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Supplemental Information

Community-integrated multi-omics facilitates screening and isolation of the organohalide dehalogenation microorganism

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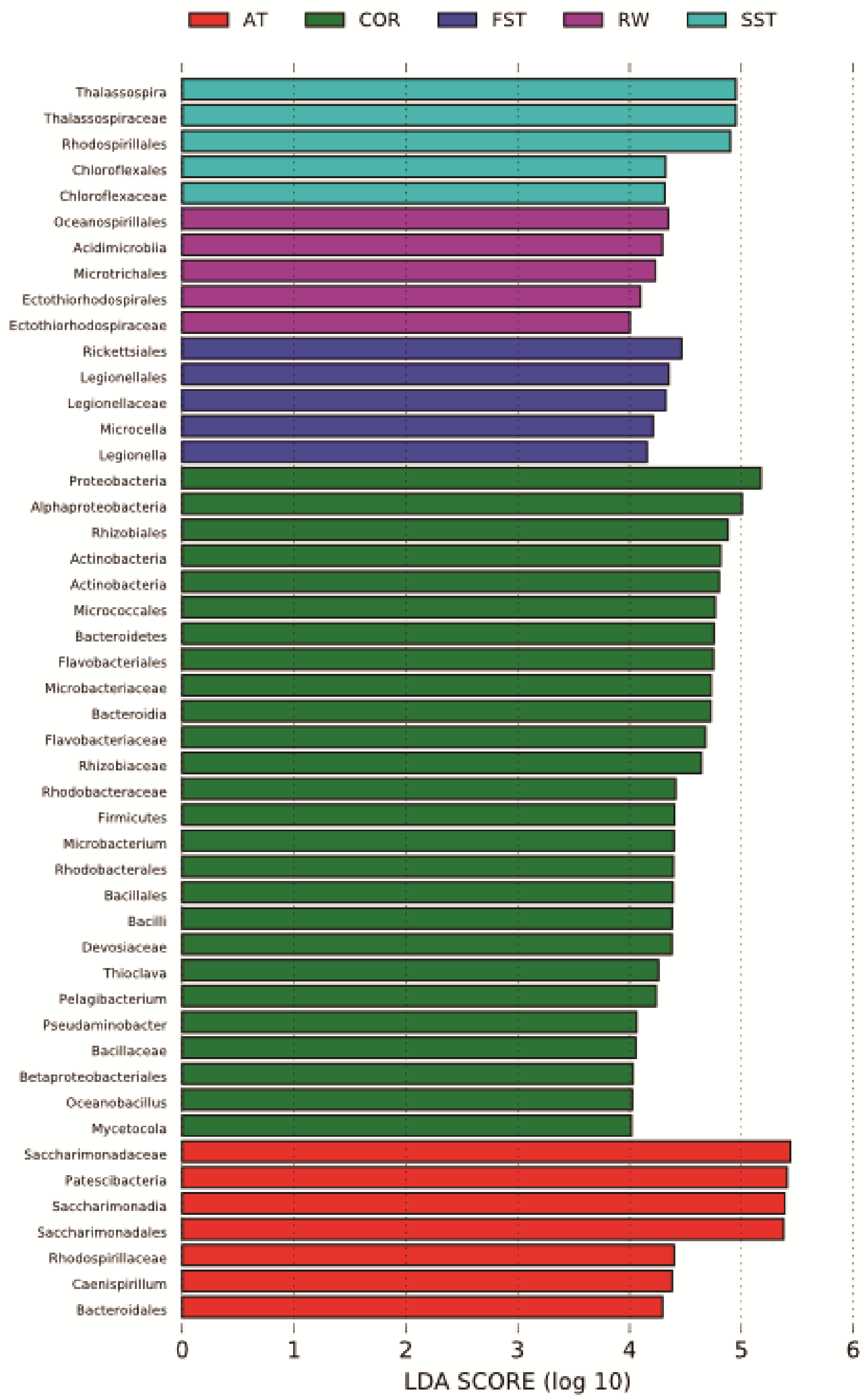


Figure S1. LEfSe results of wastewater treatment process.

Linear discriminant analysis effect size (LEfSe) analysis of the wastewater treatment process (LDA score>4, $p<0.05$). The indicated genera having statistically significant differences between distinct phases of the full process of wastewater treatment.

