Supplementary Table S2. List of manually annotated genes used to deduce distinct phenotypic or molecular traits of *K. glycovorans* L21-Fru-AB^T. Genes arranged in tentative operons are shaded in the same colour.

Locus tag	***Gene***	***Predicted product***	***Reference used for annotation***			
			Protein ID	***Organism***	***Identity***	***E-value***
Genome integrity						
L21SP4_00661	*hsdM*	Type I restriction enzyme M protein	WP_035413363	*Chromohalobacter israelensis*	88%	0.0
L21SP4_00662	*hsdS*	Type I restriction enzyme S protein	B2IJC7	*Beijerinckia indica* subsp. *indica*	49%	9e-116
L21SP4_00664	*hsdR_1*	Type I restriction enzyme R protein	WP_024329383	*Thioalkalivibrio* sp. ALR17-21	89%	0.0
L21SP4_01534	*hsdR_2*	Type I restriction enzyme R protein	ESR26267	*Lutibaculum baratangense*	74%	0.0
L21SP4_01535	*hsdM/S*	Type I restriction enzyme M protein	WP_008869845	*Desulfonatronospira thiodismutans*	86%	0.0
		Type I restriction enzyme S protein	GAO31177	*Geofilum rubicundum*	52%	1e-47
L21SP4_00684	*res*	Type III restriction enzyme res subunit	WP_009340046	*Afipia* sp. 1NLS2	80%	0.0
L21SP4_00685	*mod*	Type III restriction enzyme mod subunit	K9YUM0	*Dactylococcopsis salina*	67%	0.0
L21SP4_00679	*mcrC*	5-methylcytosine-specific restriction enzyme subunit C	KJF16159	*Acidithrix ferrooxidans*	71%	0.0
L21SP4_00680	*mcrB*	5-methylcytosine-specific restriction enzyme subunit B	EXI82560	“*Candidatus* Accumulibacter sp. BA-92”	62%	0.0
L21SP4_02005	*cas1_1*	subtype II CRISPR-associated endonuclease Cas1	WP_035473641	*Alistipes* sp. 627	47%	3e-81
L21SP4_02074	*cas1_2*	subtype I-E CRISPR-associated endonuclease Cas1	WP_004074392	*Desulfobacter postgatei*	65%	1e-137

Cell biology

L21SP4_02172	*lpxB*	Lipid-A-disaccharide synthase	A0A0D6QG30	*Anaeromyxobacter* sp. PSR-1	41%	3.2e-82
L21SP4_01206	*rfaF*	Lipopolysaccharide heptosyltransferase	W6EGC3	*Sulfurospirillum multivorans*	46%	2.7e-84
L21SP4_01194	*lpxL*	Lipid A biosynthesis lauroyl acyltransferase	W6EGB8	*Sulfurospirillum multivorans*	36%	4.4e-45
L21SP4_00626	*wza*	Lipopolysaccharide export protein	B4SFP0	*Pelodictyon phaeoclathratiforme*	34%	9.8e-55
L21SP4_00627	*wzz/wzc*	Polysaccharide chain length determinant protein and protein tyrosine kinase	WP_028103229	*Pseudoduganella violaceinigra*	25%	4e-35
L21SP4_00629	*wcy*	O-glycosylation polymerase	EFU70009	*Arcobacter butzleri*	27%	0.033
L21SP4_00630	*wbbJ_1*	O-acetyltransferase	D6TLV5	*Ktedonobacter racemifer*	45%	2e-45
L21SP4_00631	*rfaB_1*	Glycosyl transferase family 1	WP_014067214	*Rhodothermus marinus*	34%	4e-32
L21SP4_00632	*rfaB_2*	Glycosyl transferase family 1	WP_008478365	*Nitrolancea hollandica*	41%	7e-86
L21SP4_00633	*wbbJ_2*	O-acetyltransferase	KEQ23991	*Paenibacillus* sp. MSt1	35%	2e-15
L21SP4_00634	*wbbJ_3*	O-acetyltransferase	WP_052036564	*Tumebacillus flagellatus*	37%	9e-21
L21SP4_00635	*rfaB_3*	Glycosyl transferase family 1	WP_012037009	*Methanocella arvoryzae*	39%	4e-83
L21SP4_00636	*eps?*	Glycosyl transferase	WP_031458085	*Chloroflexus* sp. MS-G	38%	2e-59
L21SP4_00637	*wbbJ_4*	O-acetyltransferase	AKU98109	*Labilithrix luteola*	46%	2e-34
L21SP4_00638	*eps?*	Glycosyl transferase family 2	WP_014400810	*Corallococcus coralloides*	45%	8e-73
L21SP4_00463	*ddl*	D-alanine--D-alanine ligase	A0A0C2HLI0	*Geoalkalibacter ferrihydriticus*	46%	8.9e-73
L21SP4_01761	*murF*	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	B4UER7	*Anaeromyxobacter* sp. (strain K)	38%	2.2e-80
L21SP4_01757	*ftsW*	Peptidoglycan lipid II flippase	B3E3Y3	*Geobacter lovleyi*	41%	7.9e-83
L21SP4_00466	*ftsZ*	Cell division protein FtsZ	B9XIG1	*Pedosphaera parvula*	29%	410E-51
L21SP4_00999	*mreB*	Cell shape determining protein	B9XG13	*Pedosphaera parvula*	74%	2.6E-177
L21SP4_01870	*tolB*	Translocation protein TolB	WP_013249867	*Nitrospira defluvii*	38%	3e-57

