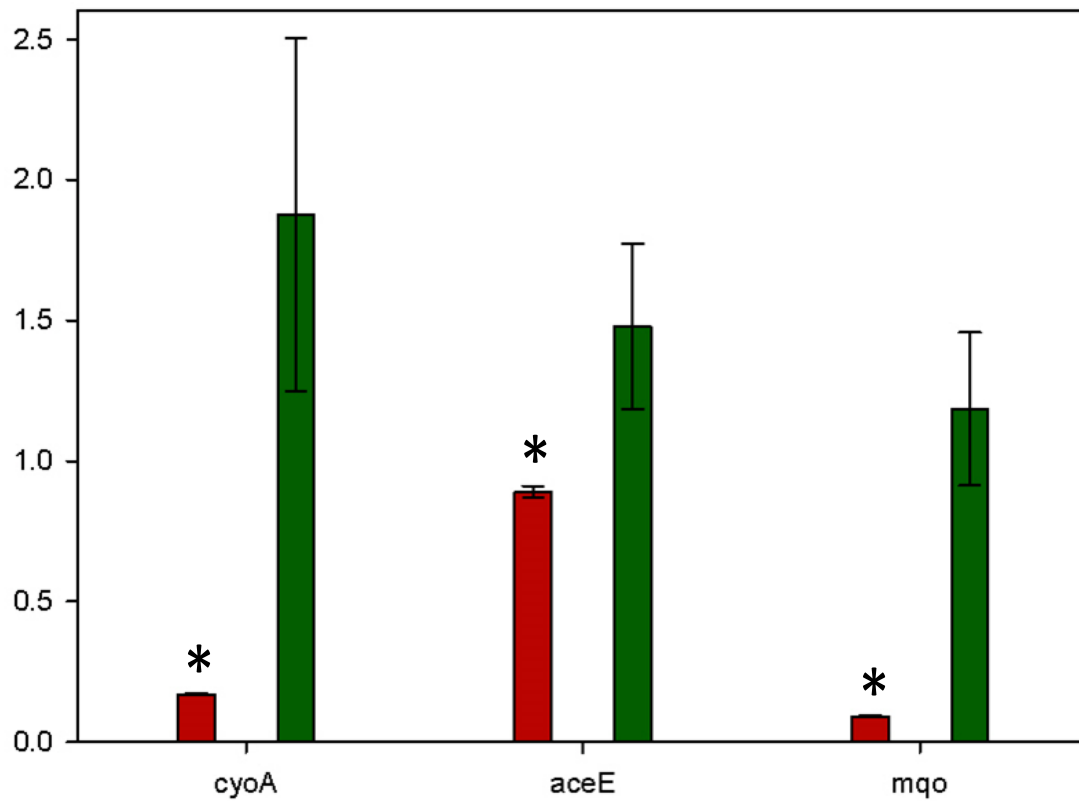


**SI Figure 1. Hierarchical cluster analysis of gene expression in MC1061 and MC1061( $\phi$ 24<sub>B</sub>) before and after norfloxacin induction.** Red and yellow indicate increased and decrease expression respectively.



**SI Figure 2. Relative q-RT-PCR ratios of *cyoA*, *aceE* and *mgo*.** Normalized against the endogenous reference genes *pdxA* and *rraB*. **Red:** MC1061(φ24<sub>B</sub>), **green:** MC1061. Error bars represent standard error of the mean ( $n=3$ ). \* represents statistically significant values in a two-sample t-test ( $p$  value < 0.05)

**SI Table 1. Bacterial strains, plasmid and phages used in the study.**

<i>E.coli</i> strains, plasmids and phages	Description	Reference
MC1061	<i>E. coli</i> K-12 derivative	(1)
φ24 <sub>B</sub> ::Kan	Stx2-phage, Δ <i>stxA</i> <sub>2</sub> :: <i>aph3</i>	(1)
TUV93-0	EDL933 with excised Stx1 and Stx2 phages	(2)
pBAD/ <i>Myc</i> -His C	araBAD, C-myc/His6 epitope, pBR322 ori, AmR	Invitrogen, Paisley, U.K.
pφ24 <sub>B</sub> -cI	pBAD carrying Φ24 <sub>B</sub> <i>cI</i>	This study
pφ24 <sub>B</sub> -cIIcIII	pBAD carrying Φ24 <sub>B</sub> <i>cII</i> and <i>cIII</i>	This study

