

Figure S1. Heatmap with Pearson correlation coefficients among SI, R-CoAD and RN samples. All positive correlations are shown in red and negative correlations are shown in blue. The numbers inside the square represent the correlation values.

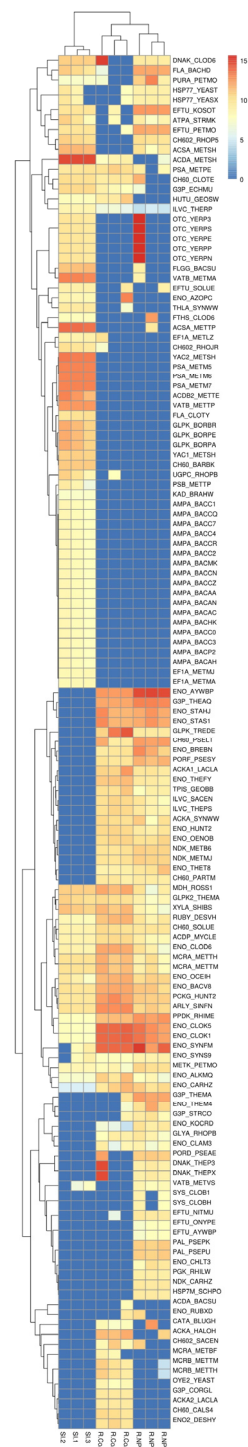


Figure S2. Hierarchical clustering analysis of the abundance profiles of the identified 139 proteins with ID of protein.

Table S1. Proteins that were differentially abundant between samples SI and R-NP.

ID protein from UNIPROT	Protein Description	significance value
ACDA_METSH		0.00
ENO_CLOK5	Enolase	0.00
ENO_CLOK1	Enolase	0.00
ENO_CLOD6	Enolase	0.04
ENO_RUMCH	Enolase	0.00
GLPK2_THEMA	Glycerol kinase 2	0.34
ENO_OCEIH	Enolase	0.38
CH60_CLOTE	60 kDa chaperonin	0.12

RUBY_DESVH	Rubrerythrin	0.01
PPDK_RICFE	Pyruvate phosphate dikinase	0.27
PPDK_RHIME		0.00
PPDK_RICPR		0.00
PPDK_RICCN	Pyruvate phosphate dikinase	0.01
PPDK_RICBR	Pyruvate phosphate dikinase	0.01
PPDK_RICTY	Pyruvate phosphate dikinase	0.01
ENO_THEAB	Enolase	0.17
PSA_METB6	Proteasome subunit alpha	0.06
PSA_METPE	Proteasome subunit alpha	0.12
PSA_METMJ	Proteasome subunit alpha	0.10
ARLY_SINFN	Argininosuccinate lyase	0.00
ARLY1_RHIME	Argininosuccinate lyase 1	0.00
ARLY_RHIE6	Argininosuccinate lyase	0.00

Table S2. Proteins that were differentially abundant between samples SI and R-CoAD.

ID protein from UNIPROT	Protein Description	Significance value
FLA_BACHD		0.04
ENO_CLOK5	Enolase	0.03
ENO_CLOK1	Enolase	0.03
CH603_BRADU	60 kDa chaperonin 3	0.36
CH602_RHOPA	60 kDa chaperonin 2	0.36
CH602_RHOP5	60 kDa chaperonin 2	0.21
CH606_BRADU	60 kDa chaperonin 6	0.36
CH602_NITHX	60 kDa chaperonin 2	0.36
ENO_BACV8	Enolase	0.05
ENO_RUMCH	Enolase	0.05
ENO_BACTN	Enolase	0.05
ENO_BACFR	Enolase	0.05
ENO_BACFN	Enolase	0.05
UGPC_BARBK	sn-glycerol-3-phosphate import ATP-binding protein UgpC OS=Bartonella bacilliformis	0.00
RUBY_DESVH	Rubrerythrin	0.14
PPDK_CLOSY		0.00
PPDK_RICFE	Pyruvate phosphate dikinase OX=315456 GN=ppdK PE=3 SV=1	0.08
PPDK_RHIME		0.00
PPDK_RICPR		0.00
PPDK_RICCN	Pyruvate phosphate dikinase	0.00
PPDK_RICBR	Pyruvate phosphate dikinase	0.00
PPDK_RICTY	Pyruvate phosphate dikinase	0.00
VATB_METPE	V-type ATP synthase beta chain	0.00
ENO_SYNSC	Enolase	0.15
ENO_THEAB	Enolase	0.00
ATPA_DECAR	ATP synthase subunit alpha	0.06
ARLY_SINFN	Argininosuccinate lyase	0.02
ARLY1_RHIME	Argininosuccinate lyase 1	0.03
ARLY_RHIE6	Argininosuccinate lyase	0.03

Table S3. Proteins that were differentially abundant between samples R-NP and R-CoAD.

