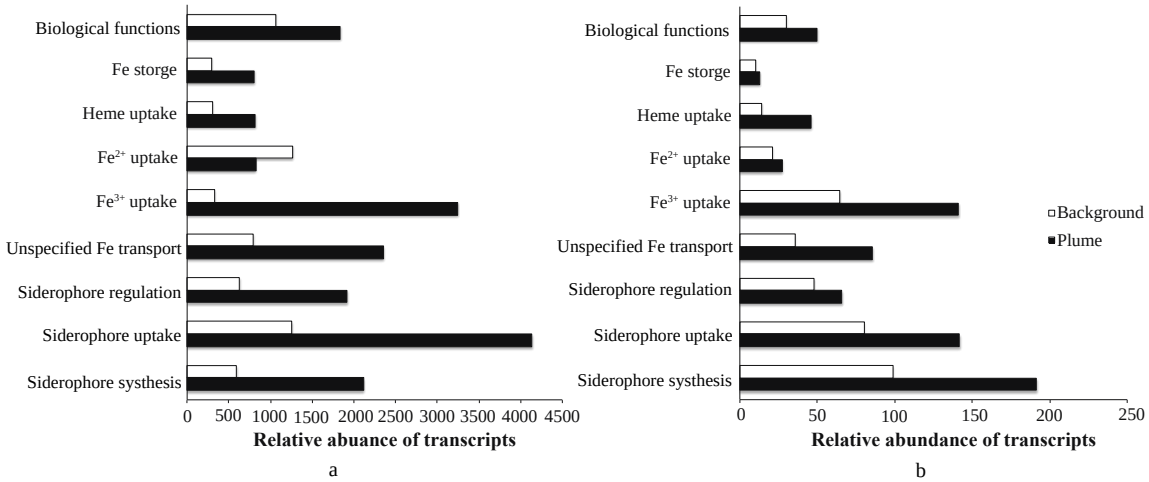
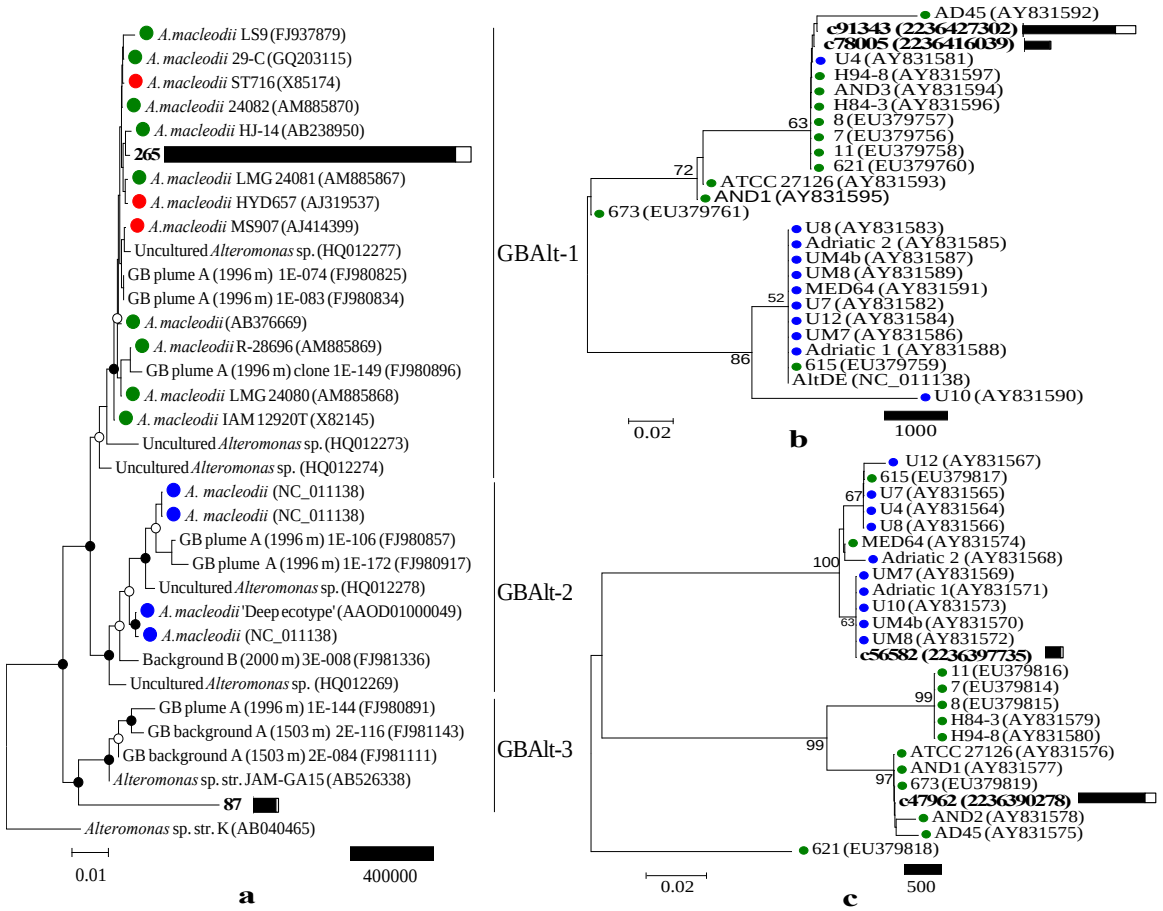