**SI Table 2. PCR and qPCR primers used in the study.**

Oligonucleotide	Sequence (5'-3')	Ref	
cI_NcoI	CCATGGTTCAGAATGAAAAAGTG	(3)	
cI_SalI	GTCGACGAAGTCACGAACCTTTTCAGC	(3)	
cII_NcoI	CCATGGAACAAACAAGTTACAGC	This study	
cII_SalI	GTCGACTTAAAATTCCATTTGTATT	This study	
cII cIII phusion	TGGAATTTTAAATGCAATATGCCATTGCAG	This study	
cIII_NcoI	CCATGGAATATGCCATTGCAG	This study	
cIII_SalI	GTCGACGTCTGGATAGC	This study	
Oligonucleotide	Sequence (5'-3')	Primer efficiency*	Ref
gadE_F	GTAGGCAATAAACCCCTTCAAGG	99.25	This study
gadE_R	TACTGATGTGATAAGGTGCC		This study
gadX_F	CACAGTTGCTTACTGAGTGTA	99.66	This study
gadX_R	GTGATATCCACAGGATACTG		This study
gadC_F	ACCGGCGTCACTCTGGA	101.03	This study
gadC_R	GTCATTCATCACAATATAGTG		This study
rraB_F	CAGAAGAGCTGGAAGTTGAAG	98.02	This study
rraB_R	TTGTTCAACCTGGGCATCGAT		This study
pdxA_F	GTACGGAAGAGATAGACACCAT	98.19	This study
pdxA_R	GCGTTATCAAGATATTTCGGCTG		This study
mqo_F	CAATACTGATGCTGCCATCG	99.76	This study
mqo_R	CGAACTCTCCTGCGCGACAC		This study
cyoA_F	CGTTGGCGATCAGATGCAG	99.73	This study
cyoA_R	CATCACGGAGTTGGAGGTCAC		This study
aceE_F	GTCTGCAGCACGAAGATGGTC	102.25	This study
aceE_R	GCTGTCATCATGCATGACG		This study
cI_F	GTGAGGGAACGGAGCTACAG	98.54	(4)
cI_R	GCGGCCTTATGCTTTCAATG		(4)
cro_F	AAAGGGCTGTCTATAAGTGG	97.15	(4)
cro_R	GCCACCAGAAATCTCTTCG		(4)
19_F	GGTGCCGGGTGCCTC	98.06	This study
19_R	GGAGGGGCGACTGG		This study
25_F	CGTCTGCTCCACACTGG	98.00	This study
25_R	CGTGACGGAAGATAACCACG		This study
28_F	CTGCTCAAAGCTTGTCGC	99.30	This study
28_R	CGGAGCACCTGAATTCA		This study

35_F	CATCACCTTTCGCCTGTGAT	97.02	This study
35_R	CACTGCGCAATAAGGACAAT		This study

\*Primer efficiency calculated applying the formula  $E=10^{(-1/\text{slope})-1}$  (5)

**SI Table 3. Complete list of bacterial genes differentially expressed in MC1061 and MC1061( $\phi$ 24<sub>B</sub>) upon treatment with norfloxacin.**

Gene	Function	Fold change MC1061 ( $\phi$ 24 <sub>B</sub> )	P value	Fold change MC1061	P value
<b>Genes upregulated</b>					
<i>entE</i>	2,3-dihydroxybenzoate-AMP ligase, enterobactin biosynthesis	110.2	0.001	429.7	0.003
<i>fhuF</i>	Ferric iron reductase Involved in the reduction of ferric iron	101.4	0.001	124.9	0.011
<i>entC</i>	Isochorismate synthase, enterobactin biosynthesis	101.1	0.000	656.6	0.000
<i>efeU</i>	Elemental ferrous iron uptake system	68.5	0.001	58.5	0.014
<i>ybdZ</i>	Putative cytoplasmic protein in enterobactin biosynthesis operon	65.0	0.001	241.0	0.005
<i>entB</i>	Isochorismatase siderophore / Apo-aryl carrier domain, enterobactin biosynthesis	48.9	0.002	116.7	0.006
<i>fes</i>	Enterobactin/Enterochelin esterase, enterobactin biosynthesis	47.4	0.001	128.0	0.004
<i>fecR</i>	Iron(III) dicitrate transmembrane sensor protein	37.8	0.002	31.6	0.038
<i>yjcB</i>	Uncharacterized protein	34.4	0.002	28.2	0.028
<i>entH</i>	Thioesterase, enterobactin biosynthesis	32.6	0.002	63.6	0.012
<i>efeO</i>	Elemental ferrous iron uptake system	28.2	0.003	36.0	0.028
<i>fepA</i>	Outer membrane receptor for ferric enterobactin and colicins B, D	26.9	0.007	89.3	0.046
<i>entS</i>	Enterobactin exporter, iron-regulated	26.7	0.003	80.4	0.009
<i>umuD</i>	Following induction of the SOS response, UmuD is proteolytically processed into UmuD' in a cleavage reaction that depends on activated RecA	25.8	0.005	25.8	0.005
<i>umuC</i>	Error-prone, lesion bypass DNA polymerase V. Binds to processed UmuD protein to form functional DNA pol V (UmuD'2UmuC	24.5	0.005	82.3	0.010
<i>fhuA</i>	Ferrichrome-iron receptor. Acts as a receptor for bacteriophage T5, T1, phi80 and colicin M.	24.1	0.006	104.7	0.007
<i>entF</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, enterobactin biosynthesis	23.6	0.011	52.7	0.031
<i>cirA</i>	Colicin I receptor precursor	22.8	0.007	106.4	0.016
<i>recX</i>	Modulates RecA activity through direct physical interaction. May have a regulatory role during the SOS response	21.8	0.009	68.5	0.019

