Supplemental Table 1. All Proteins Identified in *F. tularensis tularensis* Schu4 2D PAGE.

num	pH	band	Intensity	SD[a]	RSD[b]	FTT	gene	product	Z score[c]	% cov[d]	theo pI	theo size	est size[e]
1	4.23	2	2625	430	16	FTT0408	gcvH1	glycine cleavage system H protein	2.41	31	4.3	13.89	22
2	4.82	3	2045	97	5	FTT0188	ftsZ	cell division protein	2.32	35	4.8	39.73	38
3	4.82	4	1695	122	7	FTT0654	elbB	DJ-1/PfpI family protein	2.37	47	4.5	23.62	26
4	4.82	5	429	41	10	FTT0869		hypothetical protein	1.42	39	5.8	24.82	26
5	4.82	6	2690	233	9	FTT1747		outer membrane protein	2.41	35	5.3	20.93	24
6	4.82	7	3469	303	9	FTT0143	rplL	50S ribosomal protein L7/L12	2.37	29	4.6	12.83	19
7	4.82	8	618	117	19	FTT1102[h]		macrophage infectivity potentiator, fragment	1.87	25	5.2	10.51	19
8	5.09	1	3729	122	3	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.38	19	4.9	69.24	71
9	5.09	2	570	134	24	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.3	16	4.9	69.24	68
10	5.09	3	1797	79	4	FTT1696	groL	Chaperone protein, groEL	1.52	14	5.1	59.27	57
11	5.09	4	817	33	4	FTT0188	ftsZ	cell division protein	1.73	20	4.8	39.73	54
12	5.09	6	1202	65	5	FTT1413		Aminotransferase	1.33	13	6.8	42.2	27
13	5.09	8	2052	84	4	FTT1747		outer membrane protein	2.34	20	5.3	20.93	24
14	5.09	9	413	37	9	FTT0143	rplL	50S ribosomal protein L7/L12	2.09	29	4.6	12.83	22
15	5.09	11	ND			FTT1733		hypothetical protein	1.47	25	9.1	11.88	
16	5.09	12	718	62	9	FTT0703	rpoZ	DNA-directed RNA polymerase omega subunit	1.66	44	4.8	8.17	18
17	5.39	1	214	33	16	FTT0323	fusA	elongation factor G (EF-G)	1.79	12	5	77.68	81
18	5.39	6	4980	199	4	FTT1696	groL	Chaperone protein, groEL	2.07	26	5.1	59.27	54
19	5.39	7	677	49	7	FTT0064	atpD	ATP synthase beta chain	2.34	20	5.1	49.78	49
20	5.39	7	677	49	7	FTT0062	atpA	ATP synthase alpha chain	2.33	16	5	55.37	49
21	5.39	8	865	30	3	FTT0064	atpD	ATP synthase beta chain	2.14	29	5.1	49.78	46
22	5.39	10	1486	90	6	FTT0188	ftsZ	cell division protein	2.31	35	4.8	39	38
23	5.39	11	967	64	7	FTT1374		malonyl coA-acyl carrier protein transacylase	1.95	26	5.1	33.48	32
24	5.39	14	1086	38	3	FTT0472	accB	Acetyl-CoA carboxylase, biotin carboxyl carrierprotein subunit	2.34	62	5	16.48	22

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25	5.7	1	271	40	15	FTT0323	fusA	elongation factor G (EF-G)	1.39	14	5	77.68	81
26	5.7	2	426	11	2	FTT0715		chitinase family 18 protein	1.91	11	5	83.08	77
27	5.7	2	426	11	2	FTT0721	katG	Peroxidase/catalase	1.39	8	5.4	82.48	77
28	5.7	3	3155	59	2	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.39	21	4.9	69.24	70
29	5.7	5	3720	56	2	FTT1696	groL	Chaperone protein, groEL	2.34	26	5.1	59.27	54
30	5.7	9	582	31	5	FTT1539		conserved hypothetical protein	2.2	26	5.8	52.04	48
31	5.7	10	907	68	7	FTT1234		choloylglycine hydrolase family protein	1.8	18	8.9	42.52	45
32	5.7	11	3570	30	1	FTT0137	tufA	elongation factor Tu (EF-Tu)	2.35	41	5.1	43.39	42
33	5.7	12	834	63	8	FTT0188	ftsZ	cell division protein	2.09	20	4.8	39.73	38
34	5.7	13	1836	104	6	FTT0583	fopA1	outer membrane associated protein	2.34	26	5.6	41.38	36
35	5.7	13	1836	104	6	FTT0137	tufA	elongation factor Tu (EF-Tu)	1.58	36	5.1	43.39	36
36	5.7	14	539	42	8	FTT0137	tufA	elongation factor Tu (EF-Tu)	2.41	37	5.1	43.39	35
37	5.7	16	1747	66	4	FTT1374		malonyl coA-acyl carrier protein transacylase	2.38	29	5.1	33.48	31
38	5.7	17	1009	22	2	FTT1028	ppa	inorganic pyrophosphatase	2.05	31	4.9	19.58	24
39	5.7	17	1009	22	2	FTT1747		outer membrane protein	1.8	25	5.3	20.93	24
40	5.7	17	1009	22	2	FTT0200		hypothetical protein	1.35	20	4.8	23.14	24
41	5.7	18	1460[f]	32	2	FTT0557		AhpC/TSA family protein	1.64	20	5.1	19.68	22
42	5.7	19	954	13	1	FTT0472	accB	Acetyl-CoA carboxylase, biotin carboxyl carrierprotein subunit	2.39	62	5	16.48	22
43	5.7	21	281	19	7	FTT0630	hfq	host factor I for bacteriophage Q betareplication	1.59	24	4.9	12.51	19
44	5.7	23	348	41	12	FTT0391	cspC	cold shock protein	1.34	69	5.2	7.37	19
45	6.05	2	3360	279	8	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.35	22	4.9	69.24	70
46	6.05	3	3249	149	5	FTT1696	groL	Chaperone protein, groEL	2.41	22	5.1	59.27	54
47	6.05	4	2186	110	5	FTT1483	lpd	dihydrolipoamide dehydrogenase	1.61	12	5.6	50.47	48
48	6.05	7	4082	125	3	FTT0137	tufA	elongation factor Tu (EF-Tu)	2.4	40	5.1	43.39	42
49	6.05	8	1936	137	7	FTT1365	fbaB	Fructose-1,6-bisphosphate aldolase	2.15	14	5.3	38.13	37
50	6.05	12	2623	126	5	FTT1374		malonyl coA-acyl carrier protein transacylase	1.52	12	5.1	33.48	31

