Table S4 - Comparison of intracellular soluble proteins

					***Tevnia jerichonana* symbiont**					***Riftia pachyptila* symbiont**					
Protein	**Function**	**E.C.**	**pI**	**MW (kDa)**	**Accession number**	**%Vol**	**Peptide count**	**Mowse score**	**Sequence coverage**	**Accession number**	**%Vol**	**Peptide count**	**Mowse score**	**Sequence coverage**	**Spot ratio**
Sulfur metabolism and energetics															
SopT	ATP-sulfurylase	2.7.7.4	4.99	43.9	TevJSym_ad01200	1.249	11	268	50	Rifp1Sym_cn00110	0.737	12	329	54	-1.7
DsrC	Sulfur oxidation protein DsrC	1.8.99.3	4.81	12.4	TevJSym_aw00150	0.982	5	236	46	Rifp1Sym_am00390	1.911	5	261	46	1.9
DsrE	Sulfur oxidation protein DsrE, similar to sulfur relay protein TusD		5.28	14.3	TevJSym_aw00180	0.174	12	246	83	Rifp1Sym_am00360	0.548	13	321	94	3.1
DsrF	Putative sulfur oxidation protein DsrF, similar to sulfur relay protein TusC		4.03	15.4	TevJSym_aw00170	0.173	6	99	48	Rifp1Sym_am00370	0.394	8	193	48	2.3
Respiratory chain															
AtpD	ATP synthase beta chain	3.6.3.14	4.80	49.5	TevJSym_aq00460	0.448	33	864	83	Rifp1Sym_ae00390	0.303	30	821	81	-1.5
HdrA1	Heterodisulfide reductase, subunit A	1.8.98.1	5.28	69.9	TevJSym_ag00680	0.707	25	522	48	Rifp1Sym_dm00050	0.434	18	343	45	-1.6
HdrB2	Heterodisulfide reductase, subunit B	1.8.98.1	4.95	29.3	TevJSym_ag00710	0.410	13	213	40	Rifp1Sym_ak00380	0.279	10	184	37	-1.5
NuoD1	NADH-quinone oxidoreductase, chain D	1.6.99.5	5.59	47.3	TevJSym_ap00590	0.358	13	194	44	Rifp1Sym_bl00230	0.240	13	195	41	-1.5
NuoG	NADH-quinone oxidoreductase, chain G	1.6.99.5	5.36	82.8	TevJSym_ap00560	0.402	27	517	34	Rifp1Sym_bl00260	0.249	29	407	39	-1.6
YhfP	Putative quinone oxidoreductase	1.6.5.-	5.19	35.2	TevJSym_am00430	0.308	10	341	38	Rifp1Sym_an00090	0.108	14	556	47	-2.9

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					Tevnia jerichonana symbiont					*Riftia pachyptila* symbiont					
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Carbon metabolism															
I. Calvin-Benson-Bassham cycle															
FbaA*	Fructose-bisphosphate aldolase class-II	4.1.2.13	5.18	38.2	TevJSym_an00370	0.566	16	336	50	Rifp1Sym_dp00040	0.372	17	376	56	-1.5
GapA*	Glyceraldehyde-3-phosphate dehydrogenase	1.2.1.13	7.64	31.5	TevJSym_an00400	0.633	10	244	34	Rifp1Sym_dp00070	0.403	17	481	56	-1.6
Pgk*	Phosphoglycerate kinase	2.7.2.3	4.73	41.9	TevJSym_an00390	0.483	15	532	53	Rifp1Sym-dp00060	0.323	18	563	61	-1.5
CbbM	Ribulose-1,5-bisphosphate carboxylase/oxygenase	4.1.1.39	5.19	50.5	TevJSym_aj00630	1.080	20	467	54	Rifp1Sym_at00130	1.759	24	526	56	1.6
TpiA*	Triosephosphate isomerase	5.3.1.1	4.71	26.2	TevJSym_ap00650	0.274	11	241	37	Rifp1Sym-bl00180	0.414	11	257	35	1.5
II. Reductive TCA cycle															
AclA	ATP citrate lyase, alpha subunit	2.3.3.8	5.25	43.6	TevJSym_az00180	0.946	21	514	54	Rifp1Sym_bt00010	0.605	6	181	37	-1.6
AclB	ATP citrate lyase, beta subunit	2.3.3.8	5.59	96.7	TevJSym_az00170	0.094	19	218	30	Rifp1Sym_bt00020	0.058	21	303	32	-1.6
FumB	Fumarate hydratase class I	4.2.1.2	5.28	54.9	TevJSym_am00440	0.331	24	535	51	Rifp1Sym_an00120	0.149	16	403	61	-2.2
KorA1	2-oxoglutarate oxidoreductase, alpha subunit	1.2.7.1	5.31	42.4	TevJSym_az00290	2.125	20	475	75	Rifp1Sym_dm00080	1.266	20	470	58	-1.7
KorB1	2-oxoglutarate oxidoreductase, beta subunit	1.2.7.3	4.92	36.7	TevJSym_az00280	1.416	18	619	64	Rifp1Sym_dm00070	0.946	18	466	62	-1.5
KorG1	Putative 2-oxoglutarate oxidoreductase, gamma subunit	1.2.7.3	6.15	20.8	TevJSym_az00270	0.644	16	313	85	Rifp1Sym_dm00060	0.439	16	343	86	-1.5
SdhA1	Succinate dehydrogenase/ fumarate reductase, flavoprotein subunit	1.3.99.1	5.87	63.1	TevJSym_az00330	1.947	28	474	56	Rifp1Sym_dm00120	1.277	28	508	56	-1.5
SucC	Succinyl-CoA synthetase, beta subunit	6.2.1.5	4.83	40.5	TevJSym_aq00800	0.338	29	786	71	Rifp1Sym_aa00640	0.176	15	340	53	-1.9
SucD	Succinyl-CoA synthetase, alpha subunit	6.2.1.5	5.67	29.6	TevJSym_aq00790	0.334	10	423	49	Rifp1Sym_aa00650	0.219	11	504	53	-1.5

