

Supplemental Material For:

***Acinetobacter baumannii* OxyR regulates the transcriptional response to hydrogen peroxide**

Lillian J. Juttukonda¹, Erin R. Green¹, Zachery R. Lonergan¹, Marie C. Heffern^{2,3}, Christopher J. Chang^{3,4,5}, and Eric P. Skaar^{1#}

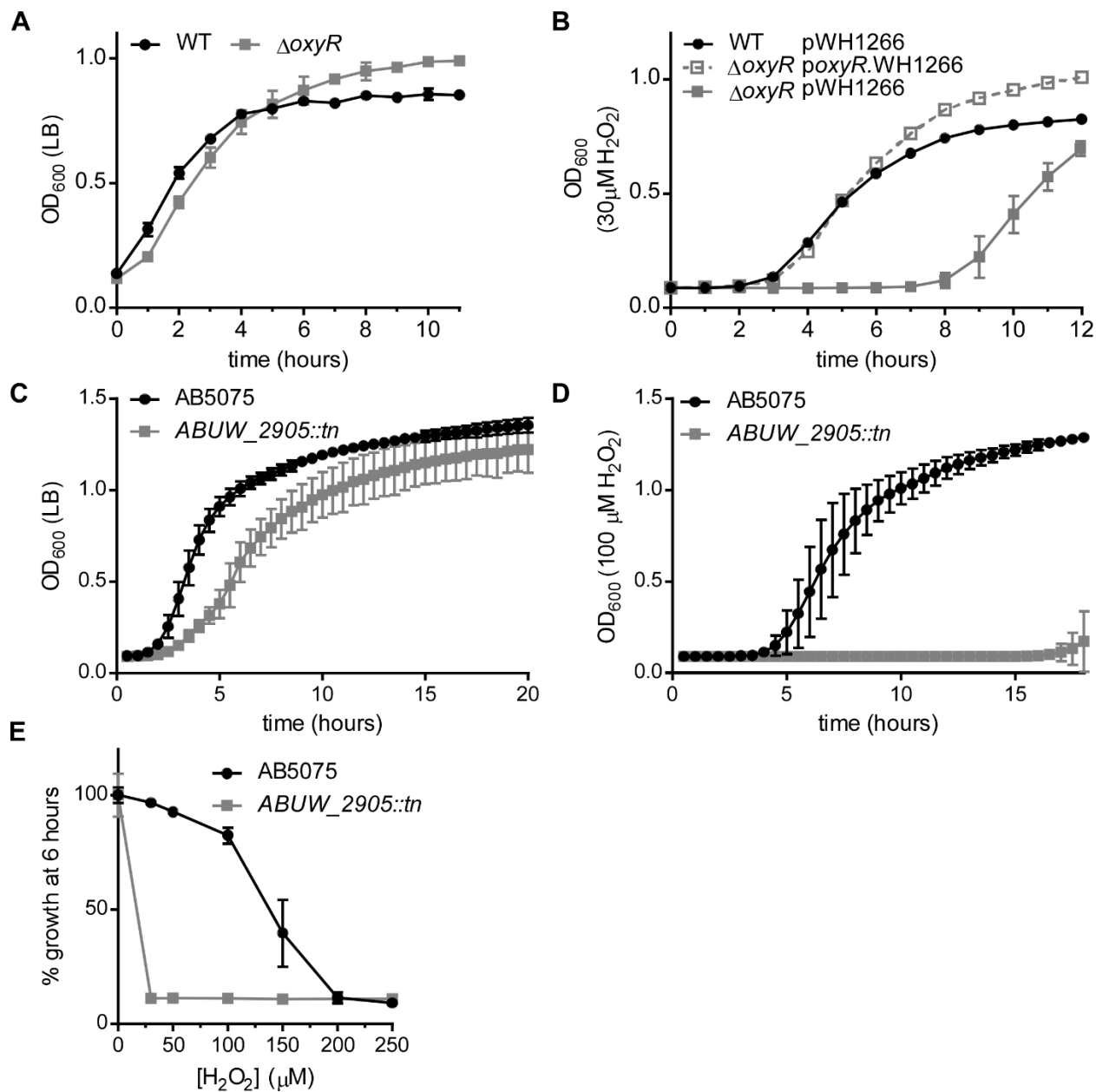
¹Vanderbilt Institute for Infection, Immunology, and Inflammation and Department of Pathology, Microbiology, and Immunology, Vanderbilt University Medical Center, Nashville, TN 37232, USA

²Present address: Department of Chemistry, University of California, Davis, CA 95616, USA.