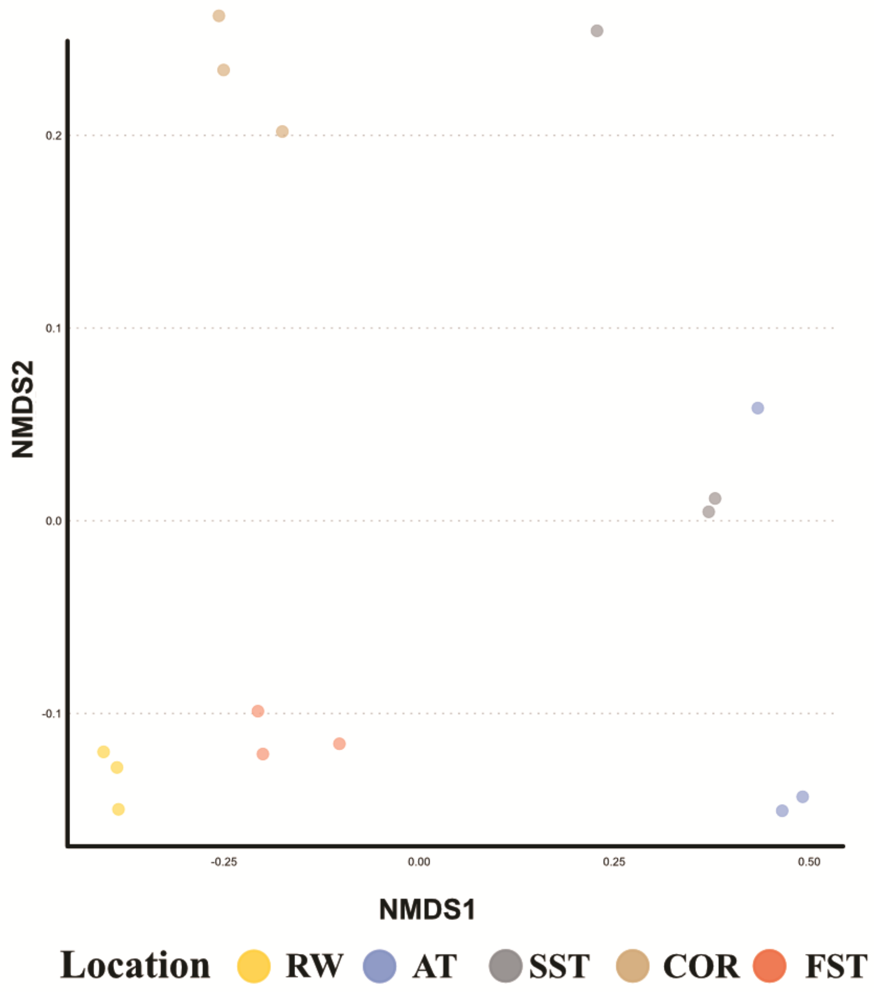


Figure S2. Beta diversity of wastewater treatment process.

Beta diversity of microbial community during the wastewater treatment process. The separation of wastewater treatment phases shows the difference in the composition of the microbial community.

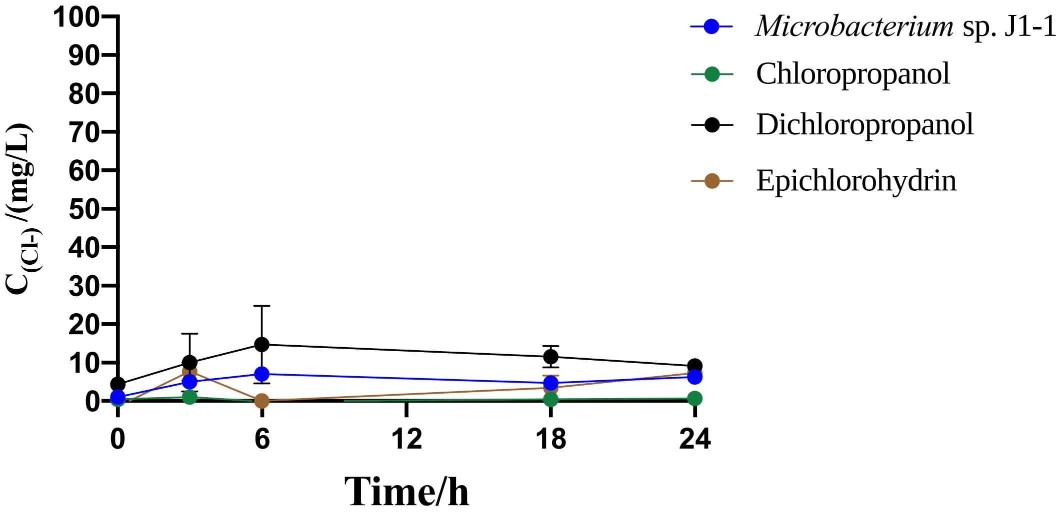
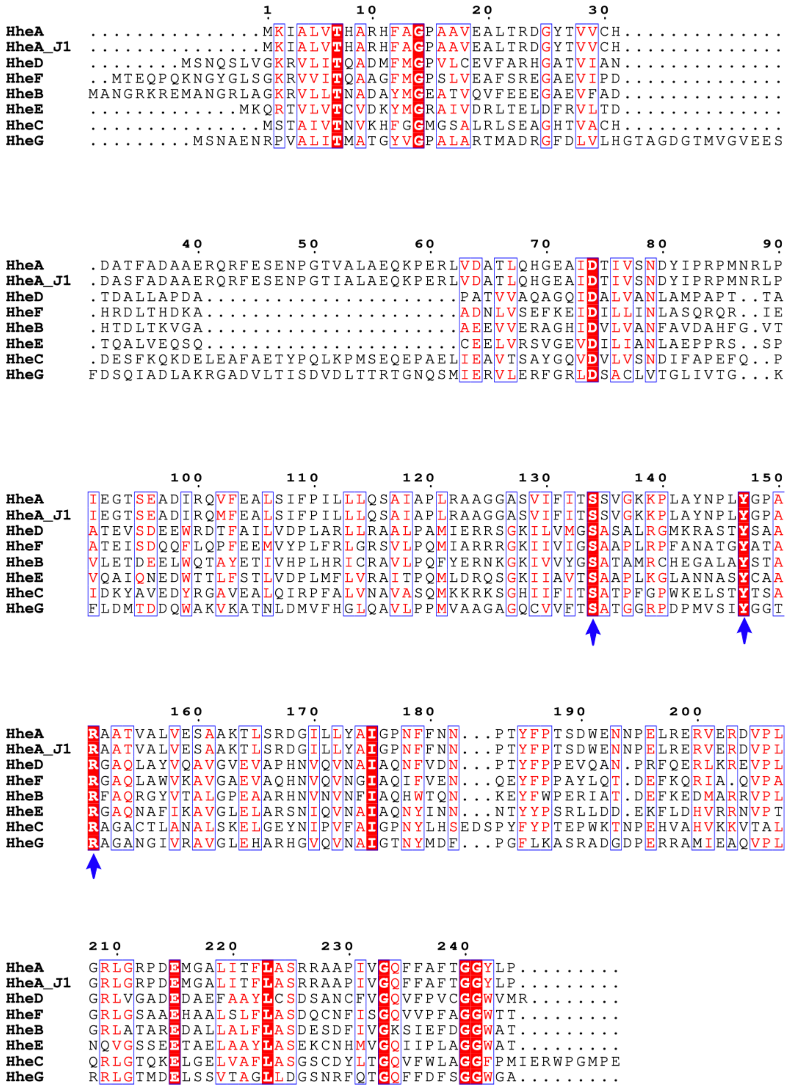


Figure S3. The halogen ion concentration of control group in 24 hours.
Blue: The halogen ion concentration of *Microbacterium* sp. J1-1 without organohalide substrates in the reaction system. Green, Black, Brown: The halogen ion concentration of organohalides without *Microbacterium* sp. J1-1 in the reaction system.



