

Supporting Information

Exploring methane capture potential in alkaline coal mine drainage: Insight from the microbial community structure and function analysis

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Figure S1 Characteristics of water samples sites from the neutral coal mine drainage in five different coal mining areas: hydrogeochemical characteristics (a) and hydrogen-oxygen isotopes (b). Colored hollow circles also indicate the coal mine drainage sampling sites ,while the diameter of the colored hollow circles indicates the content of total dissolved solids. Dark blue, red, green, yellow and light blue represent sampling points XTW01, NT01, HY01, DL01 and YTB01, respectively

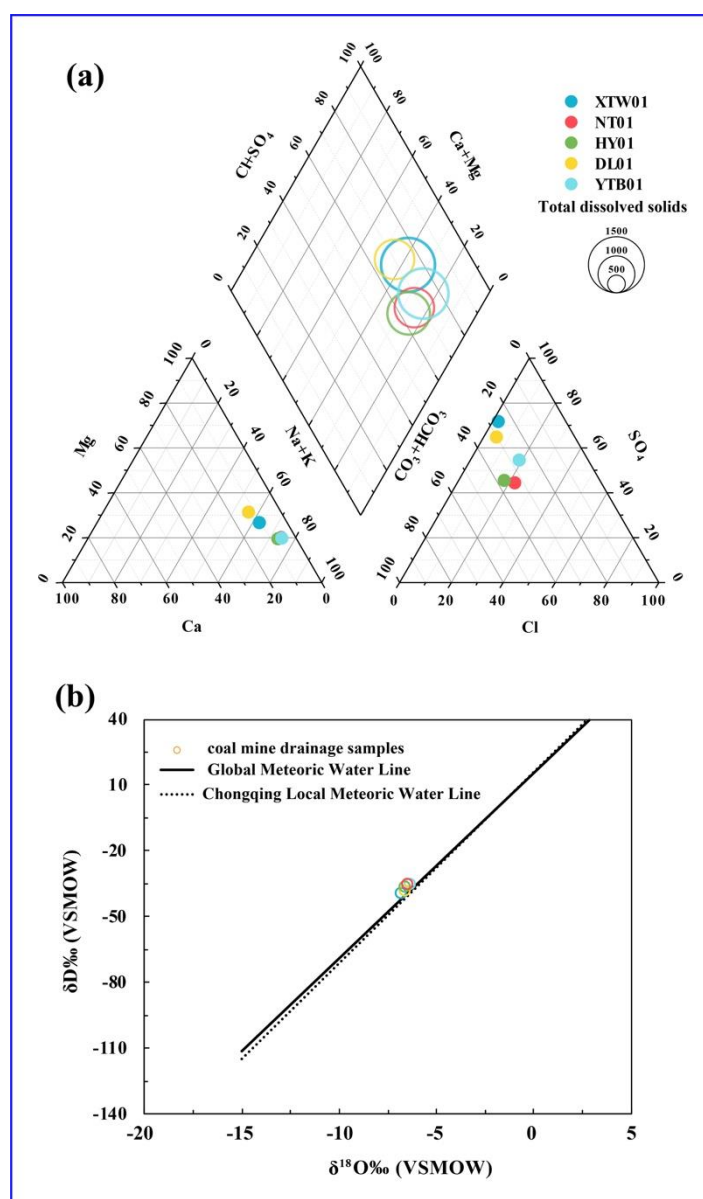


Table S1 Sequence information and alpha diversity of microbial community of water samples from alkaline coal mine drainage.

	Raw sequence	Clean sequence	coverage	Shannon	Simpson	Chao1
DL01	83847	79081	0.99	4.96	0.96	591
HY01	83867	78821	0.99	5.99	0.99	684
NT01	83972	79077	1.00	4.34	0.94	314
XTW01	84000	78012	0.99	5.70	0.99	637
YTB01	84000	78359	0.99	3.54	0.89	346

Table S2 Spearman correlations between hydrogeochemical parameters and genera occurred in at least four water samples from alkaline coal mine drainage.

