



**Figure S1.** 2D-PAGE analysis of MPF. MPF (100  $\mu$ g) was separated in the first dimension (IEF) using pH range (A) 4-7 or (B) 6-11 gradients. Following second dimension separation, polyacrylamide gels were silver stained. Data are representative of a minimum of two independent experiments. The numbered arrows indicate spots taken for LC-MS/MS analysis (Table 1 and Table S2 in the Supporting Information).

**Table S1. Proteins identified in MPF by 2D LC-MS/MS**

Protein Name	Locus	NCBI Reference Sequence	Signal Peptide	PSORTb Localization (Score) <sup>A</sup>	$\beta$ -barrel Motif	Previously Identified as Membrane (M), Secreted (T), or Surface (S) Protein and Reference	Predicted Molecular Mass (Da)	Protein Identification Probability	Number of Unique Peptides	Percentage Sequence Coverage
Chromosomal replication initiator protein dnaA	FTL_0001	YP_512811.1	-	Cyto (9.97)	-	-	55839.60	99.80%	2	6%
DNA polymerase III, beta chain	FTL_0002	YP_512812.1	-	Cyto (9.26)	-	-	41674.84	100.00%	3	9%
*Outer membrane protein	FTL_0009	YP_512819.1	NC (SP)	Peri (9.84)	-	M <sup>1,4</sup> , T <sup>5</sup>	19477.11	100.00%	3	24%
Recombinase A protein	FTL_0012	YP_512822.1	-	Cyto (9.97)	-	-	38833.58	100.00%	2	8%
Phosphate acetyltransferase	FTL_0016	YP_512826.1	-	Cyto (9.97)	-	-	77167.56	99.80%	2	4%
Aspartyl-tRNA synthetase	FTL_0020	YP_512829.1	-	Cyto (10.00)	-	-	66805.23	100.00%	6	13%
Carbamoyl phosphate synthase large subunit	FTL_0029	YP_512837.1	-	Unknown	-	-	120723.72	99.80%	2	2%
Hypothetical protein	FTL_0039	YP_512847.1	SpII	Unknown	-	-	15326.41	99.80%	2	19%
GTP-binding protein LepA	FTL_0071	YP_512875.1	-	CM (7.88)	-	-	65573.59	100.00%	5	13%
Hypothetical protein	FTL_0073	YP_512877.1	SpII	Unknown	-	M <sup>1,3,6</sup>	37517.73	100.00%	5	16%
Acetyltransferase protein	FTL_0087	YP_512888.1	-	CM (9.82)	-	-	27857.30	99.80%	2	9%
Acetyltransferase protein	FTL_0088	YP_512889.1	-	CM (10.00)	-	-	28838.19	100.00%	2	12%
ClpB protein	FTL_0094	YP_512895.1	-	Cyto (9.97)	-	M <sup>3</sup>	96047.04	100.00%	10	15%
Hypothetical protein	FTL_0097	YP_512896.1	-	Cyto (8.96)	-	-	13793.84	99.80%	2	19%
Hypothetical protein	FTL_0104	YP_512903.1	SpI	Unknown	-	-	14595.73	99.80%	2	26%
Hypothetical protein	FTL_0105	YP_512904.1	SpI	Unknown	-	M <sup>7</sup>	13728.82	100.00%	3	35%
*Intracellular growth locus, subunit A	FTL_0111	YP_512909.1	NC (SP)	Cyto (9.97)	-	M <sup>1,3</sup> , S <sup>8</sup>	20890.88	99.80%	2	14%
*Intracellular growth locus, subunit B	FTL_0112	YP_512910.1	-	Cyto (9.97)	-	M <sup>6</sup>	57917.61	100.00%	11	27%
*Intracellular growth locus, subunit C	FTL_0113	YP_512911.1	-	Unknown	-	M <sup>1,3</sup> , T <sup>9</sup>	22133.41	100.00%	6	37%
Intracellular growth locus, subunit D	FTL_0114	YP_512912.1	-	Cyto (8.96)	-	-	46401.43	100.00%	4	11%
Hypothetical protein	FTL_0116	YP_512914.1	-	Cyto (8.96)	Yes	M <sup>1</sup>	155908.31	100.00%	6	6%
Hypothetical protein	FTL_0118	YP_512916.1	-	Cyto (8.96)	-	T <sup>9</sup>	44640.56	100.00%	5	14%
Hypothetical protein	FTL_0120	YP_512918.1	-	Unknown	-	-	55363.07	99.80%	2	4%
Hypothetical protein	FTL_0125	YP_512923.1	-	Unknown	-	T <sup>9</sup>	127540.09	100.00%	10	12%
Hypothetical protein	FTL_0126	YP_512924.1	-	Cyto (9.94)	-	T <sup>9</sup>	95339.57	100.00%	4	6%

Ferrous iron transport protein	FTL_0133	YP_512931.1	-	CM (10.00)	-	-	81459.74	100.00%	5	10%
Lipopolysaccharide protein	FTL_0137	YP_512935.1	NC (SP)	Unknown	-	-	38744.36	100.00%	6	22%
ABC transporter, ATP-binding protein	FTL_0146	YP_512944.1	-	CM (7.88)	-	-	49453.15	100.00%	4	13%
Universal stress protein	FTL_0166	YP_512961.1	-	Cyto (9.97)	-	M <sup>1</sup>	30220.68	99.80%	2	14%
Inner-membrane protein	FTL_0178	YP_512973.1	SpI	CM (10.00)	-	M <sup>4</sup>	61952.44	100.00%	4	10%
Acyltransferase	FTL_0180	YP_512975.1	-	CM (10.00)	-	-	36125.96	99.80%	2	8%
Cytochrome d terminal oxidase, polypeptide subunit I	FTL_0189	YP_512984.1	-	CM (10.00)	-	M <sup>4</sup>	64275.75	100.00%	4	14%
Cytochrome O ubiquinol oxidase subunit I	FTL_0192	YP_512987.1	-	CM (10.00)	-	M <sup>4</sup>	76200.11	100.00%	3	6%
Hypothetical protein	FTL_0199	YP_512994.1	SpII	EC (9.64)	-	-	15640.67	99.80%	2	16%
Pyrrolidone-carboxylate peptidase	FTL_0207	YP_513002.1	SpI	Unknown	-	M <sup>2</sup> , T <sup>5</sup>	24215.13	100.00%	3	19%
30S ribosomal protein S2	FTL_0224	YP_513019.1	-	Cyto (9.97)	-	-	26421.69	100.00%	8	36%
Elongation factor Ts	FTL_0225	YP_513020.1	-	Cyto (10.00)	-	-	30959.65	100.00%	8	34%
30S ribosomal protein S7	FTL_0233	YP_513028.1	-	Cyto (9.97)	-	-	17807.64	100.00%	3	23%
*Elongation factor G	FTL_0234	YP_513029.1	-	Cyto (10.00)	-	-	77730.37	100.00%	9	15%
30S ribosomal protein S10	FTL_0235	YP_513030.1	-	Cyto (9.26)	-	-	11895.96	100.00%	4	31%
50S ribosomal protein L3	FTL_0236	YP_513031.1	NC (SP)	Cyto (9.26)	-	-	22307.33	100.00%	3	20%
50S ribosomal protein L4	FTL_0237	YP_513032.1	-	Cyto (9.97)	-	-	22553.16	100.00%	5	17%
50S ribosomal protein L23	FTL_0238	YP_513033.1	NC (SP)	Cyto (9.26)	-	-	11135.83	100.00%	3	40%
50S ribosomal protein L2	FTL_0239	YP_513034.1	NC (SP)	Cyto (9.97)	-	-	30401.42	100.00%	4	19%
30S ribosomal protein S3	FTL_0242	YP_513037.1	-	Cyto (9.97)	-	-	24877.10	100.00%	3	17%
50S ribosomal protein L16	FTL_0243	YP_513038.1	-	Cyto (9.97)	-	-	15710.48	100.00%	5	38%
50S ribosomal protein L14	FTL_0246	YP_513041.1	-	Cyto (9.26)	-	-	13235.48	100.00%	2	30%
50S ribosomal protein L24	FTL_0247	YP_513042.1	-	Cyto (9.97)	-	-	11476.34	100.00%	5	50%
50S ribosomal protein L5	FTL_0248	YP_513043.1	-	Cyto (9.26)	-	-	19996.34	100.00%	8	51%
30S ribosomal protein S8	FTL_0250	YP_513045.1	-	Cyto (9.26)	-	-	14410.78	100.00%	5	45%
50S ribosomal protein L6	FTL_0251	YP_513046.1	SpI	Cyto (9.26)	-	-	19075.03	99.90%	2	17%
50S ribosomal protein L18	FTL_0252	YP_513047.1	-	Cyto (9.97)	-	-	13036.06	99.80%	2	23%
50S ribosomal protein L30	FTL_0254	YP_513049.1	-	Cyto (9.26)	-	-	6871.10	99.80%	2	25%
50S ribosomal protein L15	FTL_0255	YP_513050.1	NC (SP)	Cyto (9.26)	-	-	15095.61	100.00%	4	32%
30S ribosomal protein S13	FTL_0258	YP_513053.1	-	Cyto (9.97)	-	-	13377.65	100.00%	3	20%

