

Table 2. *Y. pestis* differential gene expression during primary pneumonic plague

Chromosome*	Systematic	Common	Function	Code [†]	Fold change [‡]	SD [§]
YPO0008 [¶]	YPO0008 [¶]	rbsK	ribokinase	1.A.1	-3.334	0.130
YPO0013	YPO0013	mobA, mob, chlB	molybdopterin-guanine dinucleotide biosynthesis protein A	1.G.4	4.162	0.221
YPO0024	YPO0024	glnA	glutamine synthetase	1.D.1	5.800	0.205
YPO0026	YPO0026	bipA, typA	putative GTPase	4.1	2.306	0.254
YPO0038	YPO0038	spoT	guanosine-3',5'-bisbis(diphosphate) 3'-pyrophosphydrolase	2	3.651	0.663
YPO0042	YPO0042	----	putative membrane protein	3.C.1	2.359	0.199
YPO0063	YPO0063	----	putative membrane protein	3.C.1	2.308	0.234
YPO0108	YPO0108	cytR	transcriptional repressor	2	-4.257	3.004
YPO0114	YPO0114	metJ	transcriptional repressor protein	2	2.363	0.124
YPO0115	YPO0115	metB	cystathionine gamma-synthase (pseudogene)	1.D.2	5.068	0.022
YPO0116	YPO0116	metL, metM	bifunctional aspartokinase/homoserine dehydrogenase II	1.D.2	3.052	0.187
YPO0117	YPO0117	metF	5,10-methylenetetrahydrofolate reductase	1.D.2	14.101	2.274
YPO0131	YPO0131	----	conserved hypothetical protein	5.1	-3.775	0.230
YPO0132	YPO0132	feoB	ferrous iron transport protein B	3.C.1	-2.754	0.073
YPO0133	YPO0133	feoA	hypothetical ferrous iron transport protein A	5.1	-3.218	0.197
YPO0159	YPO0159	nirC	putative nitrite transporter	4.A.5	3.205	0.575
YPO0160	YPO0160	nirD	nitrite reductase [NAD]	1.B.7.b	5.573	0.380
YPO0163	YPO0163	----	conserved integral membrane protein	3.C.1	2.245	0.203
YPO0190	YPO0190	----	conserved hypothetical protein	5.1	3.336	0.582
YPO0231	YPO0231	rpsM	30S ribosomal protein S13	3.A.2	2.140	0.192
YPO0250	YPO0250	----	putative hydrolase (pseudogene)	5.1	-2.969	0.262
YPO0251	YPO0251	----	putative transmembrane transport protein	3.C.1	-3.387	0.053
YPO0252	YPO0252	----	putative membrane protein	3.C.1	-3.482	0.678
YPO0253	YPO0253	acs	acetyl-coenzyme A synthetase	1.A.1	-3.483	0.535
YPO0261	YPO0261	----	putative type III secretion apparatus	4.A.6	9.348	0.787
YPO0278	YPO0278	metC	cystathionine beta-lyase	1.D.2	-2.429	0.528
YPO0284	YPO0284	----	conserved hypothetical protein	5.1	2.985	0.330
YPO0286	YPO0286	----	putative coproporphyrinogen III oxidase	1.G.12	3.422	0.397
YPO0301	YPO0301	----	putative exported protein	3.C.1	-2.917	0.292
YPO0343	YPO0343	hydN	4Fe-4S ferredoxin	1.B.7.b	3.073	1.077
YPO0348	YPO0348	aspA	aspartate ammonia-lyase	1.D.2	-7.051	0.240
YPO0357	YPO0357	frdD, b4151	fumarate reductase hydrophobic protein	1.B.7.b	-2.931	0.164
YPO0358	YPO0358	frdC, b4152	fumarate reductase hydrophobic protein	1.B.7.b	-3.314	0.361
YPO0359	YPO0359	frdB, b4153	fumarate reductase iron-sulfur protein	1.B.7.b	-2.673	0.336
YPO0378	YPO0378	purA, adeK	adenylosuccinate synthetase	1.F.1	2.290	0.208
YPO0407	YPO0407	----	conserved hypothetical protein	5.1	-5.068	0.434
YPO0408	YPO0408	----	putative aldolase	5.1	-3.782	0.149
YPO0409	YPO0409	----	putative periplasmic solute-binding protein	4.A	-3.936	0.173
YPO0411	YPO0411	----	putative ABC transporter permease protein	4.A	-2.244	0.027
YPO0412	YPO0412	----	putative ABC transporter ATP-binding protein	4.A	-2.180	0.136
YPO0417	YPO0417	----	putative O-antigen biosynthesis protein	3.C.1	3.672	0.115