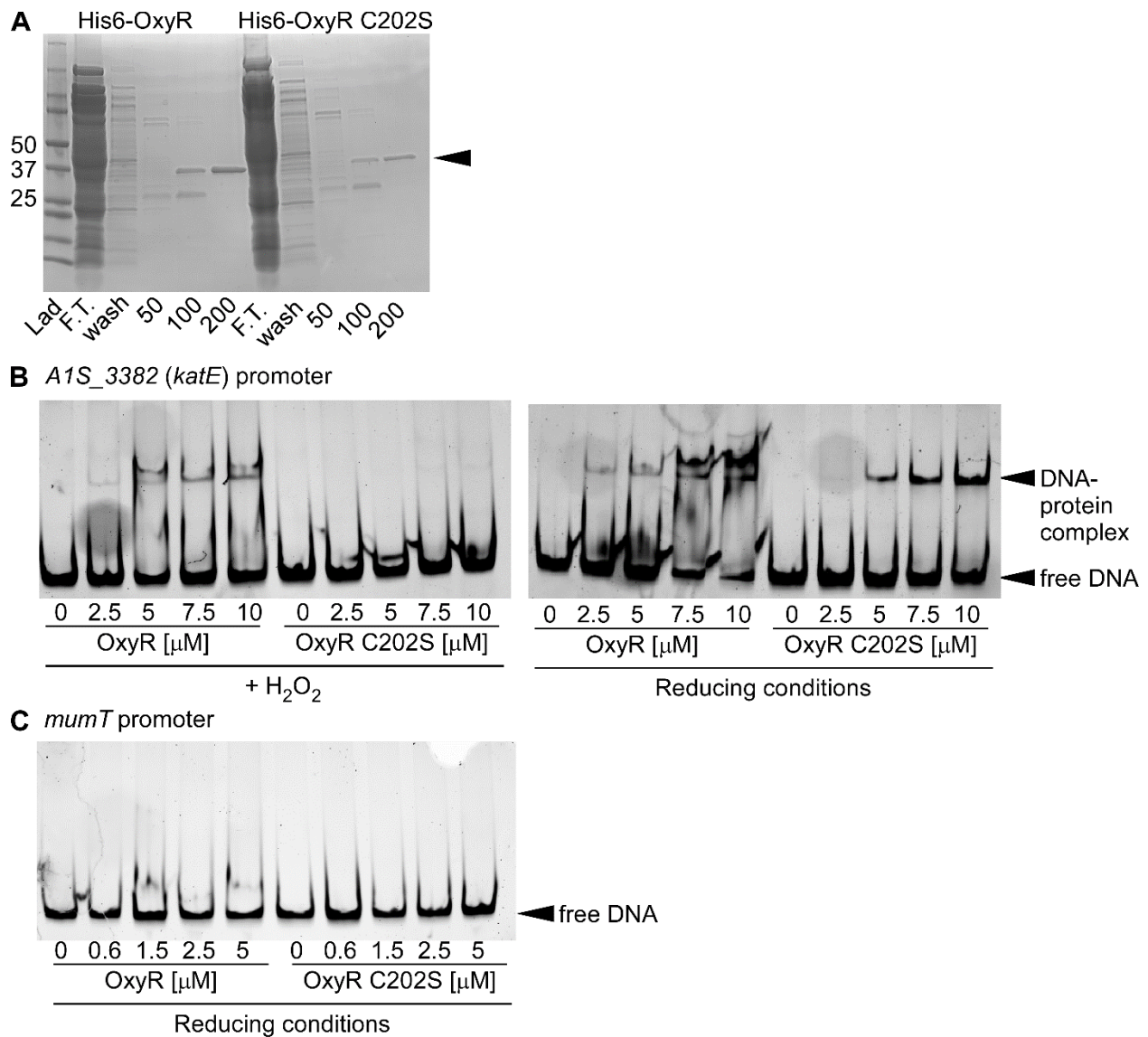
³Department of Chemistry, University of California, Berkeley, CA 94720, USA.

⁴Department of Molecular and Cell Biology University of California, Berkeley, CA 94720, USA.

⁵Howard Hughes Medical Institute, University of California, Berkeley, CA 94720, USA.



Supplemental Figure 1. Impact of *oxyR* on growth. (A-E) Growth was monitored by absorbance at 600 nm (OD_{600}) over time. (A) Growth of WT *A. baumannii* ATCC 17978 and $\Delta oxyR$ strain in LB. (B) Growth in LB containing 30 μM H_2O_2 of *A. baumannii* WT 17978 with empty vector, $\Delta oxyR$ strain with empty vector, or $\Delta oxyR$ strain constitutively expressing *oxyR* in trans. (C) Growth in LB of WT *A. baumannii* AB5075 and strains containing transposon insertions in *oxyR* ($ABUW_2905::tn$). (D) Growth of WT *A. baumannii* AB5075 and *oxyR* transposon mutants in 100 μM H_2O_2 . (E) Percent growth relative to untreated of WT *A. baumannii* AB5075 and *oxyR* transposon mutants in various concentrations of H_2O_2 at hour 6 in the growth curve. (A-E) Experiments were performed in biological triplicate and are representative of growth curves performed on at least three separate days. In (C-E), four independent transposon mutants were analyzed and the results were pooled. Data points are mean \pm standard deviation.