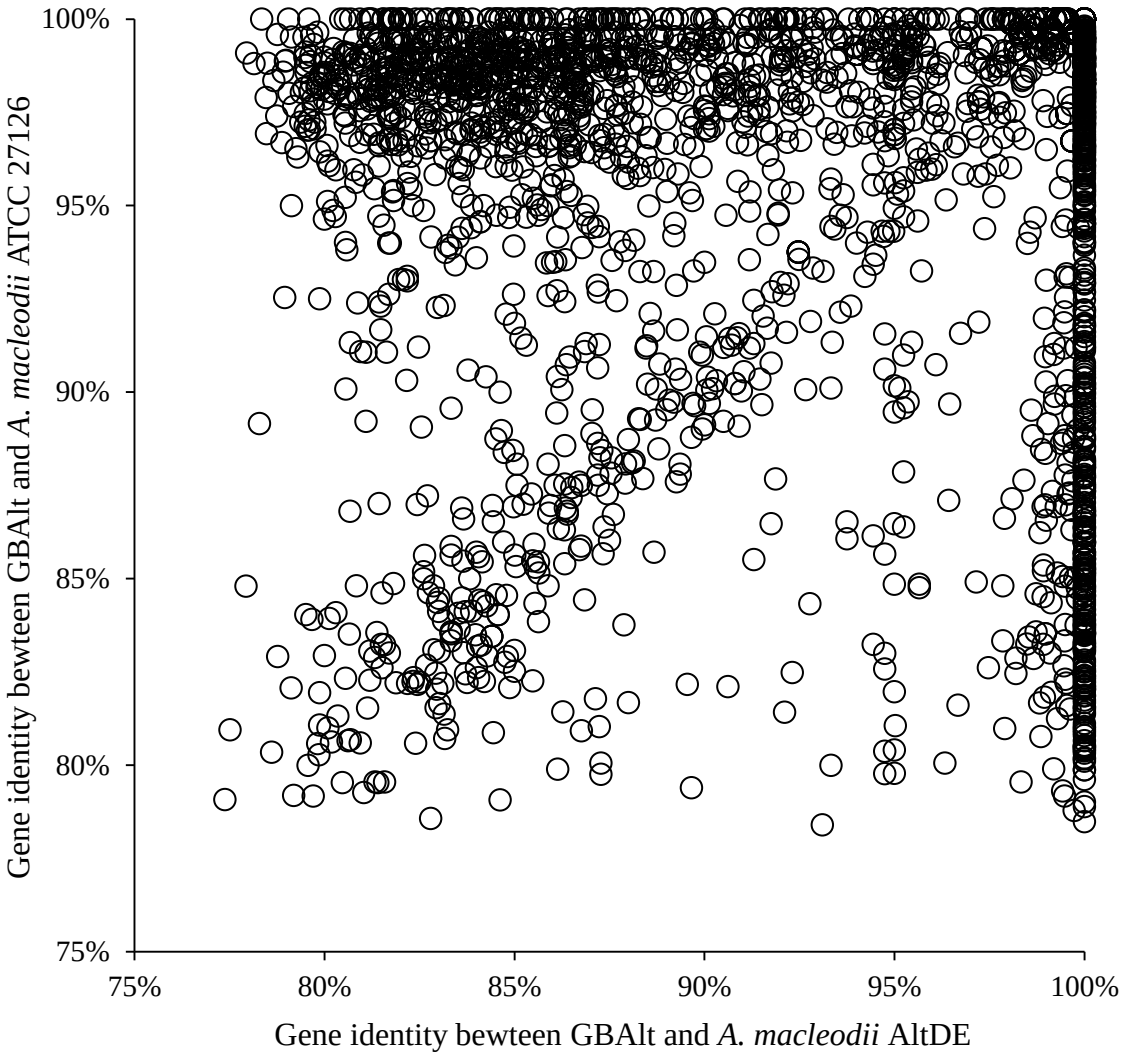
Supplementary Figures



