Table S7: COG categories, genomic islands and coverage of *P. temperata* RC23 genes from combined stations GS02-13 of the GOS data set and Norwegian fjord metagenome (Gilbert et al. 2008).

Coverages of <80% are marked pink and genomic islands gray

locus_tag	**annotation**	**COG id**	**COG category**	**genomic islands**	**GOS stations GS02-GS13 gene coverage [%]**	**Fjord gDNA gene coverage [%]**
RCA23_c00010	chromosomal replication initiatior protein DnaA	COG0593	L		100.00	100.00
RCA23_c00020	DNA polymerase III beta subunit DnaN	COG0592	L		100.00	99.55
RCA23_c00030	DNA replication and repair protein RecF	COG1195	L		100.00	100.00
RCA23_c00040	hypothetical protein, LysE type translocator	COG1280	E		100.00	100.00
RCA23_c00050	DNA gyrase subunit B	COG0187	L		100.00	99.92
RCA23_c00060	FAD dependent oxidoreductase	COG0665	E		100.00	100.00
RCA23_c00070	hypothetical protein, rhodanese-like sulphurtransferase	COG1054	R		100.00	100.00
RCA23_c00080	pyrazinamidase/nicotinamidase PncA	COG1335	Q		100.00	100.00
RCA23_c00090	nicotinate phosphoribosyltransferase PncB	COG1488	H		100.00	100.00
RCA23_c00100	aminoglycoside phosphotransferase	COG2334	R		100.00	100.00
RCA23_c00110	putative aminotransferase class III	COG0160	E		100.00	100.00
RCA23_c00120	putative peptide chain release factor	COG1186	J		100.00	100.00
RCA23_c00130	hypothetical integral membrane protein	COG1738	S		100.00	100.00
RCA23_c00140	penicillin-insensitive murein endopeptidase MepA	COG3770	M		100.00	99.57
RCA23_c00150	putative MFS-type transporter	COG2270	R		100.00	100.00
RCA23_c00160	hypothetical protein	COG0824	R		100.00	100.00
RCA23_c00170	hypothetical protein, YGGT family	COG0762	S		100.00	100.00
RCA23_c00180	ATP-dependent DNA helicase RecQ	COG0514	L		100.00	100.00
RCA23_c00190	hypothetical protein DUF328	COG3022	S		100.00	100.00
RCA23_c00200	isopentenyl-diphosphate delta-isomerase Idi	COG1443	I		100.00	100.00
RCA23_c00210	5-aminolevulinate synthase HemA	COG0156	H		100.00	100.00
RCA23_c00220	cytochrome c2	COG3474	C		100.00	100.00
RCA23_c00230	acetyl-CoA acetyltransferase PhaA	COG0183	I		100.00	100.00
RCA23_c00240	DNA polymerase III 2 alpha subunit DnaE	COG0587	L		100.00	100.00

RCA23_c00250	transcription antitermination protein NusG	COG0250	K	100.00	100.00
RCA23_c00260	putative lytic murein transglycosylase	COG2951	M	100.00	100.00
RCA23_c00270	putative ribonuclease R	COG0557	K	100.00	99.24
RCA23_c00280	hypothetical protein DUF461	COG2847	S	100.00	100.00
RCA23_c00290	chorismate synthase AroC	COG0082	E	100.00	100.00
RCA23_c00300	hypothetical protein			100.00	100.00
RCA23_c00310	thiamine-binding periplasmic protein ThiB	COG4143	H	100.00	100.00
RCA23_c00320	thiamine transport system permease protein ThiP	COG1178	P	100.00	100.00
RCA23_c00330	thiamine import ATP-binding protein ThiQ	COG3840	H	100.00	100.00
RCA23_c00340	cytochrome c1	COG2857	C	100.00	100.00
RCA23_c00350	cytochrome b	COG1290	C	100.00	97.53
RCA23_c00360	ubiquinol-cytochrome c reductase iron-sulfur subunit PetA	COG0723	C	100.00	100.00
RCA23_c00370	hypothetical protein, glutathione S-transferase	COG0625	O	100.00	100.00
RCA23_c00380	inositol 2-dehydrogenase IdhA	COG0673	R	100.00	100.00
RCA23_c00390	protein PmbA	COG0312	R	100.00	100.00
RCA23_c00400	putative inositol monophosphatase	COG0483	G	100.00	100.00
RCA23_c00410	putative 3-deoxy-D-manno-octulosonic-acid transferase	COG1519	M	100.00	100.00
RCA23_c00420	tetraacyldisaccharide 4'-kinase LpxK	COG1663	M	100.00	100.00
RCA23_c00430	hypothetical protein, thioredoxin	COG1651	O	100.00	100.00
RCA23_c00440	hypothetical protein DUF721	COG5389	S	100.00	100.00
RCA23_c00450	A/G-specific adenine glycosylase YfhQ	COG1194	L	100.00	100.00
RCA23_c00460	alkane 1-monooxygenase AlkB			100.00	100.00
RCA23_c00470	modification methylase CcrM	COG0863	L	100.00	100.00
RCA23_c00480	ribonuclease HII	COG0164	L	100.00	100.00
RCA23_c00490	putative exodeoxyribonuclease III	COG0708	L	100.00	100.00
RCA23_c00500	hypothetical protein, thioredoxin	COG3118	O	100.00	100.00
RCA23_c00510	putative ATP-dependent protease La (LON)	COG2802	R	100.00	100.00
RCA23_c00520	hypothetical protein, Trm112p-like	COG2835	S	100.00	100.00
RCA23_c00530	putative 2-octaprenyl-6-methoxyphenol hydroxylase	COG0654	H	100.00	100.00
RCA23_c00540	glutamyl-tRNA(Gln) amidotransferase subunit A	COG0154	J	100.00	98.02
RCA23_c00550	LL-diaminopimelate aminotransferase DapL	COG0436	E	100.00	100.00
RCA23_c00560	putative DNA transclocase FtsK	COG1674	D	100.00	100.00
RCA23_c00570	putative outer membrane lipoprotein carrier protein LolA	COG2834	M	100.00	93.55

RCA23_c00580	hypothetical protein	COG4764	S		100.00	100.00
RCA23_c00590	hemimethylated DNA-binding protein, YccV like	COG3785	S		100.00	100.00
RCA23_c00600	putative gamma-glutamyltransferase ywrD	COG0405	E		100.00	100.00
RCA23_c00610	acetyl-CoA acetyltransferase ThlA	COG0183	I		100.00	98.13
RCA23_c00620	hypothetical protein	COG1956	T		100.00	100.00
RCA23_c00630	putative HTH-type transcriptional regulator	COG1396	K		100.00	100.00
RCA23_c00640	hypothetical protein, homoserine/homoserine lactone efflux protein	COG1280	E		100.00	100.00
RCA23_c00650	LysE-type translocator	COG1280	E		100.00	87.72
RCA23_c00660	dimethylglycine dehydrogenase	COG0404	E		100.00	95.83
RCA23_c00670	putative homocysteine S-methyltransferase	COG2040	E		100.00	100.00
RCA23_c00680	pyridoxamine 5'-phosphate oxidase-like protein, FMN-binding	COG3576	R		100.00	99.34
RCA23_c00690	sarcosine dehydrogenase	COG0404	E		100.00	100.00
RCA23_c00700	hypothetical protein	COG0790	R		100.00	100.00
RCA23_c00710	putative agmatine deiminase AguA	COG2957	E		100.00	100.00
RCA23_c00720	Cl- channel, voltage-gated family protein	COG0038	P		100.00	85.75
RCA23_c00730	Cl- channel, voltage-gated family protein	COG0038	P		100.00	89.68
RCA23_c00750	diaminopimelate epimerase DapF	COG0253	E	GI 1	100.00	100.00
RCA23_c00760	(dimethylallyl)adenosine tRNA methylthiotransferase MiaB	COG0621	J	GI 1	100.00	100.00
RCA23_c00770	hypothetical protein, glutathione S-transferotein	COG0625	O	GI 1	100.00	100.00
RCA23_c00780	HTH-type transcriptional regulator, LacI family	COG1609	K	GI 1	71.79	100.00
RCA23_c00790	hypothetical protein			GI 1	100.00	100.00
RCA23_c00800	hypothetical protein	COG4274	S	GI 1	100.00	100.00
RCA23_c00810	hypothetical protein, phosphoglycerate mutase-like	COG0406	G	GI 1	95.68	100.00
RCA23_c00820	hypothetical protein	COG0790	R	GI 1	100.00	100.00
RCA23_c00830	hypothetical protein, glyoxalase/bleomycin resistance protein/dihydroxybiphe	COG0346	E	GI 1	100.00	100.00
RCA23_c00840	putative phage integrase	COG4974	L	GI 1	100.00	100.00
RCA23_c00850	hypothetical protein			GI 1	0.00	67.44
RCA23_c00860	hypothetical protein			GI 1	0.00	32.85
RCA23_c00870	putative endonuclease			GI 1	0.00	0.00
RCA23_c00880	DNA integration/recombination/invertion protein	COG1961	L	GI 1	0.00	100.00
RCA23_c00890	hypothetical protein			GI 1	0.00	100.00
RCA23_c00900	hypothetical protein, peptidoglycan binding-like			GI 1	0.00	0.00
RCA23_c00910	hypothetical protein			GI 1	0.00	0.00

RCA23_c00920	putative phage integrase	COG4974	L	GI 1	0.00	50.33
RCA23_c00940	putative HTH-type transcriptional repressor, ArsR family	COG0640	K		100.00	100.00
RCA23_c00950	ATP synthase protein I				100.00	100.00
RCA23_c00960	ATP synthase subunit AtpB	COG0356	C		100.00	100.00
RCA23_c00970	ATP synthase subunit c				100.00	100.00
RCA23_c01000	pyruvate dehydrogenase complex repressor	COG2186	K		100.00	100.00
RCA23_c01010	inner membrane lipoprotein YiaD	COG2885	M		100.00	100.00
RCA23_c01020	endonuclease III	COG0177	L		100.00	100.00
RCA23_c01030	putative pfkB family carbohydrate kinase	COG0524	G		100.00	100.00
RCA23_c01040	hypothetical protein				100.00	100.00
RCA23_c01050	glycosyl transferase family 14				100.00	100.00
RCA23_c01060	hypothetical protein				100.00	100.00
RCA23_c01070	HIT-like protein	COG0537	F		100.00	100.00
RCA23_c01080	ABC transporter ATP binding protein	COG1131	V		100.00	96.42
RCA23_c01090	hypothetical protein	COG4391	S		100.00	100.00
RCA23_c01100	hypothetical protein				100.00	100.00
RCA23_c01110	DNA polymerase I	COG0749	L		100.00	100.00
RCA23_c01120	cystathionine gamma-synthase MetB	COG0626	E		100.00	100.00
RCA23_c01130	ribosomal large subunit pseudouridine synthase RluE	COG1187	J		100.00	100.00
RCA23_c01140	hypothetical protein DUF1285	COG3816	S		100.00	100.00
RCA23_c01150	ATPase, MoxR type	COG0714	R		100.00	100.00
RCA23_c01160	hypothetical protein	COG1721	R		100.00	94.56
RCA23_c01170	hypothetical protein				100.00	100.00
RCA23_c01180	hypothetical protein DUF1355	COG5426	S		100.00	100.00
RCA23_c01190	glycolate oxidase subunit GlcD	COG0277	C		100.00	80.83
RCA23_c01200	glycolate oxidase subunit GlcE	COG0277	C		100.00	100.00
RCA23_c01210	glycolate oxidase iron-sulfur subunit GlcF	COG0247	C		100.00	100.00
RCA23_c01220	hypothetical protein, trypsin	COG3591	E		100.00	100.00
RCA23_c01230	putative chitinase	COG3325	G		15.64	33.69
RCA23_c01240	small heat shock protein IbpA	COG0071	O		100.00	100.00
RCA23_c01250	succinate-semialdehyde dehydrogenase GabD	COG1012	C		100.00	100.00
RCA23_c01260	hypothetical protein	COG0657	I		100.00	100.00
RCA23_c01270	hypothetical protein	COG5617	S		100.00	100.00

RCA23_c01280	putative cyclopentanol dehydrogenase CpnA	COG1028	I	100.00	100.00
RCA23_c01290	hypothetical protein			100.00	100.00
RCA23_c01300	hypothetical protein DUF1523			100.00	100.00
RCA23_c01310	aldehyde dehydrogenase	COG1012	C	100.00	100.00
RCA23_c01320	deoxyribose-phosphate aldolase DeoC	COG0274	F	100.00	100.00
RCA23_c01330	ribulose-phosphate 3-epimerase, chromosomal	COG0036	G	100.00	100.00
RCA23_c01340	hemolysin-type calcium-binding region			100.00	100.00
RCA23_c01350	5-oxoprolinase (ATP-hydrolyzing)	COG0145	E	95.58	99.00
RCA23_c01360	aminotransferase class-III	COG0161	H	100.00	100.00
RCA23_c01370	ureidoglycolate hydrolase AllA	COG3194	F	100.00	100.00
RCA23_c01380	aldose 1-epimerase GalM	COG2017	G	100.00	100.00
RCA23_c01390	beta-galactosidase BgaB	COG1874	G	100.00	96.33
RCA23_c01400	putative gluconolactonase	COG3386	G	100.00	100.00
RCA23_c01410	2-dehydro-3-deoxy-6-phosphogalactonate aldolase DgoA	COG0800	G	100.00	100.00
RCA23_c01420	2-dehydro-3-deoxygalactonokinase DgoK	COG3734	G	100.00	100.00
RCA23_c01430	short chain dehydrogenase	COG1028	I	100.00	100.00
RCA23_c01440	alpha-galactosidase RafA	COG3345	G	100.00	100.00
RCA23_c01450	putative ABC transporter inner membrane component	COG0395	G	100.00	98.89
RCA23_c01460	putative ABC transporter inner membrane component	COG1175	G	100.00	100.00
RCA23_c01470	putative extracellular solute-binding protein	COG1653	G	42.04	70.25
RCA23_c01480	HTH-type transcriptional regulator, IclR family	COG1414	K	51.78	84.73
RCA23_c01490	sugar ABC transporter ATP-binding protein	COG3839	G	100.00	87.72
RCA23_c01500	Sulfite exporter TauE/SafE			100.00	100.00
RCA23_c01510	putative transcriptional regulator, gntR family	COG1167	K	100.00	100.00
RCA23_c01520	taurine--pyruvate aminotransferase Tpa	COG0161	H	95.52	95.92
RCA23_c01530	taurine ABC transporter, periplasmic binding protein TauA	COG4521	P	100.00	100.00
RCA23_c01540	taurine ABC transport system ATP-binding protein TauB	COG1116	P	94.55	100.00
RCA23_c01550	taurine ABC transport system permease protein TauC	COG0600	P	100.00	100.00
RCA23_c01560	dimethylglycine dehydrogenase	COG0404	E	100.00	99.21
RCA23_c01570	trimethylamine methyltransferase MttB	COG5598	H	100.00	100.00
RCA23_c01580	3-hydroxyacyl-CoA dehydrogenase FadN	COG1250	I	100.00	100.00
RCA23_c01590	hypothetical protein	COG0596	R	100.00	100.00
RCA23_c01600	O-acetylhomoserine (thiol)-lyase CysD	COG2873	E	100.00	97.02

RCA23_c01610	putative signaling protein	COG2200	T	100.00	100.00
RCA23_c01620	sulfoacetaldehyde acetyltransferase Xsc	COG0028	E	100.00	100.00
RCA23_c01630	phosphate acetyltransferase Pta	COG0280	C	100.00	100.00
RCA23_c01640	DMSO reductase chain A	COG0243	C	100.00	98.54
RCA23_c01650	alpha/beta hydrolase	COG0596	R	100.00	93.42
RCA23_c01660	DMSO reductase chain B	COG0437	C	100.00	100.00
RCA23_c01670	DMSO reductase chain C	COG3302	R	100.00	100.00
RCA23_c01680	sodium:alanine symporter	COG1115	E	100.00	100.00
RCA23_c01690	thymidine kinase Tdk	COG1435	F	100.00	100.00
RCA23_c01700	NADPH-dependent FMN reductase	COG0431	R	100.00	100.00
RCA23_c01710	carbamoyl-phosphate synthase large chain CarB	COG0458	E	73.66	100.00
RCA23_c01720	HTH-type transcriptional regulator, AsnC family	COG1522	K	44.51	100.00
RCA23_c01730	hypothetical protein			100.00	100.00
RCA23_c01740	aspartyl-tRNA synthase AspS	COG0173	J	100.00	100.00
RCA23_c01750	hypothetical protein			100.00	100.00
RCA23_c01760	putative signal transduction response regulator receiver protein	COG2197	T	100.00	64.91
RCA23_c01770	methylmalonyl-CoA epimerase	COG0346	E	100.00	100.00
RCA23_c01780	hypothetical protein DUF1467	COG5454	S	100.00	100.00
RCA23_c01790	hypothetical protein DUF540	COG2981	E	39.77	100.00
RCA23_c01800	putative nitroreductase	COG0778	C	100.00	100.00
RCA23_c01810	histone deacetylase-like amidohydrolase HdaH	COG0123	B	100.00	100.00
RCA23_c01820	hypothetical protein			100.00	100.00
RCA23_c01830	hypothetical protein, peptidase family M48	COG0501	O	100.00	100.00
RCA23_c01840	hypothetical protein			100.00	100.00
RCA23_c01850	ribosomal protein S12 methylthiotransferase RimO	COG0621	J	100.00	100.00
RCA23_c01860	hypothetical protein, transmembrane			100.00	100.00
RCA23_c01870	GcrA cell cycle regulator	COG5352	S	100.00	96.34
RCA23_c01880	ABC-2 type transport system membrane protein	COG0842	V	100.00	100.00
RCA23_c01890	acetylornithine aminotransferase ArgD	COG4992	E	100.00	100.00
RCA23_c01900	ornithine carbamoyltransferase ArgF	COG0078	E	100.00	100.00
RCA23_c01910	hypothetical protein			100.00	100.00
RCA23_c01920	6-phosphogluconate dehydrogenase GntZ	COG0362	G	100.00	100.00
RCA23_c01930	ATP-dependent RNA helicase HrpB	COG1643	L	100.00	98.78

RCA23_c01940	LAO/AO transport system ATPase	COG1703	E	100.00	100.00
RCA23_c01950	50S ribosomal protein L28	COG0227	J	100.00	100.00
RCA23_c01960	hypothetical protein			100.00	100.00
RCA23_c01970	GTP-binding protein LepA	COG0481	M	100.00	93.71
RCA23_c01980	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	100.00	100.00
RCA23_c01990	putative ring-cleaving dioxygenase	COG0346	E	100.00	100.00
RCA23_c02000	serine hydroxymethyltransferase GlyA	COG0112	E	100.00	100.00
RCA23_c02010	putative inorganic polyphosphate/ATP-NAD kinase PpnK	COG0061	G	100.00	100.00
RCA23_c02020	propionate--CoA ligase PrpE	COG0365	I	100.00	100.00
RCA23_c02030	hypothetical protein	COG1917	S	86.94	100.00
RCA23_c02040	cytidine deaminase Cdd	COG0295	F	100.00	100.00
RCA23_c02050	thymidine phosphorylase DeoA	COG0213	F	100.00	93.50
RCA23_c02060	phosphopentomutase DeoB	COG1015	G	100.00	91.69
RCA23_c02070	adenosine deaminase Add	COG1816	F	100.00	100.00
RCA23_c02080	uracil phosphoribosyltransferase Upp	COG0035	F	100.00	100.00
RCA23_c02090	hypothetical protein			100.00	100.00
RCA23_c02100	3-deoxy-D-manno-octulosonic-acid transferase WaaA	COG1519	M	100.00	100.00
RCA23_c02110	L-sorbose 1-dehydrogenase	COG2303	E	100.00	100.00
RCA23_c02120	putative N-acylneuraminate cytidylyltransferase	COG1083	M	100.00	100.00
RCA23_c02130	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase ArnB	COG0399	M	100.00	100.00
RCA23_c02140	hypothetical protein	COG3119	P	0.00	77.21
RCA23_c02150	hypothetical protein, nucleoside triphosphate hydrolases-like	COG1122	P	0.00	69.70
RCA23_c02160	S-adenosyl-L-methionine-dependent methyltransferase	COG2226	H	0.00	100.00
RCA23_c02170	hypothetical protein			100.00	99.89
RCA23_c02180	medium-chain-fatty-acid--CoA ligase AlkK	COG0318	I	100.00	100.00
RCA23_c02190	hypothetical protein DUF6 transmembrane	COG0697	G	100.00	100.00
RCA23_c02200	fatty acid oxidation complex alpha subunit FadJ	COG1250	I	100.00	100.00
RCA23_c02210	hypothetical protein			100.00	96.38
RCA23_c02220	short chain dehydrogenase	COG0183	I	100.00	100.00
RCA23_c02230	putative glutathione S-transferase	COG0625	O	100.00	100.00
RCA23_c02240	acyl-CoA dehydrogenase MmgC	COG1960	I	100.00	100.00
RCA23_c02250	putative HTH-type transcriptional regulator, MerR family	COG0789	K	100.00	100.00
RCA23_c02260	putative HTH-type transcriptional regulator, MerR family	COG0789	K	100.00	100.00

RCA23_c02270	hypothetical protein, transmembrane protein DUF2899			100.00	100.00
RCA23_c02280	hypothetical protein, thioesterase	COG2050	Q	100.00	100.00
RCA23_c02290	hypothetical protein, thioesterase	COG2050	Q	100.00	100.00
RCA23_c02300	DNA-damage-inducible protein F	COG0534	V	100.00	100.00
RCA23_c02310	dihydroorotate dehydrogenase PyrD	COG0167	F	100.00	100.00
RCA23_c02320	hypothetical protein DUF952	COG3502	S	100.00	100.00
RCA23_c02330	5'-nucleotidase SurE	COG0737	F	100.00	97.26
RCA23_c02340	hypothetical protein	COG3409	M	100.00	100.00
RCA23_c02350	glycyl-tRNA synthase alpha subunit GlyQ	COG0752	J	100.00	100.00
RCA23_c02360	hypothetical protein			100.00	100.00
RCA23_c02370	glycyl-tRNA synthase beta subunit GlyS	COG0751	J	100.00	100.00
RCA23_c02380	pyruvate, phosphate dikinase PpdK	COG0574	G	100.00	98.35
RCA23_c02390	putative cell wall hydrolase	COG3773	M	100.00	100.00
RCA23_c02400	hypothetical protein, dihydroneopterin aldolase	COG1539	H	100.00	100.00
RCA23_c02410	dihydropteroate synthase FolP	COG0294	H	100.00	100.00
RCA23_c02420	putative integral membrane protein DUF6	COG0697	G	100.00	100.00
RCA23_c02430	ketol-acid reductoisomerase IlvC	COG0059	E	100.00	100.00
RCA23_c02440	putative transcriptional regulator, asnC family	COG1522	K	100.00	100.00
RCA23_c02450	putative transcriptional regulator, asnC family	COG1522	K	100.00	100.00
RCA23_c02460	hypothetical protein	COG0075	E	94.44	100.00
RCA23_c02470	2-octaprenyl-6-methoxyphenol hydroxylase UbiH	COG0654	H	100.00	100.00
RCA23_c02480	putative pyrimidine 5-nucleotidase	COG1011	R	100.00	100.00
RCA23_c02490	putative HTH-type transcriptional regulator, GntR family	COG1802	K	100.00	100.00
RCA23_c02500	uncharacterized glycosyltransferase YdaM	COG1215	M	100.00	96.52
RCA23_c02510	carbamoyl-phosphate synthase small chain CarA	COG0505	E	100.00	100.00
RCA23_c02520	GatB/YqeY family protein	COG1610	S	100.00	100.00
RCA23_c02530	hypothetical protein	COG5488	S	100.00	100.00
RCA23_c02540	cytochrome c oxidase subunit 1	COG0843	C	100.00	100.00
RCA23_c02550	octanoyltransferase LipB	COG0321	H	100.00	100.00
RCA23_c02560	hypothetical protein, LytTr transcriptional regulator	COG3279	K	100.00	99.61
RCA23_c02570	membrane protein-like	COG5395	S	100.00	100.00
RCA23_c02590	arylsulfatase	COG3119	P	100.00	100.00
RCA23_c02600	NADPH dehydrogenas	COG1902	C	100.00	100.00

RCA23_c02610	L-idonate 5-dehydrogenase IdnD	COG1063	E	100.00	100.00
RCA23_c02620	gluconate 5-dehydrogenase Gno	COG1028	I	100.00	100.00
RCA23_c02630	uncharacterized oxidoreductase YgbJ	COG2084	I	100.00	100.00
RCA23_c02640	hypothetical protein, xylose isomerase-like	COG1082	G	100.00	100.00
RCA23_c02650	glyoxylate reductase GyaR	COG1052	C	100.00	100.00
RCA23_c02660	hypothetical protein			100.00	100.00
RCA23_c02670	hypothetical protein, AzlC-like	COG1296	E	100.00	27.02
RCA23_c02680	cbbT/tktB: transketolase	COG0021	G	43.25	14.48
RCA23_c02690	hypothetical protein	COG4091	E	0.00	0.00
RCA23_c02700	transketolase, alpha subunit	COG3959	G	43.65	0.00
RCA23_c02710	transketolase, beta-subunit	COG3958	G	100.00	22.22
RCA23_c02720	putative 3-hydroxyisobutyrate dehydrogenase	COG2084	I	49.38	0.00
RCA23_c02730	putative 3-hydroxyisobutyrate dehydrogenase	COG2084	I	100.00	22.31
RCA23_c02740	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	100.00	0.00
RCA23_c02750	HTH-type transcriptional regulator, LysR family	COG0583	K	100.00	0.10
RCA23_c02760	putative HTH-type transcriptional regulator, GntR family	COG1802	K	100.00	15.72
RCA23_c02770	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	14.10	0.00
RCA23_c02780	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	100.00	44.33
RCA23_c02800	hypothetical protein	COG0240	C	100.00	0.00
RCA23_c02810	hypothetical protein DUF1537	COG3395	S	46.88	0.00
RCA23_c02820	putative ribulose bisphosphate carboxylase large chain	COG1850	G	72.70	0.00
RCA23_c02830	hypothetical protein, NAD dependent epimerase / dehydratase family	COG0451	M	100.00	0.00
RCA23_c02840	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I	100.00	26.84
RCA23_c02850	hypothetical protein			7.71	0.00
RCA23_c02860	altronate hydrolase UxaA	COG2721	G	31.20	94.15
RCA23_c02870	putative oxidoreductase	COG0673	R	100.00	100.00
RCA23_c02880	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I	100.00	98.20
RCA23_c02890	S-adenosylmethionine uptake transporter Sam	COG0697	G	100.00	100.00
RCA23_c02900	2-dehydro-3-deoxygluconokinase KdgK	COG0524	G	100.00	100.00
RCA23_c02910	D-mannonate oxidoreductase UxuB	COG0246	G	100.00	100.00
RCA23_c02920	uronate isomerase UxaC	COG1904	G	100.00	100.00
RCA23_c02930	putative oxidoreductase	COG0673	R	100.00	100.00
RCA23_c02940	putative oxidoreductase	COG0673	R	100.00	100.00

RCA23_c02950	putative oxidoreductase	COG0673	R	100.00	100.00
RCA23_c02960	mannonate dehydratase UxuA	COG1312	G	100.00	100.00
RCA23_c02970	long-chain-fatty-acid--CoA ligase	COG0318	I	100.00	100.00
RCA23_c02980	D-beta-hydroxybutyrate dehydrogenase BdhA	COG1028	I	100.00	100.00
RCA23_c02990	copper-transporting P-type ATPase ActP	COG2217	P	100.00	100.00
RCA23_c03000	HTH-type transcriptional regulator (copper efflux regulator)	COG0789	K	100.00	100.00
RCA23_c03010	hypothetical protein	COG3937	S	100.00	100.00
RCA23_c03020	hypothetical protein			100.00	100.00
RCA23_c03030	isocitrate dehydrogenase Icd	COG2838	C	91.78	100.00
RCA23_c03040	integral membrane protein DUF6	COG0697	G	100.00	100.00
RCA23_c03050	flavocytochrome c cytochrome subunit SoxE	COG3474	C	100.00	100.00
RCA23_c03060	sulfide dehydrogenase [flavocytochrome c] flavoprotein chain SoxF	COG0446	R	100.00	100.00
RCA23_c03070	hypothetical protein, OsmC-like	COG1764	O	100.00	100.00
RCA23_c03080	putative dimethyl sulfoniopropionate demethylase DmdA	COG0404	E	100.00	99.83
RCA23_c03090	transcriptional regulator, AsnC family	COG1522	K	100.00	100.00
RCA23_c03100	glutathione S-transferase	COG0625	O	0.00	0.00
RCA23_c03120	hypothetical protein, ribonuclease, E/G family	COG1530	J	87.39	100.00
RCA23_c03130	Maf-like protein	COG0424	D	100.00	100.00
RCA23_c03140	translation initiation factor IF-1	COG0361	J	100.00	100.00
RCA23_c03150	hypothetical protein, low molecular weight phosphotyrosine protein phospha	COG0394	T	76.44	100.00
RCA23_c03160	hypothetical protein UPF0262	COG5328	S	32.08	100.00
RCA23_c03170	histidinol dehydrogenase HisD	COG0141	E	100.00	100.00
RCA23_c03180	hypothetical protein			100.00	100.00
RCA23_c03190	UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA	COG0766	M	100.00	100.00
RCA23_c03210	PAS/PAC sensor hybrid histidine kinase	COG0642	T	100.00	95.59
RCA23_c03220	2OG-Fe(II) oxygenase	COG3491	R	99.62	85.93
RCA23_c03230	putative lysine exporter protein	COG1280	E	77.52	67.91
RCA23_c03240	putative carbon monoxide dehydrogenase subunit G	COG3427	S	100.00	100.00
RCA23_c03250	hypothetical protein, XdhC and CoxI family	COG1975	O	100.00	95.16
RCA23_c03260	putative MFS-type transporter	COG2814	G	93.00	100.00
RCA23_c03270	AFG1-like ATPase	COG1485	R	73.77	89.30
RCA23_c03280	bifunctional protein FolC	COG0285	H	100.00	100.00
RCA23_c03290	acetyl-coenzyme A carboxylase carboxyl transferase beta subunit AccD	COG0777	I	100.00	100.00

RCA23_c03300	hypothetical protein, CAAX amino terminal protease-like	COG1266	R	100.00	100.00
RCA23_c03310	dihydroxy-acid dehydratase IlvD	COG0129	E	100.00	96.08
RCA23_c03320	hypothetical protein			100.00	100.00
RCA23_c03330	hypothetical protein			100.00	100.00
RCA23_c03340	hypothetical protein			100.00	100.00
RCA23_c03350	hypothetical protein, OmpA family	COG2885	M	100.00	100.00
RCA23_c03360	hypothetical protein, peroxidase-like protein	COG2128	S	100.00	100.00
RCA23_c03370	hypothetical protein, acetyltransferase-like	COG0456	R	100.00	100.00
RCA23_c03380	hypothetical protein, probably molybdopterin binding	COG1058	R	100.00	100.00
RCA23_c03390	sugar fermentation stimulation protein SfsA	COG1489	R	100.00	100.00
RCA23_c03400	methionine aminopeptidase Map	COG0024	J	100.00	100.00
RCA23_c03410	ATP-dependent RNA helicase RhlE	COG0513	L	100.00	100.00
RCA23_c03420	putative ribosomal RNA small subunit methyltransferase D	COG0742	L	100.00	100.00
RCA23_c03430	rhodocoxin reductase ThcD	COG0446	R	100.00	100.00
RCA23_c03440	peroxiredoxin	COG0678	O	100.00	100.00
RCA23_c03450	pterin-4-alpha-carbinolamine dehydratase	COG2154	H	100.00	100.00
RCA23_c03460	hypothetical protein DUF482	COG3146	S	100.00	97.64
RCA23_c03470	putative glycerophosphoryl diester phosphodiesterase	COG0584	C	100.00	100.00
RCA23_c03480	putative endoribonuclease L-PSP	COG0251	J	100.00	100.00
RCA23_c03490	type I secretion system protein, HlyD family	COG1566	V	100.00	87.35
RCA23_c03500	type I secretion system ATP-binding component	COG4618	R	100.00	100.00
RCA23_c03510	putative type I secretion system protein, transmembrane domain	COG4618	R	100.00	100.00
RCA23_c03520	VacJ like lipoprotein	COG2853	M	100.00	100.00
RCA23_c03530	putative toluene tolerance protein	COG2854	Q	100.00	98.18
RCA23_c03540	penicillin-binding protein 1B	COG0744	M	100.00	97.57
RCA23_c03550	aromatic-amino-acid aminotransferase TyrB	COG1448	E	100.00	100.00
RCA23_c03560	3-mercaptopyruvate sulfurtransferase SseA	COG2897	P	100.00	100.00
RCA23_c03570	SsrA-binding protein SmpB	COG0691	O	100.00	100.00
RCA23_c03580	dihydrodipicolinate synthase DapA	COG0329	E	100.00	100.00
RCA23_c03590	soluble lytic murein transglycosylase Slt	COG0741	M	100.00	100.00
RCA23_c03600	hypothetical protein DUF6 transmembrane	COG0697	G	100.00	100.00
RCA23_c03610	hypothetical protein DUF752	COG4121	S	100.00	97.44
RCA23_c03620	putative FAD-dependent oxidoreductase	COG0665	E	100.00	100.00

RCA23_c03630	hypothetical protein, glyoxalase/dioxygenase superfamily	COG0346	E	100.00	100.00
RCA23_c03640	hypothetical protein			100.00	100.00
RCA23_c03650	hypothetical protein			100.00	100.00
RCA23_c03660	cob(I)yrinic acid a,c-diamide adenosyltransferase CobO	COG2109	H	100.00	100.00
RCA23_c03670	hypothetical protein			100.00	100.00
RCA23_c03680	oligopeptide/dipeptide ABC transporter, ATP-binding protein	COG0444	E	100.00	100.00
RCA23_c03690	oligopeptide/dipeptide ABC transporter, ATP-binding protein	COG0444	E	100.00	87.27
RCA23_c03700	oligopeptide/dipeptide ABC transporter, permease protein	COG1173	E	100.00	100.00
RCA23_c03710	oligopeptide/dipeptide ABC transporter, permease protein	COG0601	E	100.00	100.00
RCA23_c03720	oligopeptide/dipeptide ABC transporter, periplasmic substrate-binding protei	COG0747	E	100.00	90.14
RCA23_c03730	HTH-type transcriptional regulator, LysR family	COG0583	K	100.00	99.78
RCA23_c03740	putative amidohydrolase 3	COG1574	R	100.00	84.16
RCA23_c03750	cobalamin biosynthesis CobW-like	COG0523	R	100.00	100.00
RCA23_c03760	hypothetical protein, restriction endonuclease type IV-like	COG4127	S	100.00	93.58
RCA23_c03770	glycine betaine transport ATP-binding protein OpuAA	COG4175	E	100.00	97.85
RCA23_c03780	glycine betaine transport system permease protein OpuAB	COG4176	E	95.35	100.00
RCA23_c03790	glycine betaine transporter substrate-binding protein OpuAC	COG2113	E	100.00	100.00
RCA23_c03800	fatty acid desaturase	COG3239	I	100.00	100.00
RCA23_c03810	CoA-transferase family III protein involved in DMSP degradation	COG1804	C	100.00	100.00
RCA23_c03820	glyceraldehyde-3-phosphate dehydrogenase Gap	COG0057	G	100.00	100.00
RCA23_c03830	ATP-dependent Clp protease proteolytic subunit ClpP	COG0740	O	91.95	100.00
RCA23_c03840	ATP-dependent Clp protease ATP-binding subunit ClpX	COG1219	O	100.00	99.53
RCA23_c03850	putative NADH ubiquinone oxidoreductase subunit NDUFA12	COG3761	C	100.00	100.00
RCA23_c03860	ABC-type transport system involved in resistance to organic solvents, periplas	COG1463	Q	100.00	100.00
RCA23_c03870	Uncharacterized protein conserved in bacteria (DUF2155)	COG4765	S	100.00	100.00
RCA23_c03880	leucyl/phenylalanyl-tRNA--protein transferase Aat	COG2360	O	100.00	100.00
RCA23_c03890	biotin carboxylase AccC	COG4770	I	100.00	100.00
RCA23_c03900	acetyl-coenzyme A synthase AcsA	COG0365	I	100.00	100.00
RCA23_c03910	high-affinity branched-chain amino acid transport ATP-binding protein LivF	COG0410	E	100.00	100.00
RCA23_c03920	high-affinity branched-chain amino acid transport ATP-binding protein BraF	COG0411	E	14.62	100.00
RCA23_c03930	putative branched-chain amino acid transport system permease protein	COG4177	E	100.00	92.60
RCA23_c03940	putative branched-chain amino acid transport system permease protein	COG0559	E	100.00	100.00
RCA23_c03950	hypothetical protein	COG0683	E	100.00	100.00