Supplemental Figure 2. Purification of recombinant His6-OxyR and His6-OxyR C202S and electromobility shift assays with additional promoters. (A) Coomassie-stained SDS-PAGE gel of fractions collected from column purification of recombinant His6-OxyR and His6-OxyR C202S. Lad = protein ladder. F.T. = flow through. 50, 100, 200 refers to imidazole concentrations (in mM) used to wash column. The protein fraction that eluted at 200 mM was used for EMSA following buffer exchange. (B-C) The PCR amplified promoter regions for (B) *A1S_3382 (katE)* and (C) *mumT* were incubated with various amounts of recombinantly purified His6-OxyR or His6-OxyR C202S. His6-OxyR was preincubated for 10 minutes with (+H₂O₂) or without (Reducing conditions) 50 mM H₂O₂. DNA was visualized using SYBR Green. Each gel is representative of experiments performed on at least two separate days.

Supplemental Table 1: Primers used in this study

Primer	Primer Sequence	Primer description
LEJ_209	AAGTTTGAATTAATTGATGGA ATGGGGCATGATATCCCTGCC CATTTTATTCCACAGCTTAGCG GTTTATTTGCGCATCATTTTAA ATCATCATACTAGGACACTAT GGCTGCATTACCCTCACTATGA CTA ACT AGG AGG AATA	5' primer to amplify <i>aphI</i> kanamycin resistance cassette for <i>oxyR</i> recombineering
LEJ_220	AAAAAATAATTGCAGATGATA GCTTGGATTTGAGATCGGCTTG GGTATTTAAATGGGCTTCCCTA ACAGCACAGTAAAATAAAAAG GAGTCCGCAGACTCCTTTTTTTT ATTCATGTAAGTTTGTGGT TCATTATTCCCTCCAGGTA	3' primer to amplify <i>aphI</i> kanamycin resistance cassette for <i>oxyR</i> recombineering
LEJ_213	ACTGCAACTGGACCGTGAAAT	5' primer outside of <i>oxyR</i> recombineering construct to check integration
LEJ_214	GACCCTGCCAATGACTATGCA	3' primer outside of <i>oxyR</i> recombineering construct to check integration
LEJ_211	TAAGGATCCatggctgcattaccct	5' primer to amplify <i>oxyR</i> with BamHI cut site, for cloning into pP _{r01} WH1266 complementation vector
LEJ_212	GGAGTCGACTtattcatgtaagtttggtgta	3' primer to amplify <i>oxyR</i> with SalI cut site, for cloning into pP _{r01} WH1266 complementation vector
LEJ_236	cattttgettgaagaaggccacAGCttacgtgat catgtattaag	Side-directed mutagenesis primer for <i>oxyR</i> C204S
LEJ_237	cttaatacatgatcacgtaaGCTgtggccttcttc aagcaaaatg	Side-directed mutagenesis primer for <i>oxyR</i> C204S, reverse complement
LEJ_227	att CATATG gctgcattaccctcactaag	5' primer for amplifying <i>oxyR</i> with NdeI site for constructing pET15B protein expression vector
LEJ_228	gct GGATCC ttattcatgtaagtttggtg	3' primer for amplifying <i>oxyR</i> with BamHI site for constructing pET15B protein expression vector
LEJ_243	AGAGGGATTTAAAATAAGTA TTCAGTAATTTTCAG	5' primer for amplifying promoter of <i>AIS_3382</i> for EMSA
LEJ_244	AATGTAAATCCAAAAGTATA AATGCCTTTCC	3' primer for amplifying promoter of <i>AIS_3382</i> for EMSA
LEJ_370	GAAAGTACCTTTTAATGTTATG ACATAAAATC	5' primer for amplifying promoter of <i>AIS_1201</i> for EMSA
LEJ_371	CCAAATTCTTTCAATAGATGCA TAG	3' primer for amplifying promoter of <i>AIS_1201</i> for EMSA

