Table 1: Up-regulated ASM genes, normalised to BHI, using one-way ANOVA and posthoc Benjamini and Hochberg tests ($p \leq 0.05$). The corresponding ORF (Open Reading Frame), gene name and protein function are listed. The table is arranged according to the most up-regulated gene with the highest fold difference.

ORF	GENE	PROTEIN (FUNCTION)	FOLD
SaMRSA252-0153 (2L7)	**capC**	capsular polysaccharide synthesis enzyme	**64.0**
SaMRSA252-2295 (6N17)		putative exported protein	**36.6**
SaMRSA252-0154 (2M7)	**capD**	capsular polysaccharide synthesis enzyme	**33.3**
SaMRSA252-0155 (2N7)	**capE**	capsular polysaccharide synthesis enzyme	**24.5**
SaMRSA252-0225 (2E16)	**fadD**	putative acyl-CoA dehydrogenase (involved in electron transport)	**23.0**
SaMRSA252-0169 (2L9)		putative aldehyde dehydrogenase (oxidoreductase activity; metabolism)	**17.9**
SaMRSA252-0157 (2P7)	**capG**	capsular polysaccharide synthesis enzyme	**16.7**
SaMRSA252-0152 (2K7)	**capB**	capsular polysaccharide synthesis enzyme	**15.3**
SaMRSA252-0156 (2O7)	**capF**	capsular polysaccharide synthesis enzyme	**14.2**
SaMRSA252-0191 (2J12)		conserved hypothetical protein	**14.2**
SaMRSA252-0223 (2C16)	**fadA**	putative thiolase (involved in degradative pathways e.g. fatty acid beta-oxidation)	**12.8**
SaMRSA252-0193 (2L12)		sucrose-specific PTS tranporter protein (membrane component-functions as sugar transport system)	**12.7**
SaMRSA252-0227 (2G16)	**fadX**	putative acetyl-CoA transferase (fatty acid metabolism; CoA-transferase activity)	**12.4**
SaMRSA252-1773 (5B14)	**citC**	isocitrate dehydrogenase (carbohydrate metabolism; TCA cycle)	**11.6**
SaMRSA252-0919	**rocD**	ornithine aminotransferase (transaminase activity and pyridoxal phosphate binding)	**11.6**

(3A17)			
SaMRSA252-0226 (2F16)	**fadE**	putative acyl-CoA synthetase (metabolism and catalytic activity)	**11.4**
SaMRSA252-0192 (2K12)		conserved hypothetical protein	**11.4**
SaMRSA252-0194 (2M12)		RpiR family transcriptional regulator (metabolism and regulation of transcription)	**10.8**
SaMRSA252-1787 (5H15)	**ald1**	alanine dehydrogenase 1(oxidoreductase activity and electron transport)	**10.5**
SaMRSA252-0920 (3B17)		putative NAD-specific glutamate dehydrogenase (oxidoreductase activity and amino acid metabolism)	**10.4**
SaMRSA252-1774 (5C14)	**citZ**	citrate synthase II (carbohydrate metabolism: TCA)	**9.9**
SaMRSA252-0158 (2I8)	**cap8H**	capsular polysaccharide synthesis enzyme	**9.8**
SaMRSA252-0224 (2D16)	**fadB**	putative fatty oxidation complex protein (oxidoreductase activity; fatty acid metabolism)	**9.1**
SaMRSA252-0405 (2L14)		hypothetical protein	**8.8**
SaMRSA252-1614 (5G6)	**gcvT**	putative aminomethyltransferase (glycine metabolism)	**8.7**
SaMRSA252-0842 (2F7)	**clfA**	clumping factor	**8.7**
SaMRSA252-0162 (2M8)	**capL**	capsular polysaccharide synthesis enzyme	**8.6**
SaMRSA252-0161 (2L8)	**cap8K**	capsular polysaccharide synthesis enzyme	**8.5**
SaMRSA252-0151 (2J7)	**capA**	capsular polysaccharide synthesis enzyme	**8.4**
SaMRSA252-0577 (3G11)	**proP**	putative proline/betaine transporter (integral to membrane; transporter activity)	**8.3**
SaMRSA252-1362 (4M11)	**citB**	aconitate hydratase (carbohydate metabolism; TCA cycle)	**8.1**
SaMRSA252-1849 (5E23)		proline dehydrogenase (proline catabolism; glutamate biosynthesis)	**7.9**
SaMRSA252-1871 (5K14)	**pckA**	phosphoenolpyruvate carboxykinase (ATP binding; gluconeogenesis)	**7.8**
SaMRSA252-1222 (1K6)		putative succinyl-CoA ligase (catalytic activity; metabolism)	**7.4**
SaMRSA252-2688		hypothetical protein	**7.3**

(7I18)			
SaMRSA252-2109 (6J7)		putative peptidase (hydrolase; proteolysis)	**7.3**
SaMRSA252-0921 (3C17)	**glpQ**	putative glycerophosphoryl diester phosphodiesterase (glycerol metabolism)	**7.2**
SaMRSA252-1612 (5E6)		putative glycine cleavage system P-protein (lyase activity; amino acid metabolism)	**7.2**
SaMRSA252-2420 (7B9)		arginase family protein (metal ion binding)	**7.1**
SaMRSA252-1121 (4H5)	**sdhA**	putative succinate dehydrogenase flavoprotein subunit (oxidoreductase activity; electron transport)	**7.1**
SaMRSA252-2634 (7E23)		aldehyde dehydrogenase family protein (oxidoreductase activity; metabolism)	**7.0**
SaMRSA252-0163 (2N8)	**capM**	capsular polysaccharide synthesis enzyme	**6.9**
SaMRSA252-1811 (5G18)	**acsA**	acetyl-coenzyme A synthetase (catalytic activity; metabolism)	**6.8**
SaMRSA252-2559 (7C14)		putative short chain dehydrogenase (oxidoreductase activity; metabolism)	**6.8**
SaMRSA252-1425 (4C19)	**odhA, citK**	2-oxoglutarate dehydrogenase E1 component (oxidoreductase activity; metabolism)	**6.8**
SaMRSA252-2469 (7K3)		conserved hypothetical protein (Flavin mononucleotide binding))	**6.7**
SaMRSA252-0624 (3L5)		putative esterase	**6.7**
SaMRSA252-1221 (1J6)		putative CoA synthetase protein (catalytic activity; metabolism)	**6.6**
SaMRSA252-1684 (5J3)		conserved hypothetical protein	**6.6**
SaMRSA252-2275 (6J15)		putative membrane protein	**6.4**
SaMRSA252-0211 (2F14)		conserved hypothetical protein (myo-inositol catabolism)	**6.4**
SaMRSA252-0048 (1F6)		putative membrane protein -partial (integral to membrane)	**6.3**
SaMRSA252-0164 (2O8)	**capN**	capsular polysaccharide synthesis enzyme	**6.2**
SaMRSA252-0855 (2B9)		hypothetical protein	**6.0**
SaMRSA252-0208 (2C14)		putative sugar transport system permease	**5.9**

SaMRSA252-1050 (3J21)		ABC transporter ATP-binding protein (ATP binding/ATPase activity)	**5.7**
SaMRSA252-2647 (7H24)		putative membrane protein	**5.6**
SaMRSA252-1686 (5L3)		putative biotin carboxyl carrier protein of acetyl-CoA carboxylase	**5.4**
SaMRSA252-1810 (5F18)	**fhs**	formate--tetrahydrofolate ligase (folic acid and derivative biosynthesis)	**5.4**
SaMRSA252-1424 (4B19)	**odhB**	dihydrolipoamide succinyltransferase E2 component of 2-oxoglutarate dehydrogenase complex (acyltransferase activity; metabolism)	**5.3**
SaMRSA252-0996 (3M14)		conserved hypothetical protein	**5.2**
SaMRSA252-2388 (7D5)		putative exported protein	**5.2**
SaMRSA252-0938 (3D19)	**clpB**	putative ATPase subunit of an ATP-dependent protease (ATP binding; protein metabolism)	**5.1**
SaMRSA252-2558 (7B14)		conserved hypothetical protein	**5.1**
SaMRSA252-2274 (6I15)		putative membrane protein	**5.1**
SaMRSA252-2646 (7G24)		putative phytoene dehydrogenase related protein (oxidoreductase activity; electron transport)	**5.1**
SaMRSA252-0721 (1N16)		multicopper oxidase protein (oxidoreductase activity; copper ion binding)	**5.0**
SaMRSA252-2668 (7M15)		conserved hypothetical protein	**4.9**
SaMRSA252-0171 (2N9)		hypothetical protein	**4.8**
SaMRSA252-0312 (1A15)		putative N-acetylneuraminate lyase (metabolism)	**4.8**
SaMRSA252-1683 (5I3)		putative membrane protein	**4.8**
SaMRSA252-1685 (5K3)		putative biotin carboxylase subunit of acetyl-CoA carboxylase (urea cycle and biosynthesis of arginine and pyrimidines)	**4.7**
SaMRSA252-1879		putative lipoprotein	**4.7**

(5J15)			
SaMRSA252-2544 (7L12)		ABC transporter ATP-binding protein (ATP-binding/ATPase activity)	**4.7**
SaMRSA252-2661 (7N14)		putative hydrolase	**4.7**
SaMRSA252-1120 (4G5)	**sdhC**	putative succinate dehydrogenase cytochrome b558	**4.6**
SaMRSA252-0305 (1B14)		putative membrane protein	**4.6**
SaMRSA252-2645 (7F24)		putative glycosyl transferase	**4.6**
SaMRSA252-1049 (3I21)		putative cobalt transport protein (cobalamin biosynthesis)	**4.6**
SaMRSA252-0165 (2P8)	**capO**	capsular polysaccharide synthesis enzyme	**4.6**
SaMRSA252-2561 (7E14)		conserved hypothetical protein (aromatic compound metabolism)	**4.6**
SaMRSA252-1051 (3K21)		putative membrane protein	**4.6**
SaMRSA252-2543 (7K12)		putative membrane protein	**4.5**
SaMRSA252-1880 (5K15)		putative membrane protein	**4.4**
SaMRSA252-2780 (8C5)		putative membrane protein	**4.4**
SaMRSA252-2747 (8C1)	**icaA**	glucosaminyltransferase	**4.3**
SaMRSA252-2695 (7P18)	**nrdD**	anaerobic ribonucleoside-triphosphate reductase (catalytic activity; metabolism)	**4.3**
SaMRSA252-2395 (7C6)		inositol monophosphatase family protein	**4.3**
SaMRSA252-2728 (7I23)		preprotein translocase SecA subunit-like protein (membrane component)	**4.2**
SaMRSA252-1152 (4E9)		acetyltransferase (GNAT) family protein (transcription and DNA repair)	**4.2**
SaMRSA252-0985 (3J13)		conserved hypothetical protein (RNA metabolism)	**4.2**
SaMRSA252-0306 (1C14)		ABC transporter ATP-binding protein (ATPbinding/ATPase activity)	**4.2**
SaMRSA252-0210		putative oxidoreductase (oxidoreductase activity; electron transport)	**4.2**

(2E14)			
SaMRSA252-2596 (7H18)		conserved hypothetical protein	**4.1**
SaMRSA252-1344 (4K9)		catalase (response to oxidative stress)	**4.1**
SaMRSA252-1037 (3M19)	**folD**	FolD bifunctional protein (catalytic activity; folic acid and derivative biosynthesis)	**4.1**
SaMRSA252-0170 (2M9)		putative cation efflux system protein (membrane component involved in removal of divalent metal ions from cells)	**4.0**
SaMRSA252-1766 (5C13)	**gap2**	glyceraldehyde 3-phosphate dehydrogenase 2 (glycolysis)	**3.8**
SaMRSA252-1785 (5F15)		metallo-beta-lactamase superfamily protein	**3.8**
SaMRSA252-0166 (2I9)	**capP**	capsular polysaccharide synthesis enzyme	**3.8**
SaMRSA252-2182 (6B16)	**thiD**	putative phosphomethylpyrimidine kinase (thiamine pyrophosphate synthesis pathway)	**3.8**
SaMRSA252-2393 (7A6)		putative bifunctional protein (iron and molybdenum ion binding; electron transport)	**3.7**
SaMRSA252-0189 (2P11)		putative thiamine pyrophosphate enzyme (magnesium ion binding; thiamine pyrophosphate binding)	**3.7**
SaMRSA252-0311 (1H14)		sodium:solute symporter family protein (membrane transporter activity)	**3.7**
SaMRSA252-0806 (2C3)		putative S30EA family ribosomal protein	**3.7**
SaMRSA252-0279 (2B23)		conserved hypothetical protein	**3.7**
SaMRSA252-0952 (3B21)	**oppF**	putative oligopeptide transport ATP-binding protein	**3.7**
SaMRSA252-2181 (6A16)	**thiM**	putative hydroxyethylthiazole kinase (thiamine biosynthesis)	**3.7**
SaMRSA252-0675 (3N11)		putative exported protein (cell wall catabolism)	**3.6**
SaMRSA252-2568 (7D15)		hypothetical protein	**3.6**
SaMRSA252-2210 (6F19)		aldehyde dehydrogenase family protein (oxidoreductase activity; metabolism)	**3.6**

