

Supplemental Table 1. Detailed PMF and MS/MS data results for *C. caryae* EB and RB phosphoproteins identified in this study.

Phosphoproteome Spot Identification				source <sup>c</sup>	Peptide Mass Fingerprinting							Sequence(s) confirmed by Collision-Induced Dissociation						
spot number	gene	Protein function	accession #	EB	RB	spectrum file	Protein MW	Protein PI	Unique Peptides	Matched/ Searched	Seq. Coverage	Protein Score	Protein Score Confidence Interval %	Start seq.	stop seq.	peptide seq.	Total Ion Score	Total Ion Confidence Interval %
1	CCA00030	FHA domain-containing protein/CdsD T3SS	29839798			D1	90823.9	4.6	25	36/63	42%	613	100	568	576	VVNAFFTIVR	420	100
														731	743	SVVQEISSIPGVR		
														339	352	AEILSPFNVDLFR		
														552	567	EVPIENMDFQEDIER		
2	CCA00030	FHA domain-containing protein (yscD T3S structural)	29839798			D2	90823.9	4.6	22	31/67	39%	623	100	568	576	VVNAFFTIVR	479	100
														731	743	SVVQEISSIPGVR		
														339	352	AEILSPFNVDLFR		
														552	567	EVPIENMDFQEDIER		
3	CCA00030	FHA domain-containing protein (yscD T3S structural)	29839798			F1	90823.9	4.6	17	27/64	28%	303	100	568	576	VVNAFFTIVR	279	100
														731	743	SVVQEISSIPGVR		
														339	352	AEILSPFNVDLFR		
														552	567	EVPIENMDFQEDIER		
4	eno	phosphopyruvate hydratase (enolase)	29840718			D3	45424.9	4.5	12	19/62	43%	413	100	1	12	MLEVVISDIQAR	330	100
														199	215	NLATGVGDEGGFAPQLK		
														262	276	SVYEQVNLADLCDR		
														365	386	SGETEDTTIADLVAVENTGQIK		
5	CCA00015	hypothetical protein	29839784			F2	66979.9	4.8	21	30/47	45%	760	100	58	65	LSFLSSAR	679	100
														590	603	FIAQLENEFVQGSK		
														13	31	NIAPADLTLGMOASAANR		
														337	357	VSMILLTDVDSNTAAIMQGF		
7	dnaK	molecular chaperone DnaK	29840008			F3	71431.9	5.1	33	49/65	58%	573	100	463	484	SVADLSAGVGYQSLNDVYSR	409	100
														455	465	FDLTDIPPAFR		
														451	465	EIGRDLTDIPPAFR		
														327	343	LSASDIDVLLVGGMSR		
8	proS	probi-1RNA synthetase	29840011			F4	65839.1	5.3	30	36/70	63%	462	100	126	154	MKETAAYLGEFVTEAVHVPAYFVDSQR	354	100
														141	148	FRDEIRPR		
														38	48	GIVTYTFLWR		
														535	547	TFQNSGVLEESR		
9	groEL	chaperonin GroEL	29840401			C2	58118.4	5.2	19	25/68	52%	513	100	335	353	GFIGPLNCPHELVADETR	474	100
														463	474	EGAHICQVLSR		
														182	197	GFETVLDVVEGMFNFR		
														85	105	AGDGTATVLAAYNSE		
11	sucC	succinyl-CoA synthetase subunit beta	29840541			C4	42042.1	5.0	17	25/60	46%	495	100	155	161	LYNVQIR	428	100
