

Table S1. Summary of RNA-seq sequencing and data analysis.

Sample	DR1-exp	DR1-nor
Description	Exponential phase	norfloxacin 4 µg/ml treatment at exponential phase
Total no. of reads	6,583,302	19,081,119
No. of reads mapped	6,554,757 (99.57%)	18,845,931 (98.77%)
No. of genes with detectable expression	3,910/3,963	3,889/3,963
Range in expression levels (RPKM)	0.36-21,307.30	0.36-24,221.52

Table S2. Up-regulated genes under norfloxacin treatment condition in *A. oleivorans* DR1 compared with no treatment during the exponential phase.

Locus tag	Product	Fold change
Amino acid metabolism and transport		
AOLE_09730	Peptide ABC transporter membrane protein	6.29
AOLE_11685	ABC-type amino acid transport system, permease component	5.77
AOLE_08765	Shikimate dehydrogenase	5.24
AOLE_11990	2-Aminoethylphosphonate:pyruvate transaminase	3.02
Nucleotide metabolism and transport		
AOLE_04395	Deoxyguanosinetriphosphate triphosphohydrolase-like protein	3.09
AOLE_15280 (<i>dut</i>)	Deoxyuridine 5'-triphosphate nucleotidohydrolase	2.06
Carbohydrate metabolism and transport		
AOLE_11820	major facilitator transporter	2.85
Lipid metabolism		
AOLE_11230	Acyl-CoA dehydrogenase	2.75
AOLE_16945	Membrane-associated phospholipid phosphatase	2.45
AOLE_08710	3-Oxoacyl-(acyl-carrier-protein) reductase	2.10
Translation, including ribosome structure and biogenesis		
AOLE_14540	Peptide deformylase	2.75
Transcription		
AOLE_12045	Transcriptional regulator, TetR family protein	6.66
AOLE_14875	DNA polymerase V component	5.94
AOLE_07970	DNA polymerase V component	5.87
AOLE_11745	SOS-response transcriptional repressor	3.15
AOLE_14800	RNA polymerase sigma factor FecI	2.94
AOLE_12135	Redox-sensitive transcriptional activator SoxR	2.88
AOLE_08565	AraC-type DNA-binding domain-containing protein	2.10
AOLE_12595	TetR family transcriptional regulator	2.10
Replication, recombination, and repair		
AOLE_07375 (<i>recA</i>)	Recombinase A	5.17
AOLE_07965	DNA-directed DNA polymerase UmuC	4.19
AOLE_18380	DNA topoisomerase IV subunit A	2.92
AOLE_00595	DNA topoisomerase IV subunit B	2.80

Table S2. Continued.

Locus tag	Product	Fold change
AOLE_00960	ssDNA-binding protein controls activity of RecBCD nuclease	2.64
AOLE_00910	Excinuclease ABC subunit A	2.40
AOLE_14880	DNA-directed DNA polymerase UmuC	2.13
AOLE_07390	Phage integrase ^a	2.10
AOLE_04385 (<i>ruvB</i>)	Holliday junction DNA helicase RuvB	2.09
Posttranslational modification, protein turnover, chaperones		
AOLE_17410	Glutathione S-transferase	9.06
AOLE_07635	Thioredoxin	2.10
Inorganic ion transport and metabolism		
AOLE_09875	Ferric uptake regulation protein (ferric uptake regulator)	14.34
AOLE_09655	ABC transporter permease	4.19
AOLE_01565	Putative regulatory or redox component complexing with Bfr, in iron storage and mobility (BFD)	3.32
AOLE_09215	Iron ABC transporter ATP-binding protein	2.97
AOLE_12705	Substrate-binding region of ABC-type glycine betaine transport system	2.49
AOLE_11250	ABC-type metal ion transport system, periplasmic component/surface antigen	2.10
Secondary metabolites, biosynthesis, transport, and catabolism		
AOLE_12875	Phenylacetic acid degradation protein	2.10
Intracellular trafficking, secretion, and vesicular transport		
AOLE_09665	Sec-independent protein secretion pathway, translocase protein	7.63
AOLE_17090	Sec-independent protein translocase protein	2.31
General functional prediction only		
AOLE_01905	DNA-binding protein	8.65
AOLE_13495	Competence-damaged family protein	2.62
AOLE_04025	Metal-dependent hydrolase	2.45
AOLE_12115	DMT family permease	2.45
AOLE_07370	Regulatory protein	2.40
AOLE_05645	Alpha/beta superfamily hydrolase	2.38
AOLE_00590	Putative esterase	2.22
AOLE_06600	Host factor I for bacteriophage Q beta replication, a growth-related protein	2.22
No functional prediction		
AOLE_08535	Hypothetical protein	3.12
AOLE_09915	Putative MbtH family protein	3.15
AOLE_12695	Putative secreted protein	2.62
AOLE_11270	Hypothetical protein	2.45
AOLE_10675	Hypothetical protein	2.21
AOLE_03110	Hypothetical protein	2.10
Not in COGs		
AOLE_02240	Hypothetical protein	5.84
AOLE_t19518	tRNA-Leu	37.87
AOLE_04770	Hypothetical protein	13.07
AOLE_t19544	tRNA-Val	21.39
AOLE_07125	Hypothetical protein	7.04
AOLE_08980	Hypothetical protein	5.84

