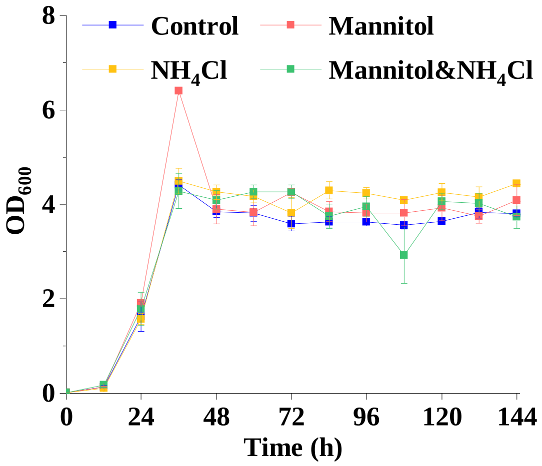

Fig. S1. Effects of external addition of mannitol or NH_4Cl with an equivalent amount of carbon or nitrogen in 0.5 g/L WSHM on the growth of *S. fredii* CCBAU45436. The data are presented as the means ± standard deviations from triplicate experiments.

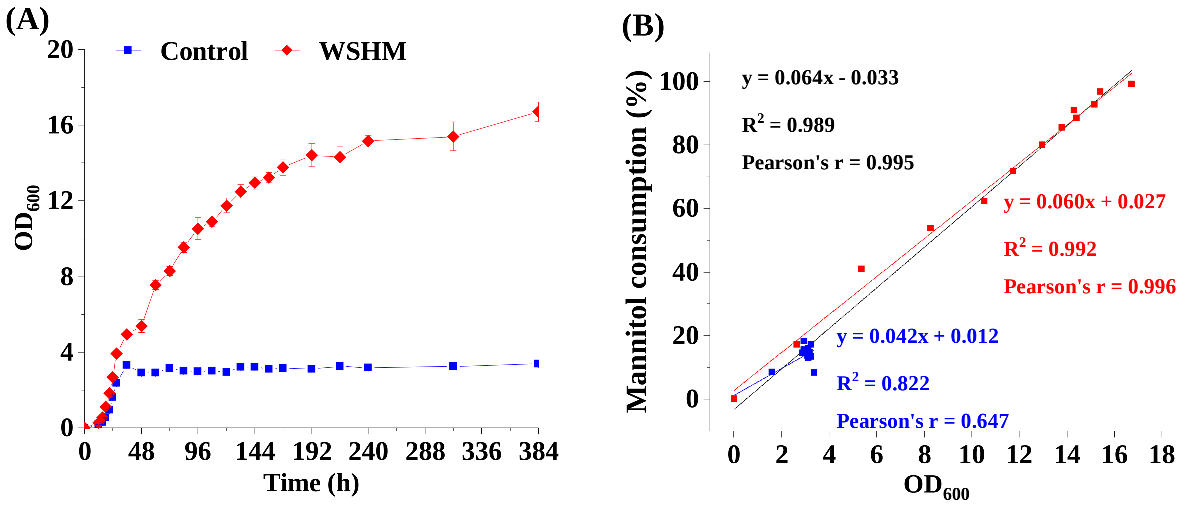

Fig. S2. Effects of WSHM on the growth and carbon source utilization efficiency of *S. fredii* CCBAU45436. (A) Effects of WSHM on the growth. (B) Correlations between mannitol consumption and OD_{600}. Blue, red and black represent samples collected from YM broth or YM broth supplied with 0.5 g/L WSHM and all, respectively. The linear model between mannitol consumption and OD_{600} were shown.

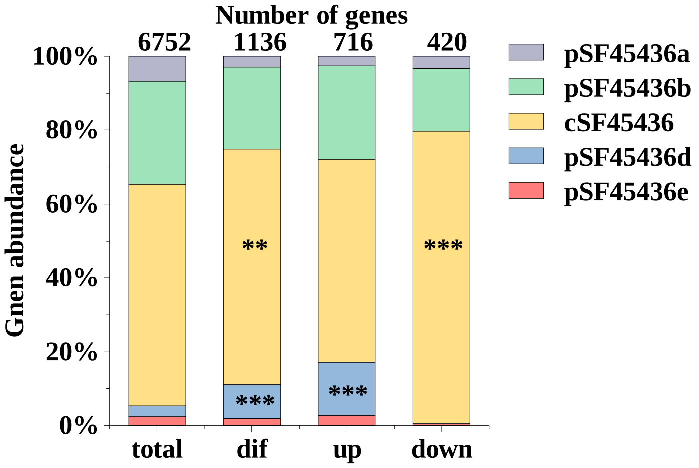

Fig. S3. Distribution of genes among replicons; total: all genes of *S. fredii* CCBAU45436, dif: differentially expressed genes, up: up-regulated genes, down: down-regulated genes; (Fisher's exact test with FDR correction, **, padj < 0.01; ***, padj < 0.001, only significantly enriched gene cluster were marked).

