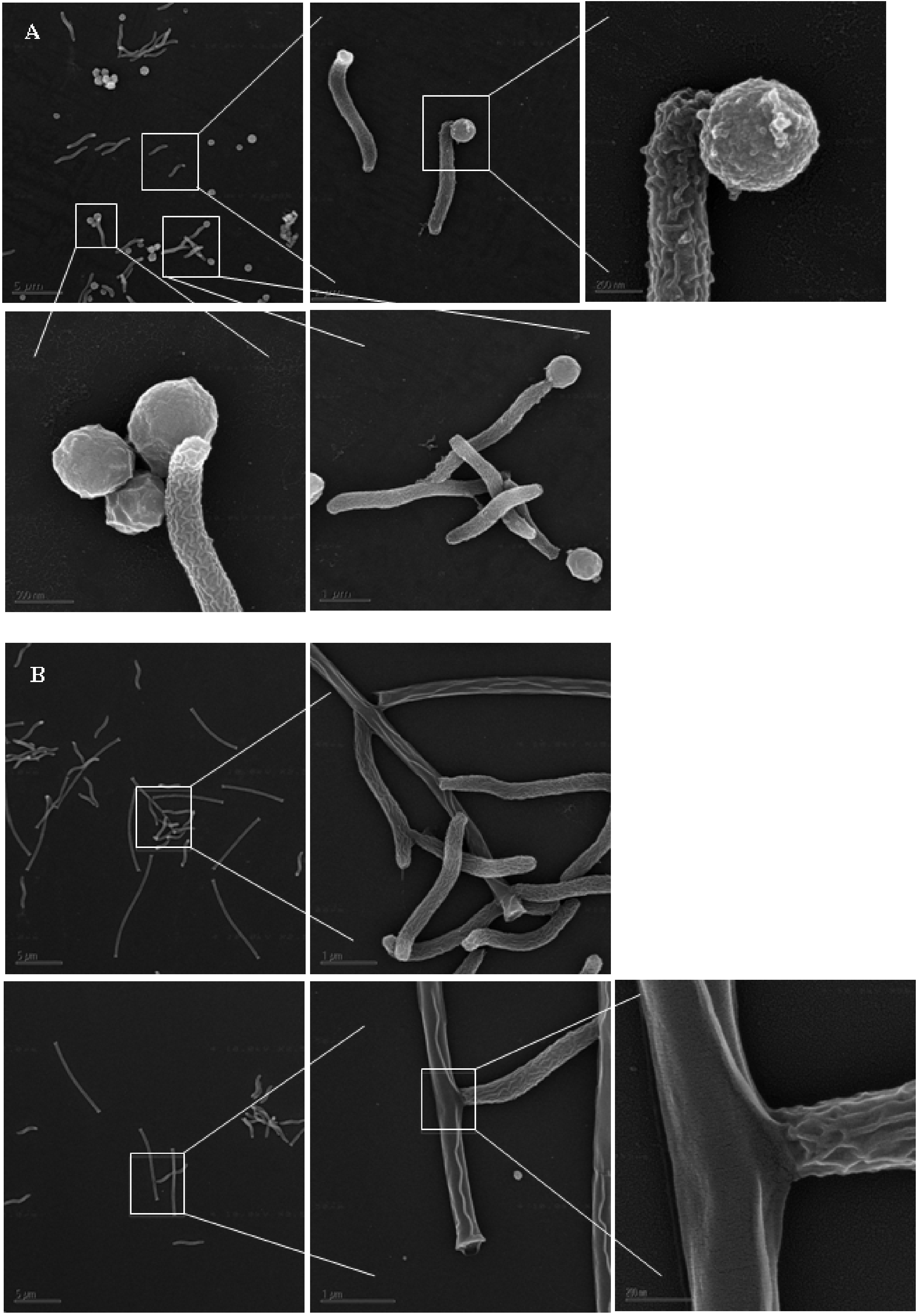
Supplemental Table S1: Detailed description of all transposon mutant strains (provided by A. Deutschbauer) used in this study

Strain ID [a]	**Insertion location** [b]	**Strand** [c]	**VIMSS ID** [d]	**Offset** [e]	**Gene Strand** [f]	**Gene ID**	**Description (as annotated in MicrobesOnline)**
JK00829	1099300	+	395608	173	+	Dde_1072	Conserved hypothetical protein
JK01112	1143756	+	395573	559	+	Dde_1114	Conserved hypothetical protein
JK01149	668339	-	392830	440	-	Dde_0649	HmcE
JK01185	697816	-	395941	188	-	Dde_0681	Oxidoreductase, iron-sulfur cluster-binding subunit
JK01905	1100971	-	395606	1461	-	Dde_1074	L-lactate permease, putative
JK01925	1290825	-	395452	1357	-	Dde_1273	Glycine radical family, pyruvate:formate lyase
JK02210	699995	+	395940	201	-	Dde_0682	Putative oxidoreductase, major subunit
JK03586	302156	+	393120	1320	+	Dde_0312	Oxidoreductase, putative
JK03700	737451	+	395910	485	+	Dde_0718	Anaerobic dimethyl sulfoxide reductase chain b
JK05672	735457	+	3334077	1524	+	Dde_0717	Formate dehydrogenase, alpha subunit
JK05969	368539	+	393064	1070	-	Dde_0374	NADH oxidase (nox)
JK07175	3231075	-	393794	83	+	Dde_3238	L-lactate permease, putative
JK07910	3474289	-	3334782	1811	+	Dde_3513	Formate dehydrogenase alpha subunit
JK08116	3235202	+	393792	943	+	Dde_3240	Glycolate oxidase iron-sulfur subunit (*E. coli*)
JK09366	3241265	+	393787	401	+	Dde_3245	Iron-sulfur cluster binding protein
JK10137	2917064	+	394059	971	+	Dde_2935	Probable Ni/Fe-hydrogenase 2 b-type cytochrome subunit
JK10695	667540	-	392831	533	-	Dde_0648	HmcF
JK11220	482572	+	3334012	305	+	Dde_0473	Formate dehydrogenase, alpha subunit
JK11401	3016773	+	393974	339	+	Dde_3029	CODH nickel-insertion accessory protein (cooC)
JK11903	2183143	-	394696	966	+	Dde_2135	Periplasmic [NiFeSe] hydrogenase, large subunit
JK12024	2185939	+	394693	246	+	Dde_2138	Probable large subunit, hydrogenase-2
JK12428	3475857	+	393590	114	+	Dde_3515	Conserved hypothetical protein
JK12756	670559	-	392828	702	-	Dde_0652	HmcB
JK13582	76078	+	393312	257	+	Dde_0081	Periplasmic (fe) hydrogenase large subunit
JK13595	2302198	-	394565	433	-	Dde_2281	Iron only hydrogenase large subunit, C-terminal domain
JK14050	834892	+	395830	1229	-	Dde_0813	Formate dehydrogenase, alpha subunit

[a] transposon mutant identifier
[b] transposon insertion location in the G20 main chromosome
[c] transposon insertion orientation, (+) is 5' to 3' while (-) is 3' to 5'
[d] gene identifier used in MicrobesOnline
[e] the location of the transposon insertion from the start of the gene
[f] (+) or (–) define whether the targeted gene is on the plus or minus strand

Supplemental Figure S2: Scanning electron microscopy (SEM) images of *D. alaskensis* str. G20 grown at low growth rate of 0.027 h^{-1} in coculture with (A) *M. maripaludis* or (B) *M. hungatei*.



Cell collection and fixation for SEM imaging: 1 ml cell suspension (anoxic) added to 5 ml fixative mix (2.5 % glutaraldehyde in 0.1% sodium cacodylate buffer) in 15 ml Falcon tube, gently mixed (3-4 times carefully flipping the tube), and stored at 4°C in the dark until further analysis.

Scanning electron microscopy (SEM) imaging: SEM sample preparation and imaging was carried out by M. Zemla at LBNL, Berkeley (M. Auer laboratory, LBNL, Berkeley; all images courteously provided by M. Auer). SEM samples of the fixed cells were prepared using poly-l-lysine coated silicon wafers followed by a post-fixation with 1% osmium tetroxide, dehydration with a graded ethanol series (20%, 40%, 60%, 80%, 100%, 100%, 100%), critical point drying using a Tousimis Auto Samdri 815 Critical Point Dryer (Tousimis, Rockville, MD, USA), and sputter coating with 10-15 nm gold-palladium using a Tousimis Sputter Coater (Tousimis, Rockville, MD, USA). Images were collected using a Hitachi S5000 Scanning Electron Microscope (Hitachi High Technologies America, Pleasanton, CA, USA). Image annotation and linear contrast optimization was performed in Adobe Illustrator CS2.

Supplemental Table S3A: Differentially expressed genes organized by their COG functional categories in *Dv. alaskensis* str. G20 grown under syntrophic conditions with *Methanococcus maripaludis* at 0.027 h^{-1}

E. Amino acid transport and metabolism

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0090		1,34	5,61	2-hydroxyglutaryl-CoA dehydratase family (Natalia Ivanova)
Dde_1326		0,49	4,94	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component
Dde_1328		0,53	4,66	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components
Dde_1329		0,52	4,13	ABC-type dipeptide transport system, periplasmic component
Dde_1692	gcvP	-0,52	-5,61	Glycine cleavage system P protein, subunit 1 (gcvP)
Dde_2166	ilvC	-0,64	-3,91	Ketol-acid reductoisomerase / Dehydropantoate reductase (Natalia Ivanova)
Dde_2306		-0,55	-4,02	Arginine ABC transporter, periplasmic arginine-binding protein, putative

G. Carbohydrate transport and metabolism

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0828		-0,50	-5,57	TPR domain protein
Dde_1091		0,91	2,29	Conserved hypothetical protein
Dde_3736	gap	-0,55	-5,27	Glyceraldehyde-3-phosphate dehydrogenase, type I

D. Cell division and chromosome partitioning

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0832		-0,51	-5,59	Polysaccharide biosynthesis protein, putative
Dde_3202	mrp	-1,71	-5,61	Mrp protein (mrp)

N. Cell motility and secretion

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_3159	flgF	0,61	5,44	Flagellar basal body rod protein

M. Cell envelope biogenesis

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0456		-0,68	-5,61	TonB-like
Dde_0829	pss	-0,59	-5,61	Exopolysaccharide production protein Pss (pss)
Dde_0830		-0,66	-5,61	Outer membrane protein, putative
Dde_2156		-1,60	-5,61	TonB-like

H. Coenzyme metabolism

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0719		1,17	5,55	Fe-S cluster domain protein
Dde_1556	thiH	-0,52	-3,78	Thiamin biosynthesis, thiazole moiety

V. Defense mechanisms

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0445		-1,40	-5,61	ABC-type multidrug transport system, ATPase component