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51	6.05	16	1905[f]	161	8	FTT0557		AhpC/TSA family protein	1.56	26	5.1	19.68	22
52	6.05	19	1570	106	7	FTT1338		translation initiation inhibitor	1.85	48	5.5	13.73	19
53	6.05	20	3040	245	8	FTT1695	groS	Chaperonin protein, groES	1.31	28	5.5	10.23	19
54	6.59	2	989	99	10	FTT0087	acnA	aconitate hydratase	2.35	22	5.4	102.6	95
55	6.59	3	280	28	10	FTT1769	clpB	ClpB protein	1.95	9	5.5	95.91	69
56	6.59	4	516	59	11	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.38	24	4.9	69.24	66
57	6.59	5	1014	91	9	FTT1696	groL	Chaperone protein, groEL	2.42	40	5.1	59.27	51
58	6.59	6	438	48	11	FTT1329	gpmI	2,3-bisphosphoglycerate-independentphosphoglycerate mutase	1.611	19	5.8	57.58	47
59	6.59	7	1064	116	11	FTT1483	lpd	dihydrolipoamide dehydrogenase	1.78	16	5.6	50.47	45
60	6.59	10	1311	110	8	FTT0137	tufA	elongation factor Tu (EF-Tu)	2.32	52	5.1	43.39	39
61	6.59	10	1311	110	8	FTT0380	gdh	NAD(P)-specific glutamate dehydrogenase	1.45	18	6.5	49.09	39
62	6.59	11	452	23	5	FTT1531	fadA	3-ketoacyl-CoA thiolase	2.16	17	5.7	41.71	38
63	6.59	12	315	15	5	FTT1234		choloylglycine hydrolase family protein	1.3	15	8.9	42.52	37
64	6.59	14	1314	120	9	FTT1365	fbaB	Fructose-1,6-bisphosphate aldolase	2.37	37	5.3	38.13	35
65	6.59	18	757	110	14	FTT0245	usp	universal stress protein	1.84	17	5.5	30.17	31
66	6.59	18	757	110	14	FTT0314	tsf	protein chain elongation factor EF-Ts	1.54	30	5.6	30.97	31
67	6.59	21	577	37	6	FTT1557		Two-component response regulator	2.11	40	6	25.49	26
68	6.59	21	577	37	6	FTT0972		ABC transporter, ATP-binding protein	1.37	32	5.8	27.43	26
69	6.59	22	195	33	17	FTT0078	apt	adenine phosphoribosyltransferase	1.55	24	5.5	18.78	25
70	6.59	23	1560	75	5	FTT1713	iglB2	intracellular growth locus, subunit B	2.43	29	8.7	24.26	25
71	6.59	24	560	79	14	FTT1060	rplI	50S ribosomal protein L9	2.09	45	5.6	16.38	24
72	6.59	26	1026	62	6	FTT1155	aroK	shikimate kinase I	2.35	48	5.5	19.72	23
73	6.59	28	2103	122	6	FTT1572	ompH	outer membrane protein OmpH	2.29	34	7.7	18.75	21
74	6.59	29	3175	135	4	FTT1060	rplI	50S ribosomal protein L9	2.23	75	5.6	16.38	21
75	6.59	29	3175	135	4	FTT1794		heat shock protein	1.67	40	5.6	16.69	21
76	6.59	30	2844	164	6	FTT1695	groS	Chaperonin protein, groES	2.37	74	5.5	10.23	19
77	6.59	31	509	21	4	FTT1060	rplI	50S ribosomal protein L9	1.95	40	5.6	16.38	19
78	6.59	32	697	51	7	FTT1281	yhbH	Sigma-54 modulation protein	2.25	63	5.9	11.16	19
79	6.59	33	524	160	30	FTT1479		conserved hypothetical protein	2.41	45	7.8	9.46	18