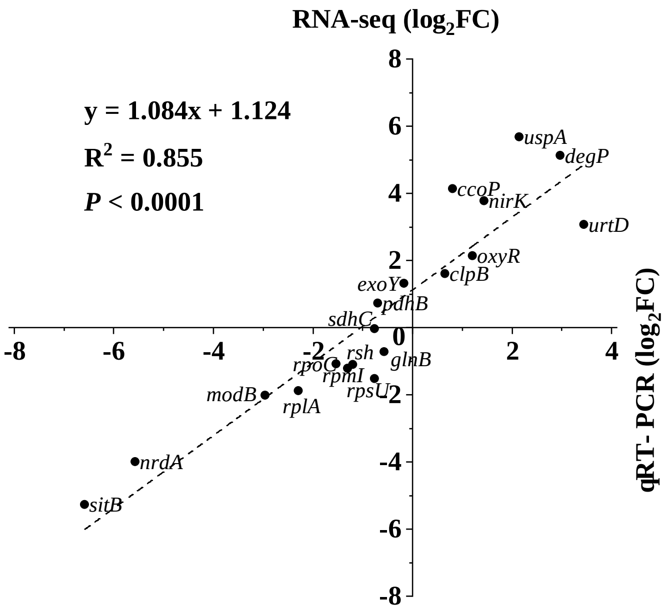

Fig. S4. Comparisons of fold change values ($\log_2$FC) of selected genes from the different functional categories measured by qRT-PCR and RNA-Seq. The R^2 indicates the square of Pearson’s correlation coefficient r.

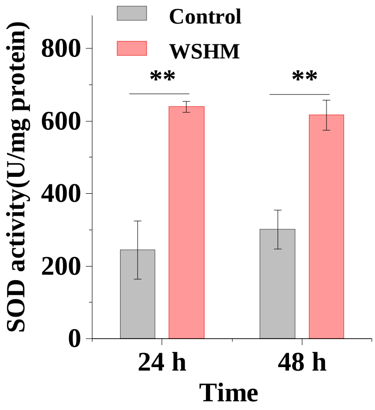

Fig. S5. Effects of WSHM on superoxide dismutase activity of *S. fredii* CCBAU45436 at 24 h and 48 h; (t-test, **, $P < 0.01$). The data are presented as the means ± standard deviations from triplicate experiments.

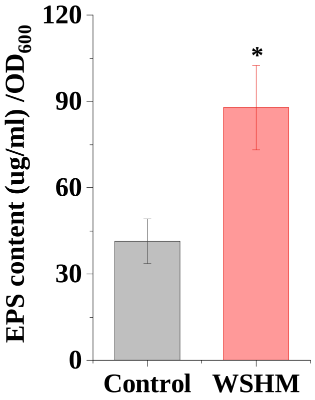

Fig. S6. Effects of WSHM on exopolysaccharides (EPS) production of *S. fredii* CCBAU45436 at 24 h; (t-test, *, $P < 0.05$). The data are presented as the means ± standard deviations from triplicate experiments.

