SUPPLEMENTAL MATERIALS

Table S1. Lists of bacterial species used in non-metric multidimensional scaling analysis.

Species	Abbreviation	Accession No.	Size of genome (Mb)	No. of CDSs	No. of COG family assigned
Deferribacteres					
Deferribacter desulfuricans SMM1	def		2.23	2,422	1,219
Deltaproteobacteria					
Desulfovibrio vulgaris subsp. vulgaris Hildenborough	dvu	NC_002937	3.57	3,531	1,327
Geobacter sulfurreducens PCA	gsu	NC_002939	3.81	3,446	1,408
Pelobacter carbinolicus	pca	NC_007498	3.67	3,352	1,405
Anaeromyxobacter dehalogenans	ade	NC_007760	5.01	4,346	1,498
Syntrophobacter fumaroxidans	sfu	NC_008554	4.99	4,064	1,389
Desulfotalea psychrophila	dps	NC_006138	3.52	3,234	1,322
Epsilonproteobacteria					
Campylobacter jejuni subsp. jejuni NCTC 11168	cje	NC_002163	1.64	1,634	1,000
Thiomicrospira denitrificans	tdn	NC_007575	2.20	2,096	1,032
Nitratiruptor sp. SB155-2	nis	NC_009662	1.88	1,843	1,011
Gammaproteobacteria					
Escherichia coli K-12	eco	NC_000913	4.64	4,133	2,084
Methylococcus capsulatus	mca	NC_002977	3.30	2,956	1,415
Pasteurella multocida	pmu	NC_002663	2.26	2,015	1,399
Pseudomonas aeruginosa	pae	NC_002516	6.26	5,568	2,164
Thiomicrospira crunogena	tcx	NC_007520	2.42	2,196	1,208
Vibrio cholerae	vch	NC_002505	2.96	3,835	1,847
Betaproteobacteria					
Thiobacillus denitrificans	tbd	NC_007404	2.91	2,827	1,395
Methylobacillus flagellatus	mfa	NC_007947	2.97	2,753	1,339
Chromobacterium violaceum	cvi	NC_005085	4.75	4,407	1,757
Dechloromonas aromatica	dar	NC_007298	4.50	4,171	1,633
Alphaproteobacteria					
Caulobacter crescentus	ccr	NC_002696	4.02	3,737	1,644
Sphingomonas wittichii	swi	NC_009511	5.38	5,345	1,568
Other proteobacteria					
Magnetococcus sp. MC-1	mgm	NC_008576	4.72	3,716	1,335
Aquificae					
Aquifex aeolicus	aae	NC_000918	1.55	1,560	1,004
Chlorobi					
Chlorobaculum tepidum	cte	NC_002932	2.15	2,252	1,052
Chlorobium chlorochromatii	cch	NC_007514	2.57	2,002	1,001
Clostridia					
Carboxydothermus hydrogenoformans	chy	NC_007503	2.40	2,620	1,261
Clostridium thermocellum	cth	NC_009012	3.84	3,191	1,255
Thermoanaerobacter tengcongensis	tte	NC_003869	2.68	2,588	1,236
Alkaliphilus oremlandii	aoe	NC_009922	3.12	2,836	1,228
Clostridium acetobutylicum	cac	NC_003030	3.94	3,848	1,463

Table S1. Continued.

Species	Abbreviation	Accession No.	Size of genome (Mb)	No. of CDSs	No. of COG family assigned
Bacillales* and *Lactobacillales					
Symbiobacterium thermophilum	sth	NC_006177	3.57	3,338	1,350
Bacillus halodurans	bha	NC_002570	4.20	4,066	1,668
Bacillus subtilis	bsu	NC_000964	4.21	4,105	1,689
Geobacillus kaustophilus	gka	NC_006510	3.54	3,540	1,541
Deinococcus-Thermus					
Thermus thermophilus	tth	NC_005835	1.89	2,210	1,154
Deinococcus radiodurans	dra	NC_001263	2.65	3,181	1,370
Thermotogae					
Thermotoga maritima	tma	NC_000853	1.86	1,858	1,097
Fervidobacterium nodosum	fno	NC_009718	1.95	1,750	976
Acidobacteria					
Acidobacteria bacterium	aba	NC_008009	5.65	4,777	1,453
Solibacter usitatus	sus	NC_008536	9.96	7,826	1,625
Bacteroidetes					
Bacteroides fragilis	bfr	NC_006347	5.28	4,625	1,159
Flavobacterium johnsoniae	fjo	NC_009441	6.10	5,017	1,334
Cyanobacteria					
Synechocystis sp. PCC 6803	syn	NC_000911	3.57	3,264	1,336
Anabaena sp. PCC 7120	ana	NC_003272	6.41	6,131	1,580
Actinobacteria					
Mycobacterium tuberculosis	mtu	NC_000962	4.41	3,989	1,382
Streptomyces coelicolor A3(2)	sco	NC_003888	8.67	8,154	1,602
Planctomycetes					
Rhodopirellula baltica	rba	NC_005027	7.15	7,325	1,300
Fusobacteria					
Fusobacterium nucleatum	fnu	NC_003454	2.17	2,067	1,072
Chloroflexi					
Chloroflexus aurantiacus	cau	NC_010175	5.26	3,853	1,377
Dehalococcoides ethenogenes	det	NC_002936	1.47	1,580	777