<i>yegD</i>	Putative heat shock protein	20.3	0.012	45.4	0.039
<i>fhuC</i>	Ferric hydroxamate ABC transporter, ATP-binding protein	20.2	0.008	24.1	0.034
<i>entD</i>	4'-phosphopantetheinyl transferase, enterobactin biosynthesis	19.5	0.007	135.4	0.004
<i>entA</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, enterobactin biosynthesis	18.5	0.009	65.4	0.013
<i>fepB</i>	ferric enterobactin (enterochelin) binding protein	18.0	0.009	34.4	0.031
<i>fecl</i>	RNA polymerase sigma factor	17.4	0.014	36.9	0.039
<i>fepD</i>	Ferric enterobactin transport system permease	17.2	0.008	47.6	0.021
<i>cspH</i>	Cold shock protein	16.7	0.058	13.0	0.058
<i>fepC</i>	Ferric enterobactin transport ATP-binding protein	16.7	0.009	39.9	0.030
<i>pstS</i>	Phosphate ABC transporter, periplasmic phosphate- binding protein	16.3	0.020	26.5	0.039
<i>nrdF</i>	Ribonucleotide reductase of class Ib (aerobic), beta subunit	16.2	0.009	39.3	0.028
<i>nrdE</i>	Ribonucleotide reductase of class Ib (aerobic), alpha subunit	16.0	0.011	67.1	0.015
<i>fepG</i>	Ferric enterobactin transport system permease	15.7	0.010	145.3	0.007
<i>pdhR</i>	Transcriptional repressor for pyruvate dehydrogenase complex	14.1	0.043	7.3	0.809
<i>rhIE</i>	ATP-dependent RNA helicase	13.7	0.047	9.7	0.277
<i>recA</i>	DNA strand exchange and recombination protein	13.7	0.576	18.7	0.706
<i>recN</i>	DNA repair protein	12.3	0.074	16.5	1.000
<i>Ferredoxin</i>	iron-sulfur proteins that transfer electrons in a wide variety of metabolic reactions	11.8	0.020	25.9	0.025
<i>wcaF</i>	colanic acid biosynthesis acetyltransferase	11.6	0.111	0.5	0.436
<i>cspA</i>	Cold-shock DEAD-box protein A	11.4	0.558	2.5	0.842
<i>nrdI</i>	Electron transport system for the ribonucleotide reductase system	11.2	0.015	67.1	0.006
<i>hycA</i>	Formate hydrogenlyase regulatory protein	10.6	0.021	39.2	0.024
<i>fhuB</i>	Ferric hydroxamate ABC transporter, permease component	10.3	0.024	12.1	0.864
<i>htpX</i>	heat shock membrane protein protein	10.1	0.213	1.1	0.197
<i>phnG</i>	Component of a carbon-phosphorous lyase enzyme	10.0	0.033	31.0	0.020
<i>suhB</i>	Inositol-1-monophosphatase	9.7	0.035	68.5	0.010
<i>carA</i>	Carbamoyl-phosphate synthase small chain	9.5	0.041	18.6	0.684
<i>iscA</i>	Iron binding protein for iron-sulfur cluster assembly	9.4	0.068	4.2	0.775
<i>rnpA</i>	Ribonuclease P protein component	9.2	0.092	5.8	0.467
<i>pspD</i>	Phage shock protein D	9.1	0.043	1.4	0.233
<i>mdtI</i>	spermidine efflux transporter	9.0	0.165	0.1	0.222

<i>nrdH</i>	Electron transport system for the ribonucleotide reductase system	8.9	0.002	65.7	0.018
<i>ansP</i>	L-asparagine permease	8.8	0.046	7.4	0.080
<i>fis</i>	DNA-binding transcriptional dual regulator	8.6	0.079	14.8	0.289
<i>hemP</i>	Hemin uptake protein	8.5	0.047	16.0	0.835
<i>apt</i>	Adenine phosphoribosyltransferase	8.4	0.056	11.6	0.707
<i>stfA</i>	Major fimbrial subunit	8.4	0.085	11.0	0.433
<i>lscS</i>	Cysteine desulfurase	8.2	0.006	6.9	1.000
<i>queD</i>	6-carboxy-5,6,7,8-tetrahydropterin synthase	8.1	0.050	5.2	1.000
<i>rpoA</i>	DNA-directed RNA polymerase alpha subunit	7.9	0.328	4.8	0.916
<i>ycfS</i>	L,D-transpeptidase	7.8	0.065	2.3	0.829
<i>cyoD</i>	Cytochrome O ubiquinol oxidase subunit IV	7.7	0.083	2.1	0.920
<i>cyoA</i>	Cytochrome O ubiquinol oxidase subunit I	7.7	0.084	1.8	0.750
<i>phnD</i>	Phosphonate ABC transporter	7.6	0.038	98.2	0.008
<i>uvrB</i>	Excinuclease ABC subunit B	7.5	0.309	6.6	0.647
<i>plsX</i>	Phosphate:acyl-ACP acyltransferase	7.1	0.110	4.5	1.000
<i>cyoC</i>	Cytochrome O ubiquinol oxidase subunit III	7.1	0.105	1.5	0.750
<i>norR</i>	transcriptional activator	7.1	0.066	2.1	0.414
<i>plsX</i>	Long-chain fatty acid transport protein	7.1	0.090	4.5	0.475
<i>pyrF</i>	Orotidine 5'-phosphate decarboxylase	7.1	0.074	12.3	0.669
<i>acfD</i>	Accessory colonization factor	7.0	0.100	1.9	0.678
	LysR family transcriptional regulator STM2281	7.0	0.040	35.0	0.013
<i>cyoB</i>	Cytochrome O ubiquinol oxidase subunit II	7.0	0.114	1.8	0.207
<i>ibpB</i>	16 kDa heat shock protein B	6.9	0.069	7.3	0.291
<i>phnC</i>	Phosphonate ABC transporter ATP-binding protein	6.8	0.068	78.0	0.904
<i>rnfD</i>	Electron transport complex protein	6.7	0.073	4.0	0.927
<i>gidC</i>	Inner membrane protein translocase	6.6	0.401	4.3	0.349
<i>rph</i>	Ribonuclease PH	6.6	0.087	5.8	0.545
<i>cspl</i>	Cold shock protein	6.6	0.072	4.7	0.895
<i>zraS</i>	Sensor protein of zinc sigma-54-dependent two- component system	6.6	0.082	0.6	0.554
<i>bioB</i>	Biotin synthase	6.5	0.071	4.8	0.973
<i>kdpA</i>	Potassium-transporting ATPase A chain	6.5	0.072	7.9	0.910
<i>dinB</i>	DNA polymerase IV	6.5	0.102	6.5	0.637
<i>fecC</i>	Iron(III) dicitrate transport system permease protein	6.5	0.073	12.0	0.298
<i>wcaB</i>	Colanic acid biosynthesis acetyltransferase	6.4	0.266	8.0	0.976