Table S2. Continued.

Locus tag	Product	Fold change
AOLE_08985	Hypothetical protein	4.50
AOLE_08995	Hypothetical protein	4.73
AOLE_09260	Hypothetical protein	5.60
AOLE_09805	Hypothetical protein	2.69
AOLE_09830	Hypothetical protein	3.48
AOLE_12455	Hypothetical protein	2.61
AOLE_12795	Hypothetical protein	3.12
AOLE_15095	Hypothetical protein	3.71
AOLE_t19592	tRNA-Lys	21.67
AOLE_18300	Hypothetical protein	8.32
AOLE_18350	Hypothetical protein	9.63
AOLE_01910	Hypothetical protein	8.54
AOLE_07875	Hypothetical protein ^a	8.39
AOLE_07415	Hypothetical protein ^a	7.34
AOLE_00460	Hypothetical protein	7.13
AOLE_07475	Hypothetical protein ^a	6.29
AOLE_08955	Hypothetical protein	6.29
AOLE_07480	Hypothetical protein ^a	6.29
AOLE_t19536	tRNA-Leu	5.77
AOLE_11750	Hypothetical protein	5.69
AOLE_t19594	tRNA-Lys	5.24
AOLE_07895	Hypothetical protein ^a	5.24
AOLE_03595	Hypothetical protein	4.59
AOLE_t19550	tRNA-Asn	4.19
AOLE_07470	Hypothetical protein ^a	4.19
AOLE_07485	Hypothetical protein ^a	4.19
AOLE_13445	Hypothetical protein	4.19
AOLE_13310	Methane/phenol/toluene hydroxylase	3.28
AOLE_04405	Hypothetical protein	3.15
AOLE_t19542	tRNA-Asn	3.15
AOLE_t19548	tRNA-Asn	3.15
AOLE_06810	Phage putative head morphogenesis protein	3.15
AOLE_07740	Hypothetical protein ^a	3.15
AOLE_07860	Hypothetical protein ^a	3.15
AOLE_13315	Phenol hydroxylase region	3.15
AOLE_09865	Coenzyme PQQ synthesis protein PqqA	2.80
AOLE_13095	Hypothetical protein	2.80
AOLE_13065	Hypothetical protein	2.73
AOLE_07395	Hypothetical protein ^a	2.62
AOLE_07930	Hypothetical protein ^a	2.62
AOLE_12600	Hypothetical protein	2.52
AOLE_09505	Hypothetical protein	2.45
AOLE_13245	Hypothetical protein	2.45

Table S2. Continued.

Locus tag	Product	Fold change
AOLE_t19526	tRNA-Val	2.39
AOLE_t19534	tRNA-Leu	2.36
AOLE_t19530	tRNA-Val	2.23
AOLE_14885	Hypothetical protein	2.16
AOLE_t19490	tRNA-Phe	2.10
AOLE_04015	Hypothetical protein	2.10
AOLE_t19546	tRNA-Asn	2.10
AOLE_05475	Hypothetical protein	2.10
AOLE_07720	Hypothetical protein ^a	2.10
AOLE_00400	Hypothetical protein	2.10
AOLE_00455	Hypothetical protein	2.10
AOLE_01705	Hypothetical protein	2.10
AOLE_07140	Hypothetical protein	2.10
AOLE_08725	NIPSNAP family protein	2.10
AOLE_09000	Hypothetical protein	2.10
AOLE_14830	Hypothetical protein	2.10
AOLE_15775	Hypothetical protein	2.10
AOLE_18460	Hypothetical protein	2.10
AOLE_18780	Hypothetical protein	2.10

^aThese are located in phage-related genomic regions.