Figure Legneds

Figure S1. Genetic reconstruction of sulfur respiration of *D. desulfuricans*. (A) Schematic model of components involved in sulfur-reduction via quinol-pool. (B) Comparison of the respiratory gene cluster between the genomes of *D. desulfuricans* and several members of *Deltaproteobacteria* including *Geobacter sulfurreducens* PCA (NC_002939), *G. metallireducens* GS-15 (NC_007517), *G. uraniireducens* Rf4 (NC_009483), *G. lovleyi* SZ (NC_010814) and *Desulfuromonas acetoxidans* DSM684 (NZ_AAEW02000014 and NZ_AAEW02000035). This locus contains genes for polysulfide reductase (blue), rhodanese-like protein (gold), porin (gold), multiheme *c*-type cytochromes (orange) and hypothetical proteins (gray).

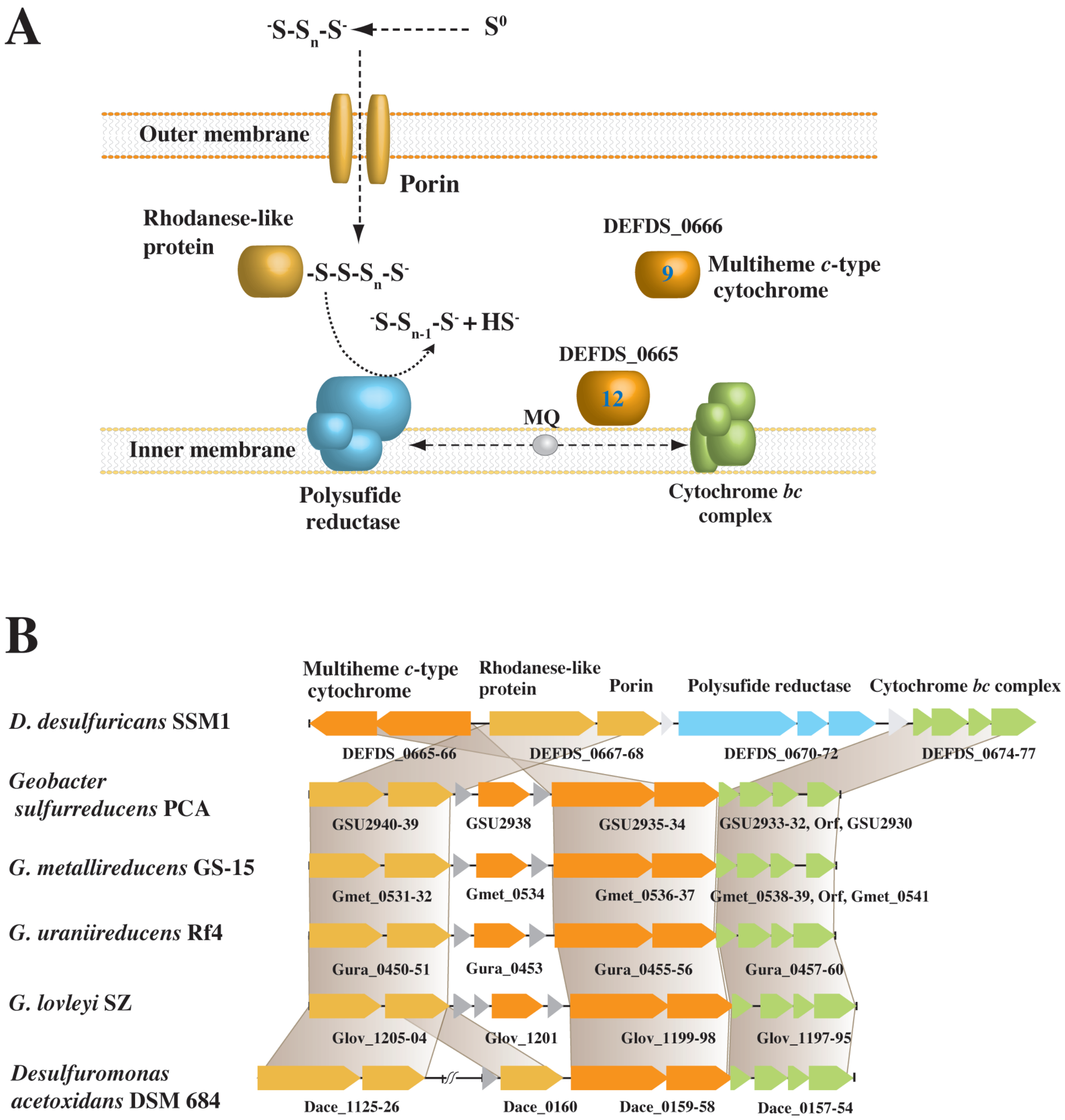
Figure S2. Subcellular distribution of products encoded in a novel multiheme *c*-type cytochrome gene cluster in the *D. desulfuricans* genome. This figure indicates the subcellular distribution of components encoded of the gene cluster (A) and the gene organization (B). Each multiheme *c*-type cytochrome (orange), two-component signal transduction proteins (gold) and other proteins (Gray) encoded in the gene clusters is depicted according to the subcellular location predicted by SOSUIgramN[1] and PSORTb[2] programs. Number in the multiheme *c*-type cytochrome represents CXXCH heme-binding motifs.