<i>hold</i>	DNA polymerase III psi subunit	6.4	0.082	6.9	0.559
<i>hscB</i>	Chaperone protein	6.3	0.113	4.8	0.913
<i>mrda</i>	Penicillin-binding protein 2	6.3	0.120	5.3	0.448
<i>ssb</i>	Single-stranded DNA-binding protein	6.3	0.167	2.1	0.948
<i>ligT</i>	2'-5' RNA ligase	6.3	0.074	2.7	0.500
<i>kdpB</i>	Potassium-transporting ATPase B chain	6.2	0.082	2.8	0.836
<i>typA</i>	GTP-binding protein TypA/BipA	6.1	0.329	2.7	0.604
<i>cspB</i>	Cold shock protein	6.0	0.099	23.4	0.206
<i>piuC</i>	Iron-uptake factor	6.0	0.086	17.3	0.516
<i>cmk</i>	Cytidylate kinase	6.0	0.130	8.2	0.753
<i>iscU</i>	Iron-sulfur cluster assembly scaffold protein	5.9	0.128	7.5	0.715
<i>betT</i>	High-affinity choline uptake protein	5.9	0.119	5.5	0.764
<i>betI</i>	HTH-type transcriptional regulator	5.9	0.125	3.3	0.889
<i>zraR</i>	Response protein of zinc sigma-54-dependent two- component system	5.8	0.085	1.0	0.826
<i>fusA</i>	Translation elongation factor G	5.8	0.252	3.4	0.605
<i>phnC</i>	Phosphonate ABC transporter	5.3	0.065	78.0	0.012
<i>piuC</i>	Iron-uptake factor	4.6	0.086	17.4	0.047
<i>yoaA</i>	DinG family ATP-dependent helicase	4.4	0.125	5.5	0.989
<i>cynT</i>	Carbonic anhydrase	4.3	0.132	6.2	0.696
<i>cspF</i>	Cold shock protein	4.3	0.092	20.8	0.412
<i>betA</i>	Choline dehydrogenase	4.3	0.135	2.9	0.586
<i>aceF</i>	Dihydrolipoamide dehydrogenase	4.3	0.368	3.6	0.822
<i>nth</i>	Endonuclease III	4.2	0.093	4.1	0.870
<i>glpE</i>	Thiosulfate sulfurtransferase	4.2	0.097	2.7	0.592
<i>rnfE</i>	Electron transport complex protein	4.2	0.096	2.9	0.295
<i>kdpF</i>	Potassium-transporting ATPase C chain	4.2	0.097	3.5	0.726
<i>hscA</i>	Chaperone protein	4.1	0.144	2.9	0.627
<i>cyoE</i>	Heme O synthase, protoheme IX farnesyltransferase	4.1	0.139	1.8	0.127
<i>dgoT</i>	D-galactonate transporter	4.1	0.114	4.4	0.366
<i>betB</i>	Betaine aldehyde dehydrogenase	4.0	0.146	3.4	0.891
<i>slp</i>	Starvation lipoprotein Slp paralog	4.0	0.115	4.2	0.998
	Protein Implicated in DNA repair function with RecA and MutS	4.0	0.117	7.1	0.685
<i>phoH</i>	Phosphate starvation-inducible protein	3.9	0.107	3.1	0.063
<i>pstB</i>	Phosphate transport ATP-binding protein	3.9	0.129	5.2	0.837



<i>ruvC</i>	Crossover junction endodeoxyribonuclease	3.9	0.127	3.0	0.896
<i>sixA</i>	Phosphohistidine phosphatase	3.8	0.134	3.1	0.508
<i>speE</i>	Spermidine synthase	3.8	0.148	3.7	0.584
<i>fecB</i>	Iron(III) dicitrate transport system	3.7	0.120	19.6	0.047
<i>hycC</i>	Formate hydrogen lyase	3.7	0.117	23.4	0.041
<i>hycB</i>	Formate hydrogen lyase	3.7	0.136	31.1	0.039
<i>rnfG</i>	Electron transport complex protein	3.5	0.095	2.4	0.411
	proteinase inhibitor	3.2	0.686	42.0	0.028
<i>hycD</i>	Formate hydrogen lyase	3.0	0.168	16.3	0.049
<i>phnH</i>	Component of a carbon-phosphorous lyase enzyme	2.5	0.237	78.0	0.003
<i>phnF</i>	Transcriptional regulator of phosphonate uptake	2.3	0.305	92.0	0.009
<i>ygeP</i>	Uncharacterized protein	2.1	0.281	28.4	0.045
<i>phnE</i>	Phosphonate ABC transporter	2.0	0.369	115.0	0.017
<i>phnI</i>	Component of a carbon-phosphorous lyase enzyme	1.8	0.358	82.5	0.011
<i>phnK</i>	Component of a carbon-phosphorous lyase enzyme	1.5	0.494	42.5	0.019
<b>Genes downregulated</b>					
<i>gutA</i>	PTS system, glucitol/sorbitol-specific IIA component	202.5	0.000	169.5	0.000
<i>malE</i>	Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein	162.7	0.975	413.4	0.974
<i>gutD</i>	Sorbitol-6-phosphate 2-dehydrogenase	157.3	0.988	138.5	0.004
<i>malK</i>	Maltose/maltodextrin transport ATP-binding protein	143.9	0.100	251.2	0.001
<i>srlE</i>	PTS system, glucitol/sorbitol-specific IIB component	138.9	0.990	197.9	0.002
<i>lamB</i>	Maltoporin	115.3	0.982	254.5	0.956
<i>treB</i>	PTS system, trehalose-specific IIB component	113.8	0.934	147.6	0.944
<i>treC</i>	Trehalose-6-phosphate hydrolase	111.2	0.972	174.1	0.966
<i>ompW</i>	Outer membrane protein W precursor	109.4	0.986	66.6	0.007
<i>fliA</i>	RNA polymerase sigma factor for flagellar operon	104.0	0.005	141.0	0.002
<i>fliL</i>	Flagellar biosynthesis protein	99.0	0.005	28.4	0.010
<i>tnaA</i>	Tryptophanase	98.6	0.837	658.6	0.919
<i>malF</i>	Maltose/maltodextrin ABC transporter, permease protein	94.0	0.037	91.8	0.004
<i>gatC</i>	PTS system, galactitol-specific IIB component	92.0	0.004	99.4	0.001
<i>ygeV</i>	Uncharacterized sigma-54-dependent transcriptional regulator	86.2	0.005	48.0	0.004
	Pyridine nucleotide-disulphide oxidoreductase family	83.1	0.005	52.2	0.004

