

## SUPPLEMENTARY DATA

TABLE 1. Genes differently regulated in the *sigB* mutant MS64 compared to the wild type Newman.

TIGR locus name Newman <sup>a</sup>	Gene symbol <sup>b</sup>	Description <sup>c</sup>	Newman/MS64 <sup>c</sup>
NWMN_0047		hypothetical protein, similar to aminoacylase	9.188
NWMN_0050		myosin-cross-reactive antigen	2.286
NWMN_0057	<i>sirC</i>	siderophore compound ABC transporter permease protein SirC	17.51
NWMN_0095	<i>capA</i>	capsular polysaccharide synthesis enzyme CapA	2.7795
NWMN_0096	<i>capB</i>	capsular polysaccharide synthesis enzyme CapB	2.7925
NWMN_0097	<i>capC</i>	capsular polysaccharide synthesis enzyme CapC	2.517
NWMN_0098	<i>capD</i>	capsular polysaccharide synthesis enzyme CapD	2.828
NWMN_0099	<i>capE</i>	capsular polysaccharide synthesis enzyme CapE	2.4015
NWMN_0102	<i>capH</i>	capsular polysaccharide synthesis enzyme CapH	2.095
NWMN_0103	<i>capI</i>	capsular polysaccharide synthesis enzyme CapI	2.354
NWMN_0104	<i>capJ</i>	capsular polysaccharide synthesis enzyme CapJ	2.059
NWMN_0105	<i>capK</i>	capsular polysaccharide synthesis enzyme CapK	2.099
NWMN_0107	<i>capM</i>	capsular polysaccharide synthesis enzyme CapM	2.087
NWMN_0135	<i>murQ</i>	N-acetylmuramic acid-6-phosphate etherase	0.452
NWMN_0136		sucrose-specific PTS transporter IIBC component protein	0.457
NWMN_0137		RpiR family transcriptional regulator	0.417
NWMN_0162	<i>pflB</i>	formate acetyltransferase	0.409
NWMN_0163	<i>pflA</i>	hypothetical protein, formate acetyltransferase activating enzyme	0.367
NWMN_0166	<i>coa</i>	staphylocoagulase precursor	2.751
NWMN_0196	<i>lrgA</i>	murein hydrolase regulator LrgA	0.124
NWMN_0197	<i>lrgB</i>	antiholin-like protein LrgB	0.16
NWMN_0199		PTS system, IIA component	0.418
NWMN_0200	<i>bglA</i>	6-phospho-beta-glucosidase	0.349
NWMN_0202	<i>rbsK</i>	ribokinase	0.276
NWMN_0203	<i>rbsD</i>	ribose ABC transporter protein	0.293
NWMN_0204	<i>rbsU</i>	ribose transporter RbsU	0.289
NWMN_0215		hypothetical protein	0.379
NWMN_0218		staphyloxanthin biosynthesis protein	0.451
NWMN_0223	<i>essC</i>	ESX-1 secretion system (Ess) protein C	0.377
NWMN_0250		ABC transporter, permease protein	4.751
NWMN_0251		ABC transporter ATP-binding protein	3.705