SaMRSA252-1190 (1K2)		putative membrane protein	**3.6**
SaMRSA252-0207 (2B14)		putative sugar transport system permease (membrane; transporter function)	**3.6**
SaMRSA252-1688 (5N3)		conserved hypothetical protein	**3.6**
SaMRSA252-0824 (2D5)		putative malolactic enzyme (oxidoreductase activity)	**3.5**
SaMRSA252-0867 (2F10)		hypothetical protein (nucleic acid binding; DNA modifcation)	**3.5**
SaMRSA252-0825 (2E5)		conserved hypothetical protein (nucleotide-sugar metabolism)	**3.5**
SaMRSA252-0188 (2O11)		putative isochorismatase (catalytic activity; metabolism)	**3.5**
SaMRSA252-0333 (1F17)	**glpT**	putative glycerol-3-phosphate transporter (major facilitator superfamily)	**3.5**
SaMRSA252-1788 (5A16)		putative universal stress protein (response to stress)	**3.5**
SaMRSA252-2180 (6H15)	**thiE**	putative thiamine-phosphate pyrophosphorylase (thiamine biosynthesis)	**3.4**
SaMRSA252-2589 (7A18)		putative transporter protein (major facilitator superfamily)	**3.4**
SaMRSA252-0629 (3I6)		phage integrase family protein (DNA binding)	**3.4**
SaMRSA252-2514 (7N8)		putative 8-amino-7-oxononanoate synthase (transaminase activity; biosynthesis/metabolism)	**3.4**
SaMRSA252-0951 (3A21)	**oppD**	putative oligopeptide transport ATP-binding protein (nucleotide-triphosphate activity; nucleotide binding)	**3.4**
SaMRSA252-0821 (2A5)		conserved hypothetical protein	**3.4**
SaMRSA252-1837 (5A22)		putative exported protein	**3.3**
SaMRSA252-0850 (2E8)		hypothetical protein	**3.3**
SaMRSA252-0609 (3M3)		conserved hypothetical protein (NADPH-dependent FMN reductase)	**3.3**
SaMRSA252-0953 (3C21)		transport system extracellular binding lipoprotein (transporter activity)	**3.3**

SaMRSA252-0499 (3A2)	**spoVG**	stage V sporulation protein G	**3.3**
SaMRSA252-0209 (2D14)		putative oxidoreductase (oxidoreductase activity; electron transport)	**3.3**
SaMRSA252-0661 (3P9)		putative dihydroxyacetone kinase (glycerol metabolism)	**3.2**
SaMRSA252-1965 (6F1)		ThiJ/PfpI family protein (transcriptional regulation)	**3.2**
SaMRSA252-2413 (7D8)		putative short chain dehydrogenase (oxidoreductase activity; metabolism)	**3.2**
SaMRSA252-2120 (6M8)		conserved hypothetical protein (oxidoreductase activity; electron transport)	**3.1**
SaMRSA252-0882 (2D12)		putative membrane protein	**3.1**
SaMRSA252-0841 (2E7)		putative acetyltransferase	**3.1**
SaMRSA252-2628 (7G22)	**clpL**	putative ATP-dependent protease ATP-binding subunit ClpL (ATP binding; nucleotide-excision repair)	**3.1**
SaMRSA252-2749 (8E1)	**icaB**	intercellular adhesion protein B (carbohydrate metabolism)	**3.1**
SaMRSA252-2739 (7K24)		conserved hypothetical protein	**3.0**
SaMRSA252-0558 (3C9)		conserved hypothetical protein (catalytic activity; coenzyme binding; cellular metabolism)	**3.0**
SaMRSA252-0840 (2D7)		putative membrane protein	**3.0**
SaMRSA252-2392 (7H5)		conserved hypothetical protein	**3.0**
SaMRSA252-1772 (5A14)	**phoP**	alkaline phosphatase synthesis transcriptional regulatory protein - (regulation of transcription: DNA-dependent)	**3.0**
SaMRSA252-2748 (8D1)	**icaD**	intercellular adhesion protein D	**3.0**
SaMRSA252-0498 (3H1)	**yabJ**	putative regulatory protein	**2.9**
SaMRSA252-0757 (1J21)		putative glucosyl transferase (biosynthesis of disaccharides, oligosaccharides and polysaccharides)	**2.9**

SaMRSA252-0218 (2E15)		putative pyruvate formate-lyase activating enzyme (iron ion binding)	**2.9**
SaMRSA252-1026 (3J18)	**atl**	bifunctional autolysin precursor (peptidoglycan metabolism)	**2.9**
SaMRSA252-2224 (6D21)	**pyn; pdp**	putative pyrimidine-nucleoside phosphorylase (transferase activity; metabolism)	**2.9**
SaMRSA252-0299 (1E13)		hypothetical protein	**2.9**
SaMRSA252-2655 (7P13)		putative glyoxalase	**2.9**
SaMRSA252-1427 (4E19)	**arlR**	response regulator protein (regulation of transcription)	**2.9**
SaMRSA252-2727 (7P22)		hypothetical protein (biosynthesis of disaccharides, oligosaccharides, polysaccharides)	**2.9**
SaMRSA252-0883 (2E12)		putative dioxygenase (oxidoreductase; electron transport)	**2.8**
SaMRSA252-0111 (2J2)		putative myosin-crossreactive antigen	**2.8**
SaMRSA252-0744 (1M19)		putative DNA photolyase	**2.8**
SaMRSA252-2541 (7I12)		putative carboxylesterase	**2.8**
SaMRSA252-0334 (1G17)		putative dioxygenase	**2.8**
SaMRSA252-0944 (3B20)		putative exported protein	**2.8**
SaMRSA252-2276 (6K15)	**opuD2**	glycine betaine transporter 2 (membrane; transporter activity)	**2.8**
SaMRSA252-2184 (6D16)		putative exported protein (probable transglycosylase enzyme)	**2.8**
SaMRSA252-0735 (1L18)		putative exported protein	**2.8**
SaMRSA252-2119 (6L8)		membrane anchored protein	**2.8**
SaMRSA252-2610 (7E20)		putative L-serine dehydratase, alpha chain (gluconeogenesis)	**2.8**
SaMRSA252-0464 (2N21)		putative exported protein (cell wall catabolism)	**2.7**
SaMRSA252-0390 (1E24)		putative lipoprotein (metalloprotease activity; Zn ion binding)	**2.7**

SaMRSA252-0575 (3E11)		putative 6-phospho-3-hexuloisomerase (sugar binding; carbohydrate metabolism)	**2.7**
SaMRSA252-2454 (7L1)	**mqo1**	putative malate:quinone oxidoreductase 1 (citric acid cycle)	**2.7**
SaMRSA252-2648 (7I13)	**ssaA**	secretory antigen precursor (cell wall metabolism)	**2.7**
SaMRSA252-1564 (4N24)		hypothetical protein (partial)	**2.7**
SaMRSA252-0849 (2D8)		hypothetical protein	**2.7**
SaMRSA252-0309 (1F14)		putative membrane protein	**2.7**
SaMRSA252-2694 (7O18)	**nrdG**	putative anaerobic ribonucleotide reductase activating protein	**2.6**
SaMRSA252-2611 (7F20)		putative L-serine dehydratase, beta chain (gluconeogenesis)	**2.6**
SaMRSA252-0280 (2C23)		putative membrane protein	**2.6**
SaMRSA252-0660 (3O9)		putative dihydroxyacetone kinase (glycerol metabolism)	**2.6**
SaMRSA252-2010 (6B7)		hypothetical protein	**2.6**
SaMRSA252-0557 (3B9)		putative L-ribulokinase (carbohydrate metabolism)	**2.6**
SaMRSA252-1687 (5M3)		conserved hypothetical protein	**2.5**
SaMRSA252-0222 (2A16)	**coa**	staphylocoagulase precursor [conserved region]	**2.5**
SaMRSA252-1814 (5B19)	**ccpA**	catabolite control protein A (regulation of transcription-DNA-dependent)	**2.5**
SaMRSA252-0273 (2D22)	**lytM**	peptidoglycan hydrolase (metalloendopeptidase activity;proteolysis)	**2.5**
SaMRSA252-2660 (7M14)		conserved hypothetical protein (metabolism)	**2.5**
SaMRSA252-1274 (1O12)	**glpF**	putative glycerol uptake facilitator protein (transport)	**2.5**
SaMRSA252-0574 (3D11)		putative hexulose-6-phosphate synthase ('de novo' pyrimidine base biosynthesis)	**2.5**
SaMRSA252-2444		putative membrane protein	**2.5**

(7B12)			
SaMRSA252-2642 (7D24)	**crtN**	squalene synthase (oxidoreductase activity; electron transport)	**2.5**
SaMRSA252-0630 (3J6)		putative NADH-Ubiquinone/plastoquinone (complex I) oxidoreductase protein (ATP synthesis coupled electron transport)	**2.5**
SaMRSA252-2233 (6E22)	**czrA; rzcA**	zinc and cobalt transport repressor protein (regulation of transcription-DNA-dependent)	**2.5**
SaMRSA252-0138 (2M5)	**deoD1**	putative purine nucleoside phosphorylase (nucleoside metabolism)	**2.5**
SaMRSA252-1857 (5E24)		putative exported protein (peptidoglycan metabolism)	**2.5**
SaMRSA252-2560 (7D14)		putative transport protein	**2.4**
SaMRSA252-2517 (7I9)		putative dethiobiotin synthetase	**2.4**
SaMRSA252-1426 (4D19)	**arlS**	sensor kinase protein (signal transduction)	**2.4**
SaMRSA252-1289 (4M2)		putative exported protein	**2.4**
SaMRSA252-2740 (7L24)		conserved hypothetical protein	**2.4**
SaMRSA252-2273 (6P14)	**asp23**	alkaline shock protein 23 (possible role in stress response)	**2.4**
SaMRSA252-2781 (8D5)	**vraD**	ABC transporter ATP-binding protein (ATP-binding/ATPase activity)	**2.4**
SaMRSA252-0813 (2B4)	**uvrA**	excinuclease ABC subunit A (ATP-binding/ATPase activity)	**2.4**
SaMRSA252-2612 (7G20)		putative membrane protein	**2.4**
SaMRSA252-0206 (2A14)		putative extracellular sugar-binding lipoprotein (transporter activity)	**2.4**
SaMRSA252-1290 (4N2)		putative exported protein (possible role in peptidoglycan hydrolysis)	**2.4**
SaMRSA252-0277 (2H22)		putative exported protein	**2.4**
SaMRSA252-0950 (3H20)	**oppC**	putative oligopeptide transport system permease protein (transporter activity)	**2.3**
SaMRSA252-0625 (3M5)	**sarA**	staphylococcal accessory regulator A	**2.3**

SaMRSA252-1440 (4B21)	**thyA;thyE**	thymidylate synthase	**2.3**
SaMRSA252-2752 (8G1)		conserved hypothetical protein	**2.3**
SaMRSA252-0222v (2B16)	**coa**	staphylocoagulase precursor [variable region]	**2.3**
SaMRSA252-2667 (7L15)		hypothetical protein	**2.3**
SaMRSA252-2602 (7F19)		glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	**2.2**
SaMRSA252-2223 (6C21)		putative membrane protein	**2.2**
SaMRSA252-2656 (7I14)		conserved hypothetical protein (regulation of nitrogen utilization)	**2.2**
SaMRSA252-0839 (2C7)		putative lipoprotein	**2.2**
SaMRSA252-2245 (6G23)		putative transcriptional antiterminator (regulation of transcription, DNA-dependent)	**2.2**
SaMRSA252-0128 (2K4)		putative membrane protein	**2.2**
SaMRSA252-2665 (7J15)		conserved hypothetical protein	**2.2**
SaMRSA252-1360 (4K11)	**mscL**	large-conductance mechanosensitive channel (ion channel activity; possible role in regulation of osmotic pressure changes within the cell)	**2.2**
SaMRSA252-0147 (2N6)		putative nucleotidase (nucleotide catabolism)	**2.2**
SaMRSA252-0734 (1K18)		conserved hypothetical protein	**2.2**
SaMRSA252-2228 (6H21)		conserved hypothetical protein	**2.2**
SaMRSA252-0308 (1E14)		PfkB family carbohydrate kinase (thiamine pyrophsophate synthesis)	**2.2**
SaMRSA252-2696 (7I19)		putative transporter protein (citrate transporter)	**2.2**
SaMRSA252-1813 (5A19)		histone deacetylase family protein (regulation of transcription)	**2.2**
SaMRSA252-1703 (5L5)		putative oxygenase	**2.2**

SaMRSA252-1616 (5A7)		putative membrane protein	**2.2**
SaMRSA252-0868 (2G10)		putative thioredoxin	**2.2**
SaMRSA252-0205 (2H13)		putative ABC transporter, ATP-binding protein	**2.1**
SaMRSA252-2726 (7O22)		conserved hypothetical protein	**2.1**
SaMRSA252-0581 (3B12)		putative ketoacyl-CoA thiolase	**2.1**
SaMRSA252-1615 (5H6)		putative shikimate kinase (amino acid biosynthesis)	**2.1**
SaMRSA252-2189 (6A17)		putative membrane protein	**2.1**
SaMRSA252-0555 (3H8)	**kbl**	putative 2-amino-3-ketobutyrate coenzyme A ligase (pyridoxal phosphate binding; transaminase activity)	**2.1**
SaMRSA252-1387 (4F14)	**femA**	factor essential for expression of methicillin resistance (antibiotic resistance)	**2.1**
SaMRSA252-0313 (1B15)		putative ROK family protein (transcriptional repressors)	**2.1**
SaMRSA252-2624 (7C22)		putative exported protein (cell wall metabolism)	**2.1**
SaMRSA252-2619 (7F21)		thiamine pyrophosphate enzyme (Mg ion binding; thiamin pyrophosphate binding)	**2.1**
SaMRSA252-0092 (1H11)		putative hydratase (metabolism)	**2.1**
SaMRSA252-2567 (7C15)		putative short chain dehydrogenase (oxidoreductase activity; metabolism)	**2.0**
SaMRSA252-2152 (6M12)	**sigB**	RNA polymerase sigma-B factor	**2.0**
SaMRSA252-2443 (7A12)	**tcaR**	MarR family regulatory protein (regulation of transcription)	**2.0**
SaMRSA252-0776 (1M23)		ABC transporter permease protein (transport)	**2.0**
SaMRSA252-2467 (7I3)		conserved hypothetical protein	**2.0**
SaMRSA252-2734 (7N23)	**sasA**	putative serine rich repeat containing protein (LPXTG surface protein; cell surface component)	**2.0**