<i>ansA</i>	L-asparaginase	77.3	0.959	60.1	0.676
<i>malM</i>	Maltose operon periplasmic protein	76.5	0.048	71.2	0.004
<i>tnaB</i>	tryptophan permease	75.5	0.314	670.0	0.955
<i>cstA</i>	Carbon starvation protein A paralog	73.0	0.981	77.6	0.274
<i>glpT</i>	Glycerol-3-phosphate transporte	66.1	0.779	80.8	0.010
<i>gatD</i>	Galactitol-1-phosphate 5-dehydrogenase	62.6	0.010	86.3	0.010
<i>hybA</i>	Hydrogenase-2 operon protein	62.3	0.032	55.9	0.015
<i>malG</i>	Maltose/maltodextrin ABC transporter, permease protein	59.8	0.030	46.5	0.018
<i>manX</i>	PTS system, mannose-specific IIB component	59.1	0.915	42.6	0.020
<i>psuG</i>	Pseudouridine 5'-phosphate glycosidase	58.5	0.009	7.9	0.111
<i>glpQ</i>	Glycerophosphoryl diester phosphodiesterase	57.8	0.967	26.6	0.033
<i>preA</i>	Dihydropyrimidine dehydrogenase	57.0	0.010	65.6	0.013
<i>cadB</i>	Lysine/cadaverine antiporter membrane protein	55.3	0.008	14.1	0.062
<i>potD</i>	periplasmic spermidine putrescine-binding protein	54.8	0.018	20.3	0.043
<i>tdcD</i>	propionate/acetate kinase	52.5	0.010	73.6	0.011
<i>GALNS</i>	N-acetylgalactosamine 6-sulfate sulfatase	51.4	0.011	31.9	0.027
<i>gudP</i>	D-galactarate permease	51.3	0.010	27.2	0.011
<i>aphA</i>	periplasmic phosphatase/phosphotransferase	47.5	0.011	26.3	0.033
<i>gadC</i>	glutamate/gamma-aminobutyrate antiporter	46.9	0.938	7.3	0.111
<i>dmsA</i>	Anaerobic dimethyl sulfoxide reductase chain A	46.7	0.239	64.2	0.013
<i>tdcC</i>	L-threonine transporter	45.1	0.037	21.2	0.041
<i>manY</i>	PTS system, mannose-specific IIC component	44.3	0.926	64.2	0.013
<i>garL</i>	2-dehydro-3-deoxyglucarate aldolase	44.0	0.013	32.7	0.026
<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase chain B	43.6	0.044	74.7	0.011
<i>mglB</i>	D-galactose-binding periplasmic protein	43.1	0.053	46.6	0.018
<i>nanA</i>	N-acetylneuraminate lyase	42.9	0.117	25.6	0.034
<i>ykgE</i>	L-lactate dehydrogenase, Fe-S oxidoreductase subunit	41.8	0.013	57.8	0.015
<i>tdcB</i>	Threonine dehydratase	41.3	0.027	25.4	0.034
<i>lsrB</i>	Autoinducer 2 (AI-2) ABC transport system, periplasmic AI-2 binding protein	40.7	0.013	23.4	0.037
<i>xylF</i>	Xylose ABC transporter periplasmic protein	40.5	0.015	11.1	0.079
<i>gatC</i>	PTS system, galactitol-specific IIA component	39.7	0.028	28.9	0.010
<i>potC</i>	Spermidine Putrescine ABC transporter permease	38.0	0.018	18.4	0.047
<i>yneH</i>	Glutaminase	36.9	0.083	38.5	0.022
<i>fadH</i>	2,4-dienoyl-CoA reductase [NADPH]	36.8	0.018	2.1	0.415