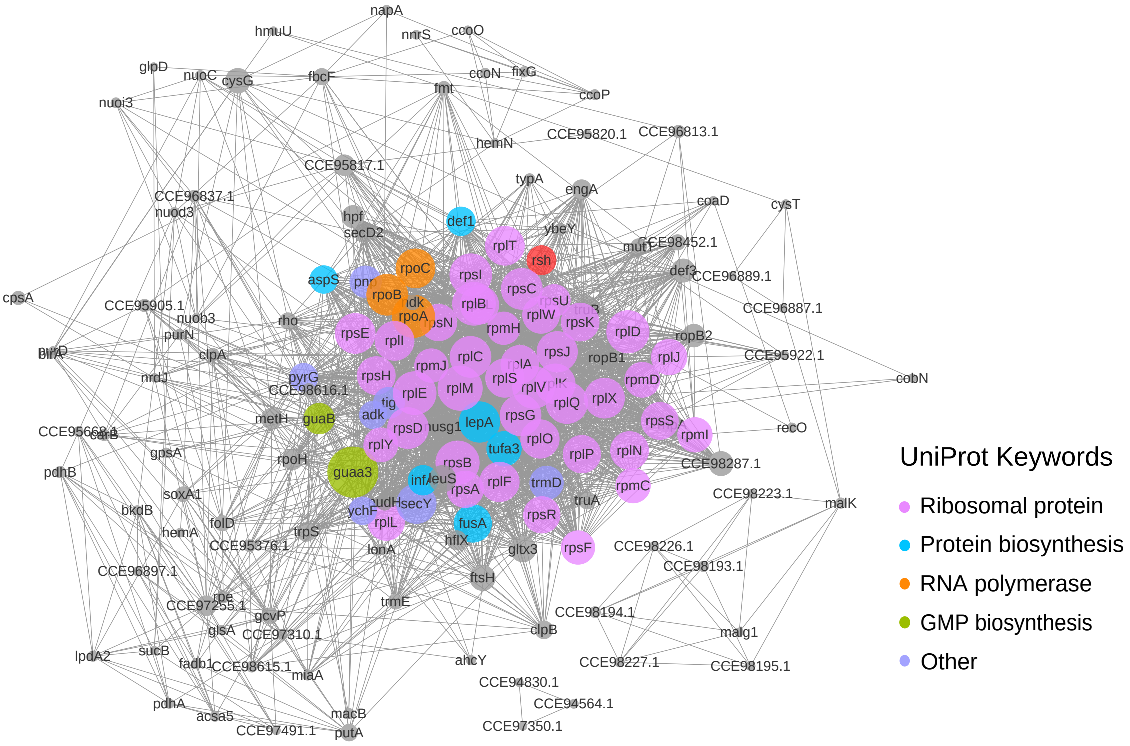

Fig. S7. STRING protein-protein interaction network for the significant differentially expressed genes, only the node with degree > 10 were shown. The size of the node is proportional to the degree, and nodes with degree ≥ 50 are colored according to the UniPort Keywords of protein expect *rsh* gene was shown in red.

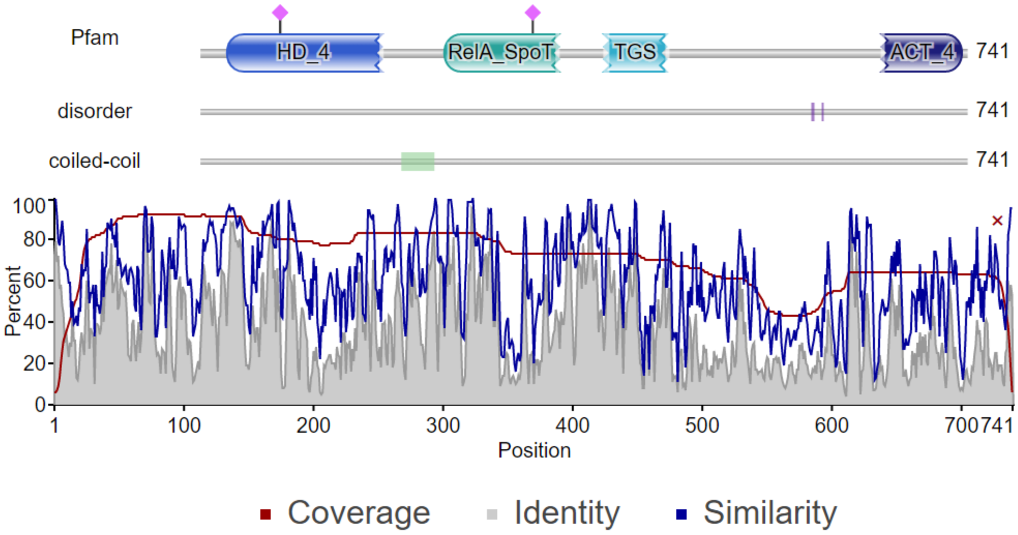

Fig. S8. Sequence matches and features of the *S. fredii* CCBAU45436 RSH protein against the Pfam database. HD: hydrolase domain; RelA-SpoT: predicted RelA-SpoT ppGpp synthase domain; TGS: Threonyl-tRNA synthetase, GTPase and SpoT; ACT: Aspartokinase, Chorismate mutase and TyrR.