YPO0424	YPO0424	----	putative pectinesterase	3.C.1	-3.921	0.910
YPO0426	YPO0426	----	putative membrane protein	3.C.1	5.333	0.434
YPO0434	YPO0434	----	putative metalloenzyme	5.1	3.556	0.204
YPO0448	YPO0448	----	putative lipoprotein	3.C.1	2.499	0.106
YPO0449	YPO0449	----	putative exported protein	3.C.1	2.459	0.242
YPO0458	YPO0458	arcA, dye, fexA	aerobic respiration control protein	2	2.413	0.168
YPO0465	YPO0465	----	putative transport protein	4.A	6.264	0.990
YPO0473	YPO0473	----	hypothetical protein	5.1	4.013	0.955
YPO0498	YPO0498	----	hypothetical protein	5.1	-2.134	0.049
YPO0531	YPO0531	leuC	3-isopropylmalate dehydratase large subunit	1.D.6	2.534	0.533
YPO0539	YPO0539	ilvI	acetolactate synthase isozyme III large subunit	1.D.6	3.739	0.428
YPO0540	YPO0540	ilvH	acetolactate synthase isozyme III small subunit	1.D.6	2.635	0.453
YPO0544	YPO0544	----	putative membrane protein	3.C.1	-4.913	0.680
YPO0569a	YPO0569a	----	conserved hypothetical protein	5.1	-2.256	0.016
YPO0570	YPO0570	yqjD	putative membrane protein	3.C.1	-3.140	0.086
YPO0579	YPO0579	uxaC	uronate isomerase	1.A.1	3.062	0.548
YPO0584	YPO0584	----	putative symporter protein	4.A	-2.229	0.026
YPO0588	YPO0588	----	putative methyltransferase	5.1	-2.378	0.003
YPO0589	YPO0589	fadH, fadH1	2,4-dienoyl-CoA reductase	1.A	-2.494	0.239
YPO0590	YPO0590	hdeD	putative membrane protein	3.C.1	-4.173	0.294
YPO0628	YPO0628	----	putative translational inhibitor protein	5.1	-2.384	0.297
YPO0711	YPO0711	fliM	putative flagellar motor switch protein	4.D	8.055	0.959
YPO0727	YPO0727	flgF	putative flagellar basal-body rod protein (pseudogene)	4.D	-2.721	0.352
YPO0728	YPO0728	flgG	putative flagellar basal-body rod protein	4.D	-2.484	0.257
YPO0781	YPO0781	----	putative surface structure protein (pseudo)	3.C.3	-2.632	0.242
YPO0819	YPO0819	----	putative carbonic anhydrase	5.1	-3.445	0.330
YPO0854	YPO0854	----	putative maltodextrin permease protein	4.A.3	5.798	0.148
YPO0858	YPO0858	----	sugar transport ATP-binding protein	4.A.3	-2.651	0.203
YPO0862	YPO0862	----	putative exported protein	3.C.1	3.086	0.228
YPO0914	YPO0914	serA	D-3-phosphoglycerate dehydrogenase	1.D.3	2.948	0.250
YPO0929	YPO0929	speA	biosynthetic arginine decarboxylase	1.E	3.575	0.740
YPO0931	YPO0931	metK	S-adenosylmethionine synthetase	1.C	9.450	0.665
YPO0932	YPO0932	----	conserved hypothetical protein	5.1	3.191	0.123
YPO0959	YPO0959	----	putative sugar ABC transporter periplasmic binding protein	4.A.3	-3.331	1.344
YPO0988	YPO0988	----	putative membrane protein	3.C.1	2.306	0.256
YPO1011	YPO1011	----	putative TonB-dependent outer membrane receptor	3.C	2.356	0.452
YPO1041	YPO1041	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1.D.2	-2.660	0.019
YPO1058	YPO1058	rhB, b0183	ribonuclease HII	3.B.1	2.315	0.152
YPO1069	YPO1069	----	conserved hypothetical protein	5.1	2.345	0.306
YPO1071	YPO1071	----	putative lipoprotein	3.C.1	4.216	0.120
YPO1072	YPO1072	----	ABC transporter permease protein	4.A	3.337	0.067
YPO1073	YPO1073	abc	ABC transporter ATP-binding protein	4.A	2.827	0.791
YPO1084	YPO1084	----	conserved hypothetical protein (pseudogene)	5.1	2.315	0.216
YPO1108	YPO1108	gltA, gltT, icdB	citrate synthase GltA	1.B.3	-2.102	0.014