Table S3. Down-regulated genes under norfloxacin treatment condition in *A. oleivorans* DR1 compared with no treatment during the exponential phase.

Locus tag	Product	Fold change
Energy production and conversion		
AOLE_11485	Monooxygenase, NtaA/SnaA/SoxA family protein	0.50
AOLE_07165	Anaerobic dehydrogenase	0.50
AOLE_04890	Phenylacetaldehyde dehydrogenase (PAD)	0.50
AOLE_09550	Putative oxidoreductase	0.50
AOLE_06670	Putative alcohol dehydrogenase	0.47
AOLE_00775	Metallo-beta-lactamase superfamily protein	0.46
AOLE_03930	Glycerophosphoryl diester phosphodiesterase	0.45
AOLE_10250	Dihydrolipoamide acetyltransferase	0.44
AOLE_10260	Acetoin:DCPIP oxidoreductase alpha subunit	0.38
AOLE_10255	Acetoin:2,6-dichlorophenolindophenoloxidoreductase subunit beta	0.37
AOLE_09740	Putative FMNH(2)-dependent alkanesulfonate monooxygenase (SsuD-like) protein	0.35
AOLE_02975	Acyl-CoA transferases/carnitine dehydratase	0.34
AOLE_09555	Nitrilotriacetate monooxygenase component A	0.30
AOLE_08645	Alkanesulfonate monooxygenase	0.23
AOLE_12940	Bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase	0.23
AOLE_12915	Flavodoxin reductase (ferredoxin-NADPH reductase) family protein 1	0.17

Table S3. Continued.

Locus tag	Product	Fold change
Amino acid metabolism and transport		
AOLE_05170	Ornithine cyclodeaminase	0.50
AOLE_11215	Binding-protein-dependent transport system inner membrane component family protein	0.50
AOLE_09500	Gamma-glutamylputrescine oxidoreductase	0.50
AOLE_13210	LysE type translocator family protein	0.49
AOLE_14280 (<i>ureA</i>)	Urease subunit gamma	0.48
AOLE_11690	ABC-type amino acid transport system, permease component	0.45
AOLE_11995	Monomeric sarcosine oxidase (MSOX)	0.45
AOLE_14415	Multifunctional protein (Includes: acyl-CoA thioesterase I; protease I; lysophospholipase(I))	0.42
AOLE_13885	Arginine <i>N</i> -succinyltransferase	0.36
AOLE_08670	Branched-chain amino acid ABC transporter ATP-binding protein	0.35
AOLE_04905	Gamma-aminobutyrate permease	0.28
Nucleotide metabolism and transport		
AOLE_08405	3-Carboxy- <i>cis,cis</i> -muconate cycloisomerase	0.50
Carbohydrate metabolism and transport		
AOLE_06155	MFS family benzoate membrane transporter	0.49
AOLE_10150	Alpha-ketoglutarate permease	0.47
AOLE_10020	Major facilitator superfamily permease	0.45
AOLE_04775	Hypothetical protein	0.44
AOLE_09290	Drug resistance MFS transporter, drug:H ⁺ antiporter-1 (14 Spanner) (DHA2) family protein	0.31
AOLE_04900	Pyruvate decarboxylase	0.17
Coenzyme metabolism		
AOLE_12025	4-Hydroxybenzoate 3-monooxygenase	0.49
AOLE_11560	Triphosphoribosyl-dephospho-CoA synthase	0.47
AOLE_07170	Molybdenum cofactor biosynthesis protein A	0.44
Lipid metabolism		
AOLE_11860	Acetyl/propionyl-CoA carboxylase, alpha subunit	0.50
AOLE_08395	Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit	0.49
AOLE_08390	3-Oxoadipate CoA-transferase subunit A	0.48
AOLE_10005	Short chain dehydrogenase	0.48
AOLE_10540	Acyl-CoA dehydrogenase	0.45
AOLE_11910	Acetyl-CoA:acetoacetyl-CoA transferase subunit alpha	0.45
AOLE_11635	3-Oxoacyl-[acyl-carrier-protein]reductase (3-ketoacyl-acyl carrier protein reductase)	0.44
AOLE_12900	3-Hydroxyacyl-CoA dehydrogenase	0.43
AOLE_11845	Isovaleryl-CoA dehydrogenase	0.43
AOLE_10110	Short-chain fatty acids transporter	0.37
AOLE_11550	Malonate decarboxylase subunit beta	0.32
AOLE_12910	Enoyl-CoA hydratase	0.29
AOLE_10105	3-Oxoadipate CoA-succinyl transferase beta subunit	0.27
AOLE_10100	Acetoacetyl-CoA transferase, alpha subunit	0.26
AOLE_18760	Phosphopantetheine attachment site family protein	0.21
Translation, including ribosome structure and biogenesis		
AOLE_16335	Probable sigma(54) modulation protein (ORF95)	0.42
AOLE_13840	Acetyltransferase	0.42

Table S3. Continued.

