

1 **Supplementary Materials**

2 **Supplementary Figures**

3 **Supplementary Figure 1. Relative expression levels of *cobB* and *yfiQ* genes in the wild-type**

4 ***Y. pestis* strain 201 grown in LB medium.** *Y. pestis* 201 was grown in LB broth and the
5 bacterial cells were harvested during the different growth phases as indicated. Relative *cobB* and
6 *yfiQ* transcript levels were determined by qRT-PCR and the expression levels were normalized
7 to 16s RNA expression.

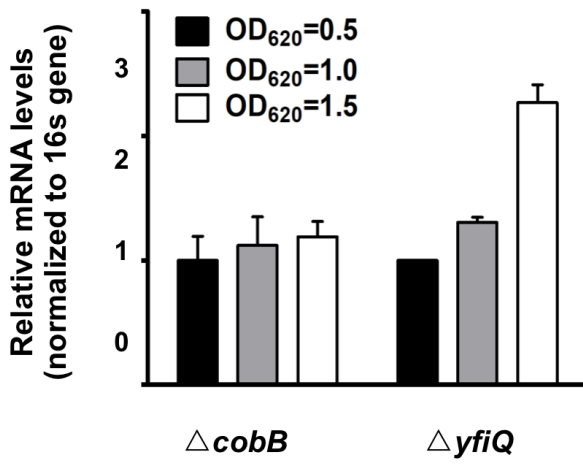
8 **Supplementary Figure 2. Mutation of *yfiQ* or *cobB* does not influence bacterial growth.**

9 The wild-type strain, along with the *cobB* and *yfiQ* mutants and the complemented strains were
10 inoculated individually into fresh LB broth (A) or TMH medium (B) at an OD₆₂₀ of 0.1, and the
11 growth curves were recorded continuously for 24 h. Each time point is the average of three
12 measurements and the error bars represent the standard deviations.

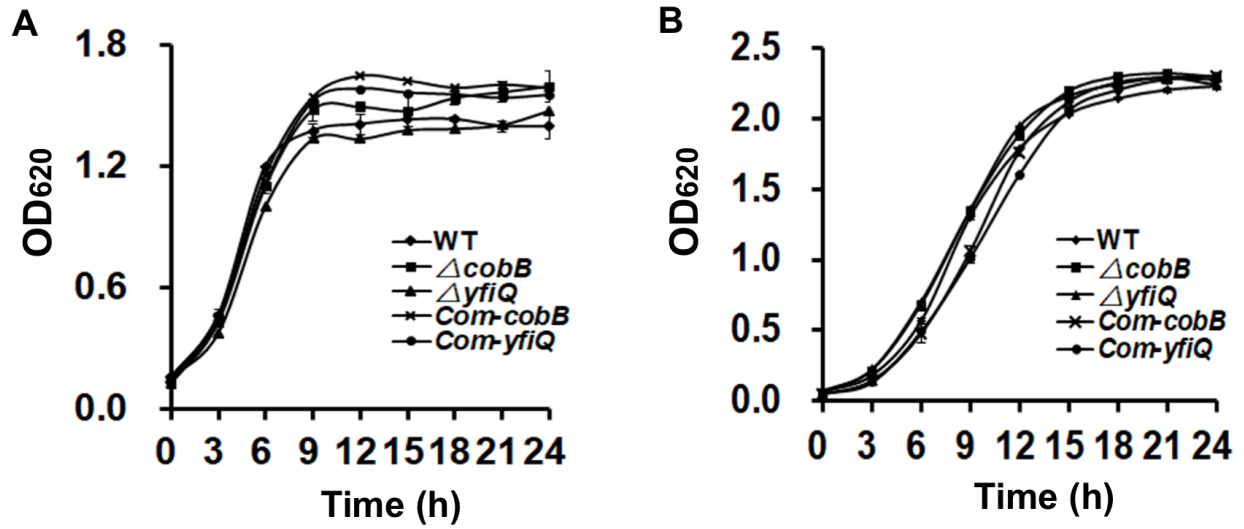
13 **Supplementary Figure 3. Functional classification of genes that were differently expressed**
14 **in the *cobB* and *yfiQ* mutants compared with the parental *Y. pestis* strain.** DEGs in $\Delta cobB$
15 (A) and $\Delta yfiQ$ (B) were classified according to their functional categories.

16 **Supplementary Figure 4. Correlations between the fold changes in gene expression**

17 **measured by qRT-PCR and RNA-seq.** Correlations between the qRT-PCR and the RNA-seq
18 data were analyzed using a linear regression method. The correlation coefficient (R^2) is shown
19 for $\Delta cobB$ /WT (A) and $\Delta yfiQ$ /WT (B).



