Table S1. Analysis of major metal ion concentrations in paddy soils in this study

Sample	Al^{3+} (μg/g)	Si^{+} (μg/g)	Mn^{2+} (μg/g)	Fe^{3+} (μg/g)	Cu^{2+} (μg/g)	Zn^{2+} (μg/g)	Ga^{3+} (μg/g)	Sr^{2+} (μg/g)	Ba^{2+} (μg/g)	Na^{+} (μg/g)	Mg^{2+} (μg/g)	Ca^{2+} (μg/g)	K^{+} (μg/g)
1H	685	775	13.75	408	0	27.4	0	97.5	85.5	181.5	1790	18400	3240
8Y	81.5	935	49.95	306	4.525	56.5	1.67	70.5	187	254	5970	49100	1510
9Y	515	885	18.25	348	46.4	30.7	7.75	43.55	415	106.5	4120	40200	1470
14Y	106.5	183.5	19.7	53.5	0	32	6.4	22.15	363.5	210	1230	6870	350
16Y	133.5	320	142	113	0	35.35	6.05	24.05	348	165	742	7100	2440
3G	186.5	980	1.21	167	2.265	44.55	6.9	23.65	380.5	150.5	3760	21600	1330
7S	466	490.5	6.2	283.5	0	21.8	7.6	202	420.5	247	2360	47700	1520
4J	170.5	600	2.525	142	2.275	35.25	5.05	28.75	313	90.5	3680	19700	981
6D	138.5	650	3.715	191	2.245	31.3	6.3	35.1	368.5	104	4930	42300	1050
5M	114	271	12.25	158	0.244	26.1	4.775	24	310	165.5	4750	15400	1290

Table S2. Mineralogical characterization of the paddy soils used in this study

Sample	Quartz (%)	Feldspar (%)	Illite (%)	Montmorillonite (%)	Kaolinite (%)	Calcite (%)	Dolomite (%)	Anatase (%)	Hornblende (%)	Iron minerals (%)	Gibbsite (%)	Chlorite (%)
8Y	√	√	√	√	√	√	√					
14Y	√		√	√	√			√				
16Y	√	√	√	√	√			√	√			
1H	86.29	1.24	1.11	3.12	√	√	√	1.02	0.62	1.55	2.62	2.43
9Y	78.81	6	2.75	1.01	0.71	1.03	8.82	0.87				
7S	70.68	6.22	8.44	2.11	√	7.35	0.55	1.02				3.01
6D	62.96	5.62	5.16	2.5		4．36	15.27		√	0.62		3.55
5M	85.64	10.65	2.15	√	0.56	√	√	1			√	
4J	77.03	11.35	5.12	1.25	√	√	1.65	0.78	√			2.82
3G	72.8	16.25	2.92	3.05	0.68	√	1.68	1.54	√			

Note: √ indicates near the detection limit or not quantified, and blanks indicate non-detectable.

Table S3. Description of 454 pyrosequencing libraries annotated in MG-RAST.

Sample	MG-RAST ID	bp Count	Sequence Count	Bacteria	Archaea	Eukaryote	Unassigned	Alpha Diversity
Bacterial primers								
14Y	4550440	2,297,360	4,757	4,152		265	250	82.6
16Y	4550442	5,762,609	11,990	10,735	0	628	530	94.4
3G	4550446	2,202,890	4,535	4,023	0	231	183	58.5
4J	4550448	2,942,967	6,102	5,132	0	396	307	67.7
5M	4550449	2,799,100	5,801	5,010	0	320	402	79.3
6D	4550451	3,768,733	7,753	6,847	0	465	235	68.3
7S	4550453	9,655,896	19,982	18,278	0	1,119	623	75.8
8Y	4550455	1,920,966	3,949	3,467	0	309	108	55.4
9Y	4550457	3,989,808	8,205	7,559	0	515	239	59.1
HX1	4550459	7,833,746	16,263	13,908	0	892	862	77.7
Archaeal primers								
14Y	4550439	2,628,956	5,368	0	4,218	0	103	6.7
16Y	4550441	3,682,737	7,497	4	6,273	0	268	6.9
3G	4550445	9,415,322	19,123	6	10,037	0	1,152	7.7
4J	4550447	10,617,696	22,366	12	13,313	0	968	13.3
5M[a]	ND	2,523	12	0	12	0	0	ND
6D	4550450	3,571,810	7,367	2	5,464	0	130	5.3
7S	4550452	7,400,267	15,174	1	12,575	0	60	2.7
8Y	4550454	4,563,757	9,376	2	6,340	0	680	8.0
9Y	4550456	4,090,531	8,479	0	7,166	0	426	6.4
HX1	4550458	4,632,285	9,494	0	6,120	0	248	5.7

