

Anaerobic carboxydrotrophy in sulfur-respiring haloarchaea from hypersaline lakes

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Discovery of anaerobic carboxydrotrophy in sulfur-respiring haloarchaea from hypersaline lakes

Dimitry Y. Sorokin, Alexander Y. Merkel, Enzo Messina, Claudia Tugui, Martin Pabst, Peter N. Golyshin, Michail M. Yakimov

Supplementary data file

Fig. S1. Macromorphology of carboxydrotrophic haloarchaea. **(a-b)** – liquid cultures grown anaerobically with CO (20% in the gas phase) + 0.2 g/L yeast extract as C source and S₈ as e-acceptor, either at pH 7 (*Halanaeroarchaeum* HSR-CO) or 9.5 (*Halalkaliarchaeum* AArc-CO). Orange color indicates high concentrations of polysulfide formed abiotically at high pH from produced sulfide and the remaining S₈. **(c-d)** colonies of *Halalkaliarchaeum* AArc-CO grown either aerobically on the surface of yeast extract/pyruvate agar **(c)** or anaerobically inside the sulfur-containing soft agar incubated under the 20% CO/80% argon atmosphere **(d)**.

Fig. S2. Phase contrast microphotographs of cells of sulfur-reducing carboxydrotrophic haloarchaea: **a,b** - *Halanaeroarchaeum* HSR-CO grown anaerobically with CO and pyruvate, respectively; **c,d** - *Halalkaliarchaeum* AArc-CO grown anaerobically with CO or aerobically with yeast extract and pyruvate, respectively.

Fig. S3. 16S rRNA gene based phylogenetic trees showing placement of **(A)** *Halanaeroarchaeum* HSR-CO within the *Halobacteriaceae* family and **(B)** *Halalkaliarchaeum* AArc-CO within the *Halorubraceae* family. The trees were built using the maximumlikelihood method by the IQ-TREE program and the approximate likelihood ratio test for branches. Bootstrap values ≥ 70 % are shown at nodes. Bar, 0.10 changes per position. GenBank accession numbers are given in parentheses.

Fig. S4. Influence of CO on growth **(a)** and sulfidogenesis **(b)** in *Halapricum desulfuricans* HSR12-2^T growing anaerobically with three different glucose concentrations (0.2, 0.4 and 0.6 g/l) and sulfur as the electron acceptor. Results represent mean values from a duplicate experiment.

Fig. S5. Anaerobic growth dynamics of *Halanaeroarchaeum* HSR-CO with H₂ as the electron donor and nitrate as the electron acceptor in presence of 0.1 g/l yeast extract as the C source. The data are mean values from a duplicate experiment.

Table S1. Genome statistics of anaerobic carboxydrotrophic haloarchaea.

Table S2. Calculation of the full genomic indexes (AAI, ANI and DDH) between the sulfur-reducing carboxydrotrophic haloarchaea and their closely related stains from the genera *Halanaeroarchaeum* and *Halalkaliarchaeum*.

Table S3. Ni₂Fe-CODH loci in haloarchaea.

Table S4. Comparison of proteins related to anaerobic glycine betaine metabolism encoded in the genomes of *Halalkaliarchaeum desulfuricum* SI^T and *Halalkaliarchaeum* AArc-CO.

Table S5. Shot-gun proteomics comparison of functional enzymes from the cells of sulfur-reducing carboxydrotrophic haloarchaea grown anaerobically with or without CO.

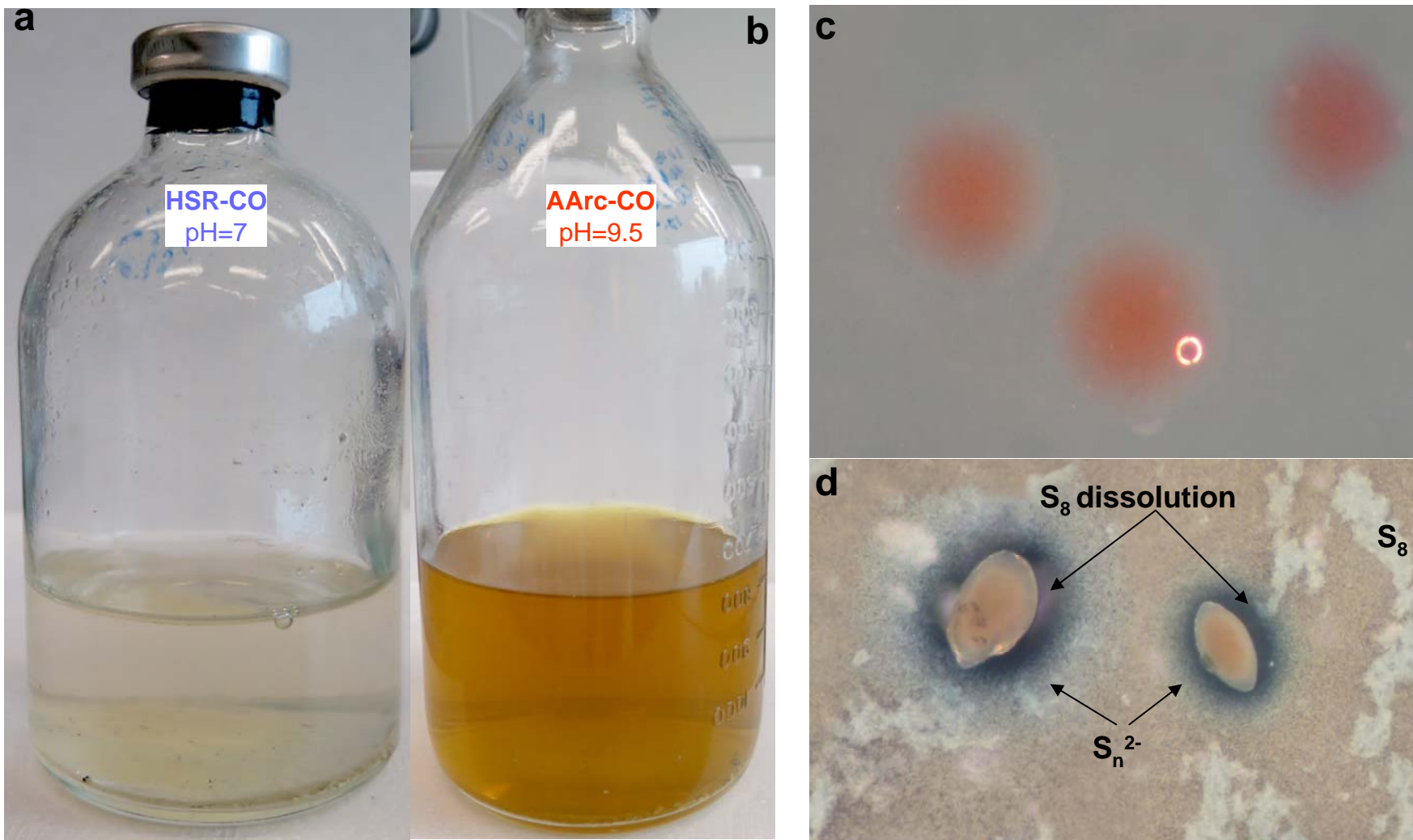


Fig. S1.