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80	6.99	2	93	16	17	FTT1060	rplI	50S ribosomal protein L9	1.54	36	5.6	16.38	107
81	6.99	3	343	28	8	FTT1703		conserved hypothetical protein.	1.89	7	8.9	68.07	97
82	6.99	3	343	28	8	FTT0087	acnA	aconitate hydratase	1.66	8	5.4	102.6	97
83	6.99	4	196	16	8	FTT1526	idh	isocitrate dehydrogenase	1.72	9	6.5	83.4	72
84	6.99	5	296	18	6	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.2	15	4.9	69.24	67
85	6.99	7	608	33	5	FTT1696	groL	Chaperone protein, groEL	2.33	24	5.1	59.27	51
86	6.99	8	654	25	4	FTT1483	lpd	dihydrolipoamide dehydrogenase	1.92	14	5.6	50.47	46
87	6.99	8	654	25	4	FTT1060	rplI	50S ribosomal protein L9	1.9	51	5.6	16.38	46
88	6.99	9	744	30	4	FTT0473	accC	Acetyl-CoA carboxylase, biotin carboxylasesubunit	1.38	22	6.5	49.95	43
89	6.99	11	1091	66	6	FTT0380	gdh	NAD(P)-specific glutamate dehydrogenase	2.11	41	6.5	49.09	39
90	6.99	12	517	20	4	FTT0149	metK	S-adenosylmethionine synthetase	1.56	13	6.1	42.12	36
91	6.99	13	554	167	30	FTT1060	rplI	50S ribosomal protein L9	2.27	55	5.6	16.38	36
92	6.99	16	859	405	47	FTT0535	mdh	lactate dehydrogenase	1.55	19	6.4	36.05	32
93	6.99	18	673	241	36	FTT0314	tsf	protein chain elongation factor EF-Ts	2.41	25	5.6	30.97	30
94	6.99	20	606	251	41	FTT1606	minD	septum site-determining protein MinD	2.32	26	6.9	30.1	28
95	6.99	21	749	237	32	FTT1127		Rhodanese-like family protein	2.1	23	6.6	28.19	27
96	6.99	21	749	237	32	FTT1060	rplI	50S ribosomal protein L9	1.35	19	5.6	16.38	27
97	6.99	22	408	87	21	FTT1557		Two-component response regulator	1.45	19	6	25.49	27
98	6.99	23	458	84	18	FTT1557		Two-component response regulator	2.37	24	6	25.49	26
99	6.99	24	794	727	91	FTT1201		Oxidoreductase, short-chain dehydrogenase familyprotein	2.23	30	6.1	25.97	25
100	6.99	25	1319	639	48	FTT1358	iglB1	intracellular growth locus, subunit B	2.4	36	8.7	24.26	25
101	6.99	26	445	28	6	FTT0061	atpH	ATP synthase delta chain	1.35	28	5.8	19.18	
102	6.99	28	950	134	14	FTT1572	ompH	outer membrane protein OmpH	1.9	34	7.7	18.75	21
103	6.99	29	933	344	37	FTT1060	rplI	50S ribosomal protein L9	2.24	42	5.6	16.38	21
104	6.99	30	629	238	38	FTT0065	atpC	ATP synthase epsilon chain	2.21	54	6.1	15.75	21
105	6.99	31	818	134	16	FTT1045		hypothetical protein	1.55	13	6.8	16.12	20
106	6.99	32	553	278	50	FTT1695	groS	Chaperonin protein, groES	2.06	57	5.5	10.23	20
107	6.99	33	315	25	8	FTT0949[h]		conserved hypothetical membraneprotein,pseudogene	2.16	38	6.6	16.1	19

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108	6.99	35	543	21	4	FTT1472	ppiC	Peptidyl-prolyl cis-trans isomerase.	1.5	28	6.5	10.22	19
109	7.5	2	384	30	8	FTT1526	idh	isocitrate dehydrogenase	2.36	27	6.5	83.4	72
110	7.5	3	321	12	4	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	1.79	10	4.9	69.24	67
111	7.5	4	ND			FTT0917	maeA	NAD-dependent malic enzyme	1.35	14	5.8	67.41	
112	7.5	5	489	24	5	FTT1696	groL	Chaperone protein, groEL	1.43	13	5.1	59.27	51
113	7.5	6	ND			FTT0473	accC	Acetyl-CoA carboxylase, biotin carboxylasesubunit	1.91	20	6.5	49.95	
114	7.5	6	ND			FTT0410	gcvP2	glycine cleavage system P protein, subunit 2	1.53	23	6.9	52.72	
115	7.5	6	ND			FTT0387	glmU	UDP-N-acetylglucosaminepyrophosphorylase/glucosamine-1-phosphateN-acetyltransferase	1.46	15	7.3	50.93	
116	7.5	7	1150	24	2	FTT0473	accC	Acetyl-CoA carboxylase, biotin carboxylasesubunit	2.32	22	6.5	49.95	43
117	7.5	8	850	12	1	FTT0380	gdh	NAD(P)-specific glutamate dehydrogenase	2.39	50	6.5	49.09	39
118	7.5	9	283	35	12	FTT0503	sucD	Succinyl-CoA synthetase, alpha subunit	2.37	29	6.1	30.08	38
119	7.5	11	297	13	4	FTT0149	metK	S-adenosylmethionine synthetase	2.27	25	6.1	42.12	35
120	7.5	13	640	29	5	FTT0535	mdh	lactate dehydrogenase	1.96	17	6.4	36.05	32
121	7.5	14	575	21	4	FTT1606	minD	septum site-determining protein MinD	1.68	25	6.9	30.1	31
122	7.5	16	224	15	7	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.36	32	7.8	35.45	30
123	7.5	17	382	18	5	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2	25	7.8	35.45	29
124	7.5	18	299	52	17	FTT0328	rplB	50S ribosomal protein L2	2.13	21	11.1	30.37	29
125	7.5	21	871	10	1	FTT1127		Rhodanese-like family protein	2.18	27	6.6	28.19	27
126	7.5	22	ND			FTT0484		hypothetical protein	2.32	34	8.8	25.66	
127	7.5	23	569	10	2	FTT1557		Two-component response regulator	2.31	25	6	25.49	26
128	7.5	24	303	12	4	FTT1713	iglB2	intracellular growth locus, subunit B	2.43	25	8.7	24.26	25
129	7.5	25	638	26	4	FTT1358	iglB1	intracellular growth locus, subunit B	2.42	30	8.7	24.26	25
130	7.5	27	247	3	1	FTT1570	fabZ	(3R)-hydroxymyristoyl-(acyl-carrier protein)dehydratase	1.36	15	6.8	18.13	22