[a] Sample 5M amplified with Archaeal primers yielded a few sequences, therefore these sequences were omitted from analyses. ND – no data.

Table S4: *hgcAB* Amplicon Identifications

Sample	Site	hgcAB identifications	Accession
1H	Huaxi	Uncultured bacterial clone hgcAW3C09 Methanomicrobia enrichment clone B2_SO4-08 Uncultured Chloroflexi hgcA clone B2-03 Methanomicrobia enrichment hgcA clone ENP3-02	KJ580802.1 KJ021083.1 KJ021119.1 KJ021112.1
3G	Gouxi	Uncultured microorganism hgcA clone 3-1-23 Uncultured bacterial clone hgcAW3C09 Uncultured microorganism hgcA clone 3-1-23	KJ184815.1 KJ580802.1 KJ184815.1
7S	Sikeng	Uncultured microorganism hgcA clone 2-3-27 Uncultured bacterial clone hgcAF1A01 Uncultured microorganism hgcA clone 2-3-27 Uncultured microorganism hgcA clone 3-1-28 Uncultured microorganism hgcA clone 3-1-28	KJ184741.1 KJ580633.1 KJ184741.1 KJ184795.1 KJ184795.1
4J	Jinjiachang	Uncultured bacterial clone hgcAW3C09	KJ580802.1
6D	Dashuixi	Uncultured Chloroflexi hgcA clone B2-03	KJ021119.1
5M	Meizixi	Uncultured microorganism hgcA clone 3-2-24 Methanoregula formicicum SMSP Uncultured bacterial clone hgcAW3H07 Uncultured microorganism hgcA clone 3-1-23 Methanomicrobia enrichment hgcA clone ENP3-07	KJ184832.1 CP003167.1 KJ580779.1 KJ184815.1 KJ021117.1
8Y	Yanwuping	Methanomicrobia enrichment hgcA clone B2_FE19 Uncultured microorganism hgcA clone 3-1-28 Desulfobulbus propionicus Uncultured microorganism hgcA clone 2-1-14	KJ021100.1 KJ184795.1 CP002364.1 KJ184754.1
9Y	Yanwuping	Uncultured bacterial clone hgcAU3B03 Desulfobulbus propionicus Uncultured microorganism hgcA clone 4-3-23 Uncultured bacterial clone hgcAW3C09	KJ580634.1 CP002364.1 KJ184710.1 KJ580802.1
14Y	Yanwuping	Uncultured microorganism hgcA clone 3-1-23 Uncultured microorganism hgcA clone 3-1-14-2 Uncultured bacterial clone hgcAU3A12 Uncultured bacterial clone hgcAF1B02 Uncultured bacterial clone hgcAF1C04	KJ184815.1 KJ184805.1 KJ580773.1 KJ580776.1 KJ580778.1
16Y	Yanwuping	Desulfobulbus propionicus Uncultured Chloroflexi hgcA clone B2-07 Methanocella paludicola Uncultured bacterial clone hgcAU3B03 Uncultured microorganism hgcA clone 4-2-54	CP002364.1 KJ021121.1 AP011532.1 KJ580634.1 KJ184670.1