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                               1        10         20         30
HheA      ...............MKIALVTHARHFAGPAAVEALTRDGYTVVCH..............
HheA_J1   ...............MKIALVTHARHFAGPAAVEALTRDGYTVVCH..............
HheD      ........MSNQSLVGKRVLITQADMFMGPVLCEVFARHGATVIAN..............
HheF      ..MTEQPQKNGYGLSGKRVVITQAAGFMGPSLVEAFSREGAEVIPD..............
HheB      MANGRKREMANGRLAGKRVLLTNADAYMGEATVQVFEEEGAEVFAD..............
HheE      .............MKQRTVLVTCVDKYMGRAIVDRLTELDFRVLTD..............
HheC      ...............MSTAIVTNVKHFGGMGSALRLSEAGHTVACH..............
HheG      .........MSNAENRPVALITMATGYVGPALARTMADRGFDLVLHGTAGDGTMVGVEES

                 40        50         60        70         80        90
HheA      .DATFADAAERQRFESENPGTVALAEQKPERLVDATLQHGEAIDTIVSNDYIPRPMNRLP
HheA_J1   .DASFADAAERQRFESENPGTIALAEQKPERLVDATLQHGEAIDTIVSNDYIPRPMNRLP
HheD      .TDALLAPDA......................PATVVAQAGQIDALVANLAMPAPT..TA
HheF      .HRDLTHDKA......................ADNLVSEFKEIDILLINLASQRQR..IE
HheB      .HTDLTKVGA......................AEEVVERAGHIDVLVANFAVDAHFG.VT
HheE      .TQALVEQSQ......................CEELVRSVGEVDILIANLAEPPRS..SP
HheC      .DESFKQKDELEAFAETYPQLKPMSEQEPAELIEAVTSAYGQVDVLVSNDIFAPEFQ..P
HheG      FDSQIADLAKRGADVLTISDVDLTTRTGNQSMIERVLERFGRLDSACLVTGLIVTG...K

                100        110        120        130        140       150
HheA      IEGTSEADIRQVFEALSIFPILLLQSAIAPLRAAGGASVIFITSSVGKKPLAYNPLYGPA
HheA_J1   IEGTSEADIRQMFEALSIFPILLLQSAIAPLRAAGGASVIFITSSVGKKPLAYNPLYGPA
HheD      ATEVSDEEWRDTFAILVDPLARLLRAALPAMIERRSGKILVMGSASALRGMKRASTYSAA
HheF      ATEISDQQFLQPFEEMVYPLFRLGRSVLPQMIARRRGKIIVIGSAAPLRPFANATGYATA
HheB      VLETDEELWQTAYETIVHPLHRICRAVLPQFYERNKGKIVVYGSATAMRCHEGALAYSTA
HheE      VQAIQNEDWTTLFSTLVDPLMFLVRAITPQMLDRQSGKIIAVTSAAPLKGLANNASYCAA
HheC      IDKYAVEDYRGAVEALQIRPFALVNAVASQMKKRKSGHIIFITSATPFGPWKELSTYTSA
HheG      FLDMTDDQWAKVKATNLDMVFHGLQAVLPPMVAAGAGQCVVFTSATGGRPDPMVSIYGGT

                160        170        180          190        200
HheA      RAATVALVESAAKTLSRDGILLYAIGPNFFNN...PTYFPTSDWENNPELRERVERDVPL
HheA_J1   RAATVALVESAAKTLSRDGILLYAIGPNFFNN...PTYFPTSDWENNPELRERVERDVPL
HheD      RGAQLAYVQAVGVEVAPHNVQVNAIAQNFVDN...PTYFPPEVQAN.PRFQERLKREVPL
HheF      RGAQLAWVKAVGAEVAQHNVQVNGIAQIFVEN...QEYFPPAYLQT.DEFKQRIA.QVPA
HheB      RFAQRGYVTALGPEAARHNVNVNFIAQHWTQN...KEYFWPERIAT.DEFKEDMARRVPL
HheE      RGAQNAFIKAVGLELARSNIQVNAIAQNYINN...NTYYPSRLLDD.EKFLDHVRRNVPT
HheC      RAGACTLANALSKELGEYNIPVFAIGPNYLHSEDSPYFYPTEPWKTNPEHVAHVKKVTAL
HheG      RAGANGIVRAVGLEHARHGVQVNAIGTNYMDF...PGFLKASRADGDPERRAMIEAQVPL

          210        220        230        240
HheA      GRLGRPDEMGALITFLASRRAAPIVGQFFAFTGGYLP.........
HheA_J1   GRLGRPDEMGALITFLASRRAAPIVGQFFAFTGGYLP.........
HheD      GRLVGADEDAEFAAYLCSDSANCFVGQVFPVCGGWVMR........
HheF      GRLGSAAEHAALSLFLASDQCNFISGQVVPFAGGWTT.........
HheB      GRLATAREDALLALFLASDESDFIVGKSIEFDGGWAT.........
HheE      NQVGSSEETAELAAYLASEKCNHMVGQIIPLAGGWAT.........
HheC      QRLGTQKELGELVAFLASGSCDYLTGQVFWLAGGFPMIERWPGMPE
HheG      RRLGTMDELSSVTAGLLDGSNRFQTGQFFDFSGGWGA.........
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Figure S4 Amino acid sequence alignment of halohydrin dehalogenases. HheA: The halohydrin dehalogenase from *Corynebacterium* sp. Strain N-1074 (GenBank Accession BAA14361.1). HheB: The halohydrin dehalogenase from *Mycobacterium* sp. GP1 (GenBank Accession AAK73175.1). HheC: The halohydrin dehalogenase from *Agrobacterium tumefaciens* (GenBank Accession AAK92099.1). HheA_J1: The putative halohydrin dehalogenase from *Microbacterium* sp. J1-1. HheD: Halohydrin dehalogenase (GenBank Accession AMQ13565.1). HheE: Halohydrin dehalogenase (GenBank Accession AMQ13570.1). HheF: Halohydrin dehalogenase (GenBank Accession AMQ13575.1). HheG: Halohydrin dehalogenase (GenBank Accession AMQ13576.1). Blue arrow: the conserve catalytic triad (Ser-Tyr-Arg) of halohydrin dehalogenases.