C. Energy production and conversion

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0082	hydB	0,57	5,53	Periplasmic (fe) hydrogenase small subunit precursor
Dde_0286	fd II	1,31	5,61	Ferredoxin II (Sean Caffrey)
Dde_0715		2,85	5,61	hypothetical protein
Dde_0717		1,40	5,61	formate dehydrogenase, alpha subunit
Dde_0718		1,10	5,61	Anaerobic dimethyl sulfoxide reductase chain b (hybA)
Dde_1074		1,30	5,61	Putative permease
Dde_1112	QmoB	-0,50	-4,29	Quinone-interacting membrane-bound oxidoreductase (Shelley Haveman)
Dde_2134		-1,33	-5,61	hydrogenase (NiFe) small subunit HydA

Dde_2135	hysA	-1,37	-5,61	periplasmic [NiFeSe] hydrogenase, large subunit, selenocysteine-containing
Dde_2137	hynB-1	1,11	5,61	periplasmic [NiFe] hydrogenase, small subunit, isozyme 1 (Sean Caffrey)
Dde_2138	hynA-1	0,94	4,23	Probable large subunit, hydrogenase-2
Dde_2274	dsrO	-0,63	-4,51	Periplasmic (Tat), binds 2[4Fe-4S] (Shelley Haveman)
Dde_2280	hydB-2	0,50	5,30	Periplasmic Fe hydrogenase small subunit (Shelley Haveman)
Dde_2562		-0,69	-4,65	Pyridine nucleotide-disulphide oxidoreductase family
Dde_2641	b0873	-0,76	-3,32	hybrid cluster protein
Dde_2701	qtpE	-0,57	-2,54	ATP synthase c chain
Dde_2749		-0,65	-3,95	rubredoxin
Dde_3182		1,22	4,11	Cytochrome c3 precursor
Dde_3200		-1,67	-5,61	Iron-sulfur cluster binding protein
Dde_3211		1,50	4,22	split soret cytochrome c precursor
Dde_3201		-1,12	-5,61	Iron-sulfur cluster binding protein
Dde_3237		0,62	5,43	Putative oxidoreductase, Fe-S subunit
Dde_3238		0,62	4,36	L-lactate permease, putative
Dde_3239	glcD	0,75	2,57	Glycolate oxidase subunit D
Dde_3240		0,63	3,72	Glycolate oxidase iron-sulfur subunit. {escherichia, putative
Dde_3242	ackA	0,56	5,45	acetate kinase
Dde_3245		0,62	3,76	Iron-sulfur cluster binding protein
Dde_3667	fld	-2,68	-5,61	Flavodoxin, iron-repressed (Dmitry Rodionov)
Dde_3707	tmcD	-1,49	-5,61	Transmembrane complex
Dde_3708	tmcC	-1,00	-5,61	Transmembrane complex, integral membrane protein (Shelley Haveman)
Dde_3709	tmcB	-1,51	-5,61	Transmembrane complex, ferredoxin, 2 [4Fe-4S] (Shelley Haveman)
Dde_3710	tmcA	-1,02	-5,61	Transmembrane complex, tetraheme cytochrome c3 (Shelley Haveman)

S. Function unknown

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0484		-0,89	-5,61	Conserved hypothetical protein
Dde_0959		0,61	4,46	Uncharacterized conserved protein
Dde_2018		1,99	5,61	HesB-like domain, putative
Dde_2020		-1,57	-5,61	Conserved hypothetical protein
Dde_2561		-0,74	-5,03	Rhodanese-like domain protein
Dde_2799		0,54	3,32	Uncharacterized phage-encoded protein
Dde_3198		-1,94	-5,61	Uncharacterized ACR, COG1433 family
Dde_3244		0,51	4,88	Uncharacterized ACR, YkgG family COG1556 family

R. General function prediction only

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0444	pqqL	-1,53	-5,61	Putative peptidase
Dde_0449		-0,69	-4,92	Putative transport system permease protein
Dde_1883		0,64	3,11	Phage protein D
Dde_2281	hydA-2	0,76	5,04	Iron only hydrogenase large subunit, C-terminal domain
Dde_2922	norQ	0,56	3,55	NorQ protein (norQ)
Dde_3033		0,49	2,46	Metal-dependent amidase/aminoacylase/carboxypeptidase
Dde_3243		0,57	5,61	Phosphate acetyltransferase, putative
Dde_3351		0,50	4,98	B protein, putative
Dde_3372		0,57	5,11	Conserved hypothetical protein
Dde_3640		-0,54	-4,49	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily
Dde_0444	pqqL	-1,53	-5,61	Putative peptidase

P. Inorganic ion transport and metabolism

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0326		-0,67	-5,54	Putative a membrane protein
Dde_0805		1,07	5,61	DoxX family protein
Dde_0806		1,14	5,61	Rhodanese-like domain protein
Dde_1312		-1,76	-5,61	Copper chaperone
Dde_2506		0,67	2,07	Orf, hypothetical protein
Dde_2669	feoB	-2,06	-5,61	ferrous iron transport protein B
Dde_2670	feoA	-2,50	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)
Dde_2673	feoA	-1,98	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)
Dde_3324	phnC	0,55	4,86	ATP-binding component of phosphonate transport
Dde_3326	phnE	0,61	4,94	ABC-type phosphate/phosphonate transport system, permease component

U. Intracellular trafficking, secretion, and vesicular transport

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0453		-0,65	-5,61	biopolymer transport proteins-like
Dde_0454		-0,54	-5,61	biopolymer transport proteins-like

Dde_0455		-0,51	-4,64	Biopolymer transport protein
Dde_2153		-2,64	-5,61	Biopolymer transport proteins
Dde_2154		-2,78	-5,61	Biopolymer transport proteins
Dde_2155		-1,90	-5,61	Biopolymer transport protein
Dde_2177	tatA	0,90	3,55	Twin-arginine translocation protein TatA
Dde_2237	secY	-0,59	-5,33	Putative ATPase subunit of translocase

I. Lipid transport and metabolism

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0089		1,17	5,61	Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)

O. Posttranslational modification, protein turnover, chaperones

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_1343	hspC	-0,50	-5,61	Small heat shock protein (class I) (hspC)
Dde_2473	mopA	-0,51	-5,61	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein
Dde_2560		-0,90	-4,19	Thioredoxin peroxidase
Dde_3054	pflA	0,65	3,48	Pyruvate formate-lyase activating enzyme (pflA)

L. Replication, recombination and repair

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0912		0,50	4,34	Site-specific recombinase XerD
Dde_1172	hrpB	0,74	2,07	ATP-dependent helicase HrpB
Dde_1921		0,49	4,76	DNA primase (bacterial type)
Dde_2323	ruvA	0,49	1,97	Holliday junction DNA helicase RuvA

T. Signal transduction mechanisms

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0227	cstA	0,75	3,19	Carbon starvation protein
Dde_0327		-0,55	-5,34	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains
Dde_0533		0,57	3,02	FOG: CheY-like receiver
Dde_1151	hdd	-0,60	-3,91	Response regulator containing a CheY-like receiver domain and an HD-GYP domain
Dde_2172		-0,60	-5,35	YGGT family superfamily
Dde_3047		-0,61	-3,20	Serine phosphatase RsbU, regulator of sigma subunit
Dde_3048	gdp	-0,75	-4,63	FOG: GGDEF domain
Dde_3712		-1,53	-5,61	Universal stress protein family family
Dde_3713	mtrA	-1,60	-5,61	DNA-binding response regulator (mtrA)
Dde_3715		-0,59	-3,07	Sensory transduction histidine kinase-related
Dde_3737		-0,70	-5,61	Phosphoenolpyruvate-protein phosphotransferase, putative

K. Transcription

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0710		0,56	2,40	Phosphoglycerate transport system transcriptional regulatory protein PgtA, putative
Dde_1611		-1,21	-5,61	AraC family transcriptional regulator
Dde_1741		0,67	2,71	Prophage antirepressor

J. Translation, ribosomal structure, and biogenesis

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0017		0,55	2,11	sun protein
Dde_2236	map	-0,56	-5,60	methionine aminopeptidase, type I
Dde_2251	rpsC	-0,49	-3,64	Ribosomal protein S3
Dde_2255	rplW	-0,60	-5,23	50S ribosomal subunit protein L23
Dde_2982	rpmE	0,78	5,00	Ribosomal protein L31
Dde_2989	tuf	0,60	4,67	Translation elongation factor Tuf
Dde_0017		0,55	2,11	sun protein

Supplemental Table S3B: Differentially expressed genes organized by their COG functional categories in *Dv. alaskensis* str. G20 grown under syntrophic conditions with *Methanospirillum hungatei* at 0.027 h^{-1}

E. Amino acid transport and metabolism

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0448		-0,64	-5,61	ABC transporter, periplasmic substrate-binding protein
Dde_0608	livF	1,00	2,54	ATP-binding component of leucine transport
Dde_2664	lysA	0,52	2,87	diaminopimelate decarboxylase

D. Cell division and chromosome partitioning

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_3029	cooC-2	0,69	4,95	CODH nickel-insertion accessory protein (cooC-2)
Dde_3202	mrp	-1,74	-5,61	Mrp protein (mrp)

N. Cell motility and secretion

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_3158	flgG	0,68	5,61	Flagellar biosynthesis, cell-distal portion of basal-body rod
Dde_3159	flgF	0,77	5,61	Flagellar basal-body rod protein FlgF (flgF)

M. Cell envelope biogenesis

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0456		-0,76	-5,61	TonB-like
Dde_2156		-1,76	-5,61	TonB-like

H. Coenzyme metabolism

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0234		1,18	5,38	Conserved hypothetical protein
Dde_0719		1,91	5,61	Fe-S cluster domain protein
Dde_0871		-0,59	-3,71	Molybdopterin-binding protein
Dde_1554		-0,56	-4,69	thiamine biosynthesis protein ThiS
Dde_3309		0,51	4,01	Conserved hypothetical protein

V. Defense mechanisms

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0445		-1,53	-5,61	ABC-type multidrug transport system, ATPase component

C. Energy production and conversion

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0715		3,60	5,61	hypothetical protein
Dde_0717		2,90	5,61	formate dehydrogenase, alpha subunit
Dde_0718		2,20	5,61	Anaerobic dimethyl sulfoxide reductase chain b (hybA)
Dde_1074		1,50	5,61	Putative permease
Dde_2562		-0,75	-5,61	Pyridine nucleotide-disulphide oxidoreductase family
Dde_2641	b0873	-0,93	-4,48	hybrid cluster protein
Dde_2749		-0,57	-4,11	rubredoxin
Dde_2933		0,64	5,61	Molybdopterin oxidoreductase, molybdopterin binding subunit, putative
Dde_2934	narH	0,60	5,47	Respiratory nitrate reductase, beta subunit (narH)
Dde_3028	cooS	0,79	5,05	carbon-monoxide dehydrogenase, catalytic subunit
Dde_3182		1,19	4,20	Cytochrome c3 precursor
Dde_3195	fprA-2	0,63	5,61	Putative flavodoxin
Dde_3200		-1,67	-5,61	Iron-sulfur cluster binding protein
Dde_3201		-1,05	-5,61	Iron-sulfur cluster binding protein
Dde_3211		1,88	4,82	split soret cytochrome c precursor
Dde_3237		0,80	5,61	Putative oxidoreductase, Fe-S subunit
Dde_3238		0,68	5,61	L-lactate permease, putative
Dde_3239	glcD	1,01	5,15	Glycolate oxidase subunit D