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					***Tevnia jerichonana* symbiont**					***Riftia pachyptila* symbiont**					
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III. Organic carbon metabolism															
Eno	Enolase	4.2.1.11	4.68	45.3	TevJSym_au00510	0.156	26	326	59	Rifp1Sym_bo00130	0.084	25	585	59	-1.9
GlgC	Glucose-1-phosphate adenylyltransferase	2.7.7.27	5.52	47.3	TevJSym_ac01030	0.193	19	488	53	Rifp1Sym_dh00120	0.104	21	357	50	-1.9
PfkA	6-Phosphofructokinase	2.7.1.11	5.28	37.8	TevJSym_by00080	0.468	11	324	40	Rifp1Sym_fe00080	0.299	7	195	47	-1.6
Por2	Pyruvate-ferredoxin oxidoreductase, homodimeric	1.2.7.1	5.11	183.9	TevJSym_br00020	0.805	40	514	31	Rifp1Sym_al00270	0.338	41	564	30	-2.4
WcaG1	Nucleoside-diphosphate-sugar epimerase	5.1.3.2	5.66	43.6	TevJSym_ai00760	0.129	11	304	43	Rifp1Sym_bu00060	0.202	14	334	50	1.6
Stress response															
AhpC	Alkyl hydroperoxide reductase, subunit C	1.11.1.15	4.64	22.0	TevJSym_ah00580	1.594	10	300	58	Rifp1Sym_ai00550	3.358	14	246	58	2.1
SodB	Superoxide dismutase [Fe]	1.15.1.1	4.74	21.5	TevJSym_an00790	0.176	7	164	60	Rifp1Sym_eb00070	0.325	5	131	42	1.8
TrxB	Thioredoxin reductase	1.8.1.9	4.89	34.5	TevJSym_ah00160	0.122	15	502	48	Rifp1Sym_ai00120	0.284	15	508	43	2.3
Protein processing, degradation and translocation															
HflK	Putative FtsH protease regulator		5.68	41.6	TevJSym_bl00180	0.297	26	533	62	Rifp1Sym_bj00120	0.433	27	580	67	1.5
PpiB	Peptidyl-prolyl cis-trans isomerase B	5.2.1.8	4.86	17.7	TevJSym_aa02180	0.126	9	330	73	Rifp1Sym_af00100	0.410	11	405	73	3.3
SecB	Preprotein translocase, chaperone subunit		4.57	17.5	TevJSym_at00230	0.126	5	252	33	Rifp1Sym_cl00120	0.203	6	319	46	1.6