RCA23_c03960	hypothetical protein, DNA binding helix-turn helix proteins	COG1396	K		100.00	100.00
RCA23_c03970	putative response regulator receiver protein, CheY like	COG0745	T		100.00	100.00
RCA23_c03980	hypothetical protein				100.00	100.00
RCA23_c03990	sensor protein kinase WalK	COG0591	E		100.00	100.00
RCA23_c04000	hypothetical protein DUF442	COG3453	S		100.00	100.00
RCA23_c04010	hypothetical protein				100.00	100.00
RCA23_c04020	hypothetical protein	COG3750	S		100.00	100.00
RCA23_c04030	hypothetical protein				100.00	100.00
RCA23_c04040	putative Fe(3+)-transport system protein SfuB	COG1178	P		100.00	100.00
RCA23_c04060	integrase	COG0582	L	GI 2	33.16	20.26
RCA23_c04070	hypothetical protein	COG3945	S	GI 2	0.00	0.00
RCA23_c04080	hypothetical protein			GI 2	0.00	22.80
RCA23_c04090	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase subunit	COG0457	R	GI 2	0.00	15.98
RCA23_c04100	esterase, SGNH hydrolase-type	COG2755	E	GI 2	0.00	0.00
RCA23_c04110	hypothetical protein			GI 2	0.00	97.49
RCA23_c04120	hypothetical protein, tetratricopeptide repeat	COG0790	R	GI 2	0.00	47.47
RCA23_c04130	hypothetical protein			GI 2	100.00	89.46
RCA23_c04140	hypothetical protein			GI 2	100.00	100.00
RCA23_c04150	hypothetical protein			GI 2	100.00	100.00
RCA23_c04160	hypothetical protein, RmlC-like cupin family	COG3450	R	GI 2	0.00	39.42
RCA23_c04170	hypothetical protein			GI 2	0.00	71.47
RCA23_c04180	hypothetical protein, DUF3127			GI 2	0.00	100.00
RCA23_c04190	putative nucleoside triphosphate hydrolase, ATPase domain	COG1066	O	GI 2	0.00	29.78
RCA23_c04200	zinc-dependent metalloprotease	COG2931	Q	GI 2	65.16	41.30
RCA23_c04210	HTH-type transcriptional regulator, AsnC family	COG1522	K	GI 2	100.00	100.00
RCA23_c04220	integrase	COG2801	L	GI 2	0.00	0.00
RCA23_c04230	putative ion channel			GI 2	96.98	100.00
RCA23_c04240	integrase	COG4974	L	GI 2	100.00	72.51
RCA23_c04250	Gcn5-like N-acetyltransferase	COG1670	J	GI 2	0.00	0.00
RCA23_c04260	integrase	COG0582	L	GI 2	36.10	94.11
RCA23_c04280	hypothetical protein, NAD dependent epimerase / dehydratase family	COG0702	M		100.00	100.00
RCA23_c04290	undecaprenyl-diphosphatase UppP	COG1968	V		100.00	100.00
RCA23_c04300	glutamate synthase [NADPH] small chain GltD	COG0493	E		100.00	100.00

RCA23_c04310	glutamate synthase [NADPH] large chain GltB	COG0069	E	100.00	99.98
RCA23_c04320	monofunctional biosynthetic peptidoglycan transglycosylase MtgA	COG0744	M	100.00	97.45
RCA23_c04330	putative glutathione S-transferase	COG0625	O	100.00	100.00
RCA23_c04340	putative electron transport protein yjeS	COG1600	C	100.00	100.00
RCA23_c04360	hypothetical protein	COG5266	P	100.00	100.00
RCA23_c04350	hypothetical protein			100.00	100.00
RCA23_c04370	branched-chain-amino-acid aminotransferase IlvE	COG0115	E	100.00	100.00
RCA23_c04380	HTH-type transcriptional regulator PetP	COG1846	K	100.00	100.00
RCA23_c04390	protein PetR	COG0745	T	100.00	100.00
RCA23_c04400	putative deacytelase, histone deacetylase superfamily protein-like	COG0123	B	100.00	100.00
RCA23_c04410	exodeoxyribonuclease 7 small subunit XseB	COG1722	L	100.00	100.00
RCA23_c04420	geranyltranstransferase IspA	COG0142	H	91.64	100.00
RCA23_c04430	1-deoxy-D-xylulose-5-phosphate synthase Dxs	COG1154	H	100.00	97.90
RCA23_c04440	hypothetical protein, NAD dependent epimerase/dehydratase	COG0451	M	100.00	100.00
RCA23_c04450	hypothetical protein			100.00	100.00
RCA23_c04460	hypothetical protein			100.00	100.00
RCA23_c04470	carnitinyl-CoA dehydratase CaiD	COG1024	I	100.00	100.00
RCA23_c04480	hypothetical protein, CoA-binding	COG1042	C	100.00	98.47
RCA23_c04490	putative acyl-CoA dehydrogenase YngJ	COG1960	I	100.00	100.00
RCA23_c04500	transcriptional regulator, AraC family	COG4977	K	100.00	100.00
RCA23_c04510	class II aldolase	COG0235	G	100.00	100.00
RCA23_c04520	arsenate reductase ArsC	COG1393	P	100.00	100.00
RCA23_c04530	adenine deaminase Ade	COG1001	F	100.00	100.00
RCA23_c04540	AMP nucleosidase Amn	COG0775	F	100.00	92.89
RCA23_c04550	DNA-binding protein HU	COG0776	L	100.00	100.00
RCA23_c04560	inner membrane protein DUF6	COG0697	G	100.00	100.00
RCA23_c04570	hypothetical protein, cytochrome C biogenesis protein	COG0785	O	100.00	100.00
RCA23_c04580	hypothetical protein, thioredoxin	COG0526	O	100.00	100.00
RCA23_c04590	hypothetical protein	COG3222	S	100.00	100.00
RCA23_c04600	succinyl-diaminopimelate desuccinylase DapE	COG0624	E	100.00	98.32
RCA23_c04610	hypothetical protein			100.00	100.00
RCA23_c04620	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase DapD	COG2171	E	100.00	100.00
RCA23_c04630	L-threonine ammonia-lyase	COG1171	E	100.00	100.00

RCA23_c04640	ribosomal RNA large subunit methyltransferase N	COG0820	R	100.00	100.00
RCA23_c04650	hypothetical protein			100.00	100.00
RCA23_c04660	L-asparaginase II	COG4448	E	100.00	100.00
RCA23_c04670	phosphoserine phosphatase SerB	COG0560	E	100.00	100.00
RCA23_c04680	hypothetical protein			100.00	100.00
RCA23_c04690	phosphoserine aminotransferase SerC	COG1932	H	100.00	100.00
RCA23_c04700	D-3-phosphoglycerate dehydrogenase SerA	COG0111	H	100.00	100.00
RCA23_c04710	metallophosphoesterase			100.00	100.00
RCA23_c04720	RNA pyrophosphohydrolase RppH	COG0494	L	100.00	100.00
RCA23_c04730	carboxy-terminal-processing protease CtpA	COG0793	M	100.00	100.00
RCA23_c04740	2,3-bisphosphoglycerate-independent phosphoglycerate mutase GpmI	COG0696	G	100.00	100.00
RCA23_c04750	putative protein ImuB			100.00	100.00
RCA23_c04760	hypothetical protein			100.00	100.00
RCA23_c04770	hypothetical protein, NlpC/P60	COG0791	M	100.00	100.00
RCA23_c04780	putative cytosol aminopeptidase PepA	COG0260	E	100.00	100.00
RCA23_c04790	hypothetical protein			100.00	100.00
RCA23_c04800	carbonic anhydrase CynT	COG0288	P	100.00	100.00
RCA23_c04810	aspartate-semialdehyde dehydrogenase Asd	COG0136	E	100.00	100.00
RCA23_c04820	MFS-type transporter	COG2223	P	100.00	93.28
RCA23_c04830	short chain dehydrogenase	COG4221	R	100.00	100.00
RCA23_c04840	FAD dependent oxidoreductase	COG0665	E	100.00	100.00
RCA23_c04850	trimethylamine methyltransferase MttB	COG5598	H	100.00	100.00
RCA23_c04860	aldehyde dehydrogenase	COG1012	C	100.00	100.00
RCA23_c04870	dihydrodipicolinate synthase DapA	COG0329	E	100.00	100.00
RCA23_c04880	transcriptional regulator, GntR family	COG1802	K	100.00	100.00
RCA23_c04890	hypothetical protein			100.00	100.00
RCA23_c04900	isopropylmalate dehydrogenase LeuB	COG0473	C	100.00	100.00
RCA23_c04910	hypothetical protein			100.00	100.00
RCA23_c04920	3-isopropylmalate dehydratase small subunit LeuD	COG0066	E	100.00	100.00
RCA23_c04930	3-isopropylmalate dehydratase large subunit LeuC	COG0065	E	100.00	99.50
RCA23_c04940	hypothetical protein, DUF2975			100.00	92.13
RCA23_c04950	hypothetical protein DUF143	COG0799	S	100.00	100.00
RCA23_c04960	ribosomal RNA large subunit methyltransferase H	COG1576	S	100.00	100.00

RCA23_c04970	alcohol dehydrogenase class-3 AdhI	COG1062	C	100.00	100.00
RCA23_c04980	putative membrane transport protein	COG0679	R	100.00	100.00
RCA23_c04990	S-formylglutathione hydrolase YeiG	COG0627	R	100.00	100.00
RCA23_c05000	soluble pyridine nucleotide transhydrogenase	COG1249	C	100.00	100.00
RCA23_c05010	hypothetical protein DUF188	COG1671	S	100.00	100.00
RCA23_c05020	putative integral membrane protein	COG0697	G	100.00	100.00
RCA23_c05030	putative HAD-superfamily hydrolase	COG1011	R	100.00	100.00
RCA23_c05040	putative ornithine cyclodeaminase	COG2423	E	100.00	97.47
RCA23_c05050	aerobic cobaltochelatase subunit CobN	COG1429	H	100.00	100.00
RCA23_c05060	hypothetical protein, acetyltransferase-like	COG0456	R	100.00	100.00
RCA23_c05070	protein CobW	COG0523	R	100.00	91.48
RCA23_c05080	hypothetical protein DUF1636	COG5469	S	100.00	100.00
RCA23_c05090	possible cobalt transporter, subunit CbtA	COG5446	S	100.00	100.00
RCA23_c05100	Cytochrome c peroxidase	COG1858	P	100.00	100.00
RCA23_c05110	hypothetical protein	COG4188	R	100.00	87.50
RCA23_c05120	hypothetical protein			42.94	100.00
RCA23_c05130	xylose repressor XylR	COG1940	K	90.90	100.00
RCA23_c05140	D-xylose-binding periplasmic protein XylF	COG4213	G	100.00	100.00
RCA23_c05150	xylose transport system permease protein XylH	COG4214	G	100.00	100.00
RCA23_c05160	xylose ABC transporter, ATP-binding protein XylG	COG1129	G	100.00	100.00
RCA23_c05170	xylulose kinase XylB	COG1070	G	100.00	100.00
RCA23_c05180	xylose isomerase XylA	COG2115	G	100.00	95.85
RCA23_c05190	long-chain-fatty-acid--CoA ligase LcfB	COG0318	I	100.00	98.16
RCA23_c05200	malonyl-CoA decarboxylase			100.00	98.72
RCA23_c05210	acyl-CoA dehydrogenase	COG1960	I	100.00	98.98
RCA23_c05220	hypothetical protein DUF81			100.00	99.63
RCA23_c05230	phosphoenolpyruvate carboxykinase PckA	COG1866	C	100.00	98.71
RCA23_c05240	two component signal transduction response regulator receiver protein ChvI	COG0745	T	100.00	96.15
RCA23_c05250	two component signal transduction histidine kinase ChvG	COG0642	T	100.00	100.00
RCA23_c05260	hypothetical protein, HPr serine kinase	COG1493	T	100.00	76.41
RCA23_c05270	putative P-loop containing ATPase	COG1660	R	100.00	100.00
RCA23_c05280	hypothetical protein, PTS system mannose-specific EIIA component	COG2893	G	100.00	100.00
RCA23_c05290	phosphocarrier protein NPr	COG1925	G	100.00	100.00

RCA23_c05300	electron transfer flavoprotein alpha subunit EtfA	COG2025	C	100.00	93.66
RCA23_c05310	electron transfer flavoprotein beta subunit EtfB	COG2086	C	100.00	100.00
RCA23_c05320	cob(I)yrinic acid a,c-diamide adenosyltransferase CobO	COG2096	S	100.00	100.00
RCA23_c05330	putative short chain dehydrogenase	COG4221	R	100.00	100.00
RCA23_c05340	DNA topoisomerase 4 subunit A	COG0188	L	100.00	100.00
RCA23_c05350	hypothetical protein DUF898	COG4269	S	54.73	98.47
RCA23_c05360	peptidase M48 Ste24p	COG4783	R	96.95	93.73
RCA23_c05370	hypothetical protein			100.00	100.00
RCA23_c05380	elongation factor Tu (EF-Tu)	COG0050	J	100.00	34.35
RCA23_c05400	hypothetical protein, DUF560			100.00	100.00
RCA23_c05410	hippurate hydrolase HipO	COG1473	R	100.00	98.89
RCA23_c05420	glutathione import ATP-binding protein GsiA	COG1123	R	100.00	90.41
RCA23_c05430	oligopeptide-binding protein AppA	COG0747	E	100.00	100.00
RCA23_c05440	oligopeptide transport system permease protein AppB	COG0601	E	100.00	100.00
RCA23_c05450	oligopeptide transport system permease protein AppC	COG1173	E	100.00	100.00
RCA23_c05460	ABC transporter ATP-binding protein	COG1131	V	100.00	100.00
RCA23_c05470	inner membrane transport permease	COG0842	V	100.00	95.54
RCA23_c05480	hypothetical protein, peptidase family S49	COG0616	O	100.00	99.75
RCA23_c05490	putative sodium/calcium exchanger protein	COG0530	P	100.00	100.00
RCA23_c05500	putative short cprotein	COG1028	I	100.00	100.00
RCA23_c05510	UvrABC system protein C	COG0322	L	100.00	100.00
RCA23_c05520	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	COG0558	I	100.00	100.00
RCA23_c05530	molybdopterin-converting factor subunit MoaD	COG1977	H	100.00	100.00
RCA23_c05540	molybdopterin synthase catalytic subunit MoaE	COG0314	H	100.00	100.00
RCA23_c05550	hypothetical protein			100.00	89.09
RCA23_c05560	hypothetical protein, OmpA	COG2885	M	100.00	100.00
RCA23_c05570	UbiA prenyltransferase	COG0382	H	100.00	100.00
RCA23_c05580	RNA methyltransferase	COG1385	S	100.00	100.00
RCA23_c05590	hypothetical protein			100.00	100.00
RCA23_c05600	glutamate--cysteine ligase	COG3572	H	100.00	100.00
RCA23_c05610	glycerol-3-phosphate acyltransferase PlsY	COG0344	S	100.00	100.00
RCA23_c05620	dihydroorotase PyrC	COG0044	F	100.00	95.87
RCA23_c05630	aspartate carbamoyltransferase PyrB	COG0540	F	100.00	100.00

RCA23_c05640	uracil DNA glycosylase family protein	COG1573	L	100.00	100.00
RCA23_c05650	molybdenum cofactor biosynthesis protein MoaB	COG0521	H	100.00	100.00
RCA23_c05660	putative efflux transporter, RND family, membrane fusion protein	COG1566	V	100.00	100.00
RCA23_c05670	transporter, AcrB/AcrD/AcrF family	COG0841	V	100.00	98.97
RCA23_c05680	hypothetical protein	COG4233	O	100.00	100.00
RCA23_c05690	hypothetical protein DUF179	COG1678	K	100.00	100.00
RCA23_c05700	acyl-CoA dehydrogenase	COG1960	I	100.00	98.18
RCA23_c05710	putative metallo-beta-lactamase family protein	COG0491	R	100.00	100.00
RCA23_c05720	hypothetical protein			100.00	100.00
RCA23_c05730	putative branched-chain amino acid transport protein	COG4392	S	100.00	100.00
RCA23_c05740	protein AzlC	COG1296	E	100.00	85.33
RCA23_c05750	formate dehydrogenase accessory protein FdhD	COG1526	C	100.00	100.00
RCA23_c05760	molybdopterin-guanine dinucleotide biosynthesis protein MobA	COG0746	H	100.00	100.00
RCA23_c05770	molybdopterin-guanine dinucleotide biosynthesis protein MobB	COG1763	H	100.00	97.79
RCA23_c05780	molybdopterin biosynthesis protein MoeA	COG0303	H	54.18	100.00
RCA23_c05790	transcription elongation factor GreA	COG0782	K	100.00	100.00
RCA23_c05800	electron transfer flavoprotein-ubiquinone oxidoreductase	COG0644	C	100.00	100.00
RCA23_c05810	tetratricopeptide repeat-containing protein	COG0457	R	100.00	100.00
RCA23_c05820	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase IspE	COG1947	I	100.00	100.00
RCA23_c05830	octaprenyl-diphosphate synthase IspB	COG0142	H	100.00	99.80
RCA23_c05840	hypothetical protein, methyltransferase	COG4123	R	100.00	100.00
RCA23_c05850	acetoacetyl-CoA reductase PhaB	COG1028	I	100.00	100.00
RCA23_c05860	acetyl-CoA acetyltransferase PhaA	COG0183	I	100.00	100.00
RCA23_c05870	signaling protein	COG2200	T	100.00	100.00
RCA23_c05880	DNA-3-methyladenine glycosylase 1	COG2818	L	100.00	100.00
RCA23_c05890	thiol:disulfide interchange protein TlpA	COG0526	O	100.00	100.00
RCA23_c05900	argininosuccinate lyase ArgH	COG0165	E	100.00	100.00
RCA23_c05910	hypothetical protein			100.00	100.00
RCA23_c05920	diaminopimelate decarboxylase LysA	COG0019	E	100.00	100.00
RCA23_c05930	hypothetical protein	COG1196	D	86.19	99.92
RCA23_c05940	putative acyltransferase	COG0204	I	100.00	100.00
RCA23_c05950	glyoxalase/bleomycin resistance protein	COG2764	S	100.00	100.00
RCA23_c05960	hypothetical protein, pyridoxamine 5'-phosphate oxidase	COG3576	R	100.00	100.00

RCA23_c05970	acetyl-coenzyme A carboxylase carboxyl transferase alpha subunit AccA	COG0825	I	100.00	100.00
RCA23_c05980	malyl-CoA ligase	COG2301	G	100.00	92.08
RCA23_c05990	hypothetical protein DUF1611	COG3367	S	100.00	100.00
RCA23_c06000	L-Ala-D/L-Glu epimerase YcjG	COG4948	M	100.00	100.00
RCA23_c06010	D-alanine aminotransferase Dat	COG0115	E	100.00	100.00
RCA23_c06020	hypothetical, OmpA-like			93.16	100.00
RCA23_c06030	hypothetical protein	COG3743	S	100.00	100.00
RCA23_c06040	hypothetical protein DUF1244	COG3492	S	100.00	98.35
RCA23_c06050	N-formylglutamate amidohydrolase	COG3931	E	100.00	100.00
RCA23_c06060	pyruvate kinase PykF	COG0469	G	100.00	100.00
RCA23_c06070	hypothetical protein			100.00	100.00
RCA23_c06080	50S ribosomal protein L35	COG0291	J	100.00	100.00
RCA23_c06090	50S ribosomal protein L20	COG0292	J	100.00	100.00
RCA23_c06100	putative subtilase family protein	COG1404	O	74.74	100.00
RCA23_c06110	hypothetical protein			100.00	100.00
RCA23_c06120	hypothetical protein, lipid A biosynthesis acyltransferase	COG1560	M	100.00	94.50
RCA23_c06130	phenylalanyl-tRNA synthase alpha chain PheS	COG0016	J	100.00	91.34
RCA23_c06140	glutamine amidotransferase class-I	COG0518	F	100.00	100.00
RCA23_c06150	phenylalanyl-tRNA synthase beta chain PheT	COG0072	J	100.00	100.00
RCA23_c06160	putative HTH-type transcriptional regulator	COG1522	K	100.00	100.00
RCA23_c06170	ribsomal protein S21	COG0828	J	100.00	100.00
RCA23_c06180	putative ubiquinone biosynthesis protein COQ9	COG5590	S	100.00	100.00
RCA23_c06190	putative quinone oxidoreductase	COG0604	C	100.00	100.00
RCA23_c06200	hypothetical protein DUF1013	COG3820	S	100.00	93.10
RCA23_c06210	recombination protein RecR	COG0353	L	100.00	100.00
RCA23_c06220	hypothetical protein	COG0718	S	100.00	100.00
RCA23_c06230	DNA polymerase III subunit tau	COG2812	L	100.00	98.44
RCA23_c06240	NADH pyrophosphatase Nudc	COG2816	L	100.00	100.00
RCA23_c06250	hypothetical protein	COG3832	S	100.00	100.00
RCA23_c06260	prephenate dehydratase PheA	COG0077	E	100.00	100.00
RCA23_c06270	cytochrome c-552	COG3474	C	100.00	100.00
RCA23_c06280	ABC transporter extracellular solute-binding protein	COG4166	E	100.00	100.00
RCA23_c06290	ABC transporter permease protein	COG4174	R	100.00	100.00

RCA23_c06300	ABC transporter permease protein	COG4239	R		100.00	100.00
RCA23_c06310	putative oligopeptide ABC transporter ATP-binding protein	COG4172	R		100.00	98.99
RCA23_c06320	fumarylacetoacetate hydrolase family protein	COG0179	Q		100.00	98.68
RCA23_c06330	D-alanyl-D-alanine carboxypeptidase DacF	COG1686	M		100.00	100.00
RCA23_c06340	haloacid dehalogenase domain protein hydrolase	COG1011	R		100.00	100.00
RCA23_c06350	ATP-dependent Clp protease adapter protein ClpS	COG2127	S		100.00	100.00
RCA23_c06360	putative methyltransferase	COG2813	J		100.00	100.00
RCA23_c06370	putative short chain dehydrogenase	COG1028	I		100.00	99.50
RCA23_c06380	coproporphyrinogen 3 oxidase, aerobic	COG0408	H		100.00	100.00
RCA23_c06390	oxidoreductase, FAD-binding protein	COG4097	P		100.00	93.60
RCA23_c06400	D-lactate dehydrogenase	COG0277	C		100.00	100.00
RCA23_c06420	integrase			GI 3	98.18	62.52
RCA23_c06430	mandelate racemase	COG4948	M	GI 3	0.00	0.00
RCA23_c06440	fumarylacetoacetate hydrolase family protein	COG0179	Q	GI 3	0.00	0.00
RCA23_c06450	short-chain dehydrogenase/reductase	COG1028	I	GI 3	0.00	0.00
RCA23_c06460	amidohydrolase	COG3618	R	GI 3	0.00	0.00
RCA23_c06470	aldo/keto reductase	COG0667	C	GI 3	0.00	0.00
RCA23_c06480	ABC transporter, permease protein	COG0600	P	GI 3	0.00	0.00
RCA23_c06490	ABC transporter, permease protein	COG0600	P	GI 3	0.00	0.00
RCA23_c06500	hypothetical protein			GI 3	0.00	0.00
RCA23_c06510	sulfonate/nitrate ABC transporter, ATPase	COG1116	P	GI 3	0.00	0.00
RCA23_c06520	ABC transporter, periplasmic substrate-binding protein	COG0715	P	GI 3	0.00	0.00
RCA23_c06530	arylsulfatase	COG3119	P	GI 3	51.23	0.00
RCA23_c06540	transcriptional regulator, GntR family	COG1802	K	GI 3	100.00	0.00
RCA23_c06550	hypothetical protein	COG4974	L	GI 3	1.94	0.00
RCA23_c06560	hypothetical protein	COG1618	F	GI 3	100.00	0.00
RCA23_c06570	hypothetical protein			GI 3	100.00	99.63
RCA23_c06580	hypothetical protein			GI 3	100.00	56.03
RCA23_c06590	hypothetical protein			GI 3	100.00	89.19
RCA23_c06600	hypothetical protein			GI 3	94.99	100.00
RCA23_c06610	hypothetical protein			GI 3	100.00	100.00
RCA23_c06620	hypothetical protein			GI 3	100.00	100.00
RCA23_c06630	hypothetical protein	COG3000	I	GI 3	0.00	72.84

RCA23_c06640	transcriptional regulator, AsnC family	COG1522	K	GI 3	100.00	100.00
RCA23_c06650	aspartate aminotransferase AspC	COG0436	E	GI 3	100.00	94.71
RCA23_c06660	3-hydroxybutyrate dehydrogenase Bdh	COG1028	I	GI 3	99.20	100.00
RCA23_c06670	putative fumarylacetoacetate hydrolase	COG0179	Q	GI 3	0.00	67.72
RCA23_c06680	oxidoreductase, short chain dehydrogenase/reductase family protein	COG1028	I	GI 3	0.00	75.17
RCA23_c06690	dimethylmenaquinone methyltransferase	COG0684	H	GI 3	0.00	98.95
RCA23_c06700	hypothetical protein	COG3970	R	GI 3	0.00	94.60
RCA23_c06710	NADP-dependent fatty aldehyde dehydrogenase AldH	COG1012	C	GI 3	0.00	75.96
RCA23_c06720	putative dihydrodipicolinate synthase	COG0329	E	GI 3	0.00	70.75
RCA23_c06730	transcriptional regulator protein, LacI family	COG1609	K	GI 3	0.00	73.33
RCA23_c06740	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	GI 3	0.00	80.34
RCA23_c06750	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	GI 3	0.00	62.24
RCA23_c06760	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	GI 3	0.00	78.96
RCA23_c06770	D-amino acid dehydrogenase small subunit DadA	COG0665	E	GI 3	0.00	83.92
RCA23_c06780	mandelate racemase/muconate lactonizing protein	COG4948	M	GI 3	53.61	78.24
RCA23_c06790	dihydrodipicolinate synthase DapA	COG0329	E	GI 3	100.00	64.59
RCA23_c06800	uncharacterized oxidoreductase, YjmC	COG2055	C	GI 3	57.07	88.13
RCA23_c06810	sarcosine oxidase beta subunit SoxB	COG0665	E	GI 3	82.58	81.90
RCA23_c06820	sarcosine oxidase delta subunit SoxD	COG4311	E	GI 3	0.00	100.00
RCA23_c06830	sarcosine oxidase alpha subunit SoxA	COG0404	E	GI 3	41.21	75.69
RCA23_c06840	sarcosine oxidase gamma subunit SoxG	COG4583	E	GI 3	100.00	77.66
RCA23_c06850	hypothetical protein, DUF6 transmembrane protein	COG0697	G	GI 3	100.00	78.68
RCA23_c06860	putative phage integrase			GI 3	46.25	27.23
RCA23_c06870	putative amidase	COG0154	J	GI 3	0.00	0.00
RCA23_c06880	integrase	COG4974	L	GI 3	100.00	55.20
RCA23_c06890	putative helicase			GI 3	48.29	0.00
RCA23_c06900	transposase	COG3316	L	GI 3	0.00	99.00
RCA23_c06910	HTH-type transcriptional regulator, LuxR family	COG2197	T	GI 3	0.00	100.00
RCA23_c06920	putative oxidoreductase, molybdopterin binding	COG3915	S	GI 3	0.00	100.00
RCA23_c06930	signal transduction histidine kinase	COG0642	T	GI 3	0.00	73.12
RCA23_c06940	glucose-1-phosphate thymidylyltransferase RfbA	COG1209	M	GI 3	0.00	61.33
RCA23_c06950	hypothetical protein, chain length determinant protein	COG0489	D	GI 3	0.00	69.96
RCA23_c06960	polysaccharide export protein	COG1596	M	GI 3	0.00	79.68

RCA23_c06970	hypothetical protein, VanZ-like	COG5652	S	GI 3	0.00	100.00
RCA23_c06980	type I secretion system membrane fusion protein, HlyD family	COG1566	V	GI 3	0.00	22.42
RCA23_c06990	type I secretion system ATP-binding component, HlyB family	COG2274	V	GI 3	0.00	67.28
RCA23_c07000	type I secretion outer membrane protein, TolC family	COG1538	M	GI 3	0.00	52.58
RCA23_c07010	putative serralysin-like metalloprotease	COG2931	Q	GI 3	0.00	26.87
RCA23_c07020	dTDP-4-dehydrorhamnose reductase RfbD	COG1091	M	GI 3	0.00	79.65
RCA23_c07030	dTDP-glucose 4,6-dehydratase RfbB	COG1088	M	GI 3	0.00	23.63
RCA23_c07040	dTDP-4-dehydrorhamnose 3,5-epimerase RfbC	COG1898	M	GI 3	0.00	88.30
RCA23_c07050	hypothetical protein			GI 3	0.00	80.02
RCA23_c07060	glycosyltransferase	COG0438	M	GI 3	0.00	21.48
RCA23_c07070	putative glycosyltransferase	COG0438	M	GI 3	0.00	46.21
RCA23_c07080	hypothetical protein, UDP-glycosyltransferase/glycogen phosphorylase-like	COG0438	M	GI 3	0.00	23.52
RCA23_c07090	polysaccharide biosynthesis protein			GI 3	0.00	31.69
RCA23_c07100	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase ArnB	COG0399	M	GI 3	0.00	0.00
RCA23_c07110	hypothetical, WxcM-like	COG0110	R	GI 3	0.00	53.54
RCA23_c07120	hypothetical protein, WxcM-like			GI 3	0.00	0.00
RCA23_c07130	hypothetical protein, acyltransferase-like	COG1670	J	GI 3	0.00	0.00
RCA23_c07140	UDP-glucose/GDP-mannose dehydrogenase family protein	COG0677	M	GI 3	0.00	68.17
RCA23_c07150	S-adenosyl-L-methionine-dependent methyltransferase			GI 3	0.00	25.41
RCA23_c07160	UDP-glucoronate 5'-epimerase LspL	COG0451	M	GI 3	0.00	53.53
RCA23_c07170	transcriptional regulator, MarR family	COG1846	K	GI 3	0.00	62.43
RCA23_c07180	transcription antitermination protein NusG	COG0250	K	GI 3	0.00	87.33
RCA23_c07190	hypothetical protein	COG1434	S	GI 3	0.00	81.82
RCA23_c07200	lipopolysaccharide core biosynthesis mannosyltransferase LpcC	COG0438	M	GI 3	0.00	69.74
RCA23_c07210	hypothetical protein			GI 3	0.00	100.00
RCA23_c07220	undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	COG0472	M	GI 3	0.00	80.44
RCA23_c07230	hypothetical protein, transmembrane			GI 3	0.00	84.12
RCA23_c07240	hypothetical protein, transmembrane			GI 3	0.00	68.70
RCA23_c07250	transposase, IS4 family protein			GI 3	0.00	100.00
RCA23_c07260	putative transposase	COG3039	L	GI 3	0.00	56.86
RCA23_c07270	hypothetical protein, transmembrane			GI 3	0.00	74.94
RCA23_c07280	hypothetical protein, transmembrane			GI 3	0.00	49.34
RCA23_c07290	transposase	COG3316	L	GI 3	0.00	0.00

RCA23_c07300	glycogen synthase GlgA	COG0297	G	GI 3	0.00	49.69
RCA23_c07310	glycogen debranching enzyme GlgX	COG1523	G	GI 3	0.00	35.65
RCA23_c07320	phosphoglucomutase Pgm	COG0033	G	GI 3	0.00	32.35
RCA23_c07330	putative alpha-glucosidase AglA	COG0366	G	GI 3	0.00	45.27
RCA23_c07340	transposase	COG3316	L	GI 3	0.00	100.00
RCA23_c07350	uncharacterized hydrolase YtnL	COG1473	R	GI 3	100.00	62.38
RCA23_c07360	glutathione-binding protein GsiB	COG0747	E	GI 3	89.85	100.00
RCA23_c07370	glutathione transport system permease protein GsiC	COG0601	E	GI 3	100.00	94.20
RCA23_c07380	dipeptide transport system permease protein	COG1173	E	GI 3	100.00	100.00
RCA23_c07390	glutathione import ATP-binding protein GsiA	COG4172	R	GI 3	100.00	97.59
RCA23_c07400	peptidase family S58	COG3191	E	GI 3	100.00	100.00
RCA23_c07410	aldehyde dehydrogenase AldA	COG1012	C	GI 3	100.00	100.00
RCA23_c07420	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	GI 3	100.00	97.71
RCA23_c07430	amidase	COG0154	J	GI 3	100.00	98.01
RCA23_c07440	MFS-type transporter	COG2807	P	GI 3	100.00	82.51
RCA23_c07450	peptidase M20D amidohydrolase	COG1473	R	GI 3	0.00	0.00
RCA23_c07460	transposase	COG3316	L	GI 3	0.00	0.00
RCA23_c07470	integrase	COG2801	L	GI 3	0.00	0.00
RCA23_c07480	transposase			GI 3	0.00	0.00
RCA23_c07490	hypothetical protein, DUF3764			GI 3	67.84	28.63
RCA23_c07500	hypothetical protein			GI 3	100.00	0.00
RCA23_c07510	hypothetical protein, beta-lactam-insensitive peptidoglycan transpeptidase Yk	COG1376	S	GI 3	100.00	56.43
RCA23_c07520	hypothetical protein			GI 3	100.00	100.00
RCA23_c07530	ABC transporter, ATP-binding protein, SbmA/BacA-like family	COG1133	I	GI 3	100.00	62.26
RCA23_c07540	hypothetical protein			GI 3	100.00	50.36
RCA23_c07550	hypothetical protein			GI 3	0.00	0.00
RCA23_c07560	integrase	COG2801	L	GI 3	0.00	0.00
RCA23_c07570	hypothetical protein			GI 3	0.00	0.00
RCA23_c07580	hypothetical protein			GI 3	0.00	0.00
RCA23_c07590	flagellin FliC	COG1344	N	GI 3	0.00	0.00
RCA23_c07600	RNA polymerase sigma-54	COG1508	K	GI 3	84.01	49.32
RCA23_c07610	hypothetical protein, cyclic nucleotide-binding-like			GI 3	100.00	0.00
RCA23_c07620	hypothetical protein	COG0664	T	GI 3	100.00	51.13