SaMRSA252-1458 (4D23)		conserved hypothetical protein	**2.0**
SaMRSA252-2394 (7B6)		putative exported protein (cell envelope-related transcriptional attenuator domain)	**2.0**
SaMRSA252-1478 (4P13)	**ndk**	putative nucleoside diphosphate kinase (ATP binding)	**2.0**
SaMRSA252-1439 (4A21)	**dfrB**	dihydrofolate reductase type I (nucleotide biosynthesis)	**2.0**
SaMRSA252-0877 (2G11)		conserved hypothetical protein	**2.0**
SaMRSA252-2782 (8E5)	**vraE**	ABC transporter permease protein	**2.0**
SaMRSA252-0749 (1J20)		putative exported protein	**1.9**
SaMRSA252-0631 (3K6)		putative membrane protein	**1.9**
SaMRSA252-0576 (3F11)		putative haloacid dehalogenase-like hydrolase (catalytic activity; metabolism)	**1.9**
SaMRSA252-0965 (3F22)		conserved hypothetical protein (cell redox homeostasis)	**1.9**
SaMRSA252-1048 (3P20)	**purD**	putative phosphoribosylamine--glycine ligase	**1.9**
SaMRSA252-0580 (3A12)		putative AMP-binding enzyme	**1.9**
SaMRSA252-0837 (2A7)	**smpB**	putative tmRNA-binding protein (protein biosynthesis)	**1.9**
SaMRSA252-2689 (7J18)		hypothetical protein	**1.9**
SaMRSA252-2546 (7N12)		putative lipoprotein	**1.9**
SaMRSA252-0602 (3O2)		putative membrane protein	**1.9**
SaMRSA252-0876 (2F11)		ABC transporter ATP-binding protein	**1.8**
SaMRSA252-2256 (6H24)		conserved hypothetical protein	**1.8**
SaMRSA252-0638 (3J7)		putative membrane protein (major facilitator superfamily)	**1.8**
SaMRSA252-0317 (1F15)	**geh**	lipase precursor	**1.8**

SaMRSA252-2386 (7B5)		putative dehydrogenase (glycerol-3-phosphate catabolism)	**1.8**
SaMRSA252-2153 (6N12)	**rsbW**	anti-sigma B factor (ATP binding)	**1.8**
SaMRSA252-2666 (7K15)		hypothetical protein	**1.8**
SaMRSA252-2528 (7L10)		putative amino acid permease (transport)	**1.8**
SaMRSA252-2635 (7F23)		putative acetyltransferase	**1.8**
SaMRSA252-2641 (7C24)		putative aminotransferase (biosynthesis)	**1.8**
SaMRSA252-0598 (3K2)	**mvaK2**	phosphomevalonate kinase (ATP binding;phosphorylation)	**1.8**
SaMRSA252-2737 (7I24)		conserved hypothetical protein	**1.8**
SaMRSA252-2778 (8A5)		putative nickel transport protein (metal ion binding/transport)	**1.7**
SaMRSA252-1017 (3I17)		putative menaquinone biosynthesis bifunctional protein (thiamin pyrophosphate binding)	**1.7**
SaMRSA252-0931 (3E18)		putative membrane protein	**1.7**
SaMRSA252-2729 (7J23)		hypothetical protein	**1.7**
SaMRSA252-0140 (2O5)	**deoC1**	deoxyribose-phosphate aldolase	**1.7**
SaMRSA252-0113 (2L2)	**lldP1**	L-lactate permease 1(lactate transport)	**1.7**
SaMRSA252-0949 (3G20)	**oppB**	putative oligopeptide transport system permease protein (transporter activity)	**1.7**
SaMRSA252-2277 (6L15)		putative zinc-binding dehydrogenase	**1.7**
SaMRSA252-0314 (1C15)		putative transcription regulator (regulation of transcription, DNA-dependent)	**1.7**
SaMRSA252-0939 (3E19)		LysR family regulatory protein (regulation of transcription, DNA-dependent)	**1.7**
SaMRSA252-1220 (1I6)	**rnhB**	putative ribonuclease HII (RNA binding)	**1.6**
SaMRSA252-1021 (3M17)	**sspB**	cysteine protease precursor (proteolysis)	**1.6**

SaMRSA252-0733 (1J18)		conserved hypothetical protein	**1.6**
SaMRSA252-2730 (7K23)		conserved hypothetical protein	**1.6**
SaMRSA252-2396 (7D6)		DeoR family regulatory protein	**1.6**
SaMRSA252-0836 (2H6)	**rnr**	putative ribonuclease R (RNA binding)	**1.6**
SaMRSA252-0838 (2B7)		putative membrane protein	**1.5**
SaMRSA252-1577 (5B2)		hypothetical protein	**1.5**
SaMRSA252-0862 (2A10)		putative thioredoxin	**1.5**
SaMRSA252-2366 (7F2)		BioY family protein	**1.5**
SaMRSA252-2731 (7L23)		conserved hypothetical protein (pseudogene)	**1.4**
SaMRSA252-2735 (7O23)		conserved hypothetical protein	**1.4**
SaMRSA252-0740 (1I19)		putative cobalamin synthesis protein	**1.3**
SaMRSA252-0860 (2G9)		putative type I 3-dehydroquinase (aromatic amino acid family biosynthesis)	**1.3**

Table 4.2: Down-regulated ASM genes, normalised to BHI, using one-way ANOVA and posthoc Benjamini and Hochberg tests ($p \leq 0.05$). The corresponding ORF (Open reading frame), gene name and protein function are listed. The table is arranged according to the most down-regulated gene with the highest fold difference.

ORF	GENE	PROTEIN (FUNCTION)	FOLD
SaMW2-0754 (10A9)		hypothetical protein	**-22.2**
SaMRSA252-0259 (2F20)	**lrgA**	holin-like protein (possible role in murein hydrolysis and penicillin tolerance)	**-10.8**
SaMRSA252-0114 (2M2)	**spa**	immunoglobulin G binding protein A precursor (surface protein)	**-9.2**
SaMRSA252-2131 (6P9)		conserved hypothetical protein	**-7.3**
SaMRSA252-2504 (7L7)		extracellular solute-binding lipoprotein (transport)	**-6.4**
SaMRSA252-2438 (7D11)		putative exported protein	**-5.8**
SaMRSA252-0260 (2G20)	**lrgB**	holin-like protein (possible role in murein hydrolysis and penicillin tolerance)	**-4.9**
SaMRSA252-1060 (3L22)		putative membrane protein	**-4.9**
SaMRSA252-2437 (7C11)		putative transport protein	**-4.6**
SaMRSA252-2503 (7K7)		transport system membrane protein (major facilitator superfamily)	**-4.6**
SaMRSA252-1454 (4H22)		putative membrane protein-pseudogene (metallopeptidase activity/Zn ion binding/proteolysis)	**-4.6**
SaMRSA252-2502 (7J7)		ABC transporter ATP-binding protein (ATP binding/ATPase activity)	**-4.1**
SaMRSA252-0172 (2O9)		conserved hypothetical protein	**-4.0**
SaMRSA252-2488 (7M5)	**nasE**	assimilatory nitrite reductase small subunit (oxidoreductase ativity; electron transport)	**-3.9**
SaMRSA252-0752		putative phosphofructokinase (thiamine pyrophosphate synthesis)	**-3.9**

(1M20)			
SaMRSA252-1133 (4D7)		putative membrane protein	**-3.8**
SaMRSA252-2489 (7N5)	**nasD**	nitrite reductase large subunit (disulfide oxidoreductase activity; electron transport)	**-3.7**
SaMRSA252-0906 (3D15)		conserved hypothetical protein (catalytic activity)	**-3.7**
SaMRSA252-2508 (7P7)	**sbi**	IgG-binding protein	**-3.6**
SaMRSA252-2132 (6I10)		putative membrane protein	**-3.6**
SaMRSA252-0905 (3C15)		putative transporter protein (Sodium ion transport/regulation of pH)	**-3.6**
SaMRSA252-1237 (1J8)		putative phosphatidate cytidylyltransferase (phospholipid biosynthesis)	**-3.6**
SaMRSA252-2470 (7L3)		putative exported protein	**-3.6**
SaMRSA252-1010 (3J16)		putative membrane protein	**-3.5**
SaMRSA252-2799 (8C7)	**rnpA**	ribonuclease P protein component (ribonuclease activity/tRNA processing)	**-3.5**
SaMRSA252-2320 (6P20)	**rplF**	50S ribosomal protein L6 (structural constituent of ribosome)	**-3.5**
SaMRSA252-2476 (7J4)	**narT**	nitrite transport protein (major facilitaor superfamily)	**-3.3**
SaMRSA252-0401 (2P13)		putative sodium:dicarboxylate symporter protein	**-3.3**
SaMRSA252-2709 (7N20)	**clfB**	fibrinogen and keratin-10 binding surface anchored protein (cell surface protein)	**-3.3**
SaMRSA252-0926 (3H17)	**spsA**	putative signal peptidase Ia (proteolysis)	**-3.1**
SaMRSA252-0694 (1P13)		putative exported protein	**-3.1**
SaMRSA252-0753 (1N20)	**fruA**	PTS transport system, fructose-specific IIABC component (sugar porter activity)	**-3.1**
SaMRSA252-0212 (2G14)		putative membrane protein (C-terminal protein amino acid methylation)	**-3.1**
SaMRSA252-2168 (6E14)		putative helicase (ATP binding; helicase activity; nucleic acid binding)	**-3.1**

SaMRSA252-1235 (1P7)	**frr**	ribosome recycling factor (protein biosynthesis)	**-3.0**
SaMRSA252-0790 (2C1)	**sstD**	lipoprotein (iron ion transport activity)	**-3.0**
SaMRSA252-1052 (3L21)		hypothetical protein	**-3.0**
SaMRSA252-2316 (6L20)	**rplO**	50S ribosomal protein L15 (protein biosynthesis)	**-3.0**
SaMRSA252-1059 (3K22)		putative cytochrome ubiquinol oxidase (membrane component; oxidoreductase activity; electron transport)	**-3.0**
SaMRSA252-1777 (5F14)	**pfkA**	6-phosphofructokinase (glycolysis)	**-2.9**
SaMRSA252-1127 (4F6)		putative exported protein	**-2.9**
SaMRSA252-2328 (6P21)	**rplP**	50S ribosomal protein L16 (protein biosynthesis)	**-2.9**
SaMRSA252-0234 (2F17)	**ldh1**	L-lactate dehydrogenase 1(oxidoreductase activity; TCA intermediate metabolism)	**-2.9**
SaMRSA252-1450 (4D22)	**tdcB**	putative threonine dehydratase (pyridoxal phosphate dependent enzyme; metabolism)	**-2.9**
SaMRSA252-0827 (2G5)	**gapR**	glycolytic operon regulator (carbohydrate binding; transcription regulator activity)	**-2.8**
SaMRSA252-2020 (6D8)		putative membrane protein	**-2.8**
SaMRSA252-1186 (1O1)		conserved hypothetical protein (transcription, DNA-dependent)	**-2.8**
SaMRSA252-0543 (3D7)	**rplA**	50S ribosomal protein L1(protein biosynthesis)	**-2.8**
SaMRSA252-2321 (6I21)	**rpsH**	30S ribosomal protein S8 (protein biosynthesis)	**-2.8**
SaMRSA252-0363 (1C21)	**ssb**	putative single-strand DNA-binding protein (single-stranded DNA binding)	**-2.7**
SaMRSA252-0787 (1P24)	**sstA**	FecCD transport family protein (membrane; transporter activity)	**-2.7**
SaMRSA252-1759 (5L12)	**rpmI**	50S ribosomal protein L35 (protein biosynthesis)	**-2.7**
SaMRSA252-2219 (6G20)		hypothetical protein	**-2.7**