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Amino acid and lipid metabolism															
AcpP	Putative acyl carrier protein		3.89	8.6	TevJSym_bc00160	0.442	4	147	44	Rifp1Sym_ax00040	0.289	5	294	44	-1.5
ArgG	Argininosuccinate synthase	6.3.4.5	4.92	45.4	TevJSym_am00650	0.246	20	444	50	Rifp1Sym_an00280	0.138	22	444	54	-1.8
AroG	Phospho-2-dehydro-3-deoxyheptonate aldolase	2.5.1.54	5.72	39.5	TevJSym_aj00720	0.144	17	371	53	Rifp1Sym_at00220	0.057	15	388	48	-2.5
GlnA	Glutamine synthetase	6.3.1.2	4.76	51.8	TevJSym_aq00060	0.922	17	298	64	Rifp1Sym_ae00070	0.452	25	543	72	-2.0
GlyA	Serine hydroxymethyltransferase 1	2.1.2.1	5.49	45.6	TevJSym_ab01480	0.252	16	485	45	Rifp1Sym_bb00260	0.143	18	441	50	-1.8
IlvB	Acetolactate synthase, large subunit	2.2.1.6	6.06	62.9	TevJSym_af00570	0.139	20	372	45	Rifp1Sym_bi00090	0.086	15	165	32	-1.6
IlvC	Ketol-acid reductoisomerase	1.1.1.86	5.21	36.5	TevJSym_af00550	0.764	22	568	67	Rifp1Sym_bi00110	0.425	15	327	46	-1.8
ThrA	Homoserine dehydrogenase	1.1.1.3	4.96	46.7	TevJSym_ba00270	0.101	24	443	59	Rifp1Sym_aj00110	0.063	21	429	48	-1.6
TrpC	Indole-3-glycerol phosphate synthase	4.1.1.48	4.95	29.4	TevJSym_ag00370	0.055	11	103	47	Rifp1Sym_ak00030	0.110	12	287	52	2.0
Transcription, translation and nucleic acid metabolism															
PurA	Adenylosuccinate synthetase	6.3.4.4	5.58	46.7	TevJSym_bl00140	0.431	22	618	58	Rifp1Sym_bj00070	0.271	19	273	41	-1.6
PurH	Bifunctional phosphoribosylamino-imidazolecarboxamide formyltransferase / IMP cyclohydrolase	2.1.2.3 3.5.4.10	5.07	56.1	TevJSym_ao00430	0.399	25	648	64	Rifp1Sym_ac00130	0.252	27	666	62	-1.6
RpoB	DNA-directed RNA polymerase, subunit beta	2.7.7.6	5.40	151.0	TevJSym_bu00050	0.264	45	805	49	Rifp1Sym_di00060	0.176	47	684	45	-1.5
AdoK	Adenosine kinase	2.7.1.20	4.72	34.2	TevJSym_ao00080	0.069	12	191	44	Rifp1Sym_ac00510	0.109	11	213	37	1.6
Frr	Ribosome recycling factor		5.63	21.7	TevJSym_ba00160	0.070	9	250	41	Rifp1Sym_aj00220	0.120	13	313	62	1.7
GreA	Transcription elongation factor GreA		4.86	17.3	TevJSym_ap00690	0.101	13	337	89	Rifp1Sym_bl00120	0.331	16	427	89	3.3

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Protein	**Function**	**E.C.**	**pI**	**MW (kDa)**	**Accession number**	**%Vol**	**Peptide count**	**Mowse score**	**Sequence coverage**	**Accession number**	**%Vol**	**Peptide count**	**Mowse score**	**Sequence coverage**	**Spot ratio**
NusA	Transcription elongation factor NusA		4.40	54.9	TevJSym_ap00460	0.116	25	485	50	Rifp1Sym_cy00040	0.170	24	428	49	1.5
NusG	Transcription antitermination factor NusG		5.25	20.1	TevJSym_bu00100	0.065	11	359	58	Rifp1Sym_di00110	0.174	14	449	72	2.7
PyrF	Orotidine 5'-phosphate decarboxylase	4.1.1.23	5.89	26.4	TevJSym_ac01140	0.039	15	444	70	Rifp1Sym_da00120	0.110	7	518	35	2.8
RplI	Putative 50S ribosomal protein L9		5.17	16.3	TevJSym_ac00870	0.116	14	465	82	Rifp1Sym_cx00050	0.413	13	481	71	3.6
Ssb	Single-stranded DNA-binding protein		5.19	16.3	TevJSym_aa00340	0.057	9	153	62	Rifp1Sym_bd00110	0.307	13	211	71	5.4