SUPPLEMENTARY MATERIAL

Proteogenomic insights into the physiology of marine, sulfate-reducing, filamentous *Desulfonema limicola* and *Desulfonema magnum*

Vanessa Schnaars Lars Wöhlbrand Sabine Scheve Christina Hinrichs Richard Reinhardt Ralf Rabus

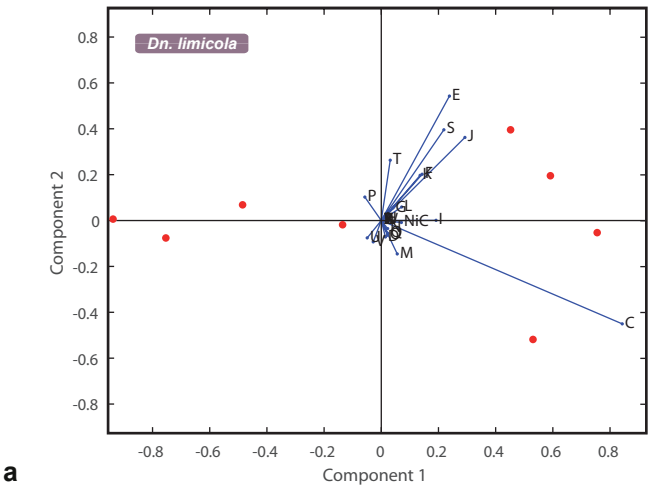
Content **Page**

Supplementary Figures

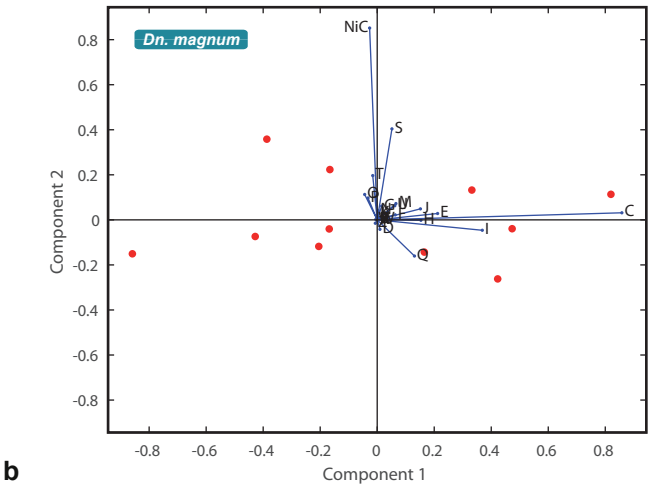
Fig S1. Biplots corresponding to the PCA analyses presented in Fig. 2b 1

Supplementary Tables

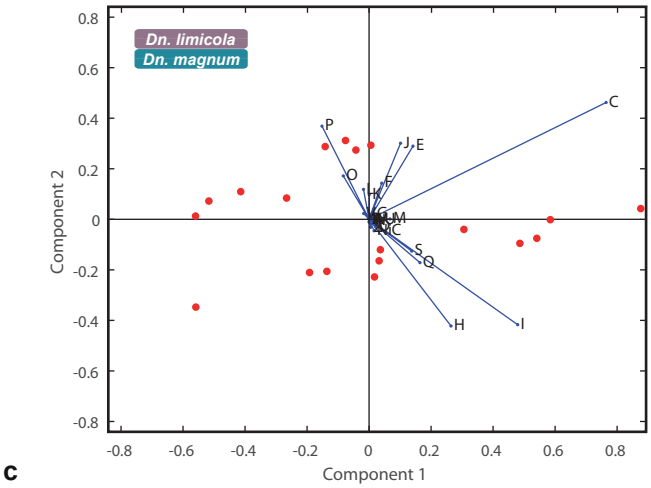
Table S1. COG representation of predicted versus detected proteins 2
Table S2. Annotations underlying the catabolic networks 3
Table S3. Differential proteomic data underlying the catabolic networks 7
Table S4. Annotations underlying the lifestyle properties 11
Table S5. Differential proteomic data underlying the lifestyle properties 13
Table S6. Annotations underlying potential members of a σ^E-regulon 15
Table S7. Differential proteomic data underlying potential members of a σ^E-regulon 17



a



b



c

Fig. S1. Biplots corresponding to the PCA analyses presented in Fig. 2b of the manuscript for *Dn. limicola* (top), *Dn. magnum* (center) and both strains combined (bottom). COG categories of the respective vectors are indicated (for abbreviations see legend to Fig. 2).

Table S1 COG representation of predicted versus detected proteins

		Dn. limicola		*Dn. magnum*	
		predicted	detected	predicted	detected
Information storage and processing					
RNA processing and modification	A	3.50	0.00	0.00	0.00
Chromatin structure and dynamics	B	2.33	0.00	2.50	0.50
Translation, ribosomal structure and biogenesis	J	178.00	75.00	177.67	93.83
Transcription	K	209.17	24.50	190.67	32.83
Replication, recombination, repair	L	408.83	27.00	454.67	25.33
Mobilome: prophages, transposons	X	0.00	0.00	0.00	0.00
Cellular processes and signaling					
Cell cycle control, cell division, chromosome partitioning	D	76.00	15.00	80.25	19.00
Cell wall/membrane/envelope biogenesis	M	263.50	49.00	312.67	75.17
Cell motility	N	93.92	30.08	104.92	22.50
Posttranslational modification, protein turnover, chaperones	O	151.33	54.33	170.58	57.00
Signal transduction mechanisms	T	524.92	96.75	496.92	107.83
Intracellular trafficking, secretion, vesicular transport	U	80.92	28.08	97.75	25.83
Defense mechanisms	V	85.00	10.50	63.00	8.00
Extracellular structures	W	1.00	0.00	3.00	1.00
Nuclear structure	Y	0.00	0.00	0.00	0.00
Cytoskeleton	Z	1.50	0.00	2.75	1.50
Metabolism					
Energy production and conversion	C	339.33	162.50	361.00	213.50
Amino acid transport and metabolism	E	264.17	84.50	262.08	92.33
Nucleotide transport and metabolism	F	87.00	22.00	83.50	33.50
Carbohydrate transport and metabolism	G	107.83	23.50	110.83	31.33
Coenzyme transport and metabolism	H	153.83	28.50	153.33	57.83
Lipid transport and metabolism	I	114.00	48.50	10800	56.50
Inorganic ion transport and metabolism	P	185.08	39.75	185.58	51.33
Secondary metabolites biosynthesis, transport and catabolism	Q	77.83	20.50	97.33	30.33
Poorly characterized					
General function prediction only	R	0.00	0.00	0.00	0.00
Function unknown	S	974.00	157.00	1,009.00	189.00
Not in COG		2,056.00	136.00	5,463.00	187.00
Total proteins		**6,441.00**	**1,133.00**	**9,991.00**	**1,413.00**

Table S2 Annotations underlying the catabolic networks

		Query used for annotation			*Dn. limicola*					*Dn. magnum*				
		Gene name	Predicted function	Length [aa]	*Gene name*	Length [aa]	Alignment lenght [aa]	Pos. [%]	e-value	*Gene name*	Length [aa]	Alignment lenght [aa]	Pos. [%]	e-value
Aromatic compound degradation	Phac	*dmul_C29130* [a]	CoA-binding domain protein	731	-					*dnm_025880*	693	692	56	1e-124
		hgdA [b]	(R)-2-hydroxyglutaryl-CoA dehydratase, subunit α	477	-					*dnm_025890*	416	303	46	1e-28
		hgdC [b]	(R)-2-hydroxyglutaryl-CoA dehydratase activating ATPase	260	-					*dnm_025900*	258	250	57	2e-39
		dmul_C24870 [a]	Putative phenylpyruvate reductase	319	-					*dnm_025910*	316	305	74	1e-108
		dctP3 [a]	Predicted C4-TRAP dicarboxylate transporter, periplasmic binding protein	318	-					*dctP1*	343	306	84	1e-135
		dctQ3 [a]	C4-TRAP dicarbooxylate transporter	170	-					*dctQ1*	164	159	71	4e-46
		dctM9 [c]	TRAP dicarboxylate transport system permease	430	-					*dctM1*	431	430	87	0
		dctM3 [c]	TRAP C4-dicarboxylate transport system permease	438	-					*dctM2*	439	438	89	0
		dctQ3 [c]	TRAP dicarboxylate transporter	164	-					*dctQ2*	163	159	72	1e-45
		dctP1 [a]	C4-TRAP dicarboxylate transporter periplasmatic binding protein	343	-					*dctP2*	340	344	76	1e-126
	p -Cre	*hbsF* [c]	Conserved uncharacterized protein	503	-					*hbsF*	570	497	68	1e-143
		hbsE [c]	Chaperone associated with benzylsuccinate synthase	287	-					*hbsE*	293	282	89	1e-124
		hbsD1 [c]	Hydroxybenzylsuccinate synthase activating enzyme	347	-					*hbsD1*	335	326	84	1e-140
		hbsD2 [c]	Hydroxybenzylsuccinate synthase activating enzyme	362	-					*hbsD2*	357	351	75	1e-124
		hbsB1 [c]	Predicted hydroxybenzylsuccinate synthase, subunitβ	68	-					*hbsB*	69	68	88	2e-29
		hbsA [c]	Hydroxybenzylsuccinate synthase, subunitα	813	-					*hbsA*	812	809	88	0
		hbsC [c]	Hydroxybenzylsuccinate synthase, subunitγ	59	-					*hbsC*	59	57	77	1e-18
		bhsA [c]	Hydroxybenzylsuccinyl-CoA thiolase, subunit A	143	-					*bhsA*	146	144	91	8e-70
		bhsB [c]	Hydroxybenzylsuccinyl-CoA thiolase, subunit B	389	-					*bhsB*	390	389	94	0
		bhsC [c]	2-[hydroxy(Phenyl)methyl]-succinyl-CoA DH	249	-					*bhsC*	251	250	66	5e-68
		bhsD [c]	2-[hydroxy(Phenyl)methyl]-succinyl-CoA DH	248	-					*bhsD*	249	248	88	1e-110
		bhsE [c]	Hydroxybenzylsuccinate CoA-transferase	414	-					*bhsE*	412	407	85	0
		bhsF [c]	Benzylsuccinate CoA-transferase	408	-					*bhsF*	410	408	88	0
		bhsG [c]	Hydroxybenzylsuccinyl-CoA dehydrogenase	410	-					*bhsG*	410	409	92	0
		bhsH [c]	Putative E-phenylitaconyl-CoA hydratase	256	-					*bhsH*	257	256	92	1e-125
		etfB2 [c]	Electron transfer flavoprotein, subunit β	251	-					*etfB4*	256	251	83	4e-98
		etfA1 [c]	Electron transfer flavoprotein, subunit α	295	-					*etfA4*	295	293	83	1e-116
		eqo [d]	ETF:quinone oxidoreductase	688	-					*eqo2*	679	639	48	6e-75
		hcrA [c]	4-hydroxybenzoyl-CoA reductase	786	-					*hcrA*	787	784	84	0
		hcrC [c]	4-hydroxybenzoyl-CoA reductase, subunit γ	154	-					*hcrC*	153	149	83	2e-60
		hcrB [c]	Predicted 4-hydroxybenzoyl-CoA reductase, subunit β	293	-					*hcrB*	294	290	71	5e-74
	3-Ppp	*dmul_C24680* [a]	Fusion protein	680	-					*dnm_055620*	680	680	80	0
		fadD3 [a]	Long-chain-fatty-acid--CoA ligase	499	-					*fadD1*	501	499	69	1e-147
		acdA12 [a]	Acyl-CoA dehydrogenase	385	-					*dnm_061160*	382	381	64	4e-95
		etfA2 [d]	EtfA2	322	-					*etfA2*	324	330	54	2e-55
		etfB2 [d]	EtfB2	262	-					*etfB2*	264	263	67	3e-64
		eqo [d]	ETF:quinone oxidoreductase	688	-					*eqo1*	664	635	49	1e-74
		fadD5 [a]	Long-chain-fatty-acid--CoA ligase	565	-					*fadD2*	566	560	83	0
	BzCoA	*bclA* [a]	Benzoate-CoA ligase	516	-					*bclA*	516	511	87	0
		HRM2_09990 [d]	Enoyl-CoA hydratase family protein	261	-					*dnm_055580*	257	256	53	3e-34
		oah [a]	Predicted 6-oxo-cyclohex-1-ene-carbonyl- CoA hydrolase	377	-					*oah*	382	382	77	1e-145
		had [c]	6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase	370	-					*had*	368	368	84	1e-160
		bamB1 [a]	Tungsten-containing aldehyde:ferredoxin oxidoreductase	665	-					*bamB*	657	656	93	0
		bamC3 [c]	4Fe-4S ferredoxin	177	-					*bamC*	178	176	91	4e-86
		bamD2 [a]	Putative heterodisulfide reductase, subunit B	383	-					*bamD*	388	383	91	0
		bamE [a]	Predicted heterodisulfide reductase, subunit A	930	-					*bamE*	930	926	89	0
		bamF [a]	Coenzyme F420 non-reducing hydrogenase, subunit δ	238	-					*bamF*	256	233	82	1e-100
		bamO [c]	Electron transfer flavoprotein, subunit β	260	-					*bamO*	261	259	93	1e-124