<i>galT</i>	Galactose-1-phosphate uridylyltransferase	36.3	0.843	19.0	0.046
<i>ybaT</i>	Inner membrane transport protein	34.7	0.090	24.7	0.035
<i>hybB</i>	Ni/Fe-hydrogenase 2 B-type cytochrome subunit	33.8	0.086	34.8	0.025
<i>galK</i>	Galactokinase	33.7	0.164	30.6	0.028
<i>caiF</i>	Transcriptional activatory protein CaiF	32.8	0.000	37.2	0.008
<i>ldcC</i>	Lysine decarboxylase	32.1	0.028	11.7	0.075
<i>flgB</i>	Flagellar basal-body rod protein	31.8	0.019	43.6	0.020
<i>nanT</i>	Sialic acid transporter	30.9	0.064	8.0	0.109
<i>cspD</i>	Cold shock protein	30.9	0.250	38.1	0.023
<i>lsrF</i>	Autoinducer 2 (AI-2) aldolase	30.8	0.021	20.6	0.042
<i>uspF</i>	Universal stress protein F	29.8	0.042	16.4	0.053
<i>patD</i>	4-aminobutyraldehyde dehydrogenase	29.4	0.051	22.8	0.038
<i>aldB</i>	Aldehyde dehydrogenase B	28.6	0.102	29.5	0.029
<i>gatZ</i>	Tagatose-6-phosphate kinase	27.8	0.886	25.8	0.034
	DUF1440 domain-containing membrane protein	27.7	0.028	23.4	0.037
<i>potA</i>	Putrescine transport ATP-binding protein	27.6	0.029	37.5	0.023
<i>uspD</i>	Universal stress protein D	26.6	0.027	16.5	0.053
<i>idnD</i>	L-idonate 5-dehydrogenase	26.5	0.033	13.1	0.028
<i>garD</i>	D-galactarate dehydratase	26.3	0.047	25.4	0.034
<i>ftnB</i>	Ferritin-like protein	25.5	0.041	35.3	0.024
<i>flgE</i>	Flagellar hook protein	25.0	0.051	46.9	0.006
<i>tdcF</i>	Hypothetical protein TdcF in cluster with anaerobic degradation of L-threonine to propionate	24.8	0.029	26.1	0.033
<i>xynT</i>	Xyloside transporter	24.8	0.033	22.3	0.013
	Putative fimbrial-like protein	24.5	0.039	7.5	0.065
<i>fliM</i>	Flagellar motor switch protein	24.3	0.030	15.1	0.030
<i>dmsC</i>	Anaerobic dimethyl sulfoxide reductase chain C	23.9	0.061	37.4	0.007
<i>yagH</i>	Beta-xylosidase	23.0	0.042	17.3	0.020
<i>tdcA</i>	Threonine catabolic operon transcriptional activator	22.8	0.043	4.8	0.144
<i>adh</i>	Alcohol dehydrogenase	22.3	0.547	20.8	0.605
<i>fndI</i>	Formate dehydrogenase N gamma subunit	22.3	0.046	36.0	0.006
<i>mglA</i>	Galactose/methyl galactoside ABC transport system, ATP-binding protein	22.0	0.048	8.5	0.064
<i>yihP</i>	Glucuronide transport protein	22.0	0.074	0.5	0.796
<i>gutM</i>	Glucitol operon activator protein	21.8	0.041	49.2	0.003

<i>rbsB</i>	Ribose ABC transport system, periplasmic ribose- binding protein	21.7	0.627	28.1	0.745
<i>gne</i>	UDP-N-acetylglucosamine 4-epimerase	21.5	0.747	15.9	0.692
<i>uxaC</i>	Uronate isomerase	21.4	0.127	7.5	0.091
<i>malT</i>	Transcriptional activator of maltose regulon	21.4	0.563	18.2	0.036
<i>fdoH</i>	Formate dehydrogenase O beta subunit	21.3	0.059	53.5	0.005
<i>agp</i>	Glucose-1-phosphatase	21.2	0.546	18.7	0.033
<i>xanP</i>	Xanthine permease	21.0	0.081	13.2	0.032
<i>gadB</i>	Glutamate decarboxylase	20.9	0.056	4.2	0.172
<i>pepE</i>	Alpha-aspartyl dipeptidase Peptidase E	20.8	0.051	31.3	0.008
<i>gutQ</i>	D-arabinose 5-phosphate isomerases	20.7	0.067	12.3	0.038
<i>agaZ</i>	Tagatose-6-phosphate kinase	20.5	0.040	2.9	0.245
<i>srlR</i>	Glucitol operon repressor	20.2	0.062	15.1	0.026
<i>talA</i>	Transaldolase	20.2	0.039	6.8	0.086
<i>fndG</i>	Formate dehydrogenase N alpha subunit	19.6	0.085	100.9	0.004
<i>gatY</i>	Tagatose-1,6-bisphosphate aldolase	19.3	0.745	19.9	0.732
<i>tdcE</i>	Pyruvate formate-lyase	19.3	0.060	32.7	0.012
<i>sdhB</i>	Succinate dehydrogenase iron-sulfur protein	19.1	0.881	19.6	0.753
<i>dcuC</i>	C4-dicarboxylate transporter	19.1	0.051	15.8	0.024
<i>gcvT</i>	Glycine cleavage system H protein	19.0	0.831	16.6	0.041
<i>yihT</i>	Aldolase	19.0	0.048	1.5	0.524
<i>fucO</i>	Lactaldehyde reductase	18.9	0.052	14.3	0.029
<i>IUNH</i>	Inosine-uridine preferring nucleoside hydrolase	18.0	0.219	7.8	0.087
<i>fliS</i>	Flagellar biosynthesis protein	18.0	0.108	4.6	0.189
<i>molR</i>	Molybdate metabolism regulator	18.0	0.108	0.7	0.959
<i>yfaW</i>	Uncharacterized protein	17.7	0.048	12.8	0.036
<i>fliN</i>	Flagellar motor switch protein	17.2	0.056	47.5	0.005
<i>glpK</i>	Glycerol kinase	16.9	0.920	26.8	0.814
<i>nanE</i>	N-acetylmannosamine-6-phosphate 2-epimerase	16.9	0.069	6.6	0.092
<i>fliF</i>	Flagellar M-ring protein	16.8	0.053	15.1	0.029
<i>lsrG</i>	Autoinducer 2 (AI-2) modifying protein	16.6	0.061	8.6	0.062
<i>araE</i>	Arabinose-proton symporter	16.2	0.878	5.6	0.112
<i>xylG</i>	D-xylose transport ATP-binding protein	16.2	0.055	5.4	0.108
<i>nrfA</i>	Cytochrome c552 precursor	16.2	0.080	24.1	0.014
<i>aldA</i>	Glycolaldehyde dehydrogenase	15.9	0.153	41.9	0.010
<i>rbsK</i>	Ribokinase	15.9	0.890	13.0	0.051