Table S1. Data quality of RNA-Seq datasets and genomic alignment results of sequencing reads

Sample name	Raw reads	Clean reads	Q20(%)	Q30(%)	Total mapped	Uniquely mapped
Control1	19532312	19005078	98.39	94.91	18790049 98.87%	18122679 95.36%
Control2	17384566	17185396	98.82	96.08	16947252 98.61	16269213 94.67%
Control3	14259850	14096340	98.81	96.04	13922282 98.77%	13394195 95.02%
WSHM1	14957640	14779534	98.82	96.08	14585780 98.69%	14225887 96.25%
WSHM2	20254278	20034488	98.82	96.06	19777881 98.72%	19282765 96.25%
WSHM3	14233518	13882542	98.5	95.22	13733661 98.93%	13406660 96.57%

Table S2. Distribution of genes among replicons, p-adjust: Fisher’s exact test with FDR correction. The p-adjust of significantly enriched gene cluster were bold.

replicons	**total gene**	**DEG**	**% of dif**	**p-adjust**	**up-regulated**	**% of up**	**p-adjust**	**down-regulated**	**% of down**	**p-adjust**
pSF45436a	452	33	2.90%	3.6E-09	19	2.65%	1.7E-06	14	3.33%	0.00405
pSF45436b	1888	252	22.18%	2.3E-06	181	25.28%	0.14	71	16.90%	1.5 E-07
cSF45436	4051	725	63.82%	**0.00484**	393	54.89%	0.00902	332	79.05%	**6.7E-17**
pSF45436d	203	104	9.15%	**1.1E-29**	103	14.39%	**6.5E-48**	1	0.24%	7.6E-05
pSF45436e	158	22	1.94%	0.38886	20	2.79%	0.36041	2	0.48%	0.00416
sum	6752	1136	100.00%		716	100.00%		420	100.00%	

Table S3. Genes selected from different functional categories and gene-specific primers for qRT-PCR analysis

Gene ID	Gene name	Primer (5'-3')	Functional categories	Gene production
AB395_RS18320	16S	GTGATAAGCCGAGAGGAAGGT CCACTGTCACCACCATTGTAG		16S rRNA gene (the reference)
AB395_RS04425	*uspA*	AGGAGGTTCTCAATCAGCAT ATCATCGCCTTCGTCACA	stress response genes	Universal stress protein UspA and related nucleotide-binding proteins
AB395_RS32460	*degP*	TCGCTTACGGAGAATACA GTTCACGACAAGCCTTAG		Trypsin-like serine proteases
AB395_RS02005	*oxyR*	TCTGGTGCCGCAACTCATTC CCTGTCGGTCAGCGATTCC		Hydrogen peroxide-inducible genes activator
AB395_RS13640	*clpB*	AATACGAGCAGCACCACAAGG CCGTGATGTAGCGATTGGATAGG		ATP-dependent chaperone ClpB
AB395_RS23120	*exoY*	CCGCAACGATGTGTCCTA CTTGAAGACGATGACGAGGT	carbon metabolism	Exopolysaccharide biosynthesis polyprenyl glycosyl phosphotransferase
AB395_RS05810	*pdhB*	GCTCTCCAAGTGGCTGAA CTCCATCGTCGCCTTGTC		pyruvate dehydrogenase complex E1 component subunit beta
AB395_RS16895	*sdhC*	CTCTCGCCGCATCTTCAA CACCAGGCAACCAGGATC		succinate dehydrogenase, cytochrome b556 subunit
AB395_RS08875	*ccoP*	CCTCGCTGGTGGGTCTAC CTTCGTCGCATCCGTCAAC		Cbb3-type cytochrome c oxidase subunit
AB395_RS04540	*nirK*	GGCGAGCAGGACTTCTATGT TTCCAGCGTATCGGCGTAG	nitrogen metabolism	Copper-containing nitrite reductase
AB395_RS21215	*urtD*	AACTCGCTCTCCTTCATC GTCCATCATCGTCGTCTT		urea ABC transporter ATP-binding protein UrtD
AB395_RS07010	*glnB*	CGGACGAGAATGCGGAAG TGCGGATTCGGATCACTT		nitrogen regulatory protein P-II
AB395_RS05290	*rpoC*	AGATTCGTGGTCGCTACAAG GGTTCTTCGGCAGGAGTT	genetic information processing	DNA-directed RNA polymerase subunit beta'
AB395_RS19775	*rpmI*	AGCGTTCCAACAAGTTCATTC CGTTCGGCAGGTAGTTCT		50S ribosomal protein L35
AB395_RS15575	*rpsU*	GCAGGTACTTGTCCGCGATAAC TGCGACGGCTTTTCATAGAAGTC		30S ribosomal protein S21
AB395_RS05270	*rplA*	GCATTGATCCGGTGAAGG GAGATTCATCGCCACTTCG		50S ribosomal protein L1
AB395_RS29160	*nrdA*	TCGCTGACGCTGTTCTTC ATGGTCTTGATGCCCTTCTT		class 1b ribonucleoside-diphosphate reductase subunit alpha
AB395_RS03645	*rsh*	GAGGAGGAACTGAGCGAACTG GCGGAAGACGGAATAGGGTTT	others	bifunctional (p)ppGpp synthetase/hydrolase