Supplementary Figures

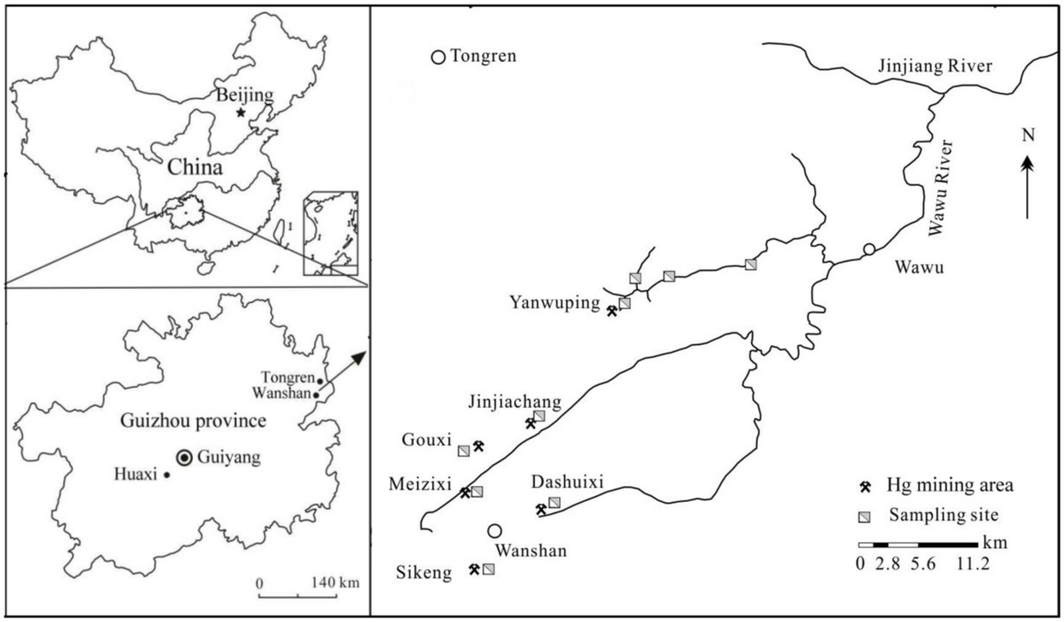

Figure S1. Map of study area and sampling sites in Guizhou province, China.

