

Additional file 1. Genes found differentially expressed in the *femAB+* backcross BB1305 compared to the wild type BB903. The selection of regulated genes is based on statistical significance of moderated *t*-scores and thus also includes genes with a $\log_2(\text{fold change}) < |1|$. The genes are clustered according to their cellular main role as in the *S. aureus* N315 genome annotation on the DOGAN website (http://www.bio.nite.go.jp/dogan/MicroTop?GENOME_ID=n315, as of September 24, 2006).

CATEGORY

Process

ORF ID	Gene	Product	$\log_2(\text{fold change})$	<i>p</i> -value
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CELL ENVELOPE AND CELLULAR PROCESSES

Cell wall

down

SA0793	<i>dltA</i>	D-alanine-D-alanyl carrier protein ligase	-1.03	0.02
SA1283	<i>pbpB</i>	PBP2	-0.47	0.04

Membrane bioenergetics (electron transport chain and ATP synthase)

down

SA0937		cytochrome D ubiquinol oxidase subunit 1 homologue	-0.70	<0.005
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up

SA0210		hypothetical protein, similar to NADH-dependent dehydrogenase	1.84	<0.005
SA0211		hypothetical protein, similar to NADH-dependent dehydrogenase	1.65	<0.005

Transport / binding proteins and lipoproteins

down

SA0617	<i>vraG</i>	ABC transporter permease	-0.80	0.04
SA0640		hypothetical protein, similar to ABC transporter required for expression of cytochrome bd	-0.57	0.04
SA0655	<i>fruA</i>	fructose specific permease	-1.28	0.01
SA0691		lipoprotein, similar to ferrichrome ABC transporter	-0.77	0.02
SA0794	<i>dltB</i>	DltB membrane protein	-1.30	0.01
SA0796	<i>dltD</i>	poly(glycerophosphate chain) D-alanine transfer protein	-1.38	<0.005
SA0950	<i>potA</i>	spermidine/putrescine ABC transporter, ATP-binding protein homologue	-0.43	0.03
SA1042	<i>pyrP</i>	uracil permease	-2.37	<0.005
SA1183	<i>opuD</i>	glycine betaine transporter	-0.83	0.03
SA1269		Blt-like protein	-1.47	<0.005
SA1270		hypothetical protein, similar to amino acid permease	-1.10	0.01
SA1505	<i>lysP</i>	lysine-specific permease	-0.92	0.01
SA1893		lipoprotein precursor	-0.75	0.02
SA1987		glycine betaine transporter <i>opuD</i> homologue	-1.07	0.02
SA2303		hypothetical protein, similar to membrane spanning protein	-1.50	0.01
SA2339		hypothetical protein, similar to antibiotic transport-associated protein	-1.68	<0.005

up

SA0186		hypothetical protein, similar to sucrose phosphotransferase enzyme II	1.40	0.02
SA0208		maltose/maltodextrin transport permease homologue	1.49	<0.005
SA0209		maltose/maltodextrin transport permease homologue	2.02	<0.005
SA0260		hypothetical protein, similar to ribose transporter RbsU	0.66	0.01
SA0318		hypothetical protein, similar to transport protein SgaT	1.53	<0.005

CATEGORY

Process					
ORF ID	Gene	Product		log ₂ (fold change)	p-value
SA0320		hypothetical protein, similar to PTS fructose-specific enzyme IIBC component		2.26	<0.005
SA0599		ATP-binding cassette transporter A		0.45	0.04
SA1140	<i>glpF</i>	glycerol uptake facilitator		1.39	<0.005
SA2167	<i>scrA</i>	PTS system, sucrose-specific IIBC component		0.70	0.02
SA2235	<i>opuCC</i>	glycine betaine/carnitine/choline ABC transporter (osmoprotec) <i>opuCC</i>		0.90	0.01
SA2426	<i>arcD</i>	arginine/ornithine antiporter		1.37	<0.005

INFORMATION PATHWAYS**DNA modification and repair**up

SA1512		hypothetical protein, similar to formamidopyrimidine-DNA glycosylase		0.51	0.04
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DNA recombinationup

SA1313		probable ATP-dependent DNA helicase RecQ		0.61	0.02
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DNA replicationup

SA1525	<i>dnaE</i>	DNA polymerase III, alpha chain		0.66	<0.005
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Protein foldingdown

SA1409	<i>dnaK</i>	DnaK protein (HSP70)		-0.71	<0.005
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up

SA1659	<i>prsA</i>	peptidyl-prolyl cis/trans isomerase homologue		1.03	0.01
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Protein synthesisdown

SA0009	<i>serS</i>	seryl-tRNA synthetase		-0.75	0.02
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SA0475	<i>lysS</i>	lysyl-tRNA synthetase		-0.56	<0.005
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SA0496	<i>rplA</i>	50S ribosomal protein L1 (BL1)		-0.62	0.04
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SA0959		GTP-binding elongation factor homologue		-0.76	0.03
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SA1456	<i>aspS</i>	aspartyl-tRNA synthetase		-0.86	0.03
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SA2041	<i>rpsC</i>	30S ribosomal protein S3		-0.73	0.01
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RNA synthesisdown