L21SP4_01871	*pal*	Peptidoglycan-associated lipoprotein	C7LX40	*Desulfomicrobium baculatum*	42%	1e-32
L21SP4_01813	*ppk*	Polyphosphate kinase	WP_012912472	*Pirellula staleyi*	54%	0.0
L21SP4_01814	*ppx*	Exopolyphosphatase	WP_012912473	*Pirellula staleyi*	50%	6e-162
L21SP4_01507	*glgC*	Glucose-1-phosphate adenylyltransferase	A0A0F2NDJ6	*Desulfobulbaceae* bacterium BRH_c16a	61%	2.6e-168
L21SP4_00491	*glgX*	Glycogen-debranching enzyme	WP_011418612	*Syntrophus aciditrophicus*	49%	0.0
L21SP4_00492	*glgP_1*	Glucan phosphorylase	WP_021760846	*Desulfovibrio gigas*	48%	0.0
L21SP4_00493	*glgA_1*	Glycogen/starch synthase	S0G459	*Desulfotignum phosphitoxidans*	58%	0.0
L21SP4_00494	*glgB*	1,4-alpha-glucan branching enzyme	WP_025324074	*Deferrisoma camini*	62	0.0
L21SP4_01037	*glgA_2*	Glycogen synthase	I4C115	*Desulfomonile tiedjei*	42%	3.6e-117
L21SP4_01270	*glgP_2*	Glycogen phosphorylase	WP_013293291	*Gallionella capsiferriformans*	52%	0.0

Nutrient uptake

L21SP4_01391	*amt_1*	Ammonium transporter	H1XV27	*Caldithrix abyssi*	69%	0.0
L21SP4_01503	*amt_2*	Ammonium transporter	S0G181	*Desulfotignum phosphitoxidans*	63%	0.0
L21SP4_00568	*gdh*	Glutamate dehydrogenase	WP_028894236	*Syntrophorhabdus aromaticivorans*	72%	0.0
L21SP4_01522	*gln*	Glutamine synthetase	D8EZN8	Deltaproteobacterium NaphS2	80%	0.0
L21SP4_02316	*cysN/cysC*	Bifunctional sulfate adenylyltransferase/ adenylylsulfate kinase	R4V6K8	*Spiribacter salinus*	66%	0.0
L21SP4_02317	*sulP*	Sulfate permease	W9V4Z0	*Thiorhodococcus* sp. AK35	58%	0.0
L21SP4_00290	*pstS*	Phosphate transporter, binding protein	CDE84321	*Coraliomargarita* sp. CAG:312	52%	7e-101
L21SP4_00291	*pstC*	Phosphate transporter, inner membrane subunit C	WP_012508404	*Pelodictyon phaeoclathratiforme*	58%	4e-150
L21SP4_00292	*pstA*	Phosphate transporter, inner membrane subunit A	WP_012502165	*Chlorobaculum parvum*	57%	3e-179