Dde_3240		0,91	5,61	Glycolate oxidase iron-sulfur subunit, putative
Dde_3242	ackA	0,93	5,61	acetate kinase
Dde_3245		0,96	5,32	Iron-sulfur cluster binding protein
Dde_3667	fld	-2,83	-5,61	Flavodoxin, iron-repressed (Dmitry Rodionov)
Dde_3707	tmcD	-1,60	-5,61	Transmembrane complex
Dde_3708	tmcC	-1,18	-5,61	Transmembrane complex, integral membrane protein (Shelley Haveman)
Dde_3709	tmcB	-1,62	-5,61	Transmembrane complex, ferredoxin, 2 [4Fe-4S] (Shelley Haveman)
Dde_3710	tmcA	-1,13	-5,61	Transmembrane complex, tetraheme cytochrome c3 (Shelley Haveman)

S. Function unknown

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0484		-1,02	-5,61	Conserved hypothetical protein
Dde_0876		0,79	5,10	Uncharacterised protein family UPF0324
Dde_2561		-0,71	-5,61	Rhodanese-like domain protein
Dde_3198		-1,88	-5,61	Uncharacterized ACR, COG1433 family
Dde_3244		0,73	5,61	Uncharacterized ACR, YkgG family COG1556 family

R. General function prediction only

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0220		-0,50	-4,12	Sel1 domain protein repeat-containing protein
Dde_0444	pqqL	-1,73	-5,61	Putative peptidase
Dde_0449		-0,73	-5,61	Putative transport system permease protein
Dde_0450	oppC	-0,66	-5,61	Putative transport system permease protein
Dde_3241	pta	0,66	5,38	Phosphotransacetylase
Dde_3243		0,88	5,61	Phosphate acetyltransferase, putative
Dde_3372		0,50	4,55	Conserved hypothetical protein

P. Inorganic ion transport and metabolism

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_1312		-1,76	-5,61	Copper chaperone
Dde_2669	feoB	-2,17	-5,61	ferrous iron transport protein B
Dde_2670	feoA	-2,45	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)
Dde_2673	feoA	-1,80	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)

U. Intracellular trafficking, secretion, and vesicular transport

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0453		-0,81	-5,61	biopolymer transport proteins-like
Dde_0454		-0,73	-5,61	biopolymer transport proteins-like
Dde_0455		-0,67	-5,61	Biopolymer transport protein
Dde_2153		-2,74	-5,61	Biopolymer transport proteins
Dde_2154		-3,06	-5,61	Biopolymer transport proteins
Dde_2155		-2,08	-5,61	Biopolymer transport protein

I. Lipid transport and metabolism

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_3217	pssA	0,77	4,21	CDP-diacylglycerol-serine O-phosphatidyltransferase

O. Posttranslational modification, protein turnover, chaperones

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_1203		0,62	2,37	thioredoxin reductase
Dde_1343	hspC	-0,59	-5,61	Small heat shock protein (class I) (hspC)
Dde_1344		-0,55	-5,61	Putative small heat shock protein hsp15
Dde_2560		-0,90	-3,90	Thioredoxin peroxidase
Dde_2946	hflK	0,57	4,43	HflK protein
Dde_3412		-0,53	-2,45	Molecular chaperone (small heat shock protein)

T. Signal transduction mechanisms

Gene ID	Gene name	Log$_2$R	Z-score	Annotation

Dde_0227	cstA	1,49	4,98	Carbon starvation protein
Dde_1151	hdd	-0,69	-3,92	Response regulator containing a CheY-like receiver domain and an HD-GYP domain
Dde_3047	Dde_3047	-0,80	-5,43	Serine phosphatase RsbU, regulator of sigma subunit
Dde_3048	gdp	-0,90	-4,84	FOG: GGDEF domain
Dde_3712	Dde_3712	-1,81	-5,61	Universal stress protein family family
Dde_3713	mtrA	-1,81	-5,61	DNA-binding response regulator (mtrA)
Dde_3715	Dde_3715	-0,70	-4,46	Sensory transduction histidine kinase-related
Dde_3737	Dde_3737	-0,73	-5,61	Phosphoenolpyruvate-protein phosphotransferase, putative

K. Transcription

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_1611		-1,21	-4,15	AraC family transcriptional regulator
Dde_3179		0,55	4,44	Putative heme biosynthesis protein (Natalia Ivanova)

J. Translation, ribosomal structure, and biogenesis

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_2982	rpmE	1,19	5,61	Ribosomal protein L31
Dde_2989	tuf	0,77	5,61	Translation elongation factor Tu

Supplemental Table S4A: TOP 50 up- or downregulated genes in *Dv. alaskensis* str. G20 grown under syntrophic conditions with *Methanococcus maripaludis* at 0.027 h^{-1} growth rate

Upregulated

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0715		2,85	5,61	hypothetical protein
Dde_2018		1,99	5,61	HesB-like domain, putative
Dde_3211		1,50	4,22	split soret cytochrome c precursor
Dde_0717		1,40	5,61	formate dehydrogenase, alpha subunit
Dde_0090		1,34	5,61	2-hydroxyglutaryl-CoA dehydratase family (Natalia Ivanova)
Dde_0286	fd II	1,31	5,61	Ferredoxin II (Sean Caffrey)
Dde_1074		1,30	5,61	Putative permease
Dde_3182		1,22	4,11	Cytochrome c3 precursor
Dde_0089		1,17	5,61	Putative enzyme
Dde_0719		1,17	5,55	Fe-S cluster domain protein
Dde_0806		1,14	5,61	Rhodanese-like domain protein
Dde_1906		1,13	2,22	hypothetical protein
Dde_2137	hynB-1	1,11	5,61	periplasmic [NiFe] hydrogenase, small subunit, isozyme 1 (Sean Caffrey)
Dde_0718		1,10	5,61	Anaerobic dimethyl sulfoxide reductase chain b (hybA)
Dde_0805		1,07	5,61	DoxX family protein
Dde_1866		1,00	3,19	hypothetical protein
Dde_2138	hynA-1	0,94	4,23	Probable large subunit, hydrogenase-2
Dde_1091		0,91	2,29	Conserved hypothetical protein
Dde_2177	TatA	0,90	3,55	twin-arginine translocation protein TatA (Kennan Kellaris Salinero)
Dde_2982	rpmE	0,78	5,00	Ribosomal protein L31
Dde_2281	hydA-2	0,76	5,04	Iron only hydrogenase large subunit, C-terminal domain
Dde_0227	cstA	0,75	3,19	Carbon starvation protein
Dde_3239	glcD	0,75	2,57	Glycolate oxidase subunit D
Dde_1172	hrpB	0,74	2,07	ATP-dependent helicase HrpB
Dde_1741		0,67	2,71	Prophage antirepressor
Dde_2506		0,67	2,07	Orf, hypothetical protein
Dde_3054	pflA	0,65	3,48	Pyruvate formate-lyase activating enzyme (pflA)
Dde_1883		0,64	3,11	Phage protein D
Dde_3240		0,63	3,72	Glycolate oxidase iron-sulfur subunit, putative
Dde_3245		0,62	3,76	Iron-sulfur cluster binding protein
Dde_3238		0,62	4,36	L-lactate permease, putative
Dde_3237		0,62	5,43	Putative oxidoreductase, Fe-S subunit
Dde_0959		0,61	4,46	Uncharacterized conserved protein
Dde_3326	phnE	0,61	4,94	ABC-type phosphate/phosphonate transport system, permease component
Dde_3159	flgF	0,61	5,44	Flagellar basal-body rod protein FlgF (flgF)
Dde_2989	tuf	0,60	4,67	Translation elongation factor Tu
Dde_2897		0,58	2,35	Transposase and inactivated derivatives
Dde_3372		0,57	5,11	Conserved hypothetical protein
Dde_0533		0,57	3,02	FOG: CheY-like receiver
Dde_0082	hydB	0,57	5,53	Periplasmic (fe) hydrogenase small subunit precursor
Dde_3243		0,57	5,61	Phosphate acetyltransferase, putative
Dde_0761		0,56	3,86	hypothetical protein
Dde_3242	ackA	0,56	5,45	acetate kinase
Dde_0894		0,56	4,43	hypothetical protein
Dde_2922	norQ	0,56	3,55	NorQ protein (norQ)
Dde_0710		0,56	2,40	Phosphoglycerate transport system transcriptional regulatory protein PgtA, putative
Dde_0947		0,55	3,47	hypothetical protein
Dde_3324	phnC	0,55	4,86	ATP-binding component of phosphonate transport
Dde_0017		0,55	2,11	sun protein
Dde_0913		0,54	4,74	hypothetical protein

Downregulated

Gene ID	Gene name	Log$_2$R	Z-score	Annotation
Dde_0283		-2,98	-5,61	Conserved hypothetical protein
Dde_2152		-2,82	-5,61	hypothetical protein
Dde_2154		-2,78	-5,61	Biopolymer transport proteins
Dde_3667	fld	-2,68	-5,61	Flavodoxin, iron-repressed (Dmitry Rodionov)
Dde_2153		-2,64	-5,61	Biopolymer transport proteins
Dde_2670	feoA	-2,50	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)
Dde_2672		-2,44	-5,61	hypothetical protein
Dde_3199		-2,29	-5,61	hypothetical protein
Dde_0111		-2,24	-5,61	Zinc resistance-associated protein precursor, putative
Dde_3197		-2,18	-5,61	hypothetical protein
Dde_2669	feoB	-2,06	-5,61	ferrous iron transport protein B
Dde_2673	feoA	-1,98	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)
Dde_3198		-1,94	-5,61	Uncharacterized ACR, COG1433 family