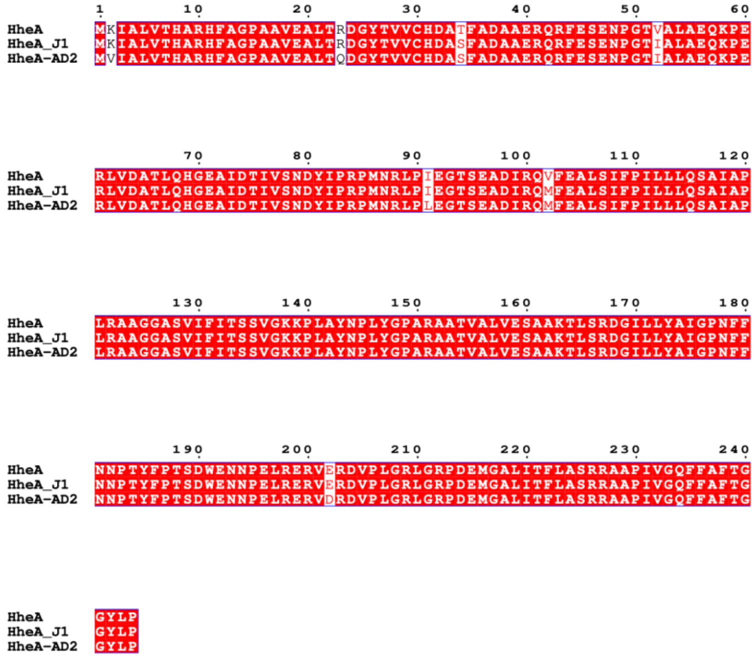

Figure S5 Amino acid sequence alignment of halohydrin dehalogenases of HheA halohydrin dehalogenases.

HheA: The halohydrin dehalogenase from *Corynebacterium* sp. Strain N-1074 (GenBank Accession BAA14361.1). HheA-AD2: The halohydrin dehalogenase from *Arthrobacter* sp. AD2 (GenBank Accession AAK92100.1). HheA_J1: The putative halohydrin dehalogenase from *Microbacterium* sp. J1-1.

Table S1 Organohalide sewage information

The physical and chemical data of organohalide sewage at different locations.

Location	Temperature (℃)	pH	COD (mg/L)	Cl^-(mg/L)
Raw water	50	>11.7	1,100–1,200	24,000–26,000
Aeration tank	35–38	6.5–6.9	280–330	23,000–24,000
Secondary sedimentation tank	33–36	6.5–6.9	230–250	23,000–24,000
Contact oxidation reactor	28–30	6.5–6.9	60–100	23,000–24,000
Final sedimentation tank	25–30	6.5–6.9	30–50	23,000–24,000

COD (Chemical oxygen demand): The amount of oxygen required for the chemical oxidation of organic compounds to inorganic products.

Table S2. Alpha diversity of organohalide sewage

The alpha diversity data of organohalide sewage at different locations.

	Simpson	Chao1	ACE	Shannon
	0.986774	1353.00	1353.00	8.36
Raw water	0.985574	1371.00	1371.00	8.35
	0.988694	1468.00	1468.00	8.49
	0.537006	583.29	589.89	2.97
Aeration tank	0.582560	496.33	525.56	3.17
	0.689960	451.00	451.00	3.61
	0.701489	818.62	821.35	3.77
Secondary sedimentation tank	0.735157	713.46	719.90	3.82
	0.942809	923.96	947.80	6.22
	0.982210	1152.00	1152.00	7.52
Contact oxidation reactor	0.974757	1447.00	1447.00	7.84
	0.982094	1224.00	1224.00	7.71
	0.973534	1529.66	1625.21	7.55
Final sedimentation tank	0.971725	1262.00	1262.00	7.54
	0.953481	1404.33	1374.26	6.70

Table S3. Quality evaluation of MAGs

The detailed information for completeness, contamination of MAG quality via MetaWRAP.

Location	Bin	Completeness	Contamination
Aeration tank	bin.10	95.93	0.949
Aeration tank	bin.11	86.17	2.482
Aeration tank	bin.12	99.18	1.434
Aeration tank	bin.13	91.39	1.728
Aeration tank	bin.14	98.65	0.223
Aeration tank	bin.15	93.25	3.184
Aeration tank	bin.16	99.41	0.904
Aeration tank	bin.17	75.86	0
Aeration tank	bin.18	78.31	1.41
Aeration tank	bin.19	92.18	4.545
Aeration tank	bin.1	74.14	0
Aeration tank	bin.20	73.93	0.561
Aeration tank	bin.21	77.43	1.442
Aeration tank	bin.22	99.5	0
Aeration tank	bin.23	98.75	0.069
Aeration tank	bin.24	74.82	0
Aeration tank	bin.25	99.05	1.342
Aeration tank	bin.26	93.93	0.202
Aeration tank	bin.27	86.24	4.267
Aeration tank	bin.28	73.48	3.636
Aeration tank	bin.29	93.76	1.006
Aeration tank	bin.2	76.3	2.808
Aeration tank	bin.30	99	2.093
Aeration tank	bin.3	77.41	0.172
Aeration tank	bin.4	72.36	1.123
Aeration tank	bin.5	94.15	0.802
Aeration tank	bin.6	88.36	2.075
Aeration tank	bin.7	98.3	4.538
Aeration tank	bin.8	93.75	2.875
Aeration tank	bin.9	93.83	2.525
Contact oxidation reactor	bin.10	70.29	1.98
Contact oxidation reactor	bin.11	96.16	2.003
Contact oxidation reactor	bin.12	95.49	0.315
Contact oxidation reactor	bin.13	94.36	1.692
Contact oxidation reactor	bin.14	95.59	3.048
Contact oxidation reactor	bin.15	98.87	0.277
Contact oxidation reactor	bin.16	98.77	0.081

