Supplementary Table S7. Genes with higher sequence identity with those of bacteria other than desulfovibrios.

gene ID	gene function	gene name of BLAST top hit	organism of BLAST top hit	sequence identity (%)	maximum identity to desulfovibrio sequences	codon adaptation index[1]	GC (%)[2]
RSDT_0009	YqeC-like putative molybdenum hydroxylase maturation	|WP_015838089.1| 4-hydroxybenzoyl-CoA thioesterase	*Geobacter* sp. M21	40	30	0.729	62.5
RSDT_0013	type II DNA restriction-modification system methylase	|WP_026767432.1| DNA methylase N-4	*Selenomonas ruminantium*	80	28	0.642	43.9
RSDT_0044	fumarate reductase subunit D	|WP_029094287.1| fumarate reductase	*Budvicia aquatica*	47	-	0.682	57.3
RSDT_0045	fumarate reductase subunit C	|WP_049277929.1| fumarate reductase	*Serratia marcescens*	47	32	0.662	50.0
RSDT_0046	fumarate reductase subunit B	|KOY60604.1| fumarate reductase	*Photorhabdus heterorhabditis*	68	33	0.722	53.9
RSDT_0047	fumarate reductase flavoprotein subunit A	|WP_038222555.1| fumarate reductase	*Xenorhabdus bovienii*	72	38	0.753	57.4
RSDT_0048	conserved hypothetical protein	|EFD25460.1| hypothetical protein	*Anaerobaculum hydrogeniformans* ATCC BAA-1850	53	29	0.741	54.6
RSDT_0052	cation efflux system protein CusA	|WP_029741280.1| cation transporter	*Enterobacter asburiae*	67	46	0.726	57.1
RSDT_0053	cation efflux system protein CusB	|WP_024908524.1| copper resistance protein	*Enterobacter asburiae*	51	26	0.734	59.0
RSDT_0054	cation efflux system protein CusF	|WP_035891064.1| hypothetical protein	*Kluyvera ascorbata*	42	36	0.713	54.6
RSDT_0055	cation efflux system protein CusC	|WP_000074222.1| cation efflux system protein CusC	*Escherichia coli*	46	37	0.734	59.2
RSDT_0056	hypothetical protein	|WP_034704395.1| hypothetical protein	*Enterococcus gallinarum*	27	-	0.742	60.3
RSDT_0058	recombination protein RmuC	|WP_035687958.1| hypothetical protein, partial	*Flavobacterium reichenbachii*	58	23	0.660	36.6
RSDT_0060	cell division protein Fic	|WP_040196958.1| cell division protein Fic	'*Candidatus* Soleaferrea massiliensis'	70	51	0.623	43.4
RSDT_0137	type II DNA DNA restriction-modification system methylase	|WP_035401565.1| restriction endonuclease subunit M	*Chlorobium* sp. GBChlB	74	28	0.616	31.2
RSDT_0154	conserved hypothetical protein	|EIC22791.1| hypothetical protein Thi970DRAFT_00426	*Thiorhodovibrio* sp. 970	53	23	0.699	52.7
RSDT_0236	conserved hypothetical protein	|GAP72491.1| hypothetical protein SAMD00024442 33 13	'*Ca.* Symbiothrix dinenymphae'	67	26	0.721	48.0
RSDT_0257	tRNA-specific 2-thiouridylase MnmA	|WP_021999269.1| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	*Acetobacter* sp. CAG:977	52	37	0.711	58.5