30S ribosomal protein S4	FTL_0260	YP_513055.1	-	Cyto (9.97)	-	-	23236.78	100.00%	6	27%
DNA-directed RNA polymerase subunit alpha	FTL_0261	YP_513056.1	-	Cyto (9.97)	-	-	35357.51	100.00%	3	14%
50S ribosomal protein L17	FTL_0262	YP_513057.1	-	Cyto (9.97)	-	-	16784.34	100.00%	7	53%
*Heat shock protein 90	FTL_0267	YP_513061.1	-	Cyto (9.97)	-	-	72371.65	100.00%	7	15%
*Glutamate dehydrogenase (Gdh)	FTL_0269	YP_513063.1	-	Unknown	-	M <sup>1</sup> , T <sup>5</sup>	49158.07	100.00%	3	10%
Heat shock protein, hsp40	FTL_0281	YP_513074.1	NC (SP)	Cyto (9.94)	-	-	33669.83	100.00%	3	13%
DNA mismatch repair protein MutS	FTL_0294	YP_513086.1	-	Cyto (9.97)	-	-	95812.74	99.80%	2	3%
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	FTL_0295	YP_513087.1	-	Cyto (9.97)	-	M <sup>3</sup>	35436.02	100.00%	10	32%
Pyruvate dehydrogenase, E1 component (AceE)	FTL_0309	YP_513101.1	-	Cyto (9.97)	-	M <sup>6,10</sup>	100268.34	100.00%	17	18%
Dihydrolipoamide acetyltransferase (AceF)	FTL_0310	YP_513102.1	NC (SP)	Cyto (9.97)	-	M <sup>1-3,6</sup>	56798.85	100.00%	8	19%
Hypothetical protein	FTL_0317	YP_513109.1	SpII	Unknown	-	M <sup>7</sup>	12214.60	100.00%	4	55%
*OmpA family protein	FTL_0325	YP_513113.1	SpII	Unknown	-	M <sup>2,3,10</sup>	46754.18	100.00%	4	13%
Hypothetical protein	FTL_0333	YP_513121.1	-	Cyto (9.97)	-	-	34654.68	99.80%	2	7%
*Peptidoglycan-associated lipoprotein	FTL_0336	YP_513124.1	SpII	OM (10.00)	-	M <sup>2,4,7,10</sup>	23291.32	100.00%	3	18%
Ribonuclease PH	FTL_0357	YP_513140.1	-	Cyto (9.26)	-	-	25440.65	99.80%	2	12%
Hypothetical protein	FTL_0358	YP_513141.1	-	Unknown	-	-	12702.64	99.80%	2	21%
LemA-like protein	FTL_0361	YP_513144.1	-	Cyto (8.96)	-	M <sup>3,7</sup>	21986.26	99.90%	2	16%
*Aspartate aminotransferase (AscP1)	FTL_0387	YP_513160.1	-	Cyto (9.97)	-	-	44382.87	99.90%	2	5%
2-polyprenylphenol 6-hydroxylase	FTL_0407	YP_513180.1	-	CM (7.88)	-	-	63814.61	100.00%	6	11%
GTP-binding protein EngA	FTL_0414	YP_513187.1	-	CM (9.82)	-	-	52468.74	99.80%	2	5%
*Lipoprotein (LpnA)	FTL_0421	YP_513194.1	SpII	OM (10.00)	-	M <sup>2-4,10</sup> , S <sup>11</sup>	15771.85	100.00%	3	30%
Hypothetical protein	FTL_0423	YP_513195.1	SpII	Unknown	-	M <sup>1</sup>	19303.26	99.80%	2	16%
Chromosome partition protein B	FTL_0428	YP_513200.1	-	Cyto (9.97)	-	-	34592.91	99.80%	2	9%
Isoleucyl-tRNA synthetase	FTL_0436	YP_513208.1	-	Cyto (9.97)	-	-	106971.95	100.00%	3	5%
Malate dehydrogenase	FTL_0438	YP_513210.1	-	Cyto (8.96)	-	-	67344.46	100.00%	3	9%
Hypothetical protein	FTL_0439	YP_513211.1	SpI	Unknown	Yes	M <sup>6,10</sup>	58445.63	99.80%	2	5%
DNA topoisomerase IV subunit A	FTL_0462	YP_513234.1	-	Cyto (9.12)	-	-	83930.88	100.00%	6	9%
Soluble lytic murein transglycosylase	FTL_0466	YP_513238.1	SpI	Peri (9.44)	Yes	-	76931.27	99.80%	2	3%
Lysine decarboxylase, inducible	FTL_0476	YP_513248.1	-	Cyto (9.97)	-	-	81935.00	100.00%	3	6%