	TDS	pH	Nitrate	Sulfate	NH4	Carbonate	Bicarbonate	DOC
<i>unclassified_Firmicutes</i>	0.10	0.36	0.31	-0.56	-0.80	-0.05	0.10	0.05
<i>Candidatus_Jorgensenbacteria</i>	-0.15	-0.05	-0.82	-0.21	-0.06	-0.21	-0.15	0.05
<i>Aeromonas</i>	-0.10	0.20	0.90	-0.40	-0.67	0.10	-0.10	-0.30
<i>Pseudorhodobacter</i>	0.36	0.10	-0.72	0.21	0.34	-0.05	0.36	0.56
<i>Pseudohongiella</i>	-0.62	0.67	0.36	-0.87	-0.80	0.67	-0.62	-0.05
<i>Geothrix</i>	-0.62	0.67	0.36	-0.87	-0.80	0.67	-0.62	-0.05
<i>Methylovulum</i>	-0.10	-0.70	-0.60	0.60	0.78	-0.40	-0.10	-0.30
<i>unclassified_Oxalobacteraceae</i>	-0.10	-0.70	-0.60	0.60	0.78	-0.40	-0.10	-0.30
<i>Thiothrix</i>	0.50	0.70	-0.10	0.10	0.22	0.60	0.50	1.00
<i>Phreatobacter</i>	0.10	-0.20	-0.60	0.60	0.89	0.10	0.10	0.30
<i>unclassified_Halothiobacillaceae</i>	0.00	0.10	-0.80	0.30	0.67	0.30	0.00	0.50
<i>Sulfurimonas</i>	0.10	0.50	-0.60	0.10	0.45	0.60	0.10	0.80
<i>unclassified_Saprospiraceae</i>	0.10	0.50	-0.60	0.10	0.45	0.60	0.10	0.80
<i>unclassified_Cytophagales</i>	0.10	0.50	-0.60	0.10	0.45	0.60	0.10	0.80
<i>unclassified_Bacteroidia</i>	0.30	0.60	-0.20	0.20	0.45	0.70	0.30	0.90
<i>Faecalibacterium</i>	0.30	0.60	-0.20	0.20	0.45	0.70	0.30	0.90
<i>Brevundimonas</i>	0.30	0.90	0.20	-0.20	-0.11	0.80	0.30	0.90
<i>Nitrospira</i>	-0.50	0.40	0.30	-0.30	-0.11	0.70	-0.50	0.00
<i>Sediminibacterium</i>	-0.50	0.40	0.30	-0.30	-0.11	0.70	-0.50	0.00
<i>unclassified_Sphingomonadacea</i>	0.20	0.50	0.30	0.20	0.34	0.70	0.20	0.60
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<i>Sulfuricurvum</i>	-0.60	0.00	0.10	-0.10	0.11	0.40	-0.60	-0.30
<i>Sporichthyaceae</i>	-0.60	0.00	0.10	-0.10	0.11	0.40	-0.60	-0.30
<i>hgcI_clade</i>	-0.60	0.00	0.10	-0.10	0.11	0.40	-0.60	-0.30
<i>Rheinheimera</i>	-0.80	-0.10	-0.30	-0.20	0.11	0.30	-0.80	-0.40
<i>A0839</i>	-0.80	-0.10	-0.30	-0.20	0.11	0.30	-0.80	-0.40
<i>Kapabacteriales</i>	-0.60	0.30	0.50	-0.50	-0.45	0.50	-0.60	-0.30
<i>Hyphomonas</i>	-0.10	0.30	0.40	0.10	0.22	0.60	-0.10	0.20
<i>Terrimonas</i>	-0.56	0.21	0.21	-0.21	0.00	0.56	-0.56	-0.15
<i>unclassified_Hydrogenophilaceae</i>	0.50	-0.80	0.40	0.60	0.22	-0.90	0.50	-0.50
<i>JGI_0000069-P22</i>	0.50	-0.80	0.40	0.60	0.22	-0.90	0.50	-0.50
<i>Candidatus_Collierbacteria</i>	0.50	-0.80	0.40	0.60	0.22	-0.90	0.50	-0.50
<i>Methylomonas</i>	0.70	0.10	0.30	0.70	0.67	0.20	0.70	0.60
<i>MM1</i>	0.80	-0.60	0.30	0.70	0.34	-0.80	0.80	-0.10
<i>Candidatus_Omnitrophus</i>	0.90	-0.50	0.10	0.90	0.67	-0.60	0.90	0.20
<i>unclassified_Burkholderiales</i>	0.40	-0.80	0.10	0.90	0.78	-0.60	0.40	-0.30
<i>Candidatus_Obscuribacter</i>	0.40	-0.80	0.10	0.90	0.78	-0.60	0.40	-0.30
<i>unclassified_Rhodocyclaceae</i>	0.70	0.00	0.80	0.20	-0.22	-0.30	0.70	0.10
<i>unclassified_Bacteria</i>	0.90	0.20	0.40	0.60	0.45	0.10	0.90	0.70
<i>Parcubacteria</i>	0.90	0.20	0.40	0.60	0.45	0.10	0.90	0.70
<i>Syntrophus</i>	0.90	0.20	0.40	0.60	0.45	0.10	0.90	0.70
<i>Candidatus_Magasanikbacteria</i>	0.90	0.20	0.40	0.60	0.45	0.10	0.90	0.70
<i>Blfdi19</i>	0.30	-0.90	0.00	0.50	0.22	-1.00	0.30	-0.60
<i>Gallionellaceae</i>	0.60	-0.30	0.10	0.90	0.89	-0.10	0.60	0.30
<i>Sideroxydans</i>	0.60	-0.30	0.10	0.90	0.89	-0.10	0.60	0.30

