Table S1. Whole-genome location analysis of OxyR in *Pseudomonas aeruginosa* (Cutoff > 0.5)

		ChIP-chip			Binding motif			
PA no. [a]	**Gene [a]**	**Max. Enrich.**	**Distance to ATG**	**Genes affected**	**Conserved motif [b]**	**Distance to ATG [b]**	**PMW score [b]**	**Gene product [a]**
PA0139	*ahpC*	1.72	171	1	ATAGATTTAGATAAT	101	7.71	Alkyl hydroperoxide reductase subunit C
PA0140	*ahpF*	1.72	127	1				Alkyl hydroperoxide reductase subunit F
PA0848	*ahpB*	0.83	-51	1	ATAGGCTGACTCTAT	117	9.21	Probable alkyl hydroperoxide reductase
PA4236	*katA*	1.61	260	2	ATTGATCTCGCTTAT	116	7.35	Catalase
PA4613	*katB*	0.53	30	2	ATTGATATTCCTAAT	97	7.26	Catalase
PA5344	*oxyR*	0.92	6	1				OxyR
PA5345	*recG*	1.59	738	1				ATP-dependent DNA helicase RecG
PA0291	*oprE*	0.63	36	1	ATTGGTATTGCTAAT	14	7.29	Anaerobically-induced outer membrane porin OprE precursor
PA0962	*dps*	1.02	107	1	ATAGGGAGAATCTAT	107	7.66	probable dna-binding stress protein
PA1289		0.64	119	1	AAAGCTGGAAACAAT	136	6.70	Hypothetical protein
PA1317	*cyoA*	0.95	304	5				Cytochrome o ubiquinol oxidase subunit II
PA2146		1.04	287	1	ATCTTTGAACCCTAT	153	7.02	Conserved hypothetical protein
PA2821		0.55	7	1	ATGAGCCTGGGTTAT	20	6.44	Probable glutathione S-transferase
PA3237		0.65	103	1	ATCGAAGCGCTCTAT	93	6.90	Hypothetical protein
PA5240	*trxA*	0.78	193	1	ATAGAGACTCTCAAT	88	7.25	Thioredoxin
PA5436		0.87	-1	2	ATAATTATTGATTTT	122	6.52	Probable biotin carboxylase subunit of a transcarboxylase
PA3450		0.52	6	1	ATAAATTCAGATTTT	62	6.60	Probable antioxidant protein
PA5319	*radC*	0.98	89	1				DNA repair protein RadC
PA1003	*mvfR*	0.74	304	1	ATATTTACCGGTTAT	364	7.20	Transcriptional regulator MvfR
PA1159		0.54	40	1	ATGGCGGCTAGCTAT	290	6.96	Probable cold-shock protein
PA1380		0.65	-12	1				Probable transcriptional regulator
PA2050		1.27	202	2	AAAAAGAATATTAAT	171	6.26	Probable sigma-70 factor. ECF subfamily