L21SP4_00293	*pstB*	Phosphate transporter, ATP-binding protein	WP_011890232	*Chlorobium phaeovibrioides*	66%	5e-132
L21SP4_01162	*nptA*	Na^{+}/phosphate symporter	WP_020614062	*Spirochaeta bajacaliforniensis*	44%	2e-165
L21SP4_01108	*fepA_1*	TonB dependent receptor plug	A0A084D6N7	*Burkholderia* sp. MSh2	38%	6.2e-7
L21SP4_01109	*fepA_2*	TonB dependent siderophore receptor	ABC76107	*Syntrophus aciditrophicus SB*	33%	6e-92
L21SP4_01110	*exbB*	Biopolymer transporter, subunit B	KHE91107	"*Ca.* Scalindua brodae"	49%	9e-64
L21SP4_01111	*exbD*	Biopolymer transporter, subunit D	KHE91106	"*Ca.* Scalindua brodae"	46%	1e-28
L21SP4_01112	*tonB*	TonB energy transducer protein	WP_045758093	*Xanthomonas albilineans*	39%	1e-16
L21SP4_01113	*fepB*	Fe^{3+}-siderophore transporter, binding protein	K6QFK1	*Thermaerobacter subterraneus*	34%	6.1e-38
L21SP4_01114	*fepC*	Fe^{3+}-siderophore transporter, ATP-binding protein	K0JZB7	*Saccharothrix espanaensis*	45%	2.6e-57
L21SP4_01115	*fepD*	Fe^{3+}-siderophore transporter, permease	I1XI55	*Methylophaga nitratireducenticrescens*	53%	2.5e-108
L21SP4_01608	*feoB*	Fe^{2+}-transporter, subunit B	KJS31893	*Desulfatitalea* sp. BRH_c12	58%	0.0
L21SP4_01609	*feoA_1*	Fe^{2+}-transporter, subunit A	WP_044249593	*Rhodobacter sphaeroides*	53%	2e-19
L21SP4_01610	*feoA_2*	Fe^{2+}-transporter, subunit A	WP_046859083	*Sedimenticola* sp. SIP-G1	40%	1e-11
L21SP4_00297	*znuB*	Zn^{2+}-transporter, permease	WP_015404094	*Desulfocapsa sulfexigens*	53%	6e-80
L21SP4_00298	*znuC*	Zn^{2+}-transporter, ATP-binding protein	WP_013257430	*Desulfarculus baarsii*	55%	1e-83
L21SP4_00299	*znuA*	Zn^{2+}-transporter, binding protein	G2FI49	Endosymbiont of *Tevnia jerichonana*	41%	5.7e-58
L21SP4_01892	*cbiM*	Cobalt transporter, permease	WP_014553677	*Halanaerobium praevalens*	47%	1e-57
L21SP4_01897	*cbiQ*	Cobalt transporter, permease	F9UFE0	*Thiocapsa marina*	40%	1.7e-39
L21SP4_01898	*cbiO*	Cobalt transporter, ATP-binding protein	KJU86287	"*Ca.* Magnetobacterium bavaricum"	50%	1e-60
L21SP4_00567	*copA*	Copper-translocating P-type ATPase	B9XQN6	*Pedosphaera parvula*	60%	0.0

L21SP4_00133	*xylE*	MFS sugar transporter	C6Y1K3	*Pedobacter heparinus*	54%	4.9e-165
L21SP4_00407	*melB*	Na^+/melibiose symporter	WP_052361845	*Diplosphaera colitermitum*	41%	5e-120
L21SP4_00607	*fucP*	Fucose permease	GAP69702	*Bacteroidales* bacterium 6E	30%	2e-17
L21SP4_00931	*rhaT*	L-rhamnose-proton symporter	I0KBJ9	*Fibrella aestuarina*	52%	2.6e-125
L21SP4_00327	*ugpBA*	Sugar transporter, binding protein and permease	CCW34240	*Chthonomonas calidirosea*	42%	0.0
L21SP4_00328	*ugpE*	Sugar transporter, permease	F4A328	*Mahella australiensis*	31%	1.9e-66
L21SP4_01748	*ugpC*	Sugar transporter, ATP-binding protein	WP_006930568	*Caldithrix abyssi*	62%	5e-159
L21SP4_00561	*dppA*	Oligopeptide transporter, binding protein	S0EYF5	*Chthonomonas calidirosea*	37%	6.4e-117
L21SP4_00562	*dppB*	Oligopeptide transporter, permease	B0BYS9	*Acaryochloris marina*	45%	2.4e-72
L21SP4_00563	*dppC*	Oligopeptide transporter, permease	WP_012472414	*“Ca.* Amoebophilus asiaticus”	47%	4e-95
L21SP4_02164	*dppF_1*	Oligopeptide transporter, ATP-binding protein	WP_009959466	*Verrucomicrobium spinosum*	53%	1e-86
L21SP4_02165	*dppF_2*	Oligopeptide transporter, ATP-binding protein	WP_024722335	*Clostridiales* bacterium VE202-01	55%	6e-92
L21SP4_00756	*potE*	Amino acid permease	WP_012571743	*Thermococcus onnurineus*	43%	0.0
L21SP4_01661	*potE/ptsN*	Amino acid permease/PTS IIA domain	WP_022947290	*Methylohalobius crimeensis*	55%	0.0
L21SP4_02424	*dctP*	TRAP C4-dicarboxylate transporter, binding protein	WP_008673150	*Rhodopirellula sallentina*	67%	2e-166
L21SP4_02425	*dctQ*	TRAP C4-dicarboxylate transporter, small permease protein	EMI43071	*Rhodopirellula* sp. SWK7	59%	1e-58
L21SP4_02426	*dctM*	TRAP C4-dicarboxylate transporter, large permease protein	WP_009100429	*Rhodopirellula* sp. SWK7	73%	0.0