Dde_2155		-1,90	-5,61	Biopolymer transport protein
Dde_1312		-1,76	-5,61	Copper chaperone
Dde_3202	mrp	-1,71	-5,61	Mrp protein (mrp)
Dde_3200		-1,67	-5,61	Iron-sulfur cluster binding protein
Dde_3713	mtrA	-1,60	-5,61	DNA-binding response regulator (mtrA)
Dde_2156		-1,60	-5,61	TonB-like
Dde_2020		-1,57	-5,61	Conserved hypothetical protein
Dde_3711		-1,55	-5,61	Conserved hypothetical protein
Dde_3712		-1,53	-5,61	Universal stress protein family family
Dde_0444	pqqL	-1,53	-5,61	Putative peptidase
Dde_3709	tmcB	-1,51	-5,61	Transmembrane complex, ferredoxin, 2 [4Fe-4S] (Shelley Haveman)
Dde_2819		-1,49	-5,42	hypothetical protein
Dde_3707		-1,49	-5,61	hypothetical protein
Dde_3146		-1,43	-5,61	hypothetical protein
Dde_0445		-1,40	-5,61	ABC transporter, ATP-binding protein, putative
Dde_2157		-1,38	-5,61	TPR repeat-containing protein
Dde_2135	hysA	-1,37	-5,61	periplasmic [NiFeSe] hydrogenase, large subunit, selenocysteine-containing
Dde_2134		-1,33	-5,61	hydrogenase (NiFe) small subunit HydA
Dde_3144		-1,27	-5,61	hypothetical protein
Dde_1611		-1,21	-5,61	AraC family transcriptional regulator
Dde_3714	divK	-1,16	-5,61	Nitrogen regulation protein NtrX (divK)
Dde_3201		-1,12	-5,61	Iron-sulfur cluster binding protein
Dde_3710	tmcA	-1,02	-5,61	Transmembrane complex, tetraheme cytochrome c3 (Shelley Haveman)
Dde_1143		-1,01	-5,55	Conserved hypothetical protein
Dde_0282		-1,01	-4,13	Conserved hypothetical protein
Dde_3708	tmcC	-1,00	-5,61	Transmembrane complex, integral membrane protein (Shelley Haveman)
Dde_3046		-0,99	-5,61	Conserved hypothetical protein
Dde_2560		-0,90	-4,19	Thioredoxin peroxidase
Dde_0484		-0,89	-5,61	Conserved hypothetical protein
Dde_3666		-0,86	-5,07	hypothetical protein
Dde_0607		-0,82	-5,61	hypothetical protein
Dde_0483		-0,80	-5,61	MoxR-like ATPases
Dde_2641	b0873	-0,76	-3,32	hybrid cluster protein
Dde_3048	gdp	-0,75	-4,63	FOG: GGDEF domain
Dde_2561		-0,74	-5,03	Rhodanese-like domain protein
Dde_3045		-0,71	-5,57	Conserved hypothetical protein

Supplemental Table S4B: TOP 30 up- or downregulated genes in *Dv. alaskensis* str. G20 grown under syntrophic conditions with *Methanospirillum hungatei* at 0.027 h^{-1} growth rate

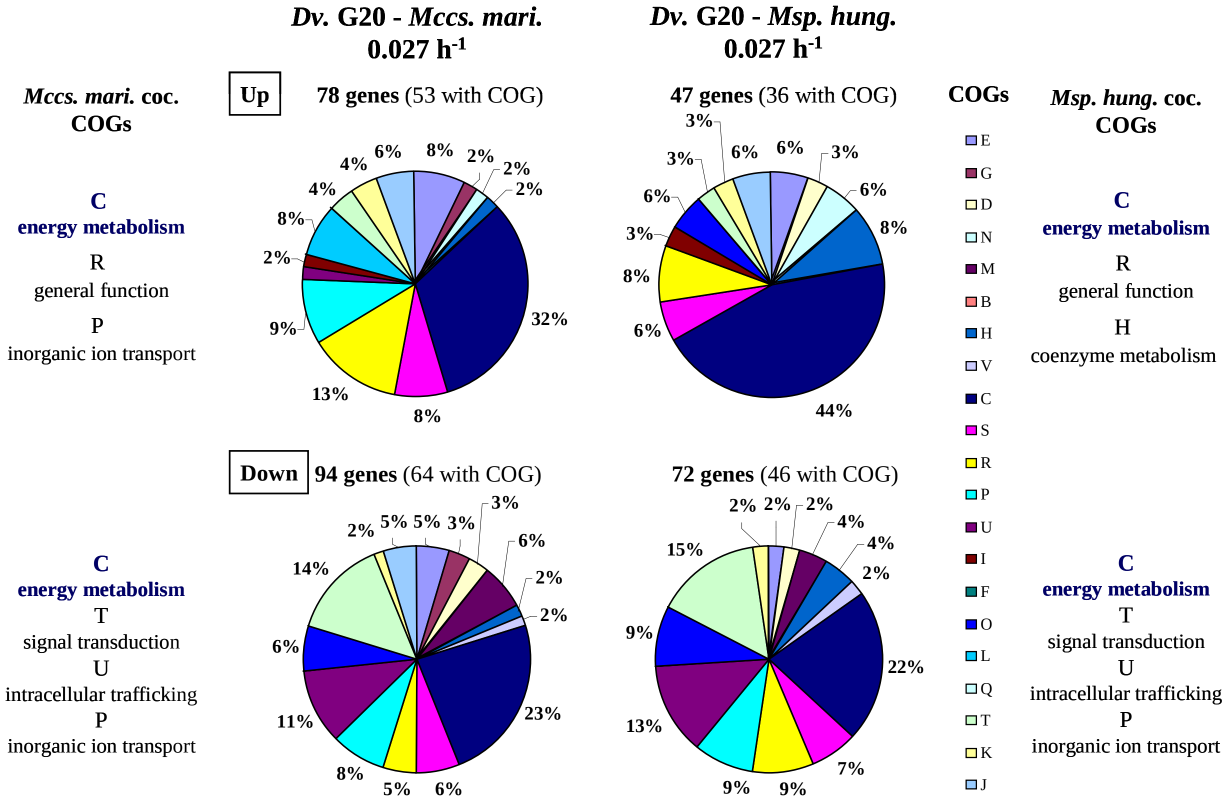
Upregulated

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_0715		3,60	5,61	hypothetical protein
Dde_0717		2,90	5,61	formate dehydrogenase, alpha subunit
Dde_0718		2,20	5,61	Anaerobic dimethyl sulfoxide reductase chain b (hybA)
Dde_0719		1,91	5,61	Fe-S cluster domain protein
Dde_3211		1,88	4,82	split soret cytochrome c precursor
Dde_1074		1,50	5,61	Putative permease
Dde_0227	cstA	1,49	4,98	Carbon starvation protein
Dde_3182		1,19	4,20	Cytochrome c_3 precursor
Dde_2982	rpmE	1,19	5,61	Ribosomal protein L31
Dde_0234		1,18	5,38	Conserved hypothetical protein
Dde_3239	glcD	1,01	5,15	Glycolate oxidase subunit D
Dde_0608	livF	1,00	2,54	ATP-binding component of leucine transport
Dde_3245		0,96	5,32	Iron-sulfur cluster binding protein
Dde_3444		0,94	4,62	hypothetical protein
Dde_3242	ackA	0,93	5,61	acetate kinase
Dde_3240		0,91	5,61	Glycolate oxidase iron-sulfur subunit, putative
Dde_0645		0,89	4,69	hypothetical protein
Dde_3243		0,88	5,61	Phosphate acetyltransferase, putative
Dde_3237		0,80	5,61	Putative oxidoreductase, Fe-S subunit
Dde_3028	cooS	0,79	5,05	carbon-monoxide dehydrogenase, catalytic subunit
Dde_0876		0,79	5,10	Uncharacterised protein family UPF0324
Dde_3217	pssA	0,77	4,21	CDP-diacylglycerol--serine O-phosphatidyltransferase
Dde_3159	flgF	0,77	5,61	Flagellar basal-body rod protein FlgF (flgF)
Dde_2989	tuf	0,77	5,61	Translation elongation factor Tu
Dde_3244		0,73	5,61	Uncharacterized ACR, YkgG family COG1556 family
Dde_3029	cooC-2	0,69	4,95	CODH nickel-insertion accessory protein (cooC-2)
Dde_3238		0,68	5,61	L-lactate permease, putative
Dde_3158	flgG	0,68	5,61	Flagellar biosynthesis, cell-distal portion of basal-body rod
Dde_1427		0,68	2,26	hypothetical protein
Dde_3241	pta	0,66	5,38	Phosphotransacetylase