PA2054	*cynR*	1.07	13	1	ATTGGTCTGGTCTAT	15	7.36	Transcriptional regulator CynR
PA2258	*ptxR*	0.61	261	1	ATGGTTTGCAATTAT	354	7.35	Transcriptional regulator PtxR
PA2259	*ptxS*	0.61	302	5	ATGGTTTGCAATTAT	195	7.35	Transcriptional regulator PtxS
PA2359		0.54	82	1	AATTTTTTAATCTAT	49	6.64	Probable transcriptional regulator
PA2426	*pvdS*	0.71	272	1	ATTGACAATCATTAT	85	7.19	Sigma factor PvdS
PA2738	*himA*	0.76	16	1				Integration host factor. alpha subunit
PA3135		1.22	-1	2	AAGTGTAGCGCCTAT	31	6.09	Probable transcriptional regulator
PA4902		0.66	-12	1	ATAGAACTGGTCTAT	1	7.38	Probable transcriptional regulator
PA5029		0.64	43	2	ATAGGTTTATATGAT	58	7.13	Probable transcriptional regulator
PA5437		0.87	215	1	ATAATTATTGATTTT	78	6.52	Probable transcriptional regulator
PA0717		1.23	306	3	ATAGAGCAAGACTAT	352	7.59	Hypothetical protein of bacteriophage Pf1
PA0984		0.52	14	1	ATTTCTAACAACGAT	70	6.71	colicin immunity protein
PA1249	*aprA*	0.57	264	1	AACGGTTTTTATAAT	225	6.25	Alkaline metalloproteinase precursor
PA1423	*bdlA*	0.77	228	1	ATATTTCCGACGAAT	213	6.81	BdlA
PA2425	*pvdG*	0.71	260	2	ATCGCTATCGCCGAT	255	6.80	PvdG
PA3064	*pelA*	0.65	298	7				PelA
PA5241	*ppx*	0.78	-9	1	ATAGAGACTCTCAAT	82	7.25	Exopolyphosphatase
PA0714.1	*phrD*	0.60		1				PhrD RNA
PA0976.1		0.88		1				tRNA-Lys
PA1030.1		0.79		1				
PA3621.1	*rsmZ*	0.57		1				Regulatory RNA RsmZ
PA4406.1		1.27		1				sRNA
PA4581.1		0.55		1				tRNA-Arg
PA0185		0.83	141	3	ATTTTTATTATTTAT	170	7.35	Probable permease of ABC transporter
PA0186		0.83	126	1	ATTTTTATTATTTAT	83	7.35	Probable binding protein component of ABC transporter
PA0195	*pntAA*	1.17	289	1	ATTAAAAACATTAAT	354	6.81	Putative NAD(P) transhydrogenase. subunit alpha part 1
PA0326		0.59	103	4	ATAGATGCGGCCAAT	111	7.37	Probable ATP-binding

								component of ABC transporter
PA0584	*cca*	0.62	23	1				tRNA nucleotidyl transferase
PA0903	*alaS*	1.42	106	1	ATAGTTATTGCCTAT	92	7.77	Alanyl-tRNA synthetase
PA0945	*purM*	0.56	5	3				phosphoribosylaminoimidazole synthetase
PA0963	*aspS*	1.02	304	2	ATAGGGAGAATCTAT	319	7.66	aspartyl-tRNA synthetase
PA1004	*nadA*	0.74	297	1	ATATTTACCGGTTAT	370	7.20	Quinolinate synthetase A
PA1054		1.48	271	6	ATAGATTGCGATAAT	138	7.45	Probable NADH dehydrogenase
PA1073	*braD*	0.63	108	4				Branched-chain amino acid transport protein BraD
PA1493	*cysP*	0.68	123	1	ATAACGTCGGGTTAT	38	6.74	Sulfate-binding protein of ABC transporter
PA1507		0.54	218	1	ATCGATTTTTTGTAT	152	7.13	Probable transporter
PA1541		1.20	308	2	ATCGATTGGCTTTTT	237	6.36	Probable drug efflux transporter
PA2015	*liuA*	0.52	6	5				Putative isovaleryl-CoA dehydrogenase
PA2042		0.52	302	1				Probable transporter (membrane subunit)
PA2053	*cynT*	1.07	102	2	ATTGGTCTGGTCTAT	86	7.36	Carbonate dehydratase
PA2165		0.64	130	6	ATTGATATTTGCAAT	223	7.30	Probable glycogen synthase
PA2975	*rluC*	0.65	-2	3	ATTGAAGCACTTAAT	28	6.94	Ribosomal large subunit pseudouridine synthase C
PA3000	*aroP1*	0.65	101	1				Aromatic amino acid transport protein AroP1
PA3032	*snr1*	1.34	282	2	ATAGACTCAGGCTAT	201	7.53	Cytochrome c Snr1
PA3136		1.22	71	2	AAGTGTAGCGCCTAT	25	6.09	Probable secretion protein
PA3236		0.65	191	1	ATCGAAGCGCTCTAT	187	6.90	Probable glycine betaine-binding protein precursor
PA3452	*mqoA*	0.55	150	1	ATAAGTTCGGTGAAT	341	8.34	Malate:quinone oxidoreductase
PA3768		0.62	108	2	AATGAGAAAATCTAT	38	6.78	Probable metallo-oxidoreductase
PA4251	*rplE*	0.56	12	2				50S ribosomal protein L5
PA4267	*rpsG*	0.60	0	3	ATATAAAAACGCTAT	86	7.16	30S ribosomal protein S7