		bamP[c]	Electron transfer flavoprotein, subunit α	319	-					*bamP*	320	318	96	1e-162
		bamD1[a]	Uncharacterized iron-sulfur cluster binding protein	702	-					*dnm_070140*	704	702	90	0
Aliphatic compound degradation	Prop	*prpE*[e]	Propionyl-CoA synthetase	634	*prpE1*	635	634	92	0	*prpE1*	635	634	93	0
		prpE[e]	Propionyl-CoA synthetase	634	*prpE2*	636	635	90	0	*prpE2*	636	634	94	0
	PropOH	*adh*[a]	Iron-containing alcohol dehydrogenase	388	*adh1*	385	394	50	6e-50	-				
		adh[c]	Iron-containing alcohol dehydrogenase	355	*adh2*	356	355	80	1e-145	*adh*	358	355	83	1e-145
	Lac	*lutR*[f]	HTH-type transcriptional regulator	219	*dnl_44850*	242	208	59	1e-29	-				
		ldhB[a]	Lactate dehydrogenase, subunit β	443	*ldhB*	431	439	83	0	-				
		ldhA[a]	Lactate dehydrogenase, subunit α	461	*ldhA*	461	461	90	0	-				
	MMP	*sucD2*[a]	Succinyl-CoA ligase, subunit α	289	*sucD*	290	289	94	1e-151	*sucD2*	291	289	87	1e-130
		sucC2[a]	Succinyl-CoA ligase, subunit γ	388	*sucC*	388	388	91	0	*sucC2*	387	387	86	1e-161
		sucC2[c]	Succinyl-CoA ligase, subunit β	377	-					*sucC1*	381	378	83	1e-144
		sucD2[c]	Succinate--CoA ligase [ADP-forming], subunit α	290	-					*sucD1*	291	289	86	1e-130
		pccB[d]	PccB	517	*pccB*	518	517	89	0	*pccB*	519	518	91	0
		sbm[a]	Methylmalonyl-CoA mutase-like	713	*sbm*	712	712	94	0	*sbm*	711	710	92	0
		mce[a]	Methylmalonyl-CoA epimerase	134	*mce*	134	133	98	8e-71	*mce*	134	133	95	1e-64
		A2Z73_06390[g]	NAD-dependent malic enzyme	535	*dnl_23190*	547	531	81	0	-				
		sdhC[a]	Succinate dehydrogenase/fumarate reductase cytochrome	213	*sdhC*	214	213	88	5e-97	*sdhC1*	213	209	79	1e-84
		sdhA[a]	Succinate dehydrogenase flavoprotein	637	*sdhA*	638	637	94	0	*sdhA1*	638	637	89	0
		sdhB[a]	Succinate dehydrogenase and fumarate reductase, iron-sulfur protein	255	*sdhB*	256	255	92	1e-127	*sdhB1*	257	253	86	1e-116
		sdhC[a]	Succinate dehydrogenase/fumarate reductase cytochrome	213	-					*sdhC2*	214	213	81	2e-88
		sdhB[a]	Succinate dehydrogenase and fumarate reductase iron-sulfur protein	255	-					*sdhB2*	255	253	87	1e-117
		sdhA[a]	Succinate dehydrogenase flavoprotein subunit	637	-					*sdhA2*	638	637	89	0
		por[a]	Pyruvate:ferredoxin oxidoreductase	1215	*por*	1187	1187	91	0	*por1*	1218	1217	85	0
		por[a]	Pyruvate:ferredoxin oxidoreductase	1215	-					*por2*	1213	1215	85	0
		fumA[a]	Fumarate hydratase class I	535	*fumA*	536	535	94	0	*fumA*	536	535	90	0
		fumC[a]	Fumarate hydratase class II	466	-					*fumC*	467	465	81	0
	WLP	*fdhA*[h]	Formate dehydrogenase, subunit α	673	*dnl_05780*	529	530	70	1e-154	*dnm_034450*	541	542	71	1e-165
		yrhE[f]	Putative formate dehydrogenase	980	*dnl_05790*	378	418	50	2e-66	*dnm_034440*	378	418	51	1e-67
		cdhA[a]	CO dehydrogenase, catalytic subunit	672	*cdhA*	655	667	67	0	*cdhA1*	676	667	87	0
		cdhA[c]	Carbon monoxide dehydrogenase	678	-					*cdhA2*	677	675	92	0
		cdhE[c]	CO dehydrogenase/acetyl-CoA synthase complex	446	*cdhE*	448	446	88	0	*cdhE*	447	445	88	0
		cdhC[c]	CO-methylating acetyl-CoA synthase	737	*cdhC*	738	737	87	0	*cdhC*	738	737	90	0
		cdhD[d]	CdhD	433	*cdhD*	520	401	82	1e-169	*cdhD*	517	394	85	1e-171
		fhs[a]	Formate--tetrahydrofolate ligase	587	*fhs*	588	587	98	0	*fhs*	588	587	95	0
		folD[a]	Bifunctional protein	303	*folD*	303	302	95	1e-155	*folD*	302	302	95	1e-153
		metF1[d]	Methylenetetrahydrofolate reductase	293	*metF*	293	291	79	1e-111	*metF*	293	291	82	1e-119
	β-Ox	*acdA12*[a]	Acyl-CoA dehydrogenase	385	*acdA1*	386	385	96	0	*acdA4*	386	385	91	0
		acsA4[a]	Acetyl-coenzyme A synthetase	676	*acsA1*	681	676	95	0	*acsA1*	678	675	89	0
		acsA6[a]	Acetyl-coenzyme A synthetase	650	*acsA2*	652	651	90	0	*acsA2*	652	651	88	0
		acdA10[a]	Acyl-CoA dehydrogenase	382	*acdA2*	383	382	96	0	*acdA3*	383	382	95	0
		acdA9[a]	Acyl-CoA dehydrogenase	604	*acdA3*	604	604	93	0	-				
		atoB2[a]	Acetyl-CoA acetyltransferase	391	*atoB*	392	391	92	0	*atoB*	392	391	91	0
		hbd2[a]	3-hydroxybutyryl-CoA dehydrogenase	283	*hbd*	284	283	95	1e-145	*hbd2*	284	283	95	1e-147
		hbd1[a]	3-hydroxybutyryl-CoA dehydrogenase	285	-					*hbd1*	286	283	87	1e-126
		bcd[i]	Acyl-CoA dehydrogenase, short-chain specific	379	*bcd*	385	377	69	1e-109	*bcd*	388	379	69	1e-111
		thlA[j]	Acetyl-CoA acetyltransferase	391	*thlA*	417	407	61	3e-91	*thlA2*	575	414	61	3e-93
					-					*thlA1*	417	414	62	1e-92
		acdA1[a]	Acyl-CoA dehydrogenase	604	*acdA4*	605	604	88	0	*acdA2*	604	604	86	0
		acdA13[a]	Acyl-CoA dehydrogenase	389	*acdA5*	390	389	91	0	*acdA1*	390	389	89	0
		acsA[c]	Acetyl-coenzyme A synthetase	655	*acsA3*	639	639	67	0	*acsA3*	637	636	70	0