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131	7.5	28	332	30	9	FTT1570	fabZ	(3R)-hydroxymyristoyl-(acyl-carrier protein)dehydratase	2.27	32	6.8	18.13	21
132	7.5	29	449	13	3	FTT1570	fabZ	(3R)-hydroxymyristoyl-(acyl-carrier protein)dehydratase	1.83	25	6.8	18.13	21
133	7.5	31	214[f]	11	5	FTT1695	groS	Chaperonin protein, groES	2.25	36	5.5	10.23	20
134	7.5	33	ND			FTT1281	yhbH	Sigma-54 modulation protein	1.95	56	5.9	11.16	
135	7.5	34	ND			FTT1472	ppiC	Peptidyl-prolyl cis-trans isomerase.	2.27	59	6.5	10.22	
136	7.84	1	214	13	6	FTT1526	idh	isocitrate dehydrogenase	2.29	19	6.5	83.4	71
137	7.84	2	165	5	3	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.24	11	4.9	69.24	67
138	7.84	3	232	16	7	FTT0919		hypothetical protein	2.38	26	5.1	59.27	51
139	7.84	4	185	10	6	FTT1317	guaB	Inosine-5-monophosphate dehydrogenase	1.93	19	7.2	52.06	44
140	7.84	5	257	37	15	FTT0473	accC	Acetyl-CoA carboxylase, biotin carboxylasesubunit	2.11	20	6.5	49.95	
141	7.84	5	257	37	15	FTT0387	glmU	UDP-N-acetylglucosaminepyrophosphorylase/glucosamine-1-phosphateN-acetyltransferase	1.64	22	7.3	50.93	
142	7.84	5	257	37	15	FTT0410	gcvP2	glycine cleavage system P protein, subunit 2	1.43	26	6.9	52.72	
143	7.84	6	354	14	4	FTT0473	accC	Acetyl-CoA carboxylase, biotin carboxylasesubunit	2.32	31	6.5	49.95	43
144	7.84	7	ND			FTT0473	accC	Acetyl-CoA carboxylase, biotin carboxylasesubunit	2.33	33	6.5	49.95	
145	7.84	8	ND			FTT0380	gdh	NAD(P)-specific glutamate dehydrogenase	2.34	27	6.5	49.09	
146	7.84	9	398	39	10	FTT0380	gdh	NAD(P)-specific glutamate dehydrogenase	2.2	19	6.5	49.09	39
147	7.84	10	95	15	16	FTT1773	trpB	tryptophan synthase beta chain	2.19	26	6.9	43.06	37
148	7.84	12	160	15	9	FTT0653	lipA	lipoic acid synthetase	1.44	20	8.4	36.82	34
149	7.84	13	218	12	6	FTT0088	pilT	Type IV pili nucleotide-binding protein	1.53	20	6.4	38.01	33
150	7.84	15	186[g]	7	4	FTT0503	sucD	Succinyl-CoA synthetase, alpha subunit	2.37	24	6.1	30.08	31
151	7.84	16	122	8	6	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	1.3	16	7.8	35.45	30
152	7.84	17	295	23	8	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.41	30	7.8	35.45	29

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153	7.84	18	278	13	5	FTT1606	minD	septum site-determining protein MinD	2.37	45	6.9	30.1	27
154	7.84	19	160	10	6	FTT1606	minD	septum site-determining protein MinD	1.83	29	6.9	30.1	27
155	7.84	21	190	30	16	FTT0331	rpsC	30S ribosomal protein S3	2.22	28	10.1	24.84	25
156	7.84	22	207	19	9	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	2.02	35	8.7	26.34	23
157	7.84	23	240	9	4	FTT1015		hypothetical protein	2.11	55	8	22.41	23
158	7.84	23	240	9	4	FTT1713	iglB2	intracellular growth locus, subunit B	1.3	26	8.7	24.26	23
159	7.84	24	165	3	2	FTT1570	fabZ	(3R)-hydroxymyristoyl-(acyl-carrier protein)dehydratase	2.33	32	6.8	18.13	22
160	7.84	26	197	21	10	FTT1060	rplI	50S ribosomal protein L9	1.56	19	5.6	16.38	21
161	7.84	26	197	21	10	FTT0332	rplP	50S ribosomal protein L16	1.36	38	11.5	15.67	21
162	7.84	27	ND			FTT1062	rpsF	30S ribosomal protein S6	1.61	21	6.5	14.2	
163	7.84	29	ND			FTT1038	rpsU3	30S ribosomal protein S21	2.12	45	11.4	7.82	
164	8.13	1	281	6	2	FTT1526	idh	isocitrate dehydrogenase	2.29	17	6.5	83.4	71
165	8.13	2	185	10	5	FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.28	14	4.9	69.24	67
166	8.13	4	408	35	9	FTT0410	gcvP2	glycine cleavage system P protein, subunit 2	1.28	18	6.9	52.72	44
167	8.13	5	431	23	5	FTT0410	gcvP2	glycine cleavage system P protein, subunit 2	1.46	11	6.9	52.72	43
168	8.13	6	437	30	7	FTT0380	gdh	NAD(P)-specific glutamate dehydrogenase	2.38	28	6.5	49.09	39
169	8.13	7	580	83	14	FTT1029	dacD	D-alanyl-D-alanine carboxypeptidase (Penicillinbinding protein) family protein	1.7	14	8.7	48.08	38
170	8.13	7	580	83	14	FTT0380	gdh	NAD(P)-specific glutamate dehydrogenase	1.62	19	6.5	49.09	38
171	8.13	8	243	12	5	FTT0653	lipA	lipoic acid synthetase	1.56	11	8.4	36.82	34
172	8.13	10	835	22	3	FTT0535	mdh	lactate dehydrogenase	2.38	24	6.4	36.05	32
173	8.13	13	203	54	26	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.26	27	7.8	35.45	30
174	8.13	14	696	47	7	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.39	43	7.8	35.45	29
175	8.13	15	416	53	13	FTT1606	minD	septum site-determining protein MinD	2.37	20	6.9	30.1	27
176	8.13	18	525	45	9	FTT0075	sdhB	succinate dehydrogenase iron-sulfur protein	1.93	30	8.4	26.58	25