<i>Methylothera</i>	0.60	-0.30	0.10	0.90	0.89	-0.10	0.60	0.30
<i>Candidatus_Komeilibacteria</i>	0.60	-0.30	0.10	0.90	0.89	-0.10	0.60	0.30
<i>unclassified_Anaerolineaceae</i>	0.30	-0.50	0.20	0.80	0.78	-0.20	0.30	-0.10
<i>unclassified_Rhizobiaceae</i>	0.30	-0.50	0.20	0.80	0.78	-0.20	0.30	-0.10
<i>Ferritrophicum</i>	0.30	-0.50	0.20	0.80	0.78	-0.20	0.30	-0.10
<i>unclassified_Methylophilaceae</i>	0.00	-0.30	-0.10	0.60	0.78	0.10	0.00	0.00
<i>unclassified_Thermodesulfovibrio</i>	0.70	-0.60	0.00	1.00	0.89	-0.50	0.70	0.10
<i>unclassified_Methylomonadaceae</i>	0.70	-0.60	0.00	1.00	0.89	-0.50	0.70	0.10
<i>unclassified_Alphaproteobacteria</i>	0.70	-0.60	0.00	1.00	0.89	-0.50	0.70	0.10
<i>unclassified_Gammaproteobacteria</i>	0.21	-0.41	0.36	0.67	0.63	-0.10	0.21	-0.15
<i>UBA9983</i>	0.90	-0.20	0.50	0.50	0.11	-0.50	0.90	0.20
<i>Candidatus_Woesebacteria</i>	0.67	-0.10	0.21	0.82	0.80	0.05	0.67	0.46
<i>unclassified_Parcubacteria</i>	0.87	-0.41	0.41	0.62	0.23	-0.67	0.87	0.05
<i>Candidatus_Moranbacteria</i>	0.41	-0.87	0.36	0.67	0.34	-0.87	0.41	-0.56
<i>unclassified_Caulobacteraceae</i>	0.50	-0.70	-0.40	0.90	0.89	-0.60	0.50	0.00
<i>Omnitrophales</i>	1.00	-0.10	0.30	0.70	0.45	-0.30	1.00	0.50
<i>unclassified_Desulfobacterota</i>	0.90	0.20	0.10	0.40	0.22	-0.10	0.90	0.70
<i>Pajaroellobacter</i>	0.90	0.20	0.10	0.40	0.22	-0.10	0.90	0.70
<i>Caulobacter</i>	0.80	0.50	0.20	0.30	0.22	0.30	0.80	0.90
<i>Candidatus_Megaira</i>	0.40	-0.20	0.90	0.10	-0.34	-0.40	0.40	-0.30
<i>Legionella</i>	0.32	-0.79	0.53	0.53	0.18	-0.79	0.32	-0.63
<i>unclassified_Holosporaceae</i>	0.00	-0.40	0.70	0.30	0.11	-0.20	0.00	-0.50