Figure S3. Comparison of components of membrane-binding and intracellular signaling proteins among the deep-sea hydrothermal vent chemolithotrophs. The numbers of potential two-component histidine kinases and cyclic diGMP signaling proteins are indicated.

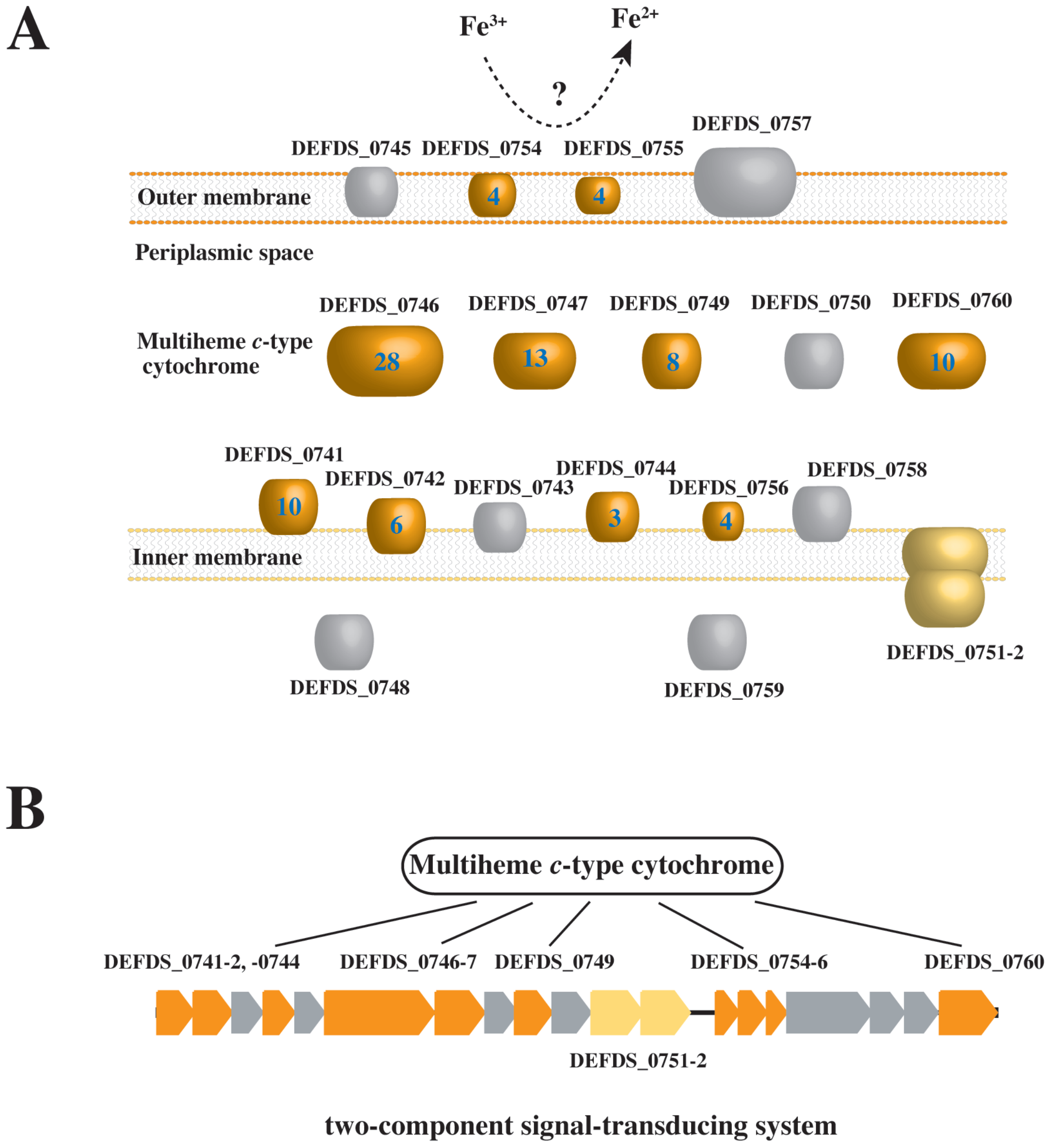
Figure S4. Residue frequency in mesophiles, thermophiles, and hyperthermophiles compared to residue frequency in *D. desulfuricans*. This analysis was performed in 135 proteomes of archaea and bacteria. According to the optimal growth temperature (OGT), these organisms were classified into: mesophiles (20 to 59°C in OGT, 108 genomes), thermophiles (60 to 80°C, 11 genomes), and hyperthermophiles (more than 81°C, 16 genomes). White boxes indicate residues necessary for thermophily of protein.