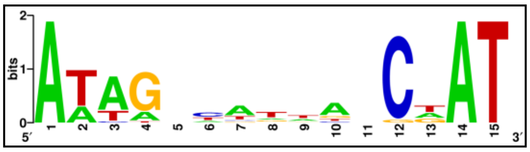
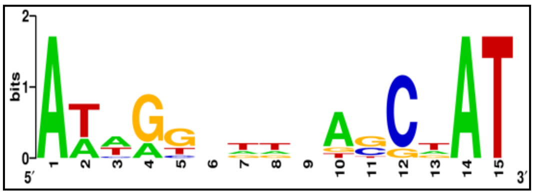
PA4268	*rpsL*	1.23	76	1	ATAGCTCCACTGATT	3	6.17	30S ribosomal protein S12
PA4406	*lpxC*	1.27	123	1	ACTGTTTTCAACAAT	30	6.50	UDP-3-O-acyl-N-acetylglucosamine deacetylase
PA4524	*nadC*	0.59	21	1	ATCTCTATAATGAAT	157	6.87	Nicotinate-nucleotide pyrophosphorylase
PA4614	*mscL*	0.53	117	1	ATTTCTTTTTACGAT	391	6.54	Conductance mechanosensitive channel
PA4901	*mdlC*	0.66	113	1	ATAGAACTGGTCTAT	86	7.38	Benzoylformate decarboxylase
PA5030		0.64	133	1	ATAGGTTTATATGAT	104	7.13	Probable major facilitator superfamily (MFS) transporter
PA5170	*arcD*	0.60	256	4	ATCGTTGATGCCGAT	265	6.87	Arginine/ornithine antiporter
PA5291		1.36	103	1	ATCGTGATAGCTAAT	64	7.12	Probable choline transporter
PA5320	*coaC*	0.98	51	2				Phosphopantothenoyl cysteine synthase/(R)-4'-phospho-N-pantothenoylcysteine decarboxylase
PA5370		0.53	16	1	ATTGTTCTCTTTATT	7	6.18	Probable major facilitator superfamily (MFS) transporter
PA5312		0.66	2	1				Probable aldehyde dehydrogenase
PA0049		0.69	312	1	ATAGGAAAAGTTGAT	364	7.02	Hypothetical protein
PA0050		0.69	236	1	ATAGGAAAAGTTGAT	232	7.02	Hypothetical protein
PA0197		0.56	191	3	AATTATTTTTGTTAT	106	6.20	Hypothetical protein
PA0327		0.59	225	1	ATAGATGCGGCCAAT	203	7.37	Hypothetical protein
PA0716		0.83	-2	1	ATAAACTACGTAAAT	93	8.43	Hypothetical protein
PA0776		0.68	79	1				Hypothetical protein
PA0861		0.53	295	2	ATTGCCGCAGCCAAT	220	6.94	Hypothetical protein
PA0938		1.27	16	1	ATCATCGGTAGTTAT	96	6.67	Hypothetical protein
PA0939		0.53	9	1				Hypothetical protein
PA0946		0.56	209	1				hypothetical protein
PA0990		0.52	164	1				conserved hypothetical protein
PA0991		0.52	301	1	AGAGGCGGAGGCAAT	134	6.25	hypothetical protein
PA1198		0.67	76	2	ATTTGCCTTCTCGAT	33	6.23	Conserved hypothetical protein
PA1383		0.58	293	1	ATGGCTTTATATAAT	200	7.09	Hypothetical protein
PA1424		0.77	68	1	ATATTTCCGACGAAT	69	6.81	Hypothetical protein
PA1656		0.86	296	4	AGCTCTTCAGACTAT	85	6.26	Hypothetical protein
PA2044		1.25	101	1	ATTGATAAAACCTAT	95	7.84	Hypothetical protein
PA2145		1.04	8	1	ATAGACCCATTCAAT	38	7.23	Hypothetical protein