1266_pro SacI	ataattGAGCTCAAAGCTGTTTTG TAGGTA AAC	5' primer for amplifying promoter of <i>mumT</i> for EMSA
1266_pro BamHI	aattctGGATCCTTAACAACGCTA TTTTCAAATTG	3' primer for amplifying promoter of <i>mumT</i> for EMSA
r01RTf	CTGTAGCGGGTCTGAGAGGAT	<i>r01</i> 5' qRT-PCR primer
r01RTr	CCATAAGGCCTTCTTCACAC	<i>r01</i> 3' qRT-PCR primer
LEJ_340	ggatgcacaaggtactccgc	<i>AIS_0104</i> 5' qRT-PCR primer
LEJ_341	cgaccaaaggcaatcagtgt	<i>AIS_0104</i> 3' qRT-PCR primer
LEJ_44	ACCCGTGGTGTAGCGTACTG	<i>AIS_1200</i> 5' qRT-PCR primer
LEJ_45	CAAGGTCAATCGCCGCTTCA	<i>AIS_1200</i> 3' qRT-PCR primer
LEJ_328	actgtccggacgtggtacag	<i>AIS_1458</i> 5' qRT-PCR primer
LEJ_329	tggaataaccatcggtacagcc	<i>AIS_1458</i> 3' qRT-PCR primer
LEJ_338	agcagcaggcgaaacagtta	<i>AIS_2150</i> 5' qRT-PCR primer
LEJ_339	ccgcacaattaaccagacca	<i>AIS_2150</i> 3' qRT-PCR primer
LEJ_318	tgttagctgctggtagtgg	<i>AIS_2459</i> 5' qRT-PCR primer
LEJ_319	tcagaacgctgtttgacca	<i>AIS_2459</i> 3' qRT-PCR primer
LEJ_330	acggtggttctggtaaacagg	<i>AIS_2531</i> 5' qRT-PCR primer
LEJ_331	tctgccagtctgttgaagc	<i>AIS_2531</i> 3' qRT-PCR primer
LEJ_46	CGAATTTGGGTACGCCTGAGA	<i>AIS_3382</i> 5' qRT-PCR primer
LEJ_47	GCCTTGTTGAGAACGCCAGT	<i>AIS_3382</i> 3' qRT-PCR primer
Pgro-172	TGAGCTTTTTAGCTCGACTAAT CCAT	Primer internal to transposon T26 in AB5075 Tn library
ERG19	tgatgggttaaaaaggatcgatcctctagAAA TTGGGAATGCTCATG	Primer 1 kb 5' to start codon of <i>oxyR</i> in AB5075; used to confirm Tn insertion site
ERG24	ttccgaagttctattctctaggggatcCAGC AAGGACTCCTTAATTATTAC	Primer 1 kb 3' to stop codon of <i>oxyR</i> in AB5075; used to confirm Tn insertion site

Supplemental Table 2: Genes with decreased expression in WT *A. baumannii* following treatment with hydrogen peroxide.

Locus	Annotation (KEGG)	Fold change
<i>Amino acid transport and metabolism</i>		
<i>AIS_1349</i>	K02614 acyl-CoA thioesterase	-51.5
<i>AIS_1702</i>	K00382 dihydrolipoamide dehydrogenase	-42.3
<i>AIS_1345</i>	K01912 phenylacetate-CoA ligase	-29.5
<i>AIS_1732</i>	K01028 3-oxoacid CoA-transferase subunit A	-26.5
<i>AIS_1344</i>	Thiolase	-23.2
<i>AIS_2449</i>	K11734 aromatic amino acid transport protein AroP	-22.4
<i>AIS_0103</i>	K00020 3-hydroxyisobutyrate dehydrogenase	-22.0
<i>AIS_1346</i>	K01912 phenylacetate-CoA ligase	-19.6
<i>AIS_1343</i>	K00074 3-hydroxybutyryl-CoA dehydrogenase	-18.4
<i>AIS_1335</i>	K02618 oxepin-CoA hydrolase	-18.2
<i>AIS_1376</i>	K00253 isovaleryl-CoA dehydrogenase	-16.7
<i>AIS_1342</i>	K15866 2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	-15.2
<i>AIS_1340</i>	K02613 ring-1,2-phenylacetyl-CoA epoxidase subunit PaaE	-12.9
<i>AIS_1731</i>	K01029 3-oxoacid CoA-transferase subunit B	-12.6
<i>AIS_1348</i>	K02617 phenylacetic acid degradation protein	-12.1
<i>AIS_1341</i>	K15866 2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	-11.5
<i>AIS_1338</i>	K02611 ring-1,2-phenylacetyl-CoA epoxidase subunit PaaC	-11.4
<i>AIS_1375</i>	K01969 3-methylcrotonyl-CoA carboxylase beta subunit	-11.3
<i>AIS_1337</i>	K02610 ring-1,2-phenylacetyl-CoA epoxidase subunit PaaB	-10.5
<i>AIS_1347</i>	K02616 phenylacetic acid degradation operon negative regulatory protein	-9.5
<i>AIS_3418</i>	K00457 4-hydroxyphenylpyruvate dioxygenase	-9.4
<i>AIS_1339</i>	K02612 ring-1,2-phenylacetyl-CoA epoxidase subunit PaaD	-9.3
<i>AIS_1373</i>	K01968 3-methylcrotonyl-CoA carboxylase alpha subunit	-8.9
<i>AIS_1372</i>	K01640 hydroxymethylglutaryl-CoA lyase	-8.9
<i>AIS_3413</i>	K11734 aromatic amino acid transport protein AroP	-8.3
<i>AIS_1336</i>	K02609 ring-1,2-phenylacetyl-CoA epoxidase subunit PaaA	-8.0
<i>AIS_2353</i>	K03305 proton-dependent oligopeptide transporter, POT family	-7.1
<i>AIS_1089</i>	K00130 betaine-aldehyde dehydrogenase	-6.8
<i>AIS_3129</i>	K01484 succinylarginine dihydrolase	-6.8
<i>AIS_3130</i>	K06447 succinylglutamic semialdehyde dehydrogenase	-6.6
<i>AIS_3414</i>	K01555 fumarylacetoacetase	-6.5
<i>AIS_3415</i>	K01800 maleylacetoacetate isomerase	-6.2
<i>AIS_1466</i>	K05597 glutamin-(asparagin-)ase	-6.2
<i>AIS_1491</i>	K10003 glutamate/aspartate transport system permease protein	-6.1
<i>AIS_3131</i>	K00673 arginine N-succinyltransferase	-6.0
<i>AIS_3402</i>	K01479 formiminoglutamase	-5.7
<i>AIS_3404</i>	K16234 histidine transporter	-5.6
<i>AIS_3132</i>	K00840 succinylornithine aminotransferase	-5.5
<i>AIS_0098</i>	K11737 D-serine/D-alanine/glycine transporter	-5.4