Glycine dehydrogenase subunit 2	FTL_0480	YP_513252.1	-	Cyto (9.97)	-	-	52781.98	99.80%	2	3%
DNA gyrase, subunit A	FTL_0533	YP_513302.1	-	Cyto (9.97)	-	-	97102.92	100.00%	5	6%
UDP-N-acetylglucosamine acyltransferase	FTL_0539	YP_513308.1	-	Cyto (9.97)	-	-	28124.64	100.00%	5	27%
Two-component response regulator	FTL_0552	YP_513318.1	-	Cyto (9.97)	-	-	25519.67	100.00%	3	21%
Ribonuclease R	FTL_0556	YP_513322.1	-	Cyto (9.97)	-	-	85994.62	100.00%	7	14%
*Hypothetical protein	FTL_0569	YP_513329.1	SpI	Unknown	-	-	19785.57	100.00%	2	14%
Hypothetical protein	FTL_0571	YP_513331.1	SpII	Unknown	-	M <sup>2</sup>	22451.65	100.00%	3	22%
*Hypothetical protein	FTL_0572	YP_513332.1	SpI	Unknown	-	M <sup>1,3</sup>	51977.34	100.00%	3	9%
Hypothetical protein	FTL_0574	YP_513334.1	SpI	OM (9.49)	Yes	-	52201.14	99.80%	2	6%
Fusion product of 3-hydroxacyl-CoA dehydrogenase and acyl-CoA-binding protein	FTL_0584	YP_513344.1	-	Cyto (9.97)	-	-	100624.28	100.00%	7	11%
Acyl-CoA dehydrogenase	FTL_0585	YP_513345.1	-	Unknown	-	-	83333.70	100.00%	7	14%
Hypothetical protein	FTL_0589	YP_513349.1	-	CM (9.82)	-	-	33263.61	99.80%	2	9%
dTDP-glucose 4,6-dehydratase	FTL_0592	YP_513352.1	-	CM (10.00)	-	-	65709.53	100.00%	4	9%
Galactosyl transferase	FTL_0593	YP_513353.1	-	CM (9.82)	-	-	23778.16	99.80%	2	7%
UDP-glucose 4-epimerase	FTL_0594	YP_513354.1	SpI	Unknown	-	-	29955.57	100.00%	4	19%
Galacturonosyl transferase	FTL_0595	YP_513355.1	-	Cyto (9.97)	-	-	41599.47	100.00%	5	13%
UDP-glucose/GDP-mannose dehydrogenase	FTL_0596	YP_513356.1	-	Cyto (9.97)	-	-	48862.13	100.00%	2	5%
Glycosyltransferase	FTL_0604	YP_513364.1	-	Cyto (8.96)	-	M <sup>4</sup>	32975.90	100.00%	3	12%
Transcription termination factor Rho	FTL_0610	YP_513370.1	-	CM (7.88)	-	-	47129.05	100.00%	4	12%
DNA-directed RNA polymerase subunit alpha	FTL_0616	YP_513375.1	-	Cyto (9.97)	-	-	35074.14	100.00%	5	15%
*Hypothetical protein	FTL_0617	YP_513376.1	-	Cyto (8.96)	-	M <sup>1,3,4</sup> , T <sup>5,12</sup> , S <sup>8</sup>	16809.36	100.00%	3	31%
ABC transporter, ATP-binding protein	FTL_0623	YP_513379.1	-	Cyto (9.12)	-	-	34827.65	100.00%	4	15%
Glycosyl transferase	FTL_0625	YP_513381.1	-	CM (9.99)	-	M <sup>4</sup>	35582.32	99.80%	2	11%
Hypothetical protein	FTL_0655	YP_513408.1	NC (SP)	Unknown	-	-	40009.17	100.00%	4	15%
Hypothetical protein	FTL_0656	YP_513409.1	-	Cyto (8.96)	-	-	44513.74	99.80%	2	7%
Pantothenate kinase	FTL_0671	YP_513423.1	-	Cyto (8.96)	-	-	27922.49	99.80%	2	5%
Pantoate-beta-alanine ligase	FTL_0673	YP_513425.1	-	Cyto (9.97)	-	-	29685.32	100.00%	5	20%
Hypothetical protein	FTL_0675	YP_513427.1	-	Unknown	-	-	27475.54	99.80%	2	11%

Polyamine transporter, ABC transporter, ATP-binding protein	FTL_0681	YP_513433.1	-	CM (10.00)	-	M <sup>2</sup>	42296.53	99.80%	2	8%
Outer membrane efflux protein	FTL_0686	YP_513437.1	SpII	OM (10.00)	-	M <sup>2,10</sup>	54535.43	100.00%	5	19%
HlyD family secretion protein	FTL_0687	YP_513438.1	NC (SP)	Unknown	-	M <sup>2</sup>	37853.27	99.80%	2	7%
Cell entry (mce) related family protein	FTL_0695	YP_513446.1	-	CM (9.82)	-	M <sup>2</sup>	26945.01	100.00%	4	19%
Ribonuclease E	FTL_0717	YP_513468.1	-	Cyto (9.94)	-	-	95948.52	100.00%	14	25%
Type IV pilin multimeric outer membrane protein	FTL_0800	YP_513532.1	SpI	OM (10.00)	-	M <sup>10</sup>	64493.72	100.00%	3	6%
Shikimate kinase I	FTL_0801	YP_513533.1	-	Cyto (9.97)	-	-	19752.84	100.00%	3	14%
Bifunctional proline dehydrogenase, pyrroline-5-carboxylate dehydrogenase	FTL_0805	YP_513537.1	-	Cyto (9.97)	-	-	150007.35	100.00%	19	18%
Type IV pili nucleotide binding protein, ABC transporter, ATP-binding protein	FTL_0828	YP_513550.1	-	Cyto (9.97)	-	-	67091.35	100.00%	5	12%
Glycerophosphoryl diester phosphodiesterase	FTL_0829	YP_513551.1	-	Cyto (9.97)	-	-	29669.29	99.80%	2	12%
Cyanophycin synthetase	FTL_0831	YP_513553.1	-	Cyto (9.97)	-	-	103993.16	100.00%	3	5%
Rhodanese-like family protein	FTL_0834	YP_513556.1	NC (SP)	Unknown	-	-	27864.42	99.80%	2	11%
D-methionine transport protein, ABC transporter, ATP-binding subunit	FTL_0838	YP_513560.1	-	CM (7.88)	-	M <sup>4</sup>	39193.40	100.00%	8	34%
Preprotein translocase family protein	FTL_0847	YP_513569.1	SpI	CM (10.00)	-	M <sup>4</sup>	12881.27	100.00%	3	33%
Preprotein translocase subunit SecD	FTL_0848	YP_513570.1	-	CM (10.00)	-	M <sup>4</sup>	69654.94	100.00%	9	23%
Major facilitator transporter	FTL_0865	YP_513587.1	-	CM (10.00)	-	M <sup>4</sup>	49728.62	100.00%	3	7%
Peptidase, M24 family protein	FTL_0877	YP_513597.1	-	Cyto (8.96)	-	-	68759.17	100.00%	2	6%
Trigger factor	FTL_0891	YP_513610.1	-	Cyto (8.96)	-	-	49570.86	100.00%	5	13%
ATP-dependent Clp protease subunit P	FTL_0892	YP_513611.1	-	Cyto (9.97)	-	-	22150.49	99.80%	2	13%
DNA-binding, ATP-dependent protease La	FTL_0894	YP_513613.1	-	Cyto (9.97)	-	-	86222.64	100.00%	9	14%
Hypothetical protein	FTL_0896	YP_513615.1	NC (SP)	CM (9.82)	-	-	54765.05	100.00%	3	9%
Protease, GTP-binding subunit	FTL_0899	YP_513618.1	-	Cyto (8.96)	-	-	50111.49	99.80%	2	7%
SPFH domain, band 7 family protein	FTL_0903	YP_513622.1	-	Cyto (8.96)	-	M <sup>4</sup>	40421.33	100.00%	4	12%
SPFH domain, band 7 family protein	FTL_0904	YP_513623.1	-	Unknown	-	M <sup>1,2,4</sup>	34589.21	100.00%	8	28%
Ketol-acid reductoisomerase	FTL_0916	YP_513629.1	NC (SP)	Cyto (9.26)	-	-	37878.69	99.80%	2	6%
Glutaredoxin 2	FTL_0923	YP_513636.1	-	Cyto (8.96)	-	-	25150.96	99.80%	2	14%
Ferritin-like protein	FTL_0926	YP_513639.1	-	Cyto (9.26)	-	M <sup>4</sup>	19073.63	100.00%	3	33%