YPO1109	sdhC, cybA	succinate dehydrogenase cytochrome b-556 subunit	1.B.3	-2.720	0.026
YPO1110	sdhD	succinate dehydrogenase hydrophobic membrane anchor protein	1.B.3	-3.132	0.093
YPO1112	sdhB	succinate dehydrogenase iron-sulfur protein	1.B.3	-2.174	0.184
YPO1113	sucA	2-oxoglutarate dehydrogenase E1 component	1.B.3	-2.493	0.288
YPO1116	sucD	succinyl-CoA synthetase alpha chain	1.B.3	-2.348	0.171
YPO1184	----	putative ABC transport membrane permease	4.A.6	11.055	2.659
YPO1187	----	putative substrate-binding periplasmic transport protein	4.A	35.300	2.832
YPO1201	----	putative amino acid decarboxylase	1.A.2	-2.609	0.568
YPO1207	katA	catalase	4.G	-3.033	0.009
YPO1221	----	putative membrane protein	3.C.1	3.003	0.055
YPO1244	----	hypothetical protein	5.I	4.372	1.405
YPO1255	----	hypothetical protein	5.I	-4.052	0.513
YPO1275	spr	putative lipoprotein	3.C.1	-2.730	0.123
YPO1277	----	putative cobalamin synthesis protein	5.I	-3.222	1.578
YPO1290	----	putative aldehyde dehydrogenase	1.A.1	-4.122	1.251
YPO1301	psaE	putative regulatory protein	2	-5.645	0.004
YPO1302	psaF	putative membrane protein	3.C.1	-4.713	0.481
YPO1303	psaA	pH 6 antigen precursor (antigen 4) (adhesin)	3.C.2	-11.980	0.428
YPO1304	psaB	chaperone protein PsaB precursor	4.B	-5.514	3.176
YPO1308	----	putative LysR-family transcriptional regulatory protein	2	-3.140	0.282
YPO1316	----	putative iron/ascorbate oxidoreductase family protein	5.I	10.036	3.116
YPO1321	sdaC, dcrA, b2796	serine transporter	4.A.1	-7.524	0.312
YPO1331	potF	putrescine-binding periplasmic protein precursor	4.A.1	3.513	0.543
YPO1332	potG	putrescine transport ATP-binding protein	4.A.1	7.279	1.771
YPO1343	----	putative periplasmic binding protein	4.A	28.117	10.914
YPO1344	----	FecCD transport family protein	4.A	10.106	1.743
YPO1345	----	putative transport ATP-binding protein	4.A	3.590	0.483
YPO1366	cspD, cspH	cold shock-like protein	5.F	-8.897	1.135
YPO1384	focA	putative formate transporter 1	4.A.3	2.066	0.089
YPO1386	ansB	putative L-asparaginase II precursor	1.A.2	2.285	0.171
YPO1392	rpsA, ssyF	30S ribosomal protein S1	3.A.2	2.274	0.296
YPO1398	cspB	cold shock-like protein	5.F	5.260	0.128
YPO1411	----	putative outer membrane porin C protein	3.C	2.684	0.138
YPO1413	pncB	putative nicotinate phosphoribosyltransferase	1.G.7	2.164	0.188
YPO1423a	rmf	putative ribosome modulation factor	3.A.3	-4.360	0.330
YPO1430	fabA	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	1.H	-2.126	0.095
YPO1501	----	putative esterase	5.I	-2.559	0.387
YPO1507	mglB	galactose-binding protein	4.A.3	-3.862	0.134
YPO1508	mglA	galactoside transport ATP-binding protein	4.A.3	-3.461	0.301
YPO1512	cdd	cytidine deaminase	1.F.4	7.792	0.718
YPO1516	----	hypothetical protein	5.I	4.588	0.296
YPO1517	----	putative sugar ABC transporter	4.A.3	7.545	0.736
YPO1542	hisI, hisIE	histidine biosynthesis bifunctional protein [includes: phosphoribosyl-amp cyclohydrolase	1.D.5	3.740	0.502
YPO1543	hisF	histidine biosynthetic protein (cyclase)	1.D.5	4.228	0.182
YPO1544	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	1.D.5	3.364	0.884