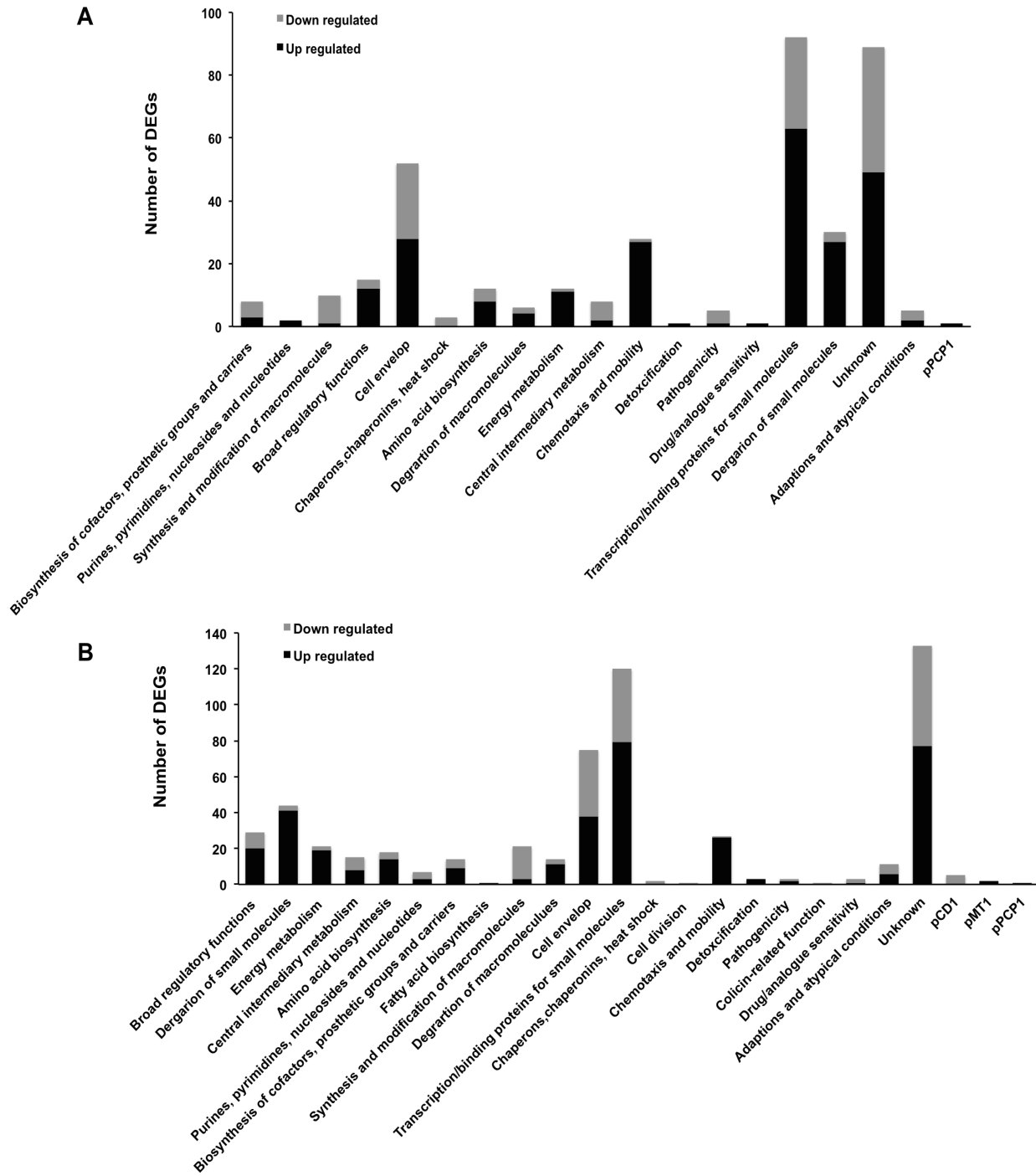
Supplementary Figure 1



Supplementary Figure 2

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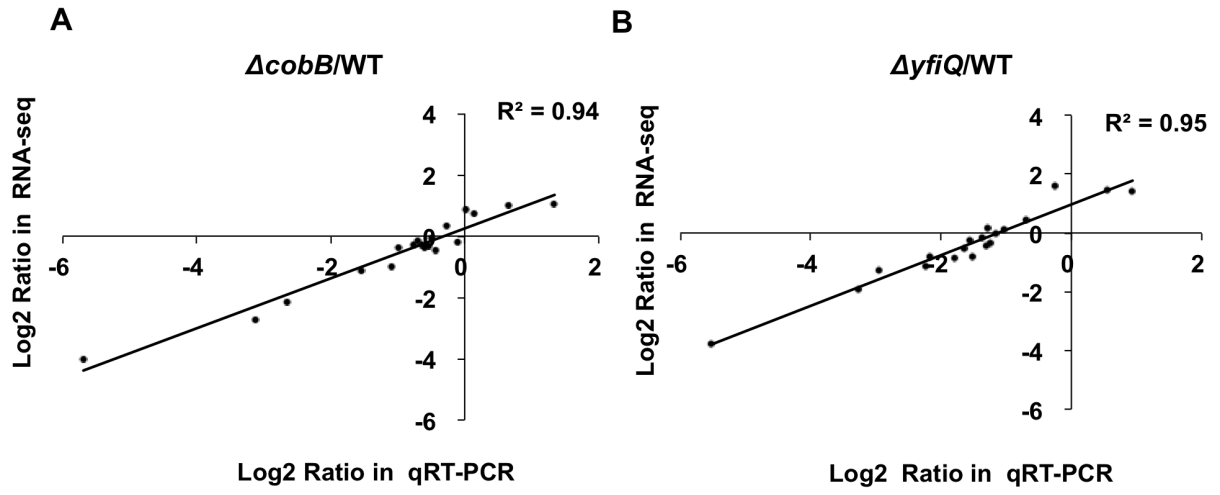
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Supplementary Figure 3

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Supplementary Figure 4

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26 **Supplementary Tables**

27 **Supplementary Table 1. Primers used in this study.**

Name	Primer (5'-3')
CobB-K-F	ATGCGCATTGCCATAGGCTGTGTCGGTTTCGTAAGAGTAGTGTAGGCTGGAGCTGCTTC
CobB-K-R	TCAATCCCCCTGACGATTCTCACCGCATGTGGTCAGAAACCATATGAATATCCTCCTTA
CobB-I-F	AGCGTTTCTGCATTTGGCAG
CobB-I-R	GACGACCTGCAACACTAATC
CobB-F	CGTTGTGCTTACTGGTGCTG
CobB-R	ATGGCCTGAAGTGCCAATTG
CobB-COM-F	CGCGCATGCGCCATCGCGGTTGTATAGAG
CobB-COM-R	ACGCGTCGACAGTTATCTGAATGAGTTGAG
CobB-EXP-F	CGCGGATCCATGCGCATTGCCATAGGCTGTG
CobB-EXP-R	ACGCGTCGACTCAATCCCCCTGACGATTCTCAC