References

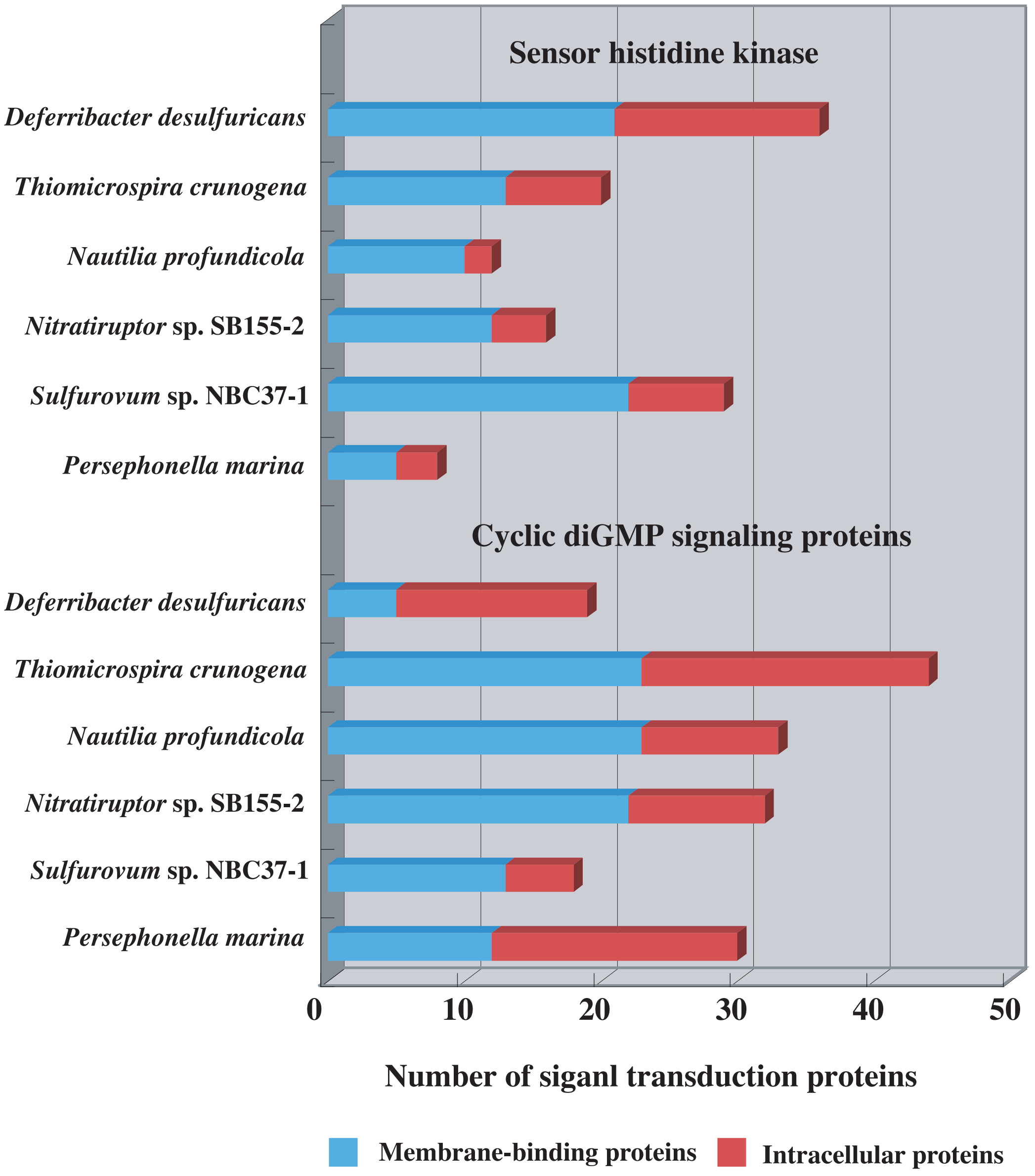
1. Imai, K., Asakawa, N., Tsuji, T. et al. 2008, SOSUI-GramN: high performance prediction for sub-cellular localization of proteins in Gram-negative bacteria, *Bioinformation*, **2**, 417-421.
2. Gardy, J. L., Spencer, C., Wang, K. et al. 2003, PSORT-B: Improving protein subcellular localization prediction for Gram-negative bacteria, *Nucleic Acids Research*, **31**, 3613-3617.