YPO1546	hisB	histidinol-phosphatase and imidazoleglycerol-phosphate dehydratase	1.D.5	3.755	0.944
YPO1547	hisC	histidinol-phosphate aminotransferase	1.D.5	5.059	1.524
YPO1549	hisG	ATP phosphoribosyltransferase	1.D.5	4.381	1.233
YPO1563	----	putative transmembrane transporter	4.A	-3.021	0.890
YPO1565	----	putative oxidoreductase	5.I	-3.063	0.270
YPO1566	----	putative hydrolase	5.I	-4.120	1.241
YPO1572	----	putative sugar transporter	4.A.3	-3.997	0.777
YPO1573	----	putative polysaccharide deacetylase	5.I	-8.028	0.018
YPO1576	----	putative GerR-family transcriptional regulatory protein	2	6.723	1.619
YPO1617	ndh	NADH dehydrogenase	1.B.7.c	2.205	0.220
YPO1649	----	conserved hypothetical protein	5.I	-3.094	0.113
YPO1683	----	probable N-acetylmuramoyl-L-alanine amidase	3.B.3	-2.176	0.174
YPO1698	----	putative exported protein	3.C.1	-3.168	1.532
YPO1699	----	putative exported protein	3.C.1	-5.613	0.440
YPO1700	----	putative exported protein	3.C.1	-6.033	0.890
YPO1718	----	putative exported protein	3.C.1	-5.511	1.047
YPO1728	----	putative transcriptional regulator of sugar transport (pseudogene)	2	-2.284	0.018
YPO1758	manX, ptsL, gptB	PTS system, mannose-specific IIAB component	4.A.3	3.003	0.212
YPO1771	sdaA	L-serine dehydratase	1.A.2	-4.156	0.229
YPO1799	flgB, flbA, fla FII	flagellar basal-body rod protein FlgB	4.D	8.529	2.599
YPO1847	yecS	putative amino-acid ABC transporter (permease)	4.A.1	3.010	0.934
YPO1848	yecC	putative amino-acid ABC transporter (ATP-binding protein)	4.A.1	2.640	0.548
YPO1906	fyuA, psn	pesticin/yersiniabactin receptor protein	3.C.3	2.318	0.345
YPO1907	ybtE, irp5	yersiniabactin siderophore biosynthetic protein	1.G.14	2.777	0.439
YPO1908	ybtT, irp4	yersiniabactin biosynthetic protein YbtT	1.G.14	2.697	0.339
YPO1910	irp1	yersiniabactin biosynthetic protein	1.G.14	2.647	0.273
YPO1911	irp2	yersiniabactin biosynthetic protein	1.G.14	2.125	0.095
YPO1913	ybtP, irp6	lipoprotein inner membrane ABC-transporter	4.A	3.340	0.511
YPO1914	ybtQ, irp7	inner membrane ABC-transporter YbtQ	4.A	4.232	0.183
YPO1915	ybtX, irp8	putative signal transducer	2	3.114	0.462
YPO1916	ybtS, irp9	putative salicylate synthetase	1.G.14	3.929	0.368
YPO1941	----	putative membrane protein	3.C.1	2.218	0.079
YPO1943	----	putative membrane protein	3.C.1	2.200	0.017
YPO1949	tehB	putative tellurite resistance protein	5.D	2.235	0.076
YPO1951	hmsH	haemin storage system, HmsH protein	1.G.14	4.374	0.124
YPO1952	hmsF	haemin storage system, HmsF protein	1.G.14	4.021	0.389
YPO1953	hmsR	haemin storage system, HmsR protein	1.G.14	3.789	0.077
YPO1954	hmsS	haemin storage system, HmsS protein	1.G.14	3.615	0.066
YPO1996	----	hypothetical protein	5.I	-2.328	0.153
YPO2012	----	putative membrane protein	3.C.1	-4.199	0.074
YPO2040	----	putative membrane protein	3.C.1	2.734	0.333
YPO2061	znuA	exported high-affinity zinc uptake system protein	4.A.2	2.118	0.008
YPO2074	fadD	long-chain-fatty-acid-CoA ligase	1.A	-4.452	0.015
YPO2080	----	conserved hypothetical protein	5.I	-2.097	0.059