Aldolase/adducin class II family protein	FTL_0939	YP_513652.1	-	Cyto (9.97)	-	-	26480.33	99.80%	2	13%
Ribose-phosphate pyrophosphokinase	FTL_0949	YP_513660.1	-	Cyto (9.97)	-	-	34909.35	99.80%	2	8%
50S ribosomal protein L25	FTL_0950	YP_513661.1	-	Cyto (9.26)	-	-	10903.65	99.80%	2	34%
Hypothetical protein	FTL_0951	YP_513662.1	-	CM (10.00)	-	-	46805.03	100.00%	3	11%
ATP-dependent protease, ATP-binding subunit	FTL_0964	YP_513675.1	-	Cyto (9.97)	-	-	51237.15	99.90%	2	5%
Lactate dehydrogenase	FTL_0987	YP_513695.1	-	Cyto (9.97)	-	T <sup>5</sup>	34076.74	100.00%	4	13%
Haloacid dehalogenase	FTL_0995	YP_513701.1	-	Cyto (8.96)	-	-	21938.39	99.80%	2	15%
Hypothetical protein	FTL_1013	YP_513714.1	-	CM (10.00)	-	-	27667.18	100.00%	3	12%
*AhpC/TSA family protein	FTL_1015	YP_513716.1	NC (SP)	Unknown	-	M <sup>3</sup> , T <sup>5,12</sup>	19668.22	100.00%	3	25%
30S ribosomal protein S6	FTL_1024	YP_513725.1	-	Cyto (9.97)	-	-	13054.09	99.90%	2	28%
*50S ribosomal protein L9 (RplI)	FTL_1026	YP_513727.1	-	Cyto (9.97)	-	T <sup>5</sup>	16087.49	100.00%	7	56%
Ribosomal large subunit pseudouridine synthase B	FTL_1030	YP_513731.1	-	Cyto (9.97)	-	-	31171.86	100.00%	3	11%
FKBP-type peptidyl-prolyl cis-trans isomerase family protein	FTL_1042	YP_513742.1	SpII	OM (9.92)	-	M <sup>1-3,10</sup>	29357.52	100.00%	6	27%
D-alanyl-D-alanine carboxypeptidase (penicillin binding protein) family protein	FTL_1046	YP_513746.1	SpI	Peri (9.44)	-	-	51339.76	100.00%	3	11%
30S ribosomal protein S21	FTL_1047	YP_513747.1	-	Cyto (9.26)	-	-	7840.30	99.80%	2	15%
RNA polymerase sigma-70 factor	FTL_1050	YP_513750.1	-	Cyto (9.97)	-	-	67646.46	99.80%	2	4%
D-alanyl-D-alanine carboxypeptidase (penicillin binding protein) family protein	FTL_1060	YP_513757.1	SpI	Unknown	-	M <sup>2,13</sup>	48033.60	100.00%	3	14%
Hypothetical protein	FTL_1064	YP_513761.1	SpI	Unknown	-	-	31675.76	100.00%	3	16%
Hypothetical protein	FTL_1067	YP_513764.1	-	Cyto (9.97)	-	-	69415.81	100.00%	3	7%
Bifunctional GMP synthase/glutamine amidotransferase protein	FTL_1071	YP_513768.1	-	Cyto (9.97)	-	-	57698.31	99.80%	2	5%
1-deoxy-D-xylulose-5-phosphate synthase	FTL_1072	YP_513769.1	-	Cyto (9.97)	-	-	67385.50	100.00%	3	10%
*Lipoprotein (DsbG)	FTL_1096	YP_513788.1	SpII	Unknown	-	M <sup>1,2,4,7,10,13</sup>	39545.19	100.00%	6	27%
Macrophage infectivity potentiator, fragment	FTL_1097	YP_513789.1	SpI	Unknown	-	-	10524.01	99.80%	2	37%
Hypothetical protein	FTL_1100	YP_513790.1	-	Cyto (9.97)	-	-	15476.99	99.80%	2	19%
3-oxoacyl-[acyl-carrier-protein] synthase II	FTL_1137	YP_513823.1	NC (SP)	Cyto (9.26)	-	-	44020.95	100.00%	3	10%
3-oxoacyl-(acyl-carrier-protein) reductase	FTL_1139	YP_513825.1	-	Cyto (9.26)	-	-	26357.24	100.00%	3	20%

Putative glycerol-3-phosphate acyltransferase PlsX	FTL_1142	YP_513828.1	-	Cyto (9.97)	-	-	37840.30	100.00%	4	22%
Pyruvate kinase	FTL_1148	YP_513834.1	-	Cyto (9.97)	-	-	51776.46	100.00%	5	13%
Fructose-1,6-bisphosphate aldolase	FTL_1149	YP_513835.1	-	Cyto (9.97)	-	-	38159.39	99.80%	2	7%
30S ribosomal protein S9	FTL_1186	YP_513869.1	NC (SP)	Cyto (9.97)	-	-	14736.01	99.80%	2	22%
50S ribosomal protein L13	FTL_1187	YP_513870.1	NC (SP)	Cyto (9.26)	-	-	15937.61	100.00%	3	30%
*Chaperone protein DnaK	FTL_1191	YP_513874.1	NC (SP)	Cyto (9.97)	-	M <sup>3,6,10</sup> , T <sup>5,12</sup> , S <sup>8</sup>	69182.22	100.00%	3	6%
Heat shock protein DnaJ	FTL_1192	YP_513875.1	-	Cyto (9.97)	-	-	41480.80	100.00%	5	14%
Phenylalanyl-tRNA synthetase subunit alpha	FTL_1197	YP_513880.1	-	Cyto (10.00)	-	-	38505.40	99.80%	2	7%
Phenylalanyl-tRNA synthetase, beta subunit	FTL_1198	YP_513881.1	-	Cyto (9.97)	-	-	88165.30	100.00%	2	3%
Hypothetical protein	FTL_1202	YP_513885.1	SpII	Unknown	-	-	36896.57	100.00%	3	13%
Lipoprotein	FTL_1211	YP_513894.1	SpII	Unknown	-	M <sup>2</sup>	21033.65	100.00%	3	22%
Hypothetical protein	FTL_1213	YP_513896.1	SpI	Cyto (8.96)	-	-	73307.99	100.00%	4	10%
Hypothetical protein	FTL_1219	YP_513902.1	-	Cyto (9.26)	-	-	47072.58	99.90%	2	5%
Signal recognition particle protein, Ffh	FTL_1239	YP_513919.1	-	CM (7.88)	-	M <sup>4</sup>	50311.00	100.00%	9	30%
2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase/dihydropteroate synthase	FTL_1265	YP_513939.1	-	Cyto (9.97)	-	-	48246.88	99.80%	2	4%
Biotin synthase	FTL_1272	YP_513943.1	-	Cyto (9.97)	-	-	34906.21	100.00%	4	17%
Dethiobiotin synthetase	FTL_1275	YP_513946.1	-	Cyto (9.26)	-	-	24502.30	99.90%	2	13%
Glutathione synthetase	FTL_1284	YP_513955.1	-	Cyto (9.97)	-	-	37159.94	99.90%	2	8%
23S rRNA m(2)G2445 methyltransferase	FTL_1287	YP_513958.1	-	Cyto (9.97)	-	-	83481.52	100.00%	3	6%
Acetyl-CoA carboxylase beta subunit	FTL_1309	YP_513980.1	-	Cyto (9.26)	-	-	33386.81	100.00%	6	14%
*Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	SpI	OM (9.93)	Yes	M <sup>2,3,7,10</sup> , T <sup>5</sup> , S <sup>8</sup> , 14	41259.65	100.00%	7	19%
Hypothetical protein	FTL_1341	YP_514006.1	-	Unknown	-	-	15407.51	99.80%	2	16%
UTP--glucose-1-phosphate uridylyltransferase	FTL_1357	YP_514018.1	-	Cyto (9.97)	-	M <sup>1</sup>	32148.15	100.00%	3	7%
Cation-efflux family protein	FTL_1358	YP_514019.1	-	CM (10.00)	-	M <sup>4</sup>	42813.45	100.00%	4	15%
Hypothetical protein	FTL_1363	YP_514024.1	NC (SP)	Unknown	-	-	36704.83	100.00%	3	9%
Hypothetical protein	FTL_1364	YP_514025.1	-	Cyto (8.96)	-	-	26430.83	100.00%	4	24%
Hypothetical protein	FTL_1384	YP_514040.1	SpI	Unknown	-	-	13313.44	99.80%	2	18%