AU	H_2/CO_2	*hynB*[d]	HynB	330	*hynB*	314	312	82	1e-132	-				
		hynA[d]	HynA	545	*hynA*	489	489	75	0	-				
		hynC[d]	HynC	169	*hynC*	164	158	72	1e-41	-				
		hynD[k]	HynD	83	*hynD*	76	77	67	5e-12	-				
Energy metabolism	ATPase	*atpH*[a]	ATP synthase, subunitδ	183	*atpH*	184	183	89	7e-76	*atpH*	182	181	83	6e-69
		atpA3[a]	ATP synthase, subunit α	505	*atpA*	506	505	95	0	*atpA*	514	513	93	0
		atpG2[a]	ATP synthase, subunit γ	297	*atpG*	300	299	88	1e-133	*atpG*	298	297	88	1e-135
		atpD2[a]	ATP synthase, subunit β	471	*atpD*	473	471	96	0	*atpD*	472	471	96	0
		atpC2[a]	ATP synthase, subunit ε	138	*atpC*	141	140	85	6e-53	*atpC*	131	130	89	2e-51
		atpB2[a]	ATP synthase, subunit α	229	*atpB1*	230	229	96	1e-121	*atpB1*	230	229	88	1e-105
		atpE4[a]	ATP synthase, subunit γ	93	*atpE1*	96	93	97	1e-44	*atpE1*	95	90	98	7e-44
		atpF2[a]	ATP synthase, subunit β	198	*atpF1*	195	172	64	7e-38	*atpF2*	195	188	65	4e-47
		atpF[1]	ATP synthase, subunit β	169	*atpF2*	151	149	66	4e-34	*atpF1*	152	143	51	2e-14
		atpE2[a]	ATP synthase, subunit γ	82	*atpE2*	83	82	93	3e-36	*atpE3*	83	82	96	5e-37
		atpE3[a]	ATP synthase, subunit γ	303	*atpE3*	325	304	76	1e-102	*atpE2*	244	221	72	3e-61
		atpB1[a]	ATP synthase, subunit α	224	*atpB2*	225	224	89	1e-101	*atpB2*	225	224	90	1e-104
		atpF3[a]	ATP synthase, subunit β	141	*atpF3*	159	141	79	1e-44	*atpF4*	142	141	81	4e-47
		atpF4[a]	ATP synthase, subunit β	208	*atpF4*	206	208	72	8e-61	*atpF3*	193	171	84	5e-60
	SO_4^{2-} Reduction	*dsrC*[a]	Sulfite reductase, dissimilatory-type, subunit γ	105	*dsrC*	106	105	92	8e-52	*dsrC*	106	105	88	9e-47
		aprB[a]	Adenylylsulfate reductase, subunit β	124	*aprB*	146	124	96	4e-68	*aprB*	146	124	95	1e-64
		aprA[a]	Adenylylsulfate reductase, subunit α	657	*aprA*	658	657	97	0	*aprA*	661	659	94	0
		dsrA[c]	Sulfite reductase, dissimilatory-type, subunit α	441	*dsrA*	437	439	86	0	*dsrA*	439	442	86	0
		dsrB[c]	Sulfite reductase, dissimilatory-type, subunit β	382	*dsrB*	382	382	90	0	*dsrB*	383	382	90	0
		dsrD[a]	Sulfite reductase, dissimilatory-type, subunit δ	80	*dsrD*	80	79	94	3e-35	*dsrD*	80	79	96	3e-35
		hppA[a]	Membrane-bound proton-translocating pyrophosphatase	669	*hppA*	679	678	91	0	*hppA*	680	679	90	0
		sulP[h]	Sulfate permease	624	*sulP*	583	578	77	0	*sulP*	586	584	79	0
		TOL2_C19470[c]	Sodium/sulfate symporter	490	*dnl_40190*	495	489	88	0	*dnm_014120*	492	488	89	0
		TOL2_C19410[c]	Sodium/sulfate symporter	526	*dnl_54150*	526	526	87	0	*dnm_051020*	527	526	88	0
		TOL2_C19300[c]	Sodium/sulfate symporter	615	*dnl_54220*	618	613	90	0	*dnm_056130*	618	614	90	0
		sat2[a]	Sulfate adenylyltransferase	423	*sat*	419	422	90	0	*sat*	425	427	87	0
	Redox complexes	*dsrM*[a]	Predicted redox complex linked to DsrAB, transmembrane subunit	333	*dsrM*	329	328	88	1e-158	*dsrM*	344	341	82	1e-139
		dsrK[a]	Predicted redox complex linked to DsrAB , iron-sulfur binding subunit	540	*dsrK*	544	541	94	0	*dsrK*	542	538	94	0
		dsrJ[a]	Predicted redox complex linked to DsrAB, cytochrome c subunit	129	*dsrJ*	136	129	89	1e-61	*dsrJ*	138	129	82	1e-54
		dsrO[a]	Predicted redox complex linked to DsrAB, iron-sulfur binding subunit	265	*dsrO*	262	265	85	1e-121	*dsrO*	277	277	78	1e-106
		dsrP[a]	Predicted redox complex linked to DsrAB, transmembrane subunit	385	*dsrP*	386	385	93	0	*dsrP*	386	385	87	1e-176
		qmoA[a]	Predicted quinone interacting membrane bound oxidoreductase, subunit A	425	*qmoA*	426	425	93	0	*qmoA*	419	418	88	0
		qmoB[a]	Quinone interacting membrane bound oxidoreductase, subunit B	778	*qmoB*	779	778	94	0	*qmoB*	779	778	91	0
		qmoC[a]	Quinone interacting membrane bound oxidoreductase, subunit C	382	*qmoC*	383	382	91	0	*qmoC*	383	382	82	1e-163
		qrcD[a]	Quinone reductase complex, subunit δ	410	*qrcD*	414	409	94	0	*qrcD*	414	409	91	0
		qrcC[a]	Quinone reductase complex, subunit γ	272	*qrcC*	272	266	91	1e-140	*qrcC*	264	262	88	1e-130
		qrcB[a]	Quinone reductase complex, subunit β	753	*qrcB*	753	753	77	0	*qrcB*	746	755	75	0
		qrcA[a]	Predicted quinone reductase complex, subunit α	215	*qrcA*	216	215	90	1e-112	*qrcA*	222	211	86	1e-102
		rnfB1[a]	Electron transport complex protein	303	*rnfB1*	304	303	90	1e-151	*rnfB1*	287	267	74	2e-96
		rnfA1[a]	Electron transport complex protein	254	*rnfA1*	249	249	93	1e-123	*rnfA1*	255	232	88	1e-105
		rnfE1[a]	Predicted electron transport complex protein	207	*rnfE1*	204	202	93	1e-101	*rnfE1*	208	204	89	1e-93
		rnfG1[a]	Electron transport complex protein	218	*rnfG1*	228	219	81	1e-82	*rnfG1*	222	203	71	2e-61
		rnfD1[a]	Electron transport complex protein	330	*rnfD1*	339	315	88	1e-148	*rnfD1*	329	323	76	1e-114
		rnfC1[a]	Predicted electron transport complex protein	454	*rnfC1*	455	455	86	0	*rnfC1*	421	419	76	1e-152
		rnfC2[a]	Electron transport complex protein	431	*rnfC2*	433	431	78	1e-157	*rnfC2*	431	430	73	1e-144
		rnfD2[a]	Electron transport complex protein	327	*rnfD2*	328	327	86	1e-143	*rnfD2*	320	325	80	1e-124
		rnfG2[a]	Electron transport complex protein	197	*rnfG2*	198	197	87	5e-86	*rnfG2*	198	197	89	8e-86
		rnfE2[a]	Electron transport complex protein	197	*rnfE2*	198	197	93	1e-96	*rnfE2*	202	201	91	7e-90
		rnfA2[a]	Electron transport complex protein	191	*rnfA2*	192	191	95	7e-93	*rnfA2*	191	189	97	3e-95
		rnfB2[a]	Electron transport complex protein	691	*rnfB2*	695	695	89	0	*rnfB2*	688	685	85	0
		rrf1[a]	Response regulator protein	117	*rrf*	121	116	87	6e-45	*rrf*	118	116	85	1e-46

tmcA1[a]	Predicted tmc redox complex, acidic cyctchrome c, class III family protein	132	*tmcA*	138	130	62	1e-30	*tmcA*	131	133	71	6e-39
tmcB1[d]	TmcB1	444	*tmcB*	445	433	82	0	*tmcB*	446	430	87	0
tmcC1[a]	Predicted tmc redox complex, uncharacterized membrane protein	219	*tmcC*	220	219	76	1e-77	*tmcC*	220	219	81	6e-87
tmcD[a]	Predicted tmc redox complex, uncharacterized protein	425	*tmcD*	385	382	70	1e-131	*tmcD*	418	421	74	1e-154

Labelled queries referred to:

[a] *Desulfococcus multivorans* (NZ_CP015381)
[b] *Acidaminococcus fermentans* (NC 013740)
[c] *Desulfobacula toluolica* Tol2 (NC 018645)
[d] *Desulfobacterium autotrophicum* HRM2 (NC_012108)
[e] *Desulfobacteraceae bacterium* (GCA 002085455.1)
[f] *Bacillus subtilis* 168 (NC 000964)
[g] *Deltaproteobacteria bacterium* (GCA_001797785.1)
[h] *Methanocaldococcus jannaschii* (NC 000909)
[i] *Clostridium acetobutylicum* (NC_015687)
[j] *Clostridioides difficile* 630 (NC 009089)
[k] *Desulfovibrio vulgaris* (NC 017310)
[l] *Heliobacterium modesticaldum* (NC_010337)