YPO2144	fadR, oleR, thdB	fatty acid metabolism regulatory protein	2	2.182	0.049
YPO2147	dadA, dadR	D-amino acid dehydrogenase small subunit	1.A.2	-7.488	0.644
YPO2157	gapA	glyceraldehyde 3-phosphate dehydrogenase A	1.B.1	2.560	0.100
YPO2174	----	putative nucleotide sugar dehydrogenase	1.C.3	-2.635	0.145
YPO2182	oppA	periplasmic oligopeptide-binding protein precursor	4.A	-3.220	0.825
YPO2185	oppD	oligopeptide transport ATP-binding protein	4.A	-2.251	0.157
YPO2191	----	hypothetical protein	5.I	-7.178	0.089
YPO2205	trpC	tryptophan biosynthesis protein TrpCF	1.D.4	3.132	1.070
YPO2206	trpD	anthranilate phosphoribosyltransferase	1.D.4	2.251	0.037
YPO2222	ribA	GTP cyclohydrolase II	1.G.9	3.308	0.038
YPO2229	osmB	osmotically inducible lipoprotein B precursor	5.F	-2.641	0.035
YPO2233	----	conserved hypothetical protein	5.I	-4.325	0.351
YPO2234	cstA	putative carbon starvation protein A	5.F	-3.919	0.179
YPO2237	----	putative integral membrane protein	4.A	-2.422	0.046
YPO2262	----	putative exported protein	3.C.1	2.107	0.025
YPO2288	amn	putative AMP nucleosidase	1.F.4	-9.332	9.778
YPO2290	----	putative virulence factor	5.I	-5.483	4.519
YPO2315	----	putative exported protein	3.C.1	-2.066	0.024
YPO2347	----	putative membrane protein	3.C.1	2.450	0.058
YPO2348	----	conserved hypothetical protein	5.I	2.172	0.034
YPO2358	sapD	peptide transport system ATP-binding protein	4.A.6	3.078	0.023
YPO2359	sapF	peptide transport system ATP-binding protein	4.A.6	2.279	0.178
YPO2360	----	conserved hypothetical protein	5.I	2.313	0.105
YPO2374	slyA	MarR-family transcriptional regulatory protein	2	-2.505	0.013
YPO2386	sodB	superoxide dismutase [Fe]	4.G	-2.604	0.099
YPO2390	cfa, cdfA	cyclopropane-fatty-acyl-phospholipid synthase	1.H	-2.303	0.162
YPO2410	----	Conserved hypothetical protein	5.I	-2.508	0.127
YPO2436	----	hypothetical protein	5.I	-2.388	0.120
YPO2439	yfeA	periplasmic-binding protein	4.A.2	2.796	0.067
YPO2443	----	putative membrane protein	3.C.1	8.657	2.161
YPO2449	----	putative LuxR-family regulatory protein	2	2.255	0.073
YPO2460	----	conserved hypothetical protein	5.I	2.373	0.144
YPO2497	----	putative LysR-family transcriptional regulatory protein	2	-2.212	0.127
YPO2501	rbsB	sugar binding protein precursor	4.A.3	-3.325	1.167
YPO2511	----	putative exported protein	3.C.1	-5.952	0.320
YPO2539	idnO	gluconate 5-dehydrogenase	1.A.1	-2.801	1.033
YPO2577	----	putative aldehyde dehydrogenase	5.I	-4.397	0.063
YPO2590	----	hypothetical protein	5.I	-7.488	0.734
YPO2592	----	putative membrane protein	3.C.1	2.256	0.145
YPO2599	lipB	lipoate-protein ligase B	1.G.3	4.379	0.061
YPO2608	holA	DNA polymerase III, delta subunit	3.A.7	3.581	0.735
YPO2615	glnH	putative amino acid-binding protein precursor	4.A.1	-4.569	0.037
YPO2616	cutE, Int	putative apolipoprotein N-acyltransferase	3.C.1	2.770	0.165
YPO2617	ybeX	putative membrane protein	3.C.1	2.578	0.283
YPO2640	trp1400A	IS1400 transposase A	5.A	3.051	0.030
YPO2659	cspB	cold shock protein	5.F	3.592	0.265
YPO2674	----	putative exported protein	3.C.1	-15.310	1.550
YPO2675	----	putative potassium channel protein	4.A.2	-2.357	0.085
YPO2732	lemA, 3	putative exported protein	3.C.1	3.730	0.355
YPO2734	ccmA	putative heme exporter protein A	4.A.6	2.649	0.284
YPO2736	ccmC	putative heme exporter protein C	4.A.6	2.531	0.105
YPO2737	ccmD	putative heme exporter protein D	4.A.6	2.627	0.184
YPO2744	fadL, ttr	putative long-chain fatty acid transport protein	4.A.3	-4.689	0.215
YPO2746	----	putative 3-ketoacyl-CoA thiolase	1.A	-2.296	0.404
YPO2757	fabB, fabC	3-oxoacyl-[acyl-carrier-protein] synthase I	1.H	-3.879	0.351
YPO2760	flk	putative flagellar assembly regulatory protein, Flk	4.D	2.492	0.285
YPO2765	asd, usg-1	putative aspartate-semialdehyde dehydrogenase	1.C	-2.151	0.139
YPO2772	purF	amidophosphoribosyltransferase	1.F.1	2.299	0.346
YPO2774	hisJ	histidine-binding periplasmic protein	4.A.1	-3.699	0.281
YPO2782	----	putative membrane protein	3.C.1	51.849	9.398
YPO2795	----	hypothetical protein	5.I	-2.116	0.097
YPO2835	pstC	putative phosphate transport system permease	4.A	5.363	0.348
YPO2846	----	putative ABC-transporter ATP-binding protein	4.A	-2.199	0.095
YPO2857	----	putative exported protein	3.C.1	-2.377	0.149
YPO2883	ndk	nucleoside diphosphate kinase	1.F.4	-3.889	0.018
YPO2894	----	conserved hypothetical protein	5.I	-2.201	0.134
YPO2895	nifU	NifU family protein	5.I	-2.400	0.075
YPO2907	glyA	serine hydroxymethyltransferase	1.C	2.324	0.054
YPO2908	hmp, hmpA, hmpX	flavohepotein	1.B.7.a	2.531	0.454
YPO2929	acpS, dpj	holo-[acyl-carrier protein] synthase	1.H	-2.212	0.160
YPO2930	pdxJ	pyridoxal phosphate biosynthetic protein PdxJ	1.G.6	-2.366	0.053
YPO2962	----	conserved hypothetical protein	5.I	-2.125	0.108
YPO2974	----	putative B-type cytochrome	1.B.7.c	3.441	0.500
YPO2976	----	conserved hypothetical protein	5.I	2.370	0.061
YPO2983	nupC, cru	nucleoside permease	4.A.6	4.623	0.331
YPO2992	cysK, cysZ	cysteine synthase A	1.D.3	3.031	0.030
YPO2994	ptsI	PTS system, enzyme I component	4.A.3	2.494	0.345
YPO3001	----	putative pyridine nucleotide-disulphide oxidoreductase	1.B.7.c	111.258	34.064
YPO3014	cysT	sulfate transport system permease protein CysT	4.A.5	3.399	0.319
YPO3015	cysP	thiosulfate-binding protein	4.A.5	5.350	0.512
YPO3040	napF	ferredoxin-type protein NapF	1.B.7.c	2.256	0.036
YPO3041	narP	nitrate/nitrite response regulator protein NarP	2	-2.384	0.115
YPO3048	----	probable ABC-transporter, ATP-binding protein	4.A	-4.203	0.423
YPO3049	----	putative binding protein-dependent transport system, inner-membrane component	4.A	-2.406	0.455
YPO3050	----	putative exported protein	3.C.1	-8.234	0.682
YPO3070	yfgD	putative arsenate reductase	5.D	-2.237	0.058
YPO3071	----	conserved hypothetical protein	5.I	4.962	0.622
YPO3120	recR	recombination protein RecR	3.A.7	2.357	0.116
YPO3128	----	conserved hypothetical protein	5.I	-2.732	0.298