SaMRSA252-1204 (1I4)		conserved hypothetical protein	**-2.7**
SaMRSA252-0910 (3H15)	**mnhE**	Na+/H+ antiporter subunit (integral to membrane; cation transport)	**-2.6**
SaMRSA252-0173 (2P9)		putative ABC transporter ATP-binding protein (ATP binding; ATPase activity)	**-2.6**
SaMRSA252-1715 (5P6)	**apt**	adenine phosphoribosyltransferase (nucleoside metabolism)	**-2.6**
SaMRSA252-0408 (2O14)	**guaB**	putative inosine-5'-monophosphate dehydrogenase (catalytic activity)	**-2.6**
SaMRSA252-0946 (3D20)	**fabH**	putative 3-oxoacyl-[acyl-carrier-protein] synthase III (fatty acid synthesis)	**-2.6**
SaMRSA252-2324 (6L21)	**rplX**	50S ribosomal protein L24	**-2.6**
SaMRSA252-0789 (2B1)	**sstC**	ABC transporter ATP-binding protein (ATP binding/ATPase activity)	**-2.6**
SaMRSA252-2315 (6K20)	**secY**	preprotein translocase SecY subunit (protein secretion)	**-2.5**
SaMRSA252-0257 (2D20)	**lytS**	autolysin sensor kinase protein (2component signal transduction (photorelay); cell wall organization and biogenesis	**-2.5**
SaMRSA252-0452 (2J20)		putative NADH-Ubiquinone/plastoquinone (complex I) protein (ATP synthesis coupled electron transport)	**-2.5**
SaMRSA252-0897 (3C14)	**dltD**	putative lipoteichoic acid biosynthesis protein (biosynthesis of D-alanyl-lipoteichoic acid)	**-2.5**
SaMRSA252-1236 (1I8)	**uppS**	undecaprenyl pyrophosphate synthetase (transferase activity; metabolism)	**-2.5**
SaMRSA252-0344 (1H18)		putative Sec-independent protein translocase protein (protein transporter activity)	**-2.5**
SaMRSA252-0454 (2L20)		conserved hypothetical protein	**-2.5**
SaMRSA252-2004 (6D6)		putative membrane protein	**-2.5**
SaMRSA252-2678 (7O16)		putative ketopantoate reductase (glycerol-3-phosphate catabolism)	**-2.5**
SaMRSA252-2344 (6P23)		putative membrane protein	**-2.5**
SaMRSA252-1836		putative peptidase (metallopeptidase activity; proteolysis)	**-2.4**

(5H21)			
SaMRSA252-1939 (5L22)		putative response regulator (regulation of transcription, DNA-dependent)	**-2.4**
SaMRSA252-0174 (2I10)		putative lipoprotein	**-2.4**
SaMRSA252-1174 (4C12)	**pyrR**	putative pyrimidine operon regulatory protein (nucleoside metabolism)	**-2.4**
SaMRSA252-0912 (3B16)	**mnhC**	Na+/H+ antiporter subunit	**-2.4**
SaMRSA252-0542 (3C7)	**rplK**	50S ribosomal protein L11(protein biosynthesis)	**-2.4**
SaMRSA252-2308 (6L19)	**rplQ**	50S ribosomal protein L17 (protein biosynthesis)	**-2.4**
SaMRSA252-0455 (2M20)		putative membrane protein	**-2.4**
SaMRSA252-1776 (5E14)	**pyk**	pyruvate kinase (phosphorylation)	**-2.4**
SaMRSA252-2675 (7L16)	**panD**	putative aspartate 1-decarboxylase precursor (alanine biosynthesis)	**-2.4**
SaMRSA252-0894 (3H13)	**dltA**	D-alanine-D-alanyl carrier protein ligase (catalytic activity; metabolism)	**-2.4**
SaMRSA252-2003 (6C6)		conserved hypothetical protein	**-2.4**
SaMRSA252-1134 (4E7)		hypothetical protein	**-2.4**
SaMRSA252-0914 (3D16)	**mnhA**	Na+/H+ antiporter subunit (electron transport)	**-2.4**
SaMRSA252-1419 (4E18)		putative branched-chain amino acid transporter protein (branched chain aliphatic amino acid transport)	**-2.4**
SaMRSA252-2669 (7N15)		putative dihydroorotate dehydrogenase ('de novo' pyrimidine base biosynthesis)	**-2.4**
SaMRSA252-2369 (7A3)		conserved hypothetical protein (electron transport)	**-2.3**
SaMRSA252-2618 (7E21)	**glcB**	PTS system, glucose-specific IIABC component (sugar porter activity)	**-2.3**
SaMRSA252-2500 (7P6)		putative lipoprotein	**-2.3**
SaMRSA252-1762	**thrS**	threonyl-tRNA synthetase (protein biosynthesis)	**-2.3**

(5O12)			
SaMRSA252-0791 (2D1)		hypothetical protein (Zn ion binding)	**-2.3**
SaMRSA252-1599 (5H4)		putative geranyltranstransferase (isoprenoid biosynthesis)	**-2.3**
SaMRSA252-2351 (6O24)		hypothetical protein (regulation of transcription)	**-2.3**
SaMRSA252-0788 (2A1)	**sstB**	FecCD transport family protein (membrane; transporter activity)	**-2.3**
SaMRSA252-2455 (7M1)	**lldP2**	putative L-lactate permease 2 (lactate transport)	**-2.3**
SaMRSA252-0546 (3G7)		conserved hypothetical protein (methyltransferase activity)	**-2.3**
SaMRSA252-1083 (4B1)		BipA family GTPase (GTP binding)	**-2.3**
SaMRSA252-2216 (6D20)	**rpoE**	DNA-directed RNA polymerase delta subunit (DNA binding;transcription)	**-2.3**
SaMRSA252-2484 (7I5)	**narJ**	respiratory nitrate reductase delta chain (nitrate reductase activity; electron transport)	**-2.3**
SaMRSA252-1206 (1K4)	**fabD**	putative malonyl CoA-acyl carrier protein transacylase (transferase activity; metabolism)	**-2.3**
SaMRSA252-1239 (1L8)	**proS**	prolyl-tRNA synthetase (protein biosynthesis)	**-2.2**
SaMRSA252-1601 (5B5)		putative exodeoxyribonuclease VII large subunit (DNA catabolism)	**-2.2**
SaMRSA252-1602 (5C5)		putative N utilization substance protein B (regulation of transcription; DNA-dependent)	**-2.2**
SaMRSA252-0063 (1E8)		hypothetical protein	**-2.2**
SaMRSA252-2341 (6M23)	**glcU**	glucose uptake protein (carbohydrate transport)	**-2.2**
SaMRSA252-2314 (6J20)	**adk**	adenylate kinase	**-2.2**
SaMRSA252-2215 (6C20)	**pyrG**	putative CTP synthase (pyrimidine nucleotide biosynthesis)	**-2.2**
SaMRSA252-0407 (2N14)	**pbuX**	putative xanthine permease (transporter activity)	**-2.2**
SaMRSA252-0256 (2C20)	**scdA**	cell wall metabolism protein	**-2.2**

SaMRSA252-1743 (5L10)	**valS**	valyl-tRNA synthetase (tRNA aminoacylation for protein translation)	**-2.2**
SaMRSA252-0799 (2D2)		putative membrane protein	**-2.2**
SaMRSA252-0909 (3G15)	**mnhF**	Na+/H+ antiporter subunit (membrane;ion transport)	**-2.2**
SaMRSA252-1711 (5L6)	**hisS**	histidyl-tRNA synthetase (tRNA aminoacylation for protein translation)	**-2.2**
SaMRSA252-1805 (5B18)		putative protease (proteolysis)	**-2.2**
SaMRSA252-0013 (1E2)		putative membrane protein	**-2.2**
SaMRSA252-1758 (5K12)	**rplT**	50S ribosomal protein L20 (protein biosynthesis)	**-2.1**
SaMRSA252-0890 (3D13)		conserved hypothetical protein	**-2.1**
SaMRSA252-2439 (7E11)		TetR family regulatory protein (regulation of transcription, DNA dependent)	**-2.1**
SaMRSA252-0681 (3K12)		conserved hypothetical protein	**-2.1**
SaMRSA252-2499 (7O6)		putative lipoprotein	**-2.1**
SaMRSA252-1778 (5G14)	**accA**	acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (fatty acid biosynthesis)	**-2.1**
SaMRSA252-1605 (5F5)	**accB; fabE**	biotin carboxyl carrier protein of acetyl-CoA carboxylase	**-2.1**
SaMRSA252-1111 (4F4)	**pheS**	putative phenylalanyl-tRNA synthetase alpha chain (phenylalanyl-tRNA aminoacylation)	**-2.1**
SaMRSA252-2621 (7H21)		putative membrane protein	**-2.1**
SaMRSA252-1404 (4F16)		ABC transporter ATP-binding protein (ATP binding/ATPase activity)	**-2.0**
SaMRSA252-0360 (1H20)		putative GTP-binding protein	**-2.0**
SaMRSA252-1551 (4I23)		hypothetical phage protein	**-2.0**
SaMRSA252-1136 (4F7)	**hla**	alpha-hemolysin precursor-pseudogene (haemolysis of red blood cells)	**-2.0**
SaMRSA252-2335	**rplC**	50S ribosomal protein L3 (protein biosynthesis)	**-2.0**

(6O22)			
SaMRSA252-1486 (4P14)	**cmk**	cytidylate kinase (nucleic acid metabolism)	**-2.0**
SaMRSA252-1207 (1L4)	**fabG**	3-oxoacyl-[acyl-carrier protein] reductase (oxidoreductase activity; metabolism)	**-2.0**
SaMRSA252-0366 (1F21)		putative integrase (family of phage integrase-DNA integration/DNA recombination)	**-2.0**
SaMRSA252-1243 (1P8)		conserved hypothetical protein	**-2.0**
SaMRSA252-2361 (7A2)	**modC**	putative molybdenum transport ATP-binding protein	**-2.0**
SaMRSA252-1780 (5A15)		NAD-dependent malic enzyme (oxidoreductase activity acting on the CH-OH group of donors NAD or NADP as acceptor)	**-2.0**
SaMRSA252-0652 (3O8)	**pbp4**	penicillin-binding protein 4 (proteolysis)	**-2.0**
SaMRSA252-0490 (2P24)		tetrapyrrole (corrin/porphyrin) methylase family protein (methyltransferase activity; metabolism)	**-2.0**
SaMRSA252-0563 (3H9)		putative deaminase (hydrolase activity; Zn ion binding)	**-2.0**
SaMRSA252-2424 (7F9)		putative aldose 1-epimerase (galactose metabolism)	**-2.0**
SaMRSA252-0891 (3E13)		haloacid dehalogenase-like hydrolase (catalytic activity; metabolism)	**-2.0**
SaMRSA252-1396 (4F15)		putative membrane protein	**-2.0**
SaMRSA252-1173 (4B12)		putative RNA pseudouridylate synthase (RNA binding)	**-2.0**
SaMRSA252-2796 (8H6)	**gidB**	putative glucose inhibited division protein B (cell cycle)	**-2.0**
SaMRSA252-0258 (2E20)	**lytR**	autolysin response regulator protein (2-component signal transduction system; regulation of transcription, DNA-dependent)	**-2.0**
SaMRSA252-1789 (5B16)	**ackA**	acetate kinase (phosphorylation; metabolism)	**-2.0**
SaMRSA252-1843 (5G22)	**leuS**	leucyl-tRNA synthetase (tRNA aminoacylation for protein translation)	**-2.0**

SaMRSA252-2207 (6C19)		putative thymidine kinase (ATP binding)	**-2.0**
SaMRSA252-0351 (1G19)	**thl;thlA**	acetyl-CoA acetyltransferase (lipid metabolism or synthesis)	**-2.0**
SaMRSA252-1719 (5L7)	**tgt**	queuine tRNA-ribosyltransferase (queuosine biosynthesis)	**-1.9**
SaMRSA252-2117 (6J8)	**groES**	hsp10-a 10 kDa chaperonin (protein folding)	**-1.9**
SaMRSA252-2338 (6J23)		xanthine/uracil permeases family protein (transporter activity)	**-1.9**
SaMRSA252-0456 (2N20)		putative membrane protein	**-1.9**
SaMRSA252-0803 (2H2)		conserved hypothetical protein (possible role in fatty acid transport or metabolism)	**-1.9**
SaMRSA252-0911 (3A16)	**mnhD**	Na+/H+ antiporter subunit (ATP synthesis coupled with electron transport)	**-1.9**
SaMRSA252-1215 (1L5)	**rimM**	16S rRNA processing protein (ribosome biogenesis)	**-1.9**
SaMRSA252-2001 (6A6)		staphopain protease (proteolysis)	**-1.9**
SaMRSA252-0979 (3D24)		putative membrane protein	**-1.9**
SaMRSA252-1923 (5L20)	**hemY**	putative protoporphyrinogen oxidase (oxidoreductase activity; electron transport)	**-1.9**
SaMRSA252-1604 (5E5)	**accC**	biotin carboxylase subunit of acetyl-CoA carboxylase (urea cycle and biosynthesis or arginine and/or pyrimidines)	**-1.9**
SaMRSA252-1803 (5H17)		PTS system IIBC component (sugar transport)	**-1.9**
SaMRSA252-0983 (3H24)		hypothetical protein	**-1.9**
SaMRSA252-1065 (3P22)		putative polypeptide deformylase 2 (peptide deformylase activity; iron and ion binding; protein biosynthesis)	**-1.9**
SaMRSA252-0646 (3I8)	**tagA**	teichoic acid biosynthesis protein (biosynthesis of teichoic acid)	**-1.9**
SaMRSA252-1804 (5A18)		putative acyltransferase (acyltransferase activity; metabolism)	**-1.9**
SaMRSA252-2170		D-alanine--D-alanine ligase (peptidoglycan biosynthesis)	**-1.9**