Cold-shock DEAD-box protein A	FTL_1392	YP_514047.1	-	Cyto (9.97)	-	-	64008.24	100.00%	14	31%
50S ribosomal protein L20	FTL_1404	YP_514059.1	NC (SP)	Cyto (9.26)	-	-	13348.57	100.00%	3	27%
Threonyl-tRNA synthetase	FTL_1407	YP_514062.1	-	Cyto (10.00)	-	-	72381.56	100.00%	2	3%
Hypothetical protein	FTL_1414	YP_514069.1	NC (SP)	Unknown	-	M <sup>4</sup>	44264.38	100.00%	3	7%
Capsule biosynthesis protein capB	FTL_1416	YP_514071.1	-	CM (7.88)	-	M <sup>4</sup>	44579.71	100.00%	4	12%
Cyanophycinase	FTL_1419	YP_514074.1	-	Unknown	-	-	29302.93	99.80%	2	9%
Carbohydrate/purine kinase pfkB family protein	FTL_1420	YP_514075.1	-	Cyto (9.26)	-	-	40313.98	99.80%	2	5%
Hypothetical protein	FTL_1426	YP_514081.1	-	Cyto (8.96)	-	-	26495.63	100.00%	3	16%
Enoyl-[acyl-carrier-protein] reductase (NADH)	FTL_1442	YP_514097.1	-	CM (9.82)	-	-	27775.17	99.80%	2	8%
50S ribosomal protein L21	FTL_1453	YP_514108.1	NC (SP)	Cyto (9.26)	-	-	11561.63	100.00%	4	34%
Preprotein translocase subunit SecA	FTL_1458	YP_514109.1	-	Cyto (9.12)	-	M <sup>4</sup>	103590.04	100.00%	5	8%
ATP-dependent metalloprotease	FTL_1464	YP_514115.1	-	CM (10.00)	-	M <sup>4</sup>	70752.29	100.00%	4	8%
Inosine-5-monophosphate dehydrogenase	FTL_1478	YP_514129.1	-	Cyto (9.97)	-	M <sup>2,3</sup>	52091.72	100.00%	3	8%
Cytosol aminopeptidase	FTL_1479	YP_514130.1	-	Cyto (9.97)	-	-	51988.90	100.00%	2	6%
FAD-binding family protein	FTL_1489	YP_514140.1	-	Cyto (9.94)	Yes	-	114567.82	100.00%	6	8%
Deoxyguanosinetriphosphate triphosphohydrolase	FTL_1503	YP_514153.1	-	Cyto (9.97)	-	-	50409.72	99.80%	2	6%
*Peroxidase/catalase (KatG)	FTL_1504	YP_514154.1	NC (SP)	Cyto (9.26)	-	M <sup>2,3,6,10</sup> , T <sup>5,12</sup>	81226.95	100.00%	5	10%
Glycerophosphoryl diester phosphodiesterase family protein	FTL_1511	YP_514160.1	SpI	Unknown	-	M <sup>1-3</sup> , T <sup>5</sup>	39076.81	100.00%	4	17%
2-amino-3-ketobutyrate coenzyme A ligase	FTL_1522	YP_514169.1	-	Cyto (9.97)	-	-	43952.33	99.80%	2	9%
*Enolase (2-phosphoglycerate dehydratase)	FTL_1527	YP_514174.1	-	Cyto (9.97)	-	-	49511.19	100.00%	6	22%
Polynucleotide phosphorylase/polyadenylase	FTL_1537	YP_514183.1	-	Cyto (9.97)	-	-	75501.74	100.00%	8	15%
Penicillin binding protein (peptidoglycan synthetase)	FTL_1539	YP_514185.1	-	CM (9.82)	-	T <sup>5</sup>	62733.93	100.00%	4	8%
Hypothetical protein	FTL_1542	YP_514188.1	-	CM (7.88)	-	-	78582.16	100.00%	6	11%
Glutamine amidotransferase subunit PdxT	FTL_1545	YP_514191.1	-	Unknown	-	-	19960.97	99.90%	2	13%
DNA gyrase subunit B	FTL_1547	YP_514193.1	-	Cyto (9.97)	-	-	89740.80	100.00%	2	3%
Hypothetical protein	FTL_1552	YP_514198.1	-	CM (10.00)	-	-	69884.07	100.00%	12	26%
*Succinyl-CoA synthetase subunit beta	FTL_1553	YP_514199.1	-	Cyto (8.96)	-	M <sup>6</sup> , T <sup>12</sup>	41541.74	100.00%	4	12%