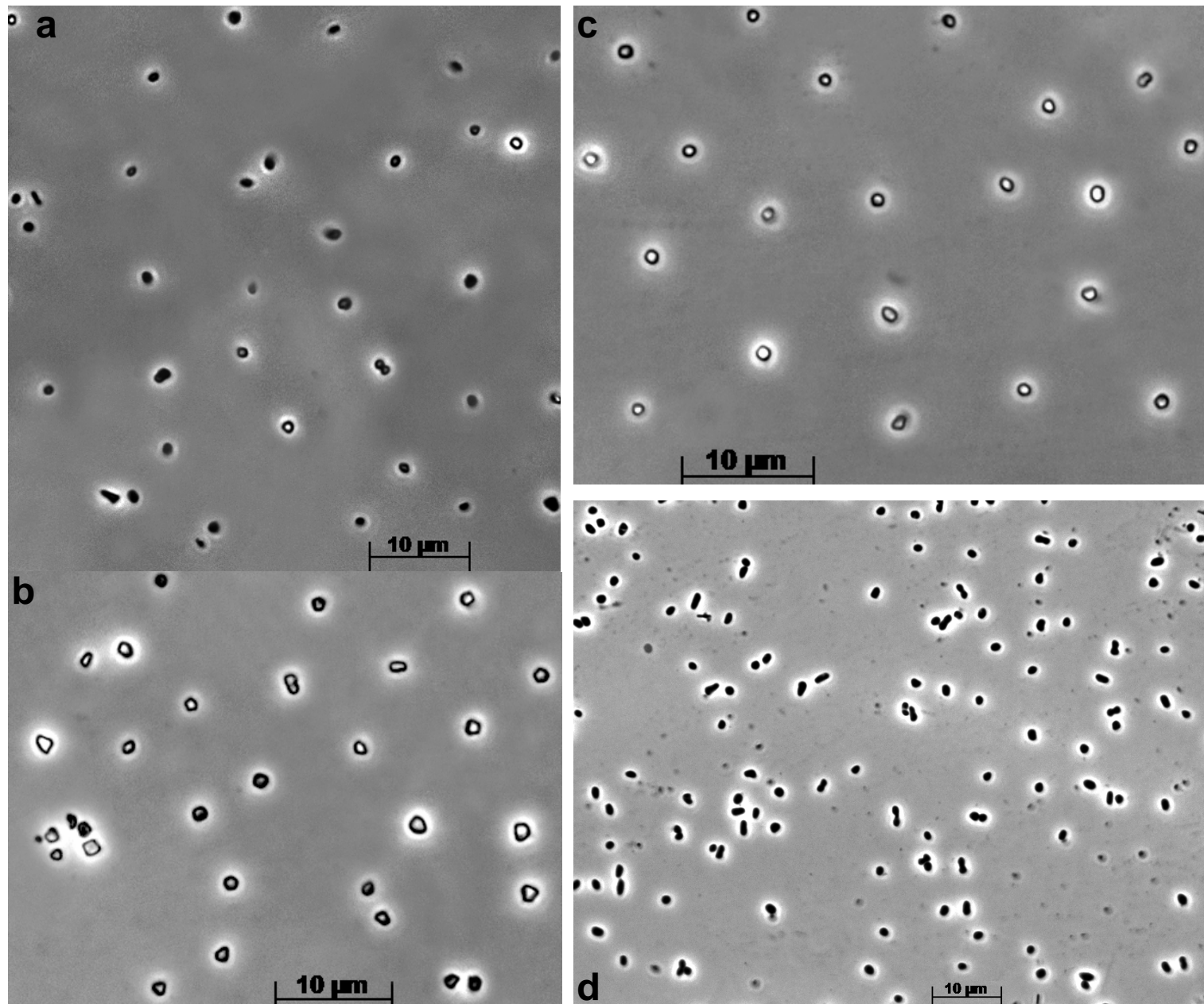


Fig.S2

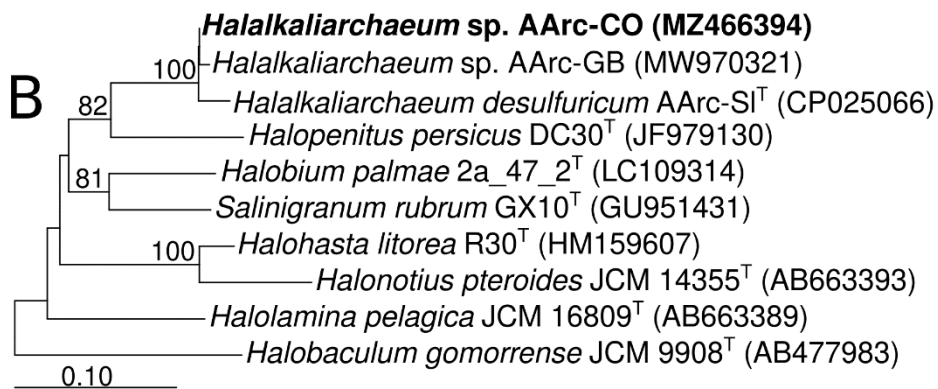