(6G14)			
SaMRSA252-0084 (1H10)		hypothetical protein	**-1.9**
SaMRSA252-0016 (1H2)	**dnaC**	DnaB-like helicase (DNA replication)	**-1.9**
SaMRSA252-0908 (3F15)	**mnhG**	Na+/H+ antiporter subunit	**-1.9**
SaMRSA252-0934 (3H18)		putative haloacid dehalogenase-like hydrolase (catalytic activity; metabolism)	**-1.9**
SaMRSA252-0357 (1E20)		putative DNA-binding protein (DNA binding)	**-1.8**
SaMRSA252-1720 (5M7)	**queA**	S-adenosylmethionine: tRNA ribosyltransferase-isomerase (quenosine biosynthesis)	**-1.8**
SaMRSA252-2411 (7B8)		putative transport protein (Na+: H antiporter; sodium ion transport; regulation of pH	**-1.8**
SaMRSA252-1677 (5M2)		putative membrane protein	**-1.8**
SaMRSA252-1268 (1I12)		conserved hypothetical protein (iron ion binding; catalytic activity)	**-1.8**
SaMRSA252-0664 (3K10)		putative membrane protein (branched chain aliphatic amino acid transport)	**-1.8**
SaMRSA252-2340 (6L23)		acetyltransferase (GNAT) family protein	**-1.8**
SaMRSA252-1793 (5F16)	**thiI**	putative thiamine biosynthesis protein (thiamin biosynthesis)	**-1.8**
SaMRSA252-0618 (3N4)		putative transport system lipoprotein (iron ion transporter)	**-1.8**
SaMRSA252-1634 (5C9)		putative endonuclease (DNA repair)	**-1.8**
SaMRSA252-0599 (3L2)		hypothetical protein	**-1.8**
SaMRSA252-1598 (5G4)	**argR**	arginine repressor (regulation of transcription, DNA-dependent)	**-1.8**
SaMRSA252-1635 (5D9)		putative helicase (nucleic acid binding)	**-1.8**
SaMRSA252-1674 (5J2)		putative GTPase (GTP binding)	**-1.8**
SaMRSA252-0343 (1G18)		putative Sec-independent protein translocase protein	**-1.8**

SaMRSA252-0494 (3D1)		ribosomal RNA adenine dimethylase (rRNA modification)	**-1.8**
SaMRSA252-2670 (7O15)		putative membrane protein	**-1.8**
SaMRSA252-0782 (1K24)		conserved hypothetical protein (aromatic compound biosynthesis)	**-1.8**
SaMRSA252-1838 (5B22)		RNA pseudouridine synthase (RNA binding)	**-1.8**
SaMRSA252-1091 (4B2)		putative membrane protein	**-1.8**
SaMRSA252-2368 (7H2)		putative ferrichrome-binding lipoprotein precursor (iron ion transporter activity)	**-1.8**
SaMRSA252-0506 (3H2)		putative tetrapyrrole (corrin/porphyrin) methylases (methyltransferase activity; metabolism)	**-1.8**
SaMRSA252-0892 (3F13)		D-isomer specific 2-hydroxyacid dehydrogenase (L-serine biosynthesis)	**-1.7**
SaMRSA252-1794 (5G16)		aminotransferase class-V protein (transaminase activity)	**-1.7**
SaMRSA252-2397 (7E6)		putative membrane protein	**-1.7**
SaMRSA252-0916 (3F16)		putative cyclophilin type peptidyl-prolyl cis-trans isomerase (protein folding)	**-1.7**
SaMRSA252-1757 (5J12)		conserved hypothetical protein	**-1.7**
SaMRSA252-0982 (3G24)		hypothetical protein	**-1.7**
SaMRSA252-2391 (7G5)		putative N-acetylmuramoyl-L-alanine amidase (peptidoglycan catabolism)	**-1.7**
SaMRSA252-1596 (5E4)	**bfmBC**	putative dihydrolipoamide dehydrogenase (disulfide oxidoreductase activity; electron transport)	**-1.7**
SaMRSA252-1241 (1N8)		conserved hypothetical protein	**-1.7**
SaMRSA252-1272 (1M12)	**mutL**	DNA mismatch repair protein MutL (ATP binding)	**-1.7**
SaMRSA252-0657 (3L9)	**fhuA**	ferrichrome transport ATP-binding protein (ATP binding/ATPase activity)	**-1.7**
SaMRSA252-1366 (4I12)		topoisomerase IV subunit B (involved in DNA modification; DNA metabolism)	**-1.7**

SaMRSA252-0367 (1G21)		DNA-binding protein (DNA binding)	**-1.7**
SaMRSA252-0686 (3P12)		putative transposase -pseudogene (transposition, DNA-mediated)	**-1.7**
SaMRSA252-0518 (3D4)	**lysS**	lysyl-tRNA synthetase (ATPbinding; aminoacyl-tRNA ligase activity; nucleic acid binding)	**-1.7**
SaMRSA252-1389 (4H14)		conserved hypothetical protein (pseudogene)	**-1.7**
SaMRSA252-1846 (5B23)		conserved hypothetical protein	**-1.7**
SaMRSA252-2795 (8G6)		putative DNA-binding protein (DNA binding)	**-1.7**
SaMRSA252-1844 (5H22)		putative membrane protein	**-1.7**
SaMRSA252-2477 (7K4)		conserved hypothetical protein	**-1.7**
SaMRSA252-0384 (1H23)		hypothetical protein	**-1.7**
SaMRSA252-0450 (2P19)		putative cobalamin synthesis protein	**-1.7**
SaMRSA252-0648 (3K8)	**tagG**	teichoic acid ABC transporter permease protein	**-1.7**
SaMRSA252-2707 (7L20)		putative regulatory protein (transcription factor activity)	**-1.7**
SaMRSA252-0925 (3G17)		putative membrane protein	**-1.7**
SaMRSA252-1334 (4I8)	**nucI**	thermonuclease (nucleic acid binding)	**-1.6**
SaMRSA252-1466 (4D24)		conserved hypothetical protein (nucleobase, nucleoside, nucleotide and nucleic acid metabolism)	**-1.6**
SaMRSA252-1195 (1P2)		putative protein phosphatase (catalytic activity)	**-1.6**
SaMRSA252-1716 (5I7)		putative single-stranded-DNA-specific exonuclease (nucleic acid binding)	**-1.6**
SaMRSA252-1094 (4E2)		putative exported protein (glycerol metabolism)	**-1.6**
SaMRSA252-0586 (3G12)	**ung**	putative uracil-DNA glycosylase	**-1.6**

SaMRSA252-1096 (4G2)		conserved hypothetical protein	**-1.6**
SaMRSA252-2363 (7C2)	**modA**	putative molybdate-binding lipoprotein precursor (transporter activity)	**-1.6**
SaMRSA252-1833 (5E21)		putative methyltransferase	**-1.6**
SaMRSA252-1267 (1P11)		conserved hypothetical protein	**-1.6**
SaMRSA252-1097 (4H2)		putative methylase	**-1.6**
SaMRSA252-1699 (5I5)		conserved hypothetical protein	**-1.6**
SaMRSA252-1167 (4D11)		conserved hypothetical protein (RNA binding)	**-1.6**
SaMRSA252-2261 (6L13)		putative membrane protein	**-1.6**
SaMRSA252-1723 (5P7)		putative DNA-binding protein (amino acid metabolism)	**-1.6**
SaMRSA252-2204 (6H18)		conserved hypothetical protein	**-1.6**
SaMRSA252-1341 (4P8)		haloacid dehalogenase-like hydrolase (catalytic activity; metabolism)	**-1.6**
SaMRSA252-1110 (4E4)		SpoU rRNA Methylase family protein (RNA processing)	**-1.5**
SaMRSA252-2671 (7P15)		conserved hypothetical protein	**-1.5**
SaMRSA252-2711 (7P20)	**arcC**	carbamate kinase (amino acid biosynthesis)	**-1.5**
SaMRSA252-0562 (3G9)		putative deoxyadenosine kinase protein (nucleobase, nucleoside, nucleotide and nucleic acid metabolism)	**-1.5**
SaMRSA252-2139 (6P10)		conserved hypothetical protein	**-1.5**
SaMRSA252-1607 (5H5)		putative peptidase (metallopeptidase activity; proteolysis)	**-1.5**
SaMRSA252-2495 (7K6)		hypothetical protein	**-1.5**
SaMRSA252-0677 (3P11)		AraC family regulatory protein -pseudogene (regulation of transcription, DNA-dependent)	**-1.5**

SaMRSA252-1756 (5I12)		hypothetical protein	**-1.5**
SaMRSA252-2703 (7P19)		response regulator protein (2-component signal transduction system; regulation of transcription, DNA-dependent)	**-1.5**
SaMRSA252-0485 (2K24)	**holB**	putative DNA polymerase III, delta' subunit	**-1.5**
SaMRSA252-1369 (4L12)		transcription antiterminator (regulation of transcription, DNA-dependent)	**-1.5**
SaMRSA252-1783 (5D15)		putative DNA-binding protein	**-1.4**
SaMRSA252-2435 (7A11)		hypothetical protein	**-1.4**
SaMRSA252-0758 (1K21)	**saeS**	histidine kinase protein (signal transduction)	**-1.4**
SaMRSA252-1581 (5F2)		conserved hypothetical protein	**-1.4**
SaMRSA252-2118 (6K8)		putative membrane protein	**-1.3**

Table 4.3: Up-regulated GASM genes, normalised to BHI, using one-way ANOVA and posthoc Benjamini and Hochberg tests ($p \leq 0.05$). The corresponding ORF (Open reading frame), gene name and protein function are listed. The table is arranged according to the most up-regulated gene with the highest fold difference.

ORF	GENE	PROTEIN (FUNCTION)	FOLD
SaMRSA252-2297 (6P17)	**SAR2297**	putative acetolactate synthase (thiamin pyrophosphate binding)	**22.8**
SaMRSA252-0129 (2L4)	**SAR0129**	putative short chain dehydrogenase (metabolism; oxidoreductase activity)	**21.9**
SaMRSA252-1852 (5H23)	**ribE**	riboflavin synthase alpha chain (riboflavin synthesis)	**21.7**
SaMRSA252-1050 (3J21)	**SAR1050**	ABC transporter ATP-binding protein (transport)	**19.3**
SaMRSA252-1851 (5G23)	**ribA**	riboflavin biosynthesis protein (riboflavin biosynthesis)	**19.2**
SaMRSA252-1051 (3K21)	**SAR1051**	putative membrane protein	**19.1**
SaMRSA252-0919 (3A17)	**rocD**	ornithine aminotransferase (pyridoxal phosphate binding)	**17.2**
SaMRSA252-1773 (5B14)	**citC**	isocitrate dehydrogenase (carbohydrate metabolism; oxidoreductase activity)	**15.5**
SaMRSA252-2296 (6O17)	**SAR2296**	conserved hypothetical protein	**15.5**
SaMRSA252-1774 (5C14)	**citZ**	citrate synthase II (carbohydrate metabolism)	**15.3**
SaMRSA252-1049 (3I21)	**SAR1049**	putative cobalt transport protein (cobalamin biosynthetic process)	**14.6**
SaMRSA252-0920 (3B17)	**SAR0920**	putative NAD-specific glutamate dehydrogenase (amino acid metabolism; oxidoreductase activity)	**14.5**
SaMRSA252-0169 (2L9)	**SAR0169**	putative aldehyde dehydrogenase (metabolism; oxidoreductase activity)	**11.5**
SaMRSA252-1425 (4C19)	**odhA**	2-oxoglutarate dehydrogenase E1 component (metabolism; oxidoreductase activity)	**11.0**
SaMRSA252-1850 (5F23)	**ribH**	6,7-dimethyl-8-ribityllumazine synthase (riboflavin biosynthetic process)	**10.9**

SaMRSA252-1853 (5A24)	**ribD**	bifunctional riboflavin biosynthesis protein (riboflavin biosynthetic process)	**10.5**
SaMRSA252-1120 (4G5)	**sdhC**	putative succinate dehydrogenase cytochrome b558	**10.2**
SaMRSA252-2697 (7J19)	**SAR2697**	conserved hypothetical protein	**10.2**
SaMRSA252-2295 (6N17)	**SAR2295**	putative exported protein	**10.1**
SaMRSA252-1614 (5G6)	**gcvT**	putative aminomethyltransferase (glycine catabolic process)	**10.0**
SaMRSA252-1121 (4H5)	**sdhA/citF**	putative succinate dehydrogenase flavoprotein subunit (electron transport; oxidoreductase activity)	**9.6**
SaMRSA252-0378 (1B23)	**SAR0378**	hypothetical protein	**9.0**
SaMRSA252-1424 (4B19)	**odhB/citM**	dihydrolipoamide succinyltransferase E2 component of 2-oxoglutarate dehydrogenase complex (metabolism; acyltransferase activity/protein binding)	**9.0**
SaMRSA252-0996 (3M14)	**SAR0996**	conserved hypothetical protein	**8.7**
SaMRSA252-0806 (2C3)	**SAR0806**	putative S30EA family ribosomal protein	**8.6**
SaMRSA252-0577 (3G11)	**proP**	putative proline/betaine transporter	**8.6**
SaMRSA252-0405 (2L14)	**SAR0405**	hypothetical protein	**8.4**
SaMRSA252-2596 (7H18)	**SAR2596**	conserved hypothetical protein	**8.3**
SaMRSA252-0153 (2L7)	**capC**	capsular polysaccharide synthesis enzyme	**8.3**
SaMRSA252-2698 (7K19)	**cysJ**	putative sulfite reductase [NADPH] flavoprotein alpha-component - (electron transport; FMN binding; oxidoreductase activity)	**8.2**
SaMRSA252-1810 (5F18)	**fhs**	formate--tetrahydrofolate ligase (folic acid & derivative biosynthetic process)	**8.1**
SaMRSA252-0661 (3P9)	**SAR0661**	putative dihydroxyacetone kinase (glycerol metabolism)	**8.1**
SaMRSA252-1787 (5H15)	**ald1**	alanine dehydrogenase 1 (aromatic amino acid family biosythesis; shikimate pathway)	**7.7**
SaMRSA252-0334 (1G17)	**SAR0334**	putative dioxygenase	**7.5**