Secretion and resistance

L21SP4_00102	*ffh*	Signal recognition particle protein	WP_013043353	*Coraliomargarita akajimensis*	50%	2e-150
L21SP4_01780	*ftsY*	Signal recognition particle receptor	WP_028388901	*Legionella fairfieldensis*	45%	4e-81
L21SP4_00353	*secA*	Preprotein translocase, subunit A	WP_006981786	*Chthoniobacter flavus*	53%	0.0
L21SP4_00551	*yidC*	Membrane protein insertase	WP_013044213	*Coraliomargarita akajimensis*	36%	9e-90
L21SP4_00560	*secG*	Preprotein translocase, subunit G	WP_032125434	*Chlamydia* sp. 'Diamant'	44%	1e-12
L21SP4_00799	*yajC*	Preprotein translocase, YajC subunit	CDE83420	*Coraliomargarita* sp. CAG:312	42%	1e-21
L21SP4_00800	*secDF*	Bifunctional preprotein translocase, subunit D and F	KJJ83209	*“Ca.* Omnitrophus sp. SKK-01”	44%	0.0
L21SP4_01696	*secY*	Preprotein translocase, subunit Y	WP_006977832	*Chthoniobacter flavus*	55%	1e-167
L21SP4_01727	*secE*	Preprotein translocase, subunit E	WP_002848632	*Ruminococcus albus*	46%	4e-09
L21SP4_01749	*tatB*	Twin-arginine translocation, subunit B	B6ISL9	*Rhodospirillum centenum*	27%	1.2e-5
L21SP4_01750	*tatC*	Twin-arginine translocation, subunit C	WP_015851434	*Desulfovibrio salexigens*	36%	8e-47
L21SP4_01751	*tatA*	Twin-arginine translocation, subunit A	Q18HC5	*Haloquadratum walsbyi*	47%	2.8e-20
L21SP4_00726	*gpsF*	General secretion pathway protein F	WP_007418780	*Pedosphaera parvula*	38%	1e-84
L21SP4_00727	*gpsG*	General secretion pathway protein G	WP_036291839	*Methylosinus* sp. PW1	48%	7e-35
L21SP4_00728	*gpsH*	General secretion pathway protein H	WP_041248570	*Geobacter* sp. M18	29%	1e-07
L21SP4_00729	*gpsI*	General secretion pathway protein I	D5MJH3	“*Ca.* Methylomirabilis oxyfera”	32%	2.3e-6
L21SP4_00730	*gpsJ*	General secretion pathway protein J	WP_017357532	*Stenotrophomonas maltophilia*	28%	2e-04
L21SP4_00731	*gpsK*	General secretion pathway protein K	KJU83711	“*Ca.* Magnetobacterium bavaricum”	32%	4e-21
L21SP4_00732	*gpsL*	General secretion pathway protein L	A0A0F6YFR7	*Sandaracinus amylolyticus*	23%	9.7e-7
L21SP4_00733	*gpsM*	General secretion pathway protein M	G2E1M1	*Thiorhodococcus drewsii*	24%	1e0
L21SP4_00734	*gpsD*	General secretion pathway protein D	A3YCA1	*Marinomonas* sp. MED121	28%	1.4e-67
L21SP4_01644	*gpsE*	General secretion pathway protein E	WP_007416861	*Pedosphaera parvula*	57%	0.0
L21SP4_01180	*bamA*	Outer membrane protein assembly	A0A0C2DQQ0	*Geoalkalibacter ferrihydriticus*	31%	2.2e-111