Contact oxidation reactor	bin.17	77.95	1.638
Contact oxidation reactor	bin.18	81.96	4.186
Contact oxidation reactor	bin.19	99.05	0.599
Contact oxidation reactor	bin.1	74.14	0
Contact oxidation reactor	bin.20	90.52	3.478
Contact oxidation reactor	bin.21	94.2	3.62
Contact oxidation reactor	bin.22	96.99	1.227
Contact oxidation reactor	bin.23	74.88	2.247
Contact oxidation reactor	bin.24	95.94	0.19
Contact oxidation reactor	bin.25	89.98	1.287
Contact oxidation reactor	bin.26	84.45	1.724
Contact oxidation reactor	bin.27	100	0.54
Contact oxidation reactor	bin.28	99.28	0
Contact oxidation reactor	bin.29	98.24	0.66
Contact oxidation reactor	bin.2	97.81	0.757
Contact oxidation reactor	bin.30	72.93	1.123
Contact oxidation reactor	bin.31	96.62	0
Contact oxidation reactor	bin.32	80.78	2.777
Contact oxidation reactor	bin.33	92.69	1.298
Contact oxidation reactor	bin.34	96.32	1.308
Contact oxidation reactor	bin.35	96.44	1.421
Contact oxidation reactor	bin.36	95.29	1.219
Contact oxidation reactor	bin.37	74.68	3.097
Contact oxidation reactor	bin.38	93.73	1.698
Contact oxidation reactor	bin.39	94.76	0.048
Contact oxidation reactor	bin.3	96.87	3.415
Contact oxidation reactor	bin.40	93.85	0.433
Contact oxidation reactor	bin.41	75.86	0
Contact oxidation reactor	bin.42	99.91	0.144
Contact oxidation reactor	bin.43	95.65	1.536
Contact oxidation reactor	bin.44	86.09	1.047
Contact oxidation reactor	bin.45	93.29	0.42
Contact oxidation reactor	bin.46	93.01	1.208
Contact oxidation reactor	bin.47	70.8	0.102
Contact oxidation reactor	bin.48	90.13	2.452
Contact oxidation reactor	bin.49	92.41	0.505
Contact oxidation reactor	bin.4	72.28	1.937
Contact oxidation reactor	bin.50	97.53	1.498
Contact oxidation reactor	bin.51	81.46	1.477
Contact oxidation reactor	bin.52	99.64	2.456
Contact oxidation reactor	bin.53	71	1.724
Contact oxidation reactor	bin.54	72.41	1.724
Contact oxidation reactor	bin.55	97.01	3.755

Contact oxidation reactor	bin.56	97.27	0.414
Contact oxidation reactor	bin.57	75.33	4.286
Contact oxidation reactor	bin.58	93.74	1.403
Contact oxidation reactor	bin.59	99.41	1.462
Contact oxidation reactor	bin.5	88.5	4.57
Contact oxidation reactor	bin.60	93.66	0.706
Contact oxidation reactor	bin.61	95.79	0
Contact oxidation reactor	bin.62	77.01	2.945
Contact oxidation reactor	bin.63	94.48	0.755
Contact oxidation reactor	bin.64	97.34	0.497
Contact oxidation reactor	bin.6	76.89	0
Contact oxidation reactor	bin.7	98.45	1.111
Contact oxidation reactor	bin.8	90.61	0
Contact oxidation reactor	bin.9	96.78	0.301

Table S4. Taxonomic assignment results of AT MAGs
The taxonomic assignment results of AT MAGs via GTDB-tk

Genome	Phylum	Class	Order	Family	Genus	Species
bin.5	*Actinobacteriota*	*Actinobacteria*	*Propionibacteriales*	*Propionibacteriaceae*	*Tessaracoccus*	*lapidicaptus*
bin.3	*Thermotogota*	*Thermotogae*	*Petrotogales*	*Petrotogaceae*	*Petrotoga*	*mobilis*
bin.13	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	koll-22	UBA5081	sp002415785
bin.14	*Firmicutes_A*	*Clostridia*	*Oscillospirales*	*Ruminococcaceae*	*Pygmaiobacter*	NA
bin.8	*Actinobacteriota*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Microbacterium*	NA
bin.23	*Actinobacteriota*	*Actinobacteria*	*Actinomycetales*	*Actinomycetaceae*	KH17	NA
bin.20	*Patescibacteria*	*Gracilibacteria*	BD1-5	UBA6164	UBA7396	NA
bin.4	*Patescibacteria*	*Microgenomatia*	UBA1406	GWC2-37-13	NA	NA
bin.19	*Chloroflexota*	*Anaerolineae*	SBR1031	UBA2029	NA	NA
bin.28	*Chloroflexota*	*Anaerolineae*	*Promineofilales*	*Promineofilaceae*	NA	NA
bin.6	*Chloroflexota*	*Chloroflexia*	*Chloroflexales*	*Chloroflexaceae*	NA	NA
bin.24	*Spirochaetota*	*Spirochaetia*	*Sphaerochaetales*	*Sphaerochaetaceae*	*Sphaerochaeta*	NA
bin.22	*Bacteroidota*	*Bacteroidia*	*Chitinophagales*	ND	NA	NA
bin.7	*Bacteroidota*	*Rhodothermia*	*Rhodothermales*	MEBICO9517	NA	NA
bin.27	*Proteobacteria*	*Gammaproteobacteria*	*Xanthomonadales*	*Wenzhouxiangellaceae*	GCA-2722315	NA
bin.17	*Proteobacteria*	*Gammaproteobacteria*	NA	NA	NA	NA
bin.25	*Proteobacteria*	*Alphaproteobacteria*	*Rickettsiales*	NA	NA	NA
bin.29	*Firmicutes_A*	*Clostridia*	*Oscillospirales*	*Oscillospiraceae*	*Intestinimonas*	NA
bin.21	*Firmicutes_A*	*Clostridia*	*Clostridiales*	*Clostridiaceae*	NA	NA
bin.2	*Patescibacteria*	*Saccharimonadia*	*Saccharimonadales*	SZUA-47	NA	NA

