Strain		Colony diameter (mm)				
		untreated	diamide (2 mmol/l)	MSB (0.12 mmol/l)	*t*BOOH (0.8 mmol/l)	H_2O_2 (6 mmol/l)
RWY 6.2	***ΔrsmA ΔnapA***	60.30 ± 0.23	8.03 ± 0.85 [ab]	n.d. [ab]	n.d. [ab]	n.d. [ab]
RWY 10.3	***ΔnapA***	61.50 ± 0.34	10.35 ± 1.17 [ab]	n.d. [ab]	n.d. [ab]	n.d. [ab]
RWY 34.30	***OErsmA ΔnapA***	61.50 ± 0.57	17.93 ± 0.13 [ab]	n.d. [ab]	n.d. [ab]	n.d. [ab]
RWY 8.5	***ΔrsmA***	60.23 ± 1.45	13.50 ± 0.68 [ab]	32.03 ± 0.26 [a]	47.10 ± 0.85 [a]	51.98 ± 1.79 [a]
RDIT 9.32	**wt**	60.53 ± 0.45	28.2 ± 0.47	33 ± 0.13	50.70 ± 1.89	55.28 ± 0.57
RWY 2.12	***OErsmA***	58.13 ± 0.56[a]	23.98 ± 0.27 [ab]	38.19 ± 0.37 [ab]	47.78 ± 0.36 [a]	49.06 ± 0.27 [ab]
RWY 35.5	***ΔrsmA OEnapA***	63.98 ± 0.47 [a]	25.28 ± 0.57 [ab]	41.10 ± 0.69 [ab]	55.65 ± 0.69 [a]	60.75 ± 0.45 [ab]
RWY 17.3	***OEnapA***	62.55 ± 0.22[a]	26.18 ± 0.47 [ab]	43.50 ± 0.47 [ab]	51.68 ± 0.47	53.70 ± 1.11[b]
RWY 32.30	***OErsmA OEnapA***	63.33 ± 0.18 [a]	23.45 ± 0.27 [ab]	47.78 ± 0.37 [ab]	52.72 ± 0.26 [a]	54.21 ± 0.18[b]

Table S1 Effects of *napA* and *rsmA* gene manipulations on the colony diameters in stress treated and untreated surface cultures. Mean±SD calculated from three independent experiments are presented.

[a] - Significant difference compared to the reference strain treated in the same way according to the Dunnatt's test ($p < 0.05$, $n = 3$).

[b] - Significant interaction between the effects of gene manipulation(s) and stress treatment on the colony diameter according to the two-way ANOVA ($p < 0.05$).

n.d. - No growth was detected.

Strain		DCM (g/l)							
		Untreated				*t*BOOH treated			
		0 h	12 h	24 h	48 h	0 h	12 h	24 h	48h
RWY 6.2	***ΔrsmA ΔnapA***	1.927 ± 0.24^{a}	4.980 ± 0.763^{a}	4.853 ± 0.411^{abc}	4.013 ± 0.284^{a}	1.580 ± 0.069^{ad}	4.640 ± 0.243^{a}	5.587 ± 0.232^{ab}	4.180 ± 0.151^{a}
RWY 10.3	***ΔnapA***	0.947 ± 0.133^{bc}	2.460 ± 0.413^{bc}	5.447 ± 0.424^{ab}	3.787 ± 1.060^{a}	0.827 ± 0.083^{b}	1.027 ± 0.264^{b}	3.953 ± 1.343^{ac}	$4.647 \pm 0.342^{a,b}$
RWY 34.30	***OErsmA ΔnapA***	1.050 ± 0.030^{bc}	2.913 ± 0.515^{bd}	5.307 ± 0.599^{ab}	3.993 ± 0.810^{a}	1.240 ± 0.122^{acd}	2.460 ± 0.781^{cd}	5.887 ± 0.629^{b}	$4.387 \pm 0.359^{a,b}$
RWY 8.5	***ΔrsmA***	1.033 ± 0.023^{bc}	3.900 ± 0.277^{ad}	5.020 ± 0.420^{abc}	3.640 ± 0.299^{a}	1.020 ± 0.171^{bcd}	3.633 ± 0.512^{ad}	5.727 ± 0.503^{bd}	$4.620 \pm 0.552^{a,b}$
RDIT 9.32	**wt**	0.747 ± 0.291^{bd}	4.507 ± 0.372^{a}	5.453 ± 0.348^{b}	3.900 ± 0.174^{a}	0.653 ± 0.172^{be}	3.233 ± 0.404^{cd}	5.753 ± 0.593^{bd}	4.333 ± 0.099^{a}
RWY 2.12	***OErmsA***	0.327 ± 0.050^{d}	1.347 ± 0.261^{c}	3.533 ± 0.081^{de}	3.640 ± 0.382^{a}	0.340 ± 0.072^{e}	0.787 ± 0.197^{b}	2.080 ± 0.203^{e}	$4.920 \pm 0.406^{a,b}$
RWY 35.5	***ΔrsmA OEnapA***	0.627 ± 0.180^{bd}	2.853 ± 0.801^{bd}	3.933 ± 0.231^{cdf}	4.580 ± 0.701^{a}	0.653 ± 0.031^{be}	3.200 ± 0.594^{cde}	4.033 ± 0.358^{ac}	$5.073 \pm 1.210^{a,b}$
RWY 17.3	***OEnapA***	1.260 ± 0.125^{c}	3.627 ± 0.280^{ab}	4.920 ± 0.203^{abf}	4.567 ± 1.485^{a}	1.347 ± 0.180^{ad}	3.860 ± 0.236^{ae}	4.793 ± 0.194^{abcd}	5.920 ± 0.733^{b}
RWY 32.30	***OErsmA OEnapA***	0.953 ± 0.095^{bc}	2.460 ± 0.440^{bc}	2.780 ± 0.579^{e}	5.120 ± 0.365^{a}	0.960 ± 0.159^{bc}	2.327 ± 0.376^{c}	3.127 ± 0.280^{ace}	$4.813 \pm 0.114^{a,b}$