YPO3134	ykgM	putative ribosomal protein	3.A.2	16.593	3.542
YPO3135	----	putative ribosomal protein L36	3.A.2	23.457	0.008
YPO3139	----	putative 6-O-methylguanine DNA methyltransferase family protein	5.I	2.346	0.189
YPO3151	----	conserved hypothetical protein	5.I	-2.108	0.033
YPO3172	thiJ	4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosynthesis enzyme	1.G.8	2.855	0.164
YPO3243	lpcA, gmhA, tfrA	phosphoheptose isomerase	3.C.2	-2.141	0.005
YPO3267	emrA	multidrug resistance protein A	5.D	6.323	0.519
YPO3319	katY	catalase-peroxidase	4.G	-3.244	0.667
YPO3320	cybC	putative cytochrome B562	1.B.7.c	-4.440	0.955
YPO3321	cybB	probable cytochrome B561	1.B.7.c	-3.068	0.532
YPO3326	araD	L-ribulose-5-phosphate 4-epimerase	1.A.1	-4.506	0.155
YPO3336	----	conserved hypothetical protein	5.I	2.780	0.344
YPO3337	map	methionine aminopeptidase	3.A.8	3.223	0.036
YPO3340	----	putative exogenous ferric siderophore receptor (pseudogene)	1.G.14	3.628	0.208
YPO3372	cysJ	sulfite reductase [NADPH] flavoprotein alpha-component	1.C.5	4.726	0.438
YPO3382	gsrA, degP, htrA	global stress requirement protein GsrA	3.B.3	-2.208	0.010
YPO3410	yacC	putative exported protein	3.C.1	2.174	0.184
YPO3420	pdhR, aceC, genA	pyruvate dehydrogenase complex repressor	2	2.128	0.071
YPO3484	----	conserved hypothetical protein	5.I	4.103	0.425
YPO3488	deaD, csdA, mssB	cold-shock dead-box protein A	5.I	2.453	0.363
YPO3498	----	conserved hypothetical protein	5.I	2.651	0.031
YPO3527	----	conserved hypothetical protein	5.I	-11.555	0.601
YPO3557	gltB, aspB	glutamate synthase [NADPH] large chain precursor	1.D.1	3.090	0.446
YPO3558	gltD, aspB	glutamate synthase [NADPH] small chain	1.D.1	2.253	0.303
YPO3582	rpoN, glnF, ntrA	RNA polymerase sigma-54 factor	3.A.9	-3.225	0.448
YPO3583	yhbH	probable sigma (54) modulation protein (pseudogene)	3.A.9	-3.521	0.132
YPO3607	----	conserved hypothetical protein	5.I	50.613	14.128
YPO3632	ddg	putative membrane protein	3.C.1	2.239	0.319
YPO3633	----	putative periplasmic binding protein	4.A	-4.165	0.091
YPO3643	cspa2	major cold shock protein Cspa2	5.F	4.249	0.350
YPO3644	cspa1	major cold shock protein Cspa1	5.F	3.178	0.479
YPO3647	----	conserved hypothetical protein	5.I	-6.347	0.095
YPO3648	----	putative 2-hydroxy-3-oxopropionate reductase	1.A.1	-5.305	0.803
YPO3649	----	putative gamma carboxymuconolactone decarboxylase	1.A	-4.632	0.468
YPO3650	----	putative metabolite transport protein	4.A	-2.684	0.326
YPO3651	----	putative GntR-family transcriptional regulatory protein	2	-2.150	0.202
YPO3661	----	putative membrane protein	3.C.1	-2.221	0.303
YPO3662	----	conserved hypothetical protein	5.I	-2.458	0.018
YPO3681	----	putative insecticidal toxin	4.I	-4.214	1.022
YPO3682	----	putative lysR-family transcriptional regulatory protein	2	-7.476	5.561
YPO3698	treR	trehalose operon repressor	2	2.163	0.156
YPO3708	----	conserved hypothetical protein	5.I	-2.443	0.069
YPO3711	lamB, malB	maltoporin	4.A.3	18.748	7.654
YPO3727	metA	homoserine O-succinyltransferase	1.D.2	21.185	7.243