Table S3 Differential proteomic data underlying the catabolic networks

		Protein in Dnl	Protein in Dnm	Predicted function	*Dn. limicola*												*Dn. magnum*																							
					H_2/CO_2		PropOH		Lac		But		Prop		FA-Mix		Suc		Fum		But		Prop		FA-Mix		Suc		Fum		Mal		Bz		Phea		3-Ppp		*p*-Cre		4-OHbenz	
					SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP
Aromatic compound degradation	Phac		Dnm_025880	CoA-binding domain-containing protein																	0	48	618	0	0	0	508	0	720	146	444	0	642	138	910	161	126	0	303	97	968	472
			Dnm_025890	2-hydroxyglutaryl-CoA dehydratase, D-component																	195	52	478	0	196	0	630	115	575	233	384	108	633	0	691	112	54	0	407	0	745	412
			Dnm_025900	CoA enzyme activase																	0	0	0	96	0	0	45	0	0	83	0	0	129	89	219	116	0	41	0	78	165	142
			Dnm_025910	Putative phenylpyruvate reductase																	277	272	210	167	84	177	299	98	99	170	127	58	333	424	291	386	193	296	240	389	316	402
			DctP1	Predicted C4-TRAP dicarboxylate transporter periplasmic binding protein																	0	0	28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
			DctQ1	C4-TRAP dicarbooxylate transporter																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
			DctM1	C4-dicarboxylate TRAP transporter, large permease protein																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
			DctM2	C4-dicarboxylate TRAP transporter large, permease protein																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
			DctQ2	C4-dicarboxylate TRAP transporter, small permease protein																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
			DctP2	C4-TRAP dicarboxylate transporter, periplasmatic binding protein																	0	191	222	345	70	0	458	231	217	121	456	175	171	168	144	267	90	55	0	45	145	128
	p-Cre		HbsF	Conserved uncharacterized protein																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68	0	0
			HbsE	Chaperone associated with benzylsuccinate synthase																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	163	0	0	0
			HbsD1	Hydroxybenzylsuccinate synthase activating enzyme																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30	0	0	0
			HbsD2	Hydroxybenzylsuccinate synthase activating enzyme																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	198	0	0	0
			HbsB	Hydroxybenzylsuccinate synthase activating enzyme																	0	0	0	0	0	0	0	0	0	0	30	0	0	0	0	93	0	0	0	181	0	31	0
			HbsA	Hydroxybenzylsuccinate synthase, subunitα																	0	0	80	0	59	0	0	0	108	0	289	0	138	0	150	77	0	0	2115	1437	296	246
			HbsC	Hydroxybenzylsuccinate synthase, subunity																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74	0	0	0	269	0	0	0
			BhsA	Hydroxybenzylsuccinyl-CoA thiolase, subunit A																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	168	0	0	0
			BhsB	Hydroxybenzylsuccinyl-CoA thiolase, subunit B																	104	0	78	78	134	26	77	0	0	0	0	0	51	32	79	0	100	31	851	1558	79	0
			BhsC	2-[hydroxy(Phenyl)methyl]-succinyl-CoA DH, subunit C																	106	0	123	0	93	0	231	0	50	0	0	0	148	0	158	0	45	0	1213	1497	105	0
			BhsD	2-[hydroxy(Phenyl)methyl]-succinyl-CoA DH, subunit D																	92	0	93	0	0	0	128	0	0	0	0	0	93	0	102	0	102	0	618	485	0	0
			BhsE	Hydroxybenzylsuccinate CoA-transferase, subunit E																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	676	563	0	0
			BhsF	Benzylsuccinate CoA-transferase, subunit F																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	460	472	0	0
			BhsG	Hydroxybenzylsuccinyl-CoA dehydrogenase																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1046	372	0	0
			BhsH	Putative E-phenylitaconyl-CoA hydratase																	124	0	0	64	0	51	111	54	0	90	0	0	103	0	85	0	0	59	765	420	87	0
			EtfB4	Electron transfer flavoprotein, subunitβ																	0	0	0	0	0	0	0	0	0	0	0	0	28	0	0	0	0	0	587	167	0	0
			EtfA4	Electron transfer flavoprotein, subunitα																	0	0	0	0	0	0	37	0	0	0	0	0	0	0	0	0	0	0	657	671	0	0
			Eqo2	ETF:quinone oxidoreductase																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	544	0	0
			HcrA	4-hydroxybenzoyl-CoA reductase, subunitα																	1260	1326	970	590	932	0	844	361	785	342	528	125	1390	1278	1100	928	957	1287	1721	1151	1776	2605
			HcrC	4-hydroxybenzoyl-CoA reductase, subunity																	392	48	373	40	318	0	355	0	308	0	273	0	402	88	390	0	363	118	576	85	504	446
			HcrB	4-hydroxybenzoyl-CoA reductase, subunitβ																	554	329	444	241	482	0	546	0	392	57	335	0	704	482	696	353	551	595	869	622	787	1760
	3-Ppp		Dnm_055620	Enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase																	1453	179	1673	305	677	252	1515	761	1692	1199	691	83	1723	337	1974	644	1688	433	1542	566	2219	1671
			FadD1	Long-chain-fatty-acid--CoA ligase																	0	0	0	32	0	0	0	0	0	0	0	0	0	0	0	0	730	547	0	0	0	0
			Dnm_061160	Acyl-CoA dehydrogenase																	0	0	0	0	0	0	0	0	0	29	0	0	0	0	0	0	486	598	0	0	0	0
			EtfA2	Electron transfer flavoprotein, subunitα																	0	0	0	0	0	0	77	0	55	0	0	0	53	0	0	0	416	142	0	0	0	0
			EtfB2	Electron transfer flavoprotein, subunitβ																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	283	0	0	0	0	0
			Eqo1	ETF:quinone oxidoreductase																	0	0	0	0	0	0	0	0	0	37	0	0	0	0	0	0	32	0	937	0	0	0
			FadD2	Long-chain-fatty-acid--CoA ligase																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	BzCoA		BclA	Benzoate-CoA ligase																	0	0	0	0	0	0	0	0	0	0	102	0	1724	1653	433	290	0	0	0	0	1529	1550
			Dnm_055580	Enoyl-CoA hydratase/isomerase																	482	0	348	0	283	0	319	123	330	134	258	0	554	122	524	105	486	114	480	85	536	196
			Oah	6-oxo-cyclohex-1-ene-carbonyl- CoA hydrolase																	988	785	959	693	646	455	978	732	882	744	708	319	1277	1479	1045	1223	898	1176	1256	1251	1168	1420
			Had	6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase																	676	458	578	506	349	223	511	287	540	486	367	190	924	928	731	954	624	582	824	954	786	841
			BamB	Tungsten-containing aldehyde:ferredoxin oxidoreductase																	373	0	295	0	184	0	66	0	309	0	161	0	904	0	613	0	452	0	674	54	1004	108
			BamC	4Fe-4S ferredoxin																	141	0	158	0	88	0	0	0	133	0	0	0	225	0	230	0	246	0	0	0	233	0
			BamD	Putative heterodisulfide reductase, subunit B																	194	0	134	0	32	0	0	0	133	0	0	0	505	0	389	0	354	0	426	0	478	0
			BamE	Predicted heterodisulfide reductase, iron-sulfur subunit A																	0	106	0	80	53	0	0	0	194	0	0	0	467	377	395	92	0	80	338	164	600	774
			BamF	Coenzyme F420 non-reducing hydrogenase, subunit delta																	0	0	0	0	0	0	0	0	0	0	0	0	54	0	0	0	60	0	31	0	170	0
			BamO	Electron transfer flavoprotein, subunitβ																	537	75	311	0	278	0	446	0	264	0	245	0	939	160	823	59	756	74	591	67	801	143

Aliphatic compound degradation
Prop
PropOH
Lac
MMP
WLP
β-Ox
BamP Electron transfer flavoprotein, subunitα
Dnm_070140 Putative heterodisulfide reductase, subunit B
PrpE1 PrpE1 Propionate-CoA ligase
PrpE2 PrpE2 Propionate-CoA ligase
Adh1
Adh Iron-containing alcohol dehydrogenase
Adh2 Iron-containing alcohol dehydrogenase
Dnl_44850 Putative HTH-type transcriptional regulator, LutR-like
LdhB Lactate dehydrogenase, subunitβ
LdhA Lactate dehydrogenase, subunitα
SucD SucD2 Succinate--CoA ligase [ADP-forming], subunitα
SucC SucC2 Succinate--CoA ligase [ADP-forming], subunitβ
SucC1 Succinate--CoA ligase [ADP-forming], subunitβ
SucD1 Succinate--CoA ligase [ADP-forming], subunitα
PccB PccB Propionyl-CoA carboxylase, carboxyltransferase subunit
Sbm Sbm Methylmalonyl-CoA mutase-like
Mce Mce Methylmalonyl-CoA epimerase
Dnl_23190 NAD-dependent malic enzyme, Mae-like
SdhC SdhC1 Succinate dehydrogenase, cytochrome b556 subunit
SdhA SdhA1 Succinate dehydrogenase flavoprotein subunit
SdhB SdhB1 Succinate dehydrogenase and fumarate reductase iron-sulfur protein
SdhC2 Succinate dehydrogenase cytochrome b556 subunit
SdhB2 Predicted succinate dehydrogenase iron-sulfur subunit
SdhA2 Succinate dehydrogenase and fumarate reductase iron-sulfur protein
Por Por1 Pyruvate:ferredoxin oxidoreductase
Por2 Pyruvate:ferredoxin oxidoreductase
FumA FumA Fumarate hydratase, class I
FumC Fumarate hydratase, class II
Dnl_05780 Dnm_034450 Formate dehydrogenase, subunitα
Dnl_05790 Dnm_034440 Formate dehydrogenase domain-containing protein
CdhA CdhA1 Acetyl-CoA decarbonylase/synthase complex, subunitα
CdhA2 Acetyl-CoA decarbonylase/synthase complex, subunitα
CdhE CdhE Acetyl-CoA decarbonylase/synthase complex, subunity
CdhC CdhC Acetyl-CoA decarbonylase/synthase complex, subunitβ
CdhD CdhD Acetyl-CoA decarbonylase/synthase complex, subunitδ
Fhs Fhs Formate-tetrahydrofolate ligase
FolD FolD Bifunctional protein
MetF MetF 5,10-methylenetetrahydrofolate reductase
AcdA1 AcdA4 Acyl-CoA dehydrogenase
AcsA1 AcsA1 Acetyl-coenzyme A synthetase
AcsA2 AcsA2 Acetyl-coenzyme A synthetase
AcdA2 AcdA3 Acyl-CoA dehydrogenase
AcdA3 Acyl-CoA dehydrogenase
AtoB AtoB Acetyl-CoA acetyltransferase
Hbd Hbd2 3-hydroxybutyryl-CoA dehydrogenase
Hbd1 3-hydroxybutyryl-CoA dehydrogenase
Bcd Bcd Acyl-CoA dehydrogenase, short-chain specific
ThlA ThlA2 Acetyl-CoA acetyltransferase
ThlA1 Acetyl-CoA acetyltransferase
AcdA4 AcdA2 Acyl-CoA dehydrogenase
AcdA5 AcdA1 Acyl-CoA dehydrogenase
AcsA3 AcsA3 Acetyl-coenzyme A synthetase