<i>AIS_3128</i>	K05526 succinylglutamate desuccinylase	-5.3
<i>AIS_1467</i>	putative glutamate symport transmembrane protein	-5.3
<i>AIS_1492</i>	K10002 glutamate/aspartate transport system permease protein	-5.3
<i>AIS_1093</i>	K00673 arginine N-succinyltransferase	-5.0
<i>AIS_1493</i>	K10004 glutamate/aspartate transport system ATP-binding protein	-5.0
<i>AIS_1882</i>	K09483 3-dehydroshikimate dehydratase	-4.8
<i>AIS_3403</i>	K01468 imidazolonepropionase	-4.8
<i>AIS_0099</i>	K11737 D-serine/D-alanine/glycine transporter	-4.6
<i>AIS_1094</i>	K11737 D-serine/D-alanine/glycine transporter	-4.5
<i>AIS_3405</i>	K01745 histidine ammonia-lyase	-4.3
<i>Ribosomal</i>		
<i>AIS_1379</i>	K15256 tRNA (cmo5U34)-methyltransferase	-11.0
<i>AIS_3078</i>	K02892 large subunit ribosomal protein L23	-5.9
<i>AIS_3075</i>	K02982 small subunit ribosomal protein S3	-5.6
<i>AIS_3079</i>	K02926 large subunit ribosomal protein L4	-5.6
<i>AIS_3076</i>	K02890 large subunit ribosomal protein L22	-5.3
<i>AIS_3077</i>	K02886 large subunit ribosomal protein L2	-5.1
<i>AIS_3080</i>	K02906 large subunit ribosomal protein L3	-4.9
<i>AIS_3074</i>	K02878 large subunit ribosomal protein L16	-4.7
<i>AIS_3081</i>	K02946 small subunit ribosomal protein S10	-4.6
<i>AIS_3063</i>	K02907 large subunit ribosomal protein L30	-4.5
<i>AIS_3072</i>	K02961 small subunit ribosomal protein S17	-4.2
<i>AIS_3073</i>	K02904 large subunit ribosomal protein L29	-4.2
<i>Fatty acid metabolism</i>		
<i>AIS_0106</i>	K01692 enoyl-CoA hydratase	-29.0
<i>AIS_1698</i>	K03644 lipoyl synthase	-18.8
<i>AIS_0107</i>	putative enoyl-CoA hydratase/isomerase family protein	-18.6
<i>AIS_1730</i>	K02106 short-chain fatty acids transporter	-17.0
<i>AIS_1378</i>	K00666 fatty-acyl-CoA synthase	-12.9
<i>AIS_1729</i>	K00626 acetyl-CoA C-acetyltransferase	-11.3
<i>AIS_0591</i>	K00666 fatty-acyl-CoA synthase	-10.8
<i>AIS_2098</i>	K13954 alcohol dehydrogenase	-8.9
<i>AIS_0721</i>	K00252 glutaryl-CoA dehydrogenase	-4.4
<i>Transport</i>		
<i>AIS_1266</i>	<i>mumT</i>	-17.7
<i>AIS_0108</i>	major facilitator superfamily (MFS) metabolite/H ⁺ symporter	-13.9
<i>AIS_3300</i>	K14393 cation/acetate symporter	-9.5
<i>AIS_1257</i>	K08195 MFS transporter, AAHS family, 4-hydroxybenzoate transporter	-7.2
<i>AIS_1810</i>	putative tartrate transporter	-6.8
<i>AIS_1724</i>	dicarboxylic acid transporter PcaT	-6.1
<i>AIS_0485</i>	K03299 gluconate:H ⁺ symporter, GntP family	-5.7
<i>AIS_2196</i>	K11103 aerobic C4-dicarboxylate transport protein	-5.2
<i>AIS_3135</i>	K16235 S-methylmethionine transporter	-5.1