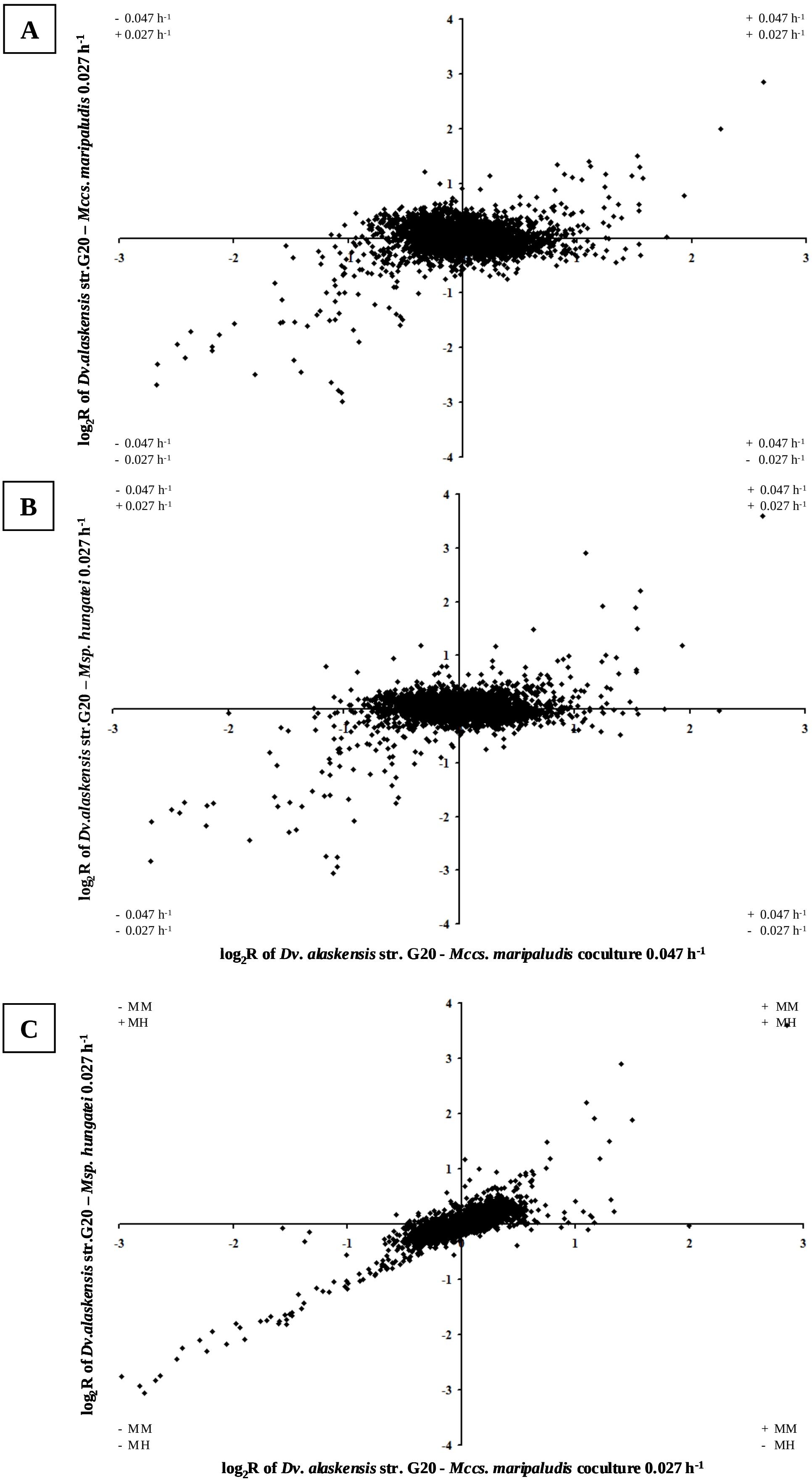
Downregulated

Gene ID	Gene name	Log_2R	Z-score	Annotation
Dde_2154		-3,06	-5,61	Biopolymer transport proteins
Dde_2152		-2,93	-5,61	hypothetical protein
Dde_3667	fld	-2,83	-5,61	Flavodoxin, iron-repressed (Dmitry Rodionov)
Dde_0283		-2,76	-5,61	Conserved hypothetical protein
Dde_2153		-2,74	-5,61	Biopolymer transport proteins
Dde_2670	feoA	-2,45	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)
Dde_0111		-2,30	-5,61	Zinc resistance-associated protein precursor. {escherichia, putative
Dde_2672		-2,25	-5,61	hypothetical protein
Dde_2669	feoB	-2,17	-5,61	ferrous iron transport protein B
Dde_3199		-2,10	-5,61	hypothetical protein
Dde_2155		-2,08	-5,61	Biopolymer transport protein
Dde_3197		-1,94	-5,61	hypothetical protein
Dde_3198		-1,88	-5,61	Uncharacterized ACR, COG1433 family
Dde_3712		-1,81	-5,61	Universal stress protein family family
Dde_3713	mtrA	-1,81	-5,61	DNA-binding response regulator (mtrA)
Dde_2673	feoA	-1,80	-5,61	ferrous iron transporter component feoA (Dmitry Rodionov)
Dde_2156		-1,76	-5,61	TonB-like
Dde_1312		-1,76	-5,61	Copper chaperone
Dde_3202	mrp	-1,74	-5,61	Mrp protein (mrp)
Dde_0444	pqqL	-1,73	-5,61	Putative peptidase
Dde_3200		-1,67	-5,61	Iron-sulfur cluster binding protein
Dde_2819		-1,65	-5,61	hypothetical protein
Dde_3711		-1,64	-5,61	Conserved hypothetical protein
Dde_3709	tmcB	-1,62	-5,61	Transmembrane complex, ferredoxin, 2 [4Fe-4S] (Shelley Haveman)
Dde_3707		-1,60	-5,61	hypothetical protein
Dde_0445		-1,53	-5,61	ABC transporter, ATP-binding protein, putative
Dde_2157		-1,43	-5,61	TPR repeat-containing protein
Dde_3146		-1,27	-5,61	hypothetical protein
Dde_3714	divK	-1,23	-5,61	Nitrogen regulation protein NtrX (divK)
Dde_1611		-1,21	-4,15	AraC family transcriptional regulator

Supplemental Figure S5: Relative number of significantly up- or downregulated genes of each COG functional category during syntrophic growth at low growth rate for each coculture pairing (absolute Z score > 2.0; absolute $\log_2 R > 0.5$; categories enriched in differentially expressed genes relative to the total number of gene in that category are listed on the side). Categories are as follows: amino acid transport (E), carbohydrate transport and metabolism (G), cell division and chromosome partitioning (D), cell motility and secretion (N), cell envelope biogenesis (M), chromatin structure and dynamics (B), coenzyme metabolism (H), defense mechanism (V), energy production and conservation (C), function unknown (S), general function prediction only (R), inorganic ion transport and metabolism (P), intracellular trafficking and secretion (U), lipid metabolism (I), nucleotide transport and metabolism (F), post-translational modification, protein turnover, chaperones (O), DNA replication, recombination and repair (L), secondary metabolites biosynthesis, transport and catabolism (Q), signal transduction mechanisms (T), transcription (K), and translation, ribosomal structures and biogenesis (J).



Supplemental Figure S6: Log_2 R data sets of *D. alaskensis* str. G20 grown syntrophically at low growth rate of 0.027 h^{-1} with *M. maripaludis* or *M. hungatei* plotted against the log_2 R data of syntrophic growth at high rate of 0.047 h^{-1} (panel A or B, respectively) and against each other (panel C).



Supplemental Table S7: Differentially up-/downregulated genes of *Desulfovibrio alaskensis* str. G20 in syntrophic coculture with *Methanococcus maripaludis* at different growth rates (0.047 h^{-1} or 0.027h^{-1}) (list is organized by G20 gene ID number)

G20 Gene ID	**$\log_2$ R 0.047 h^{-1} MM**	**Z-score**	**$\log_2$ R 0.027 h^{-1} MM**	**Z-score**	**Abs. difference $\log_2$ R**	**Abs. $\log_2$ 0.027 h^{-1} MM**	**Gene name**	**COG**	**Annotation**
Downregulated under both conditions									
Dde_0111	-0,92	-4,33	-2,24	-5,61	1,31	0,99			Zinc resistance-associated protein precursor, putative
Dde_0444	-2,37	-5,45	-1,53	-5,61	0,84	-0,63	pqqL	R	Putative peptidase
Dde_0445	-2,36	-5,52	-1,40	-5,61	0,96	-0,08		U	ABC transporter, ATP-binding protein, putative
Dde_0446	-1,59	-4,23	-0,67	-4,39	0,92	-0,42		R	hypothetical protein
Dde_0447	-1,79	-3,98	-0,65	-4,28	1,14	-0,03		R	Orf, hypothetical protein
Dde_0448	-1,19	-4,47	-0,46	-4,59	0,73	-0,21		U	ABC transporter, periplasmic substrate-binding protein
Dde_0449	-1,35	-4,54	-0,69	-4,92	0,66	-0,60		U	Putative transport system permease protein
Dde_0450	-1,15	-4,57	-0,45	-5,52	0,70	-0,30	oppC	U	Putative transport system permease protein
Dde_0451	-1,08	-3,95	-0,36	-4,72	0,72	-0,56		U	Putative ATP-binding component of a transport system
Dde_0452	-1,17	-3,23	-0,64	-4,81	0,52	-0,51		R	hypothetical protein
Dde_0453	-1,35	-4,41	-0,65	-5,61	0,70	-0,36		U	biopolymer transport proteins-like
Dde_0454	-1,26	-4,89	-0,54	-5,61	0,72	-0,46		U	biopolymer transport proteins-like
Dde_0457	-1,25	-2,29	-0,58	-4,56	0,67	-0,24		U	Putative Zn-dependent protease, contains TPR repeats
Dde_1143	-0,50	-4,04	-1,01	-5,55	0,51	2,67			Conserved hypothetical protein
Dde_1150	-0,77	-2,57	-0,25	-2,93	0,53	1,51		M	17 kDa surface antigen
Dde_1151	-1,10	-1,93	-0,60	-3,91	0,50	-0,10	hdd	T	Response regulator containing a CheY-like receiver domain and an HD-GYP domain
Dde_1175	-1,01	-3,03	-0,44	-4,28	0,57	4,45			RNA-binding protein
Dde_1178	-1,13	-4,24	-0,47	-4,87	0,65	2,92	B1200	G	Putative dihydroxyacetone kinase
Dde_1312	-2,48	-5,02	-1,76	-5,61	0,72	0,76		P	Copper chaperone
Dde_2067	-0,73	-2,05	-0,15	-2,70	0,58	3,42	trx		thioredoxin
Dde_2155	-2,43	-4,89	-1,90	-5,61	0,53	-0,20		U	Biopolymer transport protein
Dde_2170	-1,45	-5,10	-0,14	-3,03	1,31	4,09		S	Uncharacterized conserved protein
Dde_2241	-0,74	-5,61	-0,25	-5,47	0,49	2,00	rplR	J	Ribosomal protein L18
Dde_2244	-0,97	-5,61	-0,41	-5,61	0,56	1,54	rpsN	J	Ribosomal protein S14p/S29e
Upregulated under both conditions									
Dde_0286	2,57	3,90	1,31	5,61	1,26	4,31	fd II	C	Ferredoxin II (Sean Caffrey)
Dde_0346	0,88	2,71	0,40	3,28	0,49	2,09		K	Transcriptional regulator, putative
Dde_0608	1,18	3,12	0,16	2,12	1,02	0,17	livF	E	ATP-binding component of leucine transport
Dde_0612	1,04	2,93	0,18	1,59	0,87	1,06	livK	E	High-affinity leucine-specific transport system; periplasmic binding protein
Dde_0718	1,85	5,61	1,10	5,61	0,75	1,48		C	Anaerobic dimethyl sulfoxide reductase chain b (hybA)
Dde_0806	1,77	4,63	1,14	5,61	0,62	1,62		P	Rhodanese-like domain protein
Dde_2906	0,94	3,05	0,44	3,29	0,50	0,31		K	Fis family transcriptional regulator
Dde_2956	0,73	1,95	0,20	2,39	0,54	1,62		K	Orf, hypothetical protein
Dde_2982	1,83	4,98	0,78	5,00	1,06	3,95	rpmE	J	Ribosomal protein L31
Dde_2986	1,10	2,61	0,24	2,72	0,86	1,48	lpxC	M	UDP-3-0-acyl N-acetylglucosamine deacetylase
Dde_3004	0,57	2,04	0,04	2,05	0,53	0,18	gpmA	G	Phosphoglyceromutase 1
Dde_3149	0,60	4,46	0,09	2,58	0,51	0,68	yviF	S	Uncharacterized BCR, COG1699 family (yviF)
Dde_3150	1,30	4,73	0,23	2,79	1,07	1,86	csrA	T	carbon storage regulator
Dde_3184	0,85	3,98	0,23	2,21	0,62	2,08			Conserved hypothetical protein
Dde_3215	0,81	3,31	0,21	1,97	0,60	1,18		R	Haloacid dehalogenase-like hydrolase superfamily
Dde_3324	0,06	-1,29	0,55	4,86	0,49	-0,12	phnC	P	ATP-binding component of phosphonate transport
Dde_3337	1,57	4,02	0,39	2,10	1,18	3,81		C	nigerythrin
Dde_3492	0,70	2,80	0,09	1,98	0,61	-0,29	amt	P	ammonium transporter
Dde_3493	1,17	2,98	0,29	2,04	0,88	-0,05		E	Nitrogen regulatory protein PII
Differently regulated between both conditions									
Dde_0098	0,68	1,48	-0,29	-2,53	0,97	0,21		T	Universal stress protein family family
Dde_0099	0,33	1,93	-0,17	-2,13	0,50	0,64	asnS	J	asparaginyl-tRNA synthetase
Dde_0150	0,21	1,90	-0,31	-3,42	0,51	0,98	ubiX	H	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
Dde_0151	0,29	2,04	-0,46	-3,92	0,75	0,34		R	Unnamed protein product
Dde_0153	-0,34	-2,49	0,38	3,71	0,71	-0,19			hypothetical protein
Dde_0154	-0,61	-3,60	0,27	4,54	0,88	-0,67	modB	O	Molybdenum ABC transporter, permease protein (modB)
Dde_0155	-0,71	-3,26	0,31	3,66	1,02	-0,45	modA	P	molybdenum ABC transporter, periplasmic molybdate-binding protein
Dde_0186	0,61	2,82	-0,33	-3,92	0,94	1,80	artJ	ET	Arginine 3rd transport system periplasmic binding protein
Dde_0188	-0,39	-2,32	0,30	2,93	0,69	-0,18	ablB		Beta-lysine N-acetyltransferase (Natalia Ivanova)
Dde_0189	-0,37	-2,29	0,26	2,93	0,63	-0,05	ablA	E	Lysine 2,3-aminomutase (Natalia Ivanova)
Dde_0194	0,64	2,88	-0,25	-1,94	0,89	0,60			Glycophorin-binding protein family
Dde_0223	-0,40	-2,52	0,29	4,54	0,69	-0,55		R	Flavoprotein reductase
Dde_0224	-0,50	-3,26	0,36	3,33	0,86	-0,51	rrf2	K	Rrf2 protein (rrf2)
Dde_0232	-0,50	-3,24	0,32	3,75	0,83	-0,34	cysA	V	Sulfate ABC transporter, ATP-binding protein (cysA)
Dde_0233	-0,51	-1,96	0,30	3,62	0,81	-0,26	cysW	H	ABC transporter, permease protein (cysW)