														216	225	ITIDNLYR		
														229	241	LEVLYDPSQENVR		
														10	23	DLLVSYDIAIPYR		
12	prfB	peptide chain release factor 2	29839933			C5	38678	5.1	13	14/70	43%	77	91	128	154	AGGVDEEVAQKVPDQLLTVPLTPFAR	279	100
														377	390	ELNIPILCSQLSR		
														407	423	ESGSEQSDSLVMFLLR		
														101	109	IHLLAPEGR		
16	dnaB	replicative DNA helicase	29839892			C6	53017.5	5.9	21	31/70	56%	336	100	36	43	LSPLTYWR	319	100
														90	100	TYFYHGVLDQR		
														110	124	EGSQVWYQGTADAIR		
														1	20	MIENDFQGSYSPVQASHFYR		
17	glgC	glucose-1-phosphate adenylyltransferase	29839901			D4	50082.2	5.9	24	34/69	59%	543	100	285	297	AGYTPSVFTLPR	546	100
														120	133	GPLYDVNETYPVFR		
														237	251	LNAAYVGTAEVYFR		
														187	202	NAEEDVNVIALIGER		
18	CCA00035	T3SS ATPase CdsN	29839803			C7	48202.4	5.5	23	36/70	63%	640	100	106	133	VNLGEGPIDTELKGLVDVNETYPVFR	385	100
														112	119	VLLLENLR		
														193	203	RPFTAILGGAK		
														156	169	HASVYHVPQAFPGR		
19	pgk	phosphoglycerate kinase	29839829			D5	43231.5	5.7	18	24/52	57%	561	100	238	253	SVGNSLVEESGIELAR	265	100
														155	169	KHASVYHVPQAFPGR		
														112	119	VLLLENLR		
														193	203	RPFTAILGGAK		
20	pgk	phosphoglycerate kinase	29839829			C8	43231.5	5.7	17	23/70	51%	314	100	156	169	HASVYHVPQAFPGR	265	100
														238	253	SVGNSLVEESGIELAR		
														112	119	VLLLENLR		
														193	203	RPFTAILGGAK		
21	tuf	elongation factor Tu	29840456			C9	43199.1	5.4	20	30/68	55%	465	100	265	280	ELPEQAGENVGLLLR	390	100
														60	75	GITINASHVEYETPNR		
														320	334	HKPFTGYRPFQFFR		
														206	224	EVDKFLMPEDVFSISGR		
26	CCA00041	ATP:guanoide phosphotransferase	29839809			F5	39938.7	5.5	9	11/55	30%	181	100	23	33	TWPITFSLSR	157	100
														223	237	YSLGLTEEQHLSLR		
														44	55	VNQLVAPTSGR		
														213	225	VNAYIEGDEIVYR		
28	sucB	dihydroloamide acetyltransferase	29840183			F6	40027.8	5.1	15	23/50	52%	603	100	56	74	IWVSSEGDVVAVGGGVAK	535	100
														75	105	IYDANEAVPESAIENISSVDAEHCIFPR		
														80	89	ALNIPVLSR		
														107	120	RVEEFPNEVEWEEK		
30	CCA00732	DadA family oxidoreductase	29840489			C10	37818.5	5.3	13	19/69	43%	205	100	90	106	GHRPAVDDEQAEIFMK	177	100
														57	79	ASKPPLADLGTSTHGLTEASK		
														199	206	LPSELFSR		
														12	21	TARPPVWFLR		
31	hemE	uroporphyrinogen decarboxylase	29840635			F7	37150.3	5.5	12	17/70	48%	293	100	199	206	LPSELFSR	264	100
														12	21	TARPPVWFLR		