Table S2 Comparison of biomass production of the mutants.

Biomass production was characterized with DCM (g/l) values. Data are presented as mean ± SD values calculated from three independent experiments at each time point. Effects of gene manipulations were analysed by one way ANOVA followed by Tukey post-hoc test. Means marked with the same letter do not differ significantly (adj. p value < 0.05) from each other.

Strain		DCF (pmol/mg DCM)		Catalase (mkat/kg protein)	
		Untreated	***t*BOOH treated**	**Untreated**	***t*BOOH treated**
RWY 6.2	***ΔrsmA ΔnapA***	0.641 ± 0.227^{a}	$10.856 \pm 3.397^{a*}$	8850 ± 907^{a}	5937 ± 1154^{acd}
RWY 10.3	***ΔnapA***	0.541 ± 0.244^{a}	$45.909 \pm 14.209^{b*}$	5597 ± 55^{ab}	4661 ± 613^{acd}
RWY 34.30	***OErsmA ΔnapA***	3.096 ± 1.169^{b}	$5.751 \pm 1.223^{ac*}$	5733 ± 1587^{ab}	6857 ± 441^{ad}
RWY 8.5	***ΔrsmA***	0.593 ± 0.181^{a}	0.703 ± 0.270^{c}	13142 ± 381^{c}	15762 ± 971^{b}
RDIT 9.32	**wt**	0.521 ± 0.221^{a}	0.570 ± 0.216^{c}	1579 ± 195^{d}	897 ± 895^{acd}
RWY 2.12	***OErsmA***	0.293 ± 0.183^{a}	$1.213 \pm 0.434^{c*}$	4393 ± 569^{bde}	3878 ± 202^{c}
RWY 35.5	***ΔrsmA OEnapA***	0.615 ± 0.379^{a}	0.257 ± 0.075^{c}	15836 ± 473^{f}	16007 ± 1779^{b}
RWY 17.3	***OEnapA***	0.829 ± 0.269^{a}	0.499 ± 0.251^{c}	7555 ± 437^{ae}	8474 ± 788^{d}
RWY 32.30	***OErsmA OEnapA***	0.769 ± 0.250^{a}	0.928 ± 0.276^{c}	12341 ± 2967^{c}	17642 ± 643^{b}

Table S3 Comparison of DCF (RS) production and catalase activities of the mutants.

Data are presented as mean ± SD values calculated from three independent experiments. Effects of the gene manipulations were analyzed by one way ANOVA followed by Tukey post-hoc test. Means marked with the same letter do not differ significantly (adj. p value < 0.05) from each other. Effects of *t*BOOH treatment were studied by Student's t-test with Holm's p-value correction. Data of *t*BOOH treated cultures marked with "*" symbol significantly (adj. $p < 0.05$) differ from those of untreated cultures.