Locus tag	Product	Fold change
AOLE_11575	Hypothetical protein	0.39
AOLE_07990	Acetyltransferase (GNAT) family protein	0.24
Transcription		
AOLE_08300	Transcriptional regulator PadR-like family protein	0.50
AOLE_11705	Putative transcriptional regulator	0.50
AOLE_16145	TetR family transcriptional regulator	0.49
AOLE_17245	HxlR-like helix-turn-helix family protein	0.48
AOLE_18545	AraC family transcriptional regulator	0.47
AOLE_05910	HxlR family transcriptional regulator	0.47
AOLE_11435	Transcriptional regulator	0.47
AOLE_13820	AraC family transcriptional regulator	0.45
AOLE_12020	Transcriptional regulator	0.44
AOLE_12615	Putative HTH-type transcriptional regulator YcjZ	0.44
AOLE_08705	Sigma54 specific transcriptional regulator, Fis family protein	0.43
AOLE_07995	Transcriptional regulator	0.42
AOLE_11145	LysR family transcriptional regulator	0.41
AOLE_06890	AsnC family transcriptional regulator	0.35
AOLE_11410	ArsR	0.35
AOLE_04060	TetR family transcriptional regulator	0.33
AOLE_04085	TetR family transcriptional regulator	0.31
AOLE_06800	Transcriptional regulator	0.31
AOLE_12380	Putative transcriptional regulator	0.31
AOLE_06160	LysR family transcriptional regulator	0.31
AOLE_03365	PaaX-like family protein	0.29
AOLE_09095	LysR family transcriptional regulator	0.28
AOLE_10025	AraC-type DNA-binding domain-containing protein	0.26
AOLE_16700	Transcriptional regulator	0.26
AOLE_01125	TetR family transcriptional regulator	0.21
AOLE_14125	CadR	0.21
AOLE_12780	Cold shock-like protein cspG	0.21
AOLE_04895	AsnC family protein	0.17
AOLE_08480	Probable HTH-type transcriptional regulator leuO	0.15
AOLE_09195	TetR family transcriptional regulator	0.14
AOLE_12440	TetR family regulatory protein	0.35
AOLE_13165	TetR family regulatory protein	0.12
AOLE_13970	TetR family transcriptional regulator	0.14
Replication, recombination, and repair		
AOLE_06575	Addiction module antitoxin, RelB/DinJ family protein	0.41
AOLE_09825	G:T/U mismatch-specific DNA glycosylase	0.39
Cell wall structure and biogenesis and outer membrane		
AOLE_05895	Secretion protein HlyD	0.50
AOLE_08950	NmrA family protein	0.49
AOLE_13130	Glycosyl transferase family 2 family protein	0.47

Table S3. Continued.

