

Table S8. Differentially expressed genes (DEGs) related to the redox balance and tolerance to oxidative stress identified by RNA-Seq in *Pseudomonas savastanoi* pv. *savastanoi* Psv- Δ gacA.

Locus tag ^a		Annotation	FPKM ^b				Fold change (log ₂) ^c	
			NCPPB 3335		Psv-ΔgacA			
			SSM	HIM	SSM	HIM		
NADH-quinone oxidoreductase complex								
PSA3335_RS14105	Subunit NuoA		36.05	909.26	84.51	415.95	1.23	-1.13
PSA3335_RS14100	Subunit NuoB		163.19	1157.36	361.80	1415.11	1.15	0.29
PSA3335_RS14095	Subunit NuoC/D		42.25	486.88	87.41	376.01	1.05	-0.37
PSA3335_RS14090	Subunit NuoE		63.34	569.61	121.32	329.01	0.94	-0.79
PSA3335_RS14085	Subunit NuoF		73.04	494.83	120.58	406.51	0.72	-0.28
PSA3335_RS14080	Subunit NuoG		66.24	606.42	101.42	402.58	0.61	-0.59
PSA3335_RS14075	Subunit NuoH		42.57	369.26	61.70	241.23	0.54	-0.61
PSA3335_RS14070	Subunit NuoI		52.23	467.11	77.29	324.13	0.57	-0.53
PSA3335_RS14065	Subunit NuoJ		41.21	452.79	57.18	234.05	0.47	-0.95
PSA3335_RS14060	Subunit NuoK		50.68	444.84	82.52	321.91	0.70	-0.47
PSA3335_RS14055	Subunit L		54.79	436.16	70.91	259.70	0.37	-0.75
PSA3335_RS14050	Subunit M		38.03	354.55	51.57	167.58	0.44	-1.08
PSA3335_RS14045	Subunit NuoN		52.98	335.16	70.67	184.54	0.42	-0.86
ATP synthase complex								
PSA3335_RS28720	Epsilon chain		1222.22	1157.67	1830.65	479.63	0.58	-1.27
PSA3335_RS28725	Subunit beta		2087.02	2287.29	2943.28	841.79	0.50	-1.44
PSA3335_RS28730	Subunit gamma		1454.80	1494.66	1853.63	562.64	0.35	-1.41

PSA3335_RS28735	Subunit alpha	2084.76	1975.35	2371.87	704.42	0.19	-1.49
PSA3335_RS28740	Subunit delta	1606.10	1351.29	1780.94	517.57	0.15	-1.38
PSA3335_RS28745	Subunit B	3251.80	2648.43	3459.11	1091.62	0.09	-1.28
PSA3335_RS28750	Subunit C	1843.91	1964.38	1798.16	547.48	-0.04	-1.84
PSA3335_RS28755	Subunit A	364.11	278.21	325.07	184.93	-0.16	-0.59
Catalase and Peroxidase							
PSA3335_RS03775	Catalase	5.69	8.19	5.97	113.99	0.07	3.80
PSA3335_RS04865	Catalase/peroxidase HPI	97.41	249.87	110.88	608.59	0.19	1.28
PSA3335_RS13270	Catalase	24.50	79.50	28.19	280.96	0.20	1.82
PSA3335_RS27350	Catalase HP11	346.68	129.21	103.96	330.58	-1.74	1.36
PSA3335_RS07525	Catalase	296.55	95.66	125.03	200.28	-1.25	1.07
PSA3335_RS09710	Peroxide stress protein YaaA	170.06	78.24	157.81	246.09	-0.11	1.65
PSA3335_RS09415	Glutathione peroxidase	241.94	114.96	174.64	189.55	-0.47	0.72
PSA3335_RS23030	Glutathione peroxidase	184.02	190.16	189.38	339.28	0.04	0.84
Transcriptional regulators in response to oxidative stress.							
PSA3335_RS17805	LysR family transcriptional regulator (SoxR)	65.14	324.03	118.29	104.23	0.86	-1.64
PSA3335_RS27020	Hydrogen peroxide-inducible genes activator (OxyR)	299.05	233.94	264.91	313.98	-0.17	0.42
PSA3335_RS07485	LysR family transcriptional regulator (FinR)	27.35	47.77	29.78	34.25	0.12	-0.48
PSA3335_RS00850	Transcriptional regulator (HexR)	87.88	215.89	85.37	145.62	-0.04	-0.57
Other proteins							
PSA3335_RS04980	Ferric iron uptake transcriptional regulator	1500.00	671.31	973.01	1016.98	-0.62	0.60
PSA3335_RS09450	Thioredoxin-disulfide reductase	306.82	218.39	296.68	966.82	-0.05	2.15
PSA3335_RS15580	Alkyl hydroperoxide reductase F	261.88	170.23	229.35	300.14	0.19	0.82

PSA3335_RS00255	OsmC family peroxiredoxin	4441.99	2275.22	1766.50	6006.12	-1.33	1.40
PSA3335_RS06880	Aquaporin	32.58	83.042	25.10	336.27	-0.38	2.02
PSA3335_RS12780	Fumarate/nitrate reduction Fnr	120.10	209.30	230.88	316.28	0.94	0.60
PSA3335_RS15575	Peroxiredoxin	1624.32	722.28	1224.03	3497.90	-0.41	2.28
PSA3335_RS15150	Metalloprotease	192.53	173.38	173.05	291.57	-0.15	0.75
PSA3335_RS15585	Lactoylglutathion lyase	1023	292.72	706.36	468.15	-0.53	0.68
PSA3335_RS00115	Trk system potassium transporter (CioA)	35.06	74.04	42.04	44.46	0.26	-0.74
PSA3335_RS01960	Peptide-methionine oxide reductase (MsrA)	320.75	436.51	342.08	413.99	0.09	0.08
PSA3335_RS15215	MCE family protein (PqiB)	176.84	130.63	118.16	77.86	-0.58	-0.75
PSA3335_RS01030	Rubredoxin (RubB)	65.70	140.17	61.62	156.93	-0.09	0.16
PSA3335_RS05570	Superoxide dismutase (SodA)	5195.87	8.73	4246.77	8.54	-0.29	-0.03
PSA3335_RS06045	Superoxide dismutase (SodB)	165.97	827.52	132.01	1894.34	-0.33	1.19
PSA3335_RS05560	Class II fumarate hydratase (FumC1)	2223.79	7.81	1720.38	8.11	-0.37	0.06
PSA3335_RS15510	Glucose-6-phosphate dehydrogenase (Zwf-1)	846.27	175.39	419.88	189.85	-1.01	0.11
PSA3335_RS07490	Ferredoxin NADP reductase (FpR)	346.44	366.53	390.65	334.24	0.17	-0.13
PSA3335_RS12900	Aconitate hydratase (AcnA)	287.26	273.53	182.49	442.20	-0.65	0.69

^a Locus tag in the genome of *Pseudomonas savastanoi* pv. *savastanoi* NCPPB 3335 (accession no. NZ_CP008742.1).

^b FPKM indicates fragments per kilobase of gene fragments per million of readings, in an RNA-Seq analysis.

^c Fold change indicates average differential gene expression (log₂ normalized) between the wild-type strain and strain Psv-ΔgacA in SSM and HIM media. Positive and negative fold change reflect an increased or decreased level, respectively, of gene expression in strain Psv-ΔgacA. Cells with grey shading and values in bold indicate genes with a significant differential expression ($q < 0.05$).