RCA23_c07630	hypothetical protein			GI 3	0.00	21.60
RCA23_c07640	hypothetical protein			GI 3	0.00	33.83
RCA23_c07650	hypothetical protein			GI 3	0.00	59.36
RCA23_c07660	flagellar biosynthesis protein FlhB	COG1377	N	GI 3	69.34	29.88
RCA23_c07670	flagellar biosynthetic protein FliR	COG1684	N	GI 3	100.00	67.52
RCA23_c07680	flagellar biosynthetic protein FliQ	COG1987	N	GI 3	100.00	56.30
RCA23_c07690	flagellar biosynthetic protein FliP	COG1338	N	GI 3	100.00	0.00
RCA23_c07700	flagellar motor switch protein FliN	COG1886	N	GI 3	100.00	34.92
RCA23_c07710	flagellar motor switch proteins FliM	COG1868	N	GI 3	100.00	42.20
RCA23_c07720	protein FliL	COG1580	N	GI 3	100.00	59.26
RCA23_c07730	putative flagellar hook-length control protein FliK	COG3144	N	GI 3	45.98	38.66
RCA23_c07740	putative flagellar export protein FliJ			GI 3	0.00	45.00
RCA23_c07750	flagellar protein export ATPase FliI	COG1157	N	GI 3	0.00	78.38
RCA23_c07760	putative flagellar assembly protein FliH			GI 3	45.29	41.18
RCA23_c07770	flagellar motor switch protein G	COG1536	N	GI 3	100.00	48.70
RCA23_c07780	flagellar M-ring protein FliF	COG1766	N	GI 3	26.08	71.29
RCA23_c07790	flagellar hook-basal body complex subunit FliE	COG1677	N	GI 3	0.00	59.68
RCA23_c07800	transcriptional regulatory protein FlbD	COG2204	T	GI 3	40.95	29.18
RCA23_c07810	protein FliL	COG1580	N	GI 3	100.00	66.48
RCA23_c07820	hypothetical protein			GI 3	100.00	71.26
RCA23_c07830	flagellar protein FliS	COG1516	N	GI 3	36.83	43.01
RCA23_c07840	hypothetical protein			GI 3	33.33	0.00
RCA23_c07850	hypothetical protein			GI 3	100.00	0.00
RCA23_c07860	flagellar basal-body rod protein FlgG	COG4786	N	GI 3	100.00	14.18
RCA23_c07870	Cl- channel, voltage-gated family protein	COG0038	P	GI 3	89.79	12.80
RCA23_c07880	hypothetical protein, lysozym-like	COG0741	M	GI 3	100.00	17.44
RCA23_c07890	flagellar hook-associated protein FlgL	COG1344	N	GI 3	96.70	40.02
RCA23_c07900	flagellar hook-associated protein FlgK	COG1256	N	GI 3	95.40	20.46
RCA23_c07910	flagellar rod assembly protein/muramidase FlgJ	COG3951	M	GI 3	100.00	71.51
RCA23_c07920	flagellar P-ring protein FlgI	COG1706	N	GI 3	100.00	54.35
RCA23_c07930	flagellar L-ring protein FlgH	COG2063	N	GI 3	100.00	45.74
RCA23_c07940	flagellar basal-body rod protein FlgG	COG4786	N	GI 3	45.75	38.28
RCA23_c07950	putative flagellar basal body rod protein FlgF	COG4786	N	GI 3	0.00	40.41

RCA23_c07960	flagellar hook protein FlgE	COG1749	N	GI 3	52.92	46.57
RCA23_c07970	flagellar basal body rod modification protein FlgD	COG1843	N	GI 3	100.00	71.27
RCA23_c07980	flagellar basal-body rod protein FlgC	COG1558	N	GI 3	83.45	49.16
RCA23_c07990	flagellar basal-body rod protein FlgB	COG1815	N	GI 3	0.00	63.31
RCA23_c08000	hypothetical protein			GI 3	0.00	68.88
RCA23_c08010	hypothetical protein			GI 3	0.00	68.35
RCA23_c08020	RNA polymerase, sigma factor for flagellar operon FliA	COG1191	K	GI 3	13.77	44.08
RCA23_c08030	putative flagellar biosynthesis protein FlhG	COG0455	D	GI 3	100.00	64.44
RCA23_c08040	flagellar biosynthesis protein FlhF	COG1419	N	GI 3	91.12	25.89
RCA23_c08050	flagellar biosynthesis protein FlhA	COG1298	N	GI 3	100.00	47.99
RCA23_c08060	hypothetical membrane lipoprotein, DUF400			GI 3	46.46	9.26
RCA23_c08070	hypothetical protein			GI 3	0.00	58.90
RCA23_c08080	flagellar basal body P-ring biosynthesis protein FlgA	COG1261	N	GI 3	95.68	41.84
RCA23_c08090	putative negative regulator of flagellin synthesis FlgM			GI 3	100.00	94.39
RCA23_c08100	hypothetical protein			GI 3	100.00	40.89
RCA23_c08110	hypothetical protein, HCP-like	COG0790	R	GI 3	100.00	60.82
RCA23_c08120	hypothetical protein			GI 3	100.00	0.00
RCA23_c08130	sigma54 specific transcriptional regulator, Fis family	COG2204	T	GI 3	100.00	70.49
RCA23_c08140	flagellar hook-associated protein FliD	COG1345	N	GI 3	15.63	57.75
RCA23_c08150	chemotaxis protein MotB	COG1360	N	GI 3	68.55	24.59
RCA23_c08160	chemotaxis protein MotA	COG1291	N	GI 3	42.13	35.70
RCA23_c08170	hypothetical protein, DUF1566			GI 3	7.69	25.85
RCA23_c08180	putative transmembrane protein, DUF6			GI 3	100.00	100.00
RCA23_c08190	putative polyketide hydroxylase SchC	COG0654	H	GI 3	67.51	100.00
RCA23_c08200	aldehyde dehydrogenase	COG1012	C		100.00	64.07
RCA23_c08210	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	COG2159	R		100.00	89.09
RCA23_c08220	transcriptional regulator, IclR family	COG1414	K		100.00	100.00
RCA23_c08230	TRAP transporter, 4TM/12TM fusion protein	COG4666	R		100.00	92.04
RCA23_c08240	TRAP transporter solute receptor, TAXI family	COG2358	R		100.00	81.43
RCA23_c08250	thiamine pyrophosphate enzyme-like TPP-binding	COG0028	E		95.75	89.62
RCA23_c08260	hypothetical protein	COG2268	S		100.00	67.72
RCA23_c08270	short chain dehydrogenase	COG1028	I		100.00	62.23
RCA23_c08280	putative aldehyde dehydrogenase yfmT	COG1012	C		4.67	92.95

RCA23_c08290	branched-chain amino acid ABC transporter, ATP-binding protein	COG0410	E	0.00	100.00
RCA23_c08300	branched-chain amino acid ABC transporter, ATP-binding protein	COG0411	E	0.00	80.97
RCA23_c08310	putative transporter, permease protein	COG4177	E	28.51	89.92
RCA23_c08320	putative transporter, permease protein	COG0559	E	100.00	80.18
RCA23_c08330	putative transporter, periplasmic binding protein	COG0683	E	0.00	75.58
RCA23_c08340	hypothetical protein, PrpF protein-like	COG2828	S	63.44	99.81
RCA23_c08350	4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase	COG0684	H	67.87	63.96
RCA23_c08360	putative N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase,	COG2120	S	26.67	73.47
RCA23_c08370	hypothetical protein			44.71	100.00
RCA23_c08380	transcriptional regulator	COG1802	K	0.00	100.00
RCA23_c08390	aminomethyltransferase GcvT	COG0404	E	92.15	95.36
RCA23_c08400	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	100.00	85.38
RCA23_c08410	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	100.00	59.65
RCA23_c08420	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	71.26	100.00
RCA23_c08430	metapyrocatechase XylE	COG2514	R	78.34	86.31
RCA23_c08440	MFS-type transporter	COG2814	G	100.00	87.79
RCA23_c08450	hypothetical protein, cytochrome c			100.00	100.00
RCA23_c08460	hypothetical protein, copper resistance protein C	COG2372	R	100.00	100.00
RCA23_c08470	hypothetical protein, copper resistance protein D	COG1276	P	24.18	100.00
RCA23_c08480	hypothetical protein	COG3613	F	100.00	100.00
RCA23_c08490	hypothetical protein			100.00	100.00
RCA23_c08500	hypothetical protein			100.00	100.00
RCA23_c08510	fumarate reductase flavoprotein subunit	COG1053	C	100.00	100.00
RCA23_c08520	methylisocitrate lyase PrpB	COG2513	G	100.00	99.54
RCA23_c08530	putative isochorismatase family protein	COG1335	Q	100.00	93.56
RCA23_c08540	hydantoin utilization protein A	COG0145	E	84.74	100.00
RCA23_c08550	hydantoin utilization protein B	COG0146	E	79.94	99.76
RCA23_c08560	hypothetical protein	COG1942	R	100.00	100.00
RCA23_c08570	HTH-type transcriptional regulator, GntR family	COG2188	K	100.00	91.76
RCA23_c08580	3-isopropylmalate dehydratase large subunit LeuC	COG0065	E	100.00	100.00
RCA23_c08590	3-isopropylmalate dehydratase small subunit LeuD	COG0066	E	100.00	100.00
RCA23_c08600	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	100.00	100.00
RCA23_c08610	TRAP transporter, subunit DctQ	COG3090	G	100.00	100.00

RCA23_c08620	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	100.00	100.00
RCA23_c08630	putative glutamate synthase [NADPH] small chain	COG0493	E	100.00	100.00
RCA23_c08640	hypothetical protein, dihydrooronate dehydrogenase	COG0167	F	100.00	98.93
RCA23_c08650	putative HTH-type transcriptional regulator	COG1309	K	100.00	100.00
RCA23_c08660	N-carbamoyl-L-amino acid hydrolase AmaB	COG0624	E	100.00	100.00
RCA23_c08670	D-hydantoinase/dihydropyrimidinase Dht	COG0044	F	100.00	99.59
RCA23_c08680	ABC transporter ATP-binding protein	COG1116	P	100.00	100.00
RCA23_c08690	putative ABC transporter permease protein	COG0600	P	100.00	100.00
RCA23_c08700	putative ABC transporter permease protein	COG0600	P	100.00	100.00
RCA23_c08710	putative thiamine biosynthesis protein	COG0715	P	100.00	100.00
RCA23_c08720	putative integral membrane proein DUF6	COG0697	G	100.00	100.00
RCA23_c08730	hypothetical protein DUF6	COG0697	G	100.00	100.00
RCA23_c08740	alkaline phosphatase synthesis sensor protein PhoR	COG5002	T	100.00	100.00
RCA23_c08750	putative phosphate binding protein PstS	COG0226	P	100.00	97.50
RCA23_c08760	putative phosphate transport system permease protein PstC	COG0573	P	93.28	100.00
RCA23_c08770	putative phosphate transport system permease protein PstA	COG0581	P	100.00	100.00
RCA23_c08780	phosphate import ATP-binding protein PstB	COG1117	P	100.00	100.00
RCA23_c08790	phosphate transport system regulatory protein PhoU	COG0704	P	100.00	96.83
RCA23_c08800	phosphate regulon transl protein PhoB	COG0745	T	100.00	100.00
RCA23_c08810	putative hippurate hydrolase protei	COG1473	R	100.00	49.13
RCA23_c08820	urease accessory protein UreD	COG0829	O	100.00	100.00
RCA23_c08830	urease gamma subunit UreA	COG0831	E	100.00	100.00
RCA23_c08840	urease beta subunit UreB	COG0832	E	100.00	100.00
RCA23_c08850	urease alpha subunit UreC	COG0804	E	100.00	98.62
RCA23_c08860	urease accessory protein UreE	COG2371	O	100.00	100.00
RCA23_c08870	urease accessory protein UreF	COG0830	O	2.83	100.00
RCA23_c08880	urease accessory protein UreG	COG0378	O	0.00	100.00
RCA23_c08890	integrase	COG2801	L	0.00	0.00
RCA23_c08900	hypothetical protein	COG4585	T	53.33	100.00
RCA23_c08910	glucose-methanol-choline oxidoreductase AlkJ	COG2303	E	92.11	100.00
RCA23_c08920	hypothetical protein, YaeQ family protein	COG4681	S	100.00	100.00
RCA23_c08930	hypothetical protein, DUF6 transmembrane protein	COG0697	G	100.00	100.00
RCA23_c08940	UDP-glucose 6-dehydrogenase Ugd	COG1004	M	100.00	100.00

RCA23_c08950	3-deoxy-D-manno-octulosonic-acid transferase WaaA	COG1519	M		100.00	100.00
RCA23_c08960	UDP-N-acetylglucosamine 2-epimerase WecB	COG0381	M		100.00	100.00
RCA23_c08970	putative N-acetylneuramic acid synthase	COG2089	M		42.44	100.00
RCA23_c08980	hypothetical protein				67.65	100.00
RCA23_c08990	hypothetical protein	COG1651	O		100.00	100.00
RCA23_c09000	choline-sulfatase BetC	COG3119	P		100.00	94.68
RCA23_c09010	permease	COG2233	F		100.00	100.00
RCA23_c09020	hypothetical protein				100.00	100.00
RCA23_c09030	membrane dipeptidase	COG2355	E		100.00	100.00
RCA23_c09040	hypothetical protein				100.00	100.00
RCA23_c09050	hypothetical protein				100.00	100.00
RCA23_c09060	tRNA pseudouridine synthase A	COG0101	J		100.00	96.38
RCA23_c09070	YcjX-like protein	COG3106	R		100.00	93.14
RCA23_c09080	hypothetical protein, acetyltransferase-like	COG0456	R		100.00	100.00
RCA23_c09090	hypothetical protein	COG3768	S		100.00	92.33
RCA23_c09100	isoleucyl-tRNA synthase IleS	COG0060	J		100.00	100.00
RCA23_c09110	putative integral membrane protein DUF6				100.00	100.00
RCA23_c09120	phosphatidylcholine synthase Pcs	COG1183	I		100.00	100.00
RCA23_c09130	putative tyrosine recombinase xerC	COG4974	L		100.00	100.00
RCA23_c09140	hypothetical protein	COG3159	S		100.00	100.00
RCA23_c09150	transaldolase	COG0176	G		100.00	100.00
RCA23_c09160	primosomal protein N'	COG1198	L		100.00	100.00
RCA23_c09170	methylmalonyl-CoA mutase McmA	COG1884	I		100.00	93.52
RCA23_c09180	glycerol-3-phosphate acyltransferase PlsB	COG2937	I		100.00	98.68
RCA23_c09190	crotonyl-CoA reductase Ccr	COG0604	C		100.00	100.00
RCA23_c09200	putative ATPase	COG0507	L		100.00	98.61
RCA23_c09210	trimethylamine methyltransferase MttB	COG5598	H		100.00	100.00
RCA23_c09220	hypothetical protein DUF1052	COG5321	S		100.00	100.00
RCA23_c09240	hypothetical protein, DUF411	COG3019	R	GI 4	0.00	0.00
RCA23_c09250	hypothetical protein			GI 4	0.00	0.00
RCA23_c09260	hypothetical protein			GI 4	0.00	0.00
RCA23_c09270	hypothetical protein	COG4642	S	GI 4	0.00	0.00
RCA23_c09280	hypothetical protein	COG3904	S	GI 4	0.00	0.00

RCA23_c09290	putative DNA-binding protein, transposase-like	COG3415	L	GI 4	0.00	0.00
RCA23_c09300	HTH-type transcriptional regulator, LysR family	COG0583	K	GI 4	0.00	0.00
RCA23_c09310	hypothetical protein			GI 4	0.00	0.00
RCA23_c09320	hypothetical protein, hydrolase-like	COG0627	R	GI 4	0.00	0.00
RCA23_c09330	putative integrase	COG2801	L	GI 4	0.00	44.52
RCA23_c09340	putative transposase			GI 4	0.00	100.00
RCA23_c09350	hypothetical protein, ornithine cyclodeaminase-like	COG2423	E		0.00	0.00
RCA23_c09360	LrgB-like protein	COG1346	M		100.00	100.00
RCA23_c09370	hypothetical protein	COG1380	R		100.00	100.00
RCA23_c09380	putative branched-chain-amino-acid aminotransferase IlvE	COG0115	E		100.00	100.00
RCA23_c09390	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I		100.00	100.00
RCA23_c09400	bicyclomycin resistance protein Bcr	COG2814	G		100.00	100.00
RCA23_c09410	hypothetical protein				100.00	71.10
RCA23_c09420	hypothetical protein, photolyase	COG3046	R		100.00	97.08
RCA23_c09430	DNA photolyase, FAD-binding/cryptochrome	COG0415	L		100.00	91.30
RCA23_c09440	carbon monoxide dehydrogenase small chain CoxS	COG2080	C		100.00	100.00
RCA23_c09450	carbon monoxide dehydrogenase large chain CoxL	COG1529	C		100.00	100.00
RCA23_c09460	carbon monoxide dehydrogenase medium chain CoxM	COG1319	C		100.00	100.00
RCA23_c09470	MoxR-like ATPase	COG0714	R		100.00	100.00
RCA23_c09480	CoxE-like protein	COG3552	R		100.00	89.68
RCA23_c09490	5-deoxy-glucuronate isomerase IolB	COG3718	G		100.00	100.00
RCA23_c09500	branched-chain amino acid transport protein, AzlD-like	COG4392	S		100.00	100.00
RCA23_c09510	branched-chain amino acid transport protein, AzlC-like	COG1296	E		100.00	100.00
RCA23_c09520	alpha-IPM synthase/homocitrate synthase	COG0119	E		100.00	95.84
RCA23_c09530	cytochrome P450	COG2124	Q		93.18	94.13
RCA23_c09540	TRAP dicarboxylate transporter, subunit DctP	COG1638	G		100.00	100.00
RCA23_c09550	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G		100.00	100.00
RCA23_c09560	TRAP dicarboxylate transporter, subunit DctM	COG1593	G		100.00	99.40
RCA23_c09570	putative citrate transporter	COG0471	P		100.00	100.00
RCA23_c09580	triosephosphate isomerase TpiA	COG0149	G		100.00	100.00
RCA23_c09590	putative regulator protein of competence-specific genes TfoX	COG3070	K		100.00	98.11
RCA23_c09600	hypothetical protein, iron-sulfur cluster assembly protein	COG0316	S		100.00	100.00
RCA23_c09610	hypothetical protein DUF59	COG2151	R		100.00	100.00

RCA23_c09620	queuine tRNA-ribosyltransferase Tgt	COG0343	J	100.00	100.00
RCA23_c09630	hypothetical protein			100.00	100.00
RCA23_c09640	ATP-dependent protease La	COG0466	O	100.00	99.83
RCA23_c09650	putative phosphoglycerate mutase family protein	COG0406	G	100.00	100.00
RCA23_c09670	protein-L-isoaspartate O-methyltransferase Pcm	COG2518	O	100.00	100.00
RCA23_c09680	outer membrane efflux protein	COG1538	M	100.00	100.00
RCA23_c09690	hypothetical protein			100.00	100.00
RCA23_c09700	cobyric acid synthase CobQ	COG1492	H	100.00	100.00
RCA23_c09710	hypothetical protein			100.00	100.00
RCA23_c09720	translation elongation factor P	COG0231	J	100.00	100.00
RCA23_c09730	hypothetical protein tRNA modifying protein YgfZ	COG0354	R	100.00	100.00
RCA23_c09740	putative glycosyltransferase, family 2	COG0463	M	100.00	100.00
RCA23_c09750	lipid A export ATP-binding/permease protein MsbA	COG1132	V	100.00	100.00
RCA23_c09760	serine--glyoxylate aminotransferase SgaA	COG0075	E	100.00	93.37
RCA23_c09770	histidinol-phosphate aminotransferase HisC	COG0079	E	100.00	100.00
RCA23_c09780	valyl-tRNA synthase ValS	COG0525	J	100.00	98.26
RCA23_c09790	hypothetical protein, metal-dependent phosphohydrolase	COG4341	R	100.00	100.00
RCA23_c09800	putative phytanoyl-CoA dioxygenase family protein	COG5285	Q	100.00	96.68
RCA23_c09810	molybdenum-containing hydroxylase	COG1529	C	100.00	99.43
RCA23_c09820	hypothetical protein DUF2235	COG3673	S	100.00	100.00
RCA23_c09830	5,10-methylenetetrahydrofolate reductase MetF	COG0685	E	100.00	100.00
RCA23_c09840	HTH-type transcriptional regulator MetR	COG0583	K	100.00	100.00
RCA23_c09850	inositol-1-monophosphatase SuhB	COG0483	G	100.00	100.00
RCA23_c09860	hypothetical protein	COG3063	N	100.00	100.00
RCA23_c09880	transcriptional regulator, HxlR family	COG1733	K	100.00	100.00
RCA23_c09890	hypothetical protein, DUF3764			100.00	100.00
RCA23_c09900	hypothetical protein			100.00	100.00
RCA23_c09910	hypothetical protein, DsrE/F-like	COG1553	P	100.00	100.00
RCA23_c09920	glutathione peroxidase Gpo	COG0386	O	100.00	100.00
RCA23_c09930	putative ion channel			100.00	100.00
RCA23_c09950	hypothetical protein			34.50	100.00
RCA23_c09940	ribosomal large subunit pseudouridine synthase D	COG0564	J	100.00	91.09
RCA23_c09960	RNA polymerase sigma-32 factor RpoH	COG0568	K	100.00	100.00

RCA23_c09970	putative oxidoreductase	COG0673	R	100.00	100.00
RCA23_c09980	oligoendopeptidase F	COG1164	E	100.00	97.87
RCA23_c09990	2-keto-3-deoxy-L-rhamnonate aldolase RhmA	COG3836	G	100.00	100.00
RCA23_c10000	hypothetical protein, lysophospholipase L2	COG2267	I	100.00	100.00
RCA23_c10010	putative sterol-binding protein	COG3255	I	100.00	100.00
RCA23_c10020	hypothetical protein			100.00	86.99
RCA23_c10030	ATP-dependent RNA helicase RhlB	COG4581	L	100.00	99.79
RCA23_c10040	putative heat shock protein	COG1188	J	100.00	100.00
RCA23_c10050	ferredoxin FdxA	COG1146	C	87.02	100.00
RCA23_c10060	putative transcriptional regulator, CarD family	COG1329	K	19.08	100.00
RCA23_c10070	cobalamin-5-phosphate synthase CobS	COG0368	H	100.00	100.00
RCA23_c10080	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase Cob	COG2038	H	100.00	100.00
RCA23_c10090	hypothetical protein			100.00	99.41
RCA23_c10100	glyoxalase/bleomycin resistance protein	COG3565	R	100.00	100.00
RCA23_c10110	hypothetical protein			100.00	100.00
RCA23_c10120	choline dehydrogenase BetA	COG2303	E	100.00	100.00
RCA23_c10140	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB	COG0566	J	100.00	67.11
RCA23_c10150	phosphoribosyl-ATP pyrophosphatase HisE	COG0140	E	100.00	100.00
RCA23_c10160	imidazole glycerol phosphate synthase subunit HisF	COG0107	E	100.00	100.00
RCA23_c10170	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazo	COG0106	E	100.00	100.00
RCA23_c10180	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit H	COG0118	E	100.00	87.64
RCA23_c10190	imidazoleglycerol-phosphate dehydratase HisB	COG0131	E	100.00	100.00
RCA23_c10210	hypothetical protein, calcineurin-like phosphoesterase-like	COG1409	R	100.00	100.00
RCA23_c10220	pyruvate carboxylase Pyc	COG1038	C	100.00	98.75
RCA23_c10230	L-lactate dehydrogenase IldD	COG1304	C	100.00	100.00
RCA23_c10240	putative DNA helicase II	COG0210	L	100.00	100.00
RCA23_c10250	gamma-glutamylputrescine oxidoreductase PuuB	COG0665	E	100.00	100.00
RCA23_c10260	putative cysteine/O-acetylserine efflux protein	COG1280	E	100.00	100.00
RCA23_c10270	hypothetical protein			100.00	100.00
RCA23_c10280	putative protein Mrp	COG0489	D	100.00	100.00
RCA23_c10290	hypothetical protein			100.00	100.00
RCA23_c10300	hypothetical protein, MraZ	COG2001	S	100.00	100.00
RCA23_c10310	S-adenosyl-L-methionine-dependent methyltransferase MraW	COG0275	M	100.00	100.00

RCA23_c10320	hypothetical protein	COG5462	S	100.00	100.00
RCA23_c10330	peptidoglycan synthase FtsI	COG0768	M	100.00	98.32
RCA23_c10340	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase Mu	COG0769	M	100.00	100.00
RCA23_c10350	putative UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase MurF	COG0770	M	100.00	100.00
RCA23_c10360	phospho-N-acetylmuramoyl-pentapeptide-transferase MraY	COG0472	M	100.00	100.00
RCA23_c10370	UDP-N-acetylmuramoylalanine--D-glutamate ligase MurD	COG0771	M	100.00	100.00
RCA23_c10380	putative glycosyltransferase, sugar binding region	COG3774	M	100.00	100.00
RCA23_c10390	putative galactoside 2-alpha-L-fucosyltransferase 1			100.00	100.00
RCA23_c10400	hypothetical protein			100.00	100.00
RCA23_c10410	hypothetical protein	COG3306	M	100.00	100.00
RCA23_c10420	hypothetical protein HI0933	COG2081	R	100.00	96.64
RCA23_c10430	cell division protein FtsW	COG0772	D	100.00	100.00
RCA23_c10440	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-	COG0707	M	100.00	100.00
RCA23_c10450	UDP-N-acetylmuramate--L-alanine ligase MurC	COG0773	M	100.00	100.00
RCA23_c10460	permease of the drug/metabolite transporter superfamily	COG0697	G	100.00	100.00
RCA23_c10470	UDP-N-acetylenolpyruvoylglucosamine reductase MurB	COG0812	M	100.00	85.96
RCA23_c10480	D-alanine--D-alanine ligase Ddl	COG1181	M	100.00	100.00
RCA23_c10490	putative cell division protein FtsQ			57.96	100.00
RCA23_c10500	cell division protein FtsA	COG0849	D	82.02	100.00
RCA23_c10510	cell division protein FtsZ	COG0206	D	100.00	100.00
RCA23_c10520	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC	COG0774	M	100.00	100.00
RCA23_c10530	outer membrane assembly lipoprotein	COG4105	R	100.00	100.00
RCA23_c10540	DNA repair protein RecN	COG0497	L	100.00	100.00
RCA23_c10550	hypothetical protein DUF427	COG2343	S	100.00	100.00
RCA23_c10560	putative Xaa-Pro aminopeptidase	COG0006	E	100.00	100.00
RCA23_c10570	aerobic cobaltochelatase subunit CobT	COG4547	H	100.00	100.00
RCA23_c10580	aerobic cobaltochelatase subunit CobS	COG0714	R	100.00	100.00
RCA23_c10590	hypothetical protein, DnaJ	COG0484	O	100.00	100.00
RCA23_c10600	putative stress-induced morphoprotein, BolA type	COG0271	T	54.17	100.00
RCA23_c10610	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit GatB	COG0064	J	95.11	90.54
RCA23_c10620	aminopeptidase N	COG0308	E	95.06	95.89
RCA23_c10630	malate synthase GlcB	COG2225	C	100.00	97.29
RCA23_c10640	hypothetical protein DUF336	COG3193	R	100.00	100.00

RCA23_c10650	hypothetical protein				100.00	100.00
RCA23_c10660	gamma-glutamyl-gamma-aminobutyrate hydrolase PuuD	COG2071	R		100.00	100.00
RCA23_c10670	putative D-beta-hydroxybutyrate dehydrogenase	COG1028	I		100.00	100.00
RCA23_c10680	NAD(P) transhydrogenase alpha subunit PntA	COG3288	C		100.00	100.00
RCA23_c10690	NAD(P) transhydrogenase beta subunit PntB	COG1282	C		100.00	100.00
RCA23_c10700	hypothetical protein	COG4949	S		100.00	100.00
RCA23_c10710	putative acetylornithine deacetylase ArgE	COG0624	E		100.00	100.00
RCA23_c10720	molybdenum cofactor biosynthesis protein MoaA	COG2896	H		100.00	98.21
RCA23_c10730	acetyl-coenzyme A synthase AcsA	COG0365	I		100.00	94.60
RCA23_c10740	hypothetical protein	COG4321	R		100.00	100.00
RCA23_c10750	hypothetical protein				100.00	100.00
RCA23_c10760	fumarate hydratase class II	COG0114	C		100.00	100.00
RCA23_c10770	hypothetical protein	COG3814	S		100.00	81.29
RCA23_c10780	putative chromate transport protein	COG2059	P		100.00	100.00
RCA23_c10790	hydantoinase / oxoprolinase family protein	COG0145	E		100.00	100.00
RCA23_c10800	hypothetical protein				100.00	100.00
RCA23_c10810	putative quinone oxidoreductase yhdH	COG0604	C		100.00	97.47
RCA23_c10820	cysteine desulfurase SufS	COG0520	E		100.00	100.00
RCA23_c10830	deoxyribodipyrimidine photo-lyase PhrB	COG0415	L		89.88	88.75
RCA23_c10840	cyclopropane-fatty-acyl-phospholipid synthase Cfa	COG2230	M		45.00	100.00
RCA23_c10850	ADP-ribose pyrophosphatase NudF	COG0494	L		100.00	99.46
RCA23_c10860	cysteine synthase CysK	COG0031	E		100.00	93.55
RCA23_c10870	mechanosensitive ion channel protein MscS	COG3264	M		100.00	100.00
RCA23_c10890	putative phage integrase	COG4974	L	GI 5	34.02	25.54
RCA23_c10900	hypothetical protein			GI 5	0.00	19.20
RCA23_c10910	hypothetical protein, tetratricopetide domain TPR-1	COG0457	R	GI 5	0.00	0.00
RCA23_c10920	hypothetical protein, resolvase-like	COG1961	L	GI 5	100.00	100.00
RCA23_c10930	hypothetical protein, DUF2924			GI 5	100.00	37.53
RCA23_c10940	putative TRAP transporter solute receptor	COG2358	R	GI 5	35.69	62.17
RCA23_c10950	TRAP transporter, 4TM/12TM fusion protein	COG4666	R	GI 5	100.00	57.74
RCA23_c10960	putative sulfatase YidJ	COG3119	P	GI 5	100.00	58.08
RCA23_c10970	arylsulfatase	COG1234	R	GI 5	100.00	74.80
RCA23_c10980	siderophore interactin protein, vibriobactin utilization protein-like	COG2375	P	GI 5	100.00	76.80

RCA23_c10990	hypothetical protein, metallo-beta-lactamase	COG2015	Q	GI 5	97.10	63.07
RCA23_c11000	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	GI 5	64.31	47.69
RCA23_c11010	glutathione S-transferase	COG0625	O	GI 5	99.55	62.01
RCA23_c11020	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	GI 5	100.00	19.67
RCA23_c11030	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	GI 5	100.00	20.78
RCA23_c11040	hypothetical protein, DUF6 transmembrane protein	COG0697	G	GI 5	100.00	34.32
RCA23_c11050	ferric reductase like transmembrane component family			GI 5	100.00	60.14
RCA23_c11060	hypothetical protein			GI 5	100.00	72.69
RCA23_c11070	hypothetical protein			GI 5	100.00	67.93
RCA23_c11080	sulfatase family protein	COG3119	P	GI 5	12.09	49.51
RCA23_c11090	short-chain dehydrogenase/reductase SDR	COG1028	I	GI 5	3.29	35.31
RCA23_c11100	maleylacetoacetate isomerase MaiA	COG0625	O	GI 5	100.00	8.30
RCA23_c11110	salicylaldehyde dehydrogenase	COG1012	C	GI 5	100.00	42.59
RCA23_c11120	transcriptional regulator, GntR family	COG1802	K	GI 5	100.00	47.91
RCA23_c11130	transposase	COG3316	L	GI 5	4.66	0.00
RCA23_c11140	putative phage integrase	COG4974	L	GI 5	0.00	0.00
RCA23_c11150	hypothetical protein, alginate lyase-lyase			GI 5	0.00	0.00
RCA23_c11160	HTH-type transcriptional regulator, GntR family	COG1802	K	GI 5	100.00	80.77
RCA23_c11170	branched-chain amino acid ABC transporter, periplasmic substrate-binding pr	COG0683	E	GI 5	5.22	76.60
RCA23_c11180	branched-chain amino acid ABC transporter, permease protein	COG0559	E	GI 5	91.81	90.14
RCA23_c11190	branched-chain amino acid ABC transporter, permease protein	COG4177	E	GI 5	100.00	71.25
RCA23_c11200	branched-chain amino acid ABC transporter, ATP-binding protein	COG0411	E	GI 5	77.12	44.58
RCA23_c11210	branched-chain amino acid ABC transporter, ATP-binding protein	COG0410	E	GI 5	0.00	43.98
RCA23_c11220	hydantoin racemase HyuE	COG4126	E	GI 5	0.00	62.57
RCA23_c11230	transposase	COG3316	L	GI 5	0.00	79.66
RCA23_c11240	glutamine transport ATP-binding protein GlnQ	COG1126	E	GI 5	0.00	0.00
RCA23_c11250	putative inner membrane amino-acid ABC transporter permease protein	COG0765	E	GI 5	0.00	0.00
RCA23_c11260	transposase	COG3316	L	GI 5	0.00	0.00
RCA23_c11270	transcriptional regulator CoxC	COG3300	T	GI 5	43.53	100.00
RCA23_c11280	carbon monoxide dehydrogenase medium chain CoxM	COG1319	C	GI 5	100.00	100.00
RCA23_c11290	carbon monoxide dehydrogenase small chain CoxS	COG2080	C	GI 5	100.00	91.11
RCA23_c11300	carbon monoxide dehydrogenase large chain CoxL	COG1529	C	GI 5	89.29	98.06
RCA23_c11310	AAA+ ATPase chaperone CoxD	COG0714	R	GI 5	95.43	92.47

RCA23_c11320	carbon monoxide dehydrogenase accessory protein CoxE	COG3552	R	GI 5	100.00	100.00
RCA23_c11330	carbon monoxide dehydrogenase accessory protein CoxF	COG1975	O	GI 5	100.00	91.92
RCA23_c11340	hypothetical protein	COG2068	R	GI 5	100.00	100.00
RCA23_c11350	carbon monoxide dehydrogenase protein CoxG	COG3427	S	GI 5	100.00	100.00
RCA23_c11360	carbon monoxide dehydrogenase accessory protein CoxI	COG1975	O	GI 5	100.00	86.99
RCA23_c11370	transposase	COG3316	L	GI 5	100.00	0.00
RCA23_c11380	dienelactone hydrolase	COG0412	Q	GI 5	0.00	96.25
RCA23_c11390	aldo/keto reductase	COG0667	C	GI 5	94.94	97.52
RCA23_c11400	mandelate racemase MdlA	COG4948	M	GI 5	100.00	91.07
RCA23_c11410	hypothetical protein DUF1498	COG3822	R	GI 5	100.00	100.00
RCA23_c11420	two-component system, sensor histidine kinase protein	COG0642	T	GI 5	100.00	100.00
RCA23_c11430	two-component system, response regulator protein	COG0745	T	GI 5	100.00	100.00
RCA23_c11440	hypothetical protein	COG3181	S	GI 5	100.00	100.00
RCA23_c11450	putative tripartite tricarboxylate transporter (TTT) protein TctA	COG3333	S	GI 5	100.00	99.40
RCA23_c11460	hypothetical protein	COG2828	S	GI 5	100.00	90.66
RCA23_c11470	D-isomer specific 2-hydroxyacid dehydrogenase	COG0111	H	GI 5	100.00	94.32
RCA23_c11480	putative ammonia monooxygenase	COG3180	R	GI 5	100.00	100.00
RCA23_c11490	transcriptional regulator	COG1802	K	GI 5	100.00	100.00
RCA23_c11500	fumarate reductase flavoprotein subunit FccA	COG1053	C	GI 5	100.00	100.00
RCA23_c11510	aspartate aminotransferase AspC	COG0436	E	GI 5	100.00	100.00
RCA23_c11520	hypothetical protein			GI 5	100.00	100.00
RCA23_c11530	aerobic glycerol-3-phosphate dehydrogenase GlpD	COG0578	C	GI 5	100.00	98.78
RCA23_c11540	aerobic glycerol-3-phosphate dehydrogenase GlpD	COG0578	C	GI 5	100.00	100.00
RCA23_c11550	hypothetical protein	COG1192	D	GI 5	0.00	0.00
RCA23_c11560	chemotaxis protein CheW	COG0835	N	GI 5	64.10	0.00
RCA23_c11570	methyl-accepting chemotaxis protein II	COG0840	N	GI 5	99.09	0.00
RCA23_c11580	chemotaxis histidine kinase CheA	COG0643	N	GI 5	0.00	0.00
RCA23_c11590	response regulator CheY	COG2114	T	GI 5	0.00	0.00
RCA23_c11600	chemotaxis protein methyltransferase CheR	COG1352	N	GI 5	0.00	0.00
RCA23_c11610	chemotaxis response regulator protein-glutamate methylesterase CheB	COG2201	N	GI 5	0.00	0.00
RCA23_c11620	metal-dependent hydrolase	COG1235	R	GI 5	0.00	0.00
RCA23_c11630	integrase	COG2801	L	GI 5	0.00	0.00
RCA23_c11640	methyltransferase, FkbM family			GI 5	0.00	0.00