Locus tag	Product	Fold change
AOLE_14710	High-affinity choline transport protein	0.44
AOLE_13135	Putative methyltransferase	0.43
AOLE_09165	Nucleoside-diphosphate-sugar epimerase	0.29
Secretion, motility, and chemotaxis		
AOLE_11120	P pilus assembly protein, chaperone PapD	0.31
Posttranslational modification, protein turnover, chaperones		
AOLE_02915	Peroxisredoxin	0.50
Inorganic ion transport and metabolism		
AOLE_03855	Alkaline phosphatase D precursor (APaseD)	0.49
AOLE_08650	Putative periplasmic aliphatic sulfonate-binding protein	0.47
AOLE_09650	ABC transporter permease	0.47
AOLE_11395	Chromate transport protein	0.47
AOLE_06365	Flavoprotein	0.42
AOLE_11405	Putative arsenite efflux transporter	0.40
AOLE_14615	Putative ferredoxin	0.39
AOLE_14605	Vanillate <i>O</i> -demethylase oxygenase subunit (4-hydroxy-3-methoxybenzoate demethylase)	0.29
AOLE_09750	Putative desulfurization enzyme B (dibenzothiophene)	0.22
Secondary metabolites biosynthesis, transport, and catabolism		
AOLE_04865	Hypothetical protein	0.50
AOLE_11455	Taurine dioxygenase	0.49
AOLE_06110 (<i>tauD</i>)	DSBA oxidoreductase	0.35
AOLE_09975	Small subunit of phenylpropionate dioxygenase	0.35
AOLE_01165	Isoprenoid biosynthesis protein with amidotransferase-like domain	0.23
AOLE_00845	Putative isochorismatase	0.22
AOLE_12930 (<i>paaB</i>)	Phenylacetate-CoA oxygenase subunit PaaB	0.06
Signal transduction		
AOLE_06865	Universal stress family protein	0.50
AOLE_11720	Response regulator	0.49
AOLE_09575	Putative transcriptional regulator	0.42
AOLE_07135	Response regulator protein	0.26
Intracellular trafficking, secretion, and vesicular transport		
AOLE_09670	Sec-independent protein secretion pathway, component B	0.42
AOLE_10825	General secretion pathway protein I precursor (PilD-dependent protein pddC)	0.33
AOLE_09675	Sec-independent protein secretion pathway, component C	0.26
Defense mechanisms		
AOLE_10435	ABC transporter ATP-binding protein	0.39
General functional prediction only		
AOLE_03900	Phosphohydrolase	0.50
AOLE_15360	Hypothetical protein	0.50
AOLE_06040	Hypothetical protein	0.50
AOLE_02875	Metal-dependent hydrolase	0.49
AOLE_11715	Putative signal peptide protein	0.47
AOLE_06010	Hydroxyisourate hydrolase	0.47

Table S3. Continued.

Locus tag	Product	Fold change
AOLE_08410	3-Oxoadipate enol-lactonase	0.47
AOLE_09430	Putative esterase	0.47
AOLE_06860	ABC transporter family protein	0.46
AOLE_01155	General stress protein 14 (GSP14)	0.43
AOLE_05850	Putative kinase	0.43
AOLE_04080	Short-chain dehydrogenase of various substrate specificities	0.41
AOLE_15075	Hypothetical protein	0.40
AOLE_14055	Peptide/nickel transport system permease protein	0.40
AOLE_09155	Hypothetical protein	0.39
AOLE_13625	Hypothetical protein	0.39
AOLE_06790	Lysozyme	0.39
AOLE_04050	Putative hydrolase	0.36
AOLE_08655	Cysteine dioxygenase type I	0.35
AOLE_18455	NADPH-dependent fmn reductase	0.35
AOLE_03475	Permease	0.33
AOLE_01290	Putative acetyltransferase	0.32
AOLE_19365	Matrixin family protein	0.30
AOLE_09995	Hypothetical protein	0.26
AOLE_12920	Phenylacetate-CoA oxygenase, PaaJ subunit	0.14
AOLE_14595	Metapyrocatechase 2 (MPC) (CatO2ase) (catechol 2,3-dioxygenase II)	0.14
AOLE_08465	Hypothetical protein	0.10
AOLE_12855	Uroporphyrin-III C/tetrapyrrole methyltransferase	0.09
AOLE_08865	Hypothetical protein	0.16
No functional prediction		
AOLE_05570	Hypothetical protein	0.50
AOLE_05180	Sensory box protein	0.50
AOLE_03600	Transcription factor jumonji domain-containing protein	0.49
AOLE_02785	Hypothetical protein	0.48
AOLE_18885	Hypothetical protein	0.48
AOLE_17455	Hypothetical protein	0.46
AOLE_19435	Transglycosylase-associated family protein	0.46
AOLE_06120	Hypothetical protein	0.45
AOLE_13090	Hypothetical protein	0.42
AOLE_09520	Hypothetical protein	0.40
AOLE_14765	Hypothetical protein	0.40
AOLE_01710	Hypothetical protein	0.37
AOLE_05990	Paraquat-inducible protein A	0.35
AOLE_08355	Hypothetical protein	0.35
AOLE_13270	Hypothetical protein	0.35
AOLE_13905	SnoaL-like polyketide cyclase family protein	0.35
AOLE_12430	Hypothetical protein	0.33
AOLE_11710	Hypothetical protein	0.31
AOLE_06045	Hypothetical protein	0.29

Table S3. Continued.