Supplemental Table 2. Expanded analysis of *C. caviae* phosphoprotein homologs across *Chlamydia* species.

<i>C. caviae</i> GPIC			Protein Homologs																				
spot number	gene	Phosphoproteome Spot Identification	Protein acc	source <sup>a</sup>		<i>C. trachomatis</i> A/Har-13		<i>C. trachomatis</i> B/Jali		<i>C. trachomatis</i> D/UW-3/CX		<i>C. trachomatis</i> L2 434/Bu		<i>C. muridarum</i> Nigg		<i>C. felis</i> Fe/C-56		<i>C. abortus</i> S26/3		<i>C. pneumoniae</i> AR39		<i>Candidatus</i> <i>proteochlamydia</i> UWE25	
				EB	RB	accession #	% identity	accession #	% identity	accession #	% identity	accession #	% identity	accession #	% identity	accession #	% identity	accession #	% identity	accession #	% identity	accession #	% identity
1, 2, 3	CCA00030	FHA domain-containing protein/CdsD T3SS	29839798		76789404	58	237803094	58	15605397	58	166154006	58	15834660	58	89898782	79	62184678	83	16752328	63	46447025	36	
4	<i>eno</i>	phosphopyruvate hydratase (enolase)	29840718		76789324	79	237803016	79	15605316	79	166154802	80	15835490	81	89898758	91	62185532	93	16752240	77	46445777	58	
5	CCA00015	hypothetical protein	29839784		76789361	40	237803051	39	15605353	39	166154837	39	270285711	35	89898798	76	62184662	77	16752312	44		<1e-07	
7	<i>dnaK</i>	molecular chaperone DnaK	29840008		76789127	89	237802821	89	15605121	89	166154607	89	270285464	89	89898572	94	26006347	96	16752540	89	46447133	71	
8	<i>proS</i>	poly(r)-RNA synthetase	29840011		76789124	72	237802818	72	15605118	72	166154604	72	15835287	73	89898569	90	62184882	88	16752543	75		<1e-07	
9	<i>groEL</i>	chaperonin GroEL	29840401		76788825	93	237802541	93	15604829	93	166154331	93	15835005	93	89898172	98	62185227	97	16752909	94	46446814	73	
11	<i>sucC</i>	succinyl-CoA synthetase subunit beta	29840541		76789566	69	237803253	69	15605556	69	166154165	69	15834828	69	89898036	90	62185364	90	16752058	74	46446932	45	
12	<i>prfB</i>	peptide chain release factor 2	29839933		76789195	74	237802887	74	15605186	74	166154673	74	270285531	82	89898648	90	62184808	89	16752362	81	46446965	56	
16	<i>dnaB</i>	replicative DNA helicase	29839892		76789234	76	237802926	76	15605226	77	166154712	76	15835398	76	89898689	96	62184768	95	16752424	83	46447444	62	
17	<i>glgC</i>	glucose-1-phosphate adenylyltransferase	29839901		76789226	73	237802917	73	15605217	73	166154703	73	15835390	73	89898680	92	62184777	90	16752433	75	46445743	63	
18	CCA00035	T3SS system ATPase (CdsN)	29839803		76789409	92	237803099	92	15605402	92	166154011	91	15834665	92	89898777	97	62184683	98	16752333	96	46447031	69	
19, 20	<i>pgk</i>	phosphoglycerate kinase	29839829		76789433	76	237803123	76	15605426	76	166154035	77	15834690	78	89898750	91	62184709	92	16752362	81	46445873	49	
21	<i>tuf</i>	elongation factor Tu	29840456		76789044	94	237802745	94	15605043	94	166154532	94	161579044	94	89898120	98	62185281	98	16752970	92	46446229	74	
26	CCA00041	ATP:guanine phosphotransferase	29839809		76789415	52	237803105	52	15605408	52	166154017	52	15834671	52	89898771	86	62184689	89	16752339	65	46447508	32	
28	<i>sucB</i>	dihydrolipoamide acetyltransferase	29840183		76788768	68	237802490	68	15604774	68	166154276	68	15834945	69	89898393	87	62185036	88	16752033	74	46446723	46	
30	CCA00732	DadA family oxidoreductase	29840489		76789105	71	237802799	71	15605099	71	166154585	71	15835269	72	89898091	89	62185312	89	16751995	78	46447403	35	
31	<i>hemE</i>	uroporphyrinogen decarboxylase	29840635		76789488	69	237803177	69	15605480	69	166154089	69	15834747	66	89897945	85	62185447	86	16752146	67	46447147	31	
32	<i>ompA</i>	major outer membrane protein, porin (MOMP)	29839815		76789421	68	237803111	66	15605414	66	166154023	65	15834677	69	89898765	84	62184695	86	16752345	74		<1e-07	
33, 35	CCA00005	aromatic amino acid aminotransferase	29839774		76789376	59	237803066	59	15605368	60	166153978	60	15834630	57	89898808	87	62184652	86	16752301	66	161611311	36	
38	<i>gap</i>	glyceraldehyde-3-phosphate dehydrogenase	29839884		76789242	78	237802934	78	15605234	78	166154720	79	15835406	78	89898697	95	62184760	92	16752416	81	46446069	63	
