## Table 3. Y. pestis genes downregulated in the bubo relative to in vitro growth conditions

		Fold difference relative to:		e to:		
Gene	ORF*	21°C	21°C	37°C	37°C	Function of the gene product <sup><math>\dagger</math></sup>
		Exp	Stat	Exp	Stat	
Information storage and processing						
J. Translation, ribosomal						
structure and biogenesis						
_	YPO0628	A	A	A	A	Putative translational inhibitor protein
_	YPO2018	A	A	A	A	Putative protoporphyrinogen oxidase
_	YPO3216	A	A	A	A	Putative methyltransferase
_	YPO3261	A	A	A	A	Probable amidase
K. Transcription						
_	YPO0758	A	A	A	A	LacI-family regulatory protein
_	YPO1938	A	A	A	A	Probable DeoR-family transcriptional regulatory protein
_	YPO2150	A	A	A	A	LysR-family transcriptional regulatory protein
_	YPO3259	A	A	A	A	Putative RpiR-family transcriptional regulatory protein
_	YPO3682	A	A	A	A	Putative LysR-family transcriptional regulatory protein
-	YPO3978	A	A	A	A	Putative regulatory protein
betI	YPO1167	A	A	A	A	TetR-family regulatory protein
ilvY	YPO3889	A	A	A	A	LysR-family transcriptional regulatory protein
L. DNA replication, recombination						
and repair						
_	YPO0041	A	A	A	A	Putative DNA ligase
-	YPO3736	A	A	A	A	Conserved hypothetical protein
int	YPO1917	A	A	A	A	Integrase
Cellular processes and signaling						Ť
D. Cell division and						
chromosome partitioning						
_	YPO1062	A	A	A	A	Conserved hypothetical protein
ccrB	YPO2596	A	A	A	A	Putative membrane protein
M. Cell envelope biogenesis,						
outer membrane						
-	YPO1000	A	A	A	A	Putative drug efflux protein
_	YPO1364	-2.52	-2.71	-2.27	-3.10	Putative HlyD-family secretion protein
_	YPO1672	A	A	A	A	Conserved hypothetical protein

-	YPO2174	A	A	A	A	Putative nucleotide sugar dehydrogenase
_	YPO2494	A	A	A	A	Putative BCCT-family transporter
_	YPO3609	A	A	A	A	Conserved hypothetical protein
_	YPO4112	A	A	Α	A	Putative membrane protein
ddhA	YPO3115	A	A	A	A	Glucose-1-phosphate cytidylyltransferase
mltD	YPO1078	-6.56	-9.97	-6.06	-3.08	Membrane-bound lytic murein transglycosylase D precursor
pla2	YPO1231	A	A	Α	A	Putative outer membrane-associated protease
spr	YPO1275	-2.34	-3.24	-2.24	-3.08	Putative lipoprotein
yapC	YPO2796	A	A	Α	A	Putative autotransporter protein
yapH	YPO1004	A	A	A	A	Putative autotransporter protein
N. Cell motility and secretion						
_	YPO0271	A	A	A	A	Putative type III secretion apparatus protein
_	YPO2759	A	A	A	A	Putative mannose-resistant/Proteus-like fimbrial protein
fliE	YPO1831	A	A	A	A	Flagellar hook-basal body complex protein FliE
hofC	YPO3427	A	A	A	A	Putative type II secretion system protein
tsr2	YPO1229	A	A	A	A	Putative methyl-accepting chemotaxis protein
O. Posttranslational modification,						
protein turnover, chaperones						
_	YPO3916	A	A	A	A	Putative peroxiredoxin/glutaredoxin-family protein
cysT	YPO3014	A	A	A	A	Sulfate transport system permease protein CysT
cysW	YPO3013	A	A	A	A	Sulfate transport system permease protein CysW
degS	YPO3568	A	A	A	A	Protease
P. Inorganic ion transport						
and metabolism						
_	YPO0829	A	A	A	A	Putative sulfatase
_	YPO1527	A	A	A	A	Putative membrane protein
_	YPO2068	A	A	A	A	Putative integral membrane protein
_	YPO3047	A	A	A	A	Putative sulfatase
_	YPO3049	A	A	A	A	Putative binding protein-dependent transport system component
_	YPO3050	-11.65	-55.85	-5.76	-8.50	Putative exported protein
mgtB	YPO1661	A	A	A	A	Mg(2+) transport ATPase protein B
nhaB	YPO2142	A	A	A	A	Na+/H+ antiporter
ssuB	YPO3627	A	A	A	A	Putative aliphatic sulfonates transport ATP-binding protein
tauA	YPO0182	A	A	A	A	Putative taurine-binding periplasmic protein precursor
T. Signal transduction mechanisms						
_	YPO2000	A	Α	Α	A	Putative two-component system sensor protein