Supplementary Figure 1. Abundance of Fe related gene transcripts. Abundance of Fe related gene transcripts in plume and background are calculated based on mapping transcripts from Illumina (a) and 454 (b) datasets to protein sequences involved in ten pathways of Fe uptake.

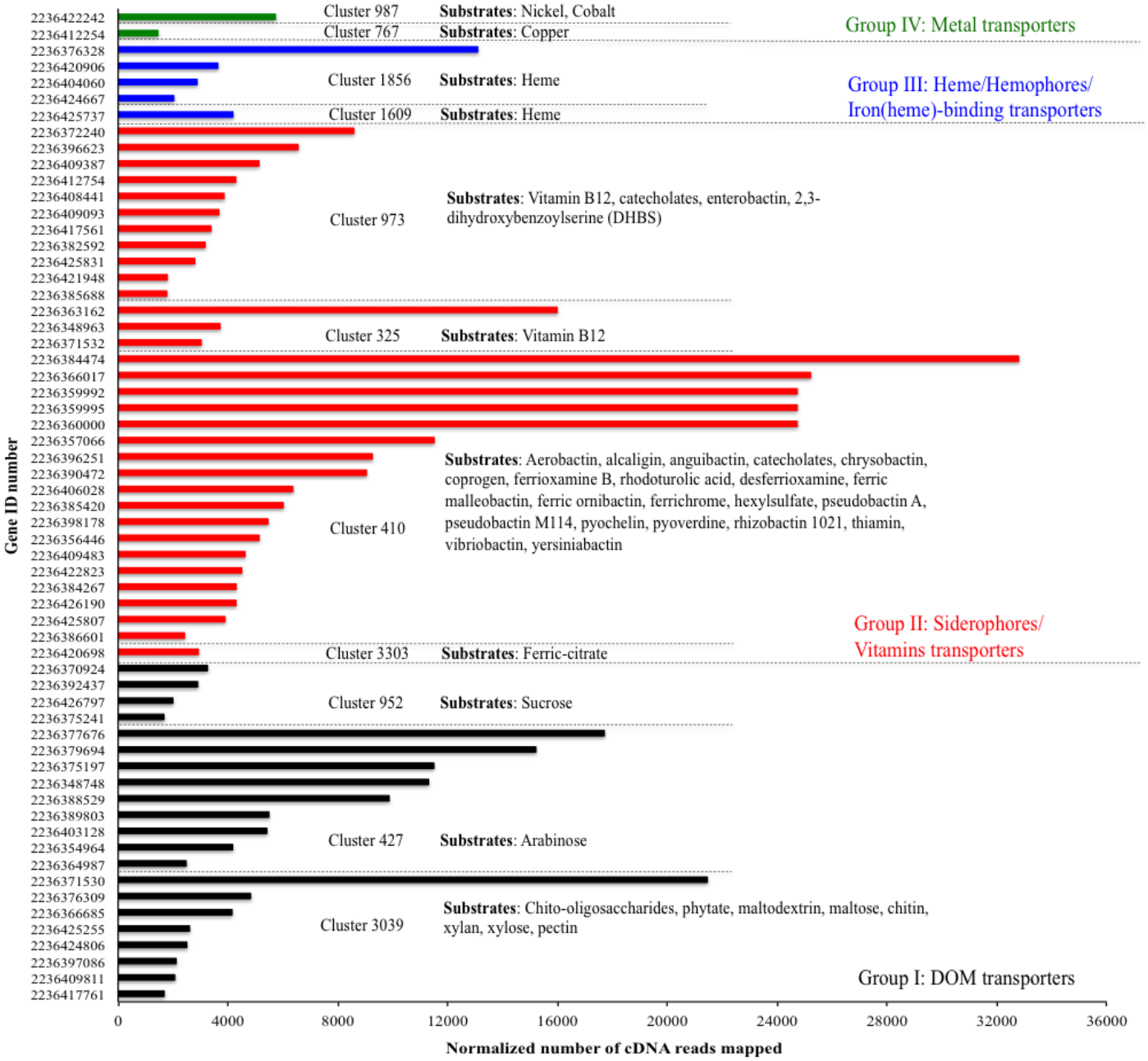


Supplementary Figure 2. Phylogeny of *Alteromonas* population. Phylogenetic analysis of *Alteromonas* population in the GB hydrothermal plume are analyzed based on 16S rRNA (a) and two housekeeping genes encoding DNA gyrase subunit B (*gyrB*, b) and RNA polymerase (*rpoB*, c). Black and white bars indicate the relative abundance of transcripts (normalized number) for each gene in the plume (black) and background (white) metatranscriptomic datasets. The red, blue and green circles indicate the environmental source of *Alteromonas* sequences, from hydrothermal vent, surface, and deep seawater, respectively. In panel (a), the identifiers of 16S rRNA gene sequences from the GB hydrothermal plume are shown in red text (265 and 87).



Supplementary Figure 3. Genome comparison of GBAlt. Gene sequence identities of GBAlt (2549 mRNA) are compared to the deep ecotype (AltDE) and surface ecotype (ATCC 27126) of *A. macleodii*. Each circle represents one gene of GBAlt with BLASTn bit score greater than 50 to genes of the other two ecotypes.