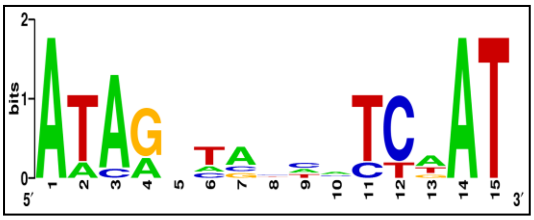
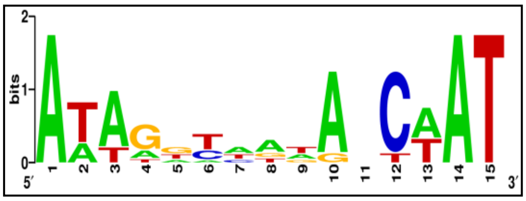
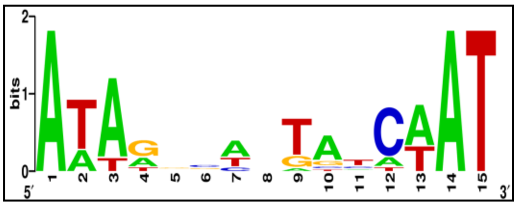
PA2166		0.64	238	1	ATTGATATTTGCAAT	131	7.30	Hypothetical protein
PA2228		0.72	5	3	ATAGATTCAGTCTTT	363	7.04	Hypothetical protein
PA2229		0.72	291	2	ATAGAGAGTACTAAT	371	7.37	Conserved hypothetical protein
PA2594		0.58	122	1	ATAGATTATTTGAAT	69	7.22	Conserved hypothetical protein
PA2595		1.13	8	1				Conserved hypothetical protein
PA2610		0.70	79	1	ATCGATCTGATCGAT	83	8.55	Conserved hypothetical protein
PA2935		0.56	85	1	ATCAAACGTATTTAT	41	6.83	Hypothetical protein
PA2936		0.56	25	1	ATCAAACGTATTTAT	55	6.83	Hypothetical protein
PA3261		0.75	-7	1				Hypothetical protein
PA3286		0.57	215	2				Hypothetical protein
PA3287		0.57	285	1				Conserved hypothetical protein
PA3340		0.72	196	1	ATGGCTTTTTGCTAT	119	7.14	Hypothetical protein
PA3446		0.59	46	1	ATAAAAAACATTTAT	89	7.16	Conserved hypothetical protein
PA3483		0.79	3	1				Hypothetical protein
PA4523		0.59	265	1	ATCTCTATAATGAAT	115	6.87	Hypothetical protein
PA5180		0.61	35	2	ATCGACGTGATCTAT	83	7.19	Conserved hypothetical protein
PA5205		0.52	74	1	TTTGAAAAAAACTAT	95	6.35	Conserved hypothetical protein
PA5545		0.60	28	1				Conserved hypothetical protein
PA5546		0.79	204	1	ATAGCAAAACTCTAT	48	7.39	Conserved hypothetical protein
PA5547		0.79	34	1	ATAGCAAAACTCTAT	176	7.39	Conserved hypothetical protein