SaMRSA252-1612 (5E6)	**SAR1612**	putative glycine cleavage system P-protein (amino acid metabolism)	**7.5**
SaMRSA252-2120 (6M8)	**SAR2120**	conserved hypothetical protein (electron transport; oxidoreductase activity)	**7.4**
SaMRSA252-2278 (6M15)	**SAR2278**	putative zinc-binding dehydrogenase	**7.1**
SaMRSA252-1222 (1K6)	**SAR1222**	putative succinyl-CoA ligase (metabolism; catalytic activity)	**7.1**
SaMRSA252-1492 (4N15)	**SAR1492**	ferredoxin	**6.9**
SaMRSA252-1344 (4K9)	**SAR1344**	catalase (response to oxidative stress)	**6.8**
SaMRSA252-0660 (3O9)	**SAR0660**	putative dihydroxyacetone kinase (glycerol metabolism)	**6.6**
SaMRSA252-0400 (2O13)	**SAR0400**	nitroreductase family protein (electron transport; oxidoreductase activity)	**6.5**
SaMRSA252-2602 (7F19)	**SAR2602**	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	**6.4**
SaMRSA252-0227 (2G16)	**fadX**	putative acetyl-CoA transferase	**6.2**
SaMRSA252-0558 (3C9)	**SAR0558**	conserved hypothetical protein (biosynthetic process; nucleotide-sugar metabolic process)	**6.2**
SaMRSA252-0135 (2J5)	**sodM**	superoxide dismutase (superoxide metabolic process; metal ion binding)	**6.2**
SaMRSA252-0420 (2J16)	**SAR0420**	putative membrane protein	**5.9**
SaMRSA252-1265 (1N11)	**SAR1265**	putative pyruvate flavodoxin/ferredoxin oxidoreductase (electron transport; oxidoreductase activity)	**5.9**
SaMRSA252-1037 (3M19)	**folD**	FolD bifunctional protein [includes: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase] (folic acid & derivative biosynthetic process)	**5.9**
SaMRSA252-2717 (7N21)	**isaB**	immunodominant antigen B	**5.9**
SaMRSA252-0225 (2E16)	**fadD**	putative acyl-CoA dehydrogenase (electron transport; oxidoreductase activity)	**5.7**
SaMRSA252-1152 (4E9)	**SAR1152**	acetyltransferase (GNAT) family protein (N-acetyltransferase activity)	**5.6**
SaMRSA252-0526 (3D5)	**SAR0526**	conserved hypothetical protein (nucleotide-excision repair; DNA binding; nuclease activity)	**5.5**
SaMRSA252-2180	**thiE**	putative thiamine-phosphate pyrophosphorylase (thiamin biosynthetic process)	**5.5**

(6H15)			
SaMRSA252-2619 (7F21)	**SAR2619**	thiamine pyrophosphate enzyme (thiamin pyrophosphate binding)	**5.5**
SaMRSA252-1849 (5E23)	**SAR1849**	proline dehydrogenase (amino acid metabolism)	**5.4**
SaMRSA252-0842 (2F7)	**clfA**	clumping factor (cell surface-virulence)	**5.4**
SaMRSA252-2621 (7H21)	**SAR2621**	putative membrane protein (lrgA family)	**5.3**
SaMRSA252-1221 (1J6)	**SAR1221**	putative CoA synthetase protein (metabolism; catalytic activity)	**5.3**
SaMRSA252-1266 (1O11)	**SAR1266**	conserved hypothetical protein (thiamin pyrophosphate)	**5.3**
SaMRSA252-0525 (3C5)	**SAR0525**	putative DNA-binding protein (family of firmicute transcriptional repressor of classIII stress genes; CtsR)	**5.2**
SaMRSA252-2372 (7D3)	**ureA**	urease gamma subunit (nitrogen compound metabolic process)	**5.1**
SaMRSA252-2181 (6A16)	**thiM**	putative hydroxyethylthiazole kinase (thiamin biosynthetic process)	**4.9**
SaMRSA252-1811 (5G18)	**acsA**	acetyl-coenzyme A synthetase (metabolism; catalytic activity)	**4.7**
SaMRSA252-1153 (4F9)	**SAR1153**	conserved hypothetical protein	**4.7**
SaMRSA252-2182 (6B16)	**thiD**	putative phosphomethylpyrimidine kinase (role in thiamin pyrophosphate phosphate pathway)	**4.7**
SaMRSA252-2290 (6I17)	**SAR2290**	aldo/keto reductase family protein (oxidoreductase activity)	**4.6**
SaMRSA252-2408 (7G7)	**SAR2408**	PTS system, arbutin-like IIBC component (transport)	**4.6**
SaMRSA252-1415 (4A18)	**SAR1415**	hypothetical protein	**4.6**
SaMRSA252-0653 (3P8)	**SAR0653**	ABC transporter ATP-binding protein (transport)	**4.5**
SaMRSA252-1312 (4I5)	**SAR1312**	hypothetical protein	**4.5**
SaMRSA252-2224 (6D21)	**pyn**	putative pyrimidine-nucleoside phosphorylase (metabolism; transferase activity)	**4.4**
SaMRSA252-1879 (5J15)	**SAR1879**	putative lipoprotein	**4.4**
SaMRSA252-0154 (2M7)	**capD**	capsular polysaccharide synthesis enzyme	**4.4**
SaMRSA252-1880 (5K15)	**SAR1880**	putative membrane protein	**4.3**

SaMRSA252-1871 (5K14)	**pckA**	phosphoenolpyruvate carboxykinase (gluconeogenesis)	**4.2**
SaMRSA252-0662 (3I10)	**SAR0662**	conserved hypothetical protein (carbohydrate transport)	**4.2**
SaMRSA252-2771 (8B4)	**SAR2771**	conserved hypothetical protein	**4.1**
SaMRSA252-0985 (3J13)	**SAR0985**	conserved hypothetical protein (RNA metabolic process)	**4.1**
SaMRSA252-2279 (6N15)	**SAR2279**	putative exported protein	**4.0**
SaMRSA252-2256 (6H24)	**SAR2256**	conserved hypothetical protein	**4.0**
SaMRSA252-2454 (7L1)	**mqo1**	putative malate:quinone oxidoreductase 1 (carbohydrate metabolism)	**4.0**
SaMRSA252-2734 (7N23)	**sasA**	putative serine rich repeat containing protein (cell surface protein)	**4.0**
SaMRSA252-1288 (4L2)	**SAR1288**	putative lipoprotein	**4.0**
SaMRSA252-1190 (1K2)	**SAR1190**	putative membrane protein	**3.9**
SaMRSA252-2378 (7B4)	**ureD**	urease accessory protein UreD (nitrogen compound metabolic process)	**3.9**
SaMRSA252-0223 (2C16)	**fadA**	putative thiolase (fatty acid metabolism)	**3.9**
SaMRSA252-0399 (2N13)	**ahpC**	alkyl hydroperoxide reductase subunit C (possible role in antioxidant activity)	**3.9**
SaMRSA252-1610 (5C6)	**SAR1610**	lipoate-protein ligase A protein (protein modification; catalytic activity)	**3.9**
SaMRSA252-1573 (5F1)	**xerD**	integrase/recombinase (DNA integration/DNA recombination)	**3.8**
SaMRSA252-1585 (5B3)	**malR**	maltose operon transcriptional repressor (regulation of transcription)	**3.8**
SaMRSA252-2637 (7H23)	**copA**	putative copper importing ATPase A (metabolism; metal ion transport)	**3.8**
SaMRSA252-0938 (3D19)	**clpB**	putative ATPase subunit of an ATP-dependent protease (protein metabolic process)	**3.8**
SaMRSA252-1574 (5G1)	**fur**	iron uptake regulatory protein (regulation of transcription)	**3.7**
SaMRSA252-2583 (7C17)	**gntK**	putative gluconokinase (carbohydrate metabolism)	**3.7**
SaMRSA252-0379 (1C23)	**SAR0379**	hypothetical protein	**3.7**

SaMRSA252-1684 (5J3)	**SAR1684**	conserved hypothetical protein	**3.7**
SaMRSA252-1362 (4M11)	**citB**	aconitate hydratase (carbohydrate metabolism)	**3.7**
SaMRSA252-0226 (2F16)	**fadE**	putative acyl-CoA synthetase (possible role in fatty acid metabolism)	**3.7**
SaMRSA252-0707 (1K15)	**SAR0707**	putative replication-associated protein (pseudogene)	**3.7**
SaMRSA252-2373 (7E3)	**ureB**	urease beta subunit (nitrogen compound metabolic process)	**3.7**
SaMRSA252-1493 (4O15)	**SAR1493**	putative membrane protein	**3.6**
SaMRSA252-1423 (4A19)	**SAR1423**	hypothetical protein	**3.6**
SaMRSA252-0969 (3B23)	**SAR0969**	conserved hypothetical protein	**3.6**
SaMRSA252-2568 (7D15)	**SAR2568**	hypothetical protein	**3.6**
SaMRSA252-0335 (1H17)	**SAR0335**	putative luciferase-like monooxygenase	**3.6**
SaMRSA252-0855 (2B9)	**SAR0855**	hypothetical protein	**3.6**
SaMRSA252-2374 (7F3)	**ureC**	urease alpha subunit (urea metabolism)	**3.6**
SaMRSA252-2359 (7G1)	**moaB**	putative molybdenum cofactor biosynthesis protein B (cofactor biosynthesis)	**3.6**
SaMRSA252-2376 (7H3)	**ureF**	urease accessory protein UreF (nitrogen compound metabolism)	**3.6**
SaMRSA252-0155 (2N7)	**capE**	capsular polysaccharide synthesis enzyme	**3.6**
SaMRSA252-1326 (4I7)	**SAR1326**	conserved hypothetical protein (amino acid metabolism)	**3.6**
SaMRSA252-1686 (5L3)	**SAR1686**	putative biotin carboxyl carrier protein of acetyl-CoA carboxylase (biotin-requiring enzyme)	**3.5**
SaMRSA252-1645 (5F10)	**cdd**	cytidine deaminase (hydrolase activity; zinc ion binding)	**3.5**
SaMRSA252-2125 (6J9)	**agrC**	autoinducer sensor protein	**3.5**
SaMRSA252-0279 (2B23)	**esxA**	conserved hypothetical protein (possible role in virulence)	**3.5**
SaMRSA252-2291 (6J17)	**SAR2291**	MerR family regulatory protein (regulation of transcription)	**3.5**
SaMRSA252-2469 (7K3)	**SAR2469**	conserved hypothetical protein (flavin mononucleotide binding)	**3.5**

SaMRSA252-2545 (7M12)	**SAR2545**	conserved hypothetical protein (enzymatic function)	**3.5**
SaMRSA252-0152 (2K7)	**capB**	capsular polysaccharide synthesis enzyme	**3.5**
SaMRSA252-1683 (5I3)	**SAR1683**	putative membrane protein	**3.4**
SaMRSA252-0168 (2K9)	**SAR0168**	putative membrane protein	**3.4**
SaMRSA252-2380 (7D4)	**SAR2380**	hypothetical protein	**3.4**
SaMRSA252-2582 (7B17)	**gntP**	putative gluconate permease (transport)	**3.4**
SaMRSA252-0528 (3F5)	**clpC**	putative stress response-related Clp ATPase (nucleotide-excision repair; protein metabolic process)	**3.4**
SaMRSA252-1864 (5L13)	**SAR1864**	putative transaldolase (carbohydrate metabolism)	**3.3**
SaMRSA252-2517 (7I9)	**SAR2517**	putative dethiobiotin synthetase	**3.3**
SaMRSA252-2389 (7E5)	**SAR2389**	putative D-isomer specific 2-hydroxyacid dehydrogenase (L-serine biosynthetic process)	**3.3**
SaMRSA252-0667 (3N10)	**SAR0667**	putative acetyltransferase	**3.3**
SaMRSA252-0622 (3J5)	**SAR0622**	putative exported protein	**3.3**
SaMRSA252-0584 (3E12)	**SAR0584**	hypothetical protein	**3.3**
SaMRSA252-1417 (4C18)	**SAR1417**	putative membrane protein	**3.3**
SaMRSA252-0031 (1F4)	**pre/mob**	plasmid recombination enzyme	**3.3**
SaMRSA252-2688 (7I18)	**SAR2688**	hypothetical protein (antibiotic biosynthesis process)	**3.3**
SaMRSA252-2396 (7D6)	**SAR2396**	DeoR family regulatory protein (regulation of transcription, DNA-dependent)	**3.2**
SaMRSA252-0824 (2D5)	**SAR0824**	putative malolactic enzyme (NAD binding; oxidoreductase activity)	**3.2**
SaMRSA252-0917 (3G16)	**SAR0917**	putative S1 RNA binding domain (RNA binding)	**3.2**
SaMRSA252-1788 (5A16)	**SAR1788**	putative universal stress protein (response to stress)	**3.2**
SaMRSA252-2223 (6C21)	**SAR2223**	putative membrane protein	**3.2**
SaMRSA252-2375	**ureE**	urease accessory protein UreE (protein complex assembly; urea metabolism)	**3.2**