AB395_RS15960	*modB*	GTGCTGCTCATCCTGTTC AGCGGAAGGAAAAGACAAG	molybdate ABC transporter permease subunit
AB395_RS12150	*tonB*	TACGCTTTACTGTCACATCCAAT GCTGCCTGGTCGAGAATT	Periplasmic protein TonB
AB395_RS16720	*sitB*	CTGAAGAAGAATCTCGTCGCCTAT GCCCATCATCACCACATCCT	manganese/iron ABC transporter ATP-binding protein

Table S4. Description of genes in Fig. 4

Gene ID	Gene name	Log$_2$FC	P-adjust	Gene production
AB395_RS12225	*mtlK*	-0.23	0.4309881	Multiple polyol-specific dehydrogenase (EC 1.1.1.-)
AB395_RS15790	*xylA*	0.01	0.9895518	Xylose isomerase (EC 5.3.1.5)
AB395_RS16435	*frk*	-0.73	0.0093495	ROK family Glucokinase with ambiguous substrate specificity
AB395_RS00575	*frk*	-0.15	0.6709546	Fructokinase (EC 2.7.1.4)
AB395_RS25675	*fbp*	1.61	7.101E-08	Fructose-1,6-bisphosphatase2C type I (EC 3.1.3.11)
AB395_RS10390	*pfp*	0.80	0.0009494	Pyrophosphate-dependent fructose 6-phosphate-1-kinase (EC 2.7.1.90)
AB395_RS32620	*pfp*	4.66	5.244E-61	Tagatose-6-phosphate kinase (EC 2.7.1.144) / 1-phosphofructokinase (EC 2.7.1.56)
AB395_RS15055	*fba*	1.80	1.906E-14	Fructose-bisphosphate aldolase class I (EC 4.1.2.13)
AB395_RS24590	*fba*	-0.45	0.1057599	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)
AB395_RS25690	*fba*	1.92	7.32E-11	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)
AB395_RS32440	*glk*	3.39	4.334E-60	Glucokinase (EC 2.7.1.2)
AB395_RS32660	*glk*	2.82	9.941E-17	Glucokinase like protein
AB395_RS18785	*glk*	-0.55	0.0499549	Glucokinase (EC 2.7.1.2)
AB395_RS00585	*pgi*	-0.29	0.3361126	Glucose-6-phosphate isomerase (EC 5.3.1.9)
AB395_RS01690	*zwf*	-0.48	0.0752833	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
AB395_RS01685	*pgl*	-0.35	0.2497178	6-phosphogluconolactonase (EC 3.1.1.31)2C eukaryotic type
AB395_RS01680	*edd*	0.07	0.8659079	Phosphogluconate dehydratase (EC 4.2.1.12)
AB395_RS15725	*eda*	-0.49	0.1408175	4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) &2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)
AB395_RS08835	*gnd*	-0.28	0.3675601	6-phosphogluconate dehydrogenase2C decarboxylating (EC 1.1.1.44)
AB395_RS25710	*rpe*	1.06	0.0051373	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)
AB395_RS07520	*rpe*	-0.48	0.1355813	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)
AB395_RS08395	*rpi*	-0.59	0.0296624	Ribose 5-phosphate isomerase A (EC 5.3.1.6)
AB395_RS23580	*rpi*	0.07	0.880628	Ribose 5-phosphate isomerase B (EC 5.3.1.6)
AB395_RS32855	*xfp*	4.27	6.022E-69	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) & Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)
AB395_RS25360	*tkt*	-0.13	0.7609231	Transketolase2C N-terminal section (EC 2.2.1.1)
AB395_RS25365	*tkt*	-0.08	0.8900902	Transketolase2C C-terminal section (EC 2.2.1.1)
AB395_RS15035	*tkt*	-0.43	0.0896349	Transketolase (EC 2.2.1.1)
AB395_RS25685	*tkt*	1.78	2.497E-12	Transketolase (EC 2.2.1.1)
AB395_RS16790	*tal*	0.18	0.5432929	Transaldolase (EC 2.2.1.2)
AB395_RS11385	*tal*	-0.26	0.6834022	Transaldolase (EC 2.2.1.2)
AB395_RS11300	*prsA*	-0.95	0.0001463	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
AB395_RS32630	*prsA*	4.93	1.805E-79	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
AB395_RS15040	*gap*	0.12	0.720159	NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
AB395_RS15050	*pgk*	-0.27	0.372946	Phosphoglycerate kinase (EC 2.7.2.3)