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177	8.13	19	505	16	3	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	2.17	33	8.7	26.34	25
178	8.13	20	255	12	5	FTT1557		Two-component response regulator	2.23	23	6	25.49	24
179	8.13	21	236	16	7	FTT1015		hypothetical protein	2.08	34	8	22.41	23
180	8.13	22	363	37	10	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	2.4	33	8.7	26.34	22
181	8.13	23	252	14	6	FTT1015		hypothetical protein	2.29	46	8	22.41	20
182	8.13	24	ND			FTT1570	fabZ	(3R)-hydroxymyristoyl-(acyl-carrier protein)dehydratase	2.34	32	6.8	18.13	
183	8.13	25	ND			FTT1570	fabZ	(3R)-hydroxymyristoyl-(acyl-carrier protein)dehydratase	2.06	26	6.8	18.13	
184	8.13	26	391[f]	36	9	FTT1570	fabZ	(3R)-hydroxymyristoyl-(acyl-carrier protein)dehydratase	2.2	32	6.8	18.13	19
185	8.13	27	ND			FTT0332	rplP	50S ribosomal protein L16	1.7	41	11.5	15.67	
186	8.6	1	ND			FTT1269	dnaK	Chaperone protein dnaK (heat shock proteinfamily 70 protein)	2.37	28	4.9	69.24	
187	8.6	2	ND			FTT1317	guaB	Inosine-5-monophosphate dehydrogenase	2.24	26	7.2	52.06	
188	8.6	4	818	17	2	FTT1029	dacD	D-alanyl-D-alanine carboxypeptidase (Penicillinbinding protein) family protein	2.3	17	8.7	48.08	39
189	8.6	5	308	25	8	FTT0607	ispG	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphatesynthase	2.37	27	8.4	43.82	35
190	8.6	7	429	13	3	FTT0535	mdh	lactate dehydrogenase	2.15	23	6.4	36.05	32
191	8.6	8	ND[g]			FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	1.87	16	7.8	35.45	
192	8.6	9	1007	33	3	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.41	47	7.8	35.45	29
193	8.6	10	261	24	9	FTT1606	minD	septum site-determining protein MinD	1.88	20	6.9	30.1	27
194	8.6	11	290	19	6	FTT0313	rpsB	30S ribosomal protein S2	1.55	18	8.5	26.45	27
195	8.6	11	290	19	6	FTT0075	sdhB	succinate dehydrogenase iron-sulfur protein	1.43	22	8.4	26.58	27
196	8.6	12	429	5	1	FTT0075	sdhB	succinate dehydrogenase iron-sulfur protein	2.23	30	8.4	26.58	27
197	8.6	14	828	15	2	FTT1161	adk	adenylate kinase	2.4	33	7.8	24.34	25
198	8.6	15	ND			FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	1.34	22	8.7	26.34	
199	8.6	16	ND			FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	1.66	22	8.7	26.34	

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200	8.6	17	ND			FTT1015		hypothetical protein	2.42	69	8	22.41	
201	8.6	18	386	30	8	FTT1542	omp26	outer membrane protein 26	1.85	29	9.1	19.77	23
202	8.6	19	357	16	4	FTT0142	rplJ	50S ribosomal protein L10	1.77	24	8.7	18.7	21
203	8.6	20	270	24	9	FTT1607	minE	cell division topological specificity factorprotein	2.03	29	8	10.17	19
204	8.88	2	66	6	8	FTT0132	glpA	anaerobic glycerol-3-phosphate dehydrogenase	1.44	13	8.4	57.8	48
205	8.88	3	83	8	9	FTT0132	glpA	anaerobic glycerol-3-phosphate dehydrogenase	1.44	13	8.4	57.8	47
206	8.88	4	263	20	8	FTT1366	pyk	pyruvate kinase	2.03	18	8.8	51.72	46
207	8.88	4	263	20	8	FTT0387	glmU	UDP-N-acetylglucosaminepyrophosphorylase/glucosamine-1-phosphateN-acetyltransferase	1.44	12	7.3	50.93	46
208	8.88	6	493	28	6	FTT1029	dacD	D-alanyl-D-alanine carboxypeptidase (Penicillinbinding protein) family protein	1.41	14	8.7	48.08	40
209	8.88	7	189	17	9	FTT0607	ispG	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphatesynthase	2.33	18	8.4	43.82	33
210	8.88	8	109	11	10	FTT0653	lipA	lipoic acid synthetase	1.63	14	8.4	36.82	32
211	8.88	9	89	3	4	FTT0369		hypothetical protein	2.11	22	8.7	39.87	31
212	8.88	10	84	12	14	FTT0535	mdh	lactate dehydrogenase	1.36	13	6.4	36.05	31
213	8.88	11	169	5	3	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.29	46	7.8	35.45	30
214	8.88	12	497	31	6	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.39	35	7.8	35.45	29
215	8.88	13	150	6	4	FTT1640[h]		ProP osmoprotectant transporter, fragment	2.38	26	9.1	27.7	28
216	8.88	15	98	5	5	FTT0313	rpsB	30S ribosomal protein S2	1.28	23	8.5	26.45	27
217	8.88	16	212	23	11	FTT0313	rpsB	30S ribosomal protein S2	2.27	34	8.5	26.45	26
218	8.88	17	132	2	2	FTT1161	adk	adenylate kinase	2.36	31	7.8	24.34	26
219	8.88	18	237	17	7	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	1.99	22	8.7	26.34	25
220	8.88	19	583	29	5	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	2.4	30	8.7	26.34	24
221	8.88	20	575	27	5	FTT1015		hypothetical protein	2.42	64	8	22.41	23
222	8.88	21	306	8	3	FTT1359	iglA1	intracellular growth locus, subunit A	2.21	43	9	22.4	23