NWMN_0321		oxidoreductase family protein	4.998
NWMN_0364		hypothetical protein (lipoprotein, putative)	17.88
NWMN_0374		sodium:dicarboxylate symporter family protein	0.282
NWMN_0393	<i>set6nm</i>	superantigen-like protein, exotoxin NM6	2.588
NWMN_0394	<i>set7nm</i>	superantigen-like protein, exotoxin NM7	2.231
NWMN_0396	<i>set9nm</i>	superantigen-like protein, exotoxin NM9	2.983
NWMN_0397	<i>set10nm</i>	superantigen-like protein, exotoxin NM10	2.048
NWMN_0429		N-acetylmuramoyl-L-alanine amidase AAA precursor	0.303
NWMN_0459	<i>purR</i>	pur operon repressor	3.658
NWMN_0460	<i>yabJ</i>	similar to translation initiation inhibitor	3.565
NWMN_0461	<i>spoVG</i>	regulatory protein SpoVG	4.127
NWMN_0513		chaperone protein HchA	4.875
NWMN_0525	<i>sdrE</i>	bone sialoprotein-binding protein	0.399
NWMN_0533		hypothetical protein, hexulose-6-phosphate synthase, putative	3.198
NWMN_0555	<i>mvaK2</i>	phosphomevalonate kinase	4.522
NWMN_0587		hypothetical protein	57.63
NWMN_0588	<i>sarA</i>	staphylococcal accessory regulator A	2.127
NWMN_0592		site-specific recombinase	21.55
NWMN_0593	<i>mnhA</i>	putative monovalent cation/H <sup>+</sup> antiporter subunit A	8.329
NWMN_0594	<i>mnhB</i>	putative monovalent cation/H <sup>+</sup> antiporter subunit B	4.749
NWMN_0595	<i>mnhC</i>	putative monovalent cation/H <sup>+</sup> antiporter subunit C	9.65
NWMN_0596	<i>mnhD</i>	putative monovalent cation/H <sup>+</sup> antiporter subunit D	7.188
NWMN_0597	<i>mnhE</i>	putative monovalent cation/H <sup>+</sup> antiporter subunit E	5.684
NWMN_0598	<i>mnhF</i>	putative monovalent cation/H <sup>+</sup> antiporter subunit F	6.812
NWMN_0599	<i>mnhG</i>	putative monovalent cation/H <sup>+</sup> antiporter subunit G	4.752
NWMN_0624	<i>lipA</i>	lipase/esterase LipA	2.185
NWMN_0651		hypothetical protein	9.587
NWMN_0695		hypothetical protein	9.395
NWMN_0696		di-/tripeptide ABC transporter	0.452
NWMN_0740	<i>gapR</i>	glycolytic operon regulator	3.436
NWMN_0756	<i>clfA</i>	clumping factor A	21.96
NWMN_0763		hypothetical protein	3.118
NWMN_0771		OsmC-like protein	12.81
NWMN_0783	<i>csbD</i>	CsbD-like superfamily protein	24.35
NWMN_0786	<i>sufD</i>	FeS assembly protein SufD	2.232

