Supplementary Tables and Figures

Table S1. Statistics of clone libraries.
The clone library sequences for ABP and DBP were compared in the RDP database (http://rdp.cme.msu.edu/comparison/). The confidence level employed in the classification was 80%. The table shows the number of clone sequences assigned to different taxonomic levels and the statistical significance of the comparisons.

Rank	Name	ABP	DBP	Significance
phylum	Deinococcus-Thermus	0	29	2.11E-09
class	Deinococci	0	29	2.11E-09
genus	Meiothermus	0	29	2.11E-09
family	Thermaceae	0	29	2.11E-09
order	Thermales	0	29	2.11E-09
class	Betaproteobacteria	97	69	6.34E-05
family	Burkholderiaceae	96	68	6.34E-05
order	Burkholderiales	97	69	6.34E-05
phylum	Proteobacteria	107	84	1.00E-04
family	Microbacteriaceae	9	0	1.87E-03
genus	Microbacterium	9	0	1.87E-03
suborder	Micrococcineae	9	0	1.87E-03
genus	Cupriavidus	80	58	2.98E-03
phylum	Actinobacteria	9	1	1.13E-02
class	Actinobacteria	9	1	1.13E-02
subclass	Actinobacteridae	9	1	1.13E-02
order	Actinomycetales	9	1	1.13E-02
genus	Ralstonia	15	5	2.53E-02
class	Bacilli	0	4	6.38E-02
phylum	Firmicutes	0	4	6.38E-02
family	Bacillaceae	0	4	6.38E-02
order	Bacillales	0	4	6.38E-02
genus	Brevundimonas	0	4	6.38E-02
family	Caulobacteraceae	0	4	6.38E-02
order	Caulobacterales	0	4	6.38E-02
genus	Acinetobacter	5	1	1.22E-01
family	Moraxellaceae	5	1	1.22E-01
order	Pseudomonadales	5	1	1.22E-01
order	Sphingomonadales	0	3	1.27E-01
genus	Wautersia	0	3	1.27E-01
class	Alphaproteobacteria	5	11	1.48E-01
genus	Bacillus	0	2	2.53E-01
family	Sphingomonadaceae	0	2	2.53E-01
genus	Sphingopyxis	0	2	2.53E-01
genus	Stenotrophomonas	0	2	2.53E-01

family	Xanthomonadaceae	0	2	2.53E-01
order	Xanthomonadales	0	2	2.53E-01
genus	Achromobacter	1	0	4.96E-01
family	Alcaligenaceae	1	0	4.96E-01
family	Bradyrhizobiaceae	1	0	4.96E-01
family	Methylobacteriaceae	1	0	4.96E-01
genus	Methylobacterium	1	0	4.96E-01
	unclassified Bacteria	1	0	NA
	unclassified Bradyrhizobiaceae	1	0	NA
class	Gammaproteobacteria	5	3	5.00E-01
genus	Anoxybacillus	0	1	5.04E-01
family	Erythrobacteraceae	0	1	5.04E-01
family	Nocardioidaceae	0	1	5.04E-01
suborder	Propionibacterineae	0	1	5.04E-01
	unclassified Proteobacteria	0	1	NA
	unclassified Bacillaceae	0	1	NA
	unclassified Burkholderiales	0	1	NA
	unclassified Erythrobacteraceae	0	1	NA
	unclassified Nocardioidaceae	0	1	NA
	unclassified Burkholderiaceae	1	2	NA
family	Phyllobacteriaceae	3	4	7.36E-01
genus	Phyllobacterium	3	4	7.36E-01
order	Rhizobiales	5	4	7.44E-01
	unclassified Root	1	1	NA
norank	Root	118	119	1.00E+00
domain	Bacteria	117	118	1.00E+00

Table S2. Chemical compounds detected in the brine water from the Atlantis II Deep brine pool identified from the brine water sample by GC-MS analysis. Rt refers to the retention time of a compound in the chromatogram, '% R' refers to the area of each peak with reference to the largest peak in the chromatogram, and '% P' is the probability of the identification. Aromatic compounds with a %P of >25% are shown in bold. The compounds were predicted based on the NIST database (http://srdata.nist.gov/).