Locus tag	Product	Fold change
AOLE_06100	Hypothetical protein	0.28
AOLE_10155	Hypothetical protein	0.26
AOLE_11420	Hypothetical protein	0.26
AOLE_15015	Putative bacteriophage protein	0.22
AOLE_12935	Phenylacetate-CoA oxygenase subunit PaaA	0.21
AOLE_12925 (<i>paaA</i>)	Phenylacetic acid degradation protein paaC	0.11
AOLE_05430	Hypothetical protein	0.13
AOLE_11010	Hypothetical protein	0.20
Not in COGs		
AOLE_05860	Hypothetical protein	0.50
AOLE_01210	Hypothetical protein	0.50
AOLE_15835	Hypothetical protein	0.50
AOLE_05060	Hypothetical protein	0.49
AOLE_18970	Hypothetical protein	0.48
AOLE_13235	Hypothetical protein	0.48
AOLE_08310	Hypothetical protein	0.48
AOLE_13855	Putative hemagglutinin protein (FhaB)	0.48
AOLE_08195	Hypothetical protein	0.47
AOLE_04725	Hypothetical protein	0.47
AOLE_07800	Hypothetical protein	0.47
AOLE_10285	Hypothetical protein	0.47
AOLE_11030	Hypothetical protein	0.47
AOLE_14960	Hypothetical protein	0.46
AOLE_05120	Hypothetical protein	0.45
AOLE_07445	Hypothetical protein	0.45
AOLE_12470	Hypothetical protein	0.45
AOLE_14165	Hypothetical protein	0.45
AOLE_15715	Hypothetical protein	0.44
AOLE_11175	Hypothetical protein	0.44
AOLE_07770	Hypothetical protein	0.44
AOLE_15140	Hypothetical protein	0.43
AOLE_05165	Peptidase M17, leucyl aminopeptidase-like protein	0.43
AOLE_07425	Hypothetical protein	0.43
AOLE_09265	Hypothetical protein	0.42
AOLE_05100	Hypothetical protein	0.42
AOLE_06815	Hypothetical protein	0.42
AOLE_14910	Hypothetical protein	0.42
AOLE_15785	Hypothetical protein	0.42
AOLE_06615	Hypothetical protein	0.42
AOLE_09760	Hypothetical protein	0.42
AOLE_13045	Hypothetical protein	0.40
AOLE_06855	Hypothetical protein	0.40
AOLE_07890	Hypothetical protein	0.39

Table S3. Continued.

Locus tag	Product	Fold change
AOLE_13770	Hypothetical protein	0.39
AOLE_16055	Hypothetical protein	0.39
AOLE_07755	Hypothetical protein	0.38
AOLE_13535	Hypothetical protein	0.37
AOLE_14820	Hypothetical protein	0.36
AOLE_07805	Hypothetical protein	0.35
AOLE_13305	Monoxygenase component MmoB/DmpM	0.35
AOLE_06700	Hypothetical protein	0.35
AOLE_10055	Hypothetical protein	0.35
AOLE_11155	Hypothetical protein	0.35
AOLE_11530	Putative malonate transporter	0.35
AOLE_12310	Hypothetical protein	0.35
AOLE_13100	Hypothetical protein	0.35
AOLE_13125	Hypothetical protein	0.35
AOLE_13385	Hypothetical protein	0.35
AOLE_13440	Hypothetical protein	0.35
AOLE_14975	Hypothetical protein	0.35
AOLE_17125	Hypothetical protein	0.35
AOLE_18430	Hypothetical protein	0.34
AOLE_07220	Hypothetical protein	0.33
AOLE_07545	Hypothetical protein	0.33
AOLE_06780	Hypothetical protein	0.33
AOLE_07515	Hypothetical protein	0.32
AOLE_08085	Hypothetical protein	0.31
AOLE_04985	Hypothetical protein	0.31
AOLE_07710	Hypothetical protein	0.30
AOLE_08790	Hypothetical protein	0.30
AOLE_09835	Hypothetical protein	0.30
AOLE_18930	Hypothetical protein	0.30
AOLE_00260	Hypothetical protein	0.30
AOLE_09330	Hypothetical protein	0.30
AOLE_10135	Hypothetical protein	0.30
AOLE_10325	Hypothetical protein	0.30
AOLE_14995	Hypothetical protein	0.29
AOLE_13490	Hypothetical protein	0.28
AOLE_13225	Hypothetical protein	0.26
AOLE_15110	Hypothetical protein	0.26
AOLE_17890	Hypothetical protein	0.26
AOLE_01330	Hypothetical protein	0.26
AOLE_01395	Hypothetical protein	0.26
AOLE_07490	Hypothetical protein	0.26
AOLE_12140	Hypothetical protein	0.26
AOLE_15790	Hypothetical protein	0.26

Table S3. Continued.