Acetyl-CoA carboxylase, biotin carboxylase subunit	FTL_1591	YP_514230.1	-	Cyto (9.97)	-	-	50050.70	100.00%	6	17%
*Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit (AccB)	FTL_1592	YP_514231.1	-	Unknown	-	M <sup>2,3</sup>	16403.98	100.00%	4	48%
Putative periplasmic protease	FTL_1605	YP_514244.1	-	CM (7.88)	-	T <sup>5</sup>	38067.40	100.00%	7	18%
Dolichyl-phosphate-mannose-protein mannosyltransferase family protein	FTL_1609	YP_514248.1	-	CM (10.00)	-	-	68148.00	99.80%	2	4%
Glycosyl transferase, group 2 family protein	FTL_1611	YP_514250.1	-	CM (9.82)	-	M <sup>4</sup>	35935.44	100.00%	4	15%
Phosphoenolpyruvate carboxykinase	FTL_1616	YP_514255.1	NC (SP)	Cyto (9.97)	-	-	60476.89	100.00%	3	9%
Hypothetical protein	FTL_1639	YP_514278.1	-	Unknown	-	-	29381.81	99.90%	2	9%
Hypothetical protein	FTL_1658	YP_514293.1	SpI	Unknown	-	S <sup>8</sup>	49321.86	100.00%	6	18%
Lipid A transport protein, ABC transporter, ATP-binding and membrane protein	FTL_1668	YP_514303.1	-	CM (10.00)	-	M <sup>4</sup>	66676.73	100.00%	6	12%
RND efflux transporter	FTL_1671	YP_514306.1	-	CM (10.00)	-	M <sup>4</sup>	50088.80	99.80%	2	5%
AcrB/AcrD/AcrF family transporter	FTL_1672	YP_514307.1	-	CM (10.00)	-	M <sup>4</sup>	112503.15	100.00%	3	4%
Hypothetical protein	FTL_1678	YP_514310.1	SpI	Unknown	-	M <sup>2</sup>	38458.69	100.00%	3	11%
Cell division protein	FTL_1705	YP_514336.1	-	CM (10.00)	-	-	92016.36	100.00%	7	10%
*Chaperonin GroEL	FTL_1714	YP_514345.1	-	Cyto (9.97)	-	M <sup>3,10,15</sup> , T <sup>5,12</sup> , S <sup>8</sup>	57402.70	100.00%	16	46%
Co-chaperonin GroES	FTL_1715	YP_514346.1	-	Cyto (9.26)	-	T <sup>5,12</sup>	10271.87	100.00%	2	24%
Hypothetical protein	FTL_1723	YP_514354.1	NC (SP)	Unknown	-	M <sup>1</sup>	23828.44	100.00%	3	17%
S-adenosylmethionine synthetase	FTL_1739	YP_514370.1	-	Cyto (10.00)	-	-	42103.04	99.80%	2	7%
DNA-directed RNA polymerase, beta subunit	FTL_1743	YP_514374.1	-	Cyto (9.97)	-	-	157387.04	100.00%	26	24%
DNA-directed RNA polymerase subunit beta	FTL_1744	YP_514376.1	-	Cyto (9.97)	-	-	151335.66	100.00%	19	19%
*50S ribosomal protein L7/L12 (RpL)	FTL_1745	YP_514376.1	-	Unknown	-	M <sup>3</sup>	12847.82	99.80%	2	20%
50S ribosomal protein L10	FTL_1746	YP_514377.1	-	Cyto (9.26)	-	M <sup>1</sup>	18731.70	100.00%	5	42%
50S ribosomal protein L1	FTL_1747	YP_514378.1	NC (SP)	Cyto (9.97)	-	-	24641.67	100.00%	11	54%
50S ribosomal protein L11	FTL_1748	YP_514379.1	NC (SP)	Cyto (9.26)	-	T <sup>5</sup>	15269.89	100.00%	3	16%
Transcription antitermination protein nusG	FTL_1749	YP_514380.1	-	Cyto (9.97)	-	T <sup>5</sup>	19981.99	100.00%	3	21%
*Elongation factor Tu (TufA)	FTL_1751	YP_514382.1	-	Cyto (9.97)	-	M <sup>3</sup>	43390.62	100.00%	13	38%
Anaerobic glycerol-3-phosphate dehydrogenase	FTL_1756	YP_514387.1	-	Unknown	-	-	57775.19	100.00%	11	26%

Sensor histidine kinase	FTL_1762	YP_514393.1	-	CM (9.99)	-	-	54752.94	100.00%	3	7%
*Aconitate hydratase	FTL_1772	YP_514399.1	-	Cyto (9.97)	-	M <sup>1,3,6</sup>	102703.80	100.00%	13	24%
Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex (SucB)	FTL_1783	YP_514408.1	-	Cyto (9.97)	-	M <sup>1,3,6</sup>	52717.94	100.00%	9	29%
Alpha-ketoglutarate decarboxylase	FTL_1784	YP_514409.1	-	Cyto (9.97)	Yes	-	105679.39	100.00%	18	24%
Succinate dehydrogenase iron-sulfur subunit	FTL_1785	YP_514410.1	-	CM (7.88)	-	M <sup>4</sup> , T <sup>5</sup>	26565.80	100.00%	5	24%
*Succinate dehydrogenase, catalytic and NAD/ flavoprotein subunit	FTL_1786	YP_514411.1	-	CM (7.88)	-	M <sup>3,4</sup>	65860.61	100.00%	7	15%
F0F1 ATP synthase subunit epsilon	FTL_1794	YP_514419.1	NC (SP)	Unknown	-	M <sup>4</sup>	15736.95	100.00%	3	30%
F0F1 ATP synthase subunit beta	FTL_1795	YP_514420.1	-	Cyto (9.12)	-	M <sup>4,10</sup>	49864.94	100.00%	10	37%
F0F1 ATP synthase subunit gamma	FTL_1796	YP_514421.1	-	Cyto (9.12)	-	M <sup>4</sup>	33235.28	100.00%	4	18%
F0F1 ATP synthase subunit alpha	FTL_1797	YP_514422.1	-	Cyto (9.97)	-	M <sup>4</sup>	55536.23	100.00%	10	23%
F0F1 ATP synthase subunit delta	FTL_1798	YP_514423.1	-	Cyto (9.26)	-	M <sup>4</sup>	19202.29	99.90%	2	20%
F0F1 ATP synthase subunit B	FTL_1799	YP_514424.1	-	CM (7.88)	-	M <sup>4</sup>	17383.26	100.00%	7	45%
Translation initiation factor IF-2	FTL_1809	YP_514434.1	-	Cyto (9.97)	-	-	92422.06	100.00%	10	20%
Transcription elongation factor NusA	FTL_1810	YP_514435.1	-	Cyto (9.97)	-	-	55178.89	100.00%	6	15%
Hypothetical protein	FTL_1811	YP_514436.1	-	Cyto (9.97)	-	-	16546.95	100.00%	4	35%
NADH dehydrogenase subunit G	FTL_1824	YP_514446.1	-	Cyto (9.12)	-	-	87340.84	100.00%	9	17%
NADH dehydrogenase I, F subunit	FTL_1825	YP_514447.1	-	Cyto (9.12)	-	M <sup>4</sup>	46282.70	100.00%	3	9%
NADH dehydrogenase subunit D	FTL_1827	YP_514449.1	-	Cyto (9.12)	-	M <sup>4</sup>	47585.74	100.00%	6	16%
NADH dehydrogenase I	FTL_1828	YP_514450.1	-	Cyto (9.12)	-	M <sup>1,4</sup>	24988.46	99.80%	2	11%
Amidophosphoribosyltransferase	FTL_1861	YP_514478.1	-	Cyto (9.97)	-	-	55417.57	100.00%	4	8%
Outer membrane protein tolC precursor	FTL_1865	YP_514482.1	SpI	OM (10.00)	-	M <sup>10</sup>	57243.63	100.00%	3	11%
Protein-L-isoaspartate O-methyltransferase	FTL_1866	YP_514483.1	-	Cyto (8.96)	-	-	23203.94	99.80%	2	11%
GTPase ObgE	FTL_1874	YP_514488.1	-	Cyto (8.96)	-	-	36887.99	99.80%	2	10%
Glutamine synthetase	FTL_1899	YP_514509.1	NC (SP)	Cyto (9.97)	-	-	38256.94	99.80%	2	9%
*Cell division protein FtsZ	FTL_1907	YP_514517.1	-	Cyto (9.12)	-	M <sup>3,4</sup>	39745.31	100.00%	11	41%
Cell division protein FtsA	FTL_1908	YP_514518.1	-	Cyto (9.97)	-	M <sup>4</sup>	44804.05	100.00%	7	20%
*30S ribosomal protein S1	FTL_1912	YP_514522.1	-	Cyto (9.97)	-	-	61669.35	100.00%	9	22%
Adenylosuccinate synthetase	FTL_1930	YP_514535.1	-	Cyto (9.97)	-	-	46879.73	100.00%	2	8%