bin.16	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Rhizobiaceae*	*Martelella*	NA
bin.26	*Proteobacteria*	*Alphaproteobacteria*	*Rhodobacterales*	*Rhodobacteraceae*	NA	NA
bin.9	*Proteobacteria*	*Alphaproteobacteria*	*Rhodobacterales*	*Rhodobacteraceae*	UBA996	NA
bin.30	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Thalassospiraceae*	*Thalassospira*	NA
bin.15	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Thalassospiraceae*	*Thalassospira*	NA
bin.18	*Campylobacterota*	*Campylobacteria*	*Campylobacterales*	NA	NA	NA
bin.12	*Campylobacterota*	*Campylobacteria*	*Campylobacterales*	*Sulfurimonadaceae*	*Sulfurimonas*	NA

Unclassified Family/Genus/Species are indicated as 'NA', not available.

Table S5. Taxonomic assignment results of COR MAGs

The taxonomic assignment results of COR MAGs via GTDB-tk.

Genome	Phylum	Class	Order	Family	Genus	Species
bin.46	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	koll-22	UBA5081	sp002415785
bin.34	*Proteobacteria*	*Gammaproteobacteria*	*Francisellales*	*Francisellaceae*	*Allofrancisella*	*guangzhouensis*
bin.23	*Patescibacteria*	*Paceibacteria*	UBA9983_A	UBA1006	UBA1006	NA
bin.26	*Patescibacteria*	*Paceibacteria*	UBA9983_A	UBA1006	UBA1006	NA
bin.47	*Patescibacteria*	*Paceibacteria*	UBA6257	UBA9933	WO2-47-17b	NA
bin.10	*Patescibacteria*	ABY1	BM507	XYC2-FULL-47-12	NA	NA
bin.30	*Patescibacteria*	*Microgenomatia*	UBA1406	GWC2-37-13	NA	NA
bin.6	*Chloroflexota*	*Dehalococcoidia*	*Dehalococcoidales*	*Dehalococcoidaceae*	*Dehalogenimonas*	NA
bin.31	*Verrucomicrobiota*	*Verrucomicrobiae*	*Opitutales*	UBA3534	NA	NA
bin.44	*VerrucomicrobiotaA*	*Chlamydiia*	*Parachlamydiales*	*Simkaniaceae*	*Simkania*	NA
bin.63	*VerrucomicrobiotaA*	*Chlamydiia*	*Parachlamydiales*	*Simkaniaceae*	NA	NA
bin.37	*Bacteroidota*	*Bacteroidia*	*Bacteroidales*	*Marinilabiliaceae*	*Marinilabilia*	NA
bin.28	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	*Cryomorphaceae*	NA	NA
bin.7	*Bacteroidota*	*Bacteroidia*	*Sphingobacteriales*	*Sphingobacteriaceae*	NA	NA
bin.51	*Bacteroidota*	*Bacteroidia*	*Chitinophagales*	*Chitinophagaceae*	*Taibaiella_B*	NA
bin.49	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacterales*	*Alteromonadaceae*	*Idiomarina*	NA
bin.3	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacterales*	*Alteromonadaceae*	*Idiomarina*	NA
bin.33	*Proteobacteria*	*Gammaproteobacteria*	UBA5158	UBA5158	2-12-FULL-43-28	NA
bin.62	*Proteobacteria*	*Gammaproteobacteria*	NA	NA	NA	NA
bin.55	*Proteobacteria*	*Gammaproteobacteria*	*Nitrococcales*	NA	NA	NA

bin.11	*Proteobacteria*	*Gammaproteobacteria*	*Nitrococcales*	NA	NA	NA
bin.52	*Proteobacteria*	*Gammaproteobacteria*	*Nitrococcales*	NA	NA	NA
bin.14	*Proteobacteria*	*Gammaproteobacteria*	*Nitrococcales*	NA	NA	NA
bin.22	*Proteobacteria*	*Gammaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Pusillimonas*	NA
bin.5	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Rhizobiaceae*	*Pararhizobium_A*	NA
bin.48	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Amorphaceae*	*Amorphus*	NA
bin.57	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Methylopilaceae*	Ga0077545	NA
bin.43	*Proteobacteria*	*Alphaproteobacteria*	*Parvibaculales*	*Parvibaculaceae*	*Parvibaculum*	NA
bin.18	*Proteobacteria*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	*Altererythrobacter_A*	NA
bin.40	*Proteobacteria*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingopyxis*	NA
bin.54	*Proteobacteria*	*Alphaproteobacteria*	Bin95	Bin95	NA	NA
bin.20	*Proteobacteria*	*Alphaproteobacteria*	*Micavibrionales*	UBA2020	NA	NA
bin.42	*Proteobacteria*	*Alphaproteobacteria*	UBA8366	GCA-2696645	NA	NA
bin.41	*Proteobacteria*	*Alphaproteobacteria*	UBA8366	GCA-2696645	NA	NA
bin.8	*Proteobacteria*	*Alphaproteobacteria*	NA	NA	NA	NA
bin.15	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Oleiphilaceae*	*Marinobacter*	*subterrani*
bin.59	*Proteobacteria*	*Gammaproteobacteria*	*Francisellales*	*Francisellaceae*	*Francisella*	*hispaniensis*
bin.36	*Proteobacteria*	*Gammaproteobacteria*	*Thiomicrospirales*	*Thiomicrospiraceae*	*Hydrogenovibrio*	sp000711305
bin.56	*Proteobacteria*	*Alphaproteobacteria*	*Rhodobacterales*	*Rhodobacteraceae*	*Thioclava*	*marina*
bin.17	*FirmicutesI*	*Bacilli_A*	*Paenibacillales*	*Paenibacillaceae*	NA	NA
bin.39	*FirmicutesI*	*Bacilli_A*	*Paenibacillales*	NA	NA	NA
bin.45	*Actinobacteriota*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Yonghaparkia*	NA
bin.2	*Actinobacteriota*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	73-13	NA
bin.25	*Actinobacteriota*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Microbacterium*	NA
bin.13	*Actinobacteriota*	*Actinobacteria*	*Propionibacteriales*	*Nocardioidaceae*	*Aeromicrobium*	NA