ID Protein from UNIPROT	Protein Description	Significance value
ENO_CLOK5	Enolase OS=Clostridium kluyveri	0.10
ENO_CLOK1	Enolase OS=Clostridium kluyveri	0.10
ENO_CLOD6	Enolase OS=Clostridioides difficile	0.07
ENO_HUNT2	Enolase	0.13
CH60_PSELT	60 kDa chaperonin	0.16
CH60_FERNB	60 kDa chaperonin	0.18

CH60_THEAB	60 kDa chaperonin	0.01
CH60_THENE	60 kDa chaperonin	0.01
CH60_THEM4	60 kDa chaperonin	0.01
CH60_THEMA	60 kDa chaperonin	0.01
CH60_THEP1	60 kDa chaperonin	0.01
CH60_THESQ	60 kDa chaperonin	0.01
ENO_THEFY	Enolase OS=Thermobifida fusca	0.19
ENO_BREBN	Enolase OS=Brevibacillus brevis	0.10
ENO_AYWBP	Enolase OS	0.00
ACKA1_LACLA		0.11
MCRA_METTH		0.04
MCRA_METTM		0.04
ACDP_MYCLE	Probable acyl-CoA dehydrogenase fadE25	0.14
ACDP_MYCBO	Probable acyl-CoA dehydrogenase fadE25	0.26
ACDP_MYCTU	Probable acyl-CoA dehydrogenase fadE25	0.26
ACDP_MYCTO	Probable acyl-CoA dehydrogenase fadE25	0.26
ENO_RUMCH	Enolase	0.04
ENO_OCEIH	Enolase	0.02
G3P_THEAQ	Glyceraldehyde-3-phosphate dehydrogenase	0.00
ENO_LACF3	Enolase OS=Lactobacillus fermentum	0.31
ENO_LACCB	Enolase OS=Lactobacillus casei	0.08
ENO_OENOB	Enolase	0.18
ENO_PEDPA	Enolase	0.05
ENO_LACP3	Enolase	0.05
ENO2_LACGA	Enolase 2	0.05
ENO_PELCD	Enolase	0.32
ENO1_LACJO	Enolase 1	0.05
ENO_LACS1	Enolase	0.05
ENO_LACSS	Enolase	0.05
ILVC_SACEN	Ketol-acid reductoisomerase (NADP (+))	0.08
ILVC_THEPS	Ketol-acid reductoisomerase (NAD (+))	0.02
RUBY_DESVH	Rubryerythrin	0.01
CH60_SOLUE	60 kDa chaperonin	0.06
PPDK_CLOSY		0.32
PPDK_RICFE	Pyruvate phosphate dikinase	0.01
PPDK_RHIME		0.01
PPDK_RICPR		0.08
PPDK_RICCN	Pyruvate phosphate dikinase	0.08
PPDK_RICBR	Pyruvate phosphate dikinase	0.00
PPDK_RICTY	Pyruvate phosphate dikinase	0.08
PORF_PSESY	Outer membrane porin F	0.03
ENO_THET8	Enolase	0.16
ENO_THET2	Enolase	0.16
GLYA_RHOP2	Serine hydroxymethyltransferase	0.14
ARLY_SINFN	Argininosuccinate lyase	0.01
ARLY1_RHIME	Argininosuccinate lyase 1	0.01
ARLY_RHIE6	Argininosuccinate lyase	0.01

Table S4. Relative abundance of identified proteins assigned to Bacterial and Archaea genera in each sample.