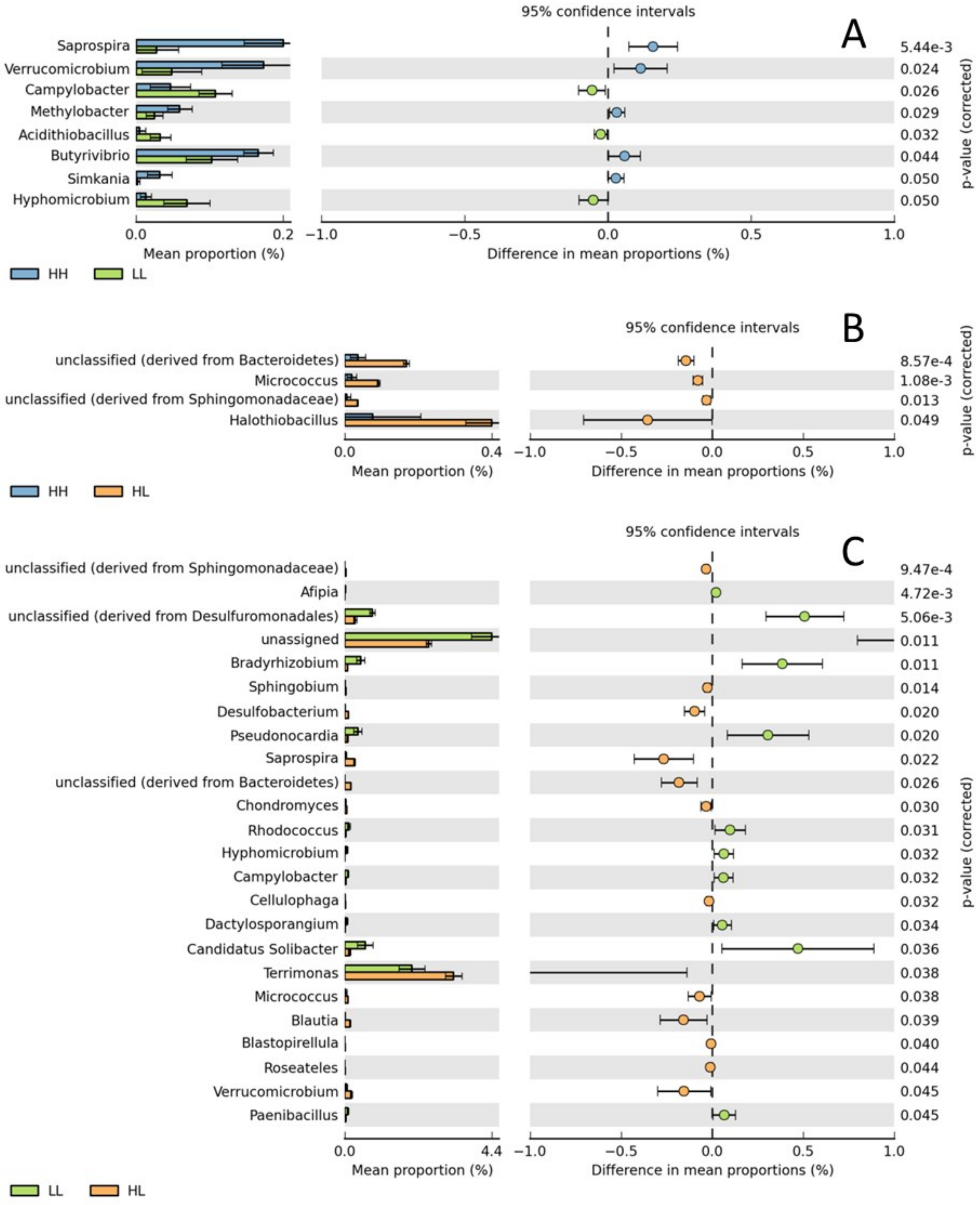

Fig. S2. Comparison of bacterial communities between sample groups: High / High (HH), Low / Low (LL), and High / Low (HL).

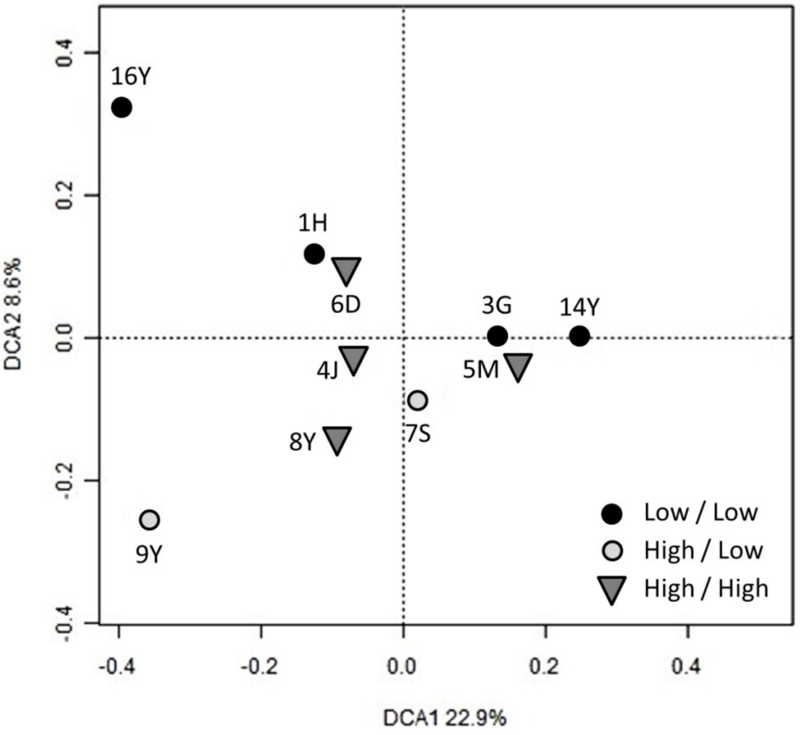

Figure S3. Detrended correspondence analysis for all rice paddy soil samples. The analysis was carried out using functional genes detected via GeoChip. Different symbols correspond to sample grouping based on THg and MeHg concentration (see Table S1).