A


Cluster 987
Substrates: Nickel, Cobalt
Cluster 767
Substrates: Copper
Group IV: Metal transporters
Cluster 1856
Substrates: Heme
Cluster 1609
Substrates: Heme
Group III: Heme/Hemophores/ Iron(heme)-binding transporters
Cluster 973
Substrates: Vitamin B12, catecholates, enterobactin, 2,3-dihydroxybenzoylserine (DHBS)
Cluster 325
Substrates: Vitamin B12
Cluster 410
Substrates: Aerobactin, alcaligin, anguibactin, catecholates, chrysobactin, coprogen, ferrioxamine B, rhodoturolic acid, desferrioxamine, ferric malleobactin, ferric ornibactin, ferrichrome, hexylsulfate, pseudobactin A, pseudobactin M114, pyochelin, pyoverdine, rhizobactin 1021, thiamin, vibriobactin, yersiniabactin
Group II: Siderophores/ Vitamins transporters
Cluster 3303
Substrates: Ferric-citrate
Cluster 952
Substrates: Sucrose
Cluster 427
Substrates: Arabinose
Cluster 3039
Substrates: Chito-oligosaccharides, phytate, maltodextrin, maltose, chitin, xylan, xylose, pectin
Group I: DOM transporters
Gene ID number
2236422242
2236412254
2236376328
2236420906
2236404060
2236424667
2236425737
2236372240
2236396623
2236409387
2236412754
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2236424806
2236397086
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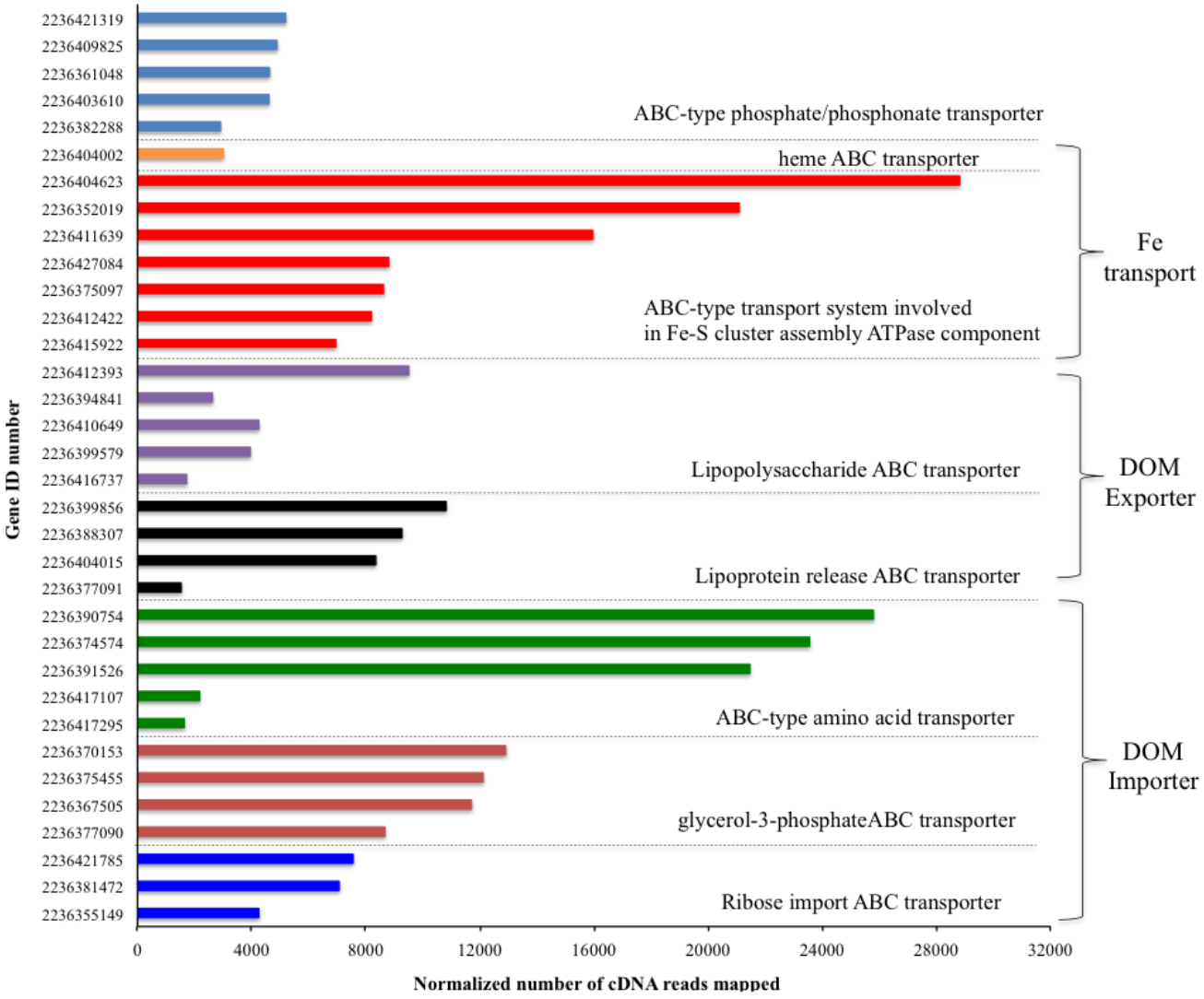
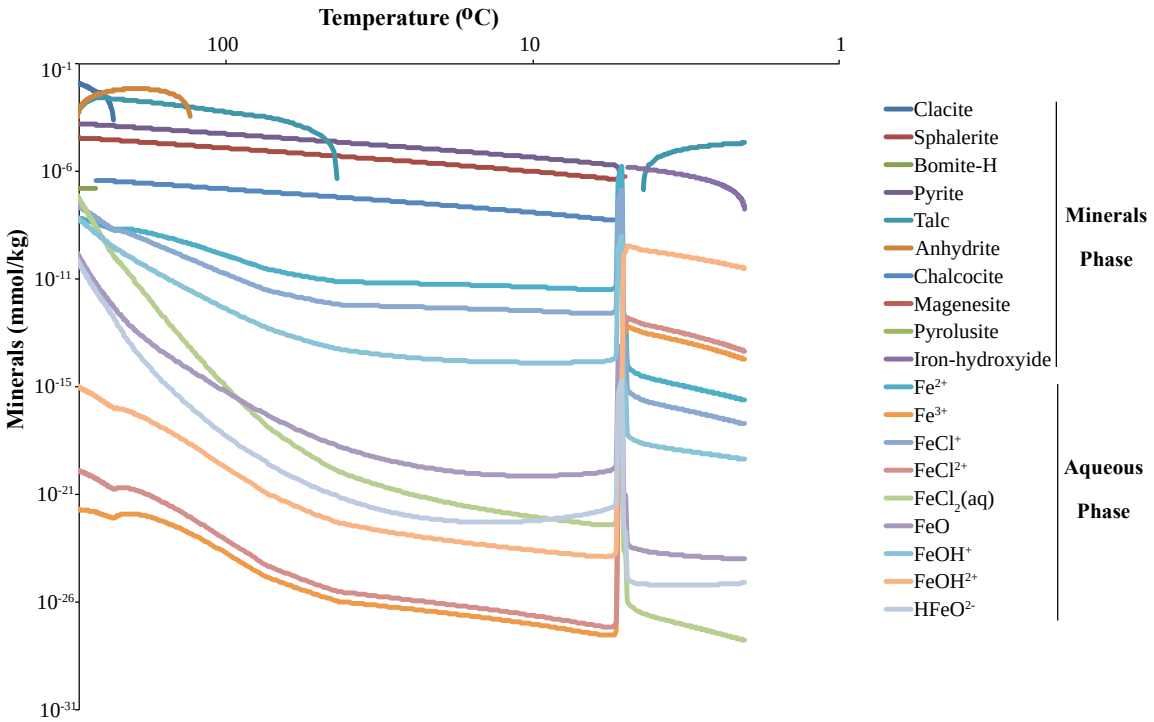
0
4000
8000
12000
16000
20000
24000
28000
32000
36000
Normalized number of cDNA reads mapped

