15981	CYP125A	cholest-4-en-3-one 26-monooxygenase [EC:1.14.15.29]
K07386	pepO	putative endopeptidase [EC:3.4.24.-]
K13571	pafA	proteasome accessory factor A [EC:6.3.1.19]
K13527	mpa	proteasome-associated ATPase
K20467	K20467	heme-binding protein
K20470	mmpL3	trehalose monomycolate/heme transporter
K20466	mmpL11	heme transporter
K12950	ctpC	manganese-transporting P-type ATPase C [EC:7.2.2.22]
K12956	ctpV	copper-transporting P-type ATPase V [EC:7.2.2.8]
K00940	ndk, NME	nucleoside-diphosphate kinase [EC:2.7.4.6]
K07768	senX3	two-component system, OmpR family, sensor histidine kinase SenX3 [EC:2.7.13.3]
K07776	regX3	two-component system, OmpR family, response regulator RegX3
K01638	aceB, glcB	malate synthase [EC:2.3.3.9]
K03530	hupB	DNA-binding protein HU-beta
K02358	tuf, TUFM	elongation factor Tu
K00162	PDHB, pdhB	pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]
K01174	nuc	micrococcal nuclease [EC:3.1.31.1]
K02032	ddpF	peptide/nickel transport system ATP-binding protein
K00134	GAPDH, gapA	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]
K18132	K18132, porA	major outer membrane protein P.IA
K03561	exbB	biopolymer transport protein ExbB
K03559	exbD	biopolymer transport protein ExbD
K02237	comEA	competence protein ComEA

K01644	citE	citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.34]
K01697	CBS	cystathionine beta-synthase [EC:4.2.1.22]
K18304	lasR	LuxR family transcriptional regulator, quorum-sensing system regulator LasR
K13015	wbpA	UDP-N-acetyl-D-glucosamine dehydrogenase [EC:1.1.1.136]
K13016	wbpB	UDP-N-acetyl-2-amino-2-deoxyglucuronate dehydrogenase [EC:1.1.1.335]
K07497	K07497	putative transposase
K00655	plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase [EC:2.3.1.51]
K07689	uvrY, gacA, varA	two-component system, NarL family, invasion response regulator UvrY
K08305	mltB	membrane-bound lytic murein transglycosylase B [EC:4.2.2.-]
K01494	dcd	dCTP deaminase [EC:3.5.4.13]
K00821	argD	acetylornithine/N-succinyldiaminopimelate aminotransferase [EC:2.6.1.11 2.6.1.17]
K00611	OTC, argF, argI	ornithine carbamoyltransferase [EC:2.1.3.3]
K10814	hcnA	hydrogen cyanide synthase HcnA [EC:1.4.99.5]
K10815	hcnB	hydrogen cyanide synthase HcnB [EC:1.4.99.5]
K10816	hcnC	hydrogen cyanide synthase HcnC [EC:1.4.99.5]
K01066	aes	acetyl esterase [EC:3.1.1.-]
K08307	mltD, dniR	membrane-bound lytic murein transglycosylase D [EC:4.2.2.-]
K10914	crp	CRP/FNR family transcriptional regulator, cyclic AMP receptor protein
K01142	E3.1.11.2, xthA	exodeoxyribonuclease III [EC:3.1.11.2]
K18093	oprD	imipenem/basic amino acid-specific outer membrane pore [EC:3.4.21.-]
K00697	otsA	trehalose 6-phosphate synthase [EC:2.4.1.15 2.4.1.347]
K17717	pld	phospholipase D [EC:3.1.4.4]
K07637	phoQ	two-component system, OmpR family, sensor histidine kinase PhoQ [EC:2.7.13.3]
K07660	phoP	two-component system, OmpR family, response regulator PhoP
K03711	fur, zur, furB	Fur family transcriptional regulator, ferric uptake regulator
K01673	cynT, can	carbonic anhydrase [EC:4.2.1.1]
K15540	ecpD	chaperone protein EcpD
K16076	nmpC, ompD	outer membrane porin protein LC
K03497	parB, spo0J	ParB family transcriptional regulator, chromosome partitioning protein
K15736	lhgO	(S)-2-hydroxyglutarate dehydrogenase [EC:1.1.5.13]
K13714	atl	bifunctional autolysin [EC:3.5.1.28 3.2.1.96]
K01738	cysK	cysteine synthase [EC:2.5.1.47]
K01750	E4.3.1.12, ocd	ornithine cyclodeaminase [EC:4.3.1.12]
K00689	E2.4.1.5	dextransucrase [EC:2.4.1.5]
K03545	tig	trigger factor
K01689	ENO, eno	enolase [EC:4.2.1.11]
K11704	mtsA	iron/zinc/manganese/copper transport system substrate-binding protein
K05946	tagA, tarA	N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase [EC:2.4.1.187]
K06024	scpB	segregation and condensation protein B

K18765	csrD	RNase E specificity factor CsrD
K08604	hap, nprV	vibriolysin [EC:3.4.24.25]
K03606	wcaJ	putative colanic acid biosysnthesis UDP-glucose lipid carrier transferase
K03933	cpbD	chitin-binding protein
K16091	fecA	Fe(3+) dicitrate transport protein
K00523	ascD, ddhD, rfbI	CDP-4-dehydro-6-deoxyglucose reductase, E3 [EC:1.17.1.1]
K10016	hisQ	histidine transport system permease protein
K12341	yadA	adhesin YadA
K19997	gnu	GlcNAc-P-P-Und epimerase [EC:5.1.3.26]
K05790	wzzE	lipopolysaccharide biosynthesis protein WzzE