bin.24	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	*Flavobacteriaceae*	NA	NA
bin.29	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	*Flavobacteriaceae*	*Galbibacter*	NA
bin.60	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*	NA
bin.32	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium_A*	NA
bin.27	*Bacteroidota*	*Bacteroidia*	*Flavobacteriales*	*Crocinitomicaceae*	UBA5422	NA
bin.61	*Bacteroidota*	*Kapabacteria*	*Kapabacteriales*	GCA-002839825	PGYR01	NA
bin.50	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacterales*	*Alteromonadaceae*	*Idiomarina*	NA
bin.4	*Proteobacteria*	*Gammaproteobacteria*	*Legionellales*	*Legionellaceae*	*Legionella_D*	NA
bin.58	*Proteobacteria*	*Gammaproteobacteria*	*Legionellales*	*Legionellaceae*	*Legionella_A*	NA
bin.53	*Proteobacteria*	*Gammaproteobacteria*	*Thiomicrospirales*	*Thiomicrospiraceae*	*Hydrogenovibrio*	NA
bin.12	*Proteobacteria*	*Gammaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Candidimonas*	NA
bin.38	*Proteobacteria*	*Gammaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Candidimonas*	NA
bin.35	*Proteobacteria*	*Gammaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	NA	NA
bin.19	*Proteobacteria*	*Gammaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	NA	NA
bin.16	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Rhizobiaceae*	*Aquamicrobium_A*	NA
bin.21	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Rhizobiaceae*	*Aliihoeflea*	NA
bin.9	*Proteobacteria*	*Alphaproteobacteria*	*Rhodobacterales*	*Rhodobacteraceae*	NA	NA
bin.64	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales_A*	*Thalassospiraceae*	*Thalassospira*	NA

Unclassified Order/Family/Genus/Species are indicated as 'NA', not available.

Table S6. The distribution of dehalogenase in MAGs

Gene numbers of four types of dehalogenases in different MAGs.

Genome	**2-haloacid dehalogenase**	**haloacetate dehalogenase**	**haloalkane dehalogenase**	**4-chlorobenzoyl coenzyme A dehalogenase**
AT_Chloroflexaceae_bin.6	1	3	2	0
AT_Rhodothermales_bin.7	0	1	4	0
AT_Microbacterium_bin.8	0	1	0	1
AT_Rhodobacteraceae_bin.9	1	1	0	2
AT_Thalassospira_bin.15	1	1	0	0
AT_Martelella_bin.16	0	2	0	0
AT_Anaerolineae_bin.19	0	1	1	0
AT_Rhodobacteraceae_bin.26	1	1	0	0
AT_Wenzhouxiangellaceae_bin.27	0	0	1	0
AT_Promineofilaceae_bin.28	1	1	2	1
AT_Thalassospira_bin.30	1	0	0	0
COR_Idiomarina_bin.3	0	0	1	1
COR_Pararhizobium_bin.5	2	1	0	0
COR_Rhodobacteraceae_bin.9	1	1	0	0
COR_Nitrococcales_bin.11	1	2	0	0
COR_Candidimonas_bin.12	2	0	0	0
COR_Nitrococcales_bin.14	1	0	2	1
COR_Marinobacter_bin.15	1	0	2	0
COR_Aquamicrobium_bin.16	1	1	2	0
COR_Altererythrobacter_bin.18	0	1	0	0
COR_Burkholderiaceae_bin.19	2	2	0	0
COR_Rhizobiaceae_bin.21	1	0	0	1
COR_Pusillimonas_bin.22	1	0	1	0
COR_Microbacterium_bin.25	0	1	0	1
COR_Opitutales_bin.31	0	0	1	0
COR_UBA5158_bin.33	0	1	1	0
COR_Marinilabilia_bin.37	2	0	0	0
COR_Candidimonas_bin.38	3	0	0	0
COR_Sphingopyxis_bin.40	0	1	0	0
COR_UBA8366_bin.41	1	1	0	0
COR_UBA8366_bin.42	1	1	0	0
COR_Parvibaculum_bin.43	0	0	1	0
COR_Simkania_bin.44	0	0	1	0
COR_Yonghaparkia_bin.45	0	0	1	0
COR_Amorphus_bin.48	1	2	0	1
COR_Idiomarina_bin.49	0	1	1	0

COR_Idiomarina_bin.50	0	0	1	0
COR_Nitrococcales_bin.52	0	1	0	1
COR_Bin95_bin.54	3	1	4	0
COR_Nitrococcales_bin.55	0	1	1	0
COR_Thioclava_bin.56	2	1	0	0
COR_Thalassospiraceae_bin.64	1	0	0	0

Table S7. The significantly different metabolism pathways between locations
The significantly different metabolism pathways between locations based on the non-targeted metabolomics data.