AU	H_2/CO_2	HynB	Periplasmic [NiFe] hydrogenase, large subunit	0	130	0	54	0	128	0	351	0	129	65	0	0	123	0	113	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		HynA	Periplasmic [NiFe] hydrogenase, small subunit	0	292	0	223	0	404	0	728	0	334	0	429	0	370	0	425	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		HynC	Periplasmic [Ni/Fe] hydrogenase, cytochrome subunit	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		HynD	ATP synthase, subunit δ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Energy metabolism	ATPase	AtpH	AtpH ATP synthase, subunit α	310	797	230	748	208	841	245	793	318	835	323	755	191	1021	294	936	136	300	165	516	153	538	646	718	706	850	243	458	79	488	60	487	56	547	430	641	139	708
		AtpA	AtpA ATP synthase, subunit γ	1622	1635	1744	1524	1781	1877	1858	1970	2034	1602	1700	1629	1735	1887	1774	2082	2246	1300	2010	1632	1826	1022	1838	1180	2130	1492	1883	1062	1923	1258	2087	1317	1996	1261	2051	1420	2025	1623
		AtpG	AtpG ATP synthase, subunit β	401	1236	380	1174	496	1082	335	1227	462	1221	274	1191	411	1272	560	1242	689	1083	671	1079	607	1359	665	1421	827	1153	559	1025	570	999	462	1131	651	1215	635	1000	721	1275
		AtpD	AtpD ATP synthase, subunit ε	1340	1426	1267	1236	1615	1801	1405	1848	1768	1471	1454	1715	1537	1841	1597	1955	1699	636	1603	868	1443	710	1771	837	1696	1041	1550	598	1632	546	1651	513	1678	611	1712	870	1661	1161
		AtpC	AtpC ATP synthase, subunit α	127	481	174	495	180	473	185	523	228	433	172	499	226	479	203	508	254	194	316	272	219	227	302	149	267	156	204	81	315	150	312	217	306	198	328	131	280	158
		AtpB1	AtpB1 ATP synthase, subunit γ	0	77	0	73	0	0	0	74	0	0	0	95	0	84	0	77	0	48	0	87	0	117	0	133	0	104	0	0	0	91	0	67	0	81	0	85	0	93
		AtpE1	AtpE1 ATP synthase, subunit β	0	125	0	94	0	103	0	108	0	120	0	116	0	109	0	108	0	104	0	88	0	0	0	73	0	70	0	68	0	66	0	73	0	92	0	108	0	91
		AtpF1	AtpF2 ATP synthase, subunit β	0	320	0	279	0	505	0	375	0	391	0	414	0	494	0	614	0	0	0	0	0	286	0	134	0	61	0	42	0	0	0	0	0	0	0	0	0	50
		AtpF2	AtpF1 ATP synthase, subunit γ	0	0	0	274	0	359	0	238	0	0	0	374	0	556	0	455	0	0	0	0	0	348	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		AtpE2	AtpE3 ATP synthase, subunit γ	0	481	0	436	0	405	0	446	0	417	0	413	0	519	63	508	0	0	0	0	0	116	0	94	0	127	0	0	0	64	0	77	0	66	0	0	0	91
		AtpE3	AtpE2 ATP synthase, subunit α	0	77	0	110	0	81	0	61	0	58	0	83	0	62	0	84	0	87	0	148	0	59	0	96	0	83	0	39	0	92	0	99	0	104	0	113	0	71
		AtpB2	AtpB2 ATP synthase, subunit β	0	90	0	45	0	0	0	50	0	60	0	54	0	38	0	72	0	0	0	0	0	0	0	0	0	0	0	29	0	0	0	0	0	0	0	0	0	0
		AtpF3	AtpF4 ATP synthase, subunit β	0	470	0	435	0	554	0	522	0	470	0	506	0	582	0	557	0	167	0	215	0	345	0	252	0	181	0	110	0	180	0	185	0	160	0	303	0	251
		AtpF4	AtpF3 Dissimilatory sulfite reductase, subunit γ	0	439	0	434	0	644	0	449	0	514	0	532	0	640	0	552	0	306	97	368	160	758	389	557	99	479	64	326	87	291	0	248	64	445	294	326	67	427
	SO_4^{2-} Reduc-tion	DsrC	DsrC Adenylylsulfate reductase, subunit β	93	74	105	75	90	80	105	82	111	135	95	81	100	95	104	107	231	30	232	0	231	50	247	0	189	0	205	0	218	58	199	0	246	0	182	61	192	0
		AprB	AprB Adenylylsulfate reductase, subunit α	242	130	311	120	430	93	321	182	461	132	413	232	399	255	391	113	691	117	749	259	788	161	732	145	566	123	564	80	772	235	687	205	727	190	740	455	607	176
		AprA	AprA Sulfite reductase, dissimilatory-type, subunit α	1985	2190	2181	2569	2415	1952	2309	2585	2418	2978	2212	3155	2547	3284	2256	2318	2625	2521	3000	2330	2345	2644	2686	2525	2010	1490	1810	1343	2427	2024	2197	1596	2083	1856	2848	1597	2500	2457
		DsrA	DsrA Sulfite reductase, dissimilatory-type, subunit β	1224	623	1382	912	1336	970	1298	573	1472	974	1368	899	1441	1087	1203	955	1925	1086	1782	1250	1724	1110	1707	1208	1242	999	1274	617	1704	1025	1629	774	1474	957	1619	753	1633	1290
		DsrB	DsrB Sulfite reductase, dissimilatory-type, subunit δ	885	992	840	867	862	946	888	999	994	1033	949	1051	993	1082	892	1041	1205	1203	1209	1065	1057	1107	1211	1128	914	851	854	564	1056	989	961	999	918	1150	1093	988	1025	1302
		DsrD	DsrD Membrane-bound proton-translocating pyrophosphatase	119	74	118	0	126	0	159	107	194	153	115	101	142	192	172	211	143	153	154	126	134	33	145	0	115	0	124	0	132	102	143	111	147	42	149	100	136	77
		HppA	HppA Sulfate permease	0	1753	0	1675	0	1646	0	1675	0	1852	0	1598	0	1854	0	1770	0	2662	0	2192	33	2492	0	2605	0	2439	0	2015	0	2137	0	2109	0	2306	0	1919	0	2056
		SulP	SulP Sodium/sulfate symporter transmembrane domain-containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Dnl_40190	Dnm_014120 Sodium/sulfate symporter	0	178	0	177	0	131	0	146	0	251	0	74	0	153	0	165	0	136	0	196	0	215	0	227	0	205	0	96	0	48	0	74	0	145	0	202	0	79
		Dnl_54150	Dnm_051020 Sodium/sulfate symporter	0	173	0	179	0	250	0	263	0	146	0	229	0	206	0	219	0	122	0	298	0	386	0	529	0	194	0	189	0	0	0	0	0	27	0	0	0	0
		Dnl_54220	Dnm_056130 Sulfate adenylyltransferase	0	0	0	0	0	130	0	155	0	0	0	0	0	0	0	0	0	0	0	129	0	193	0	286	0	30	0	0	0	0	0	0	0	43	0	0	0	0
		Sat	Sat Predicted redox complex linked to DsrAB, transmembrane subunit	1675	1335	1770	1388	1685	1645	1775	1947	1925	1840	1692	2184	1763	2092	1705	1549	1909	1537	1907	1393	1512	868	1767	1376	1491	1706	1197	452	1700	1006	1621	1149	1619	2003	1530	1301	1612	1440
	Redox com-plexes	DsrM	DsrM Predicted redox complex linked to DsrAB , iron-sulfur binding subunit	0	481	0	477	0	432	0	497	0	494	0	591	0	636	0	481	0	440	0	421	0	640	0	650	0	484	0	447	0	372	0	317	0	523	0	443	0	564
		DsrK	DsrK Predicted redox complex linked to DsrAB, cytochrome c subunit	276	1064	104	681	303	923	234	1114	192	1045	254	1103	398	1102	362	1113	81	781	114	571	0	530	0	549	83	488	209	509	0	397	29	293	0	851	0	365	27	689
		DsrJ	DsrJ Predicted redox complex linked to DsrAB, iron-sulfur binding subunit	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	48	0	56	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		DsrO	DsrO Predicted redox complex linked to DsrAB, transmembrane subunit	125	780	0	787	154	750	128	714	35	757	0	783	0	932	249	821	236	325	238	431	168	539	251	556	253	335	220	266	185	301	281	271	115	323	138	302	141	393
		DsrP	DsrP Quinone interacting membrane bound oxidoreductase, subunit A	0	179	0	164	0	154	0	126	0	153	0	151	0	175	0	169	0	146	0	136	0	155	0	147	0	97	0	114	0	152	0	97	0	115	0	152	0	129
		QmoA	QmoA Quinone interacting membrane bound oxidoreductase, subunit B	747	1202	715	657	1000	1039	791	1168	1024	939	820	1136	854	1436	873	1226	1058	2218	1135	1865	729	927	1073	1092	1059	747	910	1151	826	1518	1010	1526	713	1394	1182	1210	1084	1583
		QmoB	QmoB Quinone interacting membrane bound oxidoreductase, subunit C	1297	2173	1328	1724	1747	2270	1427	2267	1591	1687	1517	2395	1701	2632	1594	2435	1648	1346	2139	1135	1388	727	1435	1422	1776	790	1734	1205	1742	680	1883	414	1384	1029	1654	941	2084	1384
		QmoC	QmoC Menaquinone reductase, integral membrane subunit	0	887	0	991	0	897	0	964	0	1111	0	1098	0	1125	0	1076	0	776	0	794	0	1108	0	984	0	546	0	793	0	664	0	684	0	781	0	731	0	859
		QrcD	QrcD Menaquinone reductase, iron-sulfur cluster-binding subunit	0	340	0	226	0	308	0	342	0	354	0	307	0	371	0	384	0	359	0	289	0	344	0	335	0	209	0	246	0	340	0	320	0	328	0	336	0	361
		QrcC	QrcC Menaquinone reductase, molybdopterin-binding-like subunit	0	774	0	694	70	741	0	613	0	759	0	745	0	796	156	793	71	511	0	382	0	336	150	483	115	380	79	292	0	531	0	475	47	508	0	411	59	550
		QrcB	QrcB Menaquinone reductase, multiheme cytochrome c subunit	147	1716	0	1542	183	1577	129	1669	0	1571	0	1662	88	1879	200	1468	55	2159	56	1858	0	1615	0	1737	33	1679	60	1396	0	2153	0	2118	0	2016	0	1998	0	1967
		QrcA	QrcA Ion-translocating oxidoreductase complex, subunit B	0	44	0	101	0	90	0	57	0	45	0	91	0	92	0	96	0	0	0	0	0	31	0	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		RnfB1	RnfB1 Ion-translocating oxidoreductase complex, subunit A	0	532	0	523	0	333	0	421	0	442	0	523	0	519	0	471	0	0	0	84	0	64	0	115	0	0	0	0	0	0	0	0	0	33	0	29	0	0
		RnfA1	RnfA1 Ion-translocating oxidoreductase complex, subunit E	0	86	0	76	0	102	0	89	0	118	0	119	0	105	0	109	0	29	0	0	0	59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		RnfE1	RnfE1 Ion-translocating oxidoreductase complex, subunit G	0	268	0	226	0	181	0	207	0	187	0	207	0	163	0	193	0	0	0	91	0	133	0	180	0	202	0	0	0	92	0	54	0	154	0	156	0	117
		RnfG1	RnfG1 Ion-translocating oxidoreductase complex, subunit D	0	1229	0	963	0	903	0	1257	0	1238	0	1076	0	1238	0	1202	0	530	0	574	0	195	46	382	0	501	0	156	0	459	0	276	0	237	0	436	0	482
		RnfD1	RnfD1 Ion-translocating oxidoreductase complex, subunit C	0	145	0	110	0	102	0	171	0	132	0	125	0	157	0	187	0	63	0	115	0	72	0	57	0	51	0	0	0	31	0	47	0	31	0	86	0	0
		RnfC1	RnfC1 Ion-translocating oxidoreductase complex, subunit C	0	929	0	751	0	752	0	857	0	779	0	870	0	669	146	903	0	267	0	230	0	0	0	255	0	234	0	175	0	290	0	204	0	241	0	276	0	358
		RnfC2	RnfC2 Ion-translocating oxidoreductase complex, subunit D	448	1340	428	986	479	1062	440	1184	505	1150	494	1231	478	1204	530	1267	533	1344	467	974	183	605	344	751	561	713	383	934	355	1127	413	1151	391	1151	506	1104	419	1227
		RnfD2	RnfD2 Ion-translocating oxidoreductase complex, subunit G	0	174	0	116	0	100	0	142	0	153	0	144	0	148	0	143	0	294	0	321	0	323	0	326	0	297	0	273	0	341	0	298	0	289	0	260	0	309
		RnfG2	RnfG2 Ion-translocating oxidoreductase complex, subunit E	0	556	144	532	254	593	324	559	287	608	301	637	207	581	254	617	0	832	0	899	0	904	0	858	0	766	29	835	0	922	0	941	0	991	0	874	0	835
		RnfE2	RnfE2 Ion-translocating oxidoreductase complex, subunit A	0	310	0	293	0	249	0	305	0	281	0	284	0	303	0	264	0	226	0	165	0	306	0	284	0	291	0	208	0	264	0	268	0	208	0	310	0	222
		RnfA2	RnfA2 Ion-translocating oxidoreductase complex, subunit B	0	0	0	32	0	0	0	0	0	0	0	0	0	0	0	0	0	36	0	48	0	0	0	0	0	46	0	36	0	46	0	42	0	50	0	57	0	41
		RnfB2	RnfB2 Response regulator protein	0	1786	0	1303	175	1520	0	1877	134	1929	151	2145	270	2072	179	1716	114	2405	113	1872	0	1490	0	2087	0	1496	0	1497	0	2232	0	1836	0	1990	0	1746	0	2390
		Rrf	Rrf Predicted tmc redox complex, acidic cyctchrome c	188	45	153	0	120	69	280	84	407	47	235	92	265	107	45	42	0	0	0	0	31	0	35	0	0	0	49	0	0	0	0	0	47	0	0	0	0	0