AB395_RS18800	*gpm*	-0.36	0.2381711	Phosphoglycerate mutase (EC 5.4.2.1)
AB395_RS02695	*gpm*	-1.15	3.781E-05	Phosphoglycerate mutase family
AB395_RS05795	*eno*	-0.13	0.7015901	Enolase (EC 4.2.1.11)
AB395_RS15210	*pyk*	-0.69	0.0061332	Pyruvate kinase (EC 2.7.1.40)
AB395_RS32655	*pps*	3.58	9.417E-36	Phosphoenolpyruvate synthase (EC 2.7.9.2)
AB395_RS02910	*pps*	-0.07	0.8134841	Pyruvatephosphate dikinase (EC 2.7.9.1)
AB395_RS05805	*pdh*	0.87	0.000561	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)
AB395_RS05810	*pdh*	0.73	0.0032949	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)
AB395_RS32330	*pdh*	2.02	3.244E-17	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)
AB395_RS32335	*pdh*	2.11	2.893E-17	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)
AB395_RS18180	*pckA*	1.18	2.524E-08	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)
AB395_RS21690	*gltA*	0.57	0.0359065	Citrate synthase (si) (EC 2.3.3.1)
AB395_RS06120	*gltA*	0.56	0.0318637	Citrate synthase (si) (EC 2.3.3.1)
AB395_RS27600	*acnA*	-0.23	0.4264916	Aconitate hydratase (EC 4.2.1.3)
AB395_RS17375	*acnA*	0.15	0.5658562	Aconitate hydratase (EC 4.2.1.3)
AB395_RS08090	*icd*	-1.19	3.139E-07	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)
AB395_RS16840	*sucA*	0.38	0.1176081	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)
AB395_RS16835	*sucB*	0.23	0.435535	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61)
AB395_RS05830	*lpd*	0.76	0.0031442	Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)
AB395_RS15995	*lpd*	1.67	9.887E-14	Dihydrolipoamide dehydrogenase of branched-chain alpha-keto acid dehydrogenase (EC 1.8.1.4)
AB395_RS16815	*lpd*	0.32	0.2140103	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)
AB395_RS05815	*lpd*	0.68	0.0091526	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)
AB395_RS32340	*lpd*	1.60	7.382E-10	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)
AB395_RS15525	*pgm*	1.03	2.422E-05	Phosphoglucomutase (EC 5.4.2.2)
AB395_RS08840	*ccoS*	1.81	0.0010779	Type cbb3 cytochrome oxidase biogenesis protein CcoS involved in heme b insertion
AB395_RS08845	*ccoI*	4.12	1.375E-60	Type cbb3 cytochrome oxidase biogenesis protein CcoI Copper-translocating P-type ATPase (EC 3.6.3.4)
AB395_RS08850	*ccoH*	5.10	1.892E-67	Type cbb3 cytochrome oxidase biogenesis protein CcoH
AB395_RS08855	*ccoG*	5.23	5.028E-79	Type cbb3 cytochrome oxidase biogenesis protein CcoG
AB395_RS08875	*ccoP*	4.13	3.993E-58	Cytochrome c oxidase subunit CcoP (EC 1.9.3.1)
AB395_RS08880	*ccoQ*	3.08	7.577E-10	Cytochrome c oxidase subunit CcoQ (EC 1.9.3.1)
AB395_RS08885	*ccoO*	4.41	2.215E-45	Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)
AB395_RS08890	*ccoN*	5.06	9.709E-89	Cytochrome c oxidase subunit CcoN (EC 1.9.3.1)
AB395_RS04840	*nuoA*	0.41	0.2492021	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)
AB395_RS04845	*nuoB*	0.40	0.1284137	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)
AB395_RS04850	*nuoC*	0.41	0.1074975	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)
AB395_RS04855	*nuoD*	0.59	0.0240792	NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)