<i>AIS_1612</i>	K02034 peptide/nickel transport system permease protein	-4.9
<i>AIS_2773</i>	K06076 long-chain fatty acid transport protein	-4.5
<i>AIS_3283</i>	K11735 GABA permease	-4.1
<i>General metabolism</i>		
<i>AIS_1703</i>	dihydrolipoamide dehydrogenase	-96.6
<i>AIS_1700</i>	K21417 acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit beta	-96.3
<i>AIS_1699</i>	K21416 acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit alpha	-93.4
<i>AIS_1701</i>	K00627 pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	-55.1
<i>AIS_2150</i>	putative oxidoreductase short-chain dehydrogenase/reductase family	-39.2
<i>AIS_2148</i>	K01895 acetyl-CoA synthetase	-31.1
<i>AIS_0104</i>	K01895 acetyl-CoA synthetase	-29.8
<i>AIS_1704</i>	K03366 meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	-24.8
<i>AIS_0105</i>	putative acyl-CoA dehydrogenase	-22.3
<i>AIS_2149</i>	putative acyl CoA dehydrogenase oxidoreductase protein	-21.9
<i>AIS_1269</i>	<i>mumH</i>	-14.9
<i>AIS_1268</i>	<i>mumU</i>	-14.5
<i>AIS_1854</i>	K00276 Cu ²⁺ -containing amine oxidase	-14.1
<i>AIS_2450</i>	putative pyruvate decarboxylase	-12.4
<i>AIS_1267</i>	<i>mumL</i>	-11.7
<i>AIS_1270</i>	<i>mumC</i>	-10.3
<i>AIS_2102</i>	K00138 aldehyde dehydrogenase	-8.8
<i>AIS_0076</i>	K20455 2-methylcitrate dehydratase (2-methyl-trans-aconitate forming)	-8.7
<i>AIS_1374</i>	3-methylglutaconyl-CoA hydratase	-8.7
<i>AIS_1705</i>	K00004 (R,R)-butanediol dehydrogenase / meso-butanediol dehydrogenase / diacetyl reductase	-7.6
<i>AIS_0073</i>	K03417 methylisocitrate lyase	-6.7
<i>AIS_0486</i>	K00851 gluconokinase	-6.5
<i>AIS_1886</i>	K01607 4-carboxymuconolactone decarboxylase	-6.0
<i>AIS_1864</i>	Acyl-CoA dehydrogenase-like protein	-5.3
<i>AIS_1091</i>	succinylornithine transaminase (carbon starvation protein C)	-5.0
<i>AIS_0481</i>	K13788 phosphate acetyltransferase	-4.9
<i>AIS_1885</i>	K00449 protocatechuate 3,4-dioxygenase, beta subunit	-4.8
<i>AIS_0058</i>	Glycosyltransferase	-4.7
<i>AIS_1737</i>	K00019 3-hydroxybutyrate dehydrogenase	-4.4
<i>AIS_0910</i>	K00681 gamma-glutamyltranspeptidase / glutathione hydrolase	-4.2
<i>AIS_0855</i>	dioxygenase beta subunit	-4.2
<i>AIS_1092</i>	succinylornithine transaminase (carbon starvation protein C)	-4.2
<i>Hypothetical</i>		
<i>AIS_3809</i>	hypothetical protein	-24.6