RCA23_c11650	hypothetical protein, sugar transferase-like			GI 5	0.00	63.40
RCA23_c11660	aldo/keto reductase	COG0667	C	GI 5	0.00	35.84
RCA23_c11670	hypothetical protein			GI 5	0.00	92.39
RCA23_c11680	hypothetical protein	COG0790	R	GI 5	0.00	0.00
RCA23_c11690	hypothetical protein	COG4430	S	GI 5	0.00	73.65
RCA23_c11700	hypothetical protein	COG2755	E	GI 5	0.00	0.00
RCA23_c11710	phytanoyl-CoA dioxygenase family protein	COG5285	Q	GI 5	100.00	100.00
RCA23_c11720	putative bacterial extracellular solute binding protein, family 3	COG1791	S	GI 5	0.00	92.32
RCA23_c11730	hypothetical protein			GI 5	0.00	6.62
RCA23_c11740	SOUL heme-binding protein			GI 5	99.67	100.00
RCA23_c11750	arylsulfatase precursor	COG3119	P	GI 5	96.71	96.71
RCA23_c11760	hypothetical protein DUF583			GI 5	0.00	0.00
RCA23_c11770	integrase	COG2801	L	GI 5	0.00	0.00
RCA23_c11780	hypothetical protein	COG3616	E	GI 5	79.40	94.19
RCA23_c11790	glutamine synthase GlnA type I	COG0174	E	GI 5	0.00	0.00
RCA23_c11800	putative HTH-type transcriptional regulator, RpiR family	COG1737	K	GI 5	0.00	0.00
RCA23_c11810	N-formylglutamate amidohydrolase	COG3931	E	GI 5	0.00	0.00
RCA23_c11820	putative isochorismatase family protein	COG1335	Q	GI 5	0.00	0.00
RCA23_c11830	branched-chain amino acid ABC transporter, ATP-binding protein	COG0411	E	GI 5	70.26	0.00
RCA23_c11840	branched-chain amino acid ABC transporter, periplasmic binding protein	COG0683	E	GI 5	100.00	0.00
RCA23_c11850	branched-chain amino acid ABC transporter, ATP-binding protein	COG0410	E	GI 5	0.00	0.00
RCA23_c11860	branched-chain amino acid ABC transporter, permease protein	COG0559	E	GI 5	0.00	0.00
RCA23_c11870	branched-chain amino acid ABC transporter, permease protein	COG4177	E	GI 5	0.00	3.49
RCA23_c11880	acetamidase/formamidase family protein	COG2421	C	GI 5	0.00	18.96
RCA23_c11890	hypothetical protein	COG1028	I	GI 5	100.00	100.00
RCA23_c11910	putative prophage integrase	COG0582	L	GI 5	0.00	20.44
RCA23_c11920	hypothetical protein			GI 5	0.00	0.00
RCA23_c11930	hypothetical protein			GI 5	0.00	73.21
RCA23_c11940	putative AAA ATPase	COG3598	L	GI 5	0.00	73.00
RCA23_c11950	hypothetical protein			GI 5	0.00	0.00
RCA23_c11960	hypothetical protein			GI 5	0.00	0.00
RCA23_c11970	hypothetical protein			GI 5	0.00	100.00
RCA23_c11980	hypothetical protein			GI 5	0.00	32.25

RCA23_c11990	branched-chain amino acid ABC transporter, ATP-binding protein	COG0410	E	GI 5	100.00	75.68
RCA23_c12000	branched-chain amino acid ABC transporter, ATP-binding protein	COG0411	E	GI 5	100.00	0.00
RCA23_c12010	branched-chain amino acid ABC transporter, permease protein	COG4177	E	GI 5	100.00	46.14
RCA23_c12020	branched-chain amino acid ABC transporter, permease protein	COG0559	E	GI 5	92.06	14.54
RCA23_c12030	branched-chain amino acid ABC transporter, periplasmic binding protein	COG0683	E	GI 5	0.00	45.84
RCA23_c12040	enoyl-CoA hydratase/carnithine racemase	COG1024	I	GI 5	0.00	14.86
RCA23_c12050	acetyl-CoA synthase-like protein	COG0318	I	GI 5	77.41	47.70
RCA23_c12060	dehydrogenase iron-sulfur-binding subunit	COG2080	C	GI 5	100.00	23.73
RCA23_c12070	dehydrogenase FAD-binding subunit	COG1319	C	GI 5	92.00	25.70
RCA23_c12080	dehydrogenase molybdenum-binding subunit	COG1529	C	GI 5	0.00	12.86
RCA23_c12090	putative HTH-type transcriptional regulator, AraC family	COG2207	K	GI 5	0.00	0.00
RCA23_c12100	periplasmic binding protein-like	COG1879	G	GI 5	0.00	0.00
RCA23_c12110	ROK family transcriptional repressor	COG1940	K	GI 5	0.00	8.48
RCA23_c12120	xylose isomerase	COG1082	G	GI 5	0.00	0.00
RCA23_c12130	sugar ABC transporter, periplasmic binding protein	COG1879	G	GI 5	0.00	0.00
RCA23_c12140	putative oxidoreductase	COG0673	R	GI 5	0.00	0.00
RCA23_c12150	sugar ABC transporter, ATP-binding protein	COG1129	G	GI 5	0.00	6.98
RCA23_c12160	sugar ABC transporter, permease protein	COG1172	G	GI 5	0.00	0.00
RCA23_c12170	hypothetical protein, monoxygenase-like	COG1359	S	GI 5	0.00	0.00
RCA23_c12180	hypothetical protein	COG1082	G	GI 5	0.00	62.23
RCA23_c12190	putative oxidoreductase	COG0673	R	GI 5	0.00	11.02
RCA23_c12200	peptidase M20D, amidohydrolase	COG1473	R	GI 5	100.00	27.15
RCA23_c12210	X-Pro dipeptidase	COG0006	E	GI 5	46.86	29.93
RCA23_c12220	hypothetical protein			GI 5	0.00	0.00
RCA23_c12230	hypothetical protein, transmembrane			GI 5	0.00	0.00
RCA23_c12240	hypothetical protein, DNA breaking rejoining enzymes family protein-like			GI 5	88.64	0.00
RCA23_c12250	hypothetical protein			GI 5	0.00	0.00
RCA23_c12260	hypothetical protein			GI 5	0.00	17.82
RCA23_c12270	hypothetical protein			GI 5	0.00	0.00
RCA23_c12280	type I restriction-modification system, M subunit	COG0286	V	GI 5	0.00	0.00
RCA23_c12290	type I restriction-modification system, S subunit	COG0732	V	GI 5	0.00	0.00
RCA23_c12300	type I restriction-modification system, R subunit	COG0610	V	GI 5	0.00	3.78
RCA23_c12310	hypothetical protein	COG3012	S	GI 5	0.00	0.00

RCA23_c12320	hypothetical protein	COG2865	K	GI 5	0.00	0.00
RCA23_c12330	hypothetical protein			GI 5	0.00	0.00
RCA23_c12340	hypothetical protein, DNA helicase-like protein			GI 5	0.00	0.00
RCA23_c12350	hypothetical protein			GI 5	0.00	0.00
RCA23_c12360	integrase	COG0582	L	GI 5	0.00	0.00
RCA23_c12370	hypothetical protein			GI 5	0.00	0.00
RCA23_c12380	hypothetical protein			GI 5	0.00	0.00
RCA23_c12390	hypothetical protein			GI 5	0.00	0.00
RCA23_c12400	hypothetical protein			GI 5	0.00	0.00
RCA23_c12410	hypothetical protein, DUF1994			GI 5	100.00	47.10
RCA23_c12420	exonuclease I	COG2925	L	GI 5	100.00	70.01
RCA23_c12430	transpeptidase, penicillin binding protein	COG4953	M	GI 5	28.88	44.78
RCA23_c12440	hypothetical protein	COG2373	R	GI 5	22.49	26.91
RCA23_c12450	hypothetical protein			GI 5	0.00	24.93
RCA23_c12460	hypothetical protein			GI 5	0.00	0.00
RCA23_c12470	type III restriction enzyme, res subunit	COG1061	K	GI 5	0.00	31.71
RCA23_c12480	putative type III restriction system protein, mod subunit			GI 5	0.00	53.63
RCA23_c12490	putative serine/threonine protein kinase	COG0515	R	GI 5	0.00	20.27
RCA23_c12500	serine/threonine protein phosphatase PrpC	COG0631	T	GI 5	0.00	37.50
RCA23_c12510	DNA helicase, UvrD/REP type	COG0210	L	GI 5	0.00	0.00
RCA23_c12520	hypothetical protein	COG1463	Q	GI 5	0.00	0.00
RCA23_c12530	hypothetical protein, OmpA/MotB-like	COG1360	N	GI 5	0.00	0.00
RCA23_c12540	hypothetical protein			GI 5	0.00	0.00
RCA23_c12550	ATP-dependent helicase	COG0553	K	GI 5	0.00	0.00
RCA23_c12560	hypothetical protein			GI 5	0.00	0.00
RCA23_c12570	hypothetical protein			GI 5	0.00	0.00
RCA23_c12580	hypothetical protein			GI 5	0.00	0.00
RCA23_c12590	hypothetical protein			GI 5	49.19	0.00
RCA23_c12600	hypothetical protein			GI 5	89.56	0.00
RCA23_c12610	hypothetical protein			GI 5	0.00	0.00
RCA23_c12620	hypothetical protein			GI 5	0.00	0.00
RCA23_c12630	integrase	COG2801	L	GI 5	0.00	100.00
RCA23_c12640	hypothetical protein			GI 5	0.00	0.00

RCA23_c12650	hypothetical protein			GI 5	0.00	0.00
RCA23_c12660	DNA integration/recombination/invertion protein			GI 5	0.00	0.00
RCA23_c12690	putative beta-lactamase-like protein	COG0491	R		100.00	100.00
RCA23_c12680	osmolarity sensor protein EnvZ	COG0642	T		100.00	100.00
RCA23_c12700	hypothetical protein				100.00	100.00
RCA23_c12710	50S ribosomal protein L21	COG0261	J		100.00	100.00
RCA23_c12720	50S ribosomal protein L27	COG0211	J		100.00	100.00
RCA23_c12730	hypothetical protein, LysE type translocator	COG1280	E		100.00	100.00
RCA23_c12740	putative acetyltransferase	COG1670	J		100.00	100.00
RCA23_c12750	GCN5-like N-acetyltransferase	COG1670	J		100.00	100.00
RCA23_c12760	GTP-binding protein Obg	COG0536	R		100.00	100.00
RCA23_c12770	glutamate 5-kinase ProB	COG0263	E		85.73	99.01
RCA23_c12780	gamma-glutamyl phosphate reductase ProA	COG0014	E		80.35	88.94
RCA23_c12800	hypothetical protein	COG5385	S		100.00	100.00
RCA23_c12790	hypothetical protein				100.00	100.00
RCA23_c12810	hypothetical protein	COG3176	R		100.00	100.00
RCA23_c12820	putative phosphate acyltransferase	COG0204	I		100.00	98.29
RCA23_c12830	thiamine-phosphate pyrophosphorylase ThiE	COG0352	H		100.00	92.56
RCA23_c12840	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ	COG0565	J		100.00	100.00
RCA23_c12850	heme A synthase CtaA	COG1612	O		100.00	100.00
RCA23_c12860	thermostable carboxypeptidase 1	COG2317	E		100.00	97.64
RCA23_c12870	DNA gyrase subunit A	COG0188	L		100.00	98.76
RCA23_c12880	hypothetical protein	COG1495	O		100.00	100.00
RCA23_c12890	DedA family protein	COG1238	S		100.00	100.00
RCA23_c12900	hypothetical protein			GI 6	100.00	98.00
RCA23_c12910	putative snoaL-like polyketide cyclase	COG3631	R	GI 6	0.00	87.55
RCA23_c12920	hypothetical protein, DUF1330	COG5470	S	GI 6	0.00	100.00
RCA23_c12930	hypothetical protein, DUF3303			GI 6	0.00	100.00
RCA23_c12940	hypothetical protein, transmembrane			GI 6	100.00	0.00
RCA23_c12950	hypothetical protein, transmembrane			GI 6	100.00	0.00
RCA23_c12960	integrase	COG2801	L	GI 6	2.13	0.00
RCA23_c12970	hypothetical protein			GI 6	0.00	0.00
RCA23_c12980	site-specific recombinase, resolvase family protein	COG1961	L	GI 6	0.00	0.00

RCA23_c12990	hypothetical protein	COG4731	S	GI 6	0.00	100.00
RCA23_c13000	hypothetical protein			GI 6	0.00	0.00
RCA23_c13010	transposase	COG3415	L	GI 6	0.00	0.00
RCA23_c13020	ribsomal protein S21	COG0828	J	GI 6	100.00	100.00
RCA23_c13030	hypothetical protein			GI 6	100.00	45.83
RCA23_c13040	integrase	COG2801	L	GI 6	6.48	0.00
RCA23_c13050	hypothetical protein			GI 6	100.00	85.99
RCA23_c13060	putative phage integrase	COG0582	L	GI 6	100.00	100.00
RCA23_c13080	putative phage integrase	COG0582	L	GI 6	100.00	98.71
RCA23_c13090	hypothetical protein, GYD domain	COG4274	S	GI 6	0.00	0.00
RCA23_c13100	hypothetical protein			GI 6	0.00	12.95
RCA23_c13110	hypothetical protein			GI 6	0.00	100.00
RCA23_c13120	hypothetical protein			GI 6	73.28	65.53
RCA23_c13130	integrase	COG2801	L	GI 6	0.00	0.00
RCA23_c13140	hypothetical protein	COG5586	S	GI 6	90.17	100.00
RCA23_c13150	hypothetical protein			GI 6	100.00	84.93
RCA23_c13160	hypothetical protein			GI 6	100.00	100.00
RCA23_c13170	hypothetical protein	COG4274	S	GI 6	100.00	100.00
RCA23_c13180	hypothetical protein			GI 6	84.67	100.00
RCA23_c13190	hypothetical protein			GI 6	0.00	100.00
RCA23_c13210	phosphoribosylformylglycinamidine cyclo-ligase PurM	COG0150	F		90.87	100.00
RCA23_c13220	phosphoribosylglycinamide formyltransferase PurN	COG0299	F		100.00	100.00
RCA23_c13230	ribonuclease D	COG0349	J		100.00	100.00
RCA23_c13240	SufE-like protein	COG2166	R		100.00	81.51
RCA23_c13250	hypothetical protein				100.00	100.00
RCA23_c13260	putative methionine synthase (B12 dependent) subunit 2	COG5012	R		100.00	100.00
RCA23_c13270	putative methionine synthase (B12 dependent) subunit 1	COG0646	E		100.00	100.00
RCA23_c13280	phosphoribosylaminoimidazole-succinocarboxamide synthase PurC	COG0152	F		100.00	99.77
RCA23_c13290	phosphoribosylformylglycinamidine (FGAM) synthase PurS	COG1828	F		100.00	100.00
RCA23_c13300	phosphoribosylformylglycinamidine synthase PurQ	COG0047	F		100.00	100.00
RCA23_c13310	C4-dicarboxylate transport sensor protein DctB	COG4191	T		100.00	100.00
RCA23_c13320	C4-dicarboxylate transport transcriptional regulatory protein DctD	COG2204	T		100.00	100.00
RCA23_c13330	ribonuclease E	COG1530	J		100.00	99.28

RCA23_c13340	putative sulfurtransferase tusA	COG0425	O	100.00	100.00
RCA23_c13350	cytochrome C biogenesis protein transmembrane region	COG0785	O	100.00	100.00
RCA23_c13360	hypothetical protein			100.00	100.00
RCA23_c13370	putative cytochrome P450	COG2124	Q	100.00	100.00
RCA23_c13380	DNA alkylation repair enzyme	COG4912	L	100.00	100.00
RCA23_c13390	hypothetical protein	COG3153	R	100.00	100.00
RCA23_c13400	glucosamine--fructose-6-phosphate aminotransferase GlmS	COG0449	M	100.00	100.00
RCA23_c13410	bifunctional protein GlmU	COG1207	M	100.00	100.00
RCA23_c13420	putative HAD-superfamily hydrolase	COG0546	R	100.00	100.00
RCA23_c13440	MmgE/PrpD family protein	COG2079	R	100.00	99.16
RCA23_c13430	putative pyridoxal-phosphate-dependent aminotransferase	COG0399	M	94.55	87.12
RCA23_c13450	isovaleryl-CoA dehydrogenase	COG1960	I	100.00	92.78
RCA23_c13460	hypothetical protein			100.00	100.00
RCA23_c13470	methylcrotonoyl-CoA carboxylase beta subunit MccB	COG4799	I	100.00	100.00
RCA23_c13480	hypothetical protein			100.00	94.08
RCA23_c13490	methylcrotonoyl-CoA carboxylase alpha subunit MccA	COG4770	I	100.00	98.45
RCA23_c13500	hydroxymethylglutaryl-CoA lyase MvaB	COG0119	E	100.00	100.00
RCA23_c13510	putative methylglutaconyl-CoA hydratase	COG1024	I	100.00	100.00
RCA23_c13520	NADH-quinone oxidoreductase subunit A	COG0838	C	100.00	100.00
RCA23_c13530	NADH-quinone oxidoreductase subunit NuoB	COG0377	C	100.00	100.00
RCA23_c13540	hypothetical protein DUF2158	COG5475	S	100.00	100.00
RCA23_c13550	NADH-quinone oxidoreductase subunit C	COG0852	C	100.00	100.00
RCA23_c13560	hypothetical protein			100.00	100.00
RCA23_c13570	NADH-quinone oxidoreductase subunit D	COG0649	C	100.00	97.94
RCA23_c13580	NADH-quinone oxidoreductase subunit E	COG1905	C	100.00	84.88
RCA23_c13590	hypothetical protein			100.00	100.00
RCA23_c13600	NADH-quinone oxidoreductase subunit F	COG1894	C	100.00	95.14
RCA23_c13610	hypothetical protein			100.00	96.79
RCA23_c13620	NADH-quinone oxidoreductase subunit G	COG1034	C	100.00	98.27
RCA23_c13630	hypothetical protein			100.00	88.76
RCA23_c13640	NADH-quinone oxidoreductase subunit H	COG1005	C	100.00	91.62
RCA23_c13650	NADH-quinone oxidoreductase subunit I	COG1143	C	100.00	100.00
RCA23_c13660	NADH-quinone oxidoreductase subunit J	COG0839	C	100.00	100.00

RCA23_c13670	NADH-quinone oxidoreductase subunit K	COG0713	C	100.00	100.00
RCA23_c13680	NADH-quinone oxidoreductase subunit L	COG1009	C	100.00	100.00
RCA23_c13690	NADH-quinone oxidoreductase subunit M	COG1008	C	100.00	100.00
RCA23_c13700	NADH-quinone oxidoreductase subunit N	COG1007	C	100.00	100.00
RCA23_c13710	biotin-[acetyl-CoA-carboxylase] ligase	COG0340	H	100.00	100.00
RCA23_c13720	type III pantothenate kinase CoaX	COG1521	K	100.00	100.00
RCA23_c13730	putative ribonuclease	COG0595	R	100.00	100.00
RCA23_c13740	ATP-dependent RNA helicase RhlE	COG0513	L	100.00	95.14
RCA23_c13750	peptide chain release factor 3	COG4108	J	100.00	93.25
RCA23_c13760	hypothetical protein			100.00	89.10
RCA23_c13770	putative short chain dehydrogenase	COG1028	I	100.00	90.77
RCA23_c13780	arsenite methyltransferase	COG2226	H	100.00	100.00
RCA23_c13790	Fe(3+) ions import ATP-binding protein FbpC	COG3842	E	51.16	90.44
RCA23_c13800	putative helix-turn-helix protein	COG2378	K	76.75	100.00
RCA23_c13810	sec-independent protein translocase protein TatA	COG1826	U	100.00	100.00
RCA23_c13820	sec-independent protein translocase protein TatB	COG1826	U	36.47	100.00
RCA23_c13830	sec-independent protein translocase protein TatC	COG0805	U	4.94	97.98
RCA23_c13840	hypothetical protein DUF815	COG2607	R	100.00	100.00
RCA23_c13850	putative peptidoglycan-binding peptidase	COG0739	M	100.00	100.00
RCA23_c13860	protein-L-isoaspartate O-methyltransferase Pcm	COG2518	O	100.00	100.00
RCA23_c13870	5'-nucleotidase SurE	COG0496	R	100.00	100.00
RCA23_c13880	putative short chain dehydrogenase	COG1028	I	100.00	100.00
RCA23_c13890	amidophosphoribosyltransferase PurF	COG0034	F	100.00	98.57
RCA23_c13900	putative colicin V production protein			100.00	100.00
RCA23_c13910	DNA repair protein RadA	COG1066	O	100.00	100.00
RCA23_c13920	ABC transporter ATP-binding protein	COG1127	Q	100.00	100.00
RCA23_c13930	hypothetical protein DUF140	COG0767	Q	100.00	100.00
RCA23_c13940	alanine racemase, biosynthetic	COG0787	M	100.00	100.00
RCA23_c13950	replicative DNA helicase DnaB	COG0305	L	100.00	100.00
RCA23_c13960	orotate phosphoribosyltransferase PyrE	COG0461	F	100.00	100.00
RCA23_c13970	dihydroorotase PyrC	COG0418	F	100.00	95.58
RCA23_c13980	hypothetical protein			100.00	100.00
RCA23_c13990	hypothetical protein			100.00	63.96

RCA23_c14000	hypothetical protein				100.00	87.67
RCA23_c14010	malate dehydrogenase Mdh	COG0039	C		100.00	100.00
RCA23_c14020	citrate lyase beta subunit CitE	COG2301	G		100.00	100.00
RCA23_c14030	putative mesaconyl-CoA hydratase	COG2030	I		100.00	100.00
RCA23_c14040	succinate dehydrogenase cytochrome b556 subunit SdhC	COG2009	C		100.00	100.00
RCA23_c14050	succinate dehydrogenase hydrophobic membrane anchor subunit SdhD	COG2142	C		100.00	100.00
RCA23_c14060	succinate dehydrogenase flavoprotein subunit SdhA	COG1053	C		79.62	100.00
RCA23_c14070	hypothetical protein				100.00	100.00
RCA23_c14080	succinate dehydrogenase iron-sulfur subunit SdhB	COG0479	C		100.00	100.00
RCA23_c14090	purine nucleoside phosphorylase deoD-type	COG0813	F		100.00	91.91
RCA23_c14100	acetyltransferase	COG1246	E		100.00	94.56
RCA23_c14110	tryptophan synthase alpha chain TrpA	COG0159	E		100.00	95.03
RCA23_c14120	GTP-dependent nucleic acid-binding protein EngD	COG0012	J		84.61	100.00
RCA23_c14130	Non-specific ribonucleoside hydrolase rihC	COG1957	F		94.70	100.00
RCA23_c14150	hypothetical protein DUF583	COG1664	M	GI 7	100.00	61.64
RCA23_c14160	protease HtpX	COG0501	O	GI 7	100.00	82.72
RCA23_c14170	histone deacetylase	COG0123	B	GI 7	100.00	66.45
RCA23_c14180	peripheral-type benzodiazepine receptor/signal transduction protein TspO	COG3476	T	GI 7	100.00	48.84
RCA23_c14190	DNA-invertase Hin	COG1961	L	GI 7	60.90	12.61
RCA23_c14200	hypothetical protein			GI 7	0.00	0.00
RCA23_c14210	hypothetical protein			GI 7	0.00	100.00
RCA23_c14220	hypothetical protein, RmlC-like cupin family	COG3450	R	GI 7	0.00	77.25
RCA23_c14230	integrase	COG4974	L	GI 7	99.30	63.65
RCA23_c14240	hypothetical membrane protein			GI 7	100.00	89.26
RCA23_c14260	hypothetical protein	COG4530	S		100.00	100.00
RCA23_c14270	hypothetical protein DUF45	COG1451	R		100.00	100.00
RCA23_c14280	HTH-type transcriptional regulator, GntR family	COG1802	K		100.00	100.00
RCA23_c14290	dihydrolipoyl dehydrogenase Lpd	COG1249	C		100.00	100.00
RCA23_c14300	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate	COG0508	C		100.00	96.66
RCA23_c14310	2-oxoglutarate dehydrogenase E1 component SucA	COG0567	C		88.95	100.00
RCA23_c14320	succinyl-CoA ligase [ADP-forming] alpha subunit SucD	COG0074	C		100.00	100.00
RCA23_c14330	succinyl-CoA ligase [ADP-forming] beta subunit SucC	COG0045	C		100.00	100.00
RCA23_c14340	butyryl-CoA dehydrogenase	COG1960	I		100.00	100.00

RCA23_c14350	translation initiation factor IF-3	COG0290	J	100.00	100.00
RCA23_c14360	ferredoxin--NADP reductase Fpr	COG1018	C	100.00	100.00
RCA23_c14370	hypothetical protein	COG3749	S	100.00	85.29
RCA23_c14380	cysH'	COG0175	E	100.00	100.00
RCA23_c14390	cysI/sir: sulfite reductase (ferredoxin)	COG0155	P	100.00	100.00
RCA23_c14400	hypothetical protein			100.00	100.00
RCA23_c14410	siroheme synthase CysG	COG0007	H	100.00	100.00
RCA23_c14420	HTH-type transcriptional regulator, AsnC family	COG1522	K	100.00	100.00
RCA23_c14450	peptidase	COG0624	E	100.00	100.00
RCA23_c14460	hypothetical protein	COG1426	S	100.00	100.00
RCA23_c14470	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase IspG	COG0821	I	100.00	95.06
RCA23_c14480	TPR-repeat containing protein	COG4783	R	98.33	100.00
RCA23_c14490	aspartate aminotransferase	COG0436	E	100.00	89.56
RCA23_c14500	penicillin-binding protein 1A	COG5009	M	100.00	100.00
RCA23_c14510	peptide chain release factor 2	COG1186	J	41.96	93.96
RCA23_c14520	hypothetical protein DUF583	COG1664	M	0.00	100.00
RCA23_c14530	putative peptidase, M23 family	COG0739	M	55.06	100.00
RCA23_c14540	hypothetical protein DUF455	COG2833	S	100.00	100.00
RCA23_c14550	peroxiredoxin Bcp	COG1225	O	100.00	100.00
RCA23_c14560	hypothetical protein			100.00	95.00
RCA23_c14570	S-adenosylmethionine:tRNA ribosyltransferase-isomerase QueA	COG0809	J	100.00	100.00
RCA23_c14580	MFS-type transporter			100.00	100.00
RCA23_c14590	hypothetical protein DUF924	COG3803	S	100.00	100.00
RCA23_c14600	dihydrolipoyl dehydrogenase Lpd	COG1249	C	100.00	99.79
RCA23_c14610	uvrABC system protein A	COG0178	L	100.00	99.37
RCA23_c14620	MmgE/PrpD family protein	COG2079	R	100.00	100.00
RCA23_c14630	3-hydroxyisobutyrate dehydrogenase MmsB	COG2084	I	100.00	100.00
RCA23_c14640	3-hydroxyisobutyryl-CoA hydrolase	COG1024	I	100.00	100.00
RCA23_c14650	isobutyryl-CoA dehydrogenase	COG1960	I	100.00	95.32
RCA23_c14660	methylmalonate-semialdehyde dehydrogenase MmsA	COG1012	C	100.00	100.00
RCA23_c14670	putative HTH-type transcriptional regulator, LysR family	COG0583	K	100.00	100.00
RCA23_c14680	phosphopantetheine adenylyltransferase CoaD	COG0669	H	100.00	100.00
RCA23_c14690	glyceraldehyde-3-phosphate dehydrogenase Gap	COG0057	G	100.00	100.00

RCA23_c14700	glyceraldehyde-3-phosphate dehydrogenase Gap	COG0057	G	100.00	100.00
RCA23_c14710	transketolase TktA	COG0021	G	95.09	95.93
RCA23_c14720	hypothetical protein			100.00	100.00
RCA23_c14730	cell division protein ZapA	COG3027	S	100.00	100.00
RCA23_c14740	putative glutaredoxin	COG0278	O	100.00	100.00
RCA23_c14750	hypothetical protein			100.00	100.00
RCA23_c14760	hypothetical protein, BolA-like	COG0271	T	100.00	100.00
RCA23_c14770	phosphoribosylformylglycinamidine synthase PurL	COG0046	F	100.00	97.42
RCA23_c14780	HTH-type transcriptional regulator, LysR family	COG0583	K	100.00	100.00
RCA23_c14790	hypothetical protein, pyruvate ferredoxin/flavodoxin oxidoreductase	COG4231	C	100.00	97.99
RCA23_c14800	glutamate racemase MurI	COG0796	M	100.00	100.00
RCA23_c14810	N-acetyl-gamma-glutamyl-phosphate reductase ArgC	COG0002	E	86.88	98.93
RCA23_c14820	cytochrome c-type biogenesis protein CcmE	COG2332	O	54.53	100.00
RCA23_c14830	cytochrome c-type biogenesis protein CcmF	COG1138	O	100.00	99.59
RCA23_c14840	cytochrome c-type biogenesis protein CcmH	COG3088	O	100.00	100.00
RCA23_c14850	putative enoyl-CoA hydratase FadB	COG1024	I	100.00	100.00
RCA23_c14860	hypothetical protein			100.00	100.00
RCA23_c14870	citrate synthase GltA	COG0372	C	100.00	94.65
RCA23_c14880	glutamyl-tRNA synthase 2	COG0008	J	100.00	100.00
RCA23_c14890	hypothetical protein competence protein E	COG0658	R	100.00	100.00
RCA23_c14900	LexA repressor	COG1974	K	100.00	100.00
RCA23_c14910	molybdopterin biosynthesis protein MoeA	COG0303	H	100.00	95.24
RCA23_c14920	molybdenum cofactor biosynthesis protein MoaC	COG0315	H	100.00	100.00
RCA23_c14930	indole-3-glycerol phosphate synthase TrpC	COG0134	E	100.00	100.00
RCA23_c14940	anthranilate phosphoribosyltransferase TrpD	COG0547	E	100.00	91.67
RCA23_c14950	anthranilate synthase component TrpG	COG0512	E	100.00	99.48
RCA23_c14960	hypothetical protein, divergent polysaccharide deacetylase			100.00	100.00
RCA23_c14970	hypothetical protein			100.00	100.00
RCA23_c14990	hypothetical protein	COG3108	S	100.00	100.00
RCA23_c15000	putative L,D-transpeptidase YcbB	COG2989	S	100.00	100.00
RCA23_c15010	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase LpxD	COG1044	M	100.00	100.00
RCA23_c15020	acyl carrier protein	COG0236	I	100.00	100.00
RCA23_c15030	3-oxoacyl-[acyl-carrier-protein] synthase FabF	COG0304	I	100.00	100.00

RCA23_c15040	hypothetical protein, invasion protein B	COG5342	R	100.00	100.00
RCA23_c15050	inner membrane protein	COG4536	P	90.76	96.61
RCA23_c15060	tyrosine recombinase XerD	COG4974	L	100.00	100.00
RCA23_c15070	hypothetical protein			100.00	100.00
RCA23_c15080	hypothetical protein			100.00	100.00
RCA23_c15090	shikimate kinase AroK	COG0703	E	100.00	100.00
RCA23_c15100	3-dehydroquinate synthase AroB	COG0337	E	100.00	100.00
RCA23_c15110	single-stranded DNA-binding protein	COG0629	L	100.00	100.00
RCA23_c15120	glutathione import ATP-binding protein GsiA	COG0444	E	100.00	98.51
RCA23_c15130	putative ABC transporter inner membrane component	COG1173	E	100.00	94.69
RCA23_c15140	putative ABC transporter permease protein	COG0601	E	100.00	100.00
RCA23_c15150	ABC transporter extracellular solute-binding protein	COG0747	E	60.90	100.00
RCA23_c15160	tRNA delta(2)-isopentenylpyrophosphate transferase MiaA	COG0324	J	74.97	100.00
RCA23_c15170	uridylate kinase PyrH	COG0528	F	100.00	100.00
RCA23_c15180	ribosome recycling factor Frr	COG0233	J	100.00	100.00
RCA23_c15190	undecaprenyl pyrophosphate synthase UppS	COG0020	I	100.00	100.00
RCA23_c15200	putative cytidylyltransferase	COG0575	I	100.00	100.00
RCA23_c15210	1-deoxy-D-xylulose 5-phosphate reductoisomerase Dxr	COG0743	I	100.00	98.71
RCA23_c15220	RIP metalloprotease RseP	COG0750	M	100.00	100.00
RCA23_c15230	putative outer membrane assembly factor	COG4775	M	100.00	92.25
RCA23_c15240	putative outer tein			70.97	100.00
RCA23_c15250	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase FabZ	COG0764	I	0.00	100.00
RCA23_c15260	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase LpxA	COG1043	M	83.33	100.00
RCA23_c15270	hypothetical protein DUF1009	COG3494	S	100.00	94.03
RCA23_c15280	lipid-A-disaccharide synthase LpxB	COG0763	M	100.00	100.00
RCA23_c15290	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase TrmU	COG0482	J	85.49	99.56
RCA23_c15300	hypothetical protein			100.00	92.98
RCA23_c15310	cell cycle transcriptional regulator	COG0745	T	77.73	100.00
RCA23_c15320	DNA ligase LigA	COG0272	L	100.00	89.77
RCA23_c15330	ATP-dependent DNA helicase RecG	COG1200	L	98.76	100.00
RCA23_c15340	hypothetical protein			100.00	100.00
RCA23_c15350	hypothetical protein	COG0822	C	100.00	100.00
RCA23_c15360	phosphoribosyl-AMP cyclohydrolase HisI	COG0139	E	100.00	100.00