AB395_RS04865	*nuoE*	0.62	0.0088352	NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)
AB395_RS04870	*nuoF*	0.41	0.1176949	NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3)
AB395_RS04885	*nuoH*	0.29	0.3228827	NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)
AB395_RS04890	*nuoI*	0.19	0.5246981	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)
AB395_RS04895	*nuoJ*	0.26	0.3385803	NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)
AB395_RS04900	*nuoK*	-0.04	0.9198044	NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)
AB395_RS04905	*nuoL*	0.01	0.9899626	NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)
AB395_RS04910	*nuoM*	-0.02	0.9673037	NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)
AB395_RS04915	*nuoN*	0.03	0.9230476	NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)
AB395_RS10830	*nuoH*	0.54	0.0223183	NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)
AB395_RS10835	*nuoI*	1.27	5.217E-05	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)
AB395_RS10845	*nuoG*	0.94	0.00019	NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3)
AB395_RS10850	*nuoF*	0.97	0.0019513	NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3)
AB395_RS10855	*nuoE*	1.57	0.0027839	NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)
AB395_RS10860	*nuoD*	1.24	2.233E-06	NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)
AB395_RS10865	*nuoC*	1.89	1.602E-07	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)
AB395_RS10870	*nuoB*	2.04	9.417E-09	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)
AB395_RS10875	*nuoA*	1.76	4.578E-07	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)
AB395_RS10880	*nuoN*	0.17	0.6633655	NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)
AB395_RS10885	*nuoM*	0.20	0.6270663	NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)
AB395_RS10900	*mnhD*	0.28	0.5006408	NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)
AB395_RS10905	*nuoK*	0.64	0.4893503	NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)
AB395_RS10910	*nuoJ*	0.74	0.0071658	NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)
AB395_RS23060	*exoP*	1.21	3.337E-07	Succinoglycan biosynthesis transport protein exoP
AB395_RS23065	*exoN*	1.57	5.587E-12	UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
AB395_RS00880	*galE*	2.15	1.444E-34	UDP-glucose 4-epimerase (EC 5.1.3.2)
AB395_RS23070	*exoO*	1.22	6.976E-08	Succinoglycan biosynthesis protein ExoO
AB395_RS23075	*exoM*	1.26	9.182E-08	Succinoglycan biosynthesis protein ExoM
AB395_RS23080	*exoA*	1.29	5.612E-09	Succinoglycan biosynthesis protein ExoA
AB395_RS23085	*exoL*	1.54	1.493E-12	Succinoglycan biosynthesis protein ExoL
AB395_RS23090	*exoK*	2.05	1.407E-21	Endo-beta-1,3-1,4 glucanase (EC 3.2.1.73)
AB395_RS23105	*exoI*	0.59	0.027931	putative periplasmic protein
AB395_RS23110	*exoU*	1.44	1.128E-11	Succinoglycan biosynthesis protein ExoU
AB395_RS23115	*exoX*	1.22	0.0073245	Exopolysaccharide production repressor protein
AB395_RS23120	*exoY*	1.31	1.316E-09	Exopolysaccharide biosynthesis protein
AB395_RS24220	*nrtC*	2.46	5.981E-17	Nitrate ABC transporter ATP-binding protein
AB395_RS24225	*nrtB*	2.11	5.959E-10	Bicarbonate transport system permease protein
AB395_RS24230	*nrtA*	2.18	8.217E-12	Nitrate ABC transporter nitrate-binding protein
AB395_RS21200	*urtA*	2.21	2.89E-17	urea ABC transporter substrate-binding protein
AB395_RS21205	*urtB*	2.61	3.214E-25	urea ABC transporter permease subunit UrtB
AB395_RS21210	*urtC*	2.97	3.983E-39	urea ABC transporter permease subunit UrtC
AB395_RS21215	*urtD*	3.07	4.731E-31	urea ABC transporter ATP-binding protein UrtD
AB395_RS21220	*urtE*	3.42	4.016E-52	urea ABC transporter ATP-binding subunit UrtE