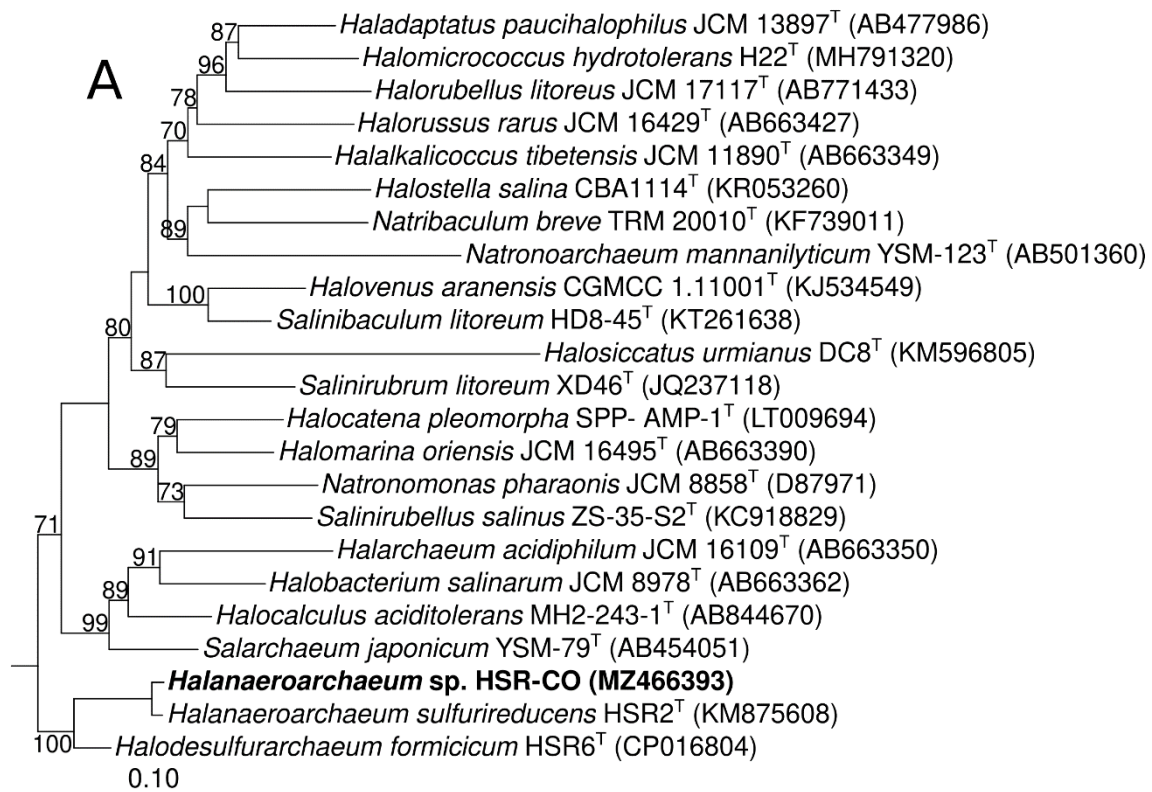
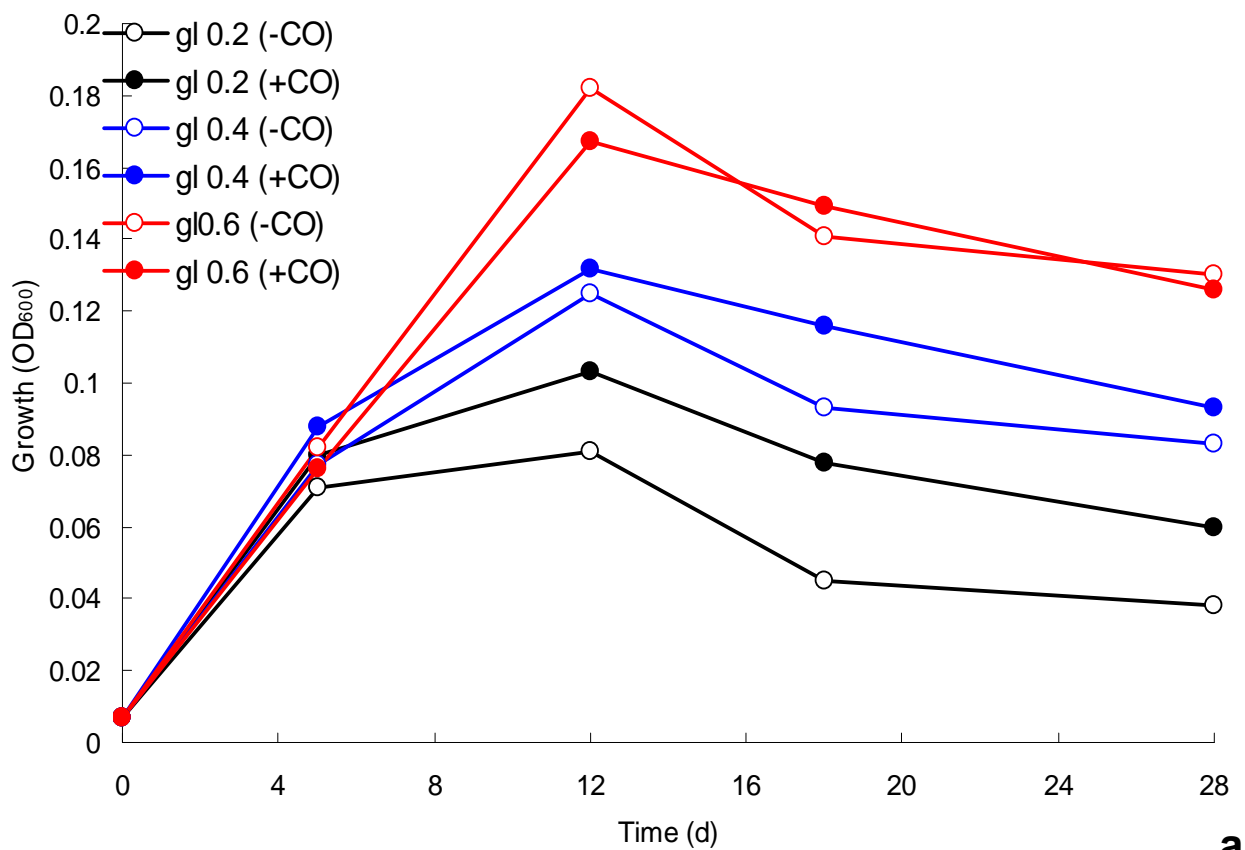
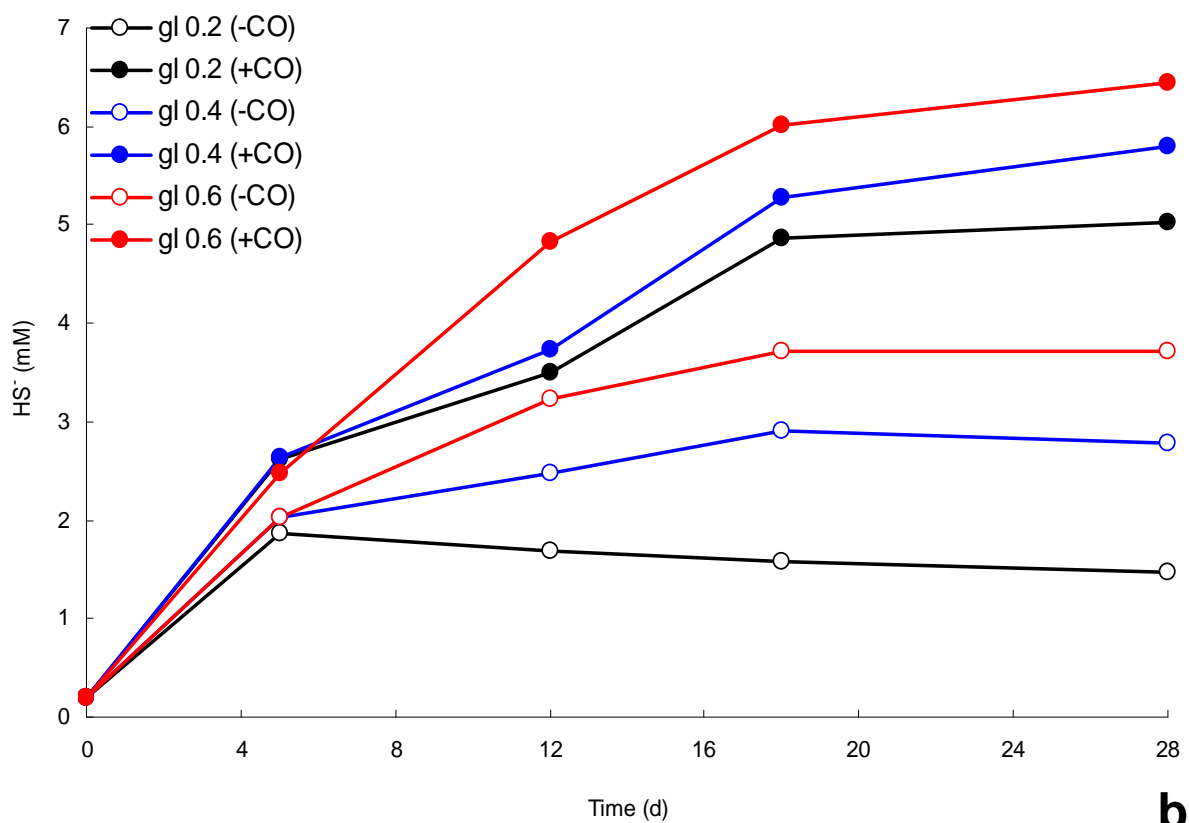