YfiQ-K-F	ATGAGCCAACGTGGATTAGAAGCACTGTTACGTCCGAAATGTGTAGGCTGGAGCTGCTTC
YfiQ-K-R	TCAAAGTGTGACGCTCCAGATTTACGATCCCATCTTCTATTCATATGAATATCCTCCTTA
YfiQ-I-F	AGTCGCCACCGCGCTGCTCC
YfiQ-I-R	ACAGTGCCTTCTTCTCTTG
YfiQ-F	GCGGTGTCTTGGCTTACGCC
YfiQ-R	GATCATCTTCTCAAGTAATG
YfiQ-COM-F	CGCGGATCCCTCTGCGTCAACCTTATGTG
YfiQ-COM-R	ACGCGTCGACATCACGCTGATTGGTGTAAC
YfiQ-EXP-F	CGCGGATCCATGAGCCAACGTGGATTAGAAGCAC
YfiQ-EXP-R	ACGCGTCGACTCAAAGTGTGACGCTCCAGATTTACG
Kana-I-R	GCCGATTGTCTGTTGTGCC
Kana-I-F	GGCTGGGTGTGGCGGACCGC
CobB-RT-F	CATCAACGTTTTTCGCTCCC
CobB-RT-R	ACGAAAAGTACGGATACCC
YfiQ-RT-F	TGCTGCGAGTACAGGATACCC
YfiQ-RT-R	CTGACAATCAACAGCCGTTCCACC
hmsS-RT-F	ACGGAACAGCGTCTGCTAC
hmsS-RT-R	GATATAATGCAATCGTCGTC
wzxE-RT-F	CACTGTCTCGGCTGAAGG
wzxE-RT-R	TTTAATACATCGCCCACC
katA-RT-F	GTGCTAAATGTCCGTTCC
katA-RT-R	AAATCAGGCTGTTCTTGG
yscL-RT-F	AGAGGTGACTGCCGATGC
yscL-RT-R	TATTGCCCGAGAAAGTGC
yscM-RT-F	AAACTAACCCTCACAGAG