ABC transporter, ATP-binding protein	FTL_1935	YP_514538.1	-	CM (9.82)	-	-	25593.76	99.80%	2	12%
Periplasmic solute binding family protein	FTL_1936	YP_514539.1	SpI	CM (9.97)	-	M <sup>1,4</sup>	33814.86	100.00%	7	40%
Heat shock protein	FTL_1957	YP_514555.1	-	Cyto (8.96)	-	M <sup>1</sup>	16739.78	99.80%	2	15%
Bifunctional indole-3-glycerol phosphate synthase/phosphoribosylanthranilate isomerase	FTL_1958	YP_514556.1	-	Cyto (9.97)	-	-	51323.54	100.00%	3	11%
Anthranilate synthase component I	FTL_1966	YP_514562.1	-	Cyto (9.97)	-	-	58066.29	100.00%	4	11%

Protein identifications were accomplished using Scaffold version 4.0.0 software. Identifications were accepted if they could be established at greater than 99% probability and contained at least two identified peptides as assigned by the protein prophet algorithm.

\*Indicates the protein was identified on the surface of *F. tularensis* LVS.

Signal peptide prediction; SpI, signal peptide cleaved by signal peptidase I; SpII, signal peptide cleaved by signal peptidase II; NC (SP), non-classical signal peptide.

<sup>^</sup>Subcellular localization predicted with PSORTb; Peri, periplasmic; Cyto, cytosol; OM, outer membrane; CM, cytoplasmic membrane.

## Table S1 References

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**Table S2. LC-MS/MS analysis of MPF spots**

Spot #	Protein Name	Locus	NCBI Reference Sequence	Predicted Molecular Mass (Da)	Protein Identification Probability	Number of Unique Peptides	Percentage Sequence Coverage
1	Dihydrolipoamide dehydrogenase (Ipd)	FTL_0311	YP_513103.1	50527.53	100.00%	6	16%
	ATP-dependent protease, ATP-binding subunit	FTL_0964	YP_513675.1	51237.15	100.00%	7	17%
	*Glyceraldehyde-3-phosphate dehydrogenase (GapA)	FTL_1146	YP_513832.1	35413.40	100.00%	2	7%
	Glutathione reductase	FTL_1248	YP_513928.1	49547.59	100.00%	4	10%
2	*Aspartate aminotransferase (AscP1)	FTL_0387	YP_513160.1	44382.87	99.80%	2	4%
	*Elongation factor Tu (TufA)	FTL_1751	YP_514382.1	43390.62	100.00%	16	49%
3	*Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	41259.65	100.00%	6	13%
4	*Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	41259.65	100.00%	6	13%
5	*Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	41259.65	100.00%	13	29%
6	*Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	41259.65	100.00%	5	10%
7	*Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	41259.65	100.00%	4	10%
8	*Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	41259.65	100.00%	8	20%
9-10	Could not be identified with confidence	-	-	-	-	-	-
11	*Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit (AccB)	FTL_1592	YP_514231.1	16403.98	100.00%	7	62%
12	*Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit (AccB)	FTL_1592	YP_514231.1	16403.98	100.00%	7	69%
13	*Hypothetical protein	FTL_0617	YP_513376.1	16809.36	100.00%	11	66%
	*50S ribosomal protein L9 (RplI)	FTL_1026	YP_513727.1	16087.49	100.00%	12	72%
14	*50S ribosomal protein L7/L12 (RplL)	FTL_1745	YP_514376.1	12847.82	100.00%	6	43%
15	Could not be identified with confidence	-	-	-	-	-	-
16	Hypothetical protein	FTL_0105	YP_512904.1	13728.82	100.00%	5	42%
17	30S ribosomal protein S7	FTL_0233	YP_513028.1	17807.64	100.00%	6	40%
	50S ribosomal protein L5	FTL_0248	YP_513043.1	19996.34	100.00%	9	54%
	30S ribosomal protein S5 (RpsE)	FTL_0253	YP_513048.1	17527.25	100.00%	3	21%
	50S ribosomal protein L15	FTL_0255	YP_513050.1	15095.61	100.00%	2	16%
	Outer membrane protein OmpH	FTL_0536	YP_513305.1	18782.40	100.00%	10	52%
	(3R)-hydroxymyristoyl-ACP dehydratase	FTL_0538	YP_513307.1	18150.25	100.00%	4	22%
	50S ribosomal protein L13	FTL_1187	YP_513870.1	15937.61	100.00%	2	13%
	Hypothetical protein	FTL_0571	YP_513331.1	22451.65	100.00%	9	60%

19	Could not be identified with confidence	-	-	-	-	-	-
	30S ribosomal protein S7	FTL_0233	YP_513028.1	17807.64	100.00%	4	33%
	50S ribosomal protein L16	FTL_0243	YP_513038.1	15710.48	100.00%	2	17%
	50S ribosomal protein L5	FTL_0248	YP_513043.1	19996.34	99.80%	7	36%
	30S ribosomal protein S5 (RpsE)	FTL_0253	YP_513048.1	17527.25	100.00%	7	51%
	50S ribosomal protein L15	FTL_0255	YP_513050.1	15095.61	100.00%	5	30%
20	50S ribosomal protein L17	FTL_0262	YP_513057.1	16784.34	100.00%	4	67%
	Peptide methionine sulfoxide reductase	FTL_0379	YP_513155.1	19632.31	100.00%	2	9%
	*Lipoprotein (LpnA)	FTL_0421	YP_513194.1	15771.85	100.00%	3	32%
	30S ribosomal protein S9	FTL_1186	YP_513869.1	14517.74	100.00%	4	39%
	50S ribosomal protein L10	FTL_1746	YP_514377.1	18731.70	100.00%	12	67%
	50S ribosomal protein L11	FTL_1748	YP_514379.1	15269.89	100.00%	7	38%
	50S ribosomal protein L15	FTL_0255	YP_513050.1	15095.61	100.00%	4	26%
21	*Lipoprotein (LpnA)	FTL_0421	YP_513194.1	15771.85	100.00%	6	46%
	Hypothetical protein	FTL_0850	YP_513572.1	20453.33	100.00%	2	7%
	*Lipoprotein (LpnA)	FTL_0421	YP_513194.1	15771.85	100.00%	8	55%
22	50S ribosomal protein L10	FTL_1746	YP_514377.1	18731.70	100.00%	5	29%
	30S ribosomal protein S10	FTL_0235	YP_513030.1	11895.96	100.00%	5	49%
23	50S ribosomal protein L24	FTL_0247	YP_513042.1	11476.34	100.00%	4	36%
	Hypothetical protein	FTL_0617	YP_513376.1	16809.36	100.00%	3	24%
	Histone-like protein HU form B (HupB)	FTL_0895	YP_513614.1	9473.90	100.00%	5	50%
24	50S ribosomal protein L31	FTL_1303	YP_513974.2	9607.09	100.00%	2	28%
	30S ribosomal protein S16	FTL_1738	YP_514369.1	9071.71	100.00%	2	20%
25	Pyruvate dehydrogenase, E1 component (AceE)	FTL_0309	YP_513101.1	100268.34	100.00%	24	27%
26	*Chitinase family 18 protein (ChiA)	FTL_1521	YP_514168.1	83595.21	100.00%	6	8%
27	*Peroxidase/catalase (KatG)	FTL_1504	YP_514154.1	81226.95	100.00%	5	6%
28	*Chaperone protein DnaK	FTL_1191	YP_513874.1	69182.22	100.00%	22	41%
29	Dihydrolipoamide acetyltransferase (AceF)	FTL_0310	YP_513102.1	56798.85	100.00%	14	29%
	*Chaperonin GroEL	FTL_1714	YP_514345.1	57402.70	100.00%	39	79%
30	Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex (SucB)	FTL_1783	YP_514408.1	52717.94	100.00%	10	26%

Protein identifications were accomplished using Scaffold version 4.0.0 software. Identifications were accepted if they could be established at greater than 99% probability and contained at least two identified peptides as assigned by the protein prophet algorithm.