41	<i>tat</i>	transaldolase B	29840447		76789035	85	237802736	86	15605034	86	166154523	86	15835204	84	89898129	95	62185272	94	16752962	85	46447325	49	
47, 48, 52	<i>pyrH</i>	uridylyl kinase	29839812		76789418	70	237803108	70	15605411	70	166154020	70	15834674	71	89898768	91	62184692	92	16752342	82	46447511	42	
49	CCA00083	hypothetical protein	29839851		76789275	85	237802967	85	15605267	85	166154753	85	15835439	84	89898730	94	62184727	96	16752382	85	46445867	51	
50	<i>tpiA</i>	triosephosphate isomerase	29840073		76789052	54	237802751	55	15605051	55	166154538	55	15835221	54	89898502	94	62184937	81	16753052	57	46446435	43	
56	<i>def</i>	peptide deformylase	29840076		76789079	64	237802778	64	15605076	64	166154565	64	15835247	65	89898499	96	62184939	84	16753049	84	46446437	45	
57	<i>adk</i>	adenylate kinase	29840294		76788843	50	237802558	50	15604847	50	166154349	50	15835023	49	89898281	76	62185147	76	16752794	56	46446675	37	
59	CCA00595	hypothetical protein	29840353		76788903	61	237802605	61	15604901	61	166154391	61	15835071	61	89898216	89	62185184	89	16753081	70	46446515	16	
60	<i>axxB</i>	arginine decarboxylase	29840487		76789101 <sup>§</sup>	89	237802798 <sup>§</sup>	89	15605097 <sup>§</sup>	90	auxB truncated	<1e-07	15835267	90	89898093	95	62185310	96	16751993	90		<1e-07	
61	<i>thiE</i>	thiamine-phosphate pyrophosphorylase	29839970			<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07	<1e-07
62	<i>ssb</i>	single-strand DNA-binding protein	29840172		76788757	64	237802479	64	15604763	64	166154265	64	15834934	66	89898405	91	62185025	88	16752652	82	46446738	29	
63	CCA00630	hypothetical protein	29840388		76788933	61	237802634	61	15604931	60	166154421	61	15835101	66	89898180	91	62185218	93	16752904	85	46447389	55	
64	<i>rsbV_2</i>	anti-anti-sigma factor	29840616		76789507	46	237803195	46	15605498	46	166154107	46	15834766	48	89897964	84	62185428	86	16752127	51	46446878	38	
65	CCA00330	hypothetical protein	29840094		76789060	75	237802759	75	15605058	75	166154546	75	15835229	75	89898479	93	62184956	89	16753005	85	46446111	31	
66	<i>rsbV_1</i>	anti-anti-sigma factor	29840000		76789157	75	237802851	75	15605151	75	166154637	75	15835322	74	89898580	92	62184871	96	16752532	80	46446878	33	
5	CCA00282	polymorphic outer membrane protein G family protein (PmpG)	29840049		76789619	29	237803305	29	15605607	29	166154217	29	15834883	27	89898532	70	62185212	53	16752590	43		<1e-07	
10	<i>fusA</i>	elongation factor G	29839959		76789171	92	237802864	92	15605164	92	166154650	92	15835336	92	89898622	96	62184832	96	16752491	93	46445841	74	
15	<i>thrS</i>	threonyl-tRNA synthetase	29840712		76789318	79	237803101	79	15605310	79	166154796	78	15835484	78	89897864	90	62185526	89	16752234	79	46447649	56	
20	<i>tkt</i>	transketolase	29840632		76789492	75	237803180	75	15605483	76	166154092	76	15834751	75	89897948	92	62185444	93	16752143	77	46447148	56	
26	<i>tig</i>	trigger factor	29840674		76789447	63	237803137	63	15605440	63	166154049	63	15834705	63	89897902	92	62185489	90	16752191	72	46447009	22	
28, 29	<i>atpB</i>	V-type ATP synthase subunit B	29840441		76789029	89	237802730	89	15605028	89	166154517	89	15835198	89	89898135	97	62185266	97	16752959	90	46447313	68	
52	<i>ispH</i>	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	29840501		76789606	70	237803293	70	15605595	70	166154205	70	15834869	68	89898079	92	62185324	93	16752009	73	46446712	60	
53	CCA00220	hypothetical protein, putative Zn-ribon	29839987		76789129	81	237802823	81	15605123	81	166154609	81	15835292	79	89898594	96	62184859	95	16752517	86	46446080	54	

<sup>a</sup>Black boxes indicate the phosphoprotein was only present in EB or RB samples, respectively. Gray boxes indicate presence of the phosphoprotein in EB and RB samples.

<sup>b</sup>*Chlamydia pneumoniae* carries a putative frameshift mutation in this gene and is not annotated *aprB* in all *C. pneumoniae* strains.

<sup>c</sup>The *axxB* gene in these strain carry a missense mutation (G115R) that inactivates the protein. Bliven et al. FEMS Micro Lett. 337(2) 2012.