Table S2. EMSA analyses of partial OxyR regulon in *P. aeruginosa*

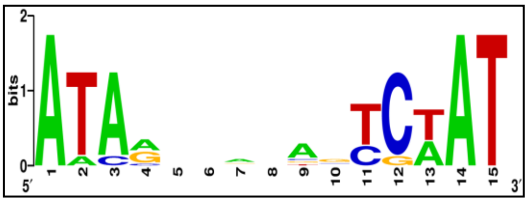
PA no.	**Gene**	**Gene product**	**EMSA**	**Upstream DNA motif**
Positive control				
PA0139	*ahpC*	Alkyl hydroperoxide reductase subunit C	**+**	ATAGATTTAGATAAT
Negative control				
PA4764	*fur*	Ferric uptake reglation protein	**-**	-
Tested targets				
PA0717	*pf4*	Hypothetical protein of bacteriophage Pf1	**++**	ATAGAGCAAGACTAT
PA0938		Hypothetical protein	**+**	ATCATCGGTAGTTAT
PA0962	*dps*	probable DNA-binding stress protein	**++**	ATAGGGAGAATCTAT
PA1003	*mvfR*	Transcriptional regulator MvfR	**-**	ATATTTACCGGTTAT
PA1423	*bdlA*	BdlA	**++**	ATATTTCCGACGAAT
PA1431	*rsaL*	RsaL	**+**	ATTTCATAATTTTAT
PA1541		Probable drug efflux transporter	**+**	ATCGATTGGCTTTTT
PA2145		Hypothetical protein	**+**	ATAGACCCATTCAAT
PA2426	*pvdS*	Sigma factor PvdS	**++**	ATTGACAATCATTAT
PA2738	*himA*	Integration host factor, alpha subunit	**-**	-
PA3032	*snr1*	Cytochrome *c* Snr1	**++**	ATAGACTCAGGCTAT
PA4268	*rpsL*	30S ribosomal protein S12	**+**	ATAGCTCCACTGATT
PA4406	*lpxC*	UDP-3-O-acyl-N-acetylglucosamine deacetylase	**++**	ACTGTTTTCAACAAT
PA4406.1		sRNA	**++**	ATTGTTGAAAACAGT
PA5240	*trxA*	Thioredoxin	**++**	ATAGAGACTCTCAAT
PA5319	*radC*	DNA repair protein RadC	**-**	-
PA5344	*oxyR*	OxyR	**-**	-
PA5345	*recG*	ATP-dependent DNA helicase RecG	**-**	-

Table S3. Potential OxyR binding sites in other bacteria on the basis of OxyR motif in *P. aeruginosa*

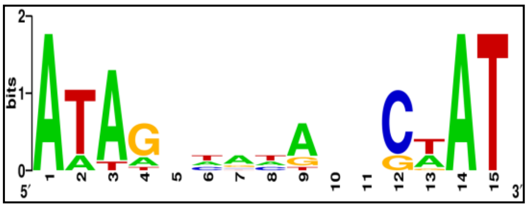
Bacterial species [a]	Gene [a]	Motif [a]	PWM Score [a]	Conserved motif [b]
***1. Bacillus subtilis* strain 168**	***katA***	AATAGTTATCTCTAT	7.95	
	trxA	AATGGGAGATGCTAT	8.06	
	alsS	ATAAGGCGAATCGAT	8.63	
	alsR	ATAAGGCGAATCGAT	8.63	
	katX	AAAGGAGAGGTCGAT	8.48	
	ahpC	ATAGCTAGAAACAAT	8.85	
***2. Escherichia coli* K12**	*cyoA*	ATTGGTATAACCAAT	8.5	
	hemH	AAAGGCCGAATGAAT	8.04	
	dsbG	AAAGGCATAACCTAT	8.76	
	ahpC	AAAGGCATAACCTAT	8.76	
	fur	ATTGGCATTATCTAT	8.86	
	dps	ATTGTTCTTATCAAT	8.73	
	grxA	ATAGCTTTTAGCAAT	8.84	
	trxB	ATCGGCAGCATCGAT	8.32	
	fhuF	ATAGGTTTACCCGAT	8.7	
	rpsL	AAAACCAGGAGCTAT	8.22	
	trxA	ATATCAGCTTACTAT	8.18	
	sodA	ATAATCATTTTCAAT	8.66	
	oxyR	ATAGCAATGAACGAT	8.65	
	trxC	AAAGCCTGCGACTAT	8.34	
	ansP	AATGGTGATAACTAT	8.18	
	ybaL	ATAGTTTATGACAAT	8.67	
	yhjA	ATAGGCACAGGCTAT	8.82	
	sufA	ATAGTCATTTTCAAT	8.93	
	flu	ATAGAATAAAACGAT	8.79	
	elbA	ATAAATATGCTCGAT	8.57	
	ydeK	AATAAGAATAACTAT	7.95	
	yceA	ATAGCAATTATCGAT	9.03	
***3. Erwinia carotovora* ATCC BAA-672**	*fur*	AAAGGTTTTACCTAT	8.72	
	katB	ATCAGGTTAAGCTAT	8.12	
	grxB	ATTGTTTGAATGTAT	8.08	
	grxA	ATTGGCTTAGCCAAT	8.33	
	dps	AAAAGAATTACCTAT	8.37	