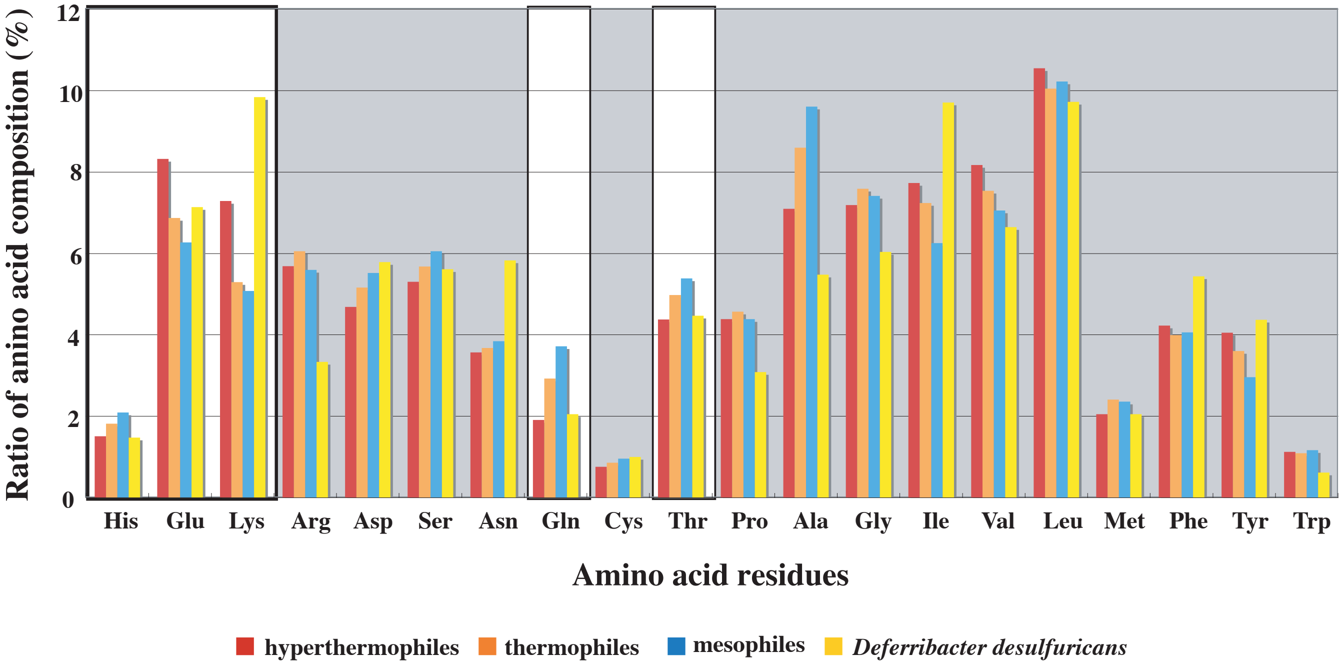
Takaki *et al.* Fig. S1



Takaki *et al.* Fig. S2



Takaki *et al.* Fig. S3



Takaki *et al*. Fig. S4