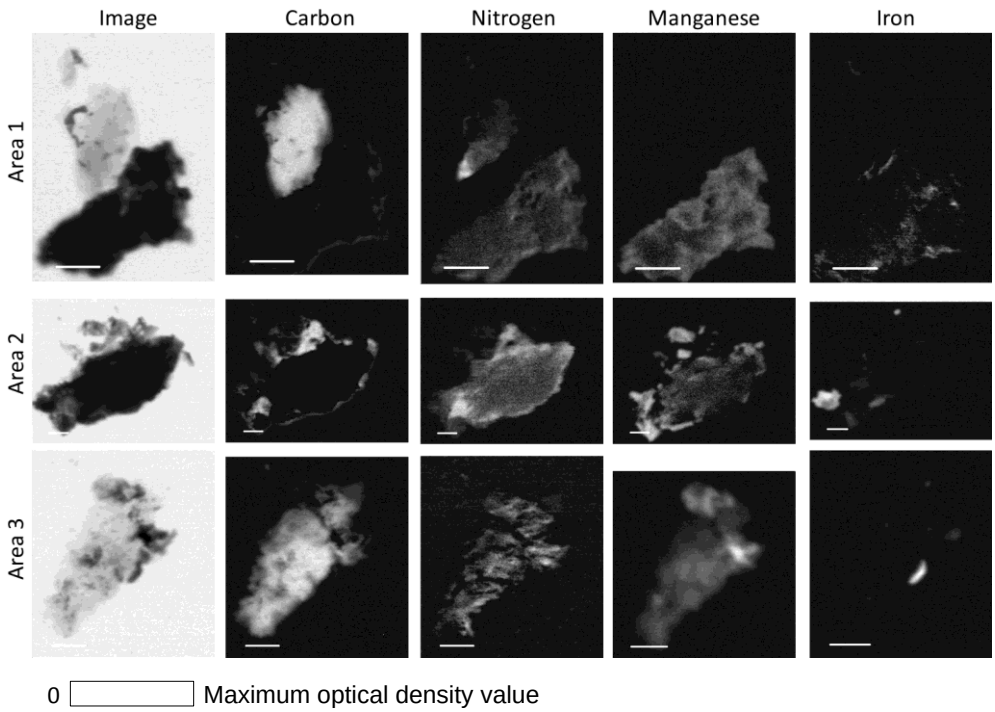
B



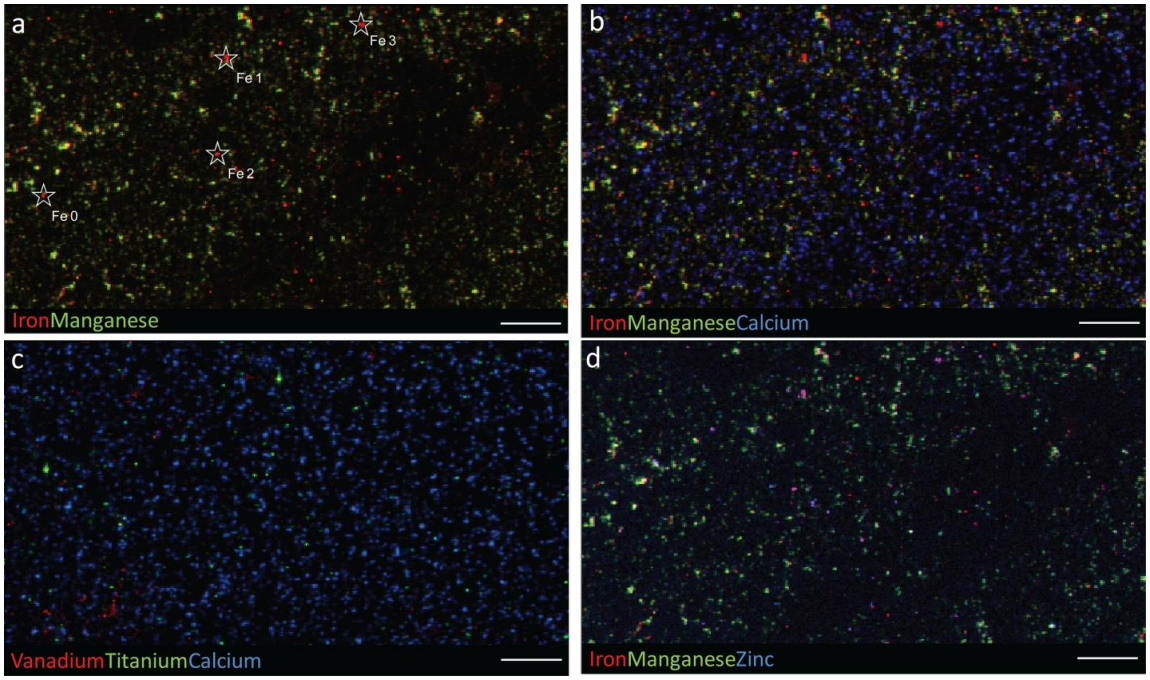
Supplementary Figure 4. TonB-dependent and ABC type transporters of GBAlt. Functional prediction of TonB-dependent (a) and ABC type transporters (b) of *Alteromonas* population in the GB hydrothermal plume is performed according to Tang et al.[41]. The relative abundance of gene transcripts was normalized to