TABLE 1. continued.

TIGR locus name Newman <sup>a</sup>	Gene symbol <sup>b</sup>	Description <sup>b</sup>	Newman/ MS64 <sup>c</sup>
NWMN_0791		hypothetical protein	3.146
NWMN_0792		hypothetical protein	2.877
NWMN_0851		truncated MHC class II analog protein	0.309
NWMN_0892	<i>htrA</i>	serine protease HtrA	2.268
NWMN_0906		glycosyl transferase, group 1 family protein	2.015
NWMN_0918	<i>sspA</i>	V8 protease, glutamyl endopeptidase precursor	0.423
NWMN_0920		hypothetical protein	2.305
NWMN_0922	<i>atl</i>	bifunctional autolysin precursor	0.422
NWMN_0927	<i>qoxD</i>	quinol oxidase polypeptide IV	0.42
NWMN_0952	<i>cydA</i>	cytochrome D ubiquinol oxidase, subunit I	2.276
NWMN_0959	<i>pdhA</i>	pyruvate dehydrogenase E1 component, alpha subunit	0.468
NWMN_0979	<i>pycA</i>	pyruvate carboxylase	0.378
NWMN_1058	<i>uvrC</i>	excinuclease ABC subunit C	2.258
NWMN_1073	<i>hla</i>	alpha-hemolysin precursor	0.239
NWMN_1077		superantigen-like protein	2.044
NWMN_1109	<i>pyrR</i>	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase	0.444
NWMN_1110	<i>uraA</i>	uracil permease	0.27
NWMN_1111	<i>pyrB</i>	aspartate carbamoyltransferase catalytic subunit	0.206
NWMN_1112	<i>pyrC</i>	dihydroorotase	0.237
NWMN_1113	<i>carA</i>	carbamoyl phosphate synthase small subunit	0.221
NWMN_1114	<i>carB</i>	carbamoyl phosphate synthase large subunit	0.307
NWMN_1115	<i>pyrF</i>	orotidine 5'-phosphate decarboxylase	0.303
NWMN_1116	<i>pyrE</i>	orotate phosphoribosyltransferase	0.298
NWMN_1180	<i>truB</i>	tRNA pseudouridine synthase B	2.377
NWMN_1314		hypothetical protein	2.245
NWMN_1328	<i>ariR</i>	two-component response regulator	2.125
NWMN_1397		hypothetical protein	0.347
NWMN_1508	<i>accB</i>	acetyl-CoA carboxylase, biotin carboxyl carrier protein	2.603
NWMN_1509		urea amidolyase-related protein	2.776
NWMN_1526		hypothetical protein	42.57
NWMN_1552		hypothetical protein	2.389
NWMN_1560	<i>abrB</i>	ammonia monooxygenase	3.322
NWMN_1575	<i>lysP</i>	lysine-specific permease	7.196
NWMN_1600		universal stress protein family protein	0.318
NWMN_1603	<i>ald2</i>	alanine dehydrogenase	0.486
NWMN_1605	<i>ackA</i>	acetate kinase	0.491
NWMN_1631		hypothetical protein	3.062
NWMN_1698		hypothetical protein	2.319
NWMN_1701	<i>spIF</i>	serine protease SplF	0.271
NWMN_1702	<i>spIE</i>	serine protease SplE	0.132
NWMN_1703	<i>spID</i>	serine protease SplD	0.121
NWMN_1704	<i>spIC</i>	serine protease SplC	0.204
NWMN_1705	<i>spIB</i>	serine protease SplB	0.187
NWMN_1706	<i>spIA</i>	serine protease SplA	0.215
NWMN_1709	<i>bsaG</i>	lantibiotic ABC transporter protein	2.5715
NWMN_1710	<i>bsaE</i>	lantibiotic ABC transporter protein	2.48
NWMN_1711	<i>bsaF</i>	lantibiotic immunity protein F	3.904
NWMN_1718	<i>lukD</i>	leukocidin LukD precursor	0.0656
NWMN_1719	<i>lukE</i>	leukocidin LukE precursor	0.0727
NWMN_1731		hypothetical protein	0.275
NWMN_1738		hypothetical protein	2.95
NWMN_1767		ThiJ/Pfpl family protein	5.071
NWMN_1819		low molecular weight phosphotyrosine protein phosphatase	2.774
NWMN_1821		ribonuclease BN	8.346
NWMN_1847	<i>sspB (2)</i>	staphopain thiol proteinase	0.263
NWMN_1927	<i>lukF</i>	leukocidin/hemolysin toxin subunit F	0.231
NWMN_1928	<i>lukS</i>	leukocidin/hemolysin toxin subunit S	0.242
NWMN_1968		metallopeptidase SprT family protein	0.0777
NWMN_1969		S1 RNA-binding domain-containing protein	0.0639
NWMN_1970	<i>sigB</i>	RNA polymerase sigma factor SigB	2.579
NWMN_1971	<i>rsbW</i>	serine-protein kinase RsbW, anti-sigma B factor	2.573
NWMN_1972	<i>rsbV</i>	anti-sigma B factor antagonist	2.695
NWMN_1999		sceD protein, putative	2.909
NWMN_2004	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	2.211
NWMN_2005		hypothetical protein	3.196
NWMN_2026		aldehyde dehydrogenase family protein	7.298
NWMN_2048		hypothetical protein	30.95
NWMN_2057	<i>mtlF</i>	PTS system, mannitol-specific IIBC component	15.41
NWMN_2058		transcriptional antiterminator BglG family protein	7.412

TABLE 1. continued.