(7G3)			
SaMRSA252-2364 (7D2)	**SAR2364**	FdhD/NarQ family protein (electron transport)	**3.1**
SaMRSA252-0565 (3B10)	**SAR0565**	conserved hypothetical protein (electron transport)	**3.1**
SaMRSA252-0970 (3C23)	**SAR0970**	protozoan/cyanobacterial globin family protein (oxygen transport)	**3.1**
SaMRSA252-1964 (6E1)	**SAR1964**	putative transglycosylase (peptidoglycan biosynthetic process)	**3.1**
SaMRSA252-0527 (3E5)	**SAR0527**	putative phosphotransferase (enzymatic)	**3.1**
SaMRSA252-0944 (3B20)	**SAR0944**	putative exported protein	**3.0**
SaMRSA252-2360 (7H1)	**moeB**	putative molybdopterin synthase sulfurylase (catalytic activity)	**3.0**
SaMRSA252-2371 (7C3)	**SAR2371**	putative membrane protein (urea transport)	**3.0**
SaMRSA252-2377 (7A4)	**ureG**	urease accessory protein UreG	**3.0**
SaMRSA252-0299 (1E13)	**SAR0299**	hypothetical protein	**3.0**
SaMRSA252-0965 (3F22)	**SAR0965**	conserved hypothetical protein (electron transport; oxidoreductase activity)	**2.9**
SaMRSA252-1739 (5P9)	**tnpA2**	transposase A 2 (DNA integration; DNA recombination; DNA binding)	**2.9**
SaMRSA252-1632 (5A9)	**mreB**	ABC transporter permease protein (transport)	**2.9**
SaMRSA252-2356 (7D1)	**mobB**	putative molybdopterin-guanine dinucleotide biosynthesis protein B (Mo-molybdopterin cofactor biosynthesis)	**2.9**
SaMRSA252-0839 (2C7)	**SAR0839**	putative lipoprotein	**2.9**
SaMRSA252-1685 (5K3)	**SAR1685**	putative biotin carboxylase subunit of acetyl-CoA carboxylase (metabolism; purine base biosynthetic process)	**2.9**
SaMRSA252-1582 (5G2)	**zwf**	putative glucose-6-phosphate 1-dehydrogenase (glucose metabolism)	**2.9**
SaMRSA252-2615 (7B21)	**SAR2615**	putative exported protein	**2.9**
SaMRSA252-0523 (3A5)	**SAR0523**	SNO glutamine amidotransferase family protein (possible role in pyridoxine biosynthesis)	**2.9**
SaMRSA252-0301 (1F13)	**SAR0301**	putative membrane protein	**2.9**

SaMRSA252-2547 (7O12)	**SAR2547**	putative membrane protein (glutamate biosynthesis)	**2.9**
SaMRSA252-1814 (5B19)	**ccpA**	catabolite control protein A (regulation of transcription, DNA-dependent)	**2.9**
SaMRSA252-2684 (7M17)	**fda**	fructose-bisphosphate aldolase class I (glycolysis)	**2.9**
SaMRSA252-1703 (5L5)	**SAR1703**	putative oxygenase	**2.9**
SaMRSA252-2263 (6N13)	**SAR2263**	putative membrane protein	**2.9**
SaMRSA252-1767 (5D13)	**coaE**	putative dephospho-CoA kinase (ATP binding)	**2.9**
SaMRSA252-1418 (4D18)	**SAR1418**	conserved hypothetical protein	**2.9**
SaMRSA252-2293 (6L17)	**SAR2293**	peptidase family M23/M37 protein (proteolysis)	**2.8**
SaMRSA252-2520 (7L9)	**SAR2520**	hypothetical protein	**2.8**
SaMRSA252-1643 (5D10)	**SAR1643**	putative recombination protein O (DNA recombination; DNA repair)	**2.8**
SaMRSA252-2653 (7N13)	**SAR2653**	hypothetical protein	**2.8**
SaMRSA252-0336 (1A18)	**SAR0336**	NADH-dependent FMN reductase (pseudogene)	**2.8**
SaMRSA252-1150 (4C9)	**SAR1150**	antibacterial protein (pathogenesis)	**2.8**
SaMRSA252-1079 (3N24)	**SAR1079**	putative manganese transport protein (transport)	**2.8**
SaMRSA252-0419 (2I16)	**SAR0419**	hypothetical protein	**2.8**
SaMRSA252-0818 (2G4)	**trxB**	putative thioredoxin reductase (electron transport)	**2.8**
SaMRSA252-2393 (7A6)	**SAR2393**	putative bifunctional protein (electron transport)	**2.8**
SaMRSA252-0385 (1A24)	**SAR0385**	putative membrane protein	**2.8**
SaMRSA252-2365 (7E2)	**SAR2365**	acetyltransferase (GNAT) family protein	**2.8**
SaMRSA252-2210 (6F19)	**SAR2210**	aldehyde dehydrogenase family protein (metabolism; oxidoreductase activity)	**2.8**
SaMRSA252-1858	**SAR1858**	hypothetical protein	**2.8**

(5F24)			
SaMRSA252-2460 (7J2)	**SAR2460**	putative acetyltransferase (GNAT) family protein	**2.8**
SaMRSA252-2611 (7F20)	**SAR2611**	putative L-serine dehydratase, beta chain (gluconeogenesis)	**2.8**
SaMRSA252-2746 (8B1)	**icaR**	ica operon transcriptional regulator (regulation of transcription, DNA-dependent)	**2.7**
SaMRSA252-1055 (3O21)	**SAR1055**	hypothetical protein	**2.7**
SaMRSA252-2467 (7I3)	**SAR2467**	conserved hypothetical protein	**2.7**
SaMRSA252-0624 (3L5)	**SAR0624**	putative esterase	**2.7**
SaMRSA252-2121 (6N8)	**SAR2121**	putative carbon-nitrogen hydrolase (nitrogen compound metabolism)	**2.7**
SaMRSA252-2357 (7E1)	**moeA**	putative molybdenum cofactor biosynthesis protein (cofactor biosynthesis)	**2.7**
SaMRSA252-1953 (5J24)	**SAR1953**	AhpC/TSA family protein	**2.7**
SaMRSA252-1151 (4D9)	**SAR1151**	putative haloacid dehalogenase-like hydrolase (metabolism; catalytic activity)	**2.7**
SaMRSA252-1333 (4P7)	**SAR1333**	putative membrane protein	**2.7**
SaMRSA252-1772 (5A14)	**phoP**	alkaline phosphatase synthesis transcriptional regulatory protein (regulation of transcription, DNA-dependent)	**2.7**
SaMRSA252-0495 (3E1)	**veg**	conserved hypothetical protein	**2.7**
SaMRSA252-0555 (3H8)	**kbl**	putative 2-amino-3-ketobutyrate coenzyme A ligase (biosynthesis)	**2.7**
SaMRSA252-0040 (1G5)	**mecR1**	methicillin resistance protein MecR1(cell wall biosynthesis)	**2.7**
SaMRSA252-1279 (4L1)	**SAR1279**	conserved hypothetical protein (mRNA processing)	**2.6**
SaMRSA252-2731 (7L23)	**SAR2731**	conserved hypothetical protein (pseudogene)	**2.6**
SaMRSA252-0663 (3J10)	**SAR0663**	hypothetical protein	**2.6**
SaMRSA252-0721 (1N16)	**SAR0721**	multicopper oxidase protein (copper ion binding; oxidoreductase activity)	**2.6**
SaMRSA252-2610 (7E20)	**SAR2610**	putative L-serine dehydratase, alpha chain (gluconeogenesis)	**2.6**
SaMRSA252-1081 (3P24)	**SAR1081**	inositol monophosphatase family protein (inositol or phosphatidylinositol phosphte activity)	**2.6**
SaMRSA252-agrIII	**agrIII**	Class III accessory gene regulator (agr) locus [3'agrB-agrD-5'agrC]	**2.6**

(8E7)			
SaMRSA252-1251 (1P9)	**SAR1251**	conserved hypothetical protein	**2.6**
SaMRSA252-1914 (5L19)	**SAR1914**	hypothetical protein (pseudogene)	**2.6**
SaMRSA252-0499 (3A2)	**spoVG**	stage V sporulation protein G (response to stress)	**2.6**
SaMRSA252-0711 (1M15)	**SAR0711**	putative replication initiation protein (pseudogene)	**2.6**
SaMRSA252-0498 (3H1)	**yabJ**	putative regulatory protein (possible role in purine biosynthesis)	**2.6**
SaMRSA252-0637 (3I7)	**SAR0637**	sodium/hydrogen exchanger family protein (regulation of pH)	**2.5**
SaMRSA252-0966 (3G22)	**SAR0966**	regulatory protein	**2.5**
SaMRSA252-rnaIII (8F7)	**rnaIII**	rnaIII accessory gene regulator (agr) locus	**2.5**
SaMRSA252-0054 (1D7)	**tnpA1**	transposase A 1 (DNA integration; DNA recombination; DNA binding)	**2.5**
SaMRSA252-2420 (7B9)	**SAR2420**	arginase family protein (urea cycle)	**2.5**
SaMRSA252-2366 (7F2)	**SAR2366**	BioY family protein	**2.5**
SaMRSA252-1197 (1J3)	**SAR1197**	conserved hypothetical protein	**2.5**
SaMRSA252-1791 (5D16)	**SAR1791**	putative thiol peroxidase	**2.5**
SaMRSA252-1633 (5B9)	**mreA**	ABC transporter ATP-binding protein (transport)	**2.5**
SaMRSA252-2715 (7L21)	**SAR2715**	arginine repressor family protein (regulation of transcription, DNA-dependent)	**2.5**
SaMRSA252-1954 (5K24)	**SAR1954**	putative glutamate-1-semialdehyde 2,1-aminomutase (pyridoxal phosphate binding)	**2.5**
SaMRSA252-0796 (2A2)	**SAR0796**	putative glycerate kinase (organic acid phosphorylation)	**2.4**
SaMRSA252-1435 (4E20)	**SAR1435**	PTS system, glucose-specific IIA component (transport)	**2.4**
SaMRSA252-0901 (3G14)	**SAR0901**	conserved hypothetical protein	**2.4**
SaMRSA252-1688 (5N3)	**SAR1688**	conserved hypothetical protein	**2.4**
SaMRSA252-2354	**moaD**	putative molybdopterin-synthase small subunit (sulfur metabolism)	**2.4**

(7B1)			
SaMRSA252-1416 (4B18)	**SAR1416**	putative acylphosphatase (acylphosphatase activity)	**2.4**
SaMRSA252-1784 (5E15)	**SAR1784**	putative universal stress protein (response to stress)	**2.4**
SaMRSA252-1769 (5F13)	**polA**	DNA polymerase I (DNA replication)	**2.4**
SaMRSA252-1054 (3N21)	**SAR1054**	conserved hypothetical protein	**2.4**
SaMRSA252-1891 (5M16)	**SAR1891**	putative exported protein (pseudogene)	**2.4**
SaMRSA252-2514 (7N8)	**SAR2514**	putative 8-amino-7-oxononanoate synthase (biosynthesis; metabolism)	**2.4**
SaMRSA252-1336 (4K8)	**SAR1336**	hypothetical protein	**2.4**
SaMRSA252-2612 (7G20)	**SAR2612**	putative membrane protein	**2.4**
SaMRSA252-2277 (6L15)	**SAR2277**	putative zinc-binding dehydrogenase	**2.4**
SaMRSA252-1085 (4D1)	**SAR1085**	conserved hypothetical protein	**2.4**
SaMRSA252-2522 (7N9)	**SAR2522**	putative glycerate kinase (organic acid phosphorylation)	**2.4**
SaMRSA252-2337 (6I23)	**SAR2337**	putative membrane protein	**2.4**
SaMRSA252-1615 (5H6)	**SAR1615**	putative shikimate kinase (amino acid biosynthesis)	**2.4**
SaMRSA252-2353 (7A1)	**mobA**	putative molybdopterin-guanine dinucleotide biosynthesis protein A	**2.4**
SaMRSA252-1459 (4E23)	**SAR1459**	conserved hypothetical protein	**2.3**
SaMRSA252-0918 (3H16)	**SAR0918**	NADH:flavin oxidoreductase / NADH oxidase family protein (electron transport; oxidoreductase activity)	**2.3**
SaMRSA252-1644 (5E10)	**era**	putative GTP-binding protein (nucleic acid binding)	**2.3**
SaMRSA252-0813 (2B4)	**uvrA**	excinuclease ABC subunit A (ATP binding/ATPase activity)	**2.3**
SaMRSA252-0862	**SAR0862**	putative thioredoxin (electron transport)	**2.3**