Rt	NIST match	% P	% R
Compounds in the DCM fraction			
9.864	Decanal dimethyl acetal	38.6	15.01
10.744	**Benzoic acid, ethyoxy ethyl ester**	38.5	11.97
11.485	8- methyl- 9- tetradecanoic acid	11.2	16.22
11.626	Tridecanoic acid	13.8	6.45
11.928	8- methyl-9- tetracen-1-olacetate	10.1	7.21
12.038	2- Bromo-tetra decanoic acid	13.5	6.05
12.47	Pentadecanoic acid- 14- methyl- methyl ester	39.3	25.25
14.526	Thiocarbamic acid, N,N-dimethyl, S-1,3-diphenyl-2-butenyl ester	10.4	58.21
16.176	**Phen-1,4-diol, 2,3-dimethyl-5-trifluoromethyl-**	30.4	6.0
17.354	Tert-Hexadecanethiol	5.62	2.6
18.219	9,10-Secocholesta-5,7,10(19)-triene-3,24,25-triol, (3á,5Z,7E)-	18.2	0.37
20.54	Oxiraneundecanoic acid, 3-pentyl-, methyl ester, cis-	10.7	0.63
20.931	Hexadecanoic acid, methyl ester	67.8	6.14
21.22	1,2-Benzenedicarboxylic acid, butyl 2-ethylhexyl ester	16.9	27.82
24.315	**2-(4-Iodo-phenyl)-5,6,7,8-tetrahydro-pyrazolo[5,1-b]quinazolin-9-ol**	36.8	100
Compounds in the methanol fraction (Derivatized)			
14.474	Silanol, trimethyl-, phosphate (3:1)	78.3	31.71
15.441	2-Dimethyl(trimethylsilyl)silyloxytridecane	6.87	3.15
16.352	Butanedioic acid, bis(trimethylsilyl) ester	81.3	69.77
20.181	Erythro-Pentonic acid, 2-deoxy-3,4,5-tris-O-(trimethylsilyl)-, trimethylsilyl ester	5.66	11.73
24.231	Hexanedioic acid, bis(trimethylsilyl) ester	89	6.26
28.09	b-D-Galactopyranoside, methyl 2,3-bis-O-(trimethylsilyl)-, cyclic	46.4	4.12
30.934	**1,2-Benzenedicarboxylic acid, bis(trimethylsilyl) ester**	97.8	44.89
33.513	**1,4-Benzenedicarboxylic acid, bis(trimethylsilyl) ester**	68.8	12.02
36.582	a-D-Glucopyranoside, methyl 2-(acetylamino)-2-deoxy-3-O-(trimethylsilyl)-, cyclic methylboronate	22.7	17.12
42.901	Hexadecanoic acid, trimethylsilyl ester	91.3	100
48.512	9,12,15-Octadecatrienoic acid, 2,3-bis[(trimethylsilyl)oxy]propyl ester, (Z,Z)	21.7	54.74

Table S3. Bacteria detected by the 16S rDNA fragments from the metareads. The classification was conducted in the RDP database without using a confidence threshold. ABP: Atlantis II Deep brine pool; DBP: Discovery Deep brine pool.

Phylum	ABP	DBP
Proteobacteria	733	175
Actinobacteria	49	11
Firmicutes	4	12
Chrysiogenetes	2	0
Dictyoglomi	1	0
Deinococcus-Thermus	0	26
Cyanobacteria	0	1
Bacteroidetes	0	3
Thermotogae	0	2
Thermodesulfobacteria	0	1
Euryarchaeota	0	208
Crenarchaeota	3	14
Total	792	453

Table S4. Average confidence (%) of classification of 16S rDNA fragments .
The 16S rDNA fragments were extracted from the metareads and classified into genera by the RDP classifier. The confidence values were obtained from the RDP database; the average and standard deviation (SD) are shown in this table.

Genus	ABP		DBP	
	Average (%)	SD (%)	Average (%)	SD (%)
Pro:Bet:Bur:Bur:Cupriavidus	90	15	93	15
Pro:Gam:Pse:Mor:Acinetobacter	91	15	94	15
Pro:Bet:Bur:Bur:Wautersia	56	14	54	20
Pro:Bet:Bur:Bur:Ralstonia	91	19	99	1
Act:Act:Mic:Mic:Microbacterium	96	10	93	12
Pro:Alp:Rhi:Bra:Bradyrhizobium	93	14	100	-
Pro:Bet:Bur:Com:Rhodoferax	45	22	65	27
Pro:Bet:Bur:Com:Malikia	9	2	8	5
Pro:Alp:Rhi:Phy:Phyllobacterium	97	4	-	-
Pro:Gam:Pse:Mor:Alkanindiges	64	13	39	-
Pro:Alp:Rhi:Bra:Afipia	66	19	-	-
Fir:Bac:Bac:Bac:Bac:Bacillus	53	32	-	-

Table S5. KEGG maps for the Atlantis II Deep brine pool-specific abundant KEGG genes.