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223	8.88	22	347	15	4	FTT1542	omp26	outer membrane protein 26	1.91	25	9.1	19.77	21
224	8.88	22	347	15	4	FTT0139	nusG	transcription antitermination protein nusG	1.65	37	8.7	20.02	21
225	8.88	23	ND			FTT0142	rplJ	50S ribosomal protein L10	1.94	24	8.7	18.7	
226	8.88	24	197	8	4	FTT0142	rplJ	50S ribosomal protein L10	2.4	45	8.7	18.7	20
227	8.88	26	127	11	8	FTT0140	rplK	50S ribosomal protein L11	2.16	34	9.5	15.74	19
228	8.88	26	127	11	8	FTT0339	rpsH	30S ribosomal protein S8	1.83	48	9.4	14.38	19
229	8.88	28	ND			FTT1607	minE	cell division topological specificity factor protein	2.37	49	8	10.17	
230	8.88	29	91	5	5	FTT0675	rplY	50S ribosomal protein L25	1.91	38	9.5	10.83	18
231	8.88	30	275	37	13	FTT1299	hitA	histidine triad (HIT) family protein	1.83	62	8	12.48	18
232	9.21	2	ND			FTT0659		DNA recombination protein RmuC family protein	2.01	22	6.3	54.32	
233	9.21	3	60	3	5	FTT0132	glpA	anaerobic glycerol-3-phosphate dehydrogenase	2.37	19	8.4	57.8	47
234	9.21	5	257	20	8	FTT1366	pyk	pyruvate kinase	2.42	32	8.8	51	44
235	9.21	6	ND			FTT0964	ffh	signal recognition particle protein, Ffh	2.07	16	9.6	50.23	
236	9.21	7	392	10	3	FTT1029	dacD	D-alanyl-D-alanine carboxypeptidase (Penicillinbinding protein) family protein	2.36	35	8.7	48.08	38
237	9.21	9	119	8	7	FTT0369		hypothetical protein	1.3	18	8.7	39.87	32
238	9.21	10	226	36	16	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	2.32	37	7.8	35.45	29
239	9.21	11	432	22	5	FTT1498	accA	Acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha	1.44	19	7.8	35.45	29
240	9.21	12	210	19	9	FTT1640		ProP osmoprotectant transporter, fragment	1.86	30	9.1	27.7	28
241	9.21	14	235	30	13	FTT0141	rplA	50S ribosomal protein L1	1.34	24	9.5	24.61	26
242	9.21	15	ND			FTT0313	rpsB	30S ribosomal protein S2	2.28	34	8.5	26.45	
243	9.21	16	173	12	7	FTT1161	adk	adenylate kinase	2.33	28	7.8	24.34	25
244	9.21	17	549	54	10	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	2.27	30	8.7	26.34	24
245	9.21	18	528	15	3	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	2.27	30	8.7	26.34	23
246	9.21	19	411	26	6	FTT1015		hypothetical protein	2.4	76	8	22.41	22
247	9.21	20	387	10	3	FTT1542	omp26	outer membrane protein 26	2.32	41	9.1	19.77	21

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248	9.21	21	ND			FTT0139	nusG	transcription antitermination protein nusG	2.33	55	8.7	20.02	
249	9.21	21	ND			FTT1542	omp26	outer membrane protein 26	1.29	23	9.1	19.77	
250	9.21	22	289	17	6	FTT0142	rplJ	50S ribosomal protein L10	2.29	63	8.7	18.7	19
251	9.21	23	206	32	16	FTT0140	rplK	50S ribosomal protein L11	2.16	30	9.5	15.74	18
252	9.21	23	206	32	16	FTT0339	rpsH	30S ribosomal protein S8	2.03	60	9.4	14.38	18
253	9.21	24	114	26	23	FTT0347	rpsM	30S ribosomal protein S13	1.88	39	11.3	13.36	18
254	9.21	24	114	26	23	FTT0336	rplX	50S ribosomal protein L24	1.6	42	9.6	11.52	18
255	9.21	26	206	55	27	FTT0675	rplY	50S ribosomal protein L25	1.91	56	9.5	10.83	
256	9.21	26	206	55	27	FTT1607	minE	cell division topological specificity factorprotein	1.77	29	8	10.17	
257	9.3	1	65	7	10	FTT0132	glpA	anaerobic glycerol-3-phosphate dehydrogenase	2.24	19	8.4	57.8	45
258	9.3	2	293	19	6	FTT1366	pyk	pyruvate kinase	2.24	38	8.8	51	43
259	9.3	2	293	19	6	FTT1305	murA	UDP-N-acetylglucosamine1-carboxyvinyltransferase	1.76	20	9	52	43
260	9.3	3	385	26	7	FTT1029	dacD	D-alanyl-D-alanine carboxypeptidase (Penicillinbinding protein) family protein	2.37	17	8.7	48.08	37
261	9.3	4	193	17	9	FTT1029	dacD	D-alanyl-D-alanine carboxypeptidase (Penicillinbinding protein) family protein	2.4	19	8.7	48.08	33
262	9.3	5	77	10	13	FTT0313	rpsB	30S ribosomal protein S2	1.65	22	8.5	26.45	32
263	9.3	8	337	30	9	FTT0372	accD	Acetyl-CoA carboxylase beta subunit	2.22	18	9.2	33.61	28
264	9.3	10	116	17	14	FTT0141	rplA	50S ribosomal protein L1	1.35	24	9.5	24.61	25
265	9.3	11	318	14	4	FTT0313	rpsB	30S ribosomal protein S2	2.38	40	8.5	26.45	25
266	9.3	12	190	7	4	FTT1161	adk	adenylate kinase	2.37	28	7.8	24.34	24
267	9.3	14	263	30	11	FTT1375	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	2.38	44	8.7	26.34	22
268	9.3	15	301	10	3	FTT1015		hypothetical protein	2.39	49	8	22.41	22
269	9.3	15	301	10	3	FTT1714	iglA2	intracellular growth locus, subunit A	1.33	41	9	22.4	22
270	9.3	16	526	16	3	FTT1015		hypothetical protein	1.55	23	8	22.41	22
271	9.3	17	497	18	4	FTT1542	omp26	outer membrane protein 26	2.37	36	9.1	19.77	20
272	9.3	19	404	6	1	FTT0142	rplJ	50S ribosomal protein L10	2.41	56	8.7	18.7	18
273	9.3	21	349	24	7	FTT0339	rpsH	30S ribosomal protein S8	1.77	37	9.4	14.38	18
274	9.3	23	363	63	17	FTT0675	rplY	50S ribosomal protein L25	1.86	36	9.5	10.83	