TIGR locus name Newman <sup>a</sup>	Gene symbol <sup>b</sup>	Description <sup>b</sup>	Newman/ MS64 <sup>c</sup>
NWMN_2059	<i>mtlA</i>	mannitol-specific IIA component	17.38
NWMN_2059	<i>mtlA</i>	mannitol-specific IIA component	17.38
NWMN_2060	<i>mtlD</i>	mannitol-1-phosphate 5-dehydrogenase	6.271
NWMN_2079		hypothetical protein	2.27
NWMN_2086	<i>asp23</i>	alkaline shock protein 23	33.94
NWMN_2087		hypothetical protein	114.5
NWMN_2088		hypothetical protein	301.8
NWMN_2089	<i>opuD2</i>	osmoprotectant transporter	115.4
NWMN_2109		truncated MHC class II analog protein	16.94
NWMN_2186		acyl-CoA dehydrogenase-related protein	2.037
NWMN_2197	<i>sarY</i>	staphylococcal accessory regulator Y	2.688
NWMN_2198		transcriptional regulator AraC family protein	4.188
NWMN_2201		dehydrogenase family protein	2.399
NWMN_2229		oxidoreductase, short chain dehydrogenase/reductase family protein	12.26
NWMN_2235	<i>hutG</i>	formimidoylglutamase	2.067
NWMN_2242		ABC transporter ATP-binding protein	0.403
NWMN_2258	<i>tcaR</i>	teicoplanin resistance operon transcriptional regulator TcaR	2.208
NWMN_2268		L-lactate permease 2	0.351
NWMN_2282		hypothetical protein	2.863
NWMN_2308	<i>dsbA</i>	protein-disulfide isomerase	2.172
NWMN_2318	<i>hlgA</i>	gamma-hemolysin component A	0.41
NWMN_2319	<i>hlgC</i>	gamma hemolysin component C	0.221
NWMN_2320	<i>hlgB</i>	gamma hemolysin component B	0.167
NWMN_2321	<i>bioX</i>	biotin biosynthesis-related protein	0.31
NWMN_2334		hypothetical protein	3.01
NWMN_2352		hypothetical protein	13.93
NWMN_2353		ABC transporter ATP-binding protein	37.71
NWMN_2360	<i>opp1F</i>	peptide ABC transporter, ATP-binding protein	0.48
NWMN_2371		alkylhydroperoxidase AhpD family protein	87.59
NWMN_2399	<i>fnbA</i>	fibronectin binding protein A precursor	2.586
NWMN_2406		hypothetical protein	14.15
NWMN_2422		D-isomer specific 2-hydroxyacid dehydrogenase	2.992
NWMN_2438	<i>poxB</i>	pyruvate oxidase	29.46
NWMN_2439	<i>cidB</i>	holin-like protein CidB	47.4
NWMN_2440	<i>cidA</i>	holin-like protein CidA	3.039
NWMN_2441		LysR family regulatory protein	2.411
NWMN_2448	<i>clpC</i>	ATP-dependent Clp protease, ATP-binding subunit ClpC	2.174
NWMN_2450	<i>feoB</i>	ferrous iron transport protein B	2.834
NWMN_2456		hypothetical protein	2.355
NWMN_2461	<i>crtN</i>	squalene synthase	5.443
NWMN_2462	<i>crtM</i>	squalene desaturase	8.444
NWMN_2463		glycosyl transferase, group 2 family protein	23.55
NWMN_2464		phytoene dehydrogenase	33.45
NWMN_2465	<i>crtI</i>	hypothetical protein	53.23
NWMN_2466	<i>oatA</i>	secretory antigen precursor SsaA homolog	2.232
NWMN_2479		amidohydrolase family protein	9.656
NWMN_2480		hydrolase, alpha/beta fold family	22.72
NWMN_2512		metallo-beta-lactamase superfamily protein	5.215
NWMN_2534	<i>arcA</i>	arginine deiminase	0.474
NWMN_2547		glycosyl transferase, group 1 family protein	2.199
NWMN_2551		accessory secretory protein Asp1	0.465
NWMN_2556		hypothetical protein	2.257
NWMN_2557		hypothetical protein	12.66
NWMN_2569	<i>geh</i>	lipase precursor	0.266
NWMN_2582		ABC transporter ATP-binding protein	2.226
NWMN_2594		hypothetical protein	29.49
NWMN_2595	<i>nixA</i> , <i>hoxN</i>	high-affinity nickel transporter	8.822
NWMN_2606		hypothetical protein	0.39

<sup>a</sup> Locus number for *S. aureus* Newman (<http://www.tigr.org>).

<sup>b</sup> Gene symbol and description of the gene based on the TIGR annotation (<http://www.tigr.org>).

<sup>c</sup> Fold change of gene transcription comparing *S. aureus* Newman with MS64.