		complex, protein A				
L21SP4_00777	*bamD*	Outer membrane protein assembly complex, protein D	Q3JD66	*Nitrosococcus oceani*	29%	1.7e-6
L21SP4_02279	*wcaJ*	UDP-glucose:undecaprenyl-phosphate glucose-1-phosphate transferase	WP_012498919	*Chloroherpeton thalassium*	31%	8e-65
L21SP4_00190	*eps?*	Glycosyl transferase family 2	KKR11054	*Microgenomates* bacterium GW2011_GWA2_39_19	30%	7e-20
L21SP4_00191	*fkbM*	Methyltransferase	WP_003436505	*Psychroflexus gondwanensis*	41%	1e-77
L21SP4_00192	*wzx*	Polysaccharide export protein	WP_013258499	*Desulfarculus baarsii*	32%	2e-37
L21SP4_00193	*eps?*	Glycosyl transferase family 2	Q116W2	*Trichodesmium erythraeum*	33%	1.3e-32
L21SP4_00194	*rfaB_4*	Glycosyl transferase family 1	WP_012870732	*Sphaerobacter thermophilus*	35%	1e-34
L21SP4_00195	*eps?*	Glycosyl transferase family 2	WP_026798035	*Planktothrix prolifica*	34%	9e-28
L21SP4_00196	*rfaB_5*	Glycosyl transferase family 1	WP_051976056	*Methylobacterium* sp. UNCCL110	39%	4e-39
L21SP4_00197	*eps?*	Glycosyl transferase	E6U648	*Ethanoligenens harbinense*	27%	3e-4
L21SP4_00198	*wcaA*	Dolichol-P-glucose synthetase	WP_012170747	*Azorhizobium caulinodans*	55%	9e-136
L21SP4_00199	*rfaB_6*	Glycosyl transferase family 1	WP_006078315	*Halococcus saccharolyticus*	35%	5e-60
L21SP4_00200	*wcy*	O-glycosylation polymerase	A0A0B0ELS5	“*Ca.* Scalindua brodae”	36%	7.5e-81
L21SP4_00201	*wzz/wzc*	Polysaccharide chain length determinant protein and protein tyrosine kinase	Q3A4J7	*Pelobacter carbinolicus*	26%	1.2e-57
L21SP4_00202	*wza*	Polysaccharide export protein	KHE92940	“*Ca.* Scalindua brodae”	29%	1e-26
L21SP4_00769	*acrB*	Multidrug efflux pump, subunit B	WP_022851495	*Geovibrio* sp. L21-Ace-BES	46%	0.0
L21SP4_00770	*acrA*	Multidrug efflux pump, subunit A	WP_026903293	*Pedobacter glucosidilyticus*	30%	1e-38
L21SP4_00771	*tolC*	Outer membrane efflux protein	WP_013041911	*Coraliomargarita akajimensis*	30%	2e-40
L21SP4_00553	*bla*	Beta-lactamase	KHD08940	“*Ca.* Thiomargarita nelsonii”	43%	7e-67
L21SP4_00571	*ars?*	Arsenical-resistance protein (fragment)	K0NHN6	*Desulfobacula toluolica*	90%	3.2e-21

L21SP4_00572	*arsC*	Arsenate reductase	WP_011341509	*Pelobacter carbinolicus*	74%	3e-72
L21SP4_00573	*arsB*	Permease	WP_015774086	*Desulfomicrobium baculatum*	69%	0.0
L21SP4_00574	*arsR*	Arsenical resistance operon repressor	WP_029458583	*Desulfovibrio alcoholivorans*	63%	2e-33

Response to environmental stress

L21SP4_00578	*nqrF*	Na^+-translocating NADH-quinone reductase, subunit F	WP_010526036	*Thermophagus xiamenensis*	58%	0.0
L21SP4_00579	*nqrE*	Na^+-translocating NADH-quinone reductase, subunit E	WP_012175956	*Desulfococcus oleovorans*	69%	3e-93
L21SP4_00580	*nqrD*	Na^+-translocating NADH-quinone reductase, subunit D	WP_012475742	*Chlorobium phaeobacteroides*	63%	1e-78
L21SP4_00581	*nqrC*	Na^+-translocating NADH-quinone reductase, subunit C	WP_012175954	*Desulfococcus oleovorans*	41%	6e-40
L21SP4_00582	*nqrB*	Na^+-translocating NADH-quinone reductase, subunit B	WP_011112869	*Nitrosomonas europaea*	52%	2e-135
L21SP4_00583	*nqrA*	Na^+-translocating NADH-quinone reductase, subunit A	WP_012475745	*Chlorobium phaeobacteroides*	39%	5e-96
L21SP4_02072	*sod*	Superoxide dismutase	A0A0F2NB26	*Desulfobulbaceae* bacterium BRH_c16a	66%	1.7e-94
L21SP4_00226	*rub*	Rubredoxin	WP_041284942	*Desulfotomaculum gibsoniae*	60%	2e-15
L21SP4_00882	*rbr*	Rubrerythrin	WP_012475810	*Chlorobium phaeobacteroides*	70%	7e-81
L21SP4_01429	*ahpC*	Alkyl hydroperoxide reductase	WP_012842556	*Rhodothermus marinus*	47%	2e-55
L21SP4_00052	*cdr_1*	Coenzyme A-disulfide reductase	G2E3F0	*Thiorhodococcus drewsii*	65%	0.0
L21SP4_02384	*cdr_2*	Coenzyme A-disulfide reductase	G2E3F0	*Thiorhodococcus drewsii*	66%	0.0
L21SP4_01626	*prx*	Peroxiredoxin	WP_012280978	*Francisella philomiragia*	65%	4e-108