Dde_0263	-0,55	-2,58	0,27	2,09	0,82	-0,35		T	Response regulator containing a CheY-like receiver domain and an HD-GYP domain
Dde_0303	0,57	2,29	-0,24	-2,45	0,81	1,30		K	Transcriptional regulator, putative
Dde_0321	0,55	2,35	-0,24	-3,07	0,79	0,57		TK	DNA-binding response regulator, putative
Dde_0325	0,31	1,98	-0,49	-4,51	0,80	0,74			hypothetical protein
Dde_0326	0,17	2,60	-0,67	-5,54	0,84	0,50		P	Putative a membrane protein
Dde_0327	0,22	2,33	-0,55	-5,34	0,76	2,45		T	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains
Dde_0348	-0,41	-2,40	0,24	2,17	0,65	-0,44		S	Conserved hypothetical protein
Dde_0384	0,63	3,12	-0,19	-3,21	0,82	1,90	cheY	T	Chemotaxis regulator transmits chemoreceptor signals to flagelllar motor components
Dde_0441	0,33	1,72	-0,18	-2,32	0,50	0,04		R	Multimeric flavodoxin WrbA
Dde_0473	-0,45	-3,51	0,19	3,07	0,65	-0,61		R	formate dehydrogenase, alpha subunit
Dde_0474	-0,61	-4,11	0,09	2,26	0,69	-0,34	fhcB	C	Hydrogenase FeS protein, cytoplasmic (Shelley Haveman)
Dde_0475	-0,49	-3,51	0,12	2,03	0,61	-0,22	fhcC	R	Fe-only hydrogenase, large & small subunits, cytoplasmic (Shelley Haveman)
Dde_0476	-0,13	-2,42	0,36	1,98	0,49	-0,73	fhcD	C	Hydrogenase FeS protein, cytoplasmic (Shelley Haveman)
Dde_0477	-0,66	-1,70	0,40	3,42	1,06	-0,13		L	transposase IS200-family protein
Dde_0561	-0,21	-1,97	0,31	2,28	0,51	-0,43			Cytochrome c subfamily, putative
Dde_0628	-0,28	-2,72	0,22	2,33	0,50	-0,45		L	DNA polymerase III, alpha subunit (gram-positive)
Dde_0629	-0,55	-3,72	0,25	2,68	0,80	-0,50		T	Predicted signal-transduction protein containing cAMP-binding and CBS domains
Dde_0630	-0,42	-3,79	0,16	2,68	0,58	-0,44		R	Putative transport protein
Dde_0631	-0,43	-2,92	0,18	2,12	0,61	-0,84		S	Predicted membrane protein
Dde_0650	0,36	3,39	-0,25	-2,23	0,61	1,10	hmcD		HmcD, 5.8 kd protein in hmc operon (voordouw)
Dde_0667	-0,27	-1,63	0,40	2,82	0,66	0,10		R	Metal-dependent hydrolase
Dde_0668	-0,72	-2,46	0,15	2,15	0,88	-0,52	bcr	G	Bicyclomycin resistance protein; transmembrane protein
Dde_0673	-0,74	-2,65	0,45	3,47	1,19	-0,17	proV	E	ATP-binding component of transport system for glycine, betaine and proline
Dde_0693	0,36	4,39	-0,35	-2,41	0,71	4,19		P	Putative transport protein
Dde_0694	0,93	4,90	-0,23	-2,31	1,16	4,28	cheYI	TK	Chemotaxis protein CheYI (cheYI)
Dde_0704	0,47	2,09	-0,20	-1,90	0,67	0,94		O	Peptide methionine sulfoxide reductase
Dde_0729	-0,55	-2,70	0,11	2,00	0,66	-0,29			hypothetical protein
Dde_0730	-0,40	-2,71	0,13	2,32	0,53	-0,41		V	ABC-type antimicrobial peptide transport system, permease component
Dde_0731	-0,39	-2,80	0,12	1,98	0,51	-0,14		V	ABC transporter, ATP-binding protein
Dde_0793	0,80	3,45	-0,37	-3,70	1,17	4,35			RNA-binding proteins (RRM domain)
Dde_0795	-0,57	-1,72	0,34	2,54	0,91	-0,18			hypothetical protein
Dde_0809	-1,27	-2,40	0,24	2,20	1,52	5,16		J	Endoribonuclease L-PSP, putative
Dde_0836	-0,46	-3,04	0,32	2,39	0,78	-0,40	capK	H	capK-related protein probably involved in cell wall biogenesis (Morgan Price)
Dde_0837	-0,51	-2,97	0,29	3,99	0,80	-0,19		M	Glycosyltransferases, probably involved in cell wall biogenesis
Dde_0838	-0,61	-3,03	0,30	4,40	0,91	-0,47		M	glycosyl transferase, group 1 family protein
Dde_0839	-0,33	-3,19	0,44	3,85	0,78	-0,08		M	Glycosyltransferase
Dde_0840	-0,48	-2,72	0,21	2,30	0,69	-0,04			hypothetical protein
Dde_0843	-0,45	-2,11	0,11	1,61	0,56	0,30		R	cell wall biosynthesis glycosyltransferase-like protein
Dde_0860	0,35	2,23	-0,16	-3,02	0,51	0,13			CRISPR-associated protein, CT1974 family
Dde_0910	-0,39	-1,92	0,52	3,82	0,92	-0,49			hypothetical protein
Dde_0933	-0,31	-2,01	0,31	2,61	0,62	-0,42			hypothetical protein
Dde_0939	-0,32	-2,53	0,25	2,81	0,57	-0,65			Uncharacterized protein conserved in bacteria
Dde_0940	-0,50	-2,66	0,23	3,36	0,73	-0,54			hypothetical protein
Dde_0941	-0,23	-2,21	0,29	2,29	0,52	-0,13			hypothetical protein
Dde_0944	-0,64	-1,84	0,30	1,98	0,94	-0,06			hypothetical protein
Dde_0947	-0,31	-2,34	0,55	3,47	0,86	-0,23			hypothetical protein
Dde_0948	-0,51	-3,65	0,40	4,13	0,91	-0,47			Phage tail protein
Dde_0949	-0,55	-3,90	0,35	4,42	0,90	-0,13			hypothetical protein
Dde_0950	-0,56	-3,19	0,46	3,80	1,02	-0,09			hypothetical protein
Dde_0954	-0,31	-1,56	0,51	3,15	0,82	0,41			hypothetical protein
Dde_0955	-0,18	-1,41	0,34	2,70	0,52	-0,41			hypothetical protein
Dde_0957	-0,37	-2,45	0,19	3,13	0,57	-0,57			hypothetical protein
Dde_0958	-0,54	-2,83	0,26	3,01	0,80	-0,79			Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
Dde_1033	0,84	2,07	-0,22	-3,11	1,06	0,76		S	Conserved hypothetical protein TIGR00242
Dde_1060	-0,51	-2,84	0,18	2,78	0,69	-0,51	pstA	P	High-affinity phosphate-specific transport system
Dde_1061	-0,59	-2,86	0,21	3,53	0,80	-0,41	pstC	P	High-affinity phosphate-specific transport system, cytoplasmic membrane component
Dde_1111	0,94	2,96	-0,31	-3,15	1,25	2,38	QmoA	C	Quinone-interacting membrane-bound oxidoreductase (Shelley Haveman)
Dde_1112	0,28	3,06	-0,50	-4,29	0,78	1,93	QmoB	C	Quinone-interacting membrane-bound oxidoreductase (Shelley Haveman)
Dde_1161	-0,71	-3,17	0,28	2,64	0,99	-0,45			hypothetical protein
Dde_1216	-0,42	-2,36	0,25	1,41	0,67	-0,23		P	alkaline phosphatase
Dde_1218	0,92	2,13	-0,26	-3,04	1,18	-0,12		E	Glutamate synthase-related protein