yscM-RT-R	TGGTAATAAGCAGGCAAT
Pla-RT-F	GGAGTGCGGGTAATAGGT
Pla-RT-R	GTGAGCCGGATGTCTTCT
adiA-RT-F	GTCACAAGAAACGCAACG
adiA-RT-R	ACAACGAAGAGTCGGAGA
hmsT-RT-F	CAGTATGCTATCATCGTCGC
hmsT-RT-R	GTAGACCGATGAGGATTG
espC3-RT-F	AGGCTTCGGTTTCATCAC
espC3-RT-R	GCAGACGGACCTTTAGCA
caf1R-RT-F	ATTCGCAACAGACATTCA
caf1R-RT-R	CCTTCTACCCAACAAACC
ilvC-RT-F	CAGCACTGGGTTACTCGC
ilvC-RT-R	CTTCGCCTTTAGGGTCGT
uspB-RT-F	GTGACCCGTTGTTGTATC
uspB-RT-R	CTAAACCACATAACGCACT
uspA2-RT-F	GCCAAACCGTACAATGCC
uspA2-RT-R	ATCACCGCTGCCGCTTAA
lytT-RT-F	GGCGAAGACACTGACACG
lytT-RT-R	GCTGGGTATAACCTGATTGC
htpG-RT-F	CTCCTCCATTTGATGATTC
htpG-RT-R	CAGGGTTAAAGTACGTTTCT
grpE-RT-F	AGAGCAGCAAGTGGAAGC
grpE-RT-R	TCAGTACGACGACGGATA
ibpB-RT-F	CCACTATCGCATCTCACTG
ibpB-RT-R	CAAACCTGGGCATTATCAAC
phoR-RT-F	GCCTGCATTATTACTGGG
rcsB-RT-F	GGGATAAGTATGGTGATGG
rcsB-RT-R	AGGTAAGTCAGCGGGTGC
phoR-RT-R	CGGTGTCATACTGCGATC
16S-RT-F	GCCCACTGGAAGTGAACACG
16S-RT-R	CGCTGAAAGTGCTTTACAACCC

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30 **Supplementary Table 2. The CobB-dependent or YfiQ-dependent genes involved in stress**
 31 **response and virulence as determined by RNA-seq and quantitative RT-PCR analyses.**

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geneID	Name	Product	log ₂ Ratio (Δ <i>cobB</i> /WT)		log ₂ Ratio (Δ <i>yfiQ</i> /WT)	
			qRT-PCR	RNA-seq	qRT-PCR	RNA-seq
YP_pCD21	<i>yscM</i>	putative type III secretion regulatory protein YscM	-0.61	-0.36	-1.16	-0.02
YP_pCD22	<i>yscL</i>	type III secretion system protein	-0.43	-0.47	-1.51	-0.79
YP_3187	<i>wzxE</i>	lipopolysaccharide biosynthesis protein	-0.53	-0.32	-2.17	-0.80
YP_3332	<i>uspB</i>	universal stress protein UspB	-0.75	-0.29	-1.29	0.15
YP_3333	<i>uspA2</i>	universal stress protein A	0.02	0.89	-0.25	1.58
YP_0919	<i>rcsB</i>	transcriptional regulator RcsB	-0.69	-0.16	-1.31	-0.42
YP_pPCP08	<i>pla</i>	outer membrane protease	1.34	1.04	0.94	1.43
YP_0728	<i>phoR</i>	phosphate regulon sensor protein	-0.10	-0.20	-1.65	-0.52
YP_0397	<i>lytT</i>	two-component response-regulatory protein YehT	0.65	1.00	0.54	1.45
YP_0931	<i>katA</i>	catalase	-0.99	-0.38	-1.03	0.11
YP_3158	<i>ilvC</i>	ketol-acid reductoisomerase	-3.11	-2.71	-2.24	-1.13
YP_3993	<i>ibpB</i>	heat shock chaperone IbpB	-1.10	-0.98	-1.24	-0.34
YP_0811	<i>htpG</i>	heat shock protein 90	-1.53	-1.15	-1.79	-0.84
YP_1698	<i>hmsS</i>	hemin storage system protein	-2.64	-2.14	-3.28	-1.94
YP_1049	<i>grpE</i>	heat shock protein GrpE	-0.64	-0.27	-1.56	-0.23
YP_0936	<i>adiA</i>	amino acid decarboxylase	-5.69	-4.00	-5.53	-3.77
YP_3756	<i>hmsT</i>	HmsT protein	0.15	0.76	-0.70	0.45
YP_1786	<i>cspC3</i>	cold shock protein	-0.50	-0.05	-2.94	-1.28
YP_pMT085	<i>caf1R</i>	putative F1 operon positive regulatory protein, caf1R	-0.27	0.34	-1.38	-0.17

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