SA0501	<i>rpoC</i>	RNA polymerase beta-prime chain		-0.55	0.01
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SA1041	<i>pyrR</i>	pyrimidine operon repressor chain A		-1.80	<0.005
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SA1956		lytic regulatory protein truncated with Tn554		-0.82	0.03
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up

SA0187		hypothetical protein, similar to transcription regulator		1.90	<0.005
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SA0321		hypothetical protein, similar to transcription antiterminator BglG family		2.52	<0.005
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SA1339	<i>malR</i>	maltose operon transcriptional repressor		2.07	<0.005
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SA1700	<i>vraR</i>	two-component response regulator		0.38	0.05
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SA1847	<i>scrR</i>	sucrose operon repressor		0.63	0.01
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SA2295	<i>gntR</i>	gluconate operon transcriptional repressor		1.49	0.02
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SA2320		hypothetical protein, similar to regulatory protein PfoR		1.08	0.03
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SA2424		hypothetical protein, similar to transcription regulator Crp/Fnr family protein		1.28	<0.005
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CATEGORY**Process**

ORF ID	Gene	Product	log₂(fold change)	p-value
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INTERMEDIARY METABOLISM**Metabolism of lipids**down

SA0548	<i>mvaD</i>	mevalonate diphosphate decarboxylase	-0.62	0.02
SA0843	<i>fab</i>	3-oxoacyl-[acyl-carrier-protein] synthase	-0.81	0.03
SA1073	<i>fabD</i>	malonyl CoA-acyl carrier protein transacylase	-0.60	0.01
SA1074	<i>fabG</i>	3-oxoacyl-(acyl-carrier protein) reductase	-0.65	<0.005

up

SA0220		hypothetical protein, similar to glycerophosphodiester phosphodiesterase	0.84	<0.005
SA0820	<i>glpQ</i>	glycerophosphoryl diester phosphodiesterase	0.59	0.03
SA2349	<i>crtM</i>	squalene synthase	0.79	0.01

Metabolism of amino acids and related moleculesdown

SA1150	<i>glnA</i>	glutamine-ammonia ligase	-1.03	<0.005
SA1271		threonine deaminase IlvA homologue	-0.99	<0.005
SA1272		alanine dehydrogenase	-1.14	<0.005
SA1608	<i>metK</i>	S-adenosylmethionine synthetase	-0.49	0.04
SA1858	<i>ilvD</i>	dihydroxy-acid dehydratase	-0.80	0.03
SA1859	<i>ilvB</i>	acetolactate synthase large subunit	-1.18	0.05
SA2125		hypothetical protein, similar to formiminoglutamase	-0.79	0.04

up

SA1012	<i>argF</i>	ornithine carbamoyltransferase	1.57	<0.005
SA2082	<i>ureA</i>	urease gamma subunit	1.73	<0.005
SA2086	<i>ureF</i>	urease accessory protein UreF	0.88	0.01
SA2121	<i>hutI</i>	imidazolonepropionase	1.39	0.04
SA2122	<i>hutU</i>	urocanate hydratase	2.00	<0.005
SA2318		hypothetical protein, similar to L-serine dehydratase	0.85	<0.005
SA2319		hypothetical protein, similar to beta-subunit of L-serine dehydratase	0.69	0.01
SA2425	<i>arcC</i>	carbamate kinase	1.49	<0.005
SA2427	<i>arcB</i>	ornithine transcarbamoylase	1.65	<0.005
SA2428	<i>arcA</i>	arginine-deiminase	2.04	<0.005

Metabolism of carbohydrates and related moleculesdown

SA1088	<i>sucC</i>	succinyl-CoA synthetase (beta subunit)	-0.99	<0.005
SA1089	<i>sucD</i>	succinyl-CoA synthetase (alpha subunit)	-0.91	<0.005

up

SA0143	<i>adhE</i>	alcohol-acetaldehyde dehydrogenase	0.85	0.01
SA0258	<i>rbsK</i>	probable ribokinase	0.71	<0.005
SA0304	<i>nanA</i>	N-acetylneuraminatase lyase subunit	1.73	<0.005
SA0305		hypothetical protein, similar to glucokinase	1.50	<0.005
SA0433		alpha-glucosidase	1.53	0.01
SA1142	<i>glpD</i>	aerobic glycerol-3-phosphate dehydrogenase	1.10	0.04
SA1338	<i>malA</i>	alpha-D-1,4-glucosidase	1.17	<0.005
SA1556	<i>acuC</i>	acetoin utilization protein	1.71	0.04
SA2294	<i>gntK</i>	gluconokinase	1.66	<0.005
SA2304	<i>fbp</i>	fructose-bisphosphatase	0.90	0.01