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275	9.3	24	208	37	18	FTT0698	rpsO	30S ribosomal protein S15	1.73	42	10.1	10.34	
276	9.95	2	ND			FTT1471	deaD	Cold-shock DEAD-box protein A	1.92	14	9.1	63.93	
277	9.95	4	219	5	2	FTT1305	murA	UDP-N-acetylglucosamine1-carboxyvinyltransferase	2.23	29	9	52.43	46
278	9.95	5	299	11	4	FTT1366	pyk	pyruvate kinase	2.38	21	8.8	51	45
279	9.95	6	167	8	5	FTT0964	ffh	signal recognition particle protein, Ffh	2.31	37	9.6	50.23	43
280	9.95	7	ND			FTT1217	visC	monooxygenase family protein	2.02	16	8.9	46.21	
281	9.95	9	152	8	5	FTT1407		hypothetical membrane protein	1.88	26	8.9	40	34
282	9.95	9	152	8	5	FTT1372	plsX	fatty acid/phospholipid synthesis protein lsX	1.44	23	9.3	37.82	34
283	9.95	10	106	10	9	FTT1372	plsX	fatty acid/phospholipid synthesis protein lsX	1.33	18	9.3	37.82	34
284	9.95	11	185	8	4	FTT0926	gshB	glutathione synthetase	2.3	25	9	37.14	33
285	9.95	13	ND			FTT0372	accD	Acetyl-CoA carboxylase beta subunit	1.52	20	9.2	33.61	
286	9.95	14	373	42	11	FTT0372	accD	Acetyl-CoA carboxylase beta subunit	2.36	22	9.2	33.61	30
287	9.95	15	371	23	6	FTT1512	dnaJ2	heat shock protein, hsp40	1.88	32	9.1	33.66	29
288	9.95	16	535	25	5	FTT0063	atpG	ATP synthase gamma chain	1.31	21	9.1	33.23	28
289	9.95	17	716	22	3	FTT0141	rplA	50S ribosomal protein L1	1.47	40	9.5	24.61	26
290	9.95	20	1262	23	2	FTT0325	rplC	50S ribosomal protein L3	2.31	49	9.6	22.48	24
291	9.95	21	636	15	2	FTT1015		hypothetical protein	1.59	30	8	22.41	23
292	9.95	23	358	8	2	FTT1714	iglA2	intracellular growth locus, subunit A	2.35	47	9	22.4	22
293	9.95	24	290	14	5	FTT0340	rplF	50S ribosomal protein L6	2.04	55	9.8	19.04	
294	9.95	24	290	14	5	FTT0818	infC	translation initiation factor IF-3	1.71	30	9.5	17.52	
295	9.95	26	ND			FTT0142	rplJ	50S ribosomal protein L10	2.07	42	8.7	18.7	
296	9.95	28	407	8	2	FTT1542	omp26	outer membrane protein 26	2.37	28	9.1	19.77	21
297	9.95	29	151	3	2	FTT1542	omp26	outer membrane protein 26	2.2	55	9.1	19.77	21
298	9.95	30	166	2	1	FTT0322	rpsG	30S ribosomal protein S7	2.27	22	10.1	17.79	20
299	9.95	31	675	25	4	FTT0342	rpsE	30S ribosomal protein S5	2.2	37	10	17.54	20
300	9.95	31	675	25	4	FTT1273	rplM	50S ribosomal subunit protein L13	1.54	54	10.1	16.9	20
301	9.95	31	675	25	4	FTT0142	rplJ	50S ribosomal protein L10	1.34	42	8.7	18.7	20
302	9.95	32	597	10	2	FTT0344	rplO	50S ribosomal protein L15	2.38	36	10.2	14.98	19