TmcA	TmcA Predicted tmc redox complex, cytoplasmic iron-sulfur protein	71	0	0	0	48	0	49	0	79	0	0	0	38	0	0	0
TmcB	TmcB Predicted tmc redox complex, uncharacterized membrane protein	154	145	199	0	137	172	162	0	150	429	136	707	243	243	0	303
TmcC	TmcC Predicted tmc redox complex, uncharacterized protein	0	414	0	0	0	402	0	445	0	400	0	411	0	442	0	464
TmcD	TmcD	486	164	365	0	416	196	350	104	542	222	452	374	400	246	0	187

TmcA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TmcB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TmcC	0	0	0	0	0	115	0	85	0	0	0	0	0	0	0	0	0	0	0	0	0	27
TmcD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S4 Annotations underlying the lifestyle properties

Query used for annotation			*Dn. limicola*					*Dn. magnum*				
Gene name	**Predicted function**	**Length [aa]**	***Gene name***	**Length [aa]**	**Alignment lenght [aa]**	**Pos. [%]**	**e-value**	***Gene name***	**Length [aa]**	**Alignment lenght [aa]**	**Pos. [%]**	**e-value**
Cytoskeleton												
ftsZ[a]	Cell division protein	383	*ftsZ*	415	403	64	3e-94	*ftsZ*	398	386	65	2e-92
minE[a]	Cell division topological specificity factor	88	*minE*	91	78	57	3e-5	*minE*	97	80	52	2e-3
minD[a]	Septum site-determining protein	270	*minD*	267	266	67	7e-57	*minD*	267	246	68	6e-56
minC[a]	Septum site-determining protein	231	*minC*	235	92	51	1e-3	*minC*	231	66	56	9e-5
ftsA[a]	Cell division protein	420	*ftsA*	411	409	64	3e-92	*ftsA*	409	410	63	2e-90
bacA[b]	Bactofilin A	161	*dnl_28030*	129	118	50	1e-9	*dnm_078840*	185	113	50	6e-8
			dnl_08050	137	130	50	8e-9	*dnm_093090*	139	118	51	8e-8
Cell division												
mreB[a]	Cell shape-determining protein	347	*mreB1*	348	339	79	1e-114	*mreB3*	347	334	78	1e-113
			mreB2	490	336	75	1e-99	*mreB2*	473	340	75	1e-101
			mreB3	336	331	61	9e-70	*mreB1*	455	331	71	2e-92
			-					*dnm_087180*	336	331	61	1e-69
mreC[a]	Cell shape-determining protein	367	*mreC*	218	166	54	1e-17	*mreC*	292	224	44	6e-18
Twitching motility												
pilA[c]	Type IV major pilin protein	149	*dnl_15920*	142	141	47	5e-7	*dnm_080970*	125	114	51	3e-7
pilD[c]	Prepilin leader peptidase/N-methyltransferase	290	*pilD*	260	268	53	3e-41	*pilD*	258	272	55	4e-45
pilB[c]	Type IV pilus assembly ATPase	566	*gspE2*	512	493	65	1e-109	*gspE*	506	495	63	1e-108
			gspE1	573	468	65	3e-95	-				
pilT[c]	Type IV pilus retractation ATPase	344	*pilT1*	382	327	58	6e-60	*pilT2*	384	332	59	1e-61
			pilT2	361	332	73	1e-102	*pilT1*	358	327	74	1e-100
pilC[c]	Type IV pilus assembly protein	374	*pilC*	403	378	62	4e-75	*pilC*	406	377	64	5e-80
pilQ[c]	Fimbrial assembly protein	714	*pilQ1*	530	436	52	3e-63	*pilQ*	570	441	50	4e-53
			pilQ2	1092	440	53	1e-62	-				
Adventurous gliding **(M. xanthus)**												
mglA[d]	Mutual gliding-motility protein	195	*mglA1*	202	197	68	9e-50	*mglA1*	202	197	69	2e-51
			mglA2	203	198	67	3e-50	*mglA2*	203	198	69	1e-53
Exposure to molecular oxygen												
sodB[a]	Superoxide dismutase	193	*sodB*	231	199	69	1e-60	-				
			-					*dnl_39890*	249	189	50	3e-28
katA[e]	Vegetative catalase	483	*katA*	484	478	73	1e-161	*katA*	488	480	74	1e-161
dfx[f]	Desulfoferrodoxin	126	*dfx*	125	124	76	3e-44	*dfx*	125	124	78	1e-46
rbr[f]	Rubrerythrin	191	*rbr*	192	191	84	1e-76	*rbr1*	192	191	78	2e-72
			-					*rbr2*	192	188	82	2e-77
rub[f]	Rubredoxin	52	*rub1*	53	50	82	3e-21	*rub1*	53	49	77	2e-19
			rub2	58	50	74	8e-16	*rub2*	55	50	70	4e-15
tpx[a]	Thiol peroxidase	168	*tpx*	172	164	57	2e-29	*tpx*	172	166	57	4e-28
trxA[a]	Thioredoxin 1	109	*trxA1*	116	84	60	2e-14	*trxA2*	152	96	77	5e-27
			trxA2	115	105	68	2e-27	*trxA1*	109	105	68	1e-24
			trxA3	125	96	55	1e-114	-				
			trxA4	152	93	65	2e-21	-				
cydA[a]	Cytochrome bd-I ubiquinol oxidase, subunit 1	522	*cydA*	441	309	69	3e-84	*cydA*	439	309	66	3e-83
cydB[a]	Cytochrome bd-I ubiquinol oxidase, subunit 2	379	*cydB*	343	365	54	2e-63	*cydB*	343	368	54	2e-64
Hyperosmotic stress												
yehZ[a]	Glycine betaine-binding protein	305	*dnl_32390*	307	308	51	5e-44	*dnm_029760*	307	296	51	2e-36
yehW[a]	Glycine betaine uptake system, permease protein	243	*dnl_32400*	247	218	55	3e-33	*dnm_029780*	246	184	65	1e-36
yehX[a]	Glycine betaine uptake system, ATP-binding protein	308	*dnl_32410*	385	286	63	3e-66	*dnm_029850*	396	213	62	5e-43
proX[a]	Glycine betaine/proline betaine-binding, periplasmic protein	330	-					*dnm_019300*	337	265	37	2e-9

proW[a]	Glycine betaine/proline betaine transport system, permease protein	354	-					*dnm_019320*	287	266	67	2e-66
proV[a]	Glycine betaine/proline betaine transport system, ATP-binding protein	400	-					*dnm_019330*	429	383	65	9e-84
proX[a]	Glycine betaine/proline betaine-binding, periplasmic protein	330	-					*dnm_029830*	285	161	42	2e-5
proW[a]	Glycine betaine/proline betaine transport system, permease protein	354	-					*dnm_029840*	278	268	64	1e-59
betT[a]	High-affinity choline transport protein	677	*dnl_48560*	510	507	57	7e-98	-				
			dnl_57710	527	514	51	1e-65	-				
Hypoosmotic stress												
mscS[a]	Small-conductance mechanosensitive channel	286	*dnl_31470*	855	286	52	2e-32	*dnm_071850*	850	258	51	4e-29
Heat shock												
lon[a]	Lon protease	784	*lon1*	783	764	68	0	*lon2*	783	764	67	0
			lon2	811	763	71	0	*lon1*	792	766	71	0
			lon3	818	770	76	0	*lon3*	815	761	75	0
hslV[a]	ATP-dependent protease	176	*hslV*	178	171	75	3e-53	*hslV*	181	171	74	3e-50
hslU[a]	ATP-dependent protease, ATPase subunit	443	*hslU*	456	455	73	1e-134	*hslU*	459	458	72	1e-135
dnaJ[a]	Chaperone protein	376	*dnaJ1*	370	344	69	1e-108	*dnaJ1*	372	367	66	1e-108
			dnaJ2	303	348	49	2e-41	*dnaJ2*	306	294	43	4e-28
grpE[a]	Protein GrpE	197	*grpE*	224	191	58	5e-27	*grpE*	249	189	57	2e-27
dnaK[a]	Chaperone protein	638	*dnaK*	642	646	79	0	*dnaK*	631	627	79	0
clpB[a]	Chaperone protein	857	*clpB2*	862	861	74	0	*clpB*	861	859	75	0
			clpB1	892	855	70	0	-				
groS[a]	10 kDa chaperonin	97	*groS*	96	96	66	4e-19	*groS*	96	96	67	5e-19
groL[a]	60 kDa chaperonin	548	*groL*	550	549	79	0	*groL*	549	548	80	0
rpoH[a]	RNA polymerase sigma factor	284	*rpoH*	317	273	59	5e-43	*rpoH2*	300	280	58	4e-44
			-					*rpoH1*	302	277	57	4e-42
Cold shock												
clpA[a]	ATP-dependent Clp protease, ATP-binding subunit	758	*clpA*	752	759	71	0	*clpA*	750	752	72	0
clpS[a]	ATP-dependent Clp protease, adapter protein	106	*clpS1*	120	109	46	2e-63	*clpS*	118	88	72	2e-21
			clpS2	105	96	67	6e-24	-				
gyrA[a]	DNA gyrase subunit A	875	*gyrA*	840	876	71	0	*gyrA*	814	842	71	0
rbfA[a]	30S ribosome-binding factor	133	*rbfA*	128	114	61	2e-15	*rbfA*	116	114	57	2e-15
Extracytoplasmic stress response												
rpoD[a]	RNA polymerase sigma factor	613	*dnl_43490*	485	529	60	1e-113					
								rpoD	589	607	60	1e-130
degP[a]	Periplasmic serine endoprotease	474	*degP*	478	452	59	2e-72	*degP*	486	462	58	3e-74
rseC[a]	Protein RseC	159	*dnl_00880*	154	92	43	3e-3	*dnm_084870*	156	135	45	8e-5
rseP[a]	Regulator of sigma-E protease	450	*dnl_48590*	355	234	54	2e-33	*dnm_090890*	357	233	57	1e-32
			dnl_10550	354	190	58	5e-31	-				
clpX[a]	ATP-dependent Clp protease, ATP-binding subunit	424	*clpX2*	415	416	82	1e-154	*clpX2*	420	418	80	1e-148
			clpX1	579	363	59	1e-62	*clpX1*	583	360	56	4e-62
clpP[a]	ATP-dependent Clp protease, proteolytic subunit	207	*clpP*	206	192	86	7e-73	*clpP*	210	192	86	1e-70