<i>Rhodobacter</i>	0.10	-0.30	0.50	0.50	0.45	0.00	0.10	-0.20
<i>Candidatus_Falkowbacteria</i>	0.82	0.15	0.36	0.67	0.57	0.15	0.82	0.67
<i>unclassified_Zavarziniales</i>	0.05	-0.36	0.62	0.41	0.29	-0.10	0.05	-0.36
<i>Novosphingobium</i>	-0.10	-0.50	0.60	-0.10	-0.45	-0.60	-0.10	-0.80
<i>unclassified_Rhodobacteraceae</i>	-0.10	0.20	0.60	-0.60	-0.89	-0.10	-0.10	-0.30
<i>unclassified_Moraxellaceae</i>	-0.50	0.80	-0.40	-0.60	-0.22	0.90	-0.50	0.50
<i>A4b</i>	-0.50	0.80	-0.40	-0.60	-0.22	0.90	-0.50	0.50
<i>Haliangium</i>	-0.50	0.80	-0.40	-0.60	-0.22	0.90	-0.50	0.50
<i>unclassified_Comamonadaceae</i>	-0.70	-0.10	-0.30	-0.70	-0.67	-0.20	-0.70	-0.60
<i>unclassified_Cryomorphaceae</i>	-0.80	0.60	-0.30	-0.70	-0.34	0.80	-0.80	0.10
<i>Thiobacillus</i>	-0.80	0.60	-0.30	-0.70	-0.34	0.80	-0.80	0.10
<i>Algoriphagus</i>	-0.80	0.60	-0.30	-0.70	-0.34	0.80	-0.80	0.10
<i>Rhodoferax</i>	-0.80	0.60	-0.30	-0.70	-0.34	0.80	-0.80	0.10
<i>Hydrogenophaga</i>	-0.90	0.50	-0.10	-0.90	-0.67	0.60	-0.90	-0.20
<i>NS11-12_marine_group</i>	-0.90	0.50	-0.10	-0.90	-0.67	0.60	-0.90	-0.20
<i>unclassified_Microbacteriaceae</i>	-0.90	0.50	-0.10	-0.90	-0.67	0.60	-0.90	-0.20
<i>Sulfurovum</i>	-0.70	0.00	-0.80	-0.20	0.22	0.30	-0.70	-0.10
<i>Marinoscillum</i>	-0.70	0.00	-0.80	-0.20	0.22	0.30	-0.70	-0.10
<i>Sphingobium</i>	-0.70	0.00	-0.80	-0.20	0.22	0.30	-0.70	-0.10
<i>Pseudomonas</i>	-0.90	-0.20	-0.40	-0.60	-0.45	-0.10	-0.90	-0.70
<i>Flavobacterium</i>	-0.30	0.90	0.00	-0.50	-0.22	1.00	-0.30	0.60
<i>Haliscomenobacter</i>	-0.30	0.90	0.00	-0.50	-0.22	1.00	-0.30	0.60
<i>Fluviicola</i>	-0.30	0.90	0.00	-0.50	-0.22	1.00	-0.30	0.60
<i>Arenimonas</i>	-0.46	0.82	0.05	-0.56	-0.29	0.97	-0.46	0.41
<i>Polynucleobacter</i>	-0.70	0.60	0.00	-1.00	-0.89	0.50	-0.70	-0.10

<i>Thiofaba</i>	-0.90	0.20	-0.50	-0.50	-0.11	0.50	-0.90	-0.20
<i>Sphingorhabdus</i>	-0.60	0.70	0.10	-0.60	-0.34	0.90	-0.60	0.20
<i>Thiovirga</i>	-1.00	0.10	-0.30	-0.70	-0.45	0.30	-1.00	-0.50
<i>Aurantimicrobium</i>	-1.00	0.10	-0.30	-0.70	-0.45	0.30	-1.00	-0.50
<i>Inhella</i>	-0.60	-0.30	-0.60	0.10	0.45	0.10	-0.60	-0.30
<i>Lentimicrobium</i>	-0.41	-0.36	-0.56	0.31	0.63	0.05	-0.41	-0.21