Fig.S3



a



b

Fig.S4

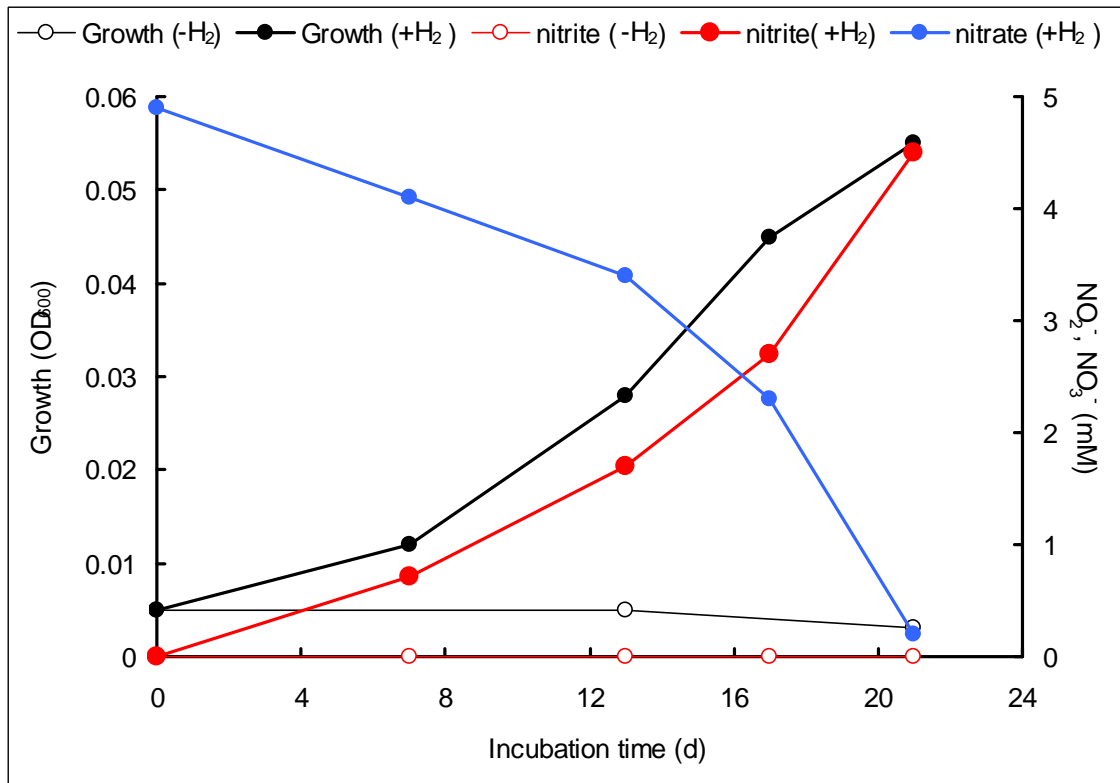


Fig.S5

Supplementary **Table S1.**

Parameter	<i>Halanaeroarchaeum</i> HSR-CO	<i>Halalkaliarchaeum</i> AArc-CO
Genome composition	1 chromosome 1 plasmid	1 chromosome 1 plasmid
Chromosome size (bp)	2,752,700 bp	3,012,260 bp
GC content	63.7%	64.0%
Total genes	2,885	3,073
rRNA genes (5S-16S-23S)	1-1-1	2-2-2 (identical operons)
tRNA genes	47 (4 with introns)	47 (3 with introns)
Protein-coding genes	2,835	3,020
CRISPR regions	0	1
Plasmid (size, bp)	34,990 bp	166,871 bp
G+ C mol%	52.8	55.2
Protein-coding genes	34	157

Supplementary **Table S2**.

Related stain (#Assembly)	ANIm*	Mean AAI (Std AAI)**	DDH***	Probability that DDH > 79%***
HSR-CO				
<i>Halanaeroarchaeum sulfurireducens</i> HSR2 (GCF_001011115.1)	84.26%	77.95% (11.95%)	22.40%	0%
<i>Halanaeroarchaeum sulfurireducens</i> M27-SA2 (GCF_001305655.1)	84.19%	77.83% (11.92%)	22.40%	0%
AArc-CO				
<i>Halalkaliarchaeum desulfuricum</i> AArc-S1 (GCF_002952775.1)	87.57%	87.45% (9.92%)	31.20%	0.17%

* ANIm (ANI with Mummer) calculated using the pyani 0.2.10
(<https://github.com/widowquinn/pyani>)

** AAI calculated using CompareM (<https://github.com/dparks1134/CompareM>)

*** DNA–DNA hybridization (DDH) estimate calculated using the Genome-to-Genome Distance Calculator 2.1 online tool (<http://ggdc.dsmz.de/ggdc.php>) formula 2 (identities / HSP length).