RCA23_c15370	glutamyl-Q tRNA(Asp) synthase GluQ	COG0008	J	86.90	100.00
RCA23_c15380	hypothetical protein, methyltransferase	COG4976	R	100.00	100.00
RCA23_c15390	tRNA uridine 5-carboxymethylaminomethyl modification enzyme Gid	COG1206	J	100.00	96.56
RCA23_c15400	putative crotonase	COG1024	I	100.00	94.04
RCA23_c15410	putative thioesterase	COG2050	Q	69.98	100.00
RCA23_c15420	50S ribosomal protein L13	COG0102	J	0.00	100.00
RCA23_c15430	30S ribosomal protein S9	COG0103	J	0.00	100.00
RCA23_c15440	integrase			0.00	64.64
RCA23_c15460	choline dehydrogenase BetA	COG2303	E	100.00	89.43
RCA23_c15470	ABC transporter, permease protein	COG4662	H	100.00	100.00
RCA23_c15480	ABC transporter, ATP-binding protein	COG1131	V	100.00	100.00
RCA23_c15490	ABC transporter, periplasmic substrate-binding protein	COG2998	H	100.00	100.00
RCA23_c15500	hypothetical membrane protein	COG1238	S	100.00	100.00
RCA23_c15510	hypothetical protein DUF6 family, transmembrane	COG2962	R	100.00	100.00
RCA23_c15520	hypothetical protein	COG2068	R	100.00	94.33
RCA23_c15530	dimethylglycine dehydrogenase	COG0404	E	100.00	95.19
RCA23_c15540	dimethylglycine dehydrogenase	COG0404	E	100.00	98.03
RCA23_c15550	short-chain dehydrogenase/reductase SDR	COG1028	I	100.00	100.00
RCA23_c15560	hypothetical transmembrane protein	COG3788	R	100.00	100.00
RCA23_c15570	hypothetical protein, tetR regulator	COG1309	K	100.00	100.00
RCA23_c15580	homoserine O-succinyltransferase MetA	COG1897	E	100.00	100.00
RCA23_c15590	hypothetical protein			100.00	100.00
RCA23_c15600	putative integral membrane protein	COG2510	S	60.07	100.00
RCA23_c15610	Gcn5-like N-acetyltransferase	COG1670	J	100.00	84.62
RCA23_c15620	GMP synthase GuaA	COG0519	F	100.00	100.00
RCA23_c15630	trimethylamine methyltransferase MttB	COG5598	H	100.00	100.00
RCA23_c15640	hypothetical protein			100.00	100.00
RCA23_c15650	lipoyl synthase LipA	COG0320	H	100.00	100.00
RCA23_c15660	hypothetical protein			100.00	100.00
RCA23_c15670	hypoxanthine phosphoribosyltransferase Hpt	COG0634	F	100.00	100.00
RCA23_c15680	hypothetical protein	COG2867	I	100.00	100.00
RCA23_c15690	ammonium transporter AmtB	COG0004	P	100.00	100.00
RCA23_c15700	putative competence-damaged protein	COG1546	R	100.00	100.00

RCA23_c15710	phosphatidylglycerophosphatase A	COG1267	I	100.00	100.00
RCA23_c15720	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF	COG0245	I	100.00	97.73
RCA23_c15730	tRNA-dihydrouridine synthase B	COG0042	J	100.00	95.22
RCA23_c15740	histidine kinase, nitrogen regulation protein NtrB	COG3852	T	100.00	100.00
RCA23_c15750	nitrogen regulation protein NtrC	COG2204	T	100.00	100.00
RCA23_c15760	histidine kinase, nitrogen regulation protein NtrY	COG5000	T	100.00	97.57
RCA23_c15770	nitrogen assimilation regulatory protein NtrX	COG2204	T	100.00	100.00
RCA23_c15780	Trk system potassium uptake protein TrkA	COG0569	P	100.00	96.80
RCA23_c15790	putative Trk system potassium uptake protein trkH	COG0168	P	100.00	99.73
RCA23_c15800	RNA-binding protein Hfq	COG1923	R	100.00	100.00
RCA23_c15810	GTP-binding protein HflX	COG2262	R	100.00	100.00
RCA23_c15820	acyl-homoserine lactone acylase QuiP	COG2366	R	100.00	96.81
RCA23_c15830	hypothetical protein	COG2930	S	100.00	93.91
RCA23_c15840	delta-aminolevulinic acid dehydratase HemB	COG0113	H	100.00	91.89
RCA23_c15850	hypothetical protein			100.00	100.00
RCA23_c15860	transcription-repair-coupling factor Mfd	COG1197	L	100.00	98.08
RCA23_c15870	putative DSBA-like thioredoxin family protein	COG2761	Q	100.00	66.67
RCA23_c15880	long-chain-fatty-acid-CoA ligase	COG0318	I	100.00	94.05
RCA23_c15890	HTH-type transcriptional regulator	COG1396	K	100.00	100.00
RCA23_c15900	aquaporin AqpZ	COG0580	G	100.00	100.00
RCA23_c15910	putative extracellular solute-binding protein	COG4166	E	100.00	100.00
RCA23_c15920	lysine exporter protein LysE	COG1279	R	100.00	100.00
RCA23_c15930	hypothetical protein DUF502	COG2928	S	100.00	99.43
RCA23_c15940	pseudouridine-5'-phosphate glycosidase PsuG	COG2313	Q	100.00	100.00
RCA23_c15950	hypothetical protein, pfkB family carbohydrate kinase	COG0524	G	100.00	100.00
RCA23_c15960	cold shock protein CspA	COG1278	K	100.00	100.00
RCA23_c15970	30S ribosomal protein S2	COG0052	J	100.00	100.00
RCA23_c15980	elongation factor Ts	COG0264	J	79.68	100.00
RCA23_c15990	hypothetical protein			95.07	79.32
RCA23_c16000	hypothetical protein, acetyltransferase-like	COG1670	J	100.00	48.43
RCA23_c16010	hypothetical protein, transcription factor NusA like			59.81	73.52
RCA23_c16020	putative phenylacetic acid degradation protein	COG0663	R	0.00	100.00
RCA23_c16030	guanylate kinase Gmk	COG0194	F	91.12	83.02

RCA23_c16040	hypothetical protein, YicC-like	COG1561	S	100.00	100.00
RCA23_c16050	hypothetical protein, DUF1457	COG5388	S	100.00	97.93
RCA23_c16060	phospho-2-dehydro-3-deoxyheptonate aldolase	COG3200	E	100.00	98.91
RCA23_c16070	putative HTH-type transcriptional regulator, AraC family	COG4977	K	100.00	98.52
RCA23_c16080	putative amino-acid binding protein	COG0683	E	100.00	80.88
RCA23_c16090	putative branched-chain amino acid transport ATP-binding protein	COG0411	E	84.49	93.46
RCA23_c16100	putative branched-chain amino acid transport ATP-binding protein	COG0410	E	100.00	79.13
RCA23_c16110	putative branched-chain amino acid transport system permease protein	COG0559	E	100.00	82.35
RCA23_c16120	putative branched-chain amino acid transport system permease protein	COG4177	E	100.00	97.53
RCA23_c16130	GTP-binding protein TypA	COG1217	T	91.58	100.00
RCA23_c16140	hypothetical protein DUF1330	COG5470	S	100.00	65.29
RCA23_c16150	alanyl-tRNA synthase AlaS	COG0013	J	77.92	100.00
RCA23_c16160	protein RecA	COG0468	L	100.00	91.02
RCA23_c16170	hypothetical protein			100.00	100.00
RCA23_c16180	sensor transduction histidine kianse	COG0642	T	71.23	100.00
RCA23_c16190	hypothetical protein			40.23	92.64
RCA23_c16200	hypothetical protein, NOL1/NOP2/sun family	COG0144	J	100.00	89.03
RCA23_c16210	inosine-5'-monophosphate dehydrogenase GuaB	COG0516	F	100.00	100.00
RCA23_c16220	hypothetical protein	COG3894	R	100.00	92.60
RCA23_c16240	cysteine desulfurase SufS	COG0520	E	100.00	100.00
RCA23_c16250	hypothetical protein			100.00	100.00
RCA23_c16260	hypothetical protein			100.00	95.60
RCA23_c16270	FeS assembly protein SufD	COG0719	O	100.00	100.00
RCA23_c16280	FeS assembly ATPase SufC	COG0396	O	100.00	100.00
RCA23_c16290	FeS assembly protein SufB	COG0719	O	59.19	100.00
RCA23_c16300	putative cysteine desulfurase	COG1104	E	100.00	100.00
RCA23_c16310	HTH-type transcriptional regulator Rrf2	COG1959	K	100.00	100.00
RCA23_c16320	hypothetical protein	COG2945	R	100.00	100.00
RCA23_c16330	putative oxidoreductase	COG0673	R	100.00	100.00
RCA23_c16340	inosose dehydratase IolE	COG1082	G	100.00	100.00
RCA23_c16350	putative oxidoreductase	COG0673	R	100.00	100.00
RCA23_c16360	HTH-type transcriptional repressor, LacI family	COG1609	K	100.00	100.00
RCA23_c16370	hypothetical protein			100.00	100.00

RCA23_c16380	sugar (ribose) ABC-transport system ATP binding protein	COG1129	G	100.00	100.00
RCA23_c16390	sugar (ribose) ABC transporter permease protein	COG1172	G	100.00	99.35
RCA23_c16400	sugar (ribose) ABC transporter periplasmic binding protein	COG1879	G	100.00	100.00
RCA23_c16410	beta-glucosidase BglA	COG2723	G	100.00	84.77
RCA23_c16420	maltose/maltodextrin import ATP-binding protein MalK	COG3839	G	100.00	100.00
RCA23_c16430	putative alpha-glucosidase AglA	COG0366	G	100.00	100.00
RCA23_c16440	alpha-glucoside transport system permease protein AglG	COG0395	G	100.00	100.00
RCA23_c16450	ABC transporter, membrane spanning protein	COG0395	G	100.00	100.00
RCA23_c16460	alpha-glucoside transport system permease protein AglF	COG1175	G	100.00	96.57
RCA23_c16470	alpha-glucosides-binding periplasmic protein AglE	COG1653	G	100.00	98.21
RCA23_c16480	HTH-type transcriptional regulator	COG1609	K	100.00	100.00
RCA23_c16490	oxidoreductase	COG4989	R	100.00	100.00
RCA23_c16500	alkanesulfonate monooxygenase SsuD	COG2141	C	100.00	87.13
RCA23_c16510	putative regulatory DNA binding protein	COG2188	K	100.00	94.56
RCA23_c16520	putative oxidoreductase	COG0673	R	100.00	100.00
RCA23_c16530	glucose-6-phosphate isomerase Pgi	COG0166	G	100.00	100.00
RCA23_c16540	6-phosphogluconolactonase Pgl	COG0363	G	100.00	100.00
RCA23_c16550	glucose-6-phosphate 1-dehydrogenase Zwf	COG0364	G	74.66	88.29
RCA23_c16560	hypothetical protein, radical SAM	COG0535	R	100.00	100.00
RCA23_c16570	putative 5-methylcytosine-specific restriction enzyme McrA	COG1403	V	100.00	100.00
RCA23_c16580	putative phospholipase/carboxylesterase	COG0400	R	94.37	98.52
RCA23_c16590	HhH-GPD superfamily base excision DNA repair protein	COG0122	L	98.24	100.00
RCA23_c16600	precorrin-6A reductase CobK	COG2099	H	100.00	97.68
RCA23_c16610	cobalamin (vitamin B12) biosynthesis CbiDprotein CbiD	COG1903	H	100.00	49.41
RCA23_c16620	uroporphyrinogen-III C-methyltransferase CobA	COG0007	H	100.00	100.00
RCA23_c16630	cobyrinic acid A,C-diamide synthase CobB	COG1797	H	100.00	100.00
RCA23_c16640	putative major facilitator superfamily transporter			100.00	95.59
RCA23_c16650	hypothetical protein	COG1562	I	100.00	100.00
RCA23_c16660	cysteinyl-tRNA synthase CysS	COG0215	J	100.00	100.00
RCA23_c16670	aspartate aminotransferase AspC	COG0436	E	100.00	100.00
RCA23_c16680	trimethylamine methyltransferase MttB	COG5598	H	100.00	100.00
RCA23_c16690	ABC transporter ATP-binding protein Uup	COG0488	R	97.63	100.00
RCA23_c16700	hypothetical protein	COG3176	R	100.00	85.60

RCA23_c16710	peptide methionine sulfoxide reductase MsrB	COG0229	O	100.00	89.22
RCA23_c16720	hypothetical protein, lipoprotein	COG2913	J	100.00	81.38
RCA23_c16730	hypothetical protein	COG1399	R	100.00	100.00
RCA23_c16740	fatty acid/phospholipid synthesis protein PlsX	COG0416	I	100.00	100.00
RCA23_c16750	3-oxoacyl-[acyl-carrier-protein] synthase FabH	COG0332	I	100.00	100.00
RCA23_c16760	integration host factor alpha subunit IhfA	COG0776	L	100.00	100.00
RCA23_c16770	hypothetical protein, MerR family regulatory protein	COG0789	K	100.00	95.91
RCA23_c16790	deoxyguanosinetriphosphate triphosphohydrolase-like protein Dcd	COG0717	F	88.73	100.00
RCA23_c16800	putative segregation and condesation protein B	COG1386	K	3.74	100.00
RCA23_c16810	hypothetical protein, segregation and condensation protein A	COG1354	S	100.00	84.61
RCA23_c16820	beta-hexosaminidase NagZ	COG1472	G	100.00	100.00
RCA23_c16830	hypothetical protein			100.00	100.00
RCA23_c16840	arginyl-tRNA synthase	COG0018	J	100.00	100.00
RCA23_c16850	deoxyguanosinetriphosphate triphosphohydrolase-like protein	COG0232	F	100.00	100.00
RCA23_c16860	putative iron-sulfur insertion protein erpA	COG0316	S	100.00	95.41
RCA23_c16870	exodeoxyribonuclease III	COG0708	L	57.16	93.92
RCA23_c16880	putative cytochrome B561	COG3038	C	100.00	99.14
RCA23_c16890	putative dnak suppressor protein dksA	COG1734	T	100.00	63.36
RCA23_c16900	hypothetical protein	COG0714	R	100.00	100.00
RCA23_c16910	hypothetical protein	COG3825	S	100.00	98.90
RCA23_c16920	putative peptidase, M48 family	COG0501	O	100.00	78.99
RCA23_c16930	hypothetical protein			100.00	100.00
RCA23_c16940	putative ribosomal RNA large subunit methyltransferase	COG1092	R	100.00	97.33
RCA23_c16950	phosphogluconate dehydratase Edd	COG0129	E	100.00	100.00
RCA23_c16960	KHG/KDPG aldolase Eda	COG0800	G	100.00	100.00
RCA23_c16970	hypothetical protein			100.00	100.00
RCA23_c16980	glutamate-ammonia-ligase adenylyltransferase GlnE	COG1391	O	100.00	100.00
RCA23_c16990	hypothetical protein	COG2606	S	100.00	100.00
RCA23_c17000	hypothetical protein			100.00	100.00
RCA23_c17010	hypothetical protein			100.00	92.89
RCA23_c17020	hypothetical protein			100.00	92.34
RCA23_c17030	putative aromatic-ring-hydroxylating dioxygenase	COG4638	P	77.49	100.00
RCA23_c17040	putative acetolactate synthase small subunit IlvH	COG0440	E	100.00	100.00

RCA23_c17050	acetolactate synthase isozyme large subunit IlvI	COG0028	E	100.00	92.98
RCA23_c17060	hypothetical membrane protein, porin-like			100.00	100.00
RCA23_c17070	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	100.00	94.50
RCA23_c17080	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	100.00	84.97
RCA23_c17090	TRAP dicarboxylate transporter, subunit DctM	COG4664	Q	100.00	100.00
RCA23_c17100	putative arginyl-tRNA--protein transferase Ate	COG2935	O	100.00	97.45
RCA23_c17110	vitamin B12-dependent ribonucleotide reductase NrdJ	COG0209	F	95.29	97.51
RCA23_c17120	hypothetical protein			100.00	100.00
RCA23_c17140	hypothetical protein DUF192	COG1430	S	100.00	100.00
RCA23_c17150	cold shock protein	COG1278	K	100.00	100.00
RCA23_c17160	pyridoxine/pyridoxamine 5'-phosphate oxidase PdxH	COG0259	H	100.00	100.00
RCA23_c17170	enoyl-[acyl-carrier-protein] reductase FabI	COG0623	I	100.00	99.11
RCA23_c17180	xanthine phosphoribosyltransferase Gpt	COG0503	F	100.00	100.00
RCA23_c17190	pyrimidine-specific ribonucleoside hydrolase RihA	COG1957	F	100.00	88.35
RCA23_c17200	hypothetical protein UPF0061	COG0397	S	100.00	100.00
RCA23_c17210	putative sodium/hydrogen exchanger	COG0025	P	100.00	100.00
RCA23_c17220	ferric uptake regulator protein Fur	COG0735	P	100.00	100.00
RCA23_c17230	putative S-adenosylmethionine uptake transporter	COG0697	G	100.00	94.63
RCA23_c17240	enolase Eno	COG0148	G	100.00	100.00
RCA23_c17250	anhydro-N-acetylmuramic acid kinase AnmK	COG2377	O	100.00	100.00
RCA23_c17260	tyrosyl-tRNA synthase TyrS	COG0162	J	100.00	100.00
RCA23_c17270	aspartate aminotransferase AspC	COG0436	E	100.00	95.63
RCA23_c17280	hypothetical protein	COG0760	O	100.00	99.35
RCA23_c17290	anthranilate synthase component TrpE	COG0147	E	100.00	99.74
RCA23_c17300	protein soxG	COG0491	R	100.00	100.00
RCA23_c17310	protein soxH	COG0491	R	100.00	96.72
RCA23_c17320	5-aminolevulinate synthase HemA	COG0156	H	100.00	72.73
RCA23_c17330	sulfide dehydrogenase flavoprotein chain SoxF	COG3439	S	100.00	100.00
RCA23_c17340	domain of unknown function DUF1791	COG1416	S	100.00	100.00
RCA23_c17350	sulfite oxidase cytochrome subunit SoxD	COG3474	C	100.00	100.00
RCA23_c17360	sulfite oxidase molybdopterin subunit SoxC	COG2041	R	100.00	100.00
RCA23_c17370	sulfur oxidation protein SoxB	COG0737	F	100.00	82.16
RCA23_c17380	diheme cytochrome c	COG3258	C	100.00	100.00

RCA23_c17390	protein SoxZ			100.00	89.09
RCA23_c17400	protein SoxY	COG5501	S	100.00	81.32
RCA23_c17410	cytochrome c	COG2010	C	100.00	64.22
RCA23_c17420	thioredoxin SoxW	COG2143	O	100.00	71.86
RCA23_c17430	cytochrome c-type biogenesis protein SoxV	COG0785	O	100.00	100.00
RCA23_c17440	protein SoxS			100.00	100.00
RCA23_c17450	HTH-type transcriptional regulator, ArsR family	COG0640	K	100.00	100.00
RCA23_c17460	putative soxT, transmembrane protein DUF395	COG2391	R	100.00	100.00
RCA23_c17470	hypothetical protein DUF395	COG2391	R	100.00	100.00
RCA23_c17480	NAD-binding protein	COG2084	I	100.00	100.00
RCA23_c17490	glyoxylate reductase GyaR	COG1052	C	100.00	96.82
RCA23_c17500	glutamyl-tRNA(Gln) amidotransferase subunit A	COG0154	J	100.00	99.25
RCA23_c17510	TRAP dicarboxylate transporter, subunit DctM	COG4664	Q	100.00	96.38
RCA23_c17520	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	100.00	100.00
RCA23_c17530	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	100.00	100.00
RCA23_c17540	hypothetical protein			100.00	100.00
RCA23_c17550	glycerol kinase GlpK	COG0554	C	100.00	100.00
RCA23_c17560	ribosomal RNA large subunit methyltransferase J	COG0293	J	100.00	100.00
RCA23_c17570	putative Ppx/GppA phosphatase family protein	COG0248	F	100.00	99.73
RCA23_c17580	hypothetical protein			100.00	100.00
RCA23_c17590	hypothetical protein	COG0685	E	100.00	100.00
RCA23_c17600	pterin domain containing enzyme	COG1410	E	100.00	97.75
RCA23_c17610	HpcH/HpaI aldolase family protein	COG3836	G	100.00	100.00
RCA23_c17620	glucokinase Glk	COG0837	G	100.00	100.00
RCA23_c17630	hypothetical protein DUF1006	COG3214	S	100.00	100.00
RCA23_c17640	reductive dehalogenase	COG1018	C	100.00	95.60
RCA23_c17650	hypothetical protein, XdhC and CoxI	COG1975	O	100.00	100.00
RCA23_c17660	2-hydroxy-3-oxopropionate reductase GlxR	COG2084	I	100.00	90.68
RCA23_c17670	3-hydroxybutyrate dehydrogenase	COG1028	I	100.00	97.71
RCA23_c17680	dihydroxy-acid dehydratase IlvD	COG0129	E	100.00	99.22
RCA23_c17690	fumarylacetoacetate hydrolase	COG0179	Q	100.00	100.00
RCA23_c17700	hypothetical protein			100.00	100.00
RCA23_c17710	nucleoside diphosphate kinase Ndk	COG0105	F	100.00	100.00

RCA23_c17720	hypothetical protein			59.55	55.34
RCA23_c17730	ABC transporter ATP-binding protein	COG0488	R	100.00	96.25
RCA23_c17740	MarC family integral membrane protein	COG2095	U	100.00	100.00
RCA23_c17750	hypothetical protein	COG3577	R	100.00	92.48
RCA23_c17760	putative DNA polymerase III chi subunit, HolC	COG2927	L	100.00	100.00
RCA23_c17770	cytosol aminopeptidase PepA	COG0260	E	100.00	100.00
RCA23_c17780	puative permease, YjgP/YjgQ family	COG0795	R	100.00	100.00
RCA23_c17790	puative permease, YjgP/YjgQ family	COG0795	R	100.00	100.00
RCA23_c17800	putative organic solvent tolerance protein	COG1452	M	91.88	100.00
RCA23_c17810	hypothetical protein, SurA	COG0760	O	100.00	92.83
RCA23_c17820	4-hydroxythreonine-4-phosphate dehydrogenase PdxA	COG1995	H	100.00	100.00
RCA23_c17830	dimethyladenosine transferase KsgA	COG0030	J	100.00	100.00
RCA23_c17840	hypothetical protein			100.00	100.00
RCA23_c17850	modification methylase, hemK family	COG2890	J	100.00	100.00
RCA23_c17860	peptide chain release factor 1	COG0216	J	100.00	100.00
RCA23_c17870	hypothetical protein	COG4446	S	100.00	100.00
RCA23_c17880	agmatinase SpeB	COG0010	E	100.00	100.00
RCA23_c17890	alpha/beta hydrolase			100.00	86.08
RCA23_c17900	agmatinase SpeB	COG0010	E	100.00	100.00
RCA23_c17910	hippurate hydrolase HipO	COG1473	R	100.00	100.00
RCA23_c17920	protein MazG	COG3956	R	100.00	96.06
RCA23_c17930	ABC transporter periplasmic iron-binding protein FutA	COG1840	P	93.77	95.75
RCA23_c17940	putative peptidyl-prolyl cis-trans isomerase Ppi	COG0652	O	100.00	78.69
RCA23_c17950	putative peptidyl-prolyl cis-trans isomerase Ppi	COG0652	O	100.00	100.00
RCA23_c17960	phosphoglycerate kinase Pgk	COG0126	G	100.00	100.00
RCA23_c17970	fructose-bisphosphate aldolase class 1	COG3588	G	100.00	100.00
RCA23_c17980	hypothetical protein, septum formation initiator	COG2919	D	100.00	100.00
RCA23_c17990	pyruvate dehydrogenase E1 component alpha subunit PdhA	COG1071	C	100.00	100.00
RCA23_c18000	pyruvate dehydrogenase E1 component beta subunit PdhB	COG0022	C	100.00	100.00
RCA23_c18010	dihydrolipoyllysine-residue acetyltransferase PdhC	COG0508	C	100.00	100.00
RCA23_c18020	serine acetyltransferase CysE	COG1045	E	100.00	97.37
RCA23_c18030	putative gene transfer agent protein			50.04	58.62
RCA23_c18040	putative gene transfer agent large terminase part 1	COG5323	S	10.00	3.73

RCA23_c18050	putative gene transfer agent large terminase part 2	COG5323	S	100.00	71.38
RCA23_c18060	aminodeoxychorismate lyase	COG1559	R	100.00	100.00
RCA23_c18070	3-oxoacyl-[acyl-carrier-protein] synthase FabF	COG0304	I	100.00	100.00
RCA23_c18080	acyl carrier protein AcpP	COG0236	I	100.00	100.00
RCA23_c18090	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	100.00	100.00
RCA23_c18100	malonyl CoA-acyl carrier protein transacylase	COG0331	I	100.00	100.00
RCA23_c18110	30S ribosomal protein S6	COG0360	J	100.00	94.81
RCA23_c18120	30S ribosomal protein S18	COG0238	J	100.00	100.00
RCA23_c18130	50S ribosomal protein L9	COG0359	J	100.00	100.00
RCA23_c18140	trigger factor (TF)	COG0544	O	100.00	100.00
RCA23_c18160	nitrogen regulatory protein P-II 1	COG0347	E	100.00	95.87
RCA23_c18170	glutamine synthase GlnA type I	COG0174	E	100.00	99.15
RCA23_c18190	hypothetical protein			100.00	100.00
RCA23_c18180	dimethylpropiothetin dethiomethylase DddP	COG0006	E	100.00	97.95
RCA23_c18200	Biotin transporter BioY	COG1268	R	100.00	87.00
RCA23_c18210	hypothetical protein			100.00	100.00
RCA23_c18220	adenylosuccinate lyase PurB	COG0015	F	100.00	100.00
RCA23_c18230	putative nitrile hydratase, beta subunit			100.00	100.00
RCA23_c18240	hypothetical protein			100.00	100.00
RCA23_c18250	nitrile hydratase alpha subunit NthA			100.00	100.00
RCA23_c18260	hypothetical protein DUF6 transmembrane	COG0697	G	100.00	100.00
RCA23_c18270	putative lipid A biosynthesis lauroyl acyltransferase	COG1560	M	100.00	100.00
RCA23_c18280	hypothetical protein	COG5429	S	100.00	100.00
RCA23_c18290	aconitate hydratase AcnA	COG1048	C	100.00	99.93
RCA23_c18300	cytochrome c biogenesis protein CcmG	COG0526	O	100.00	100.00
RCA23_c18310	cytochrome c-type biogenesis protein CcmC	COG0755	O	100.00	100.00
RCA23_c18320	cytochrome c-type biogenesis protein CcmB	COG2386	O	100.00	100.00
RCA23_c18330	cytochrome c biogenesis ATP-binding export protein CcmA	COG4133	O	100.00	100.00
RCA23_c18340	hypothetical protein	COG3737	S	100.00	100.00
RCA23_c18350	protein export membrane protein SecF	COG0341	U	100.00	100.00
RCA23_c18360	protein export membrane protein SecD	COG0342	U	100.00	96.14
RCA23_c18370	putative immunogenic membrane protein YajC	COG1862	U	100.00	100.00
RCA23_c18380	seryl-tRNA synthase SerS	COG0172	J	100.00	99.15

RCA23_c18390	hypothetical protein, alpha/beta hydrolase-like	COG2267	I	0.00	86.50
RCA23_c18400	GTP-binding protein EngA	COG1160	R	100.00	100.00
RCA23_c18410	putative quinoprotein	COG1520	S	100.00	100.00
RCA23_c18420	hypothetical protein DUF2133	COG4649	S	100.00	100.00
RCA23_c18430	RND efflux transporter, MFP subunit	COG0845	M	100.00	100.00
RCA23_c18440	RND efflux transporter, permease protein	COG0841	V	100.00	98.65
RCA23_c18450	ABC transporter ATP-binding protein	COG5265	O	100.00	97.90
RCA23_c18460	hypothetical protein, peptidoglycan-binding protein domain LysM	COG1652	S	100.00	100.00
RCA23_c18470	protein RarD	COG2962	R	100.00	100.00
RCA23_c18480	superoxide dismutase SodB	COG0605	P	100.00	100.00
RCA23_c18490	sarcosine oxidase subunit SoxG	COG4583	E	100.00	100.00
RCA23_c18500	sarcosine oxidase alpha subunit SoxA	COG0404	E	100.00	91.87
RCA23_c18510	sarcosine oxidase subunit SoxD	COG4311	E	100.00	100.00
RCA23_c18520	sarcosine oxidase beta subunit SoxB	COG0665	E	100.00	100.00
RCA23_c18530	cytochrome c-type biogenesis protein CycH	COG4235	O	100.00	100.00
RCA23_c18540	hypothetical protein	COG0816	L	100.00	100.00
RCA23_c18550	hypothetical protein DUF1289	COG3313	R	100.00	100.00
RCA23_c18560	hypothetical protein			100.00	100.00
RCA23_c18570	hypothetical protein DUF81	COG0730	R	100.00	100.00
RCA23_c18580	tRNA-dihydrouridine synthase Dus	COG0042	J	97.08	83.63
RCA23_c18590	putative peroxiredoxin (thioredoxin reductase)	COG0678	O	0.00	0.00
RCA23_c18600	benzaldehyde dehydrogenase	COG1012	C	0.00	0.00
RCA23_c18610	hypothetical protein			0.00	0.00
RCA23_c18620	hypothetical protein	COG2130	R	99.52	100.00
RCA23_c18630	MFS-type transporter	COG2814	G	100.00	100.00
RCA23_c18640	sorbitol dehydrogenase	COG1028	I	100.00	100.00
RCA23_c18650	6-hydroxynicotinate 3-monooxygenase	COG0654	H	100.00	85.61
RCA23_c18660	hypothetical protein			100.00	100.00
RCA23_c18670	glycerate kinase	COG2379	G	100.00	90.19
RCA23_c18680	putative carboxymuconolactone decarboxylase	COG0599	S	100.00	100.00
RCA23_c18690	2,4-dienoyl-CoA reductase [NADPH]	COG1902	C	100.00	97.17
RCA23_c18700	thiamine pyrophosphate protein	COG0028	E	100.00	100.00
RCA23_c18710	rffG/rfbB: dTDP-glucose 4,6-dehydratase	COG1088	M	91.97	100.00

RCA23_c18720	hypothetical protein			100.00	94.02
RCA23_c18730	choline dehydrogenase BetA	COG2303	E	100.00	94.44
RCA23_c18740	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit ScoB	COG2057	I	100.00	100.00
RCA23_c18750	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit ScoA	COG1788	I	100.00	100.00
RCA23_c18760	hypothetical membrane protein			100.00	100.00
RCA23_c18770	putative dimethyl sulfoniopropionate demethylase DmdA	COG0404	E	100.00	100.00
RCA23_c18780	hydantoin utilization protein A	COG0145	E	100.00	100.00
RCA23_c18790	hydantoin utilization protein B	COG0146	E	100.00	94.67
RCA23_c18800	FAD dependent oxidoreductase	COG0665	E	73.78	100.00
RCA23_c18810	hypothetical protein, 3-beta hydroxysteroid dehydrogenase	COG0451	M	100.00	100.00
RCA23_c18820	hypothetical protein, serine/threonine-protein kinase	COG1262	S	100.00	100.00
RCA23_c18830	hypothetical protein	COG0457	R	100.00	85.69
RCA23_c18840	hypothetical protein DUF1989	COG3665	S	100.00	100.00
RCA23_c18850	putative diaminopropionate ammonia-lyase	COG1171	E	70.99	100.00
RCA23_c18860	hypothetical protein, metallopeptidase M24	COG0006	E	100.00	91.49
RCA23_c18870	hypothetical protein, Asp/Glu/hydantoin racemase	COG3473	Q	100.00	100.00
RCA23_c18880	putative 3-oxoadipate enol-lactonase 2, alpha/beta hydrolase family	COG0596	R	100.00	100.00
RCA23_c18890	hypothetical protein DUF1185			100.00	100.00
RCA23_c18900	limonene 1,2-monooxygenase LimB	COG2141	C	100.00	100.00
RCA23_c18910	aldehyde dehydrogenase, cytosolic	COG1012	C	100.00	100.00
RCA23_c18920	ABC transporter, spermidine/putrescine import, permease protein PotC	COG1177	E	100.00	100.00
RCA23_c18930	ABC transporter, spermidine/putrescine import, permease protein PotB	COG1176	E	100.00	100.00
RCA23_c18940	ABC transporter, spermidine/putrescine import, substrate binding protein Pot	COG0687	E	100.00	92.44
RCA23_c18950	ABC transporter, spermidine/putrescine import, ATP-binding protein PotA	COG3842	E	100.00	84.06
RCA23_c18960	putative nitrilotriacetate monooxygenase component B	COG1853	R	100.00	100.00
RCA23_c18970	hypothetical protein, DUF268			70.60	99.44
RCA23_c18980	hypothetical protein DUF28	COG0217	S	100.00	100.00
RCA23_c18990	sodium/sulphate symporter	COG0471	P	100.00	96.98
RCA23_c19000	hypothetical protein	COG0697	G	95.82	99.45
RCA23_c19010	hypothetical protein	COG1692	S	33.09	100.00
RCA23_c19020	osmotically inducible OsmC-like protein	COG1764	O	100.00	100.00
RCA23_c19030	3-hydroxyacyl-CoA dehydrogenase, NAD-binding	COG1250	I	100.00	95.02
RCA23_c19040	putative transcriptional regulator	COG0703	E	100.00	97.50

RCA23_c19050	thioesterase-like protein	COG0824	R	31.07	100.00
RCA23_c19060	benzoyl-CoA oxygenase component A	COG0369	P	0.00	94.54
RCA23_c19070	benzoyl-CoA oxygenase component B	COG3396	S	86.65	98.01
RCA23_c19080	benzoyl-CoA-dihydrodiol lyase BoxC	COG1024	I	100.00	100.00
RCA23_c19090	hypothetical protein DUF309			100.00	100.00
RCA23_c19100	alpha/beta hydrolase	COG0596	R	100.00	100.00
RCA23_c19110	benzoate-coenzyme A ligase	COG0318	I	100.00	100.00
RCA23_c19120	putative 5-formyltetrahydrofolate cyclo-ligase family protein	COG0212	H	100.00	100.00
RCA23_c19130	magnesium transporter MgtE	COG2239	P	100.00	97.82
RCA23_c19140	guanine deaminase GuaD	COG0402	F	78.94	88.73
RCA23_c19150	putative hydroxydechloroatrazine ethylaminohydrolase	COG0402	F	100.00	100.00
RCA23_c19160	putative inositol monophosphatase family protein	COG0483	G	100.00	100.00
RCA23_c19170	putative helix-turn-helix protein	COG1396	K	100.00	100.00
RCA23_c19180	putative alcohol dehydrogenase	COG0604	C	100.00	100.00
RCA23_c19190	putative inner membrane protein	COG0670	R	100.00	100.00
RCA23_c19200	hypothetical protein			100.00	100.00
RCA23_c19210	putative N-acetylmuramoyl-L-alanine amidase amiD	COG3023	V	100.00	100.00
RCA23_c19220	hypothetical protein			100.00	100.00
RCA23_c19230	glutamyl-tRNA(Gln) amidotransferase subunit A	COG0154	J	100.00	100.00
RCA23_c19240	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit GatC	COG0721	J	100.00	100.00
RCA23_c19250	putative deaminase	COG0590	F	100.00	66.90
RCA23_c19260	putative ribosomal large subunit pseudouridine synthase B	COG1187	J	100.00	100.00
RCA23_c19270	molybdate ABC transporter, ATP-binding protein ModC	COG4148	P	100.00	97.94
RCA23_c19280	molybdate ABC transporter, pemease protein ModB	COG4149	P	100.00	100.00
RCA23_c19290	molybdate ABC transporter, substrate binding protein ModA	COG0725	P	92.51	100.00
RCA23_c19300	hypothetical protein, NUDIX hydrolase	COG0494	L	100.00	100.00
RCA23_c19310	hypothetical protein DUF1178	COG5319	S	100.00	100.00
RCA23_c19320	aspartokinase LysC	COG0527	E	100.00	100.00
RCA23_c19330	phosphoenolpyruvate-protein phosphotransferase PstI	COG3605	T	100.00	99.02
RCA23_c19340	hypothetical protein, acetyltransferase-like	COG3153	R	100.00	100.00
RCA23_c19350	hypothetical protein	COG1853	R	100.00	100.00
RCA23_c19360	putative sulfate transporter	COG0659	P	100.00	100.00
RCA23_c19370	methylthioadenosine phosphorylase MtnP	COG0005	F	100.00	100.00