YPO3754	tufA, tufB	elongation factor Tu	3.A.8	-2.237	0.047
YPO3766	fadB, oldB	fatty acid oxidation complex alpha subunit	1.A	-2.831	0.159
YPO3767	fadA, oldA	3-ketoacyl-CoA thiolase	1.A	-2.369	0.091
YPO3788	metE	5-methyltetrahydropteroyltriL-glutamate--homocyst eine methyltransferase	1.D.2	8.826	0.623
YPO3789	metR	lysR-family transcriptional regulatory protein	2	8.892	0.972
YPO3798	----	putative exported protein	3.C.1	18.331	2.463
YPO3803	----	hypothetical protein	5.I	8.070	2.229
YPO3804	livF	high-affinity branched-chain amino acid transport, ATP-binding protein	4.A.1	3.968	0.500
YPO3805	livG	high-affinity branched-chain amino acid transport, ATP-binding protein	4.A.1	4.617	0.245
YPO3806	livM	high-affinity branched-chain amino acid transport system, permease protein	4.A.1	3.419	0.085
YPO3807	livH	high-affinity branched-chain amino acid transport system, permease protein	4.A.1	4.292	0.227
YPO3808	livK, livJ	branched-chain amino acid-binding protein	4.A.1	3.849	0.236
YPO3820	----	putative P-type cation-translocating membrane ATPase	4.A.2	-5.437	1.102
YPO3867	rho, nitA, psuA	transcription termination factor	3.A.9	3.076	0.128
YPO3881	----	putative chaperone protein	4.B	2.609	0.097
YPO3886	----	colicin (partial)	5.B	4.176	1.152
YPO3887	----	hypothetical protein	5.I	9.823	1.219
YPO3888	ilvC	ketol-acid reductoisomerase	1.D.6	29.860	3.894
YPO3896	ilvA	threonine dehydratase	1.D.6	4.174	0.795
YPO3897	ilvD	dihydroxy-acid dehydratase	1.D.6	2.337	0.297
YPO3899	ilvE	branched-chain amino acid aminotransferase	1.D.6	2.790	0.582
YPO3900	ilvM	acetolactate synthase isozyme II small subunit	1.D.6	4.556	0.520
YPO3901	ilvG	acetolactate synthase isozyme II large subunit	1.D.6	4.047	0.470
YPO3910	----	putative vitamin B12 receptor protein	3.C	3.099	0.307
YPO3922	----	hemophore HasA	4.A.6	-2.496	0.021
YPO3927	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.D.1	-2.404	0.015
YPO3963	----	sugar transport system permease protein	4.A.3	47.131	3.026
YPO3966	----	conserved hypothetical protein	5.I	2.978	0.234
YPO3970	uspA	universal stress protein A	5.F	-2.506	0.056
YPO3986	cdh	CDP-diacylglycerol pyrophosphatase	1.H	-3.719	0.541
YPO3992	dctA	C4-dicarboxylate transport protein	4.A.3	2.435	0.049
YPO4003	dppA	periplasmic dipeptide transport protein	4.A.6	3.340	0.258
YPO4037	----	sugar-binding periplasmic protein	4.A.3	-13.584	2.105
YPO4048	mdfA, cmr	multidrug translocase	5.D	2.386	0.085
YPO4056	fdol	formate dehydrogenase, cytochrome b556 protein	1.B.7.b	-2.080	0.071
YPO4064	----	hypothetical protein	5.I	-3.580	0.070
YPO4101	rnpA	ribonuclease P protein	3.B.1	6.251	0.925
YPO4102	ydC	probable membrane protein	3.C.1	2.250	0.329
YPO4109	----	putative amino acid transport system permease	4.A.1	2.934	0.183
YPO4111	----	putative periplasmic solute-binding protein	4.A	3.218	0.152
YPO4125	atpF, uncF, papF	ATP synthase subunit B protein	1.B.9	-2.284	0.184
YPO4126	atpE, uncE, papH	ATP synthase subunit C protein	1.B.9	-2.435	0.068
YPO4127	atpB, uncB, papD	ATP synthase subunit B protein	1.B.9	-2.114	0.128