_	YPO2779	A	A	A	A	Conserved hypothetical protein
V. Defense mechanisms						
_	YPO1001	A	A	A	A	Putative integral membrane efflux protein
Metabolism						
C. Energy production and						
conversion						
_	YPO1451	A	A	A	A	Putative oxidoreductase
_	YPO3637	A	A	A	A	Putative carbohydrate kinase
_	YPO3917	A	A	A	A	Putative pyridine nucleotide-disulphide oxidoreductase
atpI	YPO4128	-6.36	-2.23	-2.53	-2.40	ATP synthase protein I
cydA	YPO1117	-2.54	-2.53	-3.30	-2.04	Cytochrome D ubiquinol oxidase subunit I
gltA	YPO1108	-2.98	-2.84	-3.07	-3.30	Citrate synthase GltA
nifJ	YPO2334	A	A	A	A	Putative pyruvate-flavodoxin oxidoreductase
ssuD	YPO3625	A	A	A	A	Alkanesulfonate monooxygenase
E. Amino acid transport						
and metabolism						
_	YPO0181	A	A	A	A	Putative ABC-transport protein
_	YPO0251	-3.07	-5.52	-2.69	-2.81	Putative transmembrane transport protein
_	YPO1061	A	A	A	A	Conserved hypothetical protein
_	YPO1193	A	A	A	A	Putative pyridoxal-dependent decarboxylase
_	YPO1848	A	A	A	A	Putative amino-acid ABC transporter (ATP-binding protein)
_	YPO2306	A	A	A	A	Putative amino acid antiporter
_	YPO2662	A	A	A	A	Binding-protein-dependent transport protein
_	YPO3048	-5.74	-8.36	-2.91	-3.19	Probable ABC-transporter, ATP-binding protein
_	YPO4110	A	A	A	A	ABC transporter permease
artP	YPO1352	A	A	A	A	Arginine transport ATP-binding protein
astA	YPO1963	A	A	A	A	Arginine N-succinyltransferase
dppC	YPO4001	A	A	A	A	Dipeptide transport system permease protein
dppD	YPO4000	A	A	A	A	Dipeptide transport ATP-binding protein
gltJ	YPO2614	A	A	A	A	Putative glutamate/aspartate transport system permease
gutB	YPO2502	A	A	A	A	Putative zinc-binding dehydrogenase
hutG	YPO1971	A	A	A	A	Putative N-formylglutamate amidohydrolase
hutH	YPO4016	A	A	A	A	Histidine ammonia-lyase
proV	YPO2647	-16.76	-4.71	-10.17	-4.53	Glycine betaine/L-proline transport ATP-binding protein
proW	YPO2646	-14.28	-3.45	-9.62	-3.75	Glycine betaine/L-proline transport system permease
proX	YPO2645	-8.76	-2.44	-4.38	-2.43	Glycine betaine-binding periplasmic protein