the length of gene fragments and total number of transcripts. The gene ID number for *Alteromonas* population of GB hydrothermal plume was assigned from gene annotation by JGI IMG/MER database.



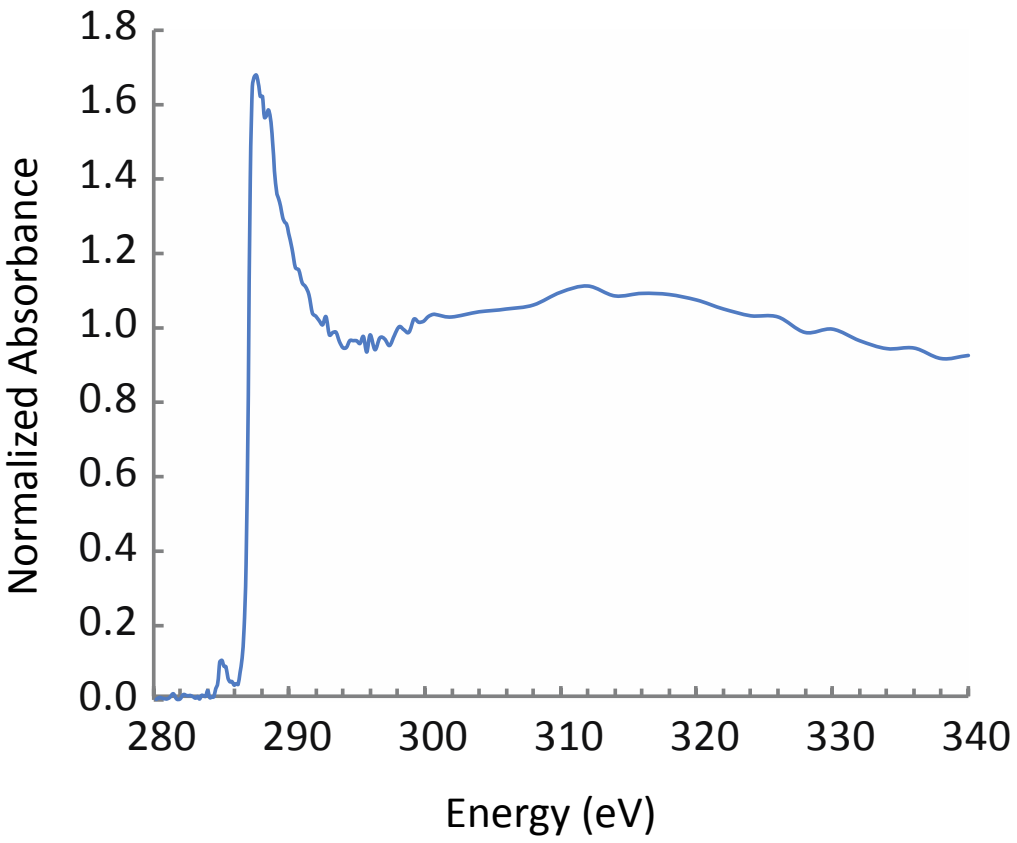
Supplementary Figure 5. Thermodynamic modeling. Mineral concentration in mineral and aqueous phase in the GB plume is predicted by thermodynamic modeling.