L21SP4_00050	*ahpD*	Alkylhydroperoxidase	WP_011375458	*Lactobacillus sakei*	54%	1e-25
L21SP4_01628	*msrA*	Peptide methionine sulfoxide reductase A	WP_048114621	*Methanoculleus* sp. MH98A	68%	2e-63
L21SP4_02069	*gsmt*	Glycine/sarcosine N-methyltransferase	A1WXN0	*Halorhodospira halophila*	70%	1.7e-138
L21SP4_02070	*sdmt*	Sarcosine/dimethylglycine N-methyltransferase	D5EA51	*Methanohalophilus mahii*	64%	1.7e-127
L21SP4_00520	*betT*	Choline/glycine betaine transporter	WP_053186822	*Sunxiuqinia dokdonensis*	62%	0.0
L21SP4_02155	*opuAC*	Glycine betaine transporter, binding protein	WP_006309190	*Caldisalinibacter kiritimatiensis*	56%	6e-102
L21SP4_02156	*opuAB*	Glycine betaine transporter, permease	WP_011100478	*Clostridium tetani*	62%	5e-118
L21SP4_02157	*opuCA*	Glycine betaine transporter, ATP-binding protein	WP_006309192	*Caldisalinibacter kiritimatiensis*	59%	9e-165
L21SP4_00973	*spp*	Sucrose-6F-phosphate phosphohydrolase	G4T022	*Methylomicrobium alcaliphilum*	36%	1.2e-42
L21SP4_02012	*sus*	Sucrose synthase	WP_008869127	*Desulfonatronospira thiodismutans*	57%	0.0
L21SP4_02013	*sps*	Sucrose-phosphate synthase	WP_008660974	*Rhodopirellula europaea*	57%	0.0
L21SP4_02014	*pfkB*	PfkB family carbohydrate kinase	WP_013034801	*Nitrosococcus halophilus*	47%	1e-84
L21SP4_02131	*sucP*	Sucrose phosphorylase	U2ER30	*Salinisphaera shabanensis*	51%	0.0
L21SP4_00167	*nhx_1*	Na^+/H^+ exchanger	WP_045088202	*Defluviitoga tunisiensis*	37%	2e-68
L21SP4_00232	*nhx_2*	Na^+/H^+ exchanger	F2JJN3	*Cellulosilyticum lentocellum*	36%	1.5e-78
L21SP4_00348	*nhx_3*	Na^+/H^+ exchanger	WP_020611771	*Spirochaeta bajacaliforniensis*	52%	7e-171
L21SP4_02045	*nhx_4*	Na^+/H^+ exchanger	WP_040847527	*Treponema lecithinolyticum*	36%	8e-99

Central metabolic pathways and regulation

L21SP4_02170	*rhaM*	L-rhamnose mutarotase	A0A081C0V9	Bacterium UASB270	70%	87e-48
L21SP4_00462	*rhaA*	L-rhamnose isomerase	B1ZR99	*Opitutus terrae*	59%	0.0
L21SP4_01498	*rhaB*	Rhamnulokinase	I0I7M4	*Caldilinea aerophila*	49%	2.7e-162
L21SP4_01948	*rhaD*	Rhamnose utilisation protein	F5Y7S7	*Treponema azotonutricium*	37%	8.6e-66

L21SP4_02182	*glk*	ROK family Glucokinase	B8CYI5	*Halothermothrix orenii*	36%	1.1e-59
L21SP4_00854	*pgi*	Glucose-6-phosphate isomerase	WP_014435059	*Caldilinea aerophila*	62%	0.0
L21SP4_01271	*pfkA*	6-Phosphofructokinase	WP_041068814	*Thiolapillus brandeum*	67%	4e-172
L21SP4_01747	*pfp*	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase	B8GUU2	*Thioalkalivibrio sulfidiphilus*	62%	5.4e-165
L21SP4_00013	*fba*	Fructose-bisphosphate aldolase	WP_043582427	*Diplosphaera colitermitum*	71%	1e-165
L21SP4_00391	*tpi*	Triosephosphate isomerase	CDE04447	*Anaerotruncus* sp. CAG:390	69%	1e-111
L21SP4_00485	*gap*	Glyceraldehyde-3-phosphate dehydrogenase	WP_006930994	*Caldithrix abyssi*	61%	2e-149
L21SP4_00558	*pgk*	Phosphoglycerate kinase	WP_014560136	*Ignavibacterium album*	59%	1e-166
L21SP4_01985	*gpmA*	2,3-Bisphosphoglycerate-dependent phosphoglycerate mutase	WP_012500693	*Chloroherpeton thalassium*	73%	1e-128
L21SP4_02068	*eno*	Enolase	WP_016779037	*Anaerophaga thermohalophila*	77%	0.0
L21SP4_01945	*ppdK*	Pyruvate phosphate dikinase	WP_006929451	*Caldithrix abyssi*	73%	0.0
L21SP4_01695	*adk*	Adenylate kinase	A8UWY7	*Hydrogenivirga* sp. 128-5-R1-1	52%	2.7e-72
L21SP4_01431	*phdE*	Pyruvate dehydrogenase complex, E1 component	B5YC76	*Dictyoglomus thermophilum*	48%	0.0
L21SP4_01432	*phdC_1*	Pyruvate dehydrogenase complex, E2 component (N-terminal subunit)	U3A8N8	*Novosphingobium tardaugens*	49%	3.6e-26
L21SP4_01433	*phdC_2*	Pyruvate dehydrogenase complex, E2 component (C-terminal subunit)	A0A023X0M2	*Rubrobacter radiotolerans*	47%	1.1e-54
L21SP4_01434	*phdD*	Pyruvate dehydrogenase complex, E3 component	WP_049954889	*Halostagnicola larsenii*	44%	5e-115
L21SP4_00338	*por*	Pyruvate:ferredoxin (flavodoxin) oxidoreductase	WP_006928237	*Caldithrix abyss*	66%	0.0