<i>AIS_3790</i>	hypothetical protein	-11.0
<i>AIS_3541</i>	hypothetical protein	-8.6
<i>AIS_3540</i>	hypothetical protein	-7.0
<i>AIS_3542</i>	hypothetical protein	-6.0
<i>AIS_1853</i>	hypothetical protein	-5.7
<i>AIS_1808</i>	hypothetical protein	-5.7
<i>AIS_2348</i>	hypothetical protein	-5.5
<i>AIS_3546</i>	hypothetical protein	-5.2
<i>AIS_1367</i>	hypothetical protein	-5.0
<i>AIS_3539</i>	hypothetical protein	-4.8
<i>AIS_3741</i>	hypothetical protein	-4.8
<i>AIS_0526</i>	hypothetical protein	-4.6
<i>AIS_1841</i>	hypothetical protein	-4.5
<i>AIS_3552</i>	hypothetical protein	-4.5
<i>AIS_3010</i>	hypothetical protein	-4.3
<i>AIS_1863</i>	hypothetical protein	-4.3
<i>AIS_2041</i>	hypothetical protein	-4.1
<i>AIS_1862</i>	hypothetical protein	-4.1
<i>AIS_3535</i>	hypothetical protein	-4.0
<i>Other</i>		
<i>AIS_1380</i>	putative protein (DcaP-like)	-22.5
<i>AIS_0891</i>	K07216 hemerythrin	-19.3
<i>AIS_3122</i>	putative membrane protein	-16.9
<i>AIS_0292</i>	K07275 outer membrane protein (GenBank) putative outer membrane protein W	-16.8
<i>AIS_3416</i>	Glyoxalase/bleomycin resistance protein/dioxygenase	-9.0
<i>AIS_1736</i>	putative membrane protein	-8.3
<i>AIS_3301</i>	putative membrane protein	-8.3
<i>AIS_0645</i>	K12213 intracellular multiplication protein IcmK	-6.0
<i>AIS_2296</i>	K08303 putative protease	-5.9
<i>AIS_0644</i>	K12204 defect in organelle trafficking protein DotC	-5.0
<i>AIS_1377</i>	transcriptional regulator acrR family	-4.6
<i>AIS_0646</i>	K12206 intracellular multiplication protein IcmB	-4.4
<i>AIS_3792</i>	K11937 biofilm PGA synthesis protein PgaD	-4.2
<i>AIS_0642</i>	K18640 plasmid segregation protein ParM	-4.2
<i>AIS_1505</i>	<i>yyaM</i>	-4.2
<i>AIS_0482</i>	K00925 acetate kinase	-4.1
<i>AIS_0201</i>	putative outer membrane protein	-4.1

Supplemental Table 3: Genes with decreased expression in $\Delta oxyR$ strain following treatment with H_2O_2 .

Locus	Annotation (KEGG)	Fold change
<i>Amino acid transport and metabolism</i>		
<i>AIS 1344</i>	Thiolase	-10.9
<i>AIS 1345</i>	K01912 phenylacetate-CoA ligase	-10.0
<i>AIS 1343</i>	K00074 3-hydroxybutyryl-CoA dehydrogenase	-9.9
<i>AIS 1346</i>	K01912 phenylacetate-CoA ligase	-8.9
<i>AIS 1342</i>	K15866 2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	-6.9
<i>AIS 1341</i>	Enoyl-CoA hydratase/carnithine racemase	-6.8
<i>AIS 1349</i>	K02614 acyl-CoA thioesterase	-6.8
<i>AIS 1941</i>	branched chain amino acid transporter	-6.7
<i>AIS 0103</i>	K00020 3-hydroxyisobutyrate dehydrogenase	-5.4
<i>AIS 2192</i>	K02071 D-methionine transport system ATP-binding protein	-5.2
<i>AIS 1340</i>	K02613 ring-1,2-phenylacetyl-CoA epoxidase subunit PaaE	-5.0
<i>AIS 1347</i>	K02616 phenylacetic acid degradation operon negative regulatory protein	-4.9
<i>AIS 2793</i>	K03310 alanine or glycine:cation symporter, AGCS family	-4.9
<i>AIS 2193</i>	K02072 D-methionine transport system permease protein	-4.5
<i>AIS 2449</i>	K11734 aromatic amino acid transport protein AroP	-4.2
<i>AIS 1335</i>	K02618 oxepin-CoA hydrolase / 3-oxo-5,6-dehydrosuberil-CoA semialdehyde dehydrogenase	-4.1
<i>AIS 0429</i>	K11102 proton glutamate symport protein	-4.0
<i>Ribosomal</i>		
<i>AIS 2171</i>	K02990 small subunit ribosomal protein S6	-6.1
<i>AIS 2172</i>	K02963 small subunit ribosomal protein S18	-6.0
<i>AIS 3081</i>	K02946 small subunit ribosomal protein S10	-5.9
<i>AIS 2173</i>	K02939 large subunit ribosomal protein L9	-5.1
<i>AIS 3080</i>	K02906 large subunit ribosomal protein L3	-4.9
<i>AIS 3079</i>	K02926 large subunit ribosomal protein L4	-4.3
<i>Fatty acid metabolism</i>		
<i>AIS 0104</i>	K01895 acetyl-CoA synthetase	-7.3
<i>AIS 1730</i>	K02106 short-chain fatty acids transporter	-4.5
<i>AIS 1729</i>	K00626 acetyl-CoA C-acetyltransferase	-4.4
<i>Transport</i>		
<i>AIS 0108</i>	major facilitator superfamily (MFS) metabolite/H ⁺ symporter	-4.4
<i>General metabolism</i>		
<i>AIS 0105</i>	putative acyl-CoA dehydrogenase	-4.7
<i>AIS 1925</i>	K00426 cytochrome d ubiquinol oxidase subunit II	-4.3
<i>Hypothetical</i>		
<i>AIS 3873</i>	hypothetical protein	-19.0
<i>AIS 3867</i>	hypothetical protein	-6.5
<i>AIS 3546</i>	hypothetical protein	-5.9