CATEGORY					
Process					
ORF ID	Gene	Product		log ₂ (fold change)	p-value
Metabolism of coenzymes and prosthetic groups					
<u>up</u>					
SA1259	<i>dfrA</i>	dihydrofolate reductase		0.62	<0.005
Metabolism of nucleotides and nucleic acids					
<u>down</u>					
SA0016	<i>purA</i>	adenylosuccinate synthase		-1.13	0.03
SA1043	<i>pyrB</i>	aspartate transcarbamoylase chain A		-2.02	<0.005
SA1044	<i>pyrC</i>	dihydroorotase		-2.67	<0.005
SA1046	<i>pyrAB</i>	carbamoyl-phosphate synthase large chain		-1.85	0.01
SA1048	<i>pyrE</i>	orotate phosphoribosyltransferase		-1.78	0.01
<u>up</u>					
SA0131	<i>pnp</i>	purine nucleoside phosphorylase		0.83	<0.005
SA1013		hypothetical protein, similar to carbamate kinase		2.18	0.01
SA2410	<i>nrdD</i>	anaerobic ribonucleoside-triphosphate reductase		0.96	<0.005
NO SIMILARITY					
<u>up</u>					
SA0663		hypothetical protein		1.13	<0.005
SA1210		hypothetical protein		0.58	0.02
SA1476		hypothetical protein		1.95	<0.005
OTHER FUNCTIONS					
Adaption to atypical conditions					
<u>up</u>					
SA0147	<i>capD</i>	capsular polysaccharide synthesis enzyme Cap5D		0.81	<0.005
Detoxification					
<u>up</u>					
SA1238		hypothetical protein, similar to tellurite resistance protein		0.54	0.04
Miscellaneous					
<u>down</u>					
SA1193	<i>fmtC</i>	oxacillin resistance-related FmtC protein		-1.12	<0.005
Pathogenic factors (toxins and colonization factors)					
<u>down</u>					
SA0587		lipoprotein, streptococcal adhesin PsaA homologue		-0.55	0.01
<u>up</u>					
SA0091	<i>plc</i>	1-phosphatidylinositol phosphodiesterase precursor		1.69	0.02
SA0900	<i>sspB</i>	cysteine protease precursor		1.07	0.02
SA1007		alpha-hemolysin precursor		1.64	0.02
SA1630	<i>spIB</i>	serine protease SpIB [Pathogenicity island SaPI _n 3]		2.48	<0.005
SA1752	<i>(hly)</i>	truncated beta-hemolysin		1.96	0.01
SA1811	<i>(hly)</i>	truncated beta-hemolysin		2.06	<0.005
SA1813		hypothetical protein, similar to leukocidin chain lukM precursor		1.64	0.04
SA2430	<i>aur</i>	zinc metalloproteinase aureolysin		2.05	0.01
SA2463	<i>lip</i>	triacylglycerol lipase precursor		1.68	<0.005

CATEGORY**Process**

ORF ID	Gene	Product	log₂(fold change)	p-value
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Phage-related functionsup

SA0252	<i>lrgA</i>	holin-like protein LrgA	1.24	0.03
SA0754		hypothetical protein, similar to lactococcal prophage ps3 protein 05	1.26	0.01
SA1782		hypothetical protein [Bacteriophage phiN315]	1.92	<0.005
SA1785		hypothetical protein [Bacteriophage phiN315]	2.27	<0.005
SA1786		hypothetical protein [Bacteriophage phiN315]	2.29	<0.005
SA1797		hypothetical protein [Bacteriophage phiN315]	2.56	<0.005
SAS063		hypothetical protein [Bacteriophage phiN315]	2.08	<0.005

Transposon and ISup

SA2387	<i>tnpB</i>	transposition regulatory protein TnpB - <i>S. aureus</i> transposon Tn554	1.21	0.04
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SIMILAR TO UNKNOWN PROTEINSdown

SA0100		conserved hypothetical protein	-0.66	<0.005
SA0477		conserved hypothetical protein	-1.47	<0.005
SA0701		conserved hypothetical protein	-0.51	0.03
SA1536		conserved hypothetical protein	-0.72	0.01
SA2143		conserved hypothetical protein	-0.82	0.02
SA2305		conserved hypothetical protein	-0.67	0.03
SA2328		conserved hypothetical protein	-0.42	0.02

up

SA0184		conserved hypothetical protein	2.35	<0.005
SA0185		conserved hypothetical protein	2.43	<0.005
SA0789		conserved hypothetical protein	0.54	0.04
SA1014		conserved hypothetical protein	1.54	<0.005
SA1258		conserved hypothetical protein	0.43	0.04
SA1661		conserved hypothetical protein	0.45	0.05
SA1690		conserved hypothetical protein	0.60	0.01