L21SP4_00414	*pflA*	Pyruvate:formate lyase activating enzyme	WP_034844058	*Clostridium cellulosi*	45%	1e-90
L21SP4_00415	*pfl*	Pyruvate:formate lyase	WP_004623430	*Clostridium termitidis*	39%	2e-179
L21SP4_02432	*fhs*	Formate--tetrahydrofolate ligase	WP_013163071	*Desulfurivibrio alkaliphilus*	67%	0.0
L21SP4_02150	*ldhA*	Lactate dehydrogenase	WP_013313365	*Spirochaeta thermophila*	63%	9e-151
L21SP4_01445	*ackA*	Acetate kinase	WP_014163260	*Thermovirga lienii*	56%	3e-153
L21SP4_01446	*pta*	Phosphate acetyltransferase	CDD36874	*Clostridium* sp. CAG:356	52%	4e-106
L21SP4_02481	*adhE*	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase	WP_024123985	*Thermosynechococcus* sp. NK55a	69%	0.0
L21SP4_01302	*hydA_1*	Fe-only hydrogenase, subunit A	F6CNN4	*Desulfotomaculum kuznetsovii*	73%	0.0
L21SP4_01303	*hydB_1*	Fe-only hydrogenase, subunit B	A0A098QYC2	*Spirochaeta* sp. JC230	61%	0.0
L21SP4_01304	*hydC_1*	Fe-only hydrogenase, subunit C	F0YTD3	*Clostridium* sp. D5	55%	6.3e-56
L21SP4_01306	*hydC_2*	Fe-only hydrogenase, subunit C	I6YYQ7	*Melioribacter roseus*	55%	1.3e-53
L21SP4_01307	*hydB_2*	Fe-only hydrogenase, subunit B	I6YYQ7	*Melioribacter roseus*	61%	5.5e-168
L21SP4_01308	*hydA_2*	Fe-only hydrogenase, subunit A	I0AG62	*Ignavibacterium album*	71%	0.0
L21SP4_01165	*rnfC*	RNF electron transport complex, subunit C	S7TC88	*Desulfococcus multivorans*	56%	6.7e-176
L21SP4_01166	*rnfD*	RNF electron transport complex, subunit D	C0QFQ5	*Desulfobacterium autotrophicum*	61%	1.7e-127
L21SP4_01167	*rnfG*	RNF electron transport complex, subunit G	A8ZSV4	*Desulfococcus oleovorans*	50%	3.7e-45
L21SP4_01168	*rnfE*	RNF electron transport complex, subunit E	C0QFQ7	*Desulfobacterium autotrophicum*	72%	4.9e-97
L21SP4_01169	*rnfA*	RNF electron transport complex, subunit A	C0QFQ8	*Desulfobacterium autotrophicum*	65%	1e-109
L21SP4_01170	*rnfB*	RNF electron transport complex, subunit B	KJS30282	*Desulfatitalea* sp. BRH_c12	58%	8e-121
L21SP4_01276	*ntpK*	V-type ATP synthase, subunit K	WP_051564474	*Desulfovermiculus halophilus*	74%	7e-62
L21SP4_01277	*ntpI*	V-type ATP synthase, subunit I	C8X3W7	*Desulfohalobium retbaense*	41%	2.2e-147
L21SP4_01278	*ntpD*	V-type ATP synthase, subunit D	S7TG39	*Desulfovibrio alkalitolerans*	66%	5.2e-82
L21SP4_01279	*ntpB*	V-type ATP synthase, subunit B	EPR36183	*Desulfovibrio alkalitolerans*	76%	0.0
L21SP4_01280	*ntpA*	V-type ATP synthase, subunit A	S7UQ59	*Desulfovibrio alkalitolerans*	70%	0.0