	ahpF	AAAGTCGGGTGCAAT	8.08	
	ahpC	ATTGGTGATAGCGAT	8.25	
	oxyR	ATAGCTAACAGCGAT	8.62	
***4. Pseudomonas entomophila* L48**	***katA***	ATAGATATTTTCAAT	9.15	
	trxB	ATAGGCAGTCTCTAT	9.1	
	ahpC	ATAGCCAAAACCAAT	8.98	
	katG	ATCGATGCCATCGAT	8.39	
	katB	ATAAAAGTTACCAAT	8.84	
	cynT-1	AAAAGTCTCATTTAT	8.49	
	cynR	AAAAGTCTCATTTAT	8.49	
	alaS	ATAGAAACCGTCGAT	8.7	
	trxA	ATAGTTACACTCAAT	9.14	
	ppx	ATAGTTACACTCAAT	9.14	
***5. P. aeruginosa* PA7**	***ahpC***	ATTATCTAAATCTAT	9.23	
	oprE	ATTAGCAATACCAAT	8.41	
	katA	AAAGTTTTTATCTAT	9.48	
	cioA	ATATTATTTGTTTAT	8.51	
	cynR	ATAGGTAGAACCAAT	8.99	
	cynT	ATAGGTAGAACCAAT	8.99	
	rsaL	AAAGATCAGAGCAAT	8.5	
	lasI	AAAGATCAGAGCAAT	8.5	
	alaS	ATAGGCAATAACTAT	9.13	
***6. P. aeruginosa* PA14**	*oprE*	ATTAGCAATACCAAT	8.4	
	rpsG	ATAGCGTTTTTATAT	8.71	
	katA	AAAGTTTTTATCTAT	9.47	
	cioA	AAAAATATTATTTAT	8.98	
	snr1	ATAGGCTCAGGCTAT	8.72	
	ohr	AAATTAACGAACAAT	8.18	
	pvdS	ATAATGATTGTCAAT	9.05	
	cynR	ATAGGCCAGACCAAT	8.69	
	cynT	ATAGGCCAGACCAAT	8.69	
	alaS	ATAGGCAATAACTAT	9.13	
	katB	ATTAGGAATATCAAT	8.87	
	recN	AAATACTGTATAAAT	8.41	
	trxA	ATAGAGACTCTCAAT	9.08	

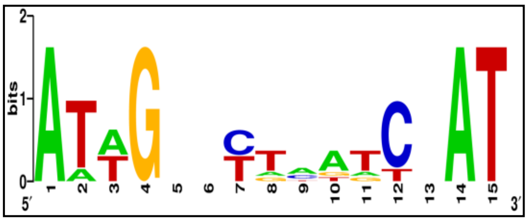
7. P. fluorescens **Pf5**	***katG***	ATCAAGCGGGTCTAT	8.19
	trxB	ATAGGCGGTCTCTAT	9
	cynR	ATAAGTACAGCCTAT	8.73
	ahpC	ATAGTCAAAACCAAT	8.99
	alaS	ATACAAACAGTCAAT	8.15
	cyoA	AAAAGTGTACTGTAT	8.24
	katA	ATAGAAATATCCAAT	8.65
	trxA	ATAGTTAGAGTCAAT	9.07
	oxyR	ATAACGTGCGTCTAT	8.83