Systematic	Common	Function	Code	Fold change	SD
yscA		type III secretion component		2.651	0.191
yscB		type III secretion component		2.699	0.021
yscC		type III secretion component		3.037	0.024
yscD		type III secretion component		3.052	0.891
yscE		type III secretion component		4.141	0.125
yscF		type III secretion component		4.074	0.095
yscH		type III secretion component		2.346	0.166
yscI		type III secretion component		2.421	0.116
yscJ		type III secretion component		2.988	0.075
yscK		type III secretion component		7.836	1.089
yscN		type III secretion component		2.141	0.013
yscO		type III secretion component		2.912	0.197
yscQ		type III secretion component		2.458	0.128
yscR		type III secretion component		2.262	0.073
yscS		type III secretion component		2.269	0.088
yscT		type III secretion component		2.554	0.138
yscU		type III secretion component		3.565	0.349
yscX		type III secretion component		3.067	0.283
yscY		type III secretion component		5.612	0.639
lcrD		type III secretion component		4.039	0.187
lcrF		type III secretion component		-2.903	0.139
lcrG		type III secretion component		4.408	0.070
lcrH		type III secretion component		3.457	0.074
lcrR		type III secretion component		5.660	0.452
lcrV		type III secretion component		4.761	0.188
sycN		type III secretion component		2.056	0.306
sycT		type III secretion component		-2.442	0.614
tyeA		type III secretion component		2.092	0.047
virG		type III secretion component		-2.205	0.021
yopB		type III secretion component		4.295	0.380
yopD		type III secretion component		2.754	0.122
yopE		type III secretion component		3.507	0.103
yopH		type III secretion component		2.390	0.108
yopK		type III secretion component		5.856	0.345
yopP		type III secretion component		2.890	0.614
yopT		type III secretion component		-3.418	0.129
ypkA		type III secretion component		3.776	0.382
YPCD1.03c				3.901	1.213
YPCD1.15c				3.347	0.197
YPCD1.16c				3.891	0.535
YPCD1.18c				3.417	0.296
YPCD1.70c				5.078	1.181
YPCD1.73c				4.196	0.153
YPCD1.75c				3.149	0.012
YPCD1.81				2.369	0.320
YPCD1.82c				3.275	0.238
YPCD1.83c				3.459	0.410
YPCD1.85				4.027	0.582

pMT1

Systematic	Common	Function	Code	Fold change	SD
YPMT1.34				-4.635	0.605
YPMT1.42				-2.539	0.121
YPMT1.86A				-2.105	0.133
YPMT1.86c				-2.237	0.072

pPCP1

Systematic	Common	Function	Code	Fold change	SD
pim		pesticin immunity protein		-4.348	0.306
pla		fibrinolysin/coagulase precursor		-6.135	0.614
rop		plasmid replication regulatory protein		-2.051	0.047
YPPCP1.06				-3.240	0.189

*Gene list is sorted by YPO number (chromosome) and the three plasmids.

†Functional classification based on CO92 chromosomal annotation (www.sanger.ac.uk/Projects/Y_pestis/Yp_gene_list_hierarchical.shtml).

‡Positive numbers indicate the mean fold change of the replicates up-regulated in the mouse lung compared to BHI broth at 37°C, and negative numbers indicate the mean fold change down-regulated.

§Standard deviation of the mean fold change of the replicates.

¶ORFs highlighted in yellow are up-regulated in the mouse lung compared with BHI broth at 37°C, and ORFs in gray are down-regulated.