RCA23_c19380	adenine phosphoribosyltransferase Apt	COG0503	F	100.00	100.00
RCA23_c19390	ribosomal-protein-alanine acetyltransferase RimJ	COG1670	J	100.00	100.00
RCA23_c19400	uncharacterized zinc protease YmxG	COG0612	R	100.00	100.00
RCA23_c19410	threonine synthase ThrC	COG0498	E	100.00	100.00
RCA23_c19420	hypothetical protein, SURF1	COG3346	S	100.00	100.00
RCA23_c19430	cytochrome c oxidase subunit 3	COG1845	C	100.00	97.64
RCA23_c19440	cytochrome c oxidase assembly protein CtaG	COG3175	O	100.00	100.00
RCA23_c19450	protoheme IX farnesyltransferase CtaB	COG0109	O	100.00	100.00
RCA23_c19460	cytochrome c oxidase subunit 2 precursor	COG1622	C	100.00	100.00
RCA23_c19470	protein TldD	COG0312	R	100.00	96.41
RCA23_c19480	SMF family protein	COG0758	L	100.00	97.57
RCA23_c19490	DNA topoisomerase TopA	COG0550	L	66.94	100.00
RCA23_c19500	fructose-bisphosphate aldolase Fba	COG0191	G	100.00	100.00
RCA23_c19510	5-deoxy-glucuronate isomerase IolB	COG3718	G	100.00	100.00
RCA23_c19520	5-dehydro-2-deoxygluconokinase IolC	COG0524	G	100.00	95.76
RCA23_c19530	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase IolD	COG3962	E	100.00	100.00
RCA23_c19540	hypothetical protein DUF989	COG3748	S	100.00	100.00
RCA23_c19550	5-hydroxyisourate hydrolase UraH	COG2351	R	100.00	100.00
RCA23_c19560	uric acid degradation bifunctional protein PucL	COG3195	S	100.00	96.32
RCA23_c19570	putative allantoin catabolism protein YlbA	COG3257	R	100.00	97.94
RCA23_c19580	sarcosine oxidase beta subunit SoxB	COG0665	E	100.00	100.00
RCA23_c19590	sarcosine oxidase subunit SoxD	COG4311	E	100.00	100.00
RCA23_c19600	sarcosine oxidase alpha subunit SoxA	COG0404	E	99.56	99.42
RCA23_c19610	sarcosine oxidase subunit SoxG	COG4583	E	100.00	100.00
RCA23_c19620	putative HTH-type transcriptional regulator, AraC family	COG4977	K	100.00	98.81
RCA23_c19630	putative DNA-binding protein	COG1396	K	100.00	99.85
RCA23_c19640	putative membrane protein			100.00	100.00
RCA23_c19650	hypothetical protein			100.00	87.92
RCA23_c19660	hypothetical protein, thioesterase	COG2050	Q	15.78	100.00
RCA23_c19670	hypothetical protein, calcineurin-like phosphoesterase-like	COG1407	R	91.10	74.81
RCA23_c19680	putative DEAD/DEAH box helicase	COG1201	R	100.00	97.90
RCA23_c19690	bidunctional enzyme FolD	COG0190	H	100.00	100.00
RCA23_c19700	formate--tetrahydrofolate ligase Fhs	COG2759	F	100.00	98.45

RCA23_c19710	hypothetical protein			100.00	100.00
RCA23_c19720	cell division protease FtsH	COG0465	O	100.00	100.00
RCA23_c19730	tRNA(Ile)-lysidine synthase TilS	COG0037	D	100.00	100.00
RCA23_c19740	hypothetical protein	COG1729	S	100.00	100.00
RCA23_c19750	peptidoglycan-associated lipoprotein Pal	COG2885	M	100.00	90.42
RCA23_c19760	Tol-Pal system beta propeller repeat protein TolB	COG0823	U	100.00	100.00
RCA23_c19770	hypothetical protein, TolA-like			100.00	86.45
RCA23_c19780	biopolymer transport protein TolR	COG0848	U	100.00	100.00
RCA23_c19790	biopolymer transport protein TolQ	COG0811	U	100.00	100.00
RCA23_c19800	acyl-CoA thioester hydrolase	COG0824	R	100.00	100.00
RCA23_c19810	hypothetical protein			100.00	100.00
RCA23_c19820	holliday junction ATP-dependent DNA helicase RuvB	COG2255	L	100.00	100.00
RCA23_c19830	holliday junction ATP-dependent DNA helicase RuvA	COG0632	L	100.00	100.00
RCA23_c19840	crossover junction endodeoxyribonuclease RuvC	COG0817	L	100.00	100.00
RCA23_c19850	putative ribosomal protein L11 methyltransferase	COG2264	J	100.00	100.00
RCA23_c19860	peptide methionine sulfoxide reductase MsrA	COG0225	O	100.00	100.00
RCA23_c19870	hypothetical protein, major facilitator superfamily transporter			100.00	100.00
RCA23_c19880	L-lactate dehydrogenase IldD	COG1304	C	100.00	100.00
RCA23_c19890	BCCT family transporter involved in DMSP uptake	COG1292	M	100.00	91.01
RCA23_c19900	putative MFS-type transporter			100.00	87.26
RCA23_c19910	50S ribosomal protein L25	COG1825	J	100.00	100.00
RCA23_c19920	peptidyl-tRNA hydrolase Pth	COG0193	J	100.00	100.00
RCA23_c19930	hypothetical protein	COG4427	S	100.00	99.22
RCA23_c19940	hypothetical protein	COG3651	S	100.00	100.00
RCA23_c19950	tryptophan synthase beta chain TrpB	COG0133	E	100.00	100.00
RCA23_c19960	N-(5'-phosphoribosyl)anthranilate isomerase TrpF	COG0135	E	100.00	100.00
RCA23_c19970	hypothetical protein			100.00	100.00
RCA23_c19980	integration host factor beta subunit IhfB	COG0776	L	100.00	100.00
RCA23_c19990	30S ribosomal protein S1	COG0539	J	100.00	100.00
RCA23_c20000	hypothetical protein			100.00	100.00
RCA23_c20010	hypothetical protein, lacI family HTH-type regulatory protein	COG1609	K	0.88	100.00
RCA23_c20020	putative phytanoyl-CoA dioxygenase	COG5285	Q	33.68	100.00
RCA23_c20030	aldo/keto reductase	COG0667	C	100.00	100.00

RCA23_c20040	cytidylate kinase Cmk	COG0283	F	15.77	94.05
RCA23_c20050	3-phosphoshikimate 1-carboxyvinyltransferase AroA	COG0128	E	100.00	100.00
RCA23_c20060	tRNA (guanine-N(7)-)-methyltransferase TrmB	COG0220	R	100.00	100.00
RCA23_c20070	S-adenosylmethionine synthase MetK	COG0192	H	100.00	100.00
RCA23_c20080	apolipoprotein N-acyltransferase Lnt	COG0815	M	100.00	100.00
RCA23_c20090	putative magnesium and cobalt efflux protein	COG1253	R	100.00	100.00
RCA23_c20100	hypothetical protein UPF0054	COG0319	R	100.00	100.00
RCA23_c20110	PhoH-like protein	COG1702	T	100.00	100.00
RCA23_c20120	RNA modification enzyme, MiaB family	COG0621	J	100.00	96.92
RCA23_c20130	hypothetical protein			100.00	100.00
RCA23_c20140	putative ferric uptake regulator family protein	COG0735	P	100.00	100.00
RCA23_c20150	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase FabA	COG0764	I	100.00	100.00
RCA23_c20160	3-oxoacyl-[acyl-carrier-protein] synthase FabB	COG0304	I	100.00	100.00
RCA23_c20170	enoyl-[acyl-carrier-protein] reductase FabI	COG0623	I	100.00	97.47
RCA23_c20180	threo-3-hydroxyaspartate ammonia-lyase SRY	COG1171	E	100.00	100.00
RCA23_c20190	2-haloalkanoic acid dehalogenase	COG1011	R	100.00	97.51
RCA23_c20200	3-oxoadipate enol-lactonase CatD	COG0596	R	100.00	100.00
RCA23_c20210	putative tetracycline resistance protein, class C	COG2814	G	100.00	97.88
RCA23_c20220	NAD/mycothiol-dependent formaldehyde dehydrogenase	COG1062	C	100.00	100.00
RCA23_c20230	D-galactonate dehydratase DgoD	COG4948	M	100.00	100.00
RCA23_c20240	dimethylglycine dehydrogenase	COG0404	E	100.00	99.88
RCA23_c20250	trimethylamine methyltransferase MttB	COG5598	H	100.00	99.42
RCA23_c20260	hypothetical protein	COG0607	P	100.00	100.00
RCA23_c20270	uncharacterized aminotransferase	COG0161	H	100.00	100.00
RCA23_c20280	aminomethyltransferase, mitochondrial	COG0404	E	100.00	98.18
RCA23_c20290	glycine cleavage system protein GcvH	COG0509	E	100.00	100.00
RCA23_c20300	glycine dehydrogenase GcvP	COG1003	E	100.00	99.96
RCA23_c20310	D-amino acid dehydrogenase small subunit DadA	COG0665	E	100.00	100.00
RCA23_c20320	putrescine ABC transport system putrescine-binding periplasmic protein PotF	COG0687	E	100.00	100.00
RCA23_c20330	putrescine ABC transport system ATP-binding protein PotG	COG3842	E	100.00	100.00
RCA23_c20340	putrescine ABC transport system permease protein PotI	COG1177	E	100.00	100.00
RCA23_c20350	putrescine ABC transport system permease protein PotB	COG1176	E	100.00	100.00
RCA23_c20360	rieske 2Fe-2S domain protein	COG4638	P	100.00	100.00

RCA23_c20370	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	100.00	100.00
RCA23_c20380	TRAP dicarboxylate transporter, subunit DctQ	COG3090	G	100.00	100.00
RCA23_c20390	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	100.00	100.00
RCA23_c20400	putative phytanoyl-CoA dioxygenase	COG5285	Q	100.00	100.00
RCA23_c20410	putative phenylacetic acid degradation NADH oxidoreductase PaaE	COG1018	C	100.00	82.96
RCA23_c20420	phenylacetate-CoA oxygenase, subunit PaaD	COG2151	R	100.00	100.00
RCA23_c20430	phenylacetate-CoA oxygenase, subunit PaaC	COG3396	S	100.00	100.00
RCA23_c20440	phenylacetate-CoA oxygenase, subunit PaaB	COG3460	Q	100.00	100.00
RCA23_c20450	phenylacetate-CoA oxygenase, subunit PaaA	COG3396	S	100.00	100.00
RCA23_c20460	phenylacetic acid degradation operon negative regulatory protein PaaX	COG3327	K	100.00	100.00
RCA23_c20470	phenylacetic acid degradation protein PaaZ	COG1012	C	100.00	100.00
RCA23_c20480	putative enoyl-CoA hydratase PaaG	COG1024	I	100.00	100.00
RCA23_c20490	acyl-coenzyme A thioesterase PaaI	COG2050	Q	100.00	100.00
RCA23_c20500	beta-ketoadipyl CoA thiolase PaaJ	COG0183	I	100.00	100.00
RCA23_c20510	phenylacetate-CoA ligase PaaK	COG1541	H	100.00	100.00
RCA23_c20520	putative HTH-type transcriptional regulator, TetR family	COG1309	K	100.00	100.00
RCA23_c20530	3-dehydroquinate dehydratase AroQ	COG0757	E	100.00	100.00
RCA23_c20540	tyrosine decarboxylase	COG0076	E	100.00	100.00
RCA23_c20550	putative short chain dehydrogenase	COG0300	R	100.00	100.00
RCA23_c20560	hypothetical protein, acetyltransferase-like	COG1247	M	100.00	100.00
RCA23_c20570	protein CsaA	COG0073	R	100.00	100.00
RCA23_c20580	pyrroline-5-carboxylate reductase ProC	COG0345	E	100.00	88.85
RCA23_c20590	hypothetical protein DUF1790	COG5465	S	100.00	100.00
RCA23_c20600	hypothetical protein DUF526	COG2960	S	100.00	82.81
RCA23_c20610	prolipoprotein diacylglyceryl transferase Lgt	COG0682	M	100.00	100.00
RCA23_c20620	hypothetical protein DUF185	COG1565	S	100.00	100.00
RCA23_c20630	multi-copper polyphenol oxidoreductase laccase	COG1496	S	100.00	100.00
RCA23_c20640	hypothetical protein			100.00	85.94
RCA23_c20650	leucine-responsive regulatory protein Lrp	COG1522	K	100.00	93.74
RCA23_c20660	thioredoxin reductase TrxB	COG0492	O	100.00	100.00
RCA23_c20670	bifunctional sulfate adenylyltransferase / adenylyl-sulfate kinase CysC	COG2046	P	100.00	100.00
RCA23_c20680	hypothetical protein DUF1150			100.00	100.00
RCA23_c20690	small heat shock protein IbpA	COG0071	O	100.00	100.00

RCA23_c20700	hypothetical protein DUF465	COG5481	S	100.00	100.00
RCA23_c20710	N5-carboxyaminoimidazole ribonucleotide mutase PurE	COG0041	F	100.00	100.00
RCA23_c20720	N5-carboxyaminoimidazole ribonucleotide synthase PurK	COG0026	F	100.00	100.00
RCA23_c20730	hypothetical protein	COG1075	R	100.00	84.51
RCA23_c20740	chaperonin GroEL	COG0459	O	77.09	97.64
RCA23_c20750	chaperonin GroS	COG0234	O	3.82	100.00
RCA23_c20760	hypothetical protein			100.00	99.68
RCA23_c20770	hypothetical protein			100.00	86.83
RCA23_c20780	hypothetical protein			100.00	100.00
RCA23_c20790	creatinase	COG0006	E	100.00	100.00
RCA23_c20800	putative membrane lipoprotein			100.00	100.00
RCA23_c20810	hypothetical protein DUF261	COG5482	S	100.00	100.00
RCA23_c20820	putative manganese-dependent inorganic pyrophosphatase PpaC	COG1227	C	100.00	100.00
RCA23_c20830	hypothetical protein, HAD family hydrolase	COG0647	G	100.00	100.00
RCA23_c20840	putative MaoC-like dehydratase	COG2030	I	100.00	100.00
RCA23_c20850	riboflavin biosynthesis protein RibF	COG0196	H	100.00	100.00
RCA23_c20860	hypothetical protein UPF0260	COG2983	S	100.00	100.00
RCA23_c20870	low specificity L-threonine aldolase ItaE	COG2008	E	100.00	100.00
RCA23_c20880	hypothetical protein, 2-hydroxychromene-2-carboxylate isomerase-like	COG3917	Q	100.00	100.00
RCA23_c20890	ribose-phosphate pyrophosphokinase Prs	COG0462	F	79.31	100.00
RCA23_c20900	hypothetical protein			100.00	80.37
RCA23_c20910	ATP synthase epsilon chain AtpC	COG0355	C	100.00	100.00
RCA23_c20920	ATP synthase beta subunit AtpD	COG0055	C	100.00	95.93
RCA23_c20930	ATP synthase gamma chain AtpG	COG0224	C	100.00	95.86
RCA23_c20940	ATP synthase alpha subunit AtpA	COG0056	C	100.00	100.00
RCA23_c20950	ATP synthase delta chain AtpH	COG0712	C	100.00	98.24
RCA23_c20960	hypothetical protein			88.98	100.00
RCA23_c20970	hydroxyacylglutathione hydrolase GloB	COG0491	R	100.00	100.00
RCA23_c20980	ATP-dependent Clp protease ATP-binding subunit ClpA	COG0542	O	100.00	100.00
RCA23_c20990	hypothetical protein, OmpA	COG1360	N	100.00	100.00
RCA23_c21000	hypothetical protein			100.00	100.00
RCA23_c21010	putative cation transport protein ChaC	COG3703	P	100.00	93.41
RCA23_c21020	hypothetical protein	COG1357	S	88.91	90.70

RCA23_c21030	protein TyrC	COG0287	E	100.00	100.00
RCA23_c21040	histidinol-phosphate aminotransferase HisC	COG0079	E	100.00	100.00
RCA23_c21050	30S ribosomal protein S4	COG0522	J	100.00	91.17
RCA23_c21060	cold-shock DEAD box protein A	COG0513	L	100.00	100.00
RCA23_c21070	hypothetical protein DUF393	COG3011	S	100.00	100.00
RCA23_c21080	vitamin B12-dependent ribonucleoside-diphosphate reductase	COG0209	F	100.00	100.00
RCA23_c21090	hypothetical protein	COG5458	S	100.00	100.00
RCA23_c21100	ATP-phosphoribosyltransferase HisG	COG0040	E	100.00	100.00
RCA23_c21110	ATP phosphoribosyltransferase regulatory subunit HisZ	COG3705	E	98.19	95.42
RCA23_c21120	histidyl-tRNA synthase HisS	COG0124	J	73.57	100.00
RCA23_c21130	hypothetical protein	COG2900	S	100.00	100.00
RCA23_c21140	DNA polymerase III 1 alpha subunit DnaE	COG0587	L	100.00	98.86
RCA23_c21150	xanthine dehydrogenase XdhA	COG4630	F	100.00	100.00
RCA23_c21160	xanthine dehydrogenase XdhB	COG4631	F	95.14	98.87
RCA23_c21170	xanthine dehydrogenase accessory protein XdhC	COG1975	O	100.00	100.00
RCA23_c21180	sugar ABC transporter, ATP-binding protein	COG3845	R	100.00	100.00
RCA23_c21190	sugar ABC transporter, permease protein	COG4603	R	100.00	91.90
RCA23_c21200	ABC transporter permease protein	COG1079	R	100.00	100.00
RCA23_c21210	putative basic membrane protein	COG1744	R	100.00	100.00
RCA23_c21220	putative FAD dependent oxidoreductase	COG0665	E	86.30	100.00
RCA23_c21230	dimethylglycine dehydrogenase	COG0404	E	99.44	100.00
RCA23_c21240	pantothenate synthase PanC	COG0414	H	100.00	80.00
RCA23_c21250	3-methyl-2-oxobutanoate hydroxymethyltransferase PanB	COG0413	H	100.00	100.00
RCA23_c21260	hypothetical protein	COG3807	S	100.00	100.00
RCA23_c21270	peptidyl-dipeptidase Dcp	COG0339	E	58.17	99.85
RCA23_c21280	molybdopterin biosynthesis protein MoeB	COG0476	H	100.00	100.00
RCA23_c21290	deoxyuridine 5'-triphosphate nucleotidohydrolase Dut	COG0756	F	100.00	100.00
RCA23_c21300	coenzyme A biosynthesis bifunctional protein CoaBC	COG0452	H	100.00	100.00
RCA23_c21310	RNA polymerase sigma-32 factor RpoH	COG0568	K	100.00	98.63
RCA23_c21320	bifunctional adenosylcobalamin biosynthesis protein CobP	COG2087	H	100.00	100.00
RCA23_c21330	putative phosphoglycerate mutase family protein	COG0406	G	100.00	100.00
RCA23_c21340	hypothetical protein, glutathione S-transferase	COG0625	O	100.00	100.00
RCA23_c21350	glutathione S-transferase family protein			100.00	100.00

RCA23_c21360	magnesium chelatase-like protein	COG0606	O	100.00	100.00
RCA23_c21370	magnesium chelatase	COG0606	O	100.00	91.27
RCA23_c21380	putative transmembrane protein			43.10	100.00
RCA23_c21390	putative sulfite exporter TauE/SafE	COG0730	R	20.92	100.00
RCA23_c21400	branched-chain amino acid transporter, permease component	COG1079	R	100.00	100.00
RCA23_c21410	branched-chain amino acid transporter, permease component	COG4603	R	100.00	100.00
RCA23_c21420	ABC transporter ATP-binding protein	COG3845	R	100.00	97.79
RCA23_c21430	putative ABC transporter, periplasmic substrate-binding protein	COG1744	R	100.00	100.00
RCA23_c21440	hypothetical protein, acetyltransferase-like	COG0456	R	100.00	100.00
RCA23_c21450	NifU-like protein	COG0694	O	100.00	100.00
RCA23_c21460	putative universal stress protein	COG0589	T	100.00	94.35
RCA23_c21470	tryptophanyl-tRNA synthase TrpS	COG0180	J	100.00	100.00
RCA23_c21480	hypothetical protein, rhomboid protease	COG0705	R	100.00	87.56
RCA23_c21490	virulence factor MviN homolg	COG0728	R	94.92	100.00
RCA23_c21500	uridylyltransferase GlnD	COG2844	O	100.00	100.00
RCA23_c21510	hypothetical protein	COG0683	E	100.00	100.00
RCA23_c21520	putative tetrapyrrole methylase	COG0313	R	100.00	100.00
RCA23_c21530	hypothetical protein UPF0102	COG0792	L	100.00	100.00
RCA23_c21540	glutathione synthase GshB	COG0189	H	100.00	100.00
RCA23_c21550	putative esterase/lipase	COG0657	I	100.00	97.46
RCA23_c21560	NusB-like protein NusB	COG0781	K	100.00	100.00
RCA23_c21570	6,7-dimethyl-8-ribityllumazine synthase RibH	COG0054	H	100.00	100.00
RCA23_c21580	riboflavin biosynthesis protein RibB	COG0108	H	100.00	100.00
RCA23_c21590	riboflavin synthase alpha chain RibE	COG0307	H	100.00	89.97
RCA23_c21600	putative capsule polysaccharide export protein	COG3562	M	100.00	98.39
RCA23_c21610	putative polysaccharide export protein	COG1596	M	100.00	89.38
RCA23_c21620	putative capsule polysaccharide export protein	COG3563	M	90.91	100.00
RCA23_c21630	riboflavin biosynthesis protein RibD	COG0117	H	100.00	100.00
RCA23_c21640	transcriptional repressor NrdR	COG1327	K	100.00	100.00
RCA23_c21650	RNA polymerase sigma factor RpoD	COG0568	K	100.00	100.00
RCA23_c21660	DNA primase DnaG	COG0358	L	100.00	100.00
RCA23_c21670	sarcosine oxidase subunit SoxG	COG4583	E	100.00	100.00
RCA23_c21680	sarcosine oxidase alpha subunit SoxA	COG0404	E	100.00	98.16

RCA23_c21690	sarcosine oxidase subunit SoxD	COG4311	E	100.00	100.00
RCA23_c21700	sarcosine oxidase beta subunit SoxB	COG0665	E	100.00	100.00
RCA23_c21710	phosphatidylserine decarboxylase proenzyme Psd	COG0688	I	100.00	100.00
RCA23_c21720	diacylglycerol kinase	COG0818	M	100.00	100.00
RCA23_c21730	putative sulfatase	COG2194	R	100.00	100.00
RCA23_c21740	hypothetical protein, CDP-alcohol phosphatidyltransferase-like	COG1183	I	100.00	100.00
RCA23_c21750	hypothetical protein	COG0671	I	100.00	100.00
RCA23_c21760	hypothetical protein	COG2194	R	100.00	100.00
RCA23_c21770	hypothetical protein, DUF1705	COG2194	R	100.00	100.00
RCA23_c21780	glutamate dehydrogenase GluD	COG0334	E	96.73	99.23
RCA23_c21790	hypothetical protein			100.00	100.00
RCA23_c21800	2-hydroxy-3-oxopropionate reductase GarR	COG2084	I	90.37	100.00
RCA23_c21810	reductive dehalogenase	COG1600	C	26.15	100.00
RCA23_c21820	pirin	COG1741	R	100.00	99.67
RCA23_c21830	transcriptional regulator	COG1309	K	100.00	100.00
RCA23_c21840	hypothetical protein			100.00	100.00
RCA23_c21850	homoserine dehydrogenase Hom	COG0460	E	91.55	100.00
RCA23_c21860	fructose-1,6-bisphosphatase class II	COG1494	G	100.00	100.00
RCA23_c21870	putative single-stranded-DNA-specific exonuclease	COG0608	L	100.00	100.00
RCA23_c21890	sulfopyruvate decarboxylase beta subunit ComE	COG0028	E	100.00	100.00
RCA23_c21900	sulfopyruvate decarboxylase alpha subunit ComD	COG4032	R	100.00	100.00
RCA23_c21910	zinc-type alcohol dehydrogenase	COG1063	E	100.00	100.00
RCA23_c21920	gluconate 5-dehydrogenase Gno	COG1028	I	100.00	100.00
RCA23_c21930	histidinol dehydrogenase HisD	COG0141	E	100.00	100.00
RCA23_c21940	HTH-type transcriptional regulator, LacI family	COG1609	K	100.00	100.00
RCA23_c21950	HTH-type transcriptional regulator, IclR family	COG1414	K	100.00	100.00
RCA23_c21960	alcohol dehydrogenase AlkJ	COG2303	E	100.00	95.01
RCA23_c21970	integral membrane protein TerC	COG0861	P	100.00	86.40
RCA23_c21980	putative TRAP transporter, DctP subunit	COG4663	Q	33.69	100.00
RCA23_c21990	TRAP transporter, DctM/DctQ subunit	COG4664	Q	89.37	100.00
RCA23_c22000	trimethylamine methyltransferase	COG5598	H	99.44	100.00
RCA23_c22010	putative HAD-family hydrolase	COG0546	R	98.57	77.40
RCA23_c22020	hypothetical protein			0.00	100.00

RCA23_c22030	hypothetical protein				0.00	100.00
RCA23_c22040	hypothetical protein				72.85	88.66
RCA23_c22050	hypothetical protein	COG5349	S		100.00	100.00
RCA23_c22060	hypothetical protein, NUDIX hydrolase	COG0494	L		100.00	100.00
RCA23_c22070	hypothetical protein				100.00	100.00
RCA23_c22080	putative fatty acid desaturase	COG3239	I		100.00	100.00
RCA23_c22090	putative helix-turn-helix protein	COG1396	K		100.00	100.00
RCA23_c22100	short chain dehydrogenase	COG1028	I		100.00	100.00
RCA23_c22110	putative 3-hydroxyacyl-CoA dehydrogenase	COG1250	I		100.00	100.00
RCA23_c22130	hypothetical protein, DUF849	COG3246	S		100.00	100.00
RCA23_c22120	transcriptional regulator, AraC family	COG4977	K		100.00	98.15
RCA23_c22140	protein Tas	COG0667	C		100.00	100.00
RCA23_c22150	hypothetical protein	COG4544	S		100.00	100.00
RCA23_c22160	putative MFS-type transporter	COG2211	G		100.00	99.35
RCA23_c22170	methionyl-tRNA synthase MetG	COG0143	J		100.00	100.00
RCA23_c22190	integrase			GI 8	65.69	100.00
RCA23_c22200	integrase	COG4974	L	GI 8	100.00	93.84
RCA23_c22210	putative nucleotidyl transferase	COG1210	M	GI 8	42.77	100.00
RCA23_c22220	hypothetical protein			GI 8	0.00	92.08
RCA23_c22230	hypothetical protein			GI 8	7.79	76.78
RCA23_c22240	putative replication factor C, small subunit	COG2256	L	GI 8	100.00	100.00
RCA23_c22250	hypothetical protein			GI 8	100.00	100.00
RCA23_c22260	hypothetical protein			GI 8	100.00	98.44
RCA23_c22270	ParB-like nuclease	COG1475	K	GI 8	100.00	97.83
RCA23_c22280	cadmium-transporting ATPase CadA	COG2217	P	GI 8	94.20	92.03
RCA23_c22290	hypothetical protein	COG3034	S	GI 8	0.00	100.00
RCA23_c22300	putative lipoprotein signal peptidase	COG0597	M	GI 8	0.00	100.00
RCA23_c22310	putative ZIP zinc transporter	COG0428	P	GI 8	3.41	100.00
RCA23_c22320	hypothetical protein DUF411	COG3019	R	GI 8	100.00	100.00
RCA23_c22330	SCO-like protein	COG1999	R	GI 8	100.00	100.00
RCA23_c22340	hypothetical protein	COG2847	S	GI 8	100.00	100.00
RCA23_c22350	hypothetical protein	COG1651	O	GI 8	100.00	100.00
RCA23_c22360	hypothetical protein, disulfide bond formation protein	COG1495	O	GI 8	100.00	100.00

RCA23_c22370	SCO-like protein	COG1999	R	GI 8	100.00	100.00
RCA23_c22380	putative HTH-type transcriptional regulator	COG0789	K	GI 8	100.00	100.00
RCA23_c22390	hypothetical protein UPF0060	COG1742	S	GI 8	26.61	100.00
RCA23_c22400	hypothetical protein			GI 8	100.00	100.00
RCA23_c22410	hypothetical protein			GI 8	90.61	88.57
RCA23_c22420	transposase	COG3316	L	GI 8	1.98	0.00
RCA23_c22430	MORN motif precursor	COG4642	S	GI 8	92.77	87.96
RCA23_c22440	transposase	COG3316	L	GI 8	87.01	0.00
RCA23_c22450	hypothetical protein			GI 8	100.00	41.98
RCA23_c22460	hypothetical protein			GI 8	0.00	100.00
RCA23_c22470	hypothetical protein	COG3295	S	GI 8	0.00	0.00
RCA23_c22480	hypothetical protein			GI 8	0.00	0.00
RCA23_c22490	hypothetical protein			GI 8	0.00	0.00
RCA23_c22500	transcriptional regulator, LuxR family	COG2197	T	GI 8	0.00	0.00
RCA23_c22510	hypothetical protein	COG3316	L	GI 8	0.00	0.00
RCA23_c22520	hypothetical protein, HTH-type transcriptional regulator, LuxR family	COG5616	S	GI 8	0.00	43.46
RCA23_c22530	cysteine synthase CysK	COG0031	E	GI 8	0.00	23.80
RCA23_c22540	hypothetical protein			GI 8	0.00	80.00
RCA23_c22550	hypothetical protein			GI 8	0.00	0.00
RCA23_c22560	hypothetical protein			GI 8	43.51	100.00
RCA23_c22570	hypothetical protein			GI 8	100.00	98.38
RCA23_c22580	hypothetical protein	COG5470	S	GI 8	100.00	15.00
RCA23_c22590	coniferyl aldehyde dehydrogenase CalB	COG1012	C	GI 8	92.50	91.22
RCA23_c22600	regulatory protein NocR	COG0583	K	GI 8	97.88	47.60
RCA23_c22610	sn-glycerol-3-phosphate-binding periplasmic protein UgpB	COG1653	G	GI 8	100.00	71.23
RCA23_c22620	sn-glycerol-3-phosphate transport system permease protein UgpA	COG1175	G	GI 8	100.00	100.00
RCA23_c22630	sn-glycerol-3-phosphate transport system permease protein UgpE	COG0395	G	GI 8	100.00	60.57
RCA23_c22640	sn-glycerol-3-phosphate import ATP-bindingprotein UgpC	COG3839	G	GI 8	100.00	30.18
RCA23_c22650	putative glycerophosphoryl diester phosphodiesterase	COG0584	C	GI 8	86.31	77.10
RCA23_c22660	aerobic glycerol-3-phosphate dehydrogenase GlpD	COG0578	C	GI 8	100.00	36.21
RCA23_c22670	hypothetical protein, Na+/Pi-cotransporter	COG1283	P	GI 8	90.48	16.94
RCA23_c22680	hypothetical protein, calcineurin-like phosphoesterase-like	COG1409	R	GI 8	100.00	27.78
RCA23_c22690	ABC transporter permease protein	COG0395	G	GI 8	95.06	30.25

RCA23_c22700	ABC transporter permease protein	COG1175	G	GI 8	21.59	0.00
RCA23_c22710	ABC transporter extracellular solute-binding protein	COG1653	G	GI 8	100.00	0.00
RCA23_c22720	ABC transporter ATP-binding protein	COG3839	G	GI 8	100.00	0.00
RCA23_c22730	HTH-type transcriptional regulator, DeoR family	COG1349	K	GI 8	100.00	28.92
RCA23_c22740	HAD-superfamily hydrolase, subfamily IIB	COG0561	R	GI 8	100.00	33.58
RCA23_c22750	putative inner membrane transporter	COG0697	G	GI 8	100.00	100.00
RCA23_c22760	soluble aldose sugar dehydrogenase YliI	COG2133	G	GI 8	100.00	97.17
RCA23_c22770	putative FKBP-type peptidyl-prolyl cis-trans isomerase	COG0545	O	GI 8	75.38	43.59
RCA23_c22780	putative NnrU family protein	COG4094	S	GI 8	81.42	81.42
RCA23_c22790	hypothetical protein			GI 8	98.28	44.44
RCA23_c22800	putative adenine methyltransferase	COG0863	L	GI 8	52.56	49.53
RCA23_c22810	hypothetical protein			GI 8	100.00	0.00
RCA23_c22820	phage uncharacterised protein	COG5410	S	GI 8	40.93	0.00
RCA23_c22830	hypothetical protein, resolvase-like	COG1961	L	GI 8	0.00	0.00
RCA23_c22840	putative prophage integrase	COG0582	L	GI 8	0.00	0.00
RCA23_c22850	hypothetical protein, putative phage-like protein			GI 8	0.00	0.00
RCA23_c22860	hypothetical protein	COG3311	K	GI 8	0.00	0.00
RCA23_c22870	hypothetical protein			GI 8	0.00	0.00
RCA23_c22880	hypothetical protein			GI 8	54.14	46.50
RCA23_c22890	DNA polymerase III	COG5545	R	GI 8	100.00	89.39
RCA23_c22900	hypothetical protein, periplasmic binding protein-like	COG2998	H	GI 8	0.00	0.00
RCA23_c22910	hypothetical protein			GI 8	0.00	81.13
RCA23_c22920	transposase	COG3316	L	GI 8	0.00	5.37
RCA23_c22930	molybdopterin biosynthesis protein MoeA	COG0303	H	GI 8	0.00	75.38
RCA23_c22940	molybdopterin-guanine dinucleotide biosynthesis protein MobB	COG1763	H	GI 8	0.00	97.39
RCA23_c22950	hypothetical protein, MobA-like	COG0746	H	GI 8	0.00	75.08
RCA23_c22960	formate dehydrogenase family accessory protein FdhD	COG1526	C	GI 8	0.00	96.01
RCA23_c22970	molybdopterin-converting factor subunit MoaE	COG0314	H	GI 8	0.00	98.42
RCA23_c22980	molybdopterin-converting factor subunit MoaD	COG1977	H	GI 8	0.00	92.68
RCA23_c22990	transposase	COG3328	L	GI 8	0.00	100.00
RCA23_c23000	molybdenum cofactor biosynthesis protein MoaA	COG2896	H	GI 8	0.00	76.98
RCA23_c23010	transposase			GI 8	0.00	89.01
RCA23_c23020	ABC transporter, ATP-binding cassette protein	COG3839	G	GI 8	0.00	76.75

RCA23_c23030	ABC transporter, permease protein	COG4662	H	GI 8	0.00	68.37
RCA23_c23040	formate dehydrogenase, gamma subunit FdhI	COG2864	C	GI 8	0.00	97.17
RCA23_c23050	formate dehydrogenase, iron-sulfur subunit FdhB	COG0437	C	GI 8	0.00	100.00
RCA23_c23060	formate dehydrogenase alpha subunit FdhA	COG0243	C	GI 8	7.36	98.65
RCA23_c23070	putative twin-arginine translocation pathway signal sequence domain			GI 8	100.00	93.23
RCA23_c23080	hypothetical protein, cytoplasmic chaperon TorD	COG3381	R	GI 8	100.00	43.89
RCA23_c23090	hypothetical protein			GI 8	100.00	81.11
RCA23_c23100	putative molybdopterin-guanine dinucleotide biosynthesis protein A			GI 8	47.65	51.60
RCA23_c23110	hypothetical protein, 4Fe-4S ferredoxin-like	COG1148	C	GI 8	53.82	95.73
RCA23_c23120	hypothetical protein			GI 8	0.00	82.64
RCA23_c23130	hypothetical protein			GI 8	0.00	100.00
RCA23_c23140	hypothetical protein, Mrp/NBP35 family protein	COG0489	D	GI 8	0.00	56.63
RCA23_c23150	hypothetical protein	COG0340	H	GI 8	0.00	100.00
RCA23_c23160	hypothetical protein			GI 8	0.00	100.00
RCA23_c23170	putative phage terminase			GI 8	0.00	0.00
RCA23_c23180	transposase	COG3316	L	GI 8	0.00	0.00
RCA23_c23190	putative phage helicase	COG3378	R	GI 8	0.00	58.97
RCA23_c23200	hypothetical protein			GI 8	0.00	100.00
RCA23_c23210	putative pyridoxal 4-dehydrogenase	COG0667	C	GI 8	0.00	0.00
RCA23_c23220	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase KduD	COG1028	I	GI 8	0.00	0.00
RCA23_c23230	putative L-rhamnonate dehydratase rhamD	COG4948	M	GI 8	0.00	0.00
RCA23_c23240	ureidoglycolate lyase	COG0179	Q	GI 8	0.00	0.00
RCA23_c23250	D-3-phosphoglycerate dehydrogenase	COG1052	C	GI 8	0.00	0.00
RCA23_c23260	uncharacterized oxidoreductase	COG1028	I	GI 8	0.00	0.00
RCA23_c23270	putative rhamnose mutarotase RhaM	COG3254	S	GI 8	0.00	0.00
RCA23_c23280	putative acetoacetate decarboxylase Adc	COG4689	Q	GI 8	0.00	0.00
RCA23_c23290	uncharacterized oxidoreductase	COG0673	R	GI 8	0.00	0.00
RCA23_c23300	transcriptional regulator, GntR family	COG2186	K	GI 8	0.00	0.00
RCA23_c23310	putative ribose ABC transport system, permease protein RbsC	COG1172	G	GI 8	0.00	0.00
RCA23_c23320	putative ribose ABC transport system, permease protein RbsC	COG1172	G	GI 8	0.00	0.00
RCA23_c23330	ribose import ABC transporter, ATP-binding protein RbsA	COG1129	G	GI 8	0.00	0.00
RCA23_c23340	putative rhamnose ABC transport system, substrate-binding protein RhaS	COG1879	G	GI 8	0.00	0.00
RCA23_c23350	galactonate dehydratase	COG4948	M	GI 8	0.00	0.00