Strain		ST (mg/g DCM)	
		Untreated	***t*BOOH treated**
RWY 6.2	***ΔrsmA ΔnapA***	0.855 ± 0.120^{a}	0.690 ± 0.229^{ab}
RWY 10.3	***ΔnapA***	0.264 ± 0.033^{bc}	0.391 ± 0.023^{ac}
RWY 34.30	***OErsmA ΔnapA***	0.330 ± 0.060^{bd}	1.020 ± 0.346^{b}
RWY 8.5	***ΔrsmA***	0.131 ± 0.039^{ce}	0.211 ± 0.031^{cd}
RDIT 9.32	**wt**	0.066 ± 0.006^{e}	0.054 ± 0.026^{cd}
RWY 2.12	***OErmsA***	0.141 ± 0.016^{ce}	0.149 ± 0.023^{c}
RWY 35.5	***ΔrsmA OEnapA***	0.329 ± 0.075^{bd}	0.283 ± 0.024^{ad}
RWY 17.3	***OEnapA***	0.048 ± 0.007^{e}	0.047 ± 0.008^{c}
RWY 32.30	***OErsmA OEnapA***	0.490 ± 0.108^{d}	0.601 ± 0.152^{abd}

Table S4 ST production of the control and mutant strains.
Data are presented as mean ± SD values calculated from three independent experiments. Effects of the gene manipulations were analyzed by one way ANOVA followed by Tukey post-hoc test. Means marked with the same letter do not differ significantly (adj. p value < 0.05) from each other. Effects of *t*BOOH treatment were studied by Student's t-test with Holm's p-value correction. No significant differences were found between the ST contents of untreated and *t*BOOH treated cultures.

	Strain	Untreated		*t*BOOH treated	
		***napA* (ΔCP)**	***rsmA* (ΔCP)**	***napA* (ΔCP)**	***rsmA* (ΔCP)**
RWY 6.2	***ΔrsmA ΔnapA***	-13.859 ± 1.530[a]	-15.558 ± 1.095[a]	-13.009 ± 0.978[a]	-13.328 ± 0.483[a]
RWY 10.3	***ΔnapA***	-12.808 ± 0.799[a]	-4.168 ± 0.350[b]	-12.818 ± 0.435[a]	-4.891 ± 0.326[b]
RWY 34.30	***OErsmA ΔnapA***	-12.804 ± 0.309[a]	2.211± 0.279[c]	-12.698 ± 0.100[a]	1.967 ± 0.130[c]
RWY 8.5	***ΔrsmA***	-2.146 ± 0.154[b]	-14.501 ± 0.838[a]	-2.191 ± 0.785[b]	-14.389 ± 1.888[ae]
RDIT 9.32	**wt**	-2.441 ± 0.439[b]	-5.149 ± 0.378[b]	-2.527 ± 0.642[b]	-4.108 ± 0.388[b,*]
RWY 2.12	***OErsmA***	1.882 ± 0.807[c]	-0.813 ± 0.469[d]	2.422 ± 0.210[c]	-1.079 ± 0.123[d]
RWY 35.5	***ΔrsmA OEnapA***	2.979 ± 0.257[c]	-14.956 ± 0.264[a]	2.982 ± 0.770[c]	-15.136 ± 0.200[e]
RWY 17.3	***OEnapA***	1.626 ± 0.527[c]	-1.109 ± 0.506[d]	1.816 ± 0.159[c]	-1.623 ± 0.212[d]
RWY 32.30	***OErsmA OEnapA***	1.582 ±0.455[c]	3.524 ± 0.475[c]	1.412 ± 0.368[c]	2.717 ± 0.028[c]

Table S5 Effects of *napA* and *rsmA* overexpression and gene deletion on the transcriptional activity of wild type *rsmA* and *napA* genes.
Data are presented as mean ± SD values calculated from three independent experiments. Effects of the gene manipulations were analyzed by one way ANOVA followed by Tukey post-hoc test. Means marked with the same letter do not differ significantly (adj. p value < 0.05) from each other. Effects of *t*BOOH treatment was studied by Student's t-test with Holm's p-value correction. Significant differences between the *t*BOOH treated and untreated cultures are marked with "*" symbol.

Table S6 Oligonucleotides used in this study.

Name	Sequence (5'→3')	Purpose
AN4562 for	TACCCCTACCCAGAACAG	forward primer of the *rsmA* gene used for rRT-PCR
AN4562rev	CCTTGGAAATCATCGCCGTG	reverse primer of the *rsmA* gene used for rRT-PCR
AN7513 for	TCTTTACCTTTCGCCTGACC	forward primer of the *napA* gene used for rRT-PCR
AN7513 rev	ACCTCGCCATTGCTGTTTG	reverse primer of the *napA* gene used for rRT-PCR
AN6542F	GAAGTCCTACGAACTGCCTGATG	forward primer of the reference gene (*actA*) used for rRT-PCR
AN6542R	AAGAACGCTGGGCTGGAA	reverse primer of the reference gene (*actA*) used for rRT-PCR
AN6700F	CCTATTCCCGAGCAAGTTC	forward primer of the reference gene used for rRT-PCR
AN6700R	TGATGTTCCTGACGATGGC	reverse primer of the reference gene used for rRT-PCR