Genus	SI	R-NP	R-CoAD
Acidovorax	0.18	0.10	0.10
Ajellomyces	0.00	0.06	0.00
Alkalilimnicola	0.18	0.05	0.05
Alkaliphilus	4.16	0.69	0.24
Amoebophilus	0.00	0.13	0.07
Aspergillus	0.09	0.11	0.00
Aster	0.00	1.11	4.46
Azobacteroides	0.08	1.81	0.12
Bacillus	2.07	0.07	0.71
Bacteroides	0.91	3.01	1.16
Bartonella	0.71	0.00	1.56
Bifidobacterium	0.18	0.04	0.07
Blumeria	0.00	0.05	0.95
Bordetella	2.37	0.34	0.00
Brachyspira	0.04	0.00	0.00
Bradyrhizobium	0.55	0.18	0.34
Brevibacillus	4.27	0.16	0.71
Burkholderia	1.79	0.51	0.31
Caldanaerobacter	0.00	5.69	0.08
Calycanthus	0.18	0.05	0.03
Carboxydotherrmus	0.01	0.36	0.34
Chelativorans	0.00	0.13	0.11
Chloroherpeton	0.00	0.00	0.11
Clavibacter	0.00	0.06	0.04
Clostridioides	0.57	6.97	1.06
Clostridium	0.70	10.94	5.08
Corynebacterium	0.00	0.14	0.00
Dechloromonas	0.27	0.05	0.04
Desulfitobacterium	0.00	0.21	0.00
Desulfovibrio	0.07	0.59	0.31
Echinococcus	0.33	0.06	0.02
Erwinia	0.17	0.00	0.00
Escherichia	0.86	0.10	0.05
Fervidobacterium	0.00	0.37	2.33
Finegoldia	0.00	0.02	0.06
Geobacillus	0.06	0.33	0.65
Geobacter	0.00	0.34	0.57
Halotheomothrix	0.00	0.58	0.24
Hungateiclostridium	0.19	1.45	0.47
Kluyveromyces	0.00	0.59	0.76
Kocuria	0.00	0.01	0.12
Kosmotoga	0.23	0.07	0.89
Lactobacillus	0.00	1.84	1.28
Lactococcus	0.00	0.73	0.13
Mannheimia	0.18	0.05	0.05
Mesorhizobium	0.12	0.00	0.00
Methanobrevibacter	1.09	0.00	0.00
Methanocaldococcus	1.11	0.03	0.00
Methanocella	0.02	0.00	0.01
Methanococcoides	2.11	0.00	0.00
Methanococcus	8.84	0.00	0.37
Methanocorpusculum	2.19	0.21	0.00
Methanoculleus	0.28	0.44	0.29
Methanoregula	0.21	0.46	0.29
Methanosarcina	14.23	0.05	0.32

Methanosphaerula	2.30	0.31	0.19
Methanospirillum	0.00	0.04	0.07
Methanothermobacter	1.61	1.56	0.22
Methanothrix	14.36	0.07	0.23
Methylococcus	0.18	0.03	0.03
Moorella	0.15	0.07	0.10
Mycobacterium	1.84	1.01	0.36
Neosartorya	0.07	0.05	0.00
Nitrobacter	0.22	0.00	0.17
Nitrosomonas	0.18	0.04	0.03
Nitrospira	0.00	0.01	0.11
Oceanobacillus	0.12	0.64	0.25
Oenococcus	0.00	0.28	0.19
Onion	0.00	0.00	0.03
Ostreococcus	0.18	0.05	0.03
Paraburkholderia	0.18	0.05	0.03
Parageobacillus	0.00	0.13	0.10
Pectobacterium	0.81	0.92	0.05
Pediococcus	0.22	0.26	0.18
Pelobacter	0.00	0.27	0.32
Petrotoga	0.34	0.12	1.59
Photorhabdus	0.00	0.30	0.00
Polynucleobacter	0.36	0.10	0.06
Prochlorococcus	0.00	0.04	0.08
Pseudomonas	0.00	1.08	1.36
Pseudothromotoga	0.00	0.34	0.79
Ralstonia	0.36	0.10	0.06
Rhizobium	0.73	3.36	1.65
Rhodococcus	0.22	0.03	0.00
Rhodopseudomonas	1.80	0.36	0.82
Rickettsia	0.76	2.46	4.51
Roseiflexus	0.42	0.72	0.09
Rubrobacter	0.00	0.14	0.22
Ruminiclostridium	0.23	0.76	0.29
Saccharomyces	0.26	0.25	0.26
Saccharopolyspora	0.00	0.43	0.36
Salmonella	6.43	6.01	0.30
Schizosaccharomyces	0.00	0.00	0.10
Serratia	0.18	0.46	0.02
Shigella	2.27	1.54	0.13
Sinorhizobium	0.23	1.43	0.25
Solibacter	0.21	0.37	0.22
Staphylococcus	1.73	2.16	1.47
Stenotrophomonas	0.43	0.10	0.12
Streptococcus	0.18	0.05	0.03
Streptomyces	0.00	0.08	0.10
Synechococcus	0.69	0.30	0.69
Syntrophobacter	0.07	2.97	3.21
Syntrophomonas	0.15	0.27	0.18
Thermacetogenium	0.00	0.26	0.08
Thermoanaerobacter	0.00	10.68	0.17
Thermobifida	0.00	0.44	0.10
Thermomicrobium	0.09	0.02	0.00
Thermosipho	0.47	5.56	4.98
Thermotoga	0.36	1.02	4.95
Thermus	0.00	1.00	1.82
Thiobacillus	0.27	0.08	0.03
Treponema	0.00	2.15	0.11
Xanthobacter	0.18	0.05	0.03

Xanthomonas	1.44	0.41	0.25
Xylella	0.18	0.05	0.03
Yarrowia	0.18	0.05	0.03
Yersinia	4.57	4.72	38.74
Zymomonas	0.18	0.05	0.03