proY	YPO3201	A	A	A	A	Probable proline-specific permease
tyrP	YPO1209	A	A	A	A	Tyrosine-specific transport protein
F. Nucleotide transport						
and metabolism						
_	YPO1296	A	A	A	A	Putative Mut-family protein
G. Carbohydrate transport						
and metabolism						
_	YPO0404	A	A	A	A	PTS system, IIC component
_	YPO0405	A	A	A	A	Putative phosphoenolpyruvate-protein phosphotransferase
_	YPO1221	A	A	A	A	Putative membrane protein
_	YPO1504	A	A	A	A	Putative exported protein
_	YPO1515	A	A	A	A	Putative multidrug resistance protein
_	YPO1563	A	A	A	A	Putative transmembrane transporter
_	YPO1572	A	A	A	A	Putative sugar transporter
_	YPO1573	A	A	A	A	Putative polysaccharide deacetylase
_	YPO1812	A	A	A	A	Putative sugar transport system permease protein
_	YPO1814	A	A	A	A	Putative sugar ABC transporter, ATP-binding protein
_	YPO1815	A	A	A	A	Putative sugar ABC transporter, permease
_	YPO1985	A	A	Α	A	Putative glycosyl transferase
_	YPO2285	A	A	A	A	Putative ribose-binding periplasmic protein (partial)
_	YPO2581	A	A	Α	A	Putative sugar-binding periplasmic protein
_	YPO3016	A	A	Α	Α	Putative sugar transporter
_	YPO3413	A	A	Α	Α	Putative membrane protein
_	YPO3472	A	A	A	Α	Putative sugar binding protein
_	YPO3620	A	A	A	A	Putative carbohydrate transport protein
_	YPO3634	A	A	A	A	ABC transporter ATP binding protein
_	YPO3906	A	A	A	A	Putative sugar transport system permease
_	YPO3907	A	A	A	A	Putative sugar transport system ATP-binding protein
_	YPO3962	A	A	A	A	Sugar-binding transport protein
agaY	YPO0844	A	A	A	A	Putative aldolase
agaZ	YPO0832	A	A	A	A	Putative tagatose 6-phosphate kinase
araF	YPO2255	A	A	A	A	L-arabinose-binding periplasmic protein precursor
araH	YPO2257	A	A	A	A	L-arabinose transport system permease protein
dhaK	YPO3350	A	A	A	A	Putative dihydroxyacetone kinase
mtlK	YPO2480	A	A	A	A	Putative mannitol transport ATP-binding protein
rosA	YPO3093	A	A	A	A	Putative membrane efflux protein

H. Coenzyme metabolism						
_	YPO1288	A	A	A	A	Putative D-isomer specific 2-hydroxyacid dehydrogenase
I. Lipid metabolism			1	1		
_	YPO1565	A	A	A	A	Putative oxidoreductase
_	YPO2817	A	A	A	A	Putative CDP-alcohol phosphatidyltransferase
acs	YPO0253	-3.90	-7.60	-3.73	-5.56	Acetyl-coenzyme A synthetase
Q. Secondary metabolites						
biosynthesis, transport and						
catabolism						
_	YPO1080	A	A	A	A	Conserved hypothetical protein
_	YPO1580	A	A	A	A	Putative phosphopantetheinyl transferase
_	YPO3079	A	A	A	A	Putative ABC transporter ATP-binding protein
pncA	YPO2160	Α	A	A	A	Putative pyrazinamidase/nicotinamidase
Poorly characterized						
R. General function						
prediction only						
_	YPO0004	A	A	A	A	Conserved hypothetical protein
_	YPO0128	A	A	A	A	Conserved hypothetical protein
_	YPO1140	A	A	A	A	Putative membrane protein
_	YPO1325	A	A	A	A	Putative membrane protein
_	YPO1496	A	A	A	A	Putative heme-binding protein
_	YPO1716	A	A	A	A	Putative transport protein
_	YPO2260	A	A	A	A	Putative membrane protein
_	YPO2467	A	A	A	A	Conserved hypothetical protein
_	YPO3051	A	A	A	A	Conserved hypothetical protein
_	YPO3961	A	A	A	A	Hypothetical protein
_	YPO4108	A	A	A	A	Putative haloacid dehalogenase-like hydrolase
fadH	YPO0589	A	A	A	A	2,4-dienoyl-CoA reductase
recX	YPO3306	A	A	A	A	Putative regulatory protein
S. Function unknown						
_	YPO0252	A	A	A	A	Putative membrane protein
_	YPO0505	A	A	A	A	Conserved hypothetical protein
_	YPO0513	A	A	A	A	Conserved hypothetical protein
_	YPO1158	A	A	A	A	Conserved hypothetical protein
_	YPO1754	A	A	A	A	Putative membrane protein
_	YPO1999	A	A	A	A	Putative decarboxylase