Locus tag	Product	Fold change
AOLE_07855	Hypothetical protein	0.24
AOLE_13040	Hypothetical protein	0.23
AOLE_08505	PaaM	0.21
AOLE_13295	Phenol hydroxylase subunit DmpK	0.21
AOLE_12535	Hypothetical protein	0.19
AOLE_07435	Hypothetical protein	0.17
AOLE_16030	Hypothetical protein	0.15
AOLE_01130	Hypothetical protein	0.12
AOLE_01830	Putative signal peptide-containing protein	0.39
AOLE_03990	Hypothetical protein	0.17
AOLE_05185	Hypothetical protein	0.10
AOLE_06830	Hypothetical protein	0.17
AOLE_06870	Hypothetical protein	0.10
AOLE_07420	Hypothetical protein	0.06
AOLE_07440	Hypothetical protein	0.08
AOLE_07735	Hypothetical protein	0.15
AOLE_07885	Hypothetical protein	0.12
AOLE_08330	Hypothetical protein	0.18
AOLE_08750	Hypothetical protein	0.12
AOLE_08890	Hypothetical protein	0.08
AOLE_09050	Hypothetical protein	0.24
AOLE_09345	Hypothetical protein	0.39
AOLE_09395	Hypothetical protein	0.19
AOLE_10085	Hypothetical protein	0.49
AOLE_10095	Hypothetical protein	0.19
AOLE_11060	Hypothetical protein	0.08
AOLE_t19562	tRNA-Met	0.10
AOLE_11795	Hypothetical protein	0.18
AOLE_11800	Hypothetical protein	0.19
AOLE_11805	Hypothetical protein	0.13
AOLE_12385	Hypothetical protein	0.16
AOLE_12555	Hypothetical protein	0.22
AOLE_12770	Hypothetical protein	0.30
AOLE_12790	Hypothetical protein	0.20
AOLE_14170	Hypothetical protein	0.15
AOLE_15045	Hypothetical protein	0.24
AOLE_15085	Hypothetical protein	0.24
AOLE_t19574	tRNA-Met	0.10
AOLE_15770	Hypothetical protein	0.12
AOLE_18925	Hypothetical protein	0.26
AOLE_18985	Hypothetical protein	0.02

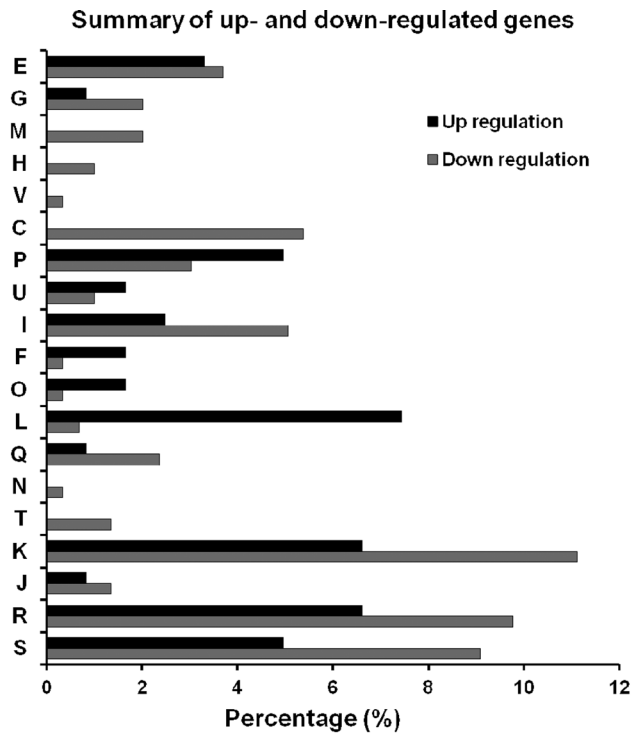


Fig. S1. A summary of up- and down-regulated genes sorted by general COGs.