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303	9.95	33	1181	41	4	FTT0140	rplK	50S ribosomal protein L11	2.13	46	9.5	15.74	19
304	9.95	33	1181	41	4	FTT0339	rpsH	30S ribosomal protein S8	1.92	72	9.4	14.38	19
305	9.95	33	1181	41	4	FTT0335	rplN	50S ribosomal protein L14	1.29	30	10.5	13.22	19
306	9.95	34	686	45	7	FTT0336	rplX	50S ribosomal protein L24	2.09	50	9.6	11.52	18
307	9.95	34	686	45	7	FTT0153	rplS	50S ribosomal protein L19	1.45	69	10.7	13.3	18
308	9.95	35	435	59	14	FTT0341	rplR	50S ribosomal protein L18	2.29	53	10.1	13.02	18
309	9.95	36	843	174	21	FTT0675	rplY	50S ribosomal protein L25	2.38	50	9.5	10.83	18
310	9.95	37	542	127	23	FTT1603	rpmB	50S ribosomal protein L28	2.13	56	11.1	8.92	
311	9.95	38	862	356	41	FTT0627	hupB	Histone-like protein HU form B	2.26	71	9.8	9.46	18
312	12	2	216	17	8	FTT1305	murA	UDP-N-acetylglucosamine1-carboxyvinyltransferase	2.4	32	9	52.43	45
313	12	3	295	18	6	FTT1305	murA	UDP-N-acetylglucosamine1-carboxyvinyltransferase	1.65	16	9	52.43	43
314	12	8	407	21	5	FTT0372	accD	Acetyl-CoA carboxylase beta subunit	1.8	15	9.2	33.61	32
315	12	10	1005	58	6	FTT0372	accD	Acetyl-CoA carboxylase beta subunit	2.28	24	9.2	33.61	29
316	12	11	463	44	9	FTT0349	rpsD	30S ribosomal protein S4	2.31	23	10	23.22	28
317	12	12	1397	74	5	FTT0141	rplA	50S ribosomal protein L1	2.33	33	9.5	24.61	26
318	12	13	ND			FTT0325	rplC	50S ribosomal protein L3	2.25	43	9.6	22.48	
319	12	14	1717	56	3	FTT0349	rpsD	30S ribosomal protein S4	1.38	27	10	23.22	24
320	12	15	423	40	9	FTT1487	coaE	Dephospho-CoA kinase	1.42	27	9.3	23.42	23
321	12	16	416	51	12	FTT1714	iglA2	intracellular growth locus, subunit A	1.9	22	9	22.4	23
322	12	17	752	27	4	FTT0340	rplF	50S ribosomal protein L6	2.34	69	9.8	19.04	22
323	12	18	412	34	8	FTT0337	rplE	50S ribosomal protein L5	2.31	43	9.7	20.01	
324	12	20	641	8	1	FTT0704		hypothetical protein	1.97	46	9.4	20.96	21
325	12	20	641	8	1	FTT0322	rpsG	30S ribosomal protein S7	1.83	15	10.1	17.79	21
326	12	21	962	38	4	FTT0142	rplJ	50S ribosomal protein L10	1.92	33	8.7	18.7	20
327	12	21	962	38	4	FTT0342	rpsE	30S ribosomal protein S5	1.52	27	10	17.54	20
328	12	22	733	41	6	FTT0344	rplO	50S ribosomal protein L15	2.11	31	10.2	14.98	19
329	12	23	748	50	7	FTT0339	rpsH	30S ribosomal protein S8	2.1	55	9.4	14.38	19
330	12	23	748	50	7	FTT0140	rplK	50S ribosomal protein L11	1.58	51	9.5	15.74	19
331	12	24	1247	175	14	FTT0140	rplK	50S ribosomal protein L11	2.36	56	9.5	15.74	18

Supplemental Table 1. All Proteins Identified in *F. tularensis tularensis* Schu4 2D PAGE.

332	12	25	858	133	16	FTT0336	rplX	50S ribosomal protein L24	1.86	42	9.6	11.52	18
333	12	26	1719	399	23	FTT0341	rplR	50S ribosomal protein L18	1.6	20	10.1	13.02	18
334	12	26	1719	399	23	FTT0330	rplV	50S ribosomal protein L22	1.38	21	10.1	12.69	18
335	12	28	824	140	17	FTT0627	hupB	Histone-like protein HU form B	1.91	50	9.8	9.46	
336	12	29	597	128	22	FTT1061	rpsR	30S ribosomal protein S18	2.25	42	10.4	8.33	
337	12.79	1	751	38	5	FTT0141	rplA	50S ribosomal protein L1	1.42	28	9.5	24.61	25
338	12.79	2	ND			FTT0331	rpsC	30S ribosomal protein S3	2.31	27	10.1	24.84	
339	12.79	2	ND			FTT0325	rplC	50S ribosomal protein L3	1.93	57	9.6	22.48	
340	12.79	2	ND			FTT0349	rpsD	30S ribosomal protein S4	1.58	35	10	23.22	
341	12.79	3	1681	76	5	FTT0349	rpsD	30S ribosomal protein S4	1.44	18	10	23.22	23
342	12.79	4	497	34	7	FTT0340	rplF	50S ribosomal protein L6	2.33	52	9.8	19.04	21
343	12.79	5	489	27	5	FTT0340	rplF	50S ribosomal protein L6	1.93	43	9.8	19.04	21
344	12.79	5	489	27	5	FTT0337	rplE	50S ribosomal protein L5	1.62	37	9.7	20.01	21
345	12.79	6	798	61	8	FTT0337	rplE	50S ribosomal protein L5	2.37	68	9.7	20.01	21
346	12.79	8	100	23	23	FTT0322	rpsG	30S ribosomal protein S7	2.36	38	10.1	17.79	
347	12.79	10	1253	13	1	FTT0344	rplO	50S ribosomal protein L15	2.27	34	10.2	14.98	19
348	12.79	11	977	80	8	FTT0140	rplK	50S ribosomal protein L11	2.31	45	9.5	15.74	18
349	12.79	12	1004	144	14	FTT0335	rplN	50S ribosomal protein L14	1.71	25	10.5	13.22	17
350	12.79	13	1141	124	11	FTT0153	rplS	50S ribosomal protein L19	1.37	46	10.7	13.3	17
351	12.79	14	606	47	8	FTT0341	rplR	50S ribosomal protein L18	1.45	40	10.1	13.02	17
352	12.79	14	606	47	8	FTT0338	rpsN	30S ribosomal protein S14	1.39	54	10.6	11.7	17
353	12.79	16	1832	150	8	FTT0150	rpsP	30S ribosomal protein S16	1.55	49	10.6	9.06	17
354	12.79	16	1832	150	8	FTT1603	rpmB	50S ribosomal protein L28	1.44	55	11.1	8.92	17

[a] Standard deviation of measured band intensity (n=3)
[b] Relative standard deviation of measured band intensity (n=3)
[c] ProFound specific quality score
[d] Percent coverage of dectected peptides across deduced amino acid sequence
[e] Estimated size of protein in kDa based on SDS-PAGE migration
[f] Silver staining of this band is proportionally *less* intense than the SYPRO Ruby staining relative to other bands.
[g] Silver staining of this band is proportionally *more* intense than the SYPRO Ruby staining relative to other bands.
[h] Protein fragment identified is annotated as a putative pseudogene in the genome annotation.
ND not determined – SYPRO Ruby measurement was indistinguishable from background