Supplementary Figure 6. STXM images and elemental maps. Scanning transmission X-ray microscopy (STXM) images and C, N, Mn, and Fe elemental maps (white scale) for three regions of a Guaymas Basin plume sample were shown. The scale bars are 2 μm are Area 1 and 1 μm for Area 2 and 3. The maximum optical density values for each elemental map, in order of C, N, Mn, and Fe, are: Area 1) 1.57, 1.28, 2.51, 0.60; Area 2) 0.90, 0.92, 1.84, and 2.21; and Area 3) 1.22, 0.29, 1.57, and 1.38.



Supplementary Figure 7. X-ray fluorescence maps. The maps are showing the distribution of: a) Fe (red) and Mn (green); b) Fe (red), Mn (green), and Ca (blue); c) V (red), Ti (green), and Ca (blue); and d) Fe (red), Mn (green), and Zn (blue). White stars labeled Fe0 to Fe3 are locations of Fe XANES spectroscopy. All scale bars are 200 μm.



Supplementary Figure 8. C 1s XANES spectrum. A representative C 1s XANES spectrum collected from Guaymas Basin plume particulates is shown**.**

Supplementary Table 1 Summary of samples and sequencing in this study.

Cast	Location	Depth (m)	Total Mn (nM)	O_2 (μM)	Temp. (°C)	Number of reads
11-2#14	27°0.823 N 111°24.654 W	1996	356	27.4	2.96	576,187 (454 DNA)
21-6#2	27°2.240 N 111°21.790 W	1963	315	26.1	2.93	664,240 (454 cDNA)
12-27a#1	**27°30.360 N 111°20.818 W**	**1950**	**288**	**27.7**	**2.93**	**894,665 (454 cDNA) 206,157,516 (Illumina cDNA)**
34-2#7	26°22.755 N 110°43.433 W	1900	21	46.5	2.59	406,533 (454 DNA) 504,086 (454 cDNA)
11-1#8	27°1.852 N 111°24.000 W	1775	257	27	2.95	563,818 (454 DNA)
12-8#12	**27°29.174 N 111°21.844 W**	**1600**	**55**	**28.5**	**2.97**	**358,335 (454 DNA) 514,607 (454 cDNA) 2,4451,9176 (Illumina cDNA)**

The bold highlighted samples are samples that are used for *de novo* metatranscriptomic assembly with Illumina cDNA sequences in the current study (after Lesniewski et al.[21] and Anantharaman et al.[34]).

Supplementary Table 2 Guaymas Basin hydrothermal plume particle elemental concentrations*

Sample	Location	Depth (m)	Vol (L)	Al/(Fe+Mn+Al)	Mn	Fe	Al	Ti	P	Zn	Ni	Cu	Cr	U
GOCAL 31-12A	27° 1.892 N 111° 25.891 W	1890	80	0.15	54.9	6.75	10.74	2.42	4.68	0.355	0.346	0.137	<DL	<DL
GOCAL 31-17A	27° 0.774 N 111° 24.984 W	1959	90	0.43	33.3	4.15	28.65	9.69	3.33	0.906	<DL	0.162	<DL	0.758
GOCAL 31-2A	27° 1.240 N 111° 24.789 W	1900	100	0.17	65.4	15.78	17.19	<DL	4.49	1.029	1.027	0.292	2.68	<DL
GOCAL 32-10A	27° 30.090 N 111° 21.210 W	1891	50	<DL	48.1	7.47	<DL	0.97	4.49	0.638	<DL	0.219	<DL	<DL

*All concentrations in nmol per kg seawater. Detection limits (DL, nmol per kg seawater): Mn (0.08), Fe (0.08), Al (1.70), Ti (0.10), P (0.30), Zn (0.04), Ni (0.04), Cu (0.01), Cr (0.18) and U (0.10).