Table S3. Ni,Fe-CODH loci in haloarchaea

CooS

Organism	Locus-tag	Protein sequence
<i>Halanaeroarchaeum</i> sp. HSR-CO	HSR-co_02698	MGsNTGTmSEKtPDPVFDfGPRDSADrTLdVQREVEYEMPVDRLEESQPQCpFGTAGSCCDIcYMGpCRVSDDDQYgQDRgVCGATpGTvVSRnLYREIAGgVSAHSHHAREAVeLLSEIADGGVADYEIKDESklRTIAADVGVQSDGDVNEVARAVADAAEDFAPGGETLNWIQRMPAEQREHLDEQGLLPLSSVDQqASRALAQTHQGNDSdTEHlLGSAlSAGIADGYAGLTMATDLQDIIFGTPTPTNAEAHLGVLEEDQVNlAVHGHSPLQSEMvVKAARELEDEAHAVGAEGINLVGICCTGNELAErHGIPLAaHSLQSELAITTTGAVDAMVVDIQCIWPGISDLMECHHTQLITTMdYVRmREAKHIPFEETALeDAKQIVREIEGYEDRQRrQKYdVNIpDRSQEAVGfSdTAIlDvLEtIDPENPAQPIVDAIQAGQLRGIvGIVGCPNPKMREAEmSEKLIENLLAADVLPVVTGCIghImAQGGYLDpGRVDELAgDGIteLLHALGDAAGLDGPLPpVLHMGsCDNSRIGNVIRAISEGSGIPTRDLpVAASAPeLIAEKAVSIGAWALTGLpVHTApTLHMDQSEEVSRIMTEdLKGITGGYAIQeEDPDAAIDALVAAVDERRLALFDEtGA
<i>Halalkaliarchaeum desulfuricum</i> AArc-S1 ^T	AArc-S1_0878	MSSQTEGEYELPEDrLEESQPQCpFGVGGCCRIcYMGpCRVTDGAHGMDRGVCGATpGTVAARNLYREIAAGAASHADHAREIAEVLEETADGGLSAYDIQDPEKLEAIAADLGI EAETDDENELAKLVAEAAIEDFQGAGETLNWLDrmPDEQREFLeeQGIQPKPSVDMEvARAMHRTTQGNdADpVHLLSGALEAGMADGYAGLTmGTDLQDVVfGRpQPvTEANLGTLEKdQVNIaVHGHSPLSEIIVEMAELEPAAREAGAEGINLVGICCTGNELAErRGIPLAAHSTQAElavTTGALDAMVADIQCIPWGIgDVIECHHTKLLTTTdyVRIpGAEHVSFDpETAeADAREIVQRGIDAYEDrNSRQeYdVEIPDERASAMVGISeDYVLEvLEAASpEDpVAVVDALeAGQLKGIvGIVGCPNPKORTADMTerLIeGLLAENVLPIVtGCIghVTAQAGYLDpARTDELAGDGLSEVLHALGNAAGLDGPLPpVWHMGsCDNSRIGNLVRAISEGADVPtRELpVAASAPeLIAEKAVSIGAWALTGLpVHTApTLHMDQSEEVSRIMTEdLKGITGGYAIQeEDPDAAIDALVAAVDERRLALFDEtGA
<i>Halalkaliarchaeum</i> sp. AArc-CO	AArc-CO_2650	MSSQPDGEYELPEDrLEESQPQCpFGVGGCCRIcYMGpCRVTDGAHGMDRGVCGATpGTVAARNLYREIAAGAASHADHAREIVEVLEETADGGLSAYDIQDPEKLEEIAADLGI EAETDDENELAKLVAEAAVEDFQGAGETLNWLDrmPDEQREFLeeQGIQPKPSVDMEvARAMHRTTQGNdADpAHLLSGALEAGMADGYAGLTmGTDLQDVVfGRpQPvTEANLGTLEADQVNIaVHGHSPLSEMI VEMADELEPAAREVGAEGINLVGICCTGNELAErRGIPLAAHSTQAElavTTGALDAMVADIQCIPWGIgDVIECHHTKLLTTTdyVRIpGAEHVSFDpETAeADAREIVQRGIAAYEDrNSRQeYdVEIPeERTSALVGISeDYVLEvLEAASpEDpVAVVDALeAGQLKGIvGIVGCPNPKORTADMTerLIeGLLEENVLPIVtGCIghVTAQAGYLDpARTDELAGDGLAEVLHALGDAAGLDGPLPpVWHMGsCDNSRIGNLVRAISEGADVPtRELpVAASAPeLIAEKAVSIGTVALTLGLpVHTApTLHMDQSEEVSRIMTEdLKEITGGYAIQeEDPDAAIDALVAAVDERRLALFDEtGA
<i>Halapricum desulfuricans</i> HSR12-1	QSG06169	MSGDpEADpVIdfGPAGSEDrTMEVQREIdYEMPADrLEESQPQCpFGVAGSCCDIcYMGpCRVSDDDQYgQDRgVCGATpGTvVSRnLYREIAGgVSAHSHHAREAVeLLEDIAEENADYIEIKDERklRDIaEDLGLDADGDVNEVAKRVAETAKEDFAPGGGETLNWVERMPAEQREHLDEQDLPLSSVDQqASRALAQTHQGNDSdTGHI LKSALsAGVADGYAGLTMATDLQDVI FGTPTPTNATAHLGVLEEDQVNlAVHGHSPELSEMvVKAaQeLEEEAYEVGAEGINLVGICCTGNELAErHGIPLAaHSLQSELAITTTGAVDAMVVDIQCIWPGISDLMECHHTRLITTMdYVRmREATHIPFEETAMeDAKEIVRQAIeGYEDRQRrQKYdVNIpDRSQEAVGfSdTALLDVLEtIDPDNPAQPIVDAIQSGQLRGIvGIVGCPNPKMREAOmSENLIENLLAADVLPVVTGCIghImAQGGYLDpGTVDELAgDGIrdLLYTLGDAAGLDGPLPpVLHMGsCDNSRIGNVIRAISEGSGIPTRDLpVAASAPeLIAEKAVSIGTVALSLGLPLHTApGLRIEASDAVtQTlTEdLKDITGGHlIQDEtPDGAaEKlIDALDERREPLLNAsAAGASegTAADD
<i>Halapricum desulfuricans</i> HSR12-2 ^T	QSG10136	MSGDpEADpVIdfGPAGSEDrTMEVQREIdYEMPADrLEESQPQCpFGVAGSCCDIcYMGpCRVSDDDQYgQDRgVCGATpGTvVSRnLYREIAGgVSAHSHHAREAVeLLEDIAEENADYIEIKDERklRDIaEDLGLDADGDVNEVAKRVAETAKEDFAPGGGETLNWVERMPAEQREHLDEQDLPLSSVDQqASRALAQTHQGNDSdTGHI LKSALsAGVADGYAGLTMATDLQDVI FGTPTPTNATAHLGVLEEDQVNlAVHGHSPELSEMvVKAaQeLEEEAYEVGAEGINLVGICCTGNELAErHGIPLAaHSLQSELAITTTGAVDAMVVDIQCIWPGISDLMECHHTRLITTMdYVRmREATHIPFEETAMeDAKEIVRQAIeGYEDRQRrQKYdVNIpDRSQEAVGfSdTALLDVLEtIDPDNPAQPIVDAIQSGQLRGIvGIVGCPNPKMREAOmSENLIENLLAADVLPVVTGCIghImAQGGYLDpGTVDELAgDGIrdLLYTLGDAAGLDGPLPpVLHMGsCDNSRIGNVIRAISEGSGIPTRDLpVAASAPeLIAEKAVSIGTVALSLGLPLHTApGLRIEASDAVtQTlTEdLKDITGGHlIQDEtPDGAaEKlIDALDERREPLLNAsAAGASegTAADD
<i>Halapricum desulfuricans</i> " HSR-Est	QSG16218	MGDpPEPVIdLGDAGDpDrTVEAQREIdYEMPADrLEEQQPQCpFGQAGSCCDIcYMGpCRVSDDDQYgDdRGVCGATpGTvVSRnLYREIAGVSSSHHAREsVELLAeIAEeEAGDFEIKDEQklRSIAEDI GLEADGDVNEVAKAVADAAMDDfGPGGETLNWLERMPDSQREVLDEQGLLPLSSVDQqAARALAQTHKGNDSdTGHI LKSALeAGVADGYAGLTMATDLQDVI FGTpSPtDATAHLGVLEEDQVNlAVHGHSPLQSEMvVKAeELEDEAREVgADGINLVGICCTGNELAErHGIPMAaHSLQSELAITTTGALDAMVVDIQCIWPGISDLIECHHTRLITTVdYVRmEEATHIPDEETAMeDAKklVREAIeGYQDRKRrQKYeVNIpDRtQeAMVGFSDSAILGVLESIDPENPAQPIVDAIQAGQLRGIvGIVGCPNPKMREANMTEKLIENLLAADVLPVVTGCIghImAQGGYLDpDRVDELAgDGLQELLYTLGDAAAGLDGPLPpVLHMGsCDNSRIGNVIRAISEGSGIPVQDLpVAASAPeLIAEKAVSIGTVALALGLPLHTApALRIEASEVVTETlTEdLKDITGGYLIQDGTpDGAeQLIDALDERRAPLVDAIDIEAAGTAD
<i>Halorubrum</i> sp. CSM-61	WP_123624322	MATSEdDEPTTPELPEERLEESQPQCpFGVGGCCRIcYMGpCRVSDGAHGMRGVCATpGTVAARNVYREIAsGAASHADHAREIATVLAETADGELSAYDIADPEKLRTIAADLGLDAEGDVSVAEeQVAEAAIEDFQEGGETLNWLDrmPDEQREYLAkQGIePLPSADKEVARAMHRTTQGNdADpKHLLTGAVEAGLTdGYAGLTmGTDLQDVVfGTpQPvQTEADLGLTLEADVNIAVHGHSPLSEMI VEMAELEPAAREAGAEGINLVGICCTGNELAErQKVPLAAHSSQAElavTTGALDAMVADIQCIPWGIgDVIECHHTRLITTVdYVRIpGAEHVSFDpETAeADAEIIVRRGIAAFGRHSRQDYtVEIPDRtTDAMVGSDDfVLNVLESANPENPSRPLVDAMEAGDLNGIVGIVGCPNPKMRTADMTeILIeLLAENVLPIVtGCIghITaQNGYLDpAMTDELAgDGLAAVLNLDGEEAGLDGPLPpVWHMGsCDNSRIGNVIRAISEGADVPtRELpVVASAPeLIAEKAVSIGTVALALGLPLHTApTLHMDHSEEVSRIMTEdLKDITGGFAIQeEDPKAAADIASALDDRtALFREeA