Dde_1222	2,10	4,35	-0,45	-3,10	2,55	0,68		C	rubrerythrin
Dde_1251	-0,34	-1,47	0,40	3,21	0,74	-0,04		HC	Oxidoreductase, FAD-binding, putative
Dde_1256	-0,51	-3,20	0,07	2,53	0,58	-0,40	frdB	C	fumarate reductase, iron sulfur protein (Jessica Butler)
Dde_1257	-0,57	-2,95	0,21	2,23	0,78	-0,17	frdA	C	Fumarate reductase, anaerobic, flavoprotein subunit
Dde_1343	0,81	-2,90	-0,50	-5,61	1,31	-0,03	hspC	O	Small heat shock protein (class I) (hspC)
Dde_1344	0,19	-2,93	-0,38	-5,22	0,57	0,32		O	Putative small heat shock protein hsp15
Dde_1371	0,58	3,02	-0,19	-2,45	0,77	1,26		M	outer membrane protein OmpH, putative
Dde_1372	0,34	3,49	-0,25	-3,45	0,59	0,35	lpxD	M	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
Dde_1384	0,52	2,57	-0,25	-3,02	0,77	2,26			Conserved hypothetical protein
Dde_1497	0,82	2,04	-0,30	-4,50	1,12	0,03		S	Uncharacterized conserved protein
Dde_1540	0,82	2,63	-0,27	-4,42	1,09	0,84			Conserved hypothetical protein
Dde_1602	-0,28	-2,26	0,26	3,66	0,53	-0,38		V	ABC-type multidrug transport system, ATPase and permease components
Dde_1603	-0,43	-2,31	0,48	4,30	0,91	-0,61			ATP-utilizing enzymes of the PP-loop superfamily
Dde_1604	-0,70	-2,88	0,45	4,01	1,15	-0,57		H	Phosphopantetheinyl transferase
Dde_1605	-0,37	-2,55	0,29	2,95	0,67	-0,17		Q	Predicted thioesterase involved in non-ribosomal peptide biosynthesis
Dde_1731	-0,55	-2,11	0,27	1,99	0,83	-0,60			Uncharacterized phage-encoded protein
Dde_1758	0,78	2,34	-0,21	-3,02	0,98	-0,23			hypothetical protein
Dde_1765	0,60	3,76	-0,27	-3,78	0,87	0,60	pyrG	F	CTP synthase
Dde_1766	0,33	2,92	-0,28	-3,78	0,61	-0,28	kdsA	M	2-dehydro-3-deoxyphosphooctonate aldolase
Dde_1769	0,32	3,24	-0,23	-3,10	0,55	0,50		S	Conserved hypothetical protein
Dde_1774	0,39	2,24	-0,28	-4,13	0,67	0,37		R	Orf, hypothetical protein
Dde_1787	0,93	4,20	-0,22	-2,23	1,15	0,85		M	putative lipoprotein
Dde_1791	0,38	1,82	-0,42	-2,91	0,80	0,78		P	Ferroxidase
Dde_1793	0,31	2,81	-0,40	-4,20	0,71	0,70	porB	C	Pyruvate ferredoxin oxidoreductase, beta subunit, putative
Dde_1794	1,00	3,73	-0,30	-3,19	1,30	1,73			hypothetical protein
Dde_1814	1,03	4,50	-0,30	-2,86	1,33	0,09	gltB-1	E	Glutamate synthase, large subunit (gltB-1)
Dde_1821	0,56	1,90	-0,22	-2,67	0,79	2,81		C	Cytochrome c-553 precursor
Dde_1842	0,57	2,67	-0,23	-2,31	0,80	0,53		C	protein of unknown function DUF224 cysteine-rich region domain protein
Dde_1844	0,44	2,65	-0,30	-2,86	0,74	-0,06		S	Uncharacterized ACR, YkgG family COG1556 family
Dde_1863	-0,44	-2,15	0,37	3,85	0,80	-0,06		S	VrlH
Dde_1864	-0,38	-3,08	0,40	4,65	0,78	-0,27		M	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
Dde_1870	-0,59	-3,61	0,21	2,81	0,81	0,09			hypothetical protein
Dde_1871	-0,74	-4,68	0,34	4,40	1,08	0,00			hypothetical protein
Dde_1872	-0,38	-4,29	0,37	5,25	0,75	-0,46			hypothetical protein
Dde_1873	-0,29	-3,52	0,33	4,17	0,61	-0,40			Phage tail protein
Dde_1874	-0,50	-2,40	0,15	2,73	0,65	-0,47			hypothetical protein
Dde_1895	0,34	3,34	-0,37	-3,49	0,71	1,60			hypothetical protein
Dde_1903	-0,24	-1,96	0,40	3,17	0,64	-0,54			hypothetical protein
Dde_1904	-0,31	-2,03	0,35	3,50	0,66	-0,41		L	Adenine-specific DNA methylase
Dde_1909	-0,77	-2,18	0,44	2,99	1,21	0,61			hypothetical protein
Dde_1910	-0,28	-1,74	0,34	3,02	0,62	-0,02			hypothetical protein
Dde_1926	-0,37	-2,19	0,19	2,66	0,56	-0,51			hypothetical protein
Dde_1927	-0,39	-2,29	0,25	3,02	0,64	-0,16			hypothetical protein
Dde_1968	0,73	3,13	-0,09	-1,62	0,83	0,39			Conserved hypothetical protein
Dde_1969	0,68	2,62	-0,13	-2,32	0,81	-0,04	folK	H	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
Dde_2005	0,62	2,39	-0,21	-2,00	0,84	0,06			hypothetical protein
Dde_2008	0,95	2,62	-0,25	-3,11	1,20	0,43	hspC	O	Heat shock protein 16.5 (hspC)
Dde_2077	0,47	2,41	-0,12	-2,03	0,59	0,39	pcm	O	protein-L-isoaspartate O-methyltransferase
Dde_2078	0,46	2,39	-0,20	-3,38	0,66	1,98		R	Acetoin utilization protein AcuB, putative
Dde_2130	0,19	3,07	-0,41	-3,74	0,61	0,42	rho	K	transcription termination factor Rho
Dde_2145	0,61	3,25	-0,10	-2,38	0,71	0,61			Periplasmic protein, putative
Dde_2148	0,91	4,29	-0,12	-2,46	1,03	1,26	CheZ	NT	CheY Protein Phosphatase (Christopher Rao)
Dde_2222	0,50	2,56	-0,35	-3,21	0,85	0,52	tig	O	trigger factor
Dde_2273	0,26	2,96	-0,35	-3,29	0,61	2,17	DsrJ		Periplasmic (Sec) triheme cytochrome c (Shelley Haveman)
Dde_2274	0,05	2,18	-0,63	-4,51	0,68	1,62	DsrO	C	Periplasmic (Tat), binds 2[4Fe-4S] (Shelley Haveman)
Dde_2300	0,29	2,27	-0,26	-4,41	0,55	0,70		Q	Orf, hypothetical protein
Dde_2354	-0,60	-3,05	0,25	2,38	0,85	-0,60		L	nuclease (SNase-like)
Dde_2358	-0,56	-2,67	0,26	3,72	0,82	-0,70		OU	Type III leader peptidase family domain protein
Dde_2359	-0,37	-3,34	0,42	5,03	0,79	-0,23		U	Conserved hypothetical protein
Dde_2360	-0,58	-3,24	0,42	4,88	1,01	-0,35	cpaC	U	Pilus assembly protein CpaC (cpaC)
Dde_2361	-0,65	-3,22	0,31	3,92	0,96	-0,18			hypothetical protein
Dde_2362	-0,32	-3,02	0,35	5,19	0,67	-0,52		U	Pilus assembly protein CpaE, putative
Dde_2363	-0,45	-3,20	0,37	5,61	0,81	-0,42		U	type II/IV secretion system protein
Dde_2364	-0,57	-3,46	0,36	5,25	0,93	-0,56		U	Conserved hypothetical protein
Dde_2365	-0,46	-3,29	0,35	4,78	0,81	-0,45		NU	Conserved hypothetical protein
Dde_2366	-0,40	-3,07	0,29	4,57	0,69	-0,28		NU	Flp pilus assembly protein TadD, contains TPR repeats
Dde_2367	-0,34	-2,41	0,25	4,53	0,59	-0,09			Conserved hypothetical protein
Dde_2462	0,59	1,69	-0,34	-3,41	0,93	-0,04			Conserved hypothetical protein
Dde_2464	0,39	2,64	-0,24	-2,59	0,63	0,25			Conserved hypothetical protein

Dde_2519	0,48	3,29	-0,29	-3,22	0,77	0,72		T	Prokaryotic dksA/traR C4-type zinc finger, putative
Dde_2561	0,08	1,92	-0,74	-5,03	0,83	1,06		S	Rhodanese-like domain protein
Dde_2562	0,02	1,58	-0,69	-4,65	0,72	0,49		C	Pyridine nucleotide-disulphide oxidoreductase family
Dde_2633	0,77	2,03	-0,17	-2,48	0,94	-0,08		K	Conserved hypothetical protein
Dde_2639	0,32	2,01	-0,28	-3,50	0,60	1,30	thrS	J	Threonyl-tRNA synthetase
Dde_2658	-0,89	-3,36	0,32	4,11	1,22	0,04		IQR	3-oxoacyl-(acyl-carrier protein) reductase
Dde_2793	0,92	4,32	-0,20	-3,29	1,12	1,15	arsC-2	T	Arsenate reductase
Dde_2819	0,23	-2,32	-1,49	-5,42	1,72	0,20			hypothetical protein
Dde_2901	0,58	3,39	-0,27	-3,41	0,85	1,12	gmd	M	GDP-mannose 4,6-dehydratase
Dde_2904	0,54	1,91	-0,27	-2,80	0,81	2,76			CopG family transcriptional regulator
Dde_3401	0,85	4,24	-0,35	-3,09	1,21	1,46			hypothetical protein
Dde_3518	-0,77	-2,98	0,19	3,36	0,96	-0,52	modA	P	molybdenum ABC transporter, periplasmic molybdate-binding protein
Dde_3528	-0,85	-3,94	0,24	3,87	1,09	-0,29			Heterodisulfide reductase subunit

Supplemental Table S8: Differentially up-/downregulated genes of *Desulfovibrio alaskensis* str. G20 in syntrophic coculture with different methanogenic partners (*Methanococcus maripaludis* or *Methanospirillum hungatei*, respectively) (list is organized by G20 gene ID number)

G20 Gene ID	**$\log_2$ R 0.027 h^{-1} MM**	**Z-score**	**$\log_2$ R 0.027 h^{-1} MH**	**Z-score**	**Abs. difference $\log_2$ R**	**Abs. $\log_2$ 0.027 h^{-1} MH**	**Gene name**	**COG**	**Annotation**
Upregulated under both conditions									
Dde_0089	1,17	5,61	0,03	1,79	1,14	-0,48		I	Putative enzyme
Dde_0090	1,34	5,61	0,23	1,85	1,11	-0,41		E	2-hydroxyglutaryl-CoA dehydratase family (Natalia Ivanova)
Dde_0227	0,75	3,19	1,49	4,98	0,73	4,47	cstA	T	Carbon starvation protein
Dde_0286	1,31	5,61	0,45	5,00	0,87	3,50	fd II	C	Ferredoxin II (Sean Caffrey)
Dde_0608	0,16	2,12	1,00	2,54	0,84	1,82	livF	E	ATP-binding component of leucine transport
Dde_0715	2,85	5,61	3,60	5,61	0,74	5,44		C	hypothetical protein
Dde_0717	1,40	5,61	2,90	5,61	1,50	4,41		C	formate dehydrogenase, alpha subunit
Dde_0718	1,10	5,61	2,20	5,61	1,10	3,43		C	Anaerobic dimethyl sulfoxide reductase chain b (hybA)
Dde_0719	1,17	5,55	1,91	5,61	0,75	3,64		H	Fe-S cluster domain protein
Dde_0805	1,07	5,61	0,23	2,10	0,84	0,28		P	DoxX family protein
Dde_0806	1,14	5,61	0,13	2,07	1,01	-0,44		P	Rhodanese-like domain protein
Dde_1866	1,00	3,19	0,41	2,91	0,59	0,01			hypothetical protein
Dde_2177	0,90	3,55	0,22	3,12	0,68	3,35	tatA	U	twin-arginine translocation protein TatA
Dde_3444	0,31	2,83	0,94	4,62	0,63	1,63			hypothetical protein
Downregulated under both conditions									
Dde_2134	-1,33	-5,61	-0,15	-4,05	1,18	2,66		C	hydrogenase (NiFe) small subunit HydA
Dde_2135	-1,37	-5,61	-0,31	-4,60	1,06	2,12	hysA	C	periplasmic [NiFeSe] hydrogenase, large subunit, selenocysteine-containing (Sean Caffrey)
Differently regulated between both conditions									
Dde_2136	-0,13	-1,74	0,57	1,33	0,70	1,51		C	Hydrogenase expression/formation protein
Dde_2137	1,11	5,61	-0,10	-1,32	1,21	0,93	hynB-1	C	periplasmic [NiFe] hydrogenase, small subunit, isozyme 1 (Sean Caffrey)
Dde_2138	0,94	4,23	0,03	0,11	0,91	0,78	hynA-1	C	Probable large subunit, hydrogenase-2
Dde_2246	-0,24	-4,34	0,24	2,44	0,48	3,00	rplX	J	Ribosomal protein L24
Dde_2247	-0,38	-4,07	0,15	2,62	0,53	2,84	rplN	J	Ribosomal protein L14
Dde_2555	0,49	2,79	-0,39	-5,35	0,88	0,57			hypothetical protein