RCA23_c23360	xylose isomerase-like	COG1082	G	GI 8	0.00	0.00
RCA23_c23370	putative aldo/keto reductase	COG0667	C	GI 8	0.00	0.00
RCA23_c23380	amidohydrolase	COG3618	R	GI 8	0.00	0.00
RCA23_c23390	hypothetical protein			GI 8	0.00	0.00
RCA23_c23400	transposase	COG3316	L	GI 8	0.00	5.79
RCA23_c23410	L-rhamnose mutarotase RhaM	COG3254	S	GI 8	0.00	31.45
RCA23_c23420	ureidoglycolate lyase	COG0179	Q	GI 8	0.00	27.06
RCA23_c23430	dihydrodipicolinate synthase DapA	COG0329	E	GI 8	0.00	0.00
RCA23_c23440	amidohydrolase	COG3618	R	GI 8	0.00	0.00
RCA23_c23450	3-ketoacyl-(acyl-carrier-protein) reductase FabG	COG1028	I	GI 8	0.00	0.00
RCA23_c23460	L-rhamnonate dehydratase RhmD	COG4948	M	GI 8	0.00	0.00
RCA23_c23470	polyamine ABC transporter, ATP-binding protein PotA	COG3842	E	GI 8	0.00	0.00
RCA23_c23480	polyamine ABC transporter, permease protein	COG1177	E	GI 8	0.00	0.00
RCA23_c23490	polyamine ABC transporter, permease protein	COG1176	E	GI 8	0.00	0.00
RCA23_c23500	polyamine ABC transporter, substrate binding protein	COG0687	E	GI 8	0.00	0.00
RCA23_c23510	hypothetical protein			GI 8	0.00	0.00
RCA23_c23520	hypothetical protein			GI 8	0.00	0.00
RCA23_c23530	uncharacterized oxidoreductase	COG1028	I	GI 8	55.29	0.00
RCA23_c23540	L-rhamnonate dehydratase	COG4948	M	GI 8	100.00	7.73
RCA23_c23550	ribose ABC transport system, permease protein RbsC	COG1172	G	GI 8	9.20	0.00
RCA23_c23560	ribose import ABC transporter, ATP-binding protein RbsA	COG1129	G	GI 8	0.00	29.44
RCA23_c23570	ribose import ABC transporter, substrate binding protein RbsC	COG1879	G	GI 8	1.80	0.00
RCA23_c23580	HTH-type transcriptional regulator, GntR family	COG1609	K	GI 8	100.00	0.00
RCA23_c23590	hypothetical protein	COG3311	K	GI 8	100.00	0.00
RCA23_c23600	putative DNA-binding protein	COG1396	K	GI 8	0.00	100.00
RCA23_c23610	glutamine amidotransferase-like protein GlxB	COG0067	E	GI 8	0.00	97.88
RCA23_c23620	glutamate synthase alpha subunit GlxC	COG0070	E	GI 8	0.00	80.68
RCA23_c23630	glutamate synthase large subunit GlxD	COG0069	E	GI 8	0.00	96.35
RCA23_c23640	glutamine synthase GlnA type III	COG0174	E	GI 8	0.00	75.58
RCA23_c23650	hypothetical protein			GI 8	0.00	0.00
RCA23_c23660	methyltrasnferase	COG0863	L	GI 8	42.40	20.00
RCA23_c23670	hypothetical protein			GI 8	100.00	4.43
RCA23_c23680	putative terminase, large subunit	COG5410	S	GI 8	94.28	41.63

RCA23_c23690	hypothetical protein, DUF2924			GI 8	0.00	0.00
RCA23_c23700	hypothetical protein, resolvase-like	COG1961	L	GI 8	9.15	0.00
RCA23_c23720	signal transduction histidine kinase	COG0642	T		100.00	97.31
RCA23_c23730	mercuric reductase MerA	COG1249	C		100.00	99.22
RCA23_c23740	hypothetical protein	COG0398	S		100.00	93.31
RCA23_c23750	putative ribonuclease P	COG0594	J		100.00	100.00
RCA23_c23760	hypothetical protein DUF37	COG0759	S		100.00	100.00
RCA23_c23770	hypothetical protein				100.00	100.00
RCA23_c23780	tRNA 2-thiocytidine biosynthesis protein TtcA	COG0037	D		100.00	100.00
RCA23_c23790	putative diguanylate phosphodiesterase	COG2200	T		100.00	100.00
RCA23_c23800	inner membrane protein OxaA	COG0706	U		100.00	99.50
RCA23_c23810	hypothetical protein, molybdenum cofactor sulfurase	COG3217	R		100.00	100.00
RCA23_c23820	putative GTP-binding protein EngB	COG0218	R		100.00	100.00
RCA23_c23830	acetylglutamate kinase ArgB	COG0548	E		100.00	100.00
RCA23_c23840	putative fatty acid hydroxylase	COG3000	I		100.00	97.35
RCA23_c23850	hypothetical protein	COG1148	C		100.00	94.52
RCA23_c23860	hypothetical protein, phosphogylcerate mutase	COG2062	T		100.00	100.00
RCA23_c23870	glutamate/glutamine/aspartate/asparagine transport ATP-binding protein Bzt	COG1126	E		100.00	100.00
RCA23_c23880	glutamate/glutamine/aspartate/asparagine transport system permease prote	COG0765	E		100.00	100.00
RCA23_c23890	glutamate/glutamine/aspartate/asparagine transport system permease prote	COG4597	E		62.65	78.89
RCA23_c23900	glutamate/glutamine/aspartate/asparagine-binding protein BztA	COG0834	E		100.00	98.19
RCA23_c23910	ATP chaperone protein	COG5387	O		93.48	100.00
RCA23_c23920	putative phosphoglycerate phosphatase	COG0546	R		100.00	100.00
RCA23_c23930	ribosomal large subunit pseudouridine synthase C	COG0564	J		100.00	100.00
RCA23_c23940	putative ccrb-like protein	COG0239	D		100.00	100.00
RCA23_c23950	replication-associated recombination protein A	COG2256	L		100.00	100.00
RCA23_c23960	HTH-type transcriptional regulator, LuxR family	COG2197	T		100.00	100.00
RCA23_c23970	50S ribosomal protein L17	COG0203	J		100.00	100.00
RCA23_c23980	DNA-directed RNA polymerase alpha subunit RpoA	COG0202	K		100.00	100.00
RCA23_c23990	30S ribosomal protein S11	COG0100	J		100.00	100.00
RCA23_c24000	30S ribosomal protein S13	COG0099	J		100.00	100.00
RCA23_c24010	adenylate kinase Adk	COG0563	F		100.00	99.38
RCA23_c24020	preprotein translocase subunit SecY	COG0201	U		100.00	100.00

RCA23_c24030	50S ribosomal protein L15	COG0200	J	100.00	100.00
RCA23_c24040	50S ribosomal protein L30	COG1841	J	100.00	100.00
RCA23_c24050	30S ribosomal protein S5	COG0098	J	100.00	100.00
RCA23_c24060	50S ribosomal protein L18	COG0256	J	100.00	100.00
RCA23_c24070	50S ribosomal protein L6	COG0097	J	100.00	100.00
RCA23_c24080	30S ribosomal protein S8	COG0096	J	100.00	100.00
RCA23_c24090	30S ribosomal protein S14	COG0199	J	100.00	100.00
RCA23_c24100	50S ribosomal protein L5	COG0094	J	100.00	100.00
RCA23_c24110	50S ribosomal protein L24	COG0198	J	100.00	100.00
RCA23_c24120	50S ribosomal protein L14	COG0093	J	100.00	100.00
RCA23_c24130	30S ribosomal protein S17	COG0186	J	100.00	100.00
RCA23_c24140	50S ribosomal protein L29	COG0255	J	70.53	100.00
RCA23_c24150	hypothetical protein			71.98	95.65
RCA23_c24160	50S ribosomal protein L23	COG0089	J	100.00	100.00
RCA23_c24170	50S ribosomal protein L4	COG0088	J	100.00	100.00
RCA23_c24180	50S ribosomal protein L3	COG0087	J	100.00	100.00
RCA23_c24190	30S ribosomal protein S10	COG0051	J	100.00	100.00
RCA23_c24200	elongation factor Tu (EF-Tu)	COG0050	J	100.00	31.12
RCA23_c24210	elongation factor FusA	COG0480	J	100.00	100.00
RCA23_c24220	30S ribosomal protein S7	COG0049	J	100.00	100.00
RCA23_c24230	30S ribosomal protein S12	COG0048	J	100.00	100.00
RCA23_c24240	hypothetical protein	COG1072	H	100.00	51.54
RCA23_c24250	ABC transporter ATP-binding protein	COG1129	G	100.00	94.47
RCA23_c24260	ABC tansporter permease protein	COG1172	G	100.00	100.00
RCA23_c24270	putative ABC transporter periplasmic binding protein	COG1879	G	100.00	96.82
RCA23_c24280	putative transcriptional repressor	COG1940	K	100.00	86.31
RCA23_c24290	hypothetical protein, acyl-CoA thioesterase-like	COG2755	E	100.00	100.00
RCA23_c24300	ABC transporter ATP-binding protein	COG1136	V	100.00	100.00
RCA23_c24310	putative ABC transporter permease protein	COG3127	Q	100.00	100.00
RCA23_c24320	hypothetical protein, gylcosyl transferase family 2	COG0463	M	95.78	100.00
RCA23_c24330	aminotransferase class-III	COG0161	H	100.00	100.00
RCA23_c24340	putative ectoine utilization protein EutD	COG0006	E	100.00	100.00
RCA23_c24350	putative integral membrane proein DUF6			100.00	100.00

RCA23_c24360	4-coumarate--CoA ligase	COG0318	I		100.00	100.00
RCA23_c24370	hypothetical protein	COG0679	R		100.00	100.00
RCA23_c24380	hypothetical protein DUF125	COG1814	S		100.00	100.00
RCA23_c24390	transcriptional regulator, AsnC family	COG1522	K		100.00	86.95
RCA23_c24400	arginase ArcA	COG0010	E		100.00	100.00
RCA23_c24410	ornithine cyclodeaminase ArcB	COG2423	E		100.00	100.00
RCA23_c24420	bifunctional protein PutA	COG4230	C		100.00	100.00
RCA23_c24430	hypothetical protein				0.00	100.00
RCA23_c24440	hypothetical protein				0.00	100.00
RCA23_c24460	hypothetical protein				100.00	100.00
RCA23_c24450	creatinase	COG0006	E		100.00	100.00
RCA23_c24470	putative hydrolase	COG0596	R		95.99	0.00
RCA23_c24480	glycine betaine/L-proline transport system permease protein ProW	COG4176	E		100.00	46.78
RCA23_c24490	glycine betaine/L-proline transport ATP-binding protein ProV	COG4175	E		19.41	5.59
RCA23_c24500	glycine betaine-binding periplasmic protein ProX	COG2113	E		13.46	13.87
RCA23_c24510	putative HTH-type transcriptional regluator, LysR family	COG0583	K		100.00	85.20
RCA23_c24520	D-cysteine desulfhydrase DcyD	COG2515	E		100.00	100.00
RCA23_c24530	hypothetical protein				100.00	86.27
RCA23_c24540	high-affinity zinc uptake system protein ZnuA	COG4531	P		100.00	100.00
RCA23_c24550	zinc uptake regulator	COG0735	P		100.00	100.00
RCA23_c24560	zinc import ATP-binding protein ZnuC	COG1121	P		100.00	100.00
RCA23_c24570	high-affinity zinc uptake system membrane protein ZnuB	COG1108	P		100.00	100.00
RCA23_c24580	4-hydroxyphenylpyruvate dioxygenase Hpd	COG3185	E		100.00	97.53
RCA23_c24590	hypothetical protein			GI 9	0.00	83.48
RCA23_c24600	hypothetical protein			GI 9	0.00	64.23
RCA23_c24610	hypothetical protein	COG1028	I	GI 9	21.14	100.00
RCA23_c24620	hypothetical protein	COG1402	R	GI 9	100.00	77.28
RCA23_c24630	putative gluconolactonase	COG3386	G	GI 9	100.00	95.04
RCA23_c24640	ribokinase RbsK	COG0524	G	GI 9	100.00	100.00
RCA23_c24650	ribose ABC transporter protein RbsD	COG4154	G	GI 9	100.00	79.69
RCA23_c24660	putative ribose ABC transporter, ATP-binding protein RbsA	COG3839	G	GI 9	100.00	96.72
RCA23_c24670	putative ribose ABC transporter, substrate binding protein RbsB	COG1653	G	GI 9	100.00	92.16
RCA23_c24680	putative ribose ABC transporter, permease protein RbsC	COG1175	G	GI 9	100.00	100.00

RCA23_c24690	putative ribose ABC transporter, permease protein RbsC	COG0395	G	GI 9	100.00	80.61
RCA23_c24700	hypothetical protein, L-fucose isomerase-like			GI 9	100.00	99.66
RCA23_c24710	sugar isomerase	COG0794	M	GI 9	100.00	81.72
RCA23_c24720	xylulose kinase XylB	COG1070	G	GI 9	24.61	100.00
RCA23_c24730	aminopeptidase SgcX	COG1363	G	GI 9	0.00	86.83
RCA23_c24740	photosystem I biogenesis protein BtpA	COG0434	R	GI 9	0.00	100.00
RCA23_c24750	pyridoxal 4-dehydrogenase Pld	COG0667	C	GI 9	17.69	100.00
RCA23_c24760	putative amidohydrolase	COG3618	R	GI 9	100.00	100.00
RCA23_c24770	putative carbohydrate kinase, pfkB family	COG0524	G	GI 9	100.00	100.00
RCA23_c24780	xylose isomerase family protein	COG4952	M	GI 9	100.00	98.89
RCA23_c24790	putative HTH-type transcriptional regulator, GntR family	COG1802	K	GI 9	100.00	100.00
RCA23_c24800	mandelate racemase/muconate lactonizing enzyme	COG4948	M	GI 9	100.00	100.00
RCA23_c24810	fatty acid desaturase	COG3239	I	GI 9	0.00	100.00
RCA23_c24820	hypothetical protein			GI 9	0.00	41.32
RCA23_c24830	transposase	COG3316	L	GI 9	0.00	0.00
RCA23_c24840	transporter, LysE family	COG1280	E	GI 9	0.00	0.00
RCA23_c24850	hypothetical protein			GI 9	0.00	68.85
RCA23_c24860	putative transporter, periplasmic binding protein	COG2358	R	GI 9	0.00	0.00
RCA23_c24870	ribitol 2-dehydrogenase RbtD	COG4221	R	GI 9	0.00	0.00
RCA23_c24880	hypothetical protein			GI 9	0.00	16.00
RCA23_c24890	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa	COG0457	R	GI 9	0.00	24.22
RCA23_c24900	putative phage integrase	COG4974	L	GI 9	100.00	50.82
RCA23_c24920	D-alanyl-D-alanine carboxypeptidase DacC	COG1686	M		69.53	100.00
RCA23_c24930	thymidylate kinase Tmk	COG0125	F		100.00	98.54
RCA23_c24940	hypothetical protein, DNA polymerase III delta subunit	COG2812	L		100.00	100.00
RCA23_c24950	TatD family deoxyribonuclease	COG0084	L		100.00	100.00
RCA23_c24960	hypothetical protein, metallo-beta-lactamase	COG1235	R		100.00	100.00
RCA23_c24970	membrane transport protein	COG0679	R		100.00	88.92
RCA23_c24980	FAD dependent oxidoreductase	COG0665	E		100.00	100.00
RCA23_c24990	UvrABC system protein B	COG0556	L		100.00	94.66
RCA23_c25000	hypothetical protein				100.00	89.12
RCA23_c25010	hypothetical protein				100.00	72.28
RCA23_c25020	hypothetical protein				100.00	100.00

RCA23_c25030	lysyl-tRNA synthase LysS	COG1384	J	100.00	93.21
RCA23_c25040	hypothetical protein			100.00	100.00
RCA23_c25050	putative D-Ala-D-Ala carboxypeptidase 3 (S13) family protein	COG2027	M	100.00	100.00
RCA23_c25060	hypothetical protein			100.00	100.00
RCA23_c25070	nicotinic acid mononucleotide adenyltransferase NadD	COG1057	H	100.00	100.00
RCA23_c25080	ABC transporter, ATP-binding cassette protein, ChvD family	COG0488	R	100.00	100.00
RCA23_c25090	cold shock protein CspA	COG1278	K	100.00	100.00
RCA23_c25100	glutamyl-tRNA synthase 1	COG0008	J	100.00	100.00
RCA23_c25110	glutamine-dependent NAD(+) synthase NadE	COG0171	H	100.00	98.47
RCA23_c25120	putative phosphatidylinositol-4-phosphate 5-kinase	COG4642	S	69.37	100.00
RCA23_c25130	hypothetical protein	COG1028	I	100.00	100.00
RCA23_c25140	2-isopropylmalate synthase LeuA	COG0119	E	100.00	100.00
RCA23_c25150	rod shape-determining protein MreB	COG1077	D	100.00	99.33
RCA23_c25160	rod shape-determining protein MreC	COG1792	M	100.00	100.00
RCA23_c25170	hypothetical protein			100.00	96.48
RCA23_c25180	penicillin-binding protein 2	COG0768	M	100.00	100.00
RCA23_c25190	rod shape-determining protein RodA	COG0772	D	100.00	100.00
RCA23_c25200	glyoxylate/hydroxypyruvate reductase GhrA	COG0111	H	100.00	100.00
RCA23_c25210	hypothetical protein			100.00	100.00
RCA23_c25220	hypothetical protein	COG1573	L	100.00	100.00
RCA23_c25230	Na+/H+ antiporter NhaA	COG3004	P	100.00	100.00
RCA23_c25240	capsule polysaccharide export protein KpsT	COG1134	G	100.00	96.36
RCA23_c25250	capsule polysaccharide export protein KpsE	COG3524	M	100.00	100.00
RCA23_c25270	hypothetical protein	COG1832	R	100.00	100.00
RCA23_c25280	ferredoxin PetF	COG0633	C	100.00	100.00
RCA23_c25290	selenium binding protein			100.00	100.00
RCA23_c25300	aldehyde dehydrogenase	COG1012	C	100.00	100.00
RCA23_c25310	CoA-transferase family III protein involved in DMSP degradation	COG1804	C	100.00	100.00
RCA23_c25320	nitrogen regulatory protein P-II 2	COG0347	E	100.00	100.00
RCA23_c25330	ammonium transporter	COG0004	P	100.00	100.00
RCA23_c25340	homoprotocatechuate degradative operon repressor	COG1846	K	100.00	100.00
RCA23_c25350	5-carboxymethyl-2-hydroxymuconic semialdehyde dehydrogenase HpaE	COG1012	C	100.00	100.00
RCA23_c25360	3,4-dihydroxyphenylacetate 2,3-dioxygenase HpaD	COG0346	E	100.00	100.00

RCA23_c25370	3-carboxy-cis,cis-muconate cycloisomerase PcaB	COG0015	F	100.00	100.00
RCA23_c25380	hypothetical protein DUF849	COG3246	S	100.00	100.00
RCA23_c25390	protocatechuate 3,4-dioxygenase alpha chain PcaG	COG3485	Q	100.00	100.00
RCA23_c25400	protocatechuate 3,4-dioxygenase beta chain PcaH	COG3485	Q	100.00	100.00
RCA23_c25410	4-carboxymuconolactone decarboxylase PcaC	COG0599	S	100.00	100.00
RCA23_c25420	hypothetical protein			100.00	100.00
RCA23_c25430	transcriptional regulatory protein	COG0745	T	100.00	99.42
RCA23_c25440	two component signal transduction histidine kinase ChvG	COG0642	T	100.00	100.00
RCA23_c25450	hypothetical protein			54.01	100.00
RCA23_c25460	Na(+)-phosphate symporter Pit	COG0306	P	100.00	100.00
RCA23_c25470	hypothetical protein			100.00	100.00
RCA23_c25480	2-dehydro-3-deoxyphosphooctonate aldolase KdsA	COG2877	M	100.00	100.00
RCA23_c25490	arabinose 5-phosphate isomerase KdsD	COG0794	M	100.00	95.21
RCA23_c25500	3-deoxy-manno-octulosonate cytidylyltransferase KdsB	COG1212	M	100.00	100.00
RCA23_c25510	hypothetical protein			51.69	66.95
RCA23_c25520	bacterial surface protein			19.09	34.25
RCA23_c25530	catalase-peroxidase KatG	COG0376	P	100.00	100.00
RCA23_c25540	hypothetical protein	COG2067	I	100.00	74.54
RCA23_c25550	thioesterase/thiol ester dehydrase-isomerase	COG0824	R	100.00	73.66
RCA23_c25560	iron-containing alcohol dehydrogenase	COG1454	C	100.00	100.00
RCA23_c25570	hypothetical protein	COG1960	I	100.00	100.00
RCA23_c25580	nodulation protein N-like protein	COG2030	I	100.00	97.22
RCA23_c25590	putative phosphotransferase, eukaryotic acyl-CoA dehydrogenase	COG3173	R	100.00	94.81
RCA23_c25600	putative HTH-type transcriptional regulator, TetR family	COG1309	K	100.00	100.00
RCA23_c25610	fatty acid oxidation complex alpha subunit FadJ	COG1250	I	100.00	100.00
RCA23_c25620	acyl-CoA dehydrogenase	COG1960	I	100.00	100.00
RCA23_c25630	acyl-CoA dehydrogenase	COG1960	I	100.00	100.00
RCA23_c25640	hypothetical protein, MarR family			100.00	95.44
RCA23_c25650	acyl-CoA dehydrogenase	COG1960	I	100.00	100.00
RCA23_c25660	quinone oxidoreductase (1.6.5.5.)	COG0604	C	100.00	100.00
RCA23_c25670	hypothetical protein			100.00	100.00
RCA23_c25680	putative DNA repair protein RecO	COG1381	L	100.00	92.32
RCA23_c25690	hypothetical protein	COG5447	S	100.00	100.00

RCA23_c25700	GTP-binding protein Era	COG1159	R	100.00	100.00
RCA23_c25710	ribonuclease 3	COG0571	K	100.00	100.00
RCA23_c25720	signal peptidase I	COG0681	U	100.00	100.00
RCA23_c25730	holo-[acyl-carrier-protein] synthase AcpS	COG0736	I	100.00	100.00
RCA23_c25740	pyridoxine 5'-phosphate synthase PdxJ	COG0854	H	89.25	100.00
RCA23_c25750	hypothetical protein DUF2062	COG3216	S	0.00	100.00
RCA23_c25760	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase SpoT	COG0317	T	97.23	96.31
RCA23_c25770	DNA-directed RNA polymerase subunit omega	COG1758	K	100.00	100.00
RCA23_c25780	putative 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphok	COG0801	H	100.00	96.41
RCA23_c25790	hypothetical protein DUF88	COG1432	S	100.00	100.00
RCA23_c25800	4-hydroxy-3-methylbut-2-enyl diphosphate reductase IspH	COG0761	I	100.00	100.00
RCA23_c25810	hypothetical protein, methyltransferase	COG2227	H	100.00	100.00
RCA23_c25820	ribonuclease H	COG0328	L	100.00	100.00
RCA23_c25830	hypothetical protein			100.00	100.00
RCA23_c25840	methionyl-tRNA formyltransferase Fmt	COG0223	J	100.00	100.00
RCA23_c25850	peptide deformylase Def	COG0242	J	100.00	100.00
RCA23_c25860	peptide deformylase Def	COG0242	J	100.00	97.46
RCA23_c25870	aminotransferase	COG1168	E	100.00	95.20
RCA23_c25880	hypothetical protein			100.00	100.00
RCA23_c25890	precorrin-4 C(11)-methyltransferase CobM	COG2875	H	100.00	100.00
RCA23_c25900	precorrin-3B C(17)-methyltransferase CobJ	COG1010	H	100.00	100.00
RCA23_c25910	precorrin-2 C(20)-methyltransferase CobI	COG2243	H	100.00	100.00
RCA23_c25920	precorrin-6Y C(5,15)-methyltransferase CobL	COG2242	H	100.00	100.00
RCA23_c25930	precorrin-8X methylmutase CobH	COG2082	H	100.00	100.00
RCA23_c25940	sirohydrochlorin cobaltochelatase CbiX	COG2138	S	100.00	100.00
RCA23_c25950	methyltransferase, FkbM family	COG3774	M	45.28	7.19
RCA23_c25960	hypothetical protein, glutathione S-transferase	COG0435	O	100.00	100.00
RCA23_c25970	hypothetical protein DUF1636	COG5469	S	100.00	100.00
RCA23_c25980	threonine-phosphate decarboxylase CobC	COG0079	E	100.00	100.00
RCA23_c25990	cobalamin biosynthesis protein CobD	COG1270	H	100.00	100.00
RCA23_c26000	putative peptidoglycan-binding lytic murein transglycosylase	COG2951	M	100.00	100.00
RCA23_c26010	putative chromosome partition protein smc	COG1196	D	100.00	98.50
RCA23_c26020	hypothetical protein			100.00	100.00

RCA23_c26030	hypothetical protein	COG1028	I		100.00	95.56
RCA23_c26040	hypothetical protein DUF81	COG0730	R		100.00	100.00
RCA23_c26050	50S ribosomal protein L2	COG0090	J		100.00	98.31
RCA23_c26060	30S ribosomal protein S19	COG0185	J		100.00	100.00
RCA23_c26070	50S ribosomal protein L22	COG0091	J		100.00	100.00
RCA23_c26080	30S ribosomal protein S3	COG0092	J		100.00	100.00
RCA23_c26090	50S ribosomal protein L16	COG0197	J		100.00	100.00
RCA23_c26100	hypothetical protein			GI 10	100.00	100.00
RCA23_c26120	hypothetcial protein	COG0666	R	GI 10	0.00	0.00
RCA23_c26130	transcriptional regulator			GI 10	0.00	61.06
RCA23_c26140	hypothetical protein			GI 10	0.00	54.41
RCA23_c26150	hypothetical protein, UPF0311			GI 10	52.81	100.00
RCA23_c26160	transcriptional regulator, MarR family	COG1846	K	GI 10	100.00	100.00
RCA23_c26170	long-chain-fatty-acid-CoA-ligase	COG0318	I	GI 10	100.00	100.00
RCA23_c26180	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	GI 10	100.00	89.01
RCA23_c26190	TRAP dicarboxylate transporter, subunit DctQ			GI 10	100.00	55.75
RCA23_c26200	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	GI 10	100.00	98.36
RCA23_c26210	3-hydroxybutyryl-CoA dehydratase Crt	COG1024	I	GI 10	100.00	92.11
RCA23_c26220	metal-dependent hydrolase	COG2159	R	GI 10	100.00	94.61
RCA23_c26230	FAD dependent monooxygenase	COG0654	H	GI 10	100.00	85.76
RCA23_c26240	arylsulfatase	COG3119	P	GI 10	100.00	82.21
RCA23_c26250	transcriptional regulator, MarR family	COG1846	K	GI 10	100.00	58.78
RCA23_c26260	putative transporter, periplasmic binding protein	COG2358	R	GI 10	100.00	86.08
RCA23_c26270	TRAP transporter, 4TM/12TM fusion protein	COG4666	R	GI 10	100.00	70.89
RCA23_c26280	hypothetical protein, UPF0261	COG5441	S	GI 10	100.00	88.29
RCA23_c26290	gamma-glutamylputrescine synthase PuuA	COG0174	E	GI 10	100.00	100.00
RCA23_c26300	cytochrome P450	COG2124	Q	GI 10	77.02	64.97
RCA23_c26310	glutamine amidotransferase class-I	COG0518	F	GI 10	0.00	90.85
RCA23_c26320	tripartite tricarboxylate transporter (TTT) protein TctC	COG3181	S	GI 10	41.28	95.46
RCA23_c26330	tripartite tricarboxylate transporter (TTT) protein TctA	COG3333	S	GI 10	47.59	100.00
RCA23_c26340	hypothetical protein, transmembrane			GI 10	0.00	64.08
RCA23_c26350	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase PuuC	COG1012	C	GI 10	51.89	100.00
RCA23_c26360	hypothetical protein			GI 10	0.00	0.00

RCA23_c26370	hypothetical protein			GI 10	0.00	0.00
RCA23_c26380	hypothetical protein			GI 10	0.00	0.00
RCA23_c26390	putative fucosyltransferase			GI 10	0.00	0.00
RCA23_c26400	integrase	COG2801	L	GI 10	0.00	91.19
RCA23_c26410	putative extracellular solute-binding protein	COG1840	P	GI 10	96.80	37.21
RCA23_c26420	two-component system, sensor histidine kinase protein	COG0642	T	GI 10	100.00	32.90
RCA23_c26430	two-component system, response regulator protein	COG0745	T	GI 10	100.00	47.68
RCA23_c26440	tripartite tricarboxylate transporter (TTT) protein TctC	COG3181	S	GI 10	80.50	100.00
RCA23_c26450	tripartite tricarboxylate transporter (TTT) protein TctB			GI 10	100.00	100.00
RCA23_c26460	tripartite tricarboxylate transporter (TTT) protein TctA	COG3333	S	GI 10	100.00	99.07
RCA23_c26470	hypothetical protein			GI 10	100.00	100.00
RCA23_c26480	hypothetical protein			GI 10	100.00	100.00
RCA23_c26490	transposase A			GI 10	7.56	86.83
RCA23_c26510	hypothetical protein			GI 10	0.00	0.00
RCA23_c26520	hypothetical protein	COG1709	K	GI 10	0.00	0.00
RCA23_c26530	hypothetical protein			GI 10	0.00	0.00
RCA23_c26540	putative RTX toxin and hemolysin-type calcium binding protein			GI 10	0.00	0.00
RCA23_c26550	putative RTX toxin and hemolysin-type calcium binding protein			GI 10	7.47	5.66
RCA23_c26560	type I secretion outer membrane protein, TolC family	COG1538	M	GI 10	94.05	90.27
RCA23_c26570	type I secretion system ATP-binding component	COG2274	V	GI 10	84.42	96.96
RCA23_c26580	type I RTX secretion system membrane fusion protein, HlyD family	COG1566	V	GI 10	100.00	100.00
RCA23_c26590	hypothetical protein			GI 10	100.00	100.00
RCA23_c26600	hypothetical protein			GI 10	100.00	99.21
RCA23_c26610	hypothetical protein			GI 10	100.00	100.00
RCA23_c26620	hypothetical protein			GI 10	100.00	100.00
RCA23_c26630	hypothetical protein DUF2125			GI 10	100.00	100.00
RCA23_c26640	Asp/Glu racemase	COG3473	Q	GI 10	88.47	100.00
RCA23_c26650	cystathionine beta-lyase	COG0626	E	GI 10	100.00	100.00
RCA23_c26660	deoxyribodipyrimidine photo-lyase PhrB	COG0415	L	GI 10	100.00	100.00
RCA23_c26670	hypothetical protein	COG3380	R	GI 10	100.00	100.00
RCA23_c26680	O-sialoglycoprotein endopeptidase Gcp	COG0533	O	GI 10	100.00	100.00
RCA23_c26690	Sua5/YciO/YrdC/YwlC family protein	COG0009	J	GI 10	100.00	100.00
RCA23_c26700	putative glycoprotease family protein	COG1214	O	GI 10	100.00	100.00

RCA23_c26710	hypothetical protein UPF0079	COG0802	R	GI 10	100.00	100.00
RCA23_c26720	xylose isomerase family protein	COG3622	G	GI 10	31.51	100.00
RCA23_c26730	putative phage integrase	COG0582	L	GI 10	0.00	79.94
RCA23_c26740	hypothetical protein			GI 10	0.00	74.23
RCA23_c26750	putative prophage regulatory protein	COG3311	K	GI 10	0.00	0.00
RCA23_c26760	hypothetical protein			GI 10	0.00	0.00
RCA23_c26770	DNA polymerase	COG0749	L	GI 10	0.00	67.34
RCA23_c26780	hypothetical protein			GI 10	0.00	0.00
RCA23_c26790	hypothetical protein, snoaL-like polyketide cyclase	COG5485	R	GI 10	0.00	0.00
RCA23_c26800	hypothetical protein			GI 10	0.00	56.96
RCA23_c26810	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein			GI 10	0.00	0.00
RCA23_c26820	hypothetical protein			GI 10	0.00	16.37
RCA23_c26830	putative ABC transporter permease protein	COG0395	G	GI 10	0.00	0.00
RCA23_c26840	putative ABC transporter permease protein	COG1175	G	GI 10	0.00	0.00
RCA23_c26850	putative ABC transporter extracellular solute binding protein	COG1653	G	GI 10	0.00	0.00
RCA23_c26860	ABC transporter ATP-binding protein	COG3839	G	GI 10	0.00	0.00
RCA23_c26870	histidinol dehydrogenase HisD	COG0141	E	GI 10	0.00	0.00
RCA23_c26880	hypothetical protein, snoaL-like polyketide cyclase	COG5485	R	GI 10	0.00	0.00
RCA23_c26890	short chain dehydrogenase	COG1028	I	GI 10	32.12	34.95
RCA23_c26900	putative HTH-type transcriptional regulator LacI family	COG1609	K	GI 10	100.00	0.00
RCA23_c26910	hypothetical protein, snoaL-like polyketide cyclase			GI 10	30.64	1.00
RCA23_c26920	hypothetical protein			GI 10	80.64	23.91
RCA23_c26930	hypothetical protein, 2-hydroxypropyl-CoM lyase-like	COG0620	E	GI 10	73.76	0.00
RCA23_c26940	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	GI 10	0.00	0.00
RCA23_c26950	hypothetical protein	COG0684	H	GI 10	0.00	0.00
RCA23_c26960	3-hydroxyisobutyrate dehydrogenase MmsB	COG2084	I	GI 10	33.55	11.59
RCA23_c26970	dihydroxy-acid dehydratase IlvD	COG0129	E	GI 10	100.00	36.50
RCA23_c26980	hypothetical protein	COG4091	E	GI 10	33.78	51.45
RCA23_c26990	putative choline (or alcohol) dehydrogenase	COG2303	E	GI 10	4.21	29.85
RCA23_c27000	aldehyde dehydrogenase	COG1012	C	GI 10	100.00	76.74
RCA23_c27010	transporter, LysE family	COG1280	E	GI 10	100.00	0.17
RCA23_c27020	TRAP dicarboxylate transporter, subunit DctM	COG4664	Q	GI 10	100.00	24.34
RCA23_c27030	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	GI 10	25.53	41.49