The ABP genes in the red part of Fig. 3 were sorted into different KEGG pathways. The number of the nodes means how many genes were identified in a KEGG pathway map.

Map	Node num	Pathway
K02020	35	Two-component system
K02010	24	ABC transporters
K00350	13	Tyrosine metabolism
K03070	13	Bacterial secretion system
K00650	12	Butanoate metabolism
K00362	12	Benzoate degradation via hydroxylation
K00360	11	Phenylalanine metabolism
K00632	11	Benzoate degradation via CoA ligation
K00361	10	Gamma-hexachlorocyclohexane degradation
K00903	10	Limonene and pinene degradation
K00071	9	Fatty acid metabolism
K00910	9	Nitrogen metabolism
K00330	9	Arginine and proline metabolism
K00280	8	Valine, leucine, and isoleucine degradation
K02030	8	Bacterial chemotaxis – general
K00380	7	Tryptophan metabolism
K00643	7	Styrene degradation
K00930	6	Caprolactam degradation
K00620	6	Pyruvate metabolism
K02040	6	Flagellar assembly
K00230	5	Purine metabolism
K00271	5	Methionine metabolism
K00630	5	Glyoxylate and dicarboxylate metabolism
K00053	5	Ascorbate and aldarate metabolism
K00260	5	Glycine, serine, and threonine metabolism
K00340	5	Histidine metabolism
K00190	5	Oxidative phosphorylation
K00920	4	Sulfur metabolism
K00623	4	2,4-Dichlorobenzoate degradation
K00480	4	Glutathione metabolism
K00564	4	Glycerophospholipid metabolism

Table S6. KEGG maps for DBP-specific abundant KEGG genes.
The DBP genes in the red part of Fig. 3 were sorted into different KEGG pathways. The number of the nodes means how many genes were identified in a KEGG pathway map.

Map	Node num	Pathway
K00240	13	Pyrimidine metabolism
K00230	12	Purine metabolism
K00790	10	Folate biosynthesis
K03010	7	Ribosome
K02010	6	ABC transporters
K00970	6	Aminoacyl-tRNA biosynthesis
K00330	5	Arginine and proline metabolism
K00190	4	Oxidative phosphorylation
K03410	4	Base excision repair
K03420	4	Nucleotide excision repair

Figure S1. Bacterial classification of the 16S rRNA clone sequences. A total of 117 and 119 clone sequences were obtained for the Atlantis II Deep (ABP) and Discovery Deep (DBP) brine pool, respectively. The classification was performed with the RDP classifier (Cole et al., 2009). The minor groups include genera accounting for less than 1% of the total.
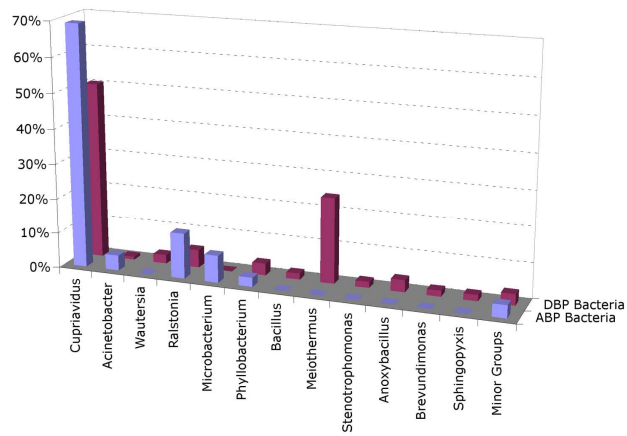
Figure S2. GC-MS results for detections of aromatic compounds and fatty acids

a Aromatic compounds

(mainlib) Benzoic acid, 4-ethoxy-, ethyl ester

(mainlib) Phen-1,4-diol, 2,3-dimethyl-5-trifluoromethyl-

(mainlib) 2-(4-Iodo-phenyl)-5,6,7,8-tetrahydro-pyrazolo[5,1-

(replib) 1,2-Benzenedicarboxylic acid, bis(trimethylsilyl) est

(replib) 1,4-Benzenedicarboxylic acid, bis(trimethylsilyl) est

b Fatty acids

(replib) Decanal dimethyl acetal

(mainlib) Pentadecanoic acid, 14-methyl-, methyl ester

(mainlib) Hexadecanoic acid, methyl ester

(mainlib) Butanedioic acid, bis(trimethylsilyl) ester

(replib) Hexanedioic acid, bis(trimethylsilyl) ester

(mainlib) Hexadecanoic acid, trimethylsilyl ester