Labelled queries referred to:

[a] *Escherichia coli* K12 (NC_000913)

[b] *Caulobacter vibrioides* (NC 011916)

[c] *Pseudomonas aeruginosa* (NC 002516)

[d] *Myxococcus xanthus* (NC_008095)

[e] *Bacillus subtilis* 168 (NC 000964)

[f] *Desulfovibrio vulgaris* (NC 017310)

Table S5 Differential proteomic data underlying the lifestyle properties

Protein in Dnl	Protein in Dnm	Predicted function	*Dn. limicola*																*Dn. magnum*																					
			H_2/CO_2		PropOH		Lac		But		Prop		FA-Mix		Suc		Fum		But		Prop		FA-Mix		Suc		Fum		Mal		Bz		Phea		3-Ppp		*p*-Cre		4-OHbenz	
			SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP
Cytoskeleton																																									
FtsZ	FtsZ	Cell division protein	138	0	0	199	0	194	212	208	219	269	160	216	190	340	0	172	0	0	0	0	0	0	0	0	0	0	0	0	75	0	0	0	0	0	0	0	0	25		
MinE	MinE	Cell division topological specificity factor	0	0	0	38	0	0	0	0	0	0	0	0	0	49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
MinD	MinD	Septum site-determining protein	0	89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
MinC	MinC	Septum site-determining protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
FtsA	FtsA	Cell division protein	0	0	0	0	0	0	0	50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Dnl_28030	Dnm_078840	Bactofilin domain-containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Dnl_08050	Dnm_093090	Putative polymer-forming cytoskeletal bactofilin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Cell division																																									
MreB1	MreB3	Cell shape-determining protein	0	186	0	249	0	212	0	155	0	210	0	145	0	0	0	91	0	35	0	285	0	74	0	52	68	81	48	0	0	49	0	118	0	27	0	159	0	88		
MreB2	MreB2	Cell shape-determining protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
MreB3	MreB1	Cell shape-determining protein	0	0	0	0	87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
	Dnm_087180	Cell shape-determining protein																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
MreC	MreC	Cell shape-determining protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Twitching motility																																									
Dnl_15920	Dnm_080970	Prepilin-type cleavage/methylation domain-containing protein	0	0	0	82	0	0	0	53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PilD	PilD	Type 4 prepilin-like proteins leader peptide-processing enzyme	0	0	0	0	0	0	0	36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
GspE2	GspE	General secretion pathway protein E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
GspE1		General secretion pathway protein E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																								
PilT1	PilT2	Twitching mobility protein	0	0	0	0	0	0	0	108	0	0	0	0	0	88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PilT2	PilT1	Twitching mobility protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PilC	PilC	Type 4 fimbrial assembly protein	0	0	0	69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	109	0	0	0	0	0	0	0	0	0	0	0	48	0	0	0	0		
PilQ1	PilQ	Type IV pilus biogenesis and competence protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PilQ2		Type IV pilus biogenesis and competence protein	0	0	0	0	0	0	0	0	0	0	132	0	0	96	0	0																								
Adventurous gliding (*M. xanthus*)																																								
MglA1	MglA1	Mutual gliding-motility protein	0	314	0	335	0	279	0	348	0	248	0	376	0	337	0	225	53	496	0	408	0	173	74	360	95	285	63	160	0	474	0	350	62	336	116	465	0	607		
MglA2	MglA2	Mutual gliding-motility protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	117	0	103	0	0	0	0	0	0	0	0	0	90	0	117	0	0	0	111	0	120		
Proteins of unkown function of COG category M																																								
Dnl_52570		Conserved uncharacterized protein	0	356	0	359	0	452	0	628	0	610	0	582	0	768	0	383																								
	Dnm_074620	Uncharacterized protein																	0	930	0	961	0	847	0	1065	148	935	0	813	0	846	0	854	0	765	0	799	0	957		
Dnl_50070		Conserved uncharacterized protein, immunoglobulin-like fold-containing	0	0	135	77	0	146	141	0	404	0	182	166	56	311	110	233																								
	Dnm_000300	Conserved uncharacterized protein, immunoglobulin-like fold-containing																	0	106	0	126	0	51	0	43	0	147	0	54	0	79	0	52	0	46	0	146	0	74		
Exposure to molecular oxygen																																								
SodB		Superoxide dismutase	0	475	0	408	0	489	0	404	0	405	0	448	0	462	0	439																								
	Dnm_072600	Superoxide dismutase																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52		
KatA	KatA	Catalase	235	0	213	0	248	0	244	72	320	0	235	83	232	0	317	0	1091	667	739	882	1255	1041	1077	784	288	363	759	485	762	1194	818	896	828	606	420	888	817	764		
Dfx	Dfx	Desulfoferrodoxin	619	102	519	149	554	189	444	110	664	109	625	136	509	138	545	96	479	0	320	0	544	57	491	0	217	0	380	0	460	29	496	0	396	0	324	0	421	0		
Rbr	Rbr1	Rubrerythrin	348	0	322	0	297	0	286	0	400	58	334	0	340	0	332	0	432	0	378	183	425	253	386	180	209	144	483	135	459	304	394	231	478	0	237	130	371	202		
	Rbr2	Rubrerythrin																	455	144	351	253	430	246	340	202	351	195	351	139	340	355	435	213	420	201	388	157	427	307		
Rub1	Rub1	Rubredoxin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Rub2	Rub2	Rubredoxin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
Tpx	Tpx	Thiol peroxidase	206	57	128	59	149	73	224	190	426	153	215	183	179	193	272	0	309	0	236	0	280	0	267	0	58	0	172	0	300	62	323	0	188	51	101	0	146	40		
TrxA1	TrxA2	Thioredoxin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55	0	0	0	0	0	29	0	0	0	0	0	0	0	0	0		
TrxA2	TrxA1	Thioredoxin	197	0	207	0	198	0	186	108	273	0	250	0	211	0	238	0	196	0	163	0	152	0	177	0	178	0	166	0	200	0	187	0	232	0	130	0	173	0		
TrxA3		Thioredoxin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																								
TrxA4		Thioredoxin	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																								

CydA	CydA	Cytochrome bd ubiquinol oxidase, subunitα	0	290	0	267	0	334	0	289	0	261	0	293	0	341	0	291	0	203	0	138	0	306	0	250	0	100	0	146	0	121	0	181	0	150	0	139	0	199
CydB	CydB	Cytochrome bd ubiquinol oxidase, subunitβ	0	0	0	0	0	46	0	0	0	0	0	46	0	33	0	0	0	0	0	0	0	63	0	0	0	0	0	38	0	29	0	0	0	38	0	28	0	0
Hyperosmotic stress																																								
Dnl_32390	Dnm_029760	Glycine betaine/proline betaine transport system, substrate-binding protein	122	0	0	117	0	377	0	561	0	67	117	207	0	143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_32400	Dnm_029780	Glycine betaine/proline betaine transport system, permease protein	0	0	0	0	0	94	0	0	0	0	0	0	0	0	0	37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_32410	Dnm_029850	Glycine betaine/proline betaine transport system, ATP-binding protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Dnm_019300	Glycine betaine/proline betaine transport system, substrate-binding protein																	194	128	91	168	87	116	224	116	51	104	125	61	79	122	0	146	117	56	77	160	116	177
	Dnm_019320	Glycine betaine/proline betaine transport system, permease protein																	0	0	0	29	0	77	0	73	0	59	0	0	0	0	0	0	0	0	0	0	0	0
	Dnm_019330	Glycine betaine/proline betaine transport system, ATP-binding protein																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Dnm_029830	Glycine betaine/proline betaine transport system, substrate-binding protein																	77	0	0	0	0	0	48	0	0	0	0	0	90	115	0	0	82	33	0	0	140	67
	Dnm_029840	Glycine betaine/proline betaine transport system, permease protein																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_48560		Transporter, BCCT family	0	0	0	0	0	0	0	57	0	0	0	172	0	116	0	99																						
Dnl_57710		Transporter, BCCT family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																						
Hypoosmotic stress																																								
Dnl_31470	Dnm_071850	Mechanosensitive ion channel	0	0	82	0	73	0	99	148	95	0	0	81	0	0	86	196	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Heat shock																																								
Lon1	Lon2	Lon protease	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95	114	115	307	72	105	0	186	0	0	103	0	0	124	0	113	170	266	279
Lon2	Lon1	Lon protease	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68	0	29	0	0	0	0	0	0	0	0	0	0	0
Lon3	Lon3	Lon protease	0	0	0	0	0	0	0	0	0	0	0	0	0	114	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75	0	0
HslV	HslV	ATP-dependent protease	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30	30	54	34	0	0	0	0	0	58	0	0	0	0	0	30	0	33
HslU	HslU	ATP-dependent hsl protease, ATP-binding subunit	0	0	0	0	0	0	0	0	0	114	0	0	0	35	75	0	46	0	0	0	92	0	218	0	269	0	0	0	0	0	0	0	0	0	0	0	0	0
DnaJ1	DnaJ1	Heat shock protein	0	116	0	86	0	0	0	57	0	0	0	0	0	0	0	137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DnaJ2	DnaJ2	Heat shock protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	29	0	0	0	0	0	0	0	0	0	82	0	0
GrpE	GrpE	HSP-70 cofactor	0	0	123	0	70	0	91	0	0	0	0	0	71	0	87	0	0	0	0	0	67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DnaK	DnaK	Chaperone Hsp70 family	814	507	965	568	1122	321	832	290	978	415	841	695	896	552	1025	456	989	332	940	224	691	123	1077	0	1354	202	1032	141	1142	186	909	114	1072	134	798	53	870	245
ClpB2	ClpB	Chaperone protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ClpB1		Chaperone protein	354	0	0	0	0	206	0	0	0	0	0	0	143	0	94	0																						
GroS	GroS	10 kDa chaperonin	280	0	399	0	422	0	294	0	325	0	300	0	283	0	396	75	318	0	286	0	345	32	325	31	342	0	298	34	333	50	291	0	292	33	265	30	298	28
GroL	GroL	60 kDa chaperonin	1886	2280	2148	2016	2323	1809	1980	2149	1879	2134	1830	2663	2046	2115	2258	2757	2100	801	1927	1027	1861	806	1919	569	2717	1579	1979	414	2061	789	2059	497	2066	547	2067	864	1937	384
RpoH	RpoH2	RNA polymerase sigma factor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	RpoH1	RNA polymerase sigma factor																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cold shock																																								
ClpA	ClpA	ATP-dependent Clp protease, ATP-binding subunit	0	0	0	0	0	0	0	0	70	0	0	0	0	0	0	0	0	0	0	33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54	0	0
ClpS1	ClpS	ATP-dependent Clp protease, adapter protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ClpS2		ATP-dependent Clp protease, adapter protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																						
GyrA	GyrA	DNA gyrase, subunit A	0	273	0	257	0	194	0	211	0	226	0	308	0	231	0	185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RbfA	RbfA	Ribosome-binding factor	0	0	0	0	0	0	0	0	0	0	0	0	0	30	0	28	0	97	0	0	0	0	0	0	0	32	0	0	0	27	0	30	0	0	0	53	0	27
Extracytoplasmic stress response																																								
Dnl_43490		RNA polymerase sigma factor protein, rpoD-like	0	0	0	0	0	0	0	0	0	0	0	0	0	128	0	0																						
	RpoD	RNA polymerase sigma factor																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DegP	DegP	Periplasmic serine endoprotease	170	0	217	0	407	0	165	0	0	0	109	0	192	0	284	295	0	32	0	0	0	0	117	26	187	91	209	26	0	0	0	0	49	0	263	46	0	0
Dnl_00880	Dnm_084870	Putative transcriptional regulator, ResC family	0	36	0	0	0	0	0	0	0	53	0	0	0	0	0	68	0	0	0	66	0	71	0	125	0	87	0	64	0	67	0	42	0	41	0	47	0	0
Dnl_48590	Dnm_090890	Zinc metallopeptidase, M50 family	0	0	0	63	0	80	0	0	0	32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_10550		Zinc metallopeptidase, M50 family	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																						
ClpX2	ClpX2	ATP-dependent Clp protease, ATP-binding subunit	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ClpX1	ClpX1	ATP-dependent Clp protease, ATP-binding subunit	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ClpP	ClpP	ATP-dependent Clp protease, proteolytic subunit	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	127	25	124	0	175	28	171	33	207	119	250	53	197	92	131	0	118	0	67	84	119	27