RSDT_0258	adenylyltransferase/sulfurtransferase MoeZ	|WP_045673096.1| molybdenum cofactor biosynthesis protein MoeB	*Paenibacillus beijingensis*	58	49	0.728	56.5
RSDT_0263	CRISPR-associated protein Csx16	|WP_038500039.1| CRISPR-associated protein	*Basilea psittacipulmonis*	53	36	0.746	60.2
RSDT_0391	multiple promoter invertase	|GAP16136.1| site-specific recombinases, DNA invertase Pin homologs	*Longilinea arvoryzae*	77	39	0.650	41.6
RSDT_0408	putative Fe2+ permease transmembrane component	|WP_034943543.1| hypothetical protein	*Gilliamella apicola*	55	49	0.680	52.7
RSDT_0409	putative Fe2+ permease periplasmic component	|WP_039129983.1| hypothetical protein	*Gilliamella apicola*	67	27	0.682	54.0
RSDT_0410	conserved membrane protein	|WP_015708650.1| membrane protein	*Treponema primitia*	37	36	0.665	53.6
RSDT_0411	ABC efflux transporter permease	|WP_042431140.1| ABC transporter permease	*Clostridium* sp. JCD	61	27	0.699	54.7
RSDT_0412	ABC efflux transporter permease	|WP_038666892.1| ABC transporter permease	*Pelosinus* sp. UFO1	51	25	0.697	54.2
RSDT_0413	ABC efflux transporter ATP-binding protein	|WP_009066059.1| GTPase	*Clostridium* sp. MSTE9	77	42	0.699	49.8
RSDT_0542	aspartate ammonia-lyase	|WP_015767470.1| aspartate ammonia-lyase	'*Ca.* Accumulibacter phosphatis'	73	57	0.732	49.8
RSDT_0543	anaerobic C4-dicarboxylate transporter DcuA	|WP_010864804.1| anaerobic c4-dicarboxylate membrane transporter family protein	*Plesiomonas* spp.	73	36	0.686	54.5
RSDT_0572	Sel1 family tetratricopeptide repeat protein	|WP_008523308.1| hypothetical protein	*Jonquetella anthropi*	41	33	0.705	56.5
RSDT_0599	uncharacterized transcriptional regulator	|WP_022204637.1| hypothetical protein	*Eubacterium* sp. CAG:248	53	39	0.517	41.8
RSDT_0600	HipA-like protein kinase	|WP_022459109.1| hypothetical protein	*Fusobacterium* sp. CAG:439	57	29	0.648	45.9
RSDT_0618	methylated-DNA-[protein]-cysteine S-methyltransferase	|WP_022000033.1| methylated-DNA--protein-cysteine methyltransferase	*Acetobacter* sp. CAG:977	58	43	0.722	59.7
RSDT_0641	conserved hypothetical protein	|WP_029462313.1| 2-hydroxyacid dehydrogenase	Comamonadaceae bacterium H1	59	52	0.699	52.4
RSDT_0673	hypothetical protein	|WP_006336104.1| ferredoxin	*Gordonia rhizosphera*	44	35	0.615	54.9
RSDT_0708	hypothetical protein	|XP_003344393.1| hypothetical protein SMAC_08986	*Sordaria macrospora* k-hell	30	28	0.652	58.3
RSDT_0726	MerR family transcriptional regulator	|WP_049817209.1| hypothetical protein	beta proteobacterium SCGC AAA027-I06	56	26	0.623	48.8
RSDT_0732	selenium-dependent molybdenum hydroxylase accessory	|CBX28760.1| hypothetical protein N47 L13580	uncultured *Desulfobacterium* sp.	53	33	0.675	58.5

RSDT_0735	putative selenate reductase	|WP_022849647.1| pyridine nucleotide-disulfide oxidoreductase	*Geovibrio* sp. L21-Ace-BES	50	29	0.699	53.3
RSDT_0737	phenylhydantoinase/dihydropyrimidinase-like protein YgeZ	|WP_023976435.1| phenylhydantoinase	*Clostridium pasteurianum*	51	35	0.698	54.8
RSDT_0784	heavy metal-resistance transcriptional regulator	|WP_037588650.1| ArsR family transcriptional regulator	*Stenoxybacter acetivorans*	80	50	0.724	51.4
RSDT_0816	O-acetylhomoserine/O-acetylserine sulfhydrylase	|WP_010075485.1| O-acetylhomoserine aminocarboxypropyltransferase	*Clostridium cellulovorans*	76	69	0.725	53.9
RSDT_0831	aromatic amino acid permease AroP	|WP_015423019.1| aromatic amino acid transporter	'*Ca.* Endomicrobium trichonymphae' Rs-D17	63	52	0.660	51.7
RSDT_0866	H+-translocating [NiFe] hydrogenase complex, transmembrane	|BAL59209.1| hydrogenase-4 component B	'*Ca.* Acetothermus autotrophicum'	39	38	0.702	58.8
RSDT_0923	putative transmembrane phospholipid methyltransferase	|KPK25183.1| hypothetical protein AMJ61_12665	Desulfobacterales bacterium SG8_35_2	48	29	0.646	46.7
RSDT_0924	glutamin-(asparagin-)ase	|WP_007874054.1| glutaminase	*Polaromonas* sp. CF318	64	38	0.634	47.3
RSDT_1015	anaerobic ribonucleoside-triphosphate reductase	|WP_027360376.1| ribonucleoside-triphosphate reductase	*Desulforegula conservatrix*	69	51	0.734	51.3
RSDT_1016	anaerobic ribonucleoside-triphosphate reductase activating	|KPJ79030.1| anaerobic ribonucleoside-triphosphate reductase activating protein	Deltaproteobacteria bacterium SG8_13	45	42	0.687	52.5
RSDT_1079	putative molybdoprotein maturation protien	|WP_032076464.1| xanthine dehydrogenase	*Clostridium drakei*	43	40	0.709	53.6

[1] Average CAI value of all CDSs was 0.72 ± 0.036. The confidence interval for 95% is 0.650-0.789.

[2] Average GC % of all CDSs was 55.93 ± 4.29. The confidence interval for 95% is 47.87-64.67.