CooC

Organism	Locus-tag	Protein sequence
<i>Halanaerarchaeum</i> sp. HSR-CO	HSR-co_02697	MKLAI TGKGGVGKSTLAAALARS IADERSLMA IDGDPDMNLA STLGVEQPSPITQENDLIEDRAGSSGGLIQMQPDEVVLEEHSATFGAAGR LITIGPPEGGGTG CMCPENNFIRALVNQALDYDDVIMDMEAGIEHLGRGTADDMDAMVVVIEPSRAS IETAHQIRSLANDVGI EHVFAFINRIREPAETEMIREHLELPVIGTFEYDQD VAAAGLQGTSPVDAS PALRDVAETLLEDLDERVL
<i>Halalkaliarchaeum</i> <i>desulfuricum</i> AArc-S1 ^T	AArc-S1_0879	MCEECEGCHDGAG HAHGHPHGHDHHDHHDH ADVETESAVDAPLR IAVTGKGGVGKTTLSAALSTR LASADDVVAVDADPDMNLAATIGCAEPPPVTEKRD LIEDR AGGDGLVRLSPDVEDVLESHSTRFGDGRGRLLTIGAPEGANTGCMCAENSFVQSLVRSALDADCAVLDMEAGIEHLGRGTAGDAMDAMIVVVGPSQSAVETAEGIR ELATEMGVEDVYAVVNRVRGEEGETVREALALPVLETVPYDEDVAAAALSGRPPVEASDRLNVAERI LRGIERRIDGESSPSARPVEGDD
<i>Halalkaliarchaeum</i> sp. AArc-CO	AArc-CO_2651	MCEECEGCHDGAG HDHDPHDHHDHDPHDHHDHDPHDHHDHDPHDHHDHDL GDDEPESVVDGPLRIAVTGKGGVGKSTLSAALSARLTREGDVVAVDADPDMNLA TIGCAEPPA ITRKRELI EDRAGGGGLVRLSPDVEDVLESHSTRFGDGRGRLLTIGAPEGANTGCLCAENSVVQSLVRSALDADYAVLDMEAGIEHLGRGTARDVD AMIVVVGPSQSAIETAKGIRELATEMGVEEVYAVVNRVREGEGEAVREALSLPVLETVPYDEDVAAAALSGTTPVDASDRLTVAVERILRGIDCRIDGADDVTSRF VSAPGSPVE
" <i>Halapricum</i> <i>desulfuricans</i> HSR12-1	QSG06168	MKLAI TGKGGVGKSTLSAAIAQHIADEREVIAIDGDPDMNLAGTLDIEQPAPITRETSLIEDRAGSSGGLLQMQPEVEDVLDKYSVFPFGAAGR LVTIGPPEGGGTG CMCPENNFIRALVNQALDADDVIMDMEAGIEHLGRGTADDMDAMIVVIEPSRAS IETAHQIQSLATDIGIDEIYGFLNKVRDEGEAE LVREQADIPIIETFGYDED VAAAGLQGTSPVEESEALRAVAVDVIDAISDAGP
<i>Halapricum</i> <i>desulfuricans</i> HSR12-2 ^T	QSG10137	MKLAI TGKGGVGKSTLSAAIAQHIADQREVIAIDGDPDMNLAGTLDIERPAPITRETSLIEDRAGSSGGLLQMQPEVEDVLDKYSVFPFGAAGR LVTIGPPEGGGTG CMCPENNFIRALVNQALDADDVIMDMEAGIEHLGRGTADDMDAMIVVIEPSRAS IETAHQIQSLANDIGIDEIYGFLNKVRDEAEAE LVREQADIPIIETFGYDED VAAAGLQGTSPVEESEALRAVAVDVLDAVSE
<i>Halapricum</i> <i>desulfuricans</i> HSR-Est	QSG16219	MKVAITGKGGVGKSTLSAAVAREIADERRMIAIDGDPDMNLSALGIDQDPDITQETDLIEDRAGSSGGLIQLRPEVTDVLESKSVAFGERGR LVTIGPPEAGGTG CMCPENNFIRSLVNQALDYDDVMDMEAGIEHLGRGTADDVDAMIVVVEPSQAS IETAHQIQLTADDIGIDATYAFLNKVRDESEAE LIEDQLALPIVETFGYD IASAGLEGVSPVEASPALRATARDVLDVSVVADIE
<i>Halorubrum</i> sp. CSM-61	WP_123624320	MCDACGRHGDGNSHDSNGSHGQDHREDHEHTHGHDHRKDHDGRVTEPDATVDTDGTVR IAITGKGGVGKSTVAAAQRLANGHETTAIDADPDMNLA TSLGVEE PSPVTDERDLIEDRAGTGGGLIRLTPDVKDVLETHSAEFGPEGRLLTIGAPAAGNTGCMCPENSFVRSLSVSSALAEYVVMMPAGIEHLGRGTAEAVDAFVVVE PSRTSIDTAERI TELAADLGVDTVRAVVKTRGNAETVADKLDVPVIATLPYDEEIAAAGLGGDSPVRASARLRDAATEVVGAFRTTSGDHDEAEGGAKPAN