Table S6 Annotations underlying potential members of a σ^E-regulon (adapted from Rowley et al., 2006)

Query used for annotation			*Dn. limicola*					*Dn. magnum*				
Gene name[a]	**Predicted function**	**Length [aa]**	***Gene name***	**Length [aa]**	**Alignment lenght [aa]**	**Pos. [%]**	**e-value**	***Gene name***	**Length [aa]**	**Alignment lenght [aa]**	**Pos. [%]**	**e-value**
σ E / σ E regulation and other σ factors												
rpoE	ECF RNA polymerase sigma-E factor	191	*rpoE*	200	193	49	7E-16	*rpoE*	221	191	51	2E-17
rpoN	RNA polymerase sigma 54 factor	477	*rpoN*	483	482	60	8E-93	*rpoN*	481	477	59	3E-89
rseA	Anti-sigma-E factor	216	-					-				
rseB	Sigma-E factor regulatory protein	318	-					-				
			dnl_10550	354	190	58	5E-31	-				
degS	Serine endoprotease	355	-					-				
sspB	Stringent starvation protein	165	-					-				
Primary metabolism, sensory-regulatory functions												
cca	Multifunctional CCA protein	412	*dnl_63570*	481	356	43	4E-19	*dnm_079450*	475	342	45	5E-28
			dnl_47670	895	223	43	4E-11	*dnm_054190*	886	224	43	3E-11
cutC	Copper homeostasis protein	248	-					-				
dnaE	DNA polymerase III subunit α	1160	*dnaE*	1179	1169	61	0	*dnaE*	1135	1135	61	0
fusA	Elongation factor G	704	*fusA3*	678	690	67	0	*fusA3*	704	690	68	0
			fusA1	696	694	65	1E-174	*fusA1*	695	698	64	1E-172
			fusA2	693	699	61	1E-147	*fusA2*	691	693	62	1E-155
greA	Transcription elongation factor	158	*greA*	156	155	70	7E-36	*greA*	156	155	70	1E-36
lhr	Probable ATP-dependent helicase	1538	-					-				
malQ	4-alpha-glucanotransferase	694	-					-				
mdoG	Glucans biosynthesis protein	511	-					-				
mdoH	Glucans biosynthesis glucosyltransferase	847	-					-				
prfB	Peptide chain release factor 2	365	*prfB*	302	298	72	1E-91	*prfB*	312	305	70	2E-93
prfA	Peptide chain release factor 1	360	*prfA*	367	348	73	1E-102	*prfA*	359	348	73	1E-104
recJ	Single-stranded-DNA-specific exonuclease	577	*recJ*	575	538	56	4E-84	*recJ*	573	562	55	4E-89
rnhB	Ribonuclease HII	198	*rnhB*	202	181	62	2E-40	*rnhB*	209	181	63	9E-40
PPs — proteases/chaperones/folding enzymes												
asnB	Asparagine synthetase B	554	*asnB1*	617	400	48	2E-38	*asnB3*	623	415	49	2E-37
			asnB2	618	390	43	1E-30	*asnB4*	627	390	50	1E-36
			-					*asnB1*	539	521	56	8E-83
			-					*asnB2*	634	368	47	4E-38
dsbC	Thiol:disulfide interchange protein	236	-					-				
fkpA	FKBP-type peptidyl-prolyl cis-trans isomerase	270	-					-				
skp	Chaperone protein	161	-					-				
surA	Chaperone	428	*dnl_13370*	334	278	47	5E-17	*dnm_040070*	329	256	49	1E-22
Phospholipid and LPS biogenesis/modification												
ahpF	Alkyl hydroperoxide reductase, subunit F	521	-					-				
fadD	Long-chain-fatty-acid--CoA ligase	561	-					*fadD2*	566	560	60	1E-106
			-					*fadD1*	501	527	53	3E-81
lpxA	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	262	*lpxA*	257	255	65	6E-69	*lpxA*	257	255	67	2E-71
lpxD	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	341	*lpxD*	343	337	55	2E-53	*dpxD*	341	336	56	5E-59
lpxP	Lipid A biosynthesis palmitoleoyltransferase	306	*dnl_24830*	310	270	44	2E-20	*dnm_003470*	296	252	46	8E-20
lpxB	Lipid-A-disaccharide synthase	382	*lpxB*	382	381	52	9E-52	*lpxB*	396	344	54	3E-52
plsB	Glycerol-3-phosphate acyltransferase	807	*plsB*	879	729	46	7E-63	*dnm_067700*	878	727	47	7E-67
psd	Phosphatidylserine decarboxylase proenzyme	322	*dnl_45450*	210	123	39	0.023	-				
rfaD	ADP-L-glycero-D-manno-heptose-6-epimerase	310	-					-				

IMPs — transport, unknown function												
uppP	ADP-L-glycero-D-manno-heptose-6-epimerase	273	*uppP*	274	267	55	1E-29	*uppP*	273	274	54	6E-32
ptsN	Nitrogen regulatory protein	163	-					-				
sbmA	Peptide antibiotic transporter	406	-					-				

[a] Labelled query referred to *Escherichia coli* K12 (NC_000913)

Table S7 Differential proteomic data underlying potential members of a σ^{E}-regulon

Protein in Dnl	Protein in Dnm	Predicted function	*Dn. limicola*																*Dn. magnum*																					
			H_2/CO_2		PropOH		Lac		But		Prop		FA-Mix		Suc		Fum		But		Prop		FA-Mix		Suc		Fum		Mal		Bz		Phea		3-Ppp		*p*-Cre		4-OHbenz	
			SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP	SG	MP
σ E / σ E regulation and other σ factors																																								
RpoE	RpoE	RNA polymerase sigma-E factor (sigma24)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RpoN	RpoN	RNA polymerase sigma 54 factor	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Primary metabolism, sensory-regulatory functions																																								
Dnl_63570	Dnm_079450	Poly A polymerase head and HD domains-containing	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_47670	Dnm_054190	Poly A polymerase head domain-containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DnaE	DnaE	DNA polymerase III, subunit α	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FusA3	FusA3	Elongation factor G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FusA1	FusA1	Elongation factor G	0	0	0	0	115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FusA2	FusA2	Elongation factor G	324	298	354	413	744	405	279	401	200	561	221	522	311	621	608	309	706	127	624	118	143	121	360	141	788	364	366	82	614	150	321	116	393	100	218	112	746	224
GreA	GreA	Transcription elongation factor	0	0	0	0	160	0	0	0	141	0	132	0	125	0	127	0	89	0	0	0	0	0	56	0	0	0	0	0	0	0	81	0	0	0	0	0	0	0
PrfB	PrfB	Peptide chain release factor 2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PrfA	PrfA	Peptide chain release factor 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	31	0	0	0	0
RecJ	RecJ	Single-stranded-DNA-specific exonuclease	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RnhB	RnhB	Ribonuclease HII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PPs — proteases/chaperones/folding enzymes																																								
AsnB1	AsnB3	Asparagine synthetase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32	0	0	0	0	0	0	0
AsnB2	AsnB4	Asparagine synthetase	0	0	0	89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	AsnB1	Asparagine synthetase																	0	0	106	0	0	0	0	0	0	0	0	0	192	0	0	0	0	0	0	0	89	0
	AsnB2	Asparagine synthetase																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_13370	Dnm_040070	Chaperone SurA N-terminal domain-containing protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phospholipid and LPS biogenesis/modification																																								
	FadD2	Long-chain-fatty-acid--CoA ligase																	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	FadD1	Long-chain-fatty-acid--CoA ligase																	0	0	0	32	0	0	0	0	0	0	0	0	0	0	0	730	547	0	0	0	0	0
LpxA	LpxA	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85	0	83	
LpxD	LpxD	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_24830	Dnm_003470	Lipid A biosynthesis acyltransferase family protein	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LpxB	LpxB	Lipid-A-disaccharide synthase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PlsB	Dnm_067700	Glycerol-3-phosphate acyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dnl_45450		Phosphatidylserine decarboxylase proenzyme	0	327	0	273	0	214	0	252	0	238	0	265	0	203	0	225																						
UppP	UppP	Undecaprenyl-diphosphatase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0