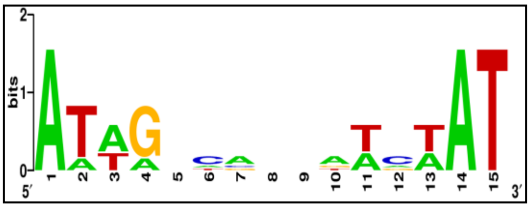
8. P. putida **KT2440**	*cynT*	AAAGATTCAGGCTAT	8.55
	oprE	ATAACCAAAAGGTAT	8.34
	katA	ATAGAAATAAACAAT	9.03
	trxB	ATAGGCGATGCCTAT	8.64
	ahpC	ATAGCCAAAACCAAT	8.96
	ptxS	ATATCAATGGCCTAT	8.24
	cioA	ATTGTTCTGTTCGAT	8.26
	recN	AAAAAAGTACTGTAT	8.16
	trx-2	ATAGTTACACTCAAT	9.11
	ppx	ATAGTTACACTCAAT	9.11



9. P. stutzeri **A1501**	***katE***	ATTGAGCAAATCCAT	8.17
	ppx	ATAGTCCTTGGCGAT	8.38
	katA	AAAGAACTAATTTAT	8.79
	lpxC	ATAGTTTTCAACAAT	8.89
	alaS	ATTGCTTGATTCAAT	8.55
	ahpC	ATTGCTTTCATCTAT	8.97

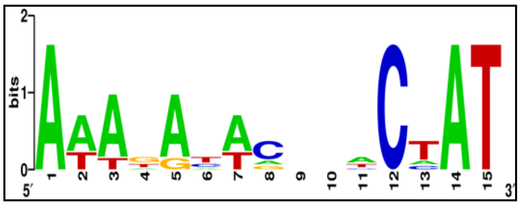


10. ***P. syringae pathovar tomato*** **DC3000**	***trx-1***	AATGCCGCCAACTAT	8.02
	trxB	ATAGGTCACTTCTAT	8.93
	cyoA	ATAGTCATTAAAAAT	8.27
	katB	ATTAAAAAAATGTAT	8.18
	trx-2	ATAGCCAGAGTCAAT	8.96



11. ***Salmonella typhimurium*** **LT2**	*cyoA*	ATTGGTATAACCAAT	8.5
	dsbG	AATGATGATGCCTAT	8.03
	fur	ATAGACAAGACCAAT	8.8
	dps	AAAAACCGGTGCTAT	8.01
	grxA	ATAACCCAGGGCTAT	8.38
	txB	ATAGCATGAACCGAT	8.75
	trxC	AAAGCTTGCGACTAT	8.32
	trxA	ATATCAGCTTACTAT	8.18
	sodA	ATAATCATTTTCAAT	8.68
	katG	AAAGGTATTAGCTAT	8.65
	oxyR	ATAGCAATGAACGAT	8.63
	hemH	AATGGCGCTAACGAT	7.98
	ybaL	ATAGTTTATGACAAT	8.66
	fhuF	ATAGCGATAAACGAT	8.81
	ansP	ATTGCGCAACGCAAT	8.18
	sufA	ATAGTCATTTTCTAT	9.07
	yceA	ATAATTAACAACAAT	8.48

12. ***Staphyloccocus aureus*** **Newman**	*sodM*	AAAGACAACTTCCAT	8.26
	ahpC	AAAGGTTGTGTCTAT	8.84
	radA	AAAGATACCGACTAT	8.78
	alaS	ATTTACACATCCTAT	8.02
	hemA	ATATATACTAACAAT	8.23
	recX	AAAAAATCACACTAT	8.09



13. ***Vibrio cholerae*** **O359**	*hemH*	ATTTCACCTATCAAT	8.13
	Qrr	ATATGGCTAGGCTAT	8.3
	luxO	ATATGGCTAGGCTAT	8.3
	grxA	ATAGATAAAAACAAT	8.9
	trxB	ATAATTGGACTCGAT	8.53
	katB	AAATTAGCTCTCTAT	8.17
	fur	ATAACAGAAGTCAAT	8.56
	recG	AAAACACAGCTCGAT	8.13
	trxA	AAATAGATGCTCTAT	8.19

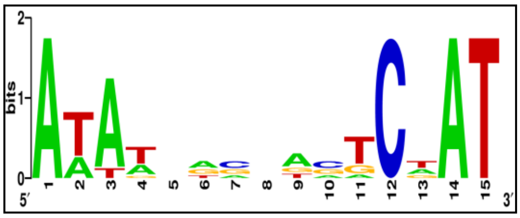


Table S4. Oligonucleotides used in this study.