56.20% of up-regulation genes and 39.73% of down-regulation genes that belong to Not in COGs do not appear in the bar graph. Total of 418 genes were expressed differentially by more than 2-fold (121 genes up-regulated and 297 genes down-regulated) in the DR1-nor, as compared with the DR1-exp. The number of total up-regulated genes and total down-regulated genes were converted into 100%. One-letter abbreviations for the functional categories: E, amino acid metabolism and transport; G, carbohydrate metabolism and transport; M, cell wall structure and biogenesis and outer membrane; H, coenzyme metabolism; V, Defense mechanisms; C, energy production and conversion; P, inorganic ion transport and metabolism; U, intracellular trafficking, secretion, and vesicular transport; I, lipid metabolism; F, nucleotide metabolism and transport; O, molecular chaperones and related functions; L, replication, recombination, and repair; Q, secondary metabolites biosynthesis, transport, and catabolism; N, secretion, motility, and chemotaxis; T, signal transduction; K, transcription; J, translation, including ribosome structure and biogenesis; R, general functional prediction only; S, no functional prediction.

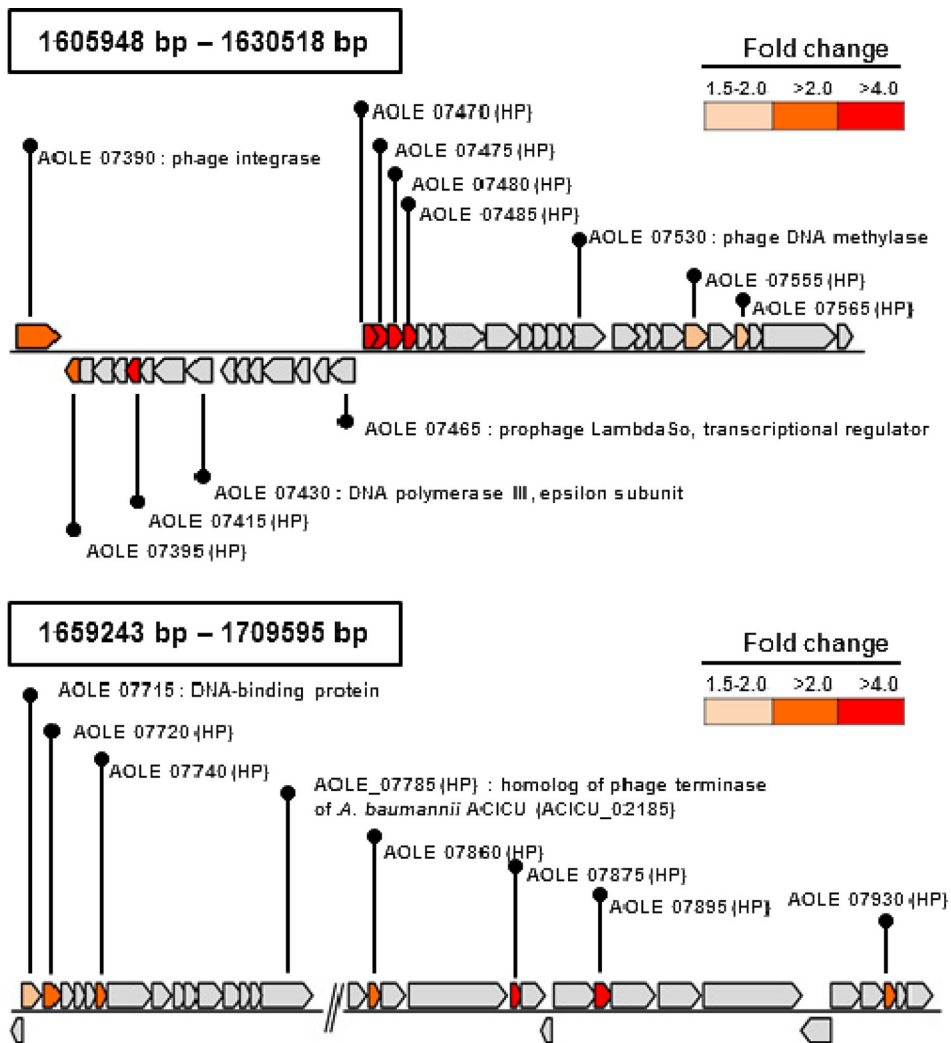


Fig. S2. Differentially expressed regions including phage-related genes.

Hypothetical proteins are designated as HP. A total of nine genes, including phage integrase (AOLE_07390), were induced by norfloxacin (upper, from 1,605,948 bp to 1,630,518 bp). In particular, expression of five of the genes increased more than four times. Seven genes were induced by norfloxacin (lower, from 1,659,243 bp to 1,709,595 bp). Expression of two of the genes increased more than four times and that of four other genes increased more than two times.