<i>ydcE</i>	Probable tautomerase	15.9	0.057	3.4	0.210
<i>hdeA</i>	chaperone	15.6	1.000	2.7	0.325
<i>rspA</i>	Starvation sensing protein	15.5	0.077	3.6	0.239
<i>flgF</i>	Flagellar basal-body rod protein	15.5	0.064	25.6	0.013
<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase chain B	15.3	0.081	47.1	0.005
<i>csiE</i>	Stationary phase inducible protein	15.2	0.323	9.2	0.070
<i>rbsC</i>	Ribose ABC transport system, permease protein	15.1	0.865	11.9	0.624
<i>gldA</i>	Glycerol dehydrogenase	15.1	0.134	14.6	0.033
<i>ygeW</i>	Aspartate/ornithine carbamoyltransferase family protein protein	15.1	0.063	91.6	0.002
<i>uxaA</i>	Altronate hydrolase	15.0	0.138	7.6	0.082
<i>hdeD</i>	Membrane transporter	14.8	0.154	1.4	0.605
<i>dapA</i>	Dihydrodipicolinate synthase	14.8	0.846	16.1	0.747
<i>yegT</i>	Putative nucleoside transporter	14.8	0.067	7.4	0.077
<i>pstI</i>	Phosphoenolpyruvate-protein phosphotransferase of PTS system	14.8	0.065	2.9	0.274
<i>zraP</i>	Zinc resistance-associated protein	14.6	0.218	5.0	0.127
<i>rhaR</i>	L-rhamnose operon transcriptional activator	14.6	0.063	1.0	0.806
<i>uidB</i>	Glucuronide transporter	14.6	0.064	6.6	0.088
<i>gntP</i>	Fructuronate transporter	14.6	0.074	7.2	0.086
<i>ykgF</i>	Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit	14.4	0.090	25.9	0.015
<i>yhjA</i>	Cytochrome c551 peroxidase	14.4	0.072	8.1	0.073
<i>fliO</i>	Flagellar biosynthesis protein	13.8	0.076	18.0	0.017
<i>hoxL</i>	Uptake hydrogenase large subunit	13.8	0.087	17.4	0.023
<i>melB</i>	Melibiose carrier protein, Na <sup>+</sup> /melibiose symporter	13.8	0.073	5.9	0.110
<i>dctA</i>	Aerobic C4-dicarboxylate transporter for fumarate, L-malate, D-malate, succinate	13.7	0.200	4.7	0.166
<i>hdeB</i>	Chaperone	13.5	0.206	2.2	0.385
<i>atoC</i>	Acetoacetate metabolism regulatory protein	13.5	0.076	13.6	0.035
<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase	13.4	0.081	13.4	0.034
<i>yfaX</i>	Uncharacterized transcriptional regulator	13.3	0.080	1.5	0.529
<i>hybF</i>	[NiFe] hydrogenase nickel incorporation protein	13.3	0.081	4.9	0.142
	Transcriptional regulator, IclR family	13.3	0.080	2.1	0.400
<i>gadA</i>	Glutamate decarboxylase	13.2	0.084	2.4	0.339
<i>ucpA</i>	Oxidoreductase	13.2	0.582	9.2	0.080
<i>gcvP</i>	Glycine dehydrogenase	13.1	0.887	22.3	0.791
<i>atoS</i>	Sensory histidine kinase	13.1	0.080	12.4	0.040

<i>cusC</i>	Cation efflux system protein	13.1	0.197	0.4	0.631
<i>gadW</i>	HTH-type transcriptional regulator	13.0	0.083	1.6	0.538
<i>frdA</i>	Fumarate reductase subunit C	12.9	0.304	13.5	0.042
<i>dppA</i>	Dipeptide-binding ABC transporter, periplasmic substrate-binding component	12.9	0.268	9.8	0.061
<i>malP</i>	Maltodextrin phosphorylase	12.9	0.998	11.3	0.063
<i>acrB</i>	Membrane fusion protein of RND family multidrug efflux pump	12.9	0.105	4.1	0.180
<i>cydA</i>	Cytochrome d ubiquinol oxidase subunit I	12.8	0.778	20.2	0.786
<i>lsrB</i>	Autoinducer 2 (AI-2) ABC transport system, fused AI2 transporter subunits and ATP-binding component	12.8	0.079	5.5	0.101
<i>melA</i>	Alpha-galactosidase	12.8	0.095	8.6	0.061
<i>uspG</i>	Universal stress protein G	12.6	0.171	15.4	0.026
<i>sdaC</i>	Serine transporter	12.6	0.123	12.8	0.035
<i>yphF</i>	Predicted sugar ABC transport system, periplasmic binding protein	12.6	0.088	5.5	0.133
<i>eutQ</i>	Ethanolamine utilization protein	12.5	0.116	3.4	0.205
<i>nikC</i>	Nickel transport system permease protein	12.4	0.085	9.0	0.058
<i>uxaB</i>	Altronate oxidoreductase	12.3	0.107	5.8	0.108
<i>tdcG</i>	Predicted L-serine dehydratase	12.2	0.087	13.9	0.030
<i>fliQ</i>	Flagellar biosynthesis protein	12.0	0.168	5.5	0.133
<i>wrbA</i>	Flavoprotein	11.8	0.878	14.2	0.053
<i>acs</i>	Acetyl-coenzyme A synthetase	11.8	0.106	20.0	0.023

SI Table 4.  $\phi 24_B$  gene expression upon norfloxacin treatment.