PA no. [a]	**Gene [a]**	**Forward primer (5'-3')**	**Reverse primer (5'-3')**
For OxyR expression in *E. coli*			
PA5344	*oxyR*	GGGAATTCCATATGACCCTCACCGAACTGCGCTAC	CCCAAGCTTTGCTATTTGCGGTTGTTCCTGG
For OxyR expression in *P. aeruginosa*			
PA5344	*oxyR*	GGAATTCATGACCCTCACCGAACTGCGCTAC	GCTCTAGATCAGTGGTGGTGGTGGTGGTGTGCTATTTGCGGTTGTTCCTGG
For EMSA analysis			
PA0139	*ahpC*	GACCATCCTGGTGCTGGTC	TGCCCTTCAGGGATTCCTC
PA0717	*pf4*	TTCCGTGCTCACGCGAATC	AGGTGCAAATCTCTACGAGGT
PA0938		TGCTCAACGTACAGAGCCAG	AGGAAGGCATACCAACGTCC
PA0962	*dps*	AATCCATGGCTTGCAGCCAG	AGGTAGAGGGTGTAGGTGTC
PA1003	*mvfR*	GCGGATTCTAACCGCATAGG	CGATGACCTGGAGGAACATG
PA1423	*bdlA*	ACGGCAAGGAGGGAATCAG	CGAGTTGCTGTTGCAAGTCG
PA1431	*rsaL*	AGGTGTTCTTCAGCATGTAGG	AGTTTCCTGGCTTTCCCGTC
PA2145		ACATCTCGGAGGAGCACCATG	GGAATCGCACTTCGTCACTG
PA2426	*pvdS*	CGATAGCGATGTACGCCATG	ATCGACGAATGCCTGGAGGA
PA2738	*himA*	CGAAGAAACTCGACCTCGAG	TGACGATGTTCTGCGTCGTG
PA3032	*snr1*	TTCCTCAGCTGCTGATGCCT	GTCAGTCCTGAAGGGAACTC
PA3841	*exoS*	GTGGATTCATGGCGTGTTCC	CCTCAATCTGTCCCAAACGC
PA4268	*rpsL*	TCTGGCTTACCACAGCGAAC	ACGCACCAGCTGGTTGATAG
PA4406	*lpxC*	AGCAGCAGTCGGTGAACTAC	AGAACACGATACCGGTGTCC
PA4406.1		AGCAGCAGTCGGTGAACTAC	AGAACACGATACCGGTGTCC
PA4764	*fur*	GCTGTCGTTGAAGAACAGGC	GCATCTGCAGGATCTTGACC
PA5240	*trxA*	TTCGCTGAGATTGCGCTCCT	GTTGACGATATGTTCGCTCATG
PA5319	*radC*	CATCACCACTCGGACTTCAG	CCTGCTCCAGAAGCTTCTC
PA5344	*oxyR*	TGTACACCAGGTAGTCGAGC	TAGCGCAGTTCGGTGAGGGT
PA5345	*recG*	ACGAGCCCTTCTATGTGCTG	AGGATGTCCTGCAGGGTTTC
For qRT-PCR analysis			
PA0139	*ahpC*	GCAAGTTCATCGAGGTGACC	CTTTCTGGAACTCGCCGTAG
PA0195	*pntAA*	CACCAGGTGATCGTCCAGAG	CGATGTTCTCGTTGTCGAAGG

PA0849	*trxB2*	TCAAGCCGCTGCTGATCAC	TCCACGGCATGAATGTGGTC
PA0962	*dps*	TGTTCGAAGGCCAGTACACC	TCCTCCTTGATGGACGACAG
PA2426	*pvdS*	GCGTTCTTCAGGCTCCAGTC	AGTTGATGTGCGAGGTTTCC
PA2853	*oprI*	ATGAACAACGTTCTGAAATTCTCTGCT	CTTGCGGCTGGCTTTTTCCAG