RCA23_c27040	TRAP dicarboxylate transporter, subunit DctP	COG4663	Q	GI 10	0.00	0.00
RCA23_c27050	transcriptional regulator, LysR family	COG0583	K	GI 10	0.00	66.37
RCA23_c27060	mandelate racemase/muconate lactonizing enzyme	COG4948	M	GI 10	100.00	100.00
RCA23_c27070	Zn-dependant oxidoreductase	COG0604	C	GI 10	56.06	97.66
RCA23_c27090	HTH-type transcriptional regulator, LysR family	COG0583	K	GI 10	0.00	70.65
RCA23_c27100	class II aldolase	COG0235	G	GI 10	0.00	29.10
RCA23_c27110	fatty acid desaturase	COG3239	I	GI 10	0.00	69.78
RCA23_c27120	3-methyl-2-oxobutanoate hydroxymethyltransferase PanB	COG0413	H	GI 10	0.00	30.86
RCA23_c27130	putative rieske [2Fe-2S] protein	COG2146	P	GI 10	0.00	89.00
RCA23_c27150	hypothetical protein	COG1396	K		100.00	100.00
RCA23_c27160	arginase family protein	COG0010	E		100.00	100.00
RCA23_c27170	hypothetical protein	COG1082	G		100.00	100.00
RCA23_c27180	putative HTH-type transcriptional regulator, AraC family	COG2169	F		100.00	100.00
RCA23_c27190	hypothetical protein. fatty acid desaturase	COG3239	I		100.00	100.00
RCA23_c27200	AMP-dependent synthase / ligase	COG0318	I		100.00	100.00
RCA23_c27210	ABC transporter ATP-binding protein	COG1132	V		100.00	100.00
RCA23_c27220	spore coat family protein				100.00	100.00
RCA23_c27230	PapD-like chaperone involved in fimbrial biogenesis	COG3121	N		100.00	100.00
RCA23_c27240	fimbrial biogenesis outer membrane usher protein	COG3188	N		100.00	100.00
RCA23_c27250	fimbrial biogenesis outer membrane usher protein	COG3188	N		100.00	100.00
RCA23_c27260	hypothetical protein				100.00	100.00
RCA23_c27280	hypothetical protein	COG0697	G		100.00	100.00
RCA23_c27290	DNA-directed RNA polymerase beta subunit RpoC	COG0086	K		86.33	100.00
RCA23_c27300	DNA-directed RNA polymerase beta subunit RpoB	COG0085	K		100.00	100.00
RCA23_c27310	50S ribosomal protein L7/L12	COG0222	J		100.00	100.00
RCA23_c27320	50S ribosomal protein L10	COG0244	J		100.00	100.00
RCA23_c27330	50S ribosomal protein L1	COG0081	J		100.00	100.00
RCA23_c27340	50S ribosomal protein L11	COG0080	J		100.00	100.00
RCA23_c27350	transcription antitermination protein NusG	COG0250	K		100.00	100.00
RCA23_c27360	preprotein translocase, subunit SecE	COG0690	U		100.00	100.00
RCA23_c27370	hypothetical protein				100.00	100.00
RCA23_c27430	hypothetical protein				100.00	100.00
RCA23_c27440	hypothetical protein, transmembrane				100.00	100.00

RCA23_c27450	hypothetical protein			74.48	100.00
RCA23_c27460	putative acetolactate synthase isozyme 1 large subunit	COG0028	E	100.00	100.00
RCA23_c27470	putative cation transporter	COG0168	P	100.00	100.00
RCA23_c27480	GTP cyclohydrolase FolE	COG1469	S	100.00	100.00
RCA23_c27490	O-succinylhomoserine sulfhydrylase MetZ	COG0626	E	100.00	100.00
RCA23_c27500	hypothetical protein	COG0625	O	100.00	100.00
RCA23_c27510	putative intracellular septation protein	COG2917	D	100.00	99.00
RCA23_c27520	hypothetical protein	COG0697	G	100.00	100.00
RCA23_c27530	putative cell division protein	COG0552	U	100.00	100.00
RCA23_c27540	NADH-quinone oxidoreductase subunits E/F (fused)	COG1894	C	100.00	100.00
RCA23_c27550	exodeoxyribonuclease 7 large subunit XseA	COG1570	L	100.00	100.00
RCA23_c27560	phosphoribosylamine--glycine ligase PurD	COG0151	F	100.00	93.19
RCA23_c27570	hypothetical protein, ferredoxin	COG0633	C	100.00	100.00
RCA23_c27580	hypothetical protein	COG0587	L	100.00	100.00
RCA23_c27590	periplasmic serine protease DO-like	COG0265	O	100.00	100.00
RCA23_c27600	putative protein hflC	COG0330	O	100.00	100.00
RCA23_c27610	protein HflK	COG0330	O	100.00	100.00
RCA23_c27620	glutathione reductase Gor	COG1249	C	100.00	100.00
RCA23_c27630	ribose-5-phosphate isomerase A	COG0120	G	100.00	100.00
RCA23_c27640	hypothetical protein			100.00	100.00
RCA23_c27650	L-serine dehydratase SdaB	COG1760	E	100.00	99.49
RCA23_c27660	putative integral membrane protein	COG0697	G	100.00	100.00
RCA23_c27670	hypothetical protein, thiamine pyrophosphokinase	COG1564	H	100.00	100.00
RCA23_c27680	hypothetical protein			100.00	100.00
RCA23_c27690	hypothetical protein			100.00	89.18
RCA23_c27700	hypothetical protein			100.00	100.00
RCA23_c27710	adenylosuccinate synthase PurA	COG0104	F	100.00	100.00
RCA23_c27720	preprotein translocase, SecG subunit SecG			100.00	100.00
RCA23_c27730	CTP synthase	COG0504	F	100.00	100.00
RCA23_c27740	hypothetical protein, DUF1330	COG5470	S	100.00	94.90
RCA23_c27750	hypothetical protein DUF1332	COG4103	S	100.00	100.00
RCA23_c27760	hypothetical protein	COG3221	P	100.00	100.00
RCA23_c27770	amino acid transport ATP-binding protein	COG4598	E	100.00	100.00

RCA23_c27780	putative amino acid transport extracellular solute binding protein	COG0834	E	100.00	100.00
RCA23_c27790	putative ABC transporter inner membrane component	COG4215	E	100.00	100.00
RCA23_c27800	putative amino acid transport permease protein	COG4160	E	100.00	100.00
RCA23_c27810	gamma-glutamylputrescine synthase PuuA	COG0174	E	100.00	98.51
RCA23_c27820	hypothetical protein, glutamine amidotransferase class I	COG0518	F	100.00	100.00
RCA23_c27830	gamma-glutamylputrescine synthase PuuA	COG0174	E	100.00	100.00
RCA23_c27840	gamma-glutamylputrescine oxidoreductase PuuB	COG0665	E	100.00	97.62
RCA23_c27850	aminotransferase class III	COG0161	H	100.00	100.00
RCA23_c27860	putative PHB synthesis repressor protein	COG5394	S	100.00	100.00
RCA23_c27870	hypothetical protein			100.00	100.00
RCA23_c27880	poly(R)-hydroxyalkanoic acid synthase PhaC	COG3243	I	100.00	100.00
RCA23_c27890	polyhydroxyalkanoate depolymerase PhaZ	COG4553	I	98.97	99.60
RCA23_c27900	putative ribosome biogenesis GTPase RsgA	COG1162	R	100.00	100.00
RCA23_c27910	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	100.00	100.00
RCA23_c27920	hypothetical protein			100.00	100.00
RCA23_c27930	hypothetical protein, alpha/beta hydrolase-like	COG0596	R	100.00	100.00
RCA23_c27940	threonyl-tRNA synthase ThrS	COG0441	J	100.00	95.74
RCA23_c27950	hypothetical protein, ArsC	COG1393	P	100.00	100.00
RCA23_c27960	thymidylate synthase	COG1351	F	100.00	100.00
RCA23_c27970	putative glyoxalase/bleomycin resistance protein/dioxygenase superfamily pr	COG0346	E	100.00	100.00
RCA23_c27980	hypothetical protein			100.00	100.00
RCA23_c27990	putative transcriptional regulatorm marR family	COG1846	K	100.00	100.00
RCA23_c28000	hypothetical protein DUF339	COG2938	S	100.00	100.00
RCA23_c28010	hypothetical protein, DNA binding	COG1813	K	100.00	100.00
RCA23_c28020	aspartate aminotransferase AatA	COG0436	E	100.00	100.00
RCA23_c28030	hypothetical protein			100.00	100.00
RCA23_c28040	multidrug resistance protein NorM	COG0534	V	100.00	100.00
RCA23_c28050	DNA topoisomerase 4 subunit B	COG0187	L	100.00	100.00
RCA23_c28060	hypothetical protein	COG3238	S	100.00	100.00
RCA23_c28070	putative malate/L-lactate dehydrogenase	COG2055	C	100.00	99.90
RCA23_c28080	lipoprotein-releasing system ATP-binding protein LolD	COG1136	V	100.00	100.00
RCA23_c28090	lipoprotein-releasing system transmembrane protein, lolC/E family	COG4591	M	100.00	100.00
RCA23_c28100	prolyl-tRNA synthase ProS	COG0442	J	100.00	100.00

RCA23_c28110	hypothetical protein DUF20	COG0628	R	100.00	100.00
RCA23_c28120	hypothetical protein	COG0593	L	100.00	100.00
RCA23_c28130	polyphosphate kinase Ppk	COG0855	P	100.00	100.00
RCA23_c28140	putative phosphatase	COG0248	F	100.00	99.16
RCA23_c28150	hypothetical protein, DnaJ	COG1076	O	100.00	100.00
RCA23_c28160	hypothetical protein			100.00	100.00
RCA23_c28170	methylmalonyl-CoA mutase McmA	COG1884	I	100.00	100.00
RCA23_c28180	hypothetical protein			100.00	100.00
RCA23_c28190	biotin carboxylase AccC	COG4770	I	100.00	100.00
RCA23_c28200	hypothetical protein			100.00	100.00
RCA23_c28210	propionyl-CoA carboxylase beta chain, mitochondrial precursor	COG4799	I	100.00	100.00
RCA23_c28220	putative major facilitator superfamily transporter	COG2814	G	100.00	100.00
RCA23_c28230	hypothetical protein	COG3800	R	100.00	100.00
RCA23_c28240	betaine aldehyde dehydrogenase BetB	COG1012	C	100.00	100.00
RCA23_c28250	hypothetical protein	COG0697	G	100.00	100.00
RCA23_c28260	TRAP dicarboxylate transporter, subunit DctM	COG1593	G	100.00	98.72
RCA23_c28270	TRAP dicarboxylate transporter, subunit DctQ	COG4665	Q	100.00	87.46
RCA23_c28280	TRAP dicarboxylate transporter, subunit DctP	COG1638	G	100.00	100.00
RCA23_c28290	transcriptional regulator, LacI family	COG1609	K	100.00	100.00
RCA23_c28300	hypothetical protein, DUF81 family	COG0730	R	100.00	100.00
RCA23_c28310	serine--glyoxylate aminotransferase SgaA	COG0075	E	100.00	99.66
RCA23_c28320	D-lactate dehydrogenase Dld	COG0277	C	100.00	90.09
RCA23_c28330	hypothetical protein			100.00	79.22
RCA23_c28340	AMP-binding enzyme	COG0318	I	100.00	80.01
RCA23_c28350	succinate-semialdehyde dehydrogenase SucD	COG1012	C	100.00	100.00
RCA23_c28360	hypothetical protein	COG3333	S	100.00	100.00
RCA23_c28370	hypothetical protein			100.00	100.00
RCA23_c28380	putative tripartite tricarboxylate transporter family receptor	COG3181	S	18.15	89.84
RCA23_c28390	putative ETC complex I subunit			100.00	100.00
RCA23_c28450	sulfoxide reductase heme-binding subunit YedZ	COG2717	S	100.00	100.00
RCA23_c28460	sulfoxide reductase catalytic subunit YedY	COG2041	R	100.00	100.00
RCA23_c28470	3-oxoacyl-[acyl-carrier-protein] reductase FabG	COG1028	I	100.00	100.00
RCA23_c28480	putative haloacid dehalogenase-like hydrolase	COG0637	R	100.00	100.00

RCA23_c28490	chaperone protein ClpB	COG0542	O	100.00	100.00
RCA23_c28500	orotidine 5'-phosphate decarboxylase PyrF	COG0284	F	100.00	100.00
RCA23_c28510	hypothetical protein			100.00	100.00
RCA23_c28520	SPFH domain/band 7 family protein	COG0330	O	100.00	100.00
RCA23_c28530	DNA polymerase IV	COG0389	L	100.00	100.00
RCA23_c28540	putative N-formylglutamate amidohydrolase	COG3741	E	100.00	100.00
RCA23_c28560	hypothetical protein, phenylacetate-coenzyme A ligase	COG1541	H	100.00	100.00
RCA23_c28570	high-affinity branched-chain amino acid transporter ATP-binding protein	COG0410	E	100.00	99.64
RCA23_c28580	hypothetical protein	COG0683	E	100.00	57.30
RCA23_c28590	high-affinity branched-chain amino acid transporter permease protein	COG4177	E	100.00	71.22
RCA23_c28600	high-affinity branched-chain amino acid transporter permease protein	COG0559	E	100.00	90.82
RCA23_c28610	high-affinity branched-chain amino acid transporter ATP-binding protein	COG0411	E	100.00	100.00
RCA23_c28620	putative long-chain-fatty-acid-CoA ligase	COG1022	I	100.00	100.00
RCA23_c28630	tRNA pseudouridine synthase B	COG0130	J	100.00	100.00
RCA23_c28650	ribosome-binding factor A	COG0858	J	100.00	100.00
RCA23_c28640	dihydrodipicolinate synthase DapA	COG0289	E	100.00	100.00
RCA23_c28660	hypothetical protein DUF1674	COG5508	S	100.00	100.00
RCA23_c28670	putative ribosomal RNA small subunit methyltransferase B	COG0144	J	100.00	100.00
RCA23_c28680	hypothetical protein, heparinase II/III	COG5360	S	79.28	100.00
RCA23_c28690	bifunctional purine biosynthesis protein PurH	COG0138	F	100.00	93.76
RCA23_c28700	signal peptidase II	COG0597	M	100.00	100.00
RCA23_c28710	uncharacterized zinc protease y4wA	COG0612	R	100.00	100.00
RCA23_c28720	uncharacterized zinc protease y4wB	COG0612	R	100.00	100.00
RCA23_c28730	DNA mismatch repair protein MutL	COG0323	L	100.00	100.00
RCA23_c28740	putative RmuC family protein	COG1322	S	100.00	100.00
RCA23_c28750	transcriptional activator ChrR	COG3806	T	100.00	100.00
RCA23_c28760	RNA polymerase sigma factor SigK	COG1595	K	100.00	100.00
RCA23_c28770	hypothetical protein	COG2907	R	100.00	100.00
RCA23_c28780	hypothetical protein DUF1365	COG3496	S	100.00	100.00
RCA23_c28790	hypothetical protein	COG2211	G	100.00	100.00
RCA23_c28800	hypothetical protein			100.00	100.00
RCA23_c28810	putative short chain dehydrogenase	COG4221	R	100.00	100.00
RCA23_c28820	saccharopine dehydrogenase (NAD+,L-lysine-forming)	COG3288	C	100.00	99.34

RCA23_c28830	putative glutathione S-transferase	COG0625	O	100.00	100.00
RCA23_c28840	putative phosphoglycerate mutase family protein	COG0406	G	100.00	100.00
RCA23_c28850	formate dehydrogenase Fdh	COG3383	R	100.00	100.00
RCA23_c28860	hypothetical protein	COG1357	S	75.52	54.92
RCA23_c28870	hypothetical protein DUF1643	COG4333	S	100.00	100.00
RCA23_c28880	haloacetate dehalogenase DehH	COG0596	R	100.00	100.00
RCA23_c28890	30S ribosomal protein S15	COG0184	J	100.00	100.00
RCA23_c28900	hypothetical protein, DUF6 transmembrane protein	COG0697	G	100.00	100.00
RCA23_c28910	polyribonucleotide nucleotidyltransferase Pnp	COG1185	J	100.00	100.00
RCA23_c28920	aldehyde dehydrogenase	COG1012	C	97.85	100.00
RCA23_c28930	ribosomal large subunit pseudouridine synthase A	COG0564	J	100.00	96.43
RCA23_c28940	protein OtnG			100.00	99.37
RCA23_c28950	hypothetical protein, DUF940 putative lipoprotein			27.08	100.00
RCA23_c28960	hypothetical protein			100.00	100.00
RCA23_c28970	UDP-glucose 4-epimerase GalE	COG1087	M	100.00	100.00
RCA23_c28980	putative FAD linked oxidase	COG0277	C	100.00	100.00
RCA23_c28990	signal recognition particle protein Ffh	COG0541	U	100.00	96.66
RCA23_c29000	putative chorismate mutase type II	COG1605	E	100.00	100.00
RCA23_c29010	30S ribosomal protein S16	COG0228	J	100.00	100.00
RCA23_c29020	ribosome maturation factor RimM	COG0806	J	100.00	100.00
RCA23_c29030	tRNA (guanine-N(1)-)-methyltransferase TrmD	COG0336	J	100.00	100.00
RCA23_c29040	50S ribosomal protein L19	COG0335	J	100.00	100.00
RCA23_c29050	50S ribosomal protein L31	COG0254	J	100.00	100.00
RCA23_c29060	ATPase MipZ	COG1192	D	100.00	100.00
RCA23_c29070	fructokinase	COG0524	G	100.00	100.00
RCA23_c29080	P-hydroxybenzoate hydroxylase PobA	COG0654	H	100.00	98.64
RCA23_c29090	kynureninase KynU	COG3844	E	100.00	100.00
RCA23_c29100	HTH-type transcriptional regulator, GntR family	COG1802	K	100.00	100.00
RCA23_c29110	hypothetical protein, glutathione S-transferase	COG0625	O	100.00	100.00
RCA23_c29120	L-threonine 3-dehydrogenase	COG0451	M	100.00	100.00
RCA23_c29130	enoyl-CoA hydratase	COG1024	I	100.00	100.00
RCA23_c29140	enoyl-CoA hydratase	COG1250	I	100.00	98.59
RCA23_c29150	3-hydroxyacyl-CoA dehydrogenase FadN	COG1028	I	100.00	100.00

RCA23_c29160	hypothetical protein			90.85	100.00
RCA23_c29170	integrase	COG4974	L	100.00	100.00
RCA23_c29180	hypothetical protein, porin-like			100.00	73.20
RCA23_c29190	leucyl-tRNA synthase LeuS	COG0495	J	100.00	100.00
RCA23_c29200	hypothetical protein DUF2159			100.00	100.00
RCA23_c29210	hypothetical protein			100.00	100.00
RCA23_c29220	hypothetical protein, glutathione S-transferase	COG0625	O	100.00	100.00
RCA23_c29230	hypothetical protein	COG2081	R	100.00	100.00
RCA23_c29240	hypothetical protein, porin			100.00	59.27
RCA23_c29250	hypothetical protein, alanine racemase-like	COG0325	R	100.00	100.00
RCA23_c29260	hypothetical protein, YkuD	COG3786	S	100.00	100.00
RCA23_c29270	GTP cyclohydrolase II RibA	COG0807	H	100.00	100.00
RCA23_c29280	response regulator receiver protein	COG0745	T	100.00	100.00
RCA23_c29290	2-oxo-hepta-3-ene-1,7-dioic acid hydratase HpcG	COG3971	Q	100.00	100.00
RCA23_c29300	fumarylacetoacetate hydrolase family protein	COG0179	Q	100.00	100.00
RCA23_c29310	5-carboxymethyl-2-hydroxymuconate isomerase	COG3232	E	100.00	100.00
RCA23_c29320	homoprotocatechuate degradation operon regulator HpaR	COG1846	K	100.00	100.00
RCA23_c29330	4-hydroxyphenylacetate 3-monooxygenase oxygenase component HpaH	COG2368	Q	100.00	98.22
RCA23_c29340	ABC sugar transporter, ATPase subunit	COG3839	G	100.00	100.00
RCA23_c29350	mannitol 2-dehydrogenase MtlK	COG0246	G	100.00	99.22
RCA23_c29360	transcriptional regulator, AraC family	COG2207	K	100.00	100.00
RCA23_c29370	ABC sugar transporter, permease protein	COG0395	G	100.00	100.00
RCA23_c29380	ABC sugar transporter, permease protein	COG1175	G	100.00	72.95
RCA23_c29390	ABC transporter, periplasmic substrate-binding protein	COG1653	G	100.00	95.16
RCA23_c29400	putative flavohemoglobin / bacterial hemoglobin	COG1017	C	0.00	73.22
RCA23_c29410	hypothetical protein			0.00	100.00
RCA23_c29420	Na+/H+ antiporter NhaA	COG3004	P	0.00	98.75
RCA23_c29430	hypothetical protein			3.54	100.00
RCA23_c29440	hypothetical protein DUF55	COG2947	S	100.00	100.00
RCA23_c29450	protein YciI	COG2350	S	100.00	100.00
RCA23_c29460	glycerol-3-phosphate dehydrogenase GpsA	COG0240	C	100.00	100.00
RCA23_c29470	hypothetical protein, uroporophyrinogen-III synthase HemD	COG1587	H	100.00	99.86
RCA23_c29480	hypothetical protein	COG3264	M	100.00	100.00

RCA23_c29490	hypothetical protein, HemY	COG3898	S	100.00	100.00
RCA23_c29500	transcriptional regulatory protein, Ars family	COG0640	K	100.00	100.00
RCA23_c29510	magnesium-chelatase subunit BchO	COG0596	R	100.00	100.00
RCA23_c29520	magnesium-chelatase subunit BchD	COG1240	H	100.00	98.79
RCA23_c29530	magnesium-chelatase subunit BchI	COG1239	H	100.00	100.00
RCA23_c29540	spheroidene monooxygenase CrtA			100.00	100.00
RCA23_c29550	phytoene dehydrogenase CrtI	COG1233	Q	100.00	100.00
RCA23_c29560	phytoene synthase CrtB	COG1562	I	100.00	100.00
RCA23_c29570	hydroxyneurosporene dehydrogenase CrtC			100.00	84.93
RCA23_c29580	methoxyneurosporene dehydrogenase CrtD	COG1233	Q	100.00	100.00
RCA23_c29590	geranylgeranyl pyrophosphate synthase CrtE	COG0142	H	100.00	91.37
RCA23_c29600	hydroxyneurosporene methyltransferase CrtF			100.00	100.00
RCA23_c29610	2-desacetyl-2-hydroxyethyl bacteriochlorophyllide A dehydrogenase BchC	COG1063	E	100.00	100.00
RCA23_c29620	chlorophyllide reductase BchX	COG1348	P	100.00	100.00
RCA23_c29630	chlorophyllide reductase BchY			100.00	100.00
RCA23_c29640	chlorophyllide reductase subunit BchZ	COG2710	C	100.00	99.38
RCA23_c29650	protein PufQ			100.00	100.00
RCA23_c29660	light-harvesting protein B-870 beta chain PufB			100.00	100.00
RCA23_c29670	light-harvesting protein B-870 alpha chain PufA			100.00	100.00
RCA23_c29680	reaction center protein L chain PufL			100.00	100.00
RCA23_c29690	reaction center protein M chain PufM			100.00	100.00
RCA23_c29700	protein PufX			100.00	100.00
RCA23_c29710	1-deoxy-D-xylulose-5-phosphate synthase Dxs	COG1154	H	100.00	100.00
RCA23_c29720	isopentenyl-diphosphate delta-isomerase Idi	COG1443	I	100.00	100.00
RCA23_c29730	geranylgeranyl reductase BchP	COG0644	C	100.00	100.00
RCA23_c29740	bacteriochlorophyll synthase 44.5 kDa chain			100.00	100.00
RCA23_c29750	bacteriochlorophyll synthase BchG	COG0382	H	100.00	100.00
RCA23_c29760	cytochrome c-551	COG3474	C	100.00	100.00
RCA23_c29770	uroporphyrinogen decarboxylase HemE	COG0407	H	100.00	100.00
RCA23_c29780	porphobilinogen deaminase HemC	COG0181	H	100.00	100.00
RCA23_c29790	hypothetical protein, NmrA-like	COG0702	M	100.00	90.83
RCA23_c29800	5-aminolevulinate synthase HemA	COG0156	H	99.67	100.00
RCA23_c29810	hypothetical protein			43.99	100.00

RCA23_c29820	aerobic Mg-protoporphyrin IX monomethyl ester oxidative cyclase AcsF			100.00	100.00
RCA23_c29830	hypothetical protein			100.00	100.00
RCA23_c29840	hypothetical protein			100.00	100.00
RCA23_c29850	hypothetical protein			90.92	100.00
RCA23_c29860	reaction center protein PuhA			22.87	100.00
RCA23_c29870	protein PucC			100.00	100.00
RCA23_c29880	magnesium-protoporphyrin O-methyltransferase BchM	COG2227	H	100.00	100.00
RCA23_c29890	light-independent protochlorophyllide reductase iron-sulfur ATP-binding prot	COG1348	P	100.00	100.00
RCA23_c29900	magnesium-chelatase subunit BchH	COG1429	H	100.00	100.00
RCA23_c29910	light-independent protochlorophyllide reductase subunit BchB	COG2710	C	100.00	100.00
RCA23_c29920	light-independent protochlorophyllide reductase subunit BchN	COG2710	C	100.00	100.00
RCA23_c29930	2-vinyl bacteriochlorophyllide hydratase BchF			100.00	100.00
RCA23_c29940	putative transcriptional regulator PpaA			100.00	100.00
RCA23_c29950	transcriptional regulator PpsR	COG3829	K	100.00	100.00
RCA23_c29960	hypothetical protein	COG5012	R	100.00	100.00
RCA23_c29970	transcriptional regulator protein FixJ	COG4566	T	100.00	100.00
RCA23_c29980	peripheral-type benzodiazepine receptor/signal transduction protein TspO	COG3476	T	100.00	100.00
RCA23_c29990	hypothetical protein, integral membrane proteins YeeE/YedE	COG2391	R	100.00	100.00
RCA23_c30000	hypothetical protein, integral membrane proteins YeeE/YedE	COG2391	R	100.00	100.00
RCA23_c30010	putative beta-lactamase hydrolase-like protein	COG0491	R	100.00	100.00
RCA23_c30020	hypothetical protein	COG3453	S	100.00	100.00
RCA23_c30030	sulphate transporter	COG0659	P	100.00	100.00
RCA23_c30040	amidase	COG0154	J	100.00	100.00
RCA23_c30050	hypothetical protein			100.00	100.00
RCA23_c30060	aminoglycoside phosphotransferase Aph			100.00	100.00
RCA23_c30070	hypothetical protein	COG2885	M	100.00	100.00
RCA23_c30080	chaperone protein DnaJ	COG0484	O	100.00	100.00
RCA23_c30090	chaperone protein DnaK	COG0443	O	100.00	100.00
RCA23_c30100	putative alpha-ketoglutarate-dependent dioxygenase AlkB	COG3145	L	100.00	100.00
RCA23_c30110	putative ABC-2 type transporter	COG1682	G	100.00	100.00
RCA23_c30120	3'(2'),5'-bisphosphate nucleotidase CysQ	COG1218	P	100.00	100.00
RCA23_c30130	UTP-glucose-1-phosphate uridylyltransferase GalU	COG1210	M	100.00	26.43
RCA23_c30140	hypothetical protein	COG0463	M	4.59	18.36

RCA23_c30150	hypothetical protein			0.00	53.82
RCA23_c30160	hypothetical protein beta-1,6-N-acetylglucosaminyltransferases			0.00	6.85
RCA23_c30170	hypothetical protein			14.99	36.27
RCA23_c30180	nitrogen regulatory protein PtsN	COG1762	G	100.00	100.00
RCA23_c30190	putative sigma 54 modulation protein	COG1544	J	100.00	100.00
RCA23_c30200	lipopolysaccharide export system ATP-binding protein LptB	COG1137	R	100.00	100.00
RCA23_c30210	putative lipopolysaccharide export system protein LptA	COG1934	S	100.00	100.00
RCA23_c30220	hypothetical protein			100.00	100.00
RCA23_c30230	putative 3'-5'-exonuclease	COG0349	J	100.00	94.63
RCA23_c30240	glycine amidinotransferase	COG1834	E	100.00	100.00
RCA23_c30250	hypothetical protein	COG4123	R	100.00	100.00
RCA23_c30260	hypothetical protein, metal-dependent phosphohydrolase	COG1896	R	100.00	100.00
RCA23_c30270	S-adenosyl-L-homocysteine hydrolase AhcY	COG0499	H	100.00	100.00
RCA23_c30280	photosynthetic apparatus regulatory protein RegA	COG4567	T	100.00	100.00
RCA23_c30290	protein SenC	COG1999	R	100.00	100.00
RCA23_c30300	sensor histidine kinase RegB	COG0642	T	100.00	100.00
RCA23_c30310	hypothetical protein			100.00	100.00
RCA23_c30320	hypothetical protein, aminoglycoside phosphotransferase	COG3178	R	100.00	98.19
RCA23_c30330	hypothetical protein, nucleotidyl transferase	COG1208	M	100.00	100.00
RCA23_c30340	double-strand break repair protein AddB	COG3893	L	100.00	100.00
RCA23_c30350	double-strand break repair helicase AddA	COG1074	L	97.97	100.00
RCA23_c30360	thioredoxin TrxA	COG3118	O	100.00	100.00
RCA23_c30370	ATP-dependent protease HslV	COG5405	O	100.00	100.00
RCA23_c30380	ATP-dependent hsl protease ATP-binding subunit HslU	COG1220	O	100.00	96.87
RCA23_c30390	MFS-type transporter	COG2814	G	100.00	100.00
RCA23_c30400	hypothetical protein, Smr protein/MutS2	COG2840	S	100.00	100.00
RCA23_c30410	putative lytic murein transglycosylase	COG2821	M	100.00	100.00
RCA23_c30420	hypothetical protein, TIM44	COG4395	S	100.00	100.00
RCA23_c30430	putative cytoplasmic membrane protein FxsA	COG3030	R	100.00	100.00
RCA23_c30440	protein-export protein SecB	COG1952	U	100.00	100.00
RCA23_c30450	DNA polymerase III subunit epsilon	COG0847	L	100.00	100.00
RCA23_c30460	dephospho-CoA kinase CoaE	COG0237	H	100.00	100.00
RCA23_c30470	shikimate 5-dehydrogenase AroE	COG0169	E	100.00	100.00

RCA23_c30480	transcription termination factor Rho	COG1158	K	100.00	100.00
RCA23_c30490	tRNA modification GTPase MnmE	COG0486	R	100.00	100.00
RCA23_c30500	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	COG0445	D	100.00	99.84
RCA23_c30510	ribosomal RNA small subunit methyltransferase G	COG0357	M	100.00	100.00
RCA23_c30520	chromosome-partitioning protein ParA	COG1192	D	100.00	100.00
RCA23_c30530	chromosome-partitioning protein ParB	COG1475	K	100.00	100.00
RCA23_c30540	oxygen-independent coproporphyrinogen III oxidase HemN	COG0635	H	100.00	100.00
RCA23_c30550	nucleoside-triphosphatase RdgB	COG0127	F	100.00	100.00
RCA23_c30560	ribonuclease PH	COG0689	J	100.00	100.00
RCA23_c30570	heat-inducible transcription repressor HrcA	COG1420	K	100.00	100.00
RCA23_c30580	protein GrpE	COG0576	O	100.00	100.00
RCA23_c30590	DNA mismatch repair protein MutS	COG0249	L	100.00	100.00
RCA23_c30600	NADP-dependent malic enzyme MaeB	COG0281	C	100.00	98.05
RCA23_c30610	pfkB family carbohydrate kinase	COG0524	G	100.00	100.00
RCA23_c30620	putative aminotransferase class IV	COG0115	E	100.00	100.00
RCA23_c30630	hypothetical protein, branched-chain-amino-acid aminotransferase-like			100.00	100.00
RCA23_c30640	argininosuccinate synthase ArgG	COG0137	E	100.00	100.00
RCA23_c30650	threonine dehydratase, biosynthetic	COG1171	E	100.00	100.00
RCA23_c30660	putative NUDIX hydrolase	COG0494	L	100.00	100.00
RCA23_c30670	heat shock protein 33	COG1281	O	100.00	100.00
RCA23_c30680	putative NUDIX hydrolase	COG0494	L	100.00	100.00
RCA23_c30690	hypothetical protein, poly A polymerase	COG0617	J	100.00	100.00
RCA23_c30700	ABC transporter ATP-binding/permease protein	COG1132	V	100.00	100.00
RCA23_c30710	hypothetical protein	COG2265	J	95.06	100.00
RCA23_c30720	ion transport protein			2.89	100.00
RCA23_c30730	hypothetical protein	COG3034	S	100.00	100.00
RCA23_c30740	hypothetical protein, SCP-like extracellular protein	COG2340	S	100.00	100.00
RCA23_c30750	hypothetical protein	COG1376	S	100.00	100.00
RCA23_c30760	ferrochelatase HemH	COG0276	H	100.00	100.00
RCA23_c30770	hypothetical protein			100.00	100.00
RCA23_c30780	hypothetical protein, ComF/GntX family	COG1040	R	100.00	100.00
RCA23_c30790	glutaredoxin GrxC	COG0695	O	100.00	100.00
RCA23_c30800	putative carbon-nitrogen hydrolase	COG0388	R	100.00	100.00

RCA23_c30810	putative HTH-type transcriptional regulator, MarR family	COG1846	K	100.00	100.00
RCA23_c30820	3-demethylubiquinone-9 3-O-methyltransferase UbiG	COG2227	H	100.00	100.00
RCA23_c30830	proline iminopeptidase Pip	COG0596	R	100.00	94.74
RCA23_c30840	putative peptide transport system permease protein	COG0601	E	100.00	100.00
RCA23_c30850	putative peptide transport system permease protein	COG1173	E	100.00	100.00
RCA23_c30860	peptide transport system ATP-binding protein	COG1123	R	100.00	100.00
RCA23_c30870	putative periplasmic peptide-binding protein	COG0747	E	100.00	97.48
RCA23_c30880	hypothetical protein UPF0090	COG0779	S	100.00	100.00
RCA23_c30890	transcription elongation protein NusA	COG0195	K	100.00	100.00
RCA23_c30900	hypothetical protein DUF448	COG2740	K	100.00	100.00
RCA23_c30910	translation initiation factor IF-2	COG0532	J	100.00	100.00
RCA23_c30920	putative mutator MutT protein	COG1051	F	100.00	100.00
RCA23_c30930	arginine biosynthesis bifunctional protein ArgJ	COG1364	E	100.00	100.00
RCA23_c30940	putative peptidylprolyl isomerase	COG0760	O	100.00	100.00
RCA23_c30950	protein translocase subunit SecA	COG0653	U	100.00	100.00
RCA23_c30960	putative O-acetyltransferase OatA	COG1835	I	87.06	100.00
RCA23_c30970	hypothetical protein	COG4922	S	100.00	100.00
RCA23_c30980	hypothetical protein, transcriptional regulator-like	COG1733	K	100.00	100.00
RCA23_c30990	UDP-glucoronate 5'-epimerase LspL	COG0451	M	62.96	96.49
RCA23_c31000	hypothetical protein			100.00	98.60
RCA23_c31010	phosphoglucosamine mutase GlmM	COG1109	G	100.00	100.00
RCA23_c31020	putative ubiquinone biosynthesis protein UbiB	COG0661	R	100.00	100.00
RCA23_c31030	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	COG2226	H	100.00	100.00
RCA23_c31040	formamidopyrimidine-DNA glycosylase MutM	COG0266	L	100.00	100.00
RCA23_c31050	enoyl-CoA hydratase/isomerase	COG1024	I	100.00	100.00
RCA23_c31060	30S ribosomal protein S20	COG0268	J	100.00	100.00