Table S1 Cultured genus most related to OTUs from *cbbL* and *cbbM* clone libraries

cbbL OTU	Closest affiliation	Max identity	cbbM OTU	Closest affiliation	Max identity
cbbL-OTU1	*Sulfobacillus acidophilus* (DQ139404)	99	cbbM-OTU1	Gamma proteobacterium (HQ675075)	98
cbbL-OTU2	*Thiohalospira halophila* (GQ888600)	83	cbbM-OTU2	*Magnetospirillum moscoviense* (KF712469)	88
cbbL-OTU3	*Chromatium vinosum* (M26396)	78	cbbM-OTU3	Gamma proteobacterium (HQ675084)	98
cbbL-OTU4	*Acidithiobacillus caldus* (GQ409763)	83	cbbM-OTU4	*Magnetospirillum magnetotacticum* (AF442517)	90
cbbL-OTU5	*Thiobacillus denitrificans* (L42940)	86	cbbM-OTU5	*Acidithiobacillus ferrooxidans* (KT884974)	98
cbbL-OTU6	*Acidithiobacillus ferrooxidans* (AB362170)	100	cbbM-OTU6	Thiobacillus sp. (AB032829)	99
cbbL-OTU7	*Chromatium vinosum* (M26396)	89			
cbbL-OTU8	*Thioalkalivibrio versutus* (KY452013)	82			
cbbL-OTU9	*Azospirillum lipoferum* (DQ787337)	100			

Table S2 The relative abundance of the main known groups in the heavy fractions of Yangshanchong mine tailings (YM) and Shuimuchong mine tailings (SM) according to DNA-SIP and 16S rRNA analysis.

	YM	SM
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Sulfobacillaceae;g__Sulfobacillus	17.18%	18.24%
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium	2.87%	3.40%
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Acetobacteraceae;g__Acidiphilium	3.05%	3.24%
k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__[Leptospirillaceae];g__Leptospirillum	1.32%	1.58%
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Sulfobacillaceae;g__YNPFFP6	1.14%	1.20%
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Alicyclobacillaceae;g__Alicyclobacillus	1.00%	1.09%
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Methyloversatilis	0.87%	1.00%
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Conexibacteraceae;g__Conexibacter	0.39%	0.43%
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Coxiellaceae;g__Aquicella	0.25%	0.38%
k__Archaea;p__Euryarchaeota;c__Thermoplasmata;o__Thermoplasmatales;f__Picrophilaceae;g__Thermogymnomonas	0.23%	0.15%
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Phenylobacterium	0.14%	0.15%
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__Methylobacterium	0.13%	0.13%
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Dok59	0.03%	0.11%
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Acidithiobacillales;f__Acidithiobacillaceae;g__Acidithiobacillus	0.11%	0.06%