<i>AIS_2982</i>	hypothetical protein	-4.5
<i>AIS_3809</i>	hypothetical protein	-4.5
<i>AIS_3908</i>	hypothetical protein	-4.2
<i>AIS_3540</i>	hypothetical protein	-4.1
<i>AIS_3535</i>	hypothetical protein	-4.1
<i>AIS_1736</i>	hypothetical protein	-4.1
<i>AIS_3541</i>	hypothetical protein	-4.0
<i>AIS_3907</i>	hypothetical protein	-4.0
<i>Other</i>		
<i>AIS_0992</i>	<i>oxyR</i>	-8.0
<i>AIS_1380</i>	putative protein (DcaP-like)	-4.8
<i>AIS_2216</i>	<i>csuB</i>	-4.7
<i>AIS_0646</i>	K12206 intracellular multiplication protein IcmB	-4.5
<i>AIS_0644</i>	K12204 defect in organelle trafficking protein DotC	-4.4
<i>AIS_2959</i>	K03687 molecular chaperone GrpE	-4.0

Supplemental Table 4. Locus tags for *oxyR* genes in sequenced *A. baumannii* strains.

Strain Name	Locus tag
ATCC 17978	<i>AIS_0992</i>
AB5075 UW	<i>ABUW_2905</i>
AB0057	<i>AB57_1071</i>
AB307-0294	<i>ABBFA_002618</i>
AYE	<i>ABAYE2801</i>
MDR-ZJ06	<i>ABZJ_01096</i>
ACICU	<i>ACICU_00953</i>
TCDC-AB0715	<i>ABTW07_1082</i>
1656-2	<i>ABK1_0978</i>
ATCC 19606	<i>HMPREF0010_01528</i>
SDF	<i>ABSDF2402</i>
D1279779	<i>ABD1_09450</i>
MDR-TJ	<i>ABTJ_02819</i>
TYTH_1	<i>M3Q_1290</i>

Supplemental Table 5: Genes with decreased expression in the $\Delta oxyR$ strain in LB

Locus	Annotation (KEGG)	Fold change
<i>Peroxide detoxification</i>		
<i>AIS 0992</i>	OxyR	-361.0
<i>Iron homeostasis</i>		
<i>AIS 0474</i>	catecholate siderophore receptor	-14.5
<i>AIS 1921</i>	catecholate siderophore receptor	-5.7
<i>Metabolism (other)</i>		
<i>AIS 1854</i>	Cu ²⁺ -containing amine oxidase	-8.8
<i>AIS 0971</i>	5-methyltetrahydrofolate--homocysteine methyltransferase	-8.5
<i>AIS 1703</i>	dihydrolipoamide dehydrogenase	-4.2
<i>Other</i>		
<i>AIS 1591</i>	phage major capsid protein HK97	-11.9
<i>AIS 3297</i>	putative outer membrane protein	-9.0
<i>AIS 2988</i>	putative membrane protein	-7.1
<i>AIS 1590</i>	peptidase U35 phage prohead HK97	-6.4
<i>AIS 1588</i>	Phage terminase-like protein large subunit	-6.0
<i>AIS 0891</i>	hemerythrin	-4.3
<i>Hypothetical</i>		
<i>AIS 3693</i>	hypothetical protein	-15.6
<i>AIS 1853</i>	hypothetical protein	-10.7
<i>AIS 3696</i>	hypothetical protein	-7.7
<i>AIS 0736</i>	hypothetical protein	-7.4
<i>AIS 3704</i>	hypothetical protein	-5.8
<i>AIS 3510</i>	hypothetical protein	-5.8
<i>AIS 3699</i>	hypothetical protein	-5.7
<i>AIS 3718</i>	hypothetical protein	-5.4
<i>AIS 3694</i>	hypothetical protein	-4.8
<i>AIS 3695</i>	hypothetical protein	-4.4