\*Indicates the protein was identified on the surface of *F. tularensis* LVS.

**Table S3. LC-MS/MS analysis of *F. tularensis* LVS surface proteins**

Protein Name	Locus	NCBI Reference Sequence	Fraction ID	Predicted MW (Da)	Protein Identification Probability	Number of Unique Peptides	Percentage Sequence Coverage
* <sup>C</sup> 50S ribosomal protein L7/L12 (RplL)	FTL_1745	YP_514376.1	10-15 kDa	12847.82	99.80%	2	22%
* <sup>CT</sup> Lipoprotein (LpnA)	FTL_0421	YP_513194.1	15-20 kDa	15771.85	100.00%	3	22%
* <sup>CT</sup> Hypothetical protein	FTL_0617	YP_513376.1	15-20 kDa	16809.36	100.00%	5	45%
* <sup>C</sup> 50S ribosomal protein L9 (RplI)	FTL_1026	YP_513727.1	15-20 kDa	16087.49	99.80%	2	19%
<sup>CT</sup> Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit (AccB)	FTL_1592	YP_514231.1	20-25 and 15-20 kDa	16403.98	100.00%	6	59%
* <sup>CT</sup> Outer membrane protein	FTL_0009	YP_512819.1	20-25 kDa	19477.11	100.00%	5	34%
* <sup>CT</sup> Intracellular growth locus, subunit A	FTL_0111	YP_512909.1	20-25 kDa	20890.88	99.80%	2	14%
* <sup>T</sup> Intracellular growth locus, subunit C	FTL_0113	YP_512911.1	20-25 kDa	22133.41	99.80%	2	13%
* <sup>C</sup> Peptidoglycan-associated lipoprotein	FTL_0336	YP_513124.1	20-25 kDa	23291.32	99.80%	2	11%
* <sup>C</sup> Hypothetical protein	FTL_0569	YP_513329.1	20-25 kDa	19785.57	99.80%	2	24%
* <sup>C</sup> AhpC/TSA family protein	FTL_1015	YP_513716.1	20-25 kDa	19668.22	100.00%	3	28%
<sup>C</sup> Hypothetical protein	FTL_1494	YP_514145.1	20-25 kDa	18158.27	99.80%	2	18%
<sup>CT</sup> Hypothetical protein	FTL_1225	YP_513908.1	25-37 kDa	25699.94	99.80%	2	11%
<sup>C</sup> Hypothetical protein	FTL_1579	YP_514218.1	25-37 kDa	25702.85	99.80%	2	11%
* <sup>C</sup> OmpA family protein	FTL_0325	YP_513113.1	37-50 kDa	46754.18	99.80%	2	6%
* <sup>C</sup> Aspartate aminotransferase (AscP1)	FTL_0387	YP_513160.1	37-50 kDa	44382.87	100.00%	4	14%
* <sup>C</sup> Glyceraldehyde-3-phosphate dehydrogenase (GapA)	FTL_1146	YP_513832.1	37-50 kDa	35413.40	99.80%	2	8%
* <sup>C</sup> Outer membrane associated protein FopA1	FTL_1328	YP_513994.1	37-50 kDa	41259.65	100.00%	5	12%
* <sup>C</sup> Succinyl-CoA synthetase subunit beta	FTL_1553	YP_514199.1	37-50 kDa	41541.74	100.00%	4	17%
<sup>C</sup> Citrate synthase	FTL_1789	YP_514414.1	37-50 kDa	46794.56	100.00%	3	10%
* <sup>CT</sup> Cell division protein FtsZ	FTL_1907	YP_514517.1	37-50 kDa	39745.31	100.00%	4	15%
* <sup>CT</sup> Elongation factor Tu (TufA)	FTL_1751	YP_514382.1	50-75 and 37-50 kDa	43390.62	100.00%	7	31%
* <sup>C</sup> Intracellular growth locus, subunit B	FTL_0112	YP_512910.1	50-75 kDa	57917.61	100.00%	7	17%
* <sup>C</sup> Glutamate dehydrogenase (Gdh)	FTL_0269	YP_513063.1	50-75 kDa	49158.07	100.00%	3	11%
* <sup>C</sup> Hypothetical protein	FTL_0572	YP_513332.1	50-75 kDa	51977.34	100.00%	3	7%
* <sup>C</sup> Lipoprotein (DsbG)	FTL_1096	YP_513788.1	50-75 kDa	39545.19	100.00%	4	18%
* <sup>C</sup> Enolase (2-phosphoglycerate dehydratase)	FTL_1527	YP_514174.1	50-75 kDa	49511.19	99.80%	2	8%
* <sup>CT</sup> Chaperonin GroEL	FTL_1714	YP_514345.1	50-75 kDa	57402.70	100.00%	8	20%
<sup>C</sup> Succinate dehydrogenase, catalytic and NAD/ flavoprotein subunit	FTL_1786	YP_514411.1	50-75 kDa	65860.61	99.90%	2	5%
* <sup>C</sup> 30S ribosomal protein S1	FTL_1912	YP_514522.1	50-75 kDa	61669.35	100.00%	5	12%
* <sup>C</sup> Elongation factor G	FTL_0234	YP_513029.1	75-100 kDa	77730.37	100.00%	6	13%
* <sup>C</sup> Heat shock protein 90	FTL_0267	YP_513061.1	75-100 kDa	72371.65	100.00%	7	13%
* <sup>CT</sup> Chaperone protein DnaK	FTL_1191	YP_513874.1	75-100 kDa	69182.22	100.00%	5	10%
* <sup>CT</sup> Peroxidase/catalase (KatG)	FTL_1504	YP_514154.1	75-100 kDa	81226.95	100.00%	3	6%
* <sup>C</sup> Chitinase family 18 protein (ChiA)	FTL_1521	YP_514168.1	75-100 kDa	83595.21	100.00%	3	5%
* <sup>C</sup> Aconitate hydratase	FTL_1772	YP_514399.1	100-150 kDa	102703.80	99.80%	2	3%



Protein identifications were accomplished using Scaffold version 4.0.0 software. Identifications were accepted if they could be established at greater than 99% probability and contained at least two identified peptides as assigned by the protein prophet algorithm.

\*Indicates the protein was identified in the MPF.

<sup>C</sup>Indicates the protein was identified using chymotrypsin digestions

<sup>T</sup>Indicates the protein was identified using trypsin digestions