Supplemental Table S9A: Commonly up-/downregulated genes of *Desulfovibrio alaskensis* str. G20 in syntrophic cocultures irrespective of methanogenic partner and growth rate (genes included have an abs. Z-score ≥ 2.0; list is organized by G20 gene ID number)

G20 Gene ID	**$\log_2$ R 0.047 h^{-1} MM**	**$\log_2$ R 0.027 h^{-1} MM**	**$\log_2$ R 0.027 h^{-1} MH**	**Gene name**	**COG**	**Annotation**
Commonly upregulated						
Dde_0227	0,76	0,75	1,48	cstA	T	Carbon starvation protein
Dde_0715	2,89	2,85	3,60		C	hypothetical protein
Dde_0717	1,46	1,40	2,90	fdhA	C	formate dehydrogenase, alpha subunit
Dde_0718	1,85	1,10	2,20	fdhB	C	Anaerobic dimethyl sulfoxide reductase chain b (hybA)
Dde_0719	1,57	1,17	1,91	fdh	H	Fe-S cluster domain protein
Dde_1074	1,32	1,30	1,50	lctP1	C	Putative permease
Dde_2982	1,83	0,78	1,19	rpmE	J	Ribosomal protein L31
Dde_3159	0,64	0,61	0,77	flgF	N	Flagellar basal-body rod protein FlgF
Dde_3211	1,15	1,50	1,88	ssc	C	split soret cytochrome c precursor
Dde_3238	0,78	0,62	0,68	lctP2	C	L-lactate permease, putative
Dde_3239	0,55	0,75	1,01	ldhA	C	Glycolate oxidase subunit D
Dde_3240	0,50	0,63	0,91	ldhB1	C	Glycolate oxidase iron-sulfur subunit
Dde_3244	0,83	0,51	0,73		C	Uncharacterized ACR, YkgG family COG1556 family
Dde_3245	0,51	0,62	0,96	ldhB2	C	Iron-sulfur cluster binding protein
Commonly downregulated						
Dde_0111	-0,92	-2,24	-2,30			Zinc resistance-associated protein precursor
Dde_0283	-2,82	-2,98	-2,76			Conserved hypothetical protein
Dde_0444	-2,37	-1,53	-1,73	pqqL	RU	Putative peptidase
Dde_0445	-2,36	-1,40	-1,53		U	ABC transporter, ATP-binding protein, putative
Dde_0446	-1,59	-0,67	-0.76		U	hypothetical protein
Dde_0447	-1,79	-0,65	-0,80		U	Orf, hypothetical protein
Dde_0449	-1,35	-0,69	-0,73		U	Putative transport system permease protein
Dde_0452	-1,17	-0,64	-0,64			hypothetical protein
Dde_0453	-1,35	-0,65	-0,81		U	biopolymer transport proteins-like
Dde_0454	-1,26	-0,54	-0,73		U	biopolymer transport proteins-like
Dde_0455	-0,90	-0,51	-0,67		U	Biopolymer transport protein
Dde_0456	-1,07	-0,68	-0,76		M	TonB-like
Dde_0457	-1,25	-0,58	-0,67		U	Putative Zn-dependent protease, contains TPR repeats
Dde_0483	-1,17	-0,80	-0,89			MoxR-like ATPases
Dde_0484	-1,18	-0,89	-1,02			Conserved hypothetical protein
Dde_0485	-0,68	-0,51	-0,55			hypothetical protein
Dde_0607	-0,56	-0,82	-0,81			hypothetical protein
Dde_1143	-0,50	-1,01	-0,56			Conserved hypothetical protein
Dde_1151	-1,10	-0,60	-0,69	hdd	T	Response regulator containing a CheY-like receiver domain and an HD-GYP domain
Dde_1312	-2,48	-1,76	-1,76		P	Copper chaperone
Dde_1611	-1,44	-1,21	-1,21	araC	K	AraC family transcriptional regulator
Dde_2152	-2,76	-2,82	-2,93			hypothetical protein
Dde_2153	-2,87	-2,64	-2,74		U	Biopolymer transport proteins
Dde_2154	-3,10	-2,78	-3,06		U	Biopolymer transport proteins
Dde_2155	-2,43	-1,90	-2,08		U	Biopolymer transport proteins
Dde_2156	-1,85	-1,60	-1,76		M	TonB-like
Dde_2157	-1,72	-1,38	-1,43			TPR repeat-containing protein
Dde_2560	-0,92	-0,90	-0,90		O	Thioredoxin peroxidase
Dde_2641	-0,61	-0,76	-0,93	b0873	C	hybrid cluster protein
Dde_2669	-3,53	-2,06	-2,17	feoB	P	ferrous iron transport protein B
Dde_2670	-3,13	-2,50	-2,45	feoA	P	ferrous iron transporter component feoA
Dde_2672	-2,67	-2,44	-2,25	feoB	P	hypothetical protein
Dde_2673	-3,13	-1,98	-1,80	feoA	P	ferrous iron transporter component feoA
Dde_3045	-0,97	-0,71	-0,82			Conserved hypothetical protein
Dde_3046	-2,05	-0,99	-1,07			Conserved hypothetical protein
Dde_3047	-0,90	-0,61	-0,80		TK	Serine phosphatase RsbU, regulator of sigma subunit
Dde_3144	-1,22	-1,27	-1,16			hypothetical protein
Dde_3197	-2,38	-2,18	-1,94			hypothetical protein
Dde_3198	-2,50	-1,94	-1,88			Uncharacterized ACR, COG1433 family
Dde_3199	-2,65	-2,29	-2,10			hypothetical protein
Dde_3200	-1,55	-1,67	-1,67		C	Iron-sulfur cluster binding protein
Dde_3201	-1,49	-1,12	-1,05		C	Iron-sulfur cluster binding protein
Dde_3202	-2,55	-1,71	-1,74	mrp	D	Mrp protein
Dde_3666	-1,59	-0,86	-1,00			hypothetical protein
Dde_3667	-4,43	-2,68	-2,83	fld	C	Flavodoxin, iron-repressed
Dde_3707	-1,07	-1,49	-1,60	tmcD	C	hypothetical protein
Dde_3708	-1,29	-1,00	-1,18	tmcC	C	Transmembrane complex, integral membrane protein
Dde_3709	-1,11	-1,51	-1,62	tmcB	C	Transmembrane complex, ferredoxin, 2 [4Fe-4S]
Dde_3710	-0,80	-1,02	-1,13	tmcA	C	Transmembrane complex, tetraheme cytochrome c_3
Dde_3711	-1,43	-1,55	-1,64			Conserved hypothetical protein

Dde_3712	-1,39	-1,53	-1,81		T	Universal stress protein family family
Dde_3713	-1,29	-1,60	-1,81	mtrA	T	DNA-binding response regulator
Dde_3714	-1,04	-1,16	-1,23	divK	T	Nitrogen regulation protein NtrX
Dde_3737	-0,49	-0,70	-0,73		T	Phosphoenolpyruvate-protein phosphotransferase, putative

Supplemental Table S9B: Commonly up-/downregulated genes of *Desulfovibrio alaskensis* str. G20 in syntrophic cocultures with *Mccs. maripaludis* irrespective of growth rate (genes included have an abs. Z-score ≥ 2.0; list is organized by G20 gene ID number)

G20 Gene ID	**$\log_2$ R 0.047 h^{-1} MM**	**$\log_2$ R 0.027 h^{-1} MM**	**Gene name**	**COG**	**Annotation**
Commonly upregulated					
Dde_0089	0,94	1,17		E	Putative enzyme
Dde_0090	0,97	1,34		E	2-hydroxyglutaryl-CoA dehydratase family
Dde_0286	2,57	1,31	fd II	C	Ferredoxin II
Dde_0761	0,96	0,56			hypothetical protein
Dde_0805	1,23	1,07		P	DoxX family protein
Dde_0806	1,77	1,14		P	Rhodanese-like domain protein
Dde_2018	2,32	1,99		S	HesB-like domain, putative
Dde_2137	0,92	1,11	hynB	C	periplasmic [NiFe] hydrogenase, small subunit
Dde_2138	1,26	0,94	hynA	C	Probable large subunit, hydrogenase-2
Dde_2280	0,90	0,50	hydB	C	Periplasmic Fe hydrogenase small subunit
Dde_2281	0,58	0,76	hydA	C	Iron only hydrogenase large subunit
Dde_2555	0,93	0,49			hypothetical protein
Dde_2897	0,50	0,58			Transposase and inactivated derivative
Dde_3230	0,81	0,51			Domain of unknown function domain protein
Commonly downregulated					
Dde_2020	-1,72	-1,57		S	conserved hypothetical protein
Dde_2134	-1,11	-1,33	hysB	C	hydrogenase (NiFe) small subunit HysB
Dde_2135	-1,17	-1,37	hysA	C	periplasmic [NiFeSe] hydrogenase, large subunit, selenocysteine-containing
Dde_2255	-0,65	-0,60	rplW	J	50S ribosomal subunit protein L23
Dde_2473	-0,96	-0,51	mopA	O	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein

Supplemental Table S9C: Commonly up-/downregulated genes of *Desulfovibrio alaskensis* str. G20 in syntrophic cocultures at low growth rate (low energy availability) irrespective of methanogenic partner (genes included have an abs. Z-score ≥ 2.0; list is organized by G20 gene ID number)

G20 Gene ID	**$\log_2$ R 0.027 h^{-1} MM**	**$\log_2$ R 0.027 h^{-1} MH**	**Gene name**	**COG**	**Annotation**
Commonly upregulated					
Dde_0645	0,52	0,89		C	Cytochrome c_3 precursor
Dde_0954	0,51	0,50	por	C	POR
Dde_2796	0,52	0,50		J	Translation elongation factor Tu
Dde_2989	0,60	0,77		R	conserved hypothetical protein
Dde_3182	1,22	1,19		C	Phosphate acetyltransferase, putative
Dde_3237	0,62	0,80	ack	C	Acetate kinase
Dde_3242	0,56	0,93			hypothetical protein
Dde_3243	0,57	0,88			hypothetical protein
Dde_3372	0,57	0,50			hypothetical protein
Commonly downregulated					
Dde_0282	-1,01	-1,03			conserved hypothetical protein
Dde_1239	-0,69	-0,66			hypothetical protein
Dde_2561	-0,74	-0,71		HS	Rhodanese-like domain protein
Dde_2562	-0,69	-0,75		C	Pyridine nucleotide-disulphide oxidoreductase family
Dde_2749	-0,65	-0,57		C	Rubredoxin

Dde_2819	-1,49	-1,65			hypothetical protein
Dde_3048	-0,75	-0,90		T	FOG:GGDEF domain
Dde_3146	-1,43	-1,27			hypothetical protein
Dde_3715	-0,59	-0,70		T	Sensory transduction histidine kinase-related