L21SP4_01281	*ntpC?*	V-type ATP synthase, subunit C (fragment)	D4VSP1	*Bacteroides xylanisolvens*	31%	4.4e0
L21SP4_01282	*ntpE*	V-type ATP synthase, subunit E	C9RNV0	*Fibrobacter succinogenes*	35%	1.3e-33
L21SP4_00987	*zwf*	Glucose-6-phosphate 1-dehydrogenase	WP_013109466	*Planctopirus limnophila*	47%	3e-150
L21SP4_00648	*gnd*	6-Phosphogluconate dehydrogenase, decarboxylating	WP_045033806	*Draconibacterium* sp. JN14CK-3	77%	0.0
L21SP4_01787	*tkt*	Transketolase	WP_015947514	*Desulfatibacillum alkenivorans*	57%	0.0
L21SP4_00829	*tal*	Transaldolase	EMI15679	*Rhodopirellula maiorica*	42%	5e-99
L21SP4_01026	*accA*	Acetyl-CoA carboxylase, carboxyl transferase subunit A	B9XC31	*Pedosphaera parvula*	62%	5e-133
L21SP4_01127	*accD*	Acetyl-CoA carboxylase, carboxyl transferase subunit B	B9XP59	*Pedosphaera parvula*	61%	4.3e-109
L21SP4_00815	*accB*	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	B4D216	*Chthoniobacter flavus*	50%	6e-43
L21SP4_00816	*accC*	Acetyl-CoA/pyruvate carboxylase, biotin carboxylase subunit	A0A0F0CK69	“*Ca.* Omnitrophus” sp. SKK-01	62%	0.0
L21SP4_00826	*pycB*	Pyruvate carboxylase, subunit B	E0RRA9	*Spirochaeta thermophila*	65%	0.0
L21SP4_00845	*gltA*	Citrate synthase (type II)	WP_012844713	*Rhodothermus marinus*	62%	0.0
L21SP4_00761	*acnA*	Aconitate hydratase	WP_026961881	*Alicyclobacillus herbarius*	54%	0.0
L21SP4_00989	*icd*	Isocitrate dehydrogenase (NADP)	WP_012843901	*Rhodothermus marinus*	74%	0.0
L21SP4_00972	*mvaA*	Class I hydroxymethylglutaryl-CoA reductase (NADPH)	S3XX46	*Dermabacter* sp. HFH0086	60%	2e-130
L21SP4_02095	*mvaD*	Diphosphomevalonate decarboxylase	WP_024850502	*Thiomicrospira kuenenii*	51%	3e-111
L21SP4_02096	*pmk*	Phosphomevalonate kinase (GHMP kinase C-terminal domain)	A9KC29	*Coxiella burnetii*	34%	1.8e-39
L21SP4_02097	*mvaK*	Mevalonate kinase (GHMP kinase N-	WP_005771666	*Coxiella burnetii*	43%	1e-92

		terminal domain)				
L21SP4_02098	*mvaS*	Hydroxymethylglutaryl-CoA synthase	WP_028471426	*Neptunomonas japonica*	55%	5e-153
L21SP4_02099	*idi*	Isopentenyl-diphosphate delta isomerase (type 2)	WP_027852820	*Marinobacterium litorale*	56%	7e-115
L21SP4_00792	*hprK*	HPr (ser) kinase/phosphatase	D5EIM8	*Coraliomargarita akajimensis*	46%	6.1e-84
L21SP4_00793	*ptsH_1*	Phosphocarrier protein HPr	D5HAE7	*Salinibacter ruber*	49%	1.9e-21
L21SP4_00794	*ptsA_1*	Phosphoenolpyruvate-protein phosphotransferase	WP_007413672	*Pedosphaera parvula*	51%	0.0
L21SP4_00014	*ptsH_2*	Phosphocarrier protein HPr	WP_007278638	*Lentisphaera araneosa*	48%	1e-20
L21SP4_01117	*ptsA_2*	Phosphoenolpyruvate-protein phosphotransferase	WP_014455518	*Spirochaeta africana*	46%	0.0
L21SP4_00166	*ptsN_1*	PTS system sugar transporter, subunit IIA	WP_025321887	*Deferrisoma camini*	42%	4e-24
L21SP4_00231	*ptsN_2*	PTS system sugar transporter, subunit IIA	Q2S4A8	*Salinibacter ruber*	30%	1.1e-14
L21SP4_00347	*ptsN_3*	PTS system sugar transporter, subunit IIA	C8PPN3	*Treponema vincentii*	53%	1.4e-44
L21SP4_01384	*ptsN_4*	PTS system sugar transporter, subunit IIA	WP_041589264	*Thermoanaerobacter wiegelii*	28%	6e-14
L21SP4_01661	*potE/ptsN*	Amino acid transporter/PTS IIA domain	S7TGJ5	*Desulfovibrio alkalitolerans*	49%	0.0
L21SP4_02044	*ptsN_5*	PTS system sugar transporter, subunit IIA	WP_009106564	*Treponema* sp. JC4	45%	1e-65
L21SP4_01616	*acyC*	Adenylate cyclase with Chase sensor	WP_014260764	*Desulfovibrio africanus*	33%	1e-92