_	YPO2080	A	A	A	A	Conserved hypothetical protein
_	YPO3057	A	A	A	A	Putative membrane protein
_	YPO3985	-2.34	-3.65	-2.33	-2.98	Putative membrane protein
mgtC	YPO1660	-4.48	-10.39	-6.57	-25.50	Mg(2+) transport ATPase protein C
Unclassified in COGs						
_	YPO0142	A	A	A	A	Putative membrane protein
_	YPO0147	A	A	A	A	Putative membrane protein
_	YPO0301	A	A	A	A	Putative exported protein
_	YPO0306	A	A	A	A	Hypothetical protein
_	YPO0384	A	A	A	A	Putative lipoprotein
_	YPO0466	A	A	A	A	Hypothetical protein
_	YPO0703	A	A	A	A	Putative lipoprotein
_	YPO0757	A	A	A	A	Conserved hypothetical protein (pseudogene)
_	YPO0760	A	Α	A	A	Putative membrane protein
_	YPO0769	A	Α	A	A	Putative exported protein
_	YPO0822	A	Α	A	A	Putative exported protein
_	YPO0870	A	Α	A	A	Conserved hypothetical protein
_	YPO0886	A	Α	A	A	Hypothetical protein
_	YPO1016	A	Α	A	A	Putative membrane protein
_	YPO1249	A	Α	A	A	Putative bacteriophage protein GP46
_	YPO1659	-2.95	-4.60	-3.14	-5.68	Hypothetical protein
_	YPO1674	A	Α	A	A	Putative membrane protein (pseudogene)
_	YPO1818	A	Α	A	A	Conserved hypothetical protein
_	YPO1933	A	Α	A	A	Putative dicarboxylic acid hydrolase
_	YPO2079	A	Α	A	A	Hypothetical protein
_	YPO2108	A	Α	A	A	Hypothetical phage protein
_	YPO2113	A	Α	A	A	Hypothetical phage protein
_	YPO2128	A	A	A	A	Putative phage-related lipoprotein
_	YPO2275	A	A	A	A	Putative phage protein
_	YPO2277	A	A	A	A	Putative phage protein
_	YPO2292	-3.84	-3.01	-2.87	-3.02	Putative lipoprotein
_	YPO2314	A	A	A	A	Putative invertase protein (partial)
_	YPO2644	A	A	A	A	Conserved hypothetical protein (pseudogene)
_	YPO2728	A	A	A	A	Conserved hypothetical protein
_	YPO2731	A	A	A	A	Putative membrane protein

_	YPO2795	-3.58	-5.82	-3.07	-4.38	Hypothetical protein
_	YPO2801	A	A	A	A	Putative membrane protein
_	YPO2802	A	A	A	A	Putative membrane protein
_	YPO3245	A	A	A	A	Hypothetical protein
_	YPO3260	A	A	A	A	Hypothetical protein
_	YPO3468	A	A	A	A	Hypothetical protein
_	YPO3473	A	A	A	A	Putative exported protein
_	YPO3486	A	A	A	A	Conserved hypothetical protein
_	YPO3611	A	A	A	A	Hypothetical protein
_	YPO3681	-2.53	-17.54	-2.48	-5.76	Putative insecticidal toxin
_	YPO3738	A	A	A	A	Hypothetical protein
_	YPO4020	A	A	A	A	Putative membrane protein
_	YPMT1.04c	A	A	A	A	Putative phage tail protein
_	YPMT1.45c	A	A	A	A	Hypothetical protein
_	YPMT1.68a	A	A	A	A	Unknown
-	y0065	A	A	A	A	Putative transposase
_	y0200	A	A	A	A	Hypothetical protein
-	y0930	A	A	A	A	Hypothetical protein
_	y1172	A	A	A	A	Hypothetical protein
_	y1259	A	A	A	A	Hypothetical protein
_	y1327	A	A	A	A	Hypothetical protein
_	y3533	A	A	A	A	Hypothetical protein
_	y4068	A	A	A	A	Hypothetical protein
flk	YPO2760	A	A	A	A	Putative flagellar assembly regulatory protein, Flk
hpaG	YPO1761	A	A	A	A	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (pseudogene)
leuL	y3643	A	A	A	A	Leu operon leader peptide
ompC2	YPO1967	A	A	A	A	Porin (pseudogene)
yehZ	YPO1195	A	A	A	A	Periplasmic choline/glycine/betaine binding protein (pseudogene)

Genes in bold type were also reported to be downregulated during pneumonic plague in mice (1). –, gene name not assigned; A, signal not detected *in vivo*.

\*YPO and y numbers refer to the *Y. pestis* CO92 and KIM genome annotations, respectively. YPO numbers are given unless the gene was annotated only in KIM

<sup>†</sup>Genes are categorized according to Clusters of Orthologous Groups (COG) database.

1. Lathem, W. W., Crosby, S. D., Miller, V. L. & Goldman, W. E. (2005) Proc. Natl. Acad. Sci. USA 102, 17786-17791.