Table S4: Comparison of proteins related to the anaerobic glycine betaine metabolism encoded in the genomes of *Halalkaliarchaeum desulfuricum* SI^T and *Halalkaliarchaeum* sp. AArc-CO

Gene	Protein	Function	Locus tag in the genome		
			AArc-SI ^T	AArc-CO	
<i>soxB1</i>	Monomeric sarcosine oxidase	THF-dependent sarcosine demethylation	2131	2416	
<i>soxB2</i>			2132	2420	
<i>soxB3</i>			0243	2052	
<i>soxB4</i>			2824	-	
<i>dmg1</i>	Dimethylglycine dehydrogenase	THF/EtfAB-dependent DMG demethylation	0459	2191	
<i>dmg2</i>			-	2258	
<i>etfA</i>	Electron transfer flavoproteins	Transfer of electrons from DMG and possibly from sarcosine oxidative demethylation to quinone	0457	2256	
<i>etfB</i>			0458	2257	
<i>mtgA1</i>	GB-specific methyl-transferases	Cobalamin-dependent anaerobic glycine betaine demethylation	0459	2263	
<i>mtgB1</i>			0468	2267	
<i>mtgC</i>			0470	2269	
<i>mtgB2</i>			1175	0698	
<i>mtgB3</i>			-	2184	
<i>mtgB4</i>			-	2419	
<i>metF1</i>	Methyl-group oxidation	NAD(P)-dependent 5,10-methylene-THF reductase	0463	2262	
<i>metF2</i>			-	1684	
<i>fdhH</i>		NAD-dependent formate dehydrogenase	0465	2264	
<i>fhs</i>		Formate-THF ligase	0467	2266	
<i>folD</i>		Methenyl-THF cyclohydrolase/dehydrogenase	0469	2268	
<i>mch</i>		Methenyl-THP cyclohydrolase	1968	1967	
<i>metH/E</i>		Methyl-group assimilation	5-methyl-THF-homocysteine methyltransferase	0456	2255
<i>glyA1</i>			Glycine hydroxymethyltransferase	1001	0928
<i>glyA2</i>	(glycine>>serine)		2531	-	
<i>betA1</i>	Choline oxidation to GB	Choline dehydrogenase (choline>GB aldehyde)	0622	2408	
<i>betB1</i>		GB aldehyde dehydrogenase (GBA>GB)	0623	2409	
<i>betA2</i>		Choline dehydrogenase	2225	-	
<i>betB2</i>		GB aldehyde dehydrogenase	2226	2292	
<i>betB3</i>			0486	-	
<i>betT1</i>		GB-choline uptake	Choline/GB/carnithine family transporter	0477	2270
<i>betT2</i>	-			2276	
<i>betT3</i>	-			2407	
<i>betT4</i>	-			2418	
<i>opuCB</i>	ABC type of GB/choline transporter		2214	2186	
<i>opuCA</i>			2215	2187	
<i>opuCD</i>			2216	2188	
<i>opuAC</i>			2217	2189	

Hypothetical pathway of choline-GB metabolism in *Halalkaliarchaeum*:

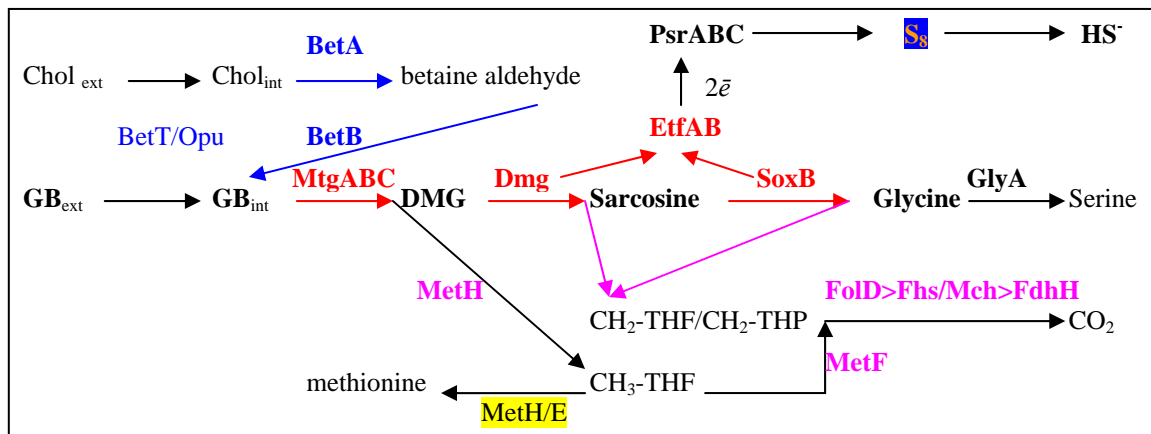


Table S5

<i>Halanaeroarchaeum</i> HSR-CO							<i>Halalkaliarchaeum</i> AArc-CO						
locus-tag	(-)CO		(+)CO		Mass	protein	locus-tag	(-)CO		(+)CO		Mass	protein
	-10lgP	#Peptides	-10lgP	#Peptides				-10lgP	#Peptides	-10lgP	#Peptides		
HSR-CO_02512	92.0	1	57.6	1	35659	HypE; hydrogenase expression/formation protein	AArc-CO_2392			363	12	55265	HyaB membrane Ni,Fe hydrogenase, large subunit
							AArc-CO_2393			65	1	6504	HyaC, membrane subunit
HSR-CO_02685	236.6	14	86.0	3	82187	HypF; hydrogenase maturation	AArc-CO_2394			190	4	19699	HyaD hydrogenase maturation factors
HSR-CO_02686	140.0	4	138.0	4	32133	HypB; hydrogenase nickel incorporation protein	AArc-CO_2397	59	2	41	1	38732	HypD
HSR-CO_02687	46.8	1			13907	HypA, hybF; hydrogenase nickel incorporation protein	AArc-CO_2398	117	4	241	10	38267	HypE
HSR-CO_02689	226.4	8	155.6	6	39483	HypD; hydrogenase expression/formation protein	AArc-CO_2399			50	1	14260	HypA
HSR-CO_02690	74.5	1			10483	HypC; hydrogenase expression/formation protein	AArc-CO_2400	98	2	172	4	30758	HypB
HSR-CO_02695	208.8	5	158.9	4	38842	HyaA hydrogenase small subunit	AArc-CO_2401	45	1	150	3	82822	HypF
							AArc-CO_2635	183	5	186	5	33764	EtfA1 ; electron transfer flavoprotein, subunit A
							AArc-CO_2636	132	3	178	2	28875	EtfB1; electron transfer flavoprotein, subunit B
HSR-CO_02697	354.2	17	278.4	15	70189	CooS; CODH, catalytic subunit	AArc-CO_2650	200	7	185	5	66419	CooS, CODH, catalytic subunit
HSR-CO_02698	272.6	11	140.4	2	26137	CooC; CODH, Ni-incorporating maturation protein	AArc-CO_2651						CooC, CODH Ni-incorporating maturation protein
							AArc-CO_00408	359	31	391	21	74039	FdhH1; formate dehydrogenase (coenzyme F ₄₂₀) alpha
							AArc-CO_2264	282	22	309	18	79020	FdhH2; formate dehydrogenase (coenzyme F ₄₂₀) alpha (GB locus)
HSR-CO_02242	86.1	2	90.2	2	19599	FdoH iron-sulfur subunit	AArc-CO_1939	240	15	341	21	108463	FdoG, membrane formate dehydrogenase, major subunit
HSR-CO_02243	402.1	32	347.5	33	108611	FdoG major subunit	AArc-CO_1940	77	2			18653	FdoH; iron-sulfur subunit
							AArc-CO_1942			69	1	36063	FdoI; membrane diheme cyt.b subunit
HSR-CO_02658	327.8	25	302.8	25	125707	TtrA; tetrathionate reductase subunit A	AArc-CO_1111			37	1	119958	TtrA; tetrathionate reductase, catalytic subunit
HSR-CO_01917	442.8	33	346.8	27	84633	PsrA1	AArc-CO_1245	246	10	281	7	86130	SseA; sulfur transferase (extracellular)
	258.7	9	145.6	5	22283	PsrB1	AArc-CO_1246	344	23	448	27	87661	PsrA; polysulfide reductase, catalytic
HSR-CO_02118	113.4	2			32646	SseA1; thiosulfate/3-mercaptopyruvate sulfurtransferase	AArc-CO_1247			117	2	23143	PsrB; iron sulfur subunit
HSR-CO_02851	377.2	19	302.0	13	45230	SseA2;							
HSR-CO_02852	510.7	38	337.4	30	84411	PsrA2							
HSR-CO_01281	362.3	27	295.5	26	90300	DmsA1	AArc-CO_2906	135	3	122	2	48339	DmsC; dimethyl sulfoxide reductase membrane subunit
HSR-CO_01282	258.7	10	154.5	4	27604	DmsB1; dimethyl sulfoxide reductase iron-sulfur subunit	AArc-CO_2907	193	7	206	5	27541	DmsB; iron-sulfur subunit
							AArc-CO_2908	248	18	247.5	13	93065	DmsA; catalytic subunit
HSR-CO_02129	103.1	3	122.6	5	90803	DmsA2							
HSR-CO_02131			70.4	1	48200	DmsC2	AArc-CO_1207			78	1	44872	PsrB/NrfC(1)
HSR-CO_02137	389.2	31	276.4	25	91962	DmsA3	AArc-CO_1208			64	1	48711	PsrC/NrfD, polysulfide reductase, membrane subunit
HSR-CO_02138	223.8	9	150.7	4	27964	DmsB3	AArc-CO_1210			125	3	45337	PsrB/NrfC (2)
HSR-CO_02139			151.8	5	46042	DmsC3	AArc-CO_1518			63	1	46158	PsrB/NrfC (3)
							AArc-CO_1758			142	2	42649	PsrB/NrfC (4)
							AArc-CO_00216	278	18	269	10	125084	hdrA2; heterodisulfide reductase subunit
							AArc-CO_00218	160	3	215	4	35377	EtfA2
							AArc-CO_00219			204	4	28576	EtfB2
HSR-CO_02148	229.3	9	228.5	7	33330	EtfA1; electron transfer flavoprotein, subunit A	AArc-CO_1725	63	2	116	2	31710	EtfB3
HSR-CO_02149	224.3	4	178.3	3	28651	EtfB1; electron transfer flavoprotein, subunit B	AArc-CO_1726			53	1	62125	EtfA3
							AArc-CO_1727			182	4	59763	EtfC1
HSR-CO_01647	308.3	9	228.8	7	27550	etfB2	AArc-CO_1914			156	4	12899	EtfX electron transfer flavoprotein, ferredoxin subunit
HSR-CO_01648	300.4	13	244.0	10	36751	etfA2	AArc-CO_1915	285	20	303	13	49205	EtfC2
HSR-CO_01649	425.8	24	264.5	15	48743	EtfC	AArc-CO_1916	255	12	318	13	37254	EtfA4
HSR-CO_01651	139.2	3	76.8	1	12134	EtfX; ferredoxin like protein	AArc-CO_1917	199	8	230	8	27238	EtfB4
HSR-CO_01652	74.24	1	74.24	1	59502	Fhs, formate-tetrahydrofolate ligase/foprmyl-THF synthase							
							AArc-CO_2094	179	6	239	6	50756	EtfD electron transfer flavoprotein quinol dehydrogenase
							AArc-CO_2256	233	9	306	9	33671	EtfA5 (part of the glycine-betaine oxidation (GB locus)
							AArc-CO_2257	214	7	197	5	26199	EtfB5
HSR-CO_00269	91.6	1	108.1	2	12085	NuoA; NADH-quinone oxidoreductase (ferredoxin?)	AArc-CO_1696	77	2	66	1	15245	NuoA; NADH-quinone oxidoreductase (ferredoxin-oxidizing?)
HSR-CO_00270	246.2	9	177.4	10	26189	NuoB	AArc-CO_1697	151	9	166	8	26138	NuoB
HSR-CO_00271	400.1	34	311.3	27	64375	NuoCD	AArc-CO_1698	261	19	312	15	63323	NuoCD
HSR-CO_00272	141.8	5	136.2	6	36881	NuoH	AArc-CO_1699	98	2	76	1	37665	NuoH
HSR-CO_00273	196.7	6	104.9	2	17739	NuoI	AArc-CO_1700	50	1	104	2	17716	NuoI
HSR-CO_00274			53.3	1	11031	NuoK							
HSR-CO_00275	133.2	2	127.4	3	74148	NuoL	AArc-CO_1704	131	3	109	1	71925	NuoL
HSR-CO_00276	48.2	1	74.7	2	54461	NuoM	AArc-CO_1705	73	2			54461	NuoM
							AArc-CO_0005			356	17	45675	Ferredoxin-NAD ⁺ reductase
							AArc-CO_1942			101	2	22138	Fpr, flavodoxin-NADP ⁺ reductase
							AArc-CO_1942			54	1	42698	Ndh1; NADH:quinone reductase (H+-translocating)
							AArc-CO_1942	212	8	261	8	43718	Ndh2; NADH:quinone reductase (H+-translocating)
HSR-CO_00988	236.9	7	88	2	33731	Qor1; NADPH:quinone reductase	AArc-CO_1942			190	4	36846	QorA1, NADPH-quinone reductase, proton
HSR-CO_00276	67.4	1	139.7	4	33301	Qor2	AArc-CO_1942	229	10	259	8	33507	QorA2, NADPH-quinone reductase, proton
HSR-CO_02418	192	3	147	5	23440	Fno, F ₄₂₀ -NADP ⁺ reductase							
							AArc-CO_2388			150	3	18234	PhaC, PHA synthase type III