AB395_RS04560	*napE*	3.34	9.481E-27	Periplasmic nitrate reductase component NapE
AB395_RS04565	*napF*	2.24	2.215E-20	Ferredoxin-type protein NapF (periplasmic nitrate reductase)
AB395_RS04570	*napD*	1.80	0.0046529	Periplasmic nitrate reductase component NapD
AB395_RS04575	*napA*	2.02	4.6E-27	Periplasmic nitrate reductase precursor (EC 1.7.99.4)
AB395_RS04580	*napB*	1.88	6.78E-12	Nitrate reductase cytochrome c550-type subunit
AB395_RS04585	*napC*	1.53	9.234E-11	Cytochrome c-type protein NapC
AB395_RS26435	*nasA*	0.81	0.0197989	Assimilatory nitrate reductase large subunit (EC:1.7.99.4)
AB395_RS04535	*nnrS*	3.56	2.219E-32	NnrS protein involved in response to NO
AB395_RS04540	*nirK*	3.77	1.707E-59	Copper-containing nitrite reductase (EC 1.7.2.1)
AB395_RS04545	*nirV*	2.32	1.074E-18	Nitrite reductase accessory protein NirV
AB395_RS04550	*nnrR*	0.18	0.5852129	Nitric oxide -responding transcriptional regulator NnrR
AB395_RS26425	*nirB*	-0.54	0.4524857	Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)
AB395_RS26430	*nirD*	0.84	0.0165051	Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4)
AB395_RS08065	*glsA*	-1.36	2.421E-05	Glutaminase (EC 3.5.1.2)
AB395_RS21835	*glnA*	1.39	4.45E-10	Glutamine synthetase type II (EC 6.3.1.2)
AB395_RS27410	*glnA*	-0.24	0.5860045	Glutamine synthetase type I (EC 6.3.1.2)
AB395_RS01700	*glnA*	0.49	0.0296624	glutamine synthetase family protein
AB395_RS07005	*glnA*	-0.11	0.7735058	Glutamine synthetase type I (EC 6.3.1.2)
AB395_RS10505	*glnA*	0.51	0.0701031	glutamine synthetase family protein
AB395_RS26035	*gdhA*	0.42	0.2775176	glutamate dehydrogenase
AB395_RS12345	*ureG*	1.06	8.612E-05	Urease accessory protein UreG
AB395_RS12350	*ureF*	-0.17	0.6804141	Urease accessory protein UreF
AB395_RS12355	*ureE*	0.29	0.3221612	Urease accessory protein UreE

Table S5. Strains, plasmids and primers used in this study

	Relevant characteristics	**Note**
Strains		
E. coli DH5α	F-φ80 lac ZΔM15 Δ(lacZYA-arg F) U169 endA1 recA1 hsdR17(rk-,mk+) supE44λ- thi -1 gyrA96 relA1 phoA	Biomed
S. fredii CCBAU45436	*S. fredii* CCBAU45436 wild type, NA^r, TMP^r	(1)
Δ*rsh*	*S. fredii* CCBAU45436 *rsh* in-frame deletion, NA^r, TMP^r	This work
Plasmids		
pJQ200SK	suicide plasmid with sacB selectable marker, Gm^r	(2)
pRK2013	Helper plasmid, IncP, Tra$^+$, Mob$^+$, ColE1, Km^r	(3)
Primers for *rsh* deletion		
rsh-UF	ATCGAATTCCTGCAGCCCTCCGGTTTCGTGTCGTTAATC	
rsh-UR	AATTCCTTGACTCGTATTGGCGCATCATTC	
rsh-DF	CCAATACGAGTCAAGGAATTGCCGAGCATC	
rsh-DR	AGAACTAGTGGATCCCCCTTGATGGGCGCAAGATATGC	
rsh-WF	CATCGCGGAAATGTCGTATTC	
rsh-WR	CCGTCATCGCATCTTGAAAC	

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