	Pathway Name	**Pathway ID**	**Pvalue**	**Compounds**
RW/AT	Tyrosine metabolism	edi00350	0.0238	C03964|(R)-3-(4-Hydroxyphenyl) lactate; C00042|Succinate
RW/AT	Oxidative phosphorylation	edi00190	0.049	C00042|Succinate
AT/COR	Tyrosine metabolism	edi00350	0.00498	C03964|(R)-3-(4-Hydroxyphenyl) lactate; C00042|Succinate
AT/COR	Oxidative phosphorylation	edi00190	0.0229	C00042|Succinate
AT/COR	Pantothenate and CoA biosynthesis	edi00770	0.0398	C01053|(R)-4-Dehydropantoate
AT/COR	Alanine, aspartate, and glutamate metabolism	edi00250	0.0398	C00042|Succinate
AT/COR	Pyruvate metabolism	edi00620	0.044	C00042|Succinate
AT/COR	Sulfur metabolism	edi00920	0.0468	C00042|Succinate

Table S8. The antibiotic resistance ontology of the MAGs.

The potential ARO genes of the MAGs were predicted via RGI and CARD.

MAG	Taxonomy_MAG	Name	ARO	Resistance Mechanism
AT_bin.12	*Campylobacterales*	*qac*J	3007014	antibiotic efflux
AT_bin.14	*Oscillospirale*	*nim*I	3007111	antibiotic inactivation
AT_bin.15	*Rhodospirillales*	*qac*J	3007014	antibiotic efflux
AT_bin.16	*Rhizobiales*	*ade*F	3000777	antibiotic efflux
AT_bin.16	*Rhizobiales*	*qac*J	3007014	antibiotic efflux
AT_bin.21	*Clostridiales*	*van*R	3003728	antibiotic target alteration
AT_bin.21	*Clostridiales*	*gyr*B	3004562	antibiotic target alteration
AT_bin.26	*Rhodobacterales*	*qac*G	3007015	antibiotic efflux
AT_bin.30	*Rhodospirillales*	*qac*J	3007014	antibiotic efflux
AT_bin.30	*Rhodospirillales*	*ade*F	3000777	antibiotic efflux
AT_bin.30	*Rhodospirillales*	*ade*F	3000777	antibiotic efflux
COR_bin.5	*Rhizobiales*	*qac*G	3007015	antibiotic efflux
COR_bin.9	*Rhodobacterales*	*qac*G	3007015	antibiotic efflux
COR_bin.12	*Burkholderiales*	*qac*G	3007015	antibiotic efflux
COR_bin.12	*Burkholderiales*	*ade*F	3000777	antibiotic efflux
COR_bin.12	*Burkholderiales*	*qac*G	3007015	antibiotic efflux
COR_bin.14	*Nitrococcales*	*ade*F	3000777	antibiotic efflux
COR_bin.15	*Pseudomonadales*	*rsm*A	3005069	antibiotic efflux
COR_bin.15	*Pseudomonadales*	*qac*G	3007015	antibiotic efflux
COR_bin.16	*Rhizobiales*	*qac*G	3007015	antibiotic efflux
COR_bin.19	*Burkholderiales*	*ade*F	3000777	antibiotic efflux
COR_bin.19	*Burkholderiales*	*qac*G	3007015	antibiotic efflux
COR_bin.21	*Rhizobiales*	*qac*G	3007015	antibiotic efflux
COR_bin.22	*Burkholderiales*	*qac*G	3007015	antibiotic efflux
COR_bin.27	*Flavobacteriales*	*ade*F	3000777	antibiotic efflux
COR_bin.29	*Flavobacteriales*	*ade*F	3000777	antibiotic efflux
COR_bin.31	*Opitutales*	*ade*F	3000777	antibiotic efflux
COR_bin.35	*Burkholderiales*	*ade*F	3000777	antibiotic efflux
COR_bin.35	*Burkholderiales*	*ade*F	3000777	antibiotic efflux
COR_bin.35	*Burkholderiales*	*qac*G	3007015	antibiotic efflux
COR_bin.36	*Thiomicrospirales*	*ade*F	3000777	antibiotic efflux
COR_bin.36	*Thiomicrospirales*	*ade*F	3000777	antibiotic efflux
COR_bin.38	*Burkholderiales*	*qac*J	3007014	antibiotic efflux
COR_bin.38	*Burkholderiales*	*qac*G	3007015	antibiotic efflux
COR_bin.40	*Sphingomonadales*	*ade*F	3000777	antibiotic efflux
COR_bin.40	*Sphingomonadales*	*ade*F	3000777	antibiotic efflux
COR_bin.43	*Parvibaculales*	*ade*F	3000777	antibiotic efflux
COR_bin.48	*Rhizobiales*	*qac*G	3007015	antibiotic efflux
COR_bin.49	*Enterobacterales*	*rsm*A	3005069	antibiotic efflux

COR_bin.50	*Enterobacterales*	*rsm*A	3005069	antibiotic efflux
COR_bin.52	*Nitrococcales*	*ade*F	3000777	antibiotic efflux
COR_bin.53	*Thiomicrospirales*	*ade*F	3000777	antibiotic efflux
COR_bin.55	*Nitrococcales*	*ade*F	3000777	antibiotic efflux
COR_bin.56	*Rhodobacterales*	*qac*G	3007015	antibiotic efflux
COR_bin.57	*Rhizobiales*	*ade*F	3000777	antibiotic efflux
COR_bin.59	*Francisellales*	*qac*J	3007014	antibiotic efflux
COR_bin.60	*Flavobacteriales*	*ade*F	3000777	antibiotic efflux
COR_bin.60	*Flavobacteriales*	*ade*F	3000777	antibiotic efflux
COR_bin.64	*Rhodospirillales*	*ade*F	3000777	antibiotic efflux
COR_bin.64	*Rhodospirillales*	*qac*J	3007014	antibiotic efflux
COR_bin.64	*Rhodospirillales*	*ade*F	3000777	antibiotic efflux