Gene	Function	Fold change	Pvalue
<i>vb 24B+1c</i>	Unknown	72.34	0.007
<i>vb 24B+2c</i>	Unknown	73.34	0.009
<i>vb 24B+4c</i>	Unknown	105.44	0.004
<i>vb 24B+5c</i>	Unknown	99.73	0.001
<i>vb 24B+7c</i>	Unknown	72.53	0.007
<i>vb 24B+8c</i>	Unknown	111.42	0.003
<i>vb 24B+9c</i>	Unknown	119.5	0.001
<i>vb 24B+14</i>	Unknown	103.38	0.001
<i>vb 24B+15</i>	Unknown	94.57	0.001
<i>vb 24B+16</i>	Unknown	141	0.000
<i>vb 24B+17</i>	Unknown	36.35	0.002
<i>vb 24B+23</i>	Unknown	38.73	0.009
<i>vb 24B+26</i>	Unknown	90.4	0.001
<i>vb 24B+31</i>	Unknown	28.12	0.011
<i>vb 24B+33</i>	adaptive-response sensory kinase	51.93	0.008
<i>vb 24B+34</i>	Unknown	51.01	0.011
<i>vb 24B+35</i>	Unknown	51.94	0.005
<i>vb 24B+36</i>	Unknown	21.75	0.023
<i>vb 24B+39</i>	Unknown	22.32	0.021
<i>vb 24B+40</i>	Unknown	15.5	0.023
<i>vb 24B+41</i>	Unknown	15.82	0.010
<i>vb 24B+41</i>	Unknown	15.72	0.011
<i>vb 24B+44</i>	Unknown	8.34	0.039
<i>vb 24B+45</i>	Unknown	7.01	0.047
<i>vb 24B+52c</i>	Unknown	10.5	0.023
<i>ninA</i>	Uncharacterized phage-encoded protein	71.33	0.000
<i>ninB</i>	putative DNA N-6-adenosine methyltransferase	68.94	0.009
<i>ninG</i>	putative recombination endonuclease	124.02	0.003
<i>ninH</i>	Uncharacterized phage-encoded protein	89.9	0.000
<i>ninE</i>	Uncharacterized phage-encoded protein	143.07	0.000
<i>S</i>	Host cell lysis	133.64	0.002
<i>R</i>	Associated with endolysin/autolysin	118	0.003
<i>Q</i>	Antiterminator	50.93	0.005
<i>stx</i>	Shiga toxin	95.77	0.000
<i>cII</i>	Transcriptional activator	47.45	0.002
<i>cIII</i>	Regulatory protein	70.35	0.002
<i>cro</i>	Transcriptional activator/repressor	44.9	0.008
<i>d ant</i>		95.60	0.004
<i>ant</i>	Uncharacterized protein	27.32	0.018
<i>roi</i>	Uncharacterized protein	88.55	0.003
<i>Rz</i>	Host cell lysis	49.73	0.005
<i>Rz1</i>	Host cell lysis	86.33	0.000
<i>kil</i>	Host killing; lambda Kil superfamily	83.63	0.003
<i>hyp+c4-zinc+finger</i>	Unknown	76.01	0.006
<i>Sterm</i>	Terminase, small subunit	74.9	0.004
<i>lar</i>	putative restriction alleviation protein	63.84	0.004
<i>hyp+33</i>	Unknown	49.84	0.005
<i>xis</i>	excisionase	51.16	0.002
<i>hyp+DAM</i>	Unknown	101.17	0.004
<i>vb 24B+3c</i>	Unknown	76.35	0.272

<i>vb_24B+10</i>	Unknown	0.6	0.272
<i>vb_24B+11c</i>	Unknown	43.17	0.273
<i>vb_24B+12c</i>	Unknown	3.63	0.141
<i>vb_24B+19c</i>	Unknown	1.63	0.400
<i>vb_24B+20c</i>	Unknown	3.44	0.136
<i>vb_24B+24</i>	Unknown	47.3	0.626
<i>vb_24B+27c</i>	Unknown	1	1
<i>vb_24B+28</i>	Unknown	49.01	0.837
<i>vb_24B+29</i>	Unknown	31.71	0.623
<i>vb_24B+30c</i>	Unknown	0.81	0.848
<i>vb_24B+32c</i>	Unknown	1	0.797
<i>Lterm</i>	Terminase, large subunit	39.17	0.132
<i>vb_24B+37c</i>	Unknown	1.63	0.400
<i>vb_24B+47</i>	Unknown	7.30	0.059
<i>vb_24B+48</i>	Unknown	5.63	0.309
<i>vb_24B+51c</i>	Unknown	0.71	0.879
<i>Int</i>	Integrase	1.73	0.271
<i>vb_24B+6c</i>	Unknown	87.75	0.272
<i>res</i>	putative holliday junction resolvase	1.16	0.532
<i>vb_24B+13c</i>	Unknown	0.65	0.908
<i>exo</i>	Exonuclease	98.02	0.273
<i>bet</i>	possesses large RecT domain	89.25	0.273
<i>gam</i>	Host nuclease inhibitor protein	136.73	0.273
<i>ssb</i>	putative single-stranded DNA binding protein	78.65	0.273
<i>stk</i>	Serine/Threonine protein kinases	1.81	0.329
<i>bor</i>	lambda <i>bor</i> increases the resistance of <i>E. coli</i> to serum	1.43	0.443
<i>cI</i>	repressor protein	1.23	0.446
<i>lom</i>	Outer membrane protein beta-barrel domain	3.00	0.140
<i>port</i>	putative portal protein	29.89	0.526
<i>O</i>	DNA replication protein	64.99	0.606
<i>N</i>	anti-terminator	47.46	0.736
<i>vb_24B+21</i>	Unknown	23.99	0.745
<i>P</i>	DNA replication protein	42.22	0.804



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