(2A10)			
SaMRSA252-0280 (2C23)	**SAR0280**	putative membrane protein	**2.3**
SaMRSA252-2127 (6L9)	**SAR2127**	putative fructokinase (carbohydrate metabolism)	**2.3**
SaMRSA252-1436 (4F20)	**SAR1436**	conserved hypothetical protein	**2.3**
SaMRSA252-2730 (7K23)	**SAR2730**	conserved hypothetical protein	**2.3**
SaMRSA252-1360 (4K11)	**mscL**	large-conductance mechanosensitive channel (transport)	**2.3**
SaMRSA252-1611 (5D6)	**SAR1611**	putative membrane protein	**2.3**
SaMRSA252-2392 (7H5)	**SAR2392**	conserved hypothetical protein	**2.3**
SaMRSA252-0807 (2D3)	**secA**	preprotein translocase SecA subunit (protein import)	**2.3**
SaMRSA252-0921 (3C17)	**glpQ**	putative glycerophosphoryl diester phosphodiesterase (glycerol metabolism)	**2.3**
SaMRSA252-1706 (5O5)	**SAR1706**	conserved hypothetical protein (transcriptional regulator)	**2.3**
SaMRSA252-0706 (1J15)	**SAR0706**	putative membrane protein	**2.3**
SaMRSA252-0682 (3L12)	**SAR0682**	hypothetical protein	**2.3**
SaMRSA252-1987 (6C4)	**SAR1987**	putative membrane protein	**2.3**
SaMRSA252-1391 (4A15)	**SAR1391**	hypothetical protein	**2.3**
SaMRSA252-2729 (7J23)	**SAR2729**	hypothetical protein	**2.3**
SaMRSA252-0167 (2J9)	**SAR0167**	conserved hypothetical protein (antibiotic biosynthetic process)	**2.3**
SaMRSA252-1589 (5F3)	**gnd**	6-phosphogluconate dehydrogenase, decarboxylating (pentose phosphate shunt)	**2.2**
SaMRSA252-0569 (3G10)	**SAR0569**	putative glycosyl transferase (biosynthetic process)	**2.2**
SaMRSA252-1363 (4N11)	**SAR1363**	conserved hypothetical protein (catalytic activity)	**2.2**
SaMRSA252-2428 (7B10)	**SAR2428**	putative membrane protein	**2.2**

SaMRSA252-0724 (1I17)	**cadC**	putative cadmium efflux system accessory protein (regulation of transcription, DNA-dependent)	**2.2**
SaMRSA252-1018 (3J17)	**SAR1018**	putative hydrolase	**2.2**
SaMRSA252-0600 (3M2)	**SAR0600**	pyridine nucleotide-disulphide oxidoreductase protein (electron transport)	**2.2**
SaMRSA252-1647 (5H10)	**SAR1647**	conserved hypothetical protein	**2.2**
SaMRSA252-2395 (7C6)	**SAR2395**	inositol monophosphatase family protein (inositol or phosphatidylinositol phosphte activity)	**2.2**
SaMRSA252-0854 (2A9)	**SAR0854**	hypothetical protein	**2.2**
SaMRSA252-1437 (4G20)	**msrA2**	peptide methionine sulfoxide reductase II (protein metabolic process)	**2.2**
SaMRSA252-0581 (3B12)	**SAR0581**	putative ketoacyl-CoA thiolase	**2.2**
SaMRSA252-2641 (7C24)	**SAR2641**	putative aminotransferase (biosynthesis)	**2.2**
SaMRSA252-2687 (7P17)	**SAR2687**	putative AMP-binding enzyme (metabolism)	**2.2**
SaMRSA252-2399 (7G6)	**SAR2399**	putative transcription regulator (carbohydrate metabolism; regulation of transcription, DNA-dependent)	**2.2**
SaMRSA252-1198 (1K3)	**SAR1198**	putative ribulose-phosphate 3-epimerase (carbohydrate metabolism)	**2.2**
SaMRSA252-1641 (5B10)	**SAR1641**	putative DNA-binding protein [pseudogene]; (regulation of transcription, DNA-dependent)	**2.2**
SaMRSA252-2358 (7F1)	**moaC**	putative molybdenum cofactor biosynthesis protein C	**2.1**
SaMRSA252-0445 (2K19)	**SAR0445**	putative lipoprotein	**2.1**
SaMRSA252-0812 (2A4)	**uvrB**	excinuclease ABC subunit B (nucleotide-excision repair)	**2.1**
SaMRSA252-1057 (3I22)	**ptsI**	phosphoenolpyruvate-protein phosphotransferase (carbohydrate metabolism)	**2.1**
SaMRSA252-0151 (2J7)	**capA**	capsular polysaccharide synthesis enzyme	**2.1**
SaMRSA252-2225 (6E21)	**deoC2**	putative deoxyribose-phosphate aldolase (nucleoside metabolism)	**2.1**
SaMRSA252-0147 (2N6)	**SAR0147**	putative nucleotidase (nucleotide catabolism)	**2.1**

SaMRSA252-2515 (7O8)	**bioB**	putative biotin synthase (biotin biosynthesis)	**2.1**
SaMRSA252-1086 (4E1)	**SAR1086**	conserved hypothetical protein	**2.1**
SaMRSA252-1203 (1P3)	**recG**	ATP-dependent DNA helicase (ATP binding/helicase activity/nucleic acid binding)	**2.1**
SaMRSA252-2274 (6I15)	**SAR2274**	putative membrane protein	**2.1**
SaMRSA252-2780 (8C5)	**SAR2780**	putative membrane protein	**2.1**
SaMRSA252-2728 (7I23)	**SAR2728**	preprotein translocase SecA subunit-like protein (protein binding)	**2.1**
SaMRSA252-1877 (5P14)	**SAR1877**	AMP-binding enzyme (metabolism)	**2.1**
SaMRSA252-1884 (5O15)	**SAR1884**	hypothetical protein	**2.1**
SaMRSA252-1847 (5C23)	**rot**	repressor of toxins	**2.1**
SaMRSA252-1591 (5H3)	**SAR1591**	putative membrane protein	**2.1**
SaMRSA252-0802 (2G2)	**SAR0802**	putative membrane protein	**2.1**
SaMRSA252-1379 (4F13)	**SAR1379**	putative peptidase	**2.1**
SaMRSA252-2451 (7I1)	**SAR2451**	putative membrane protein (regulation of transcription-DNA-dependent)	**2.1**
SaMRSA252-2516 (7P8)	**bioA**	putative adenosylmethionine-8-amino-7-oxononanoate aminotransferase (pyridoxal phosphate binding)	**2.1**
SaMRSA252-0381 (1E23)	**SAR0381**	hypothetical protein	**2.1**
SaMRSA252-1053 (3M21)	**SAR1053**	putative membrane protein	**2.1**
SaMRSA252-1260 (1I11)	**SAR1260**	conserved hypothetical protein (Mo-molybdopterin cofactor biosynthesis)	**2.1**
SaMRSA252-1350 (4I10)	**SAR1350**	putative membrane protein	**2.1**
SaMRSA252-0305 (1B14)	**SAR0305**	putative membrane protein	**2.1**
SaMRSA252-2546 (7N12)	**SAR2546**	putative lipoprotein	**2.1**
SaMRSA252-0559 (3D9)	**SAR0559**	putative aminotransferase (metabolism)	**2.1**

SaMRSA252-1785 (5F15)	**SAR1785**	metallo-beta-lactamase superfamily protein	**2.1**
SaMRSA252-0380 (1D23)	**SAR0380**	hypothetical protein	**2.0**
SaMRSA252-2413 (7D8)	**SAR2413**	putative short chain dehydrogenase	**2.0**
SaMRSA252-2655 (7P13)	**SAR2655**	putative glyoxalase	**2.0**
SaMRSA252-1183 (1L1)	**SAR1183**	conserved hypothetical protein	**2.0**
SaMRSA252-2379 (7C4)	**sarR**	staphylococcal accessory regulator A homologue	**2.0**
SaMRSA252-0580 (3A12)	**SAR0580**	putative AMP-binding enzyme (metabolism)	**2.0**
SaMRSA252-0020 (1D3)	**yycH**	putative exported protein	**2.0**
SaMRSA252-1985 (6A4)	**SAR1985**	putative exonuclease	**2.0**
SaMRSA252-2532 (7P10)	**SAR2532**	hypothetical protein	**2.0**
SaMRSA252-0448 (2N19)	**SAR0448**	hypothetical protein	**2.0**
SaMRSA252-2369 (7A3)	**SAR2369**	conserved hypothetical protein (electron transport)	**2.0**
SaMRSA252-0735 (1L18)	**SAR0735**	putative exported protein	**2.0**
SaMRSA252-1782 (5C15)	**SAR1782**	conserved hypothetical protein	**2.0**
SaMRSA252-1813 (5A19)	**SAR1813**	histone deacetylase family protein	**2.0**
SaMRSA252-2640 (7B24)	**SAR2640**	D-isomer specific 2-hydroxyacid dehydrogenase (L-serine biosynthesis; metabolism)	**2.0**
SaMRSA252-2658 (7K14)	**SAR2658**	TetR family regulatory protein (regulation of transcription, DNA-dependent)	**2.0**
SaMRSA252-0869 (2H10)	**SAR0869**	hypothetical protein	**2.0**
SaMRSA252-0876 (2F11)	**SAR0876**	ABC transporter ATP-binding protein- (ATP binding/ATPase activity/nucleoside-triphosphatase activity/ nucleotide binding)	**2.0**
SaMRSA252-1766	**gap2**	glyceraldehyde 3-phosphate dehydrogenase 2 (glycolysis)	**2.0**

(5C13)			
SaMRSA252-1816 (5D19)	**SAR1816**	putative membrane protein	**2.0**
SaMRSA252-0986 (3K13)	**SAR0986**	putative membrane protein	**2.0**
SaMRSA252-1707 (5P5)	**SAR1707**	putative ATPase (ATP binding; nucleoside-triphosphatase activity; nucleotide binding)	**1.9**
SaMRSA252-0987 (3L13)	**SAR0987**	conserved hypothetical protein (biosynthetic process)	**1.9**
SaMRSA252-1261 (1J11)	**recA**	recombinase A (DNA metabolic process)	**1.9**
SaMRSA252-1422 (4H18)	**SAR1422**	conserved hypothetical protein	**1.9**
SaMRSA252-0128 (2K4)	**SAR0128**	putative membrane protein	**1.9**
SaMRSA252-0821 (2A5)	**SAR0821**	conserved hypothetical protein	**1.9**
SaMRSA252-0757 (1J21)	**SAR0757**	putative glucosyl transferase	**1.9**
SaMRSA252-1965 (6F1)	**SAR1965**	ThiJ/PfpI family protein	**1.9**
SaMRSA252-2294 (6M17)	**SAR2294**	hypothetical protein	**1.9**
SaMRSA252-2275 (6J15)	**SAR2275**	putative membrane protein	**1.9**
SaMRSA252-2394 (7B6)	**SAR2394**	putative exported protein	**1.9**
SaMRSA252-1458 (4D23)	**SAR1458**	conserved hypothetical protein	**1.9**
SaMRSA252-2617 (7D21)	**SAR2617**	hypothetical protein	**1.9**
SaMRSA252-0021 (1E3)	**yycI**	putative exported protein	**1.9**
SaMRSA252-1837 (5A22)	**SAR1837**	putative exported protein	**1.9**
SaMRSA252-0867 (2F10)	**SAR0867**	hypothetical protein (DNA modification)	**1.9**
SaMRSA252-0744 (1M19)	**SAR0744**	putative DNA photolyase	**1.9**
SaMRSA252-0683 (3M12)	**SAR0683**	LysR family regulatory protein (regulation of transcription, DNA-dependent)	**1.9**

SaMRSA252-2352 (6P24)	**moaA**	putative molybdenum cofactor biosynthesis protein A	**1.9**
SaMRSA252-2128 (6M9)	**scrB**	sucrose-6-phosphate hydrolase (carbohydrate metabolism)	**1.9**
SaMRSA252-2627 (7F22)	**SAR2627**	putative 6-O-methylguanine DNA methyltransferase (DNA repair)	**1.9**
SaMRSA252-1048 (3P20)	**purD**	putative phosphoribosylamine--glycine ligase (purine base biosynthesis)	**1.9**
SaMRSA252-0743 (1L19)	**SAR0743**	putative sodium:sulfate symporter protein (transport)	**1.8**
SaMRSA252-2262 (6M13)	**SAR2262**	putative UTP--glucose-1-phosphate uridylyltransferase (metabolism)	**1.8**
SaMRSA252-2618 (7E21)	**glcB**	PTS system, glucose-specific IIABC component (sugar transport)	**1.8**
SaMRSA252-1876 (5O14)	**SAR1876**	hypothetical protein	**1.8**
SaMRSA252-1696 (5N4)	**SAR1696**	conserved hypothetical protein	**1.8**
SaMRSA252-0048 (1F6)	**SAR0048**	putative membrane protein (partial)	**1.8**
SaMRSA252-1017 (3I17)	**SAR1017**	putative menaquinone biosynthesis bifunctional protein	**1.8**
SaMRSA252-2749 (8E1)	**icaB**	intercellular adhesion protein B (carbohydrate metabolism)	**1.8**
SaMRSA252-0583 (3D12)	**SAR0583**	hypothetical protein	**1.8**
SaMRSA252-1651 (5D11)	**SAR1651**	putative membrane protein	**1.8**
SaMRSA252-0669 (3P10)	**SAR0669**	putative response regulator protein (regulation of transcription, DNA-dependent)	**1.8**
SaMRSA252-0024 (1H3)	**SAR0024**	conserved hypothetical protein	**1.8**
SaMRSA252-2126 (6K9)	**agrA**	autoinducer sensor protein response regulator protein	**1.8**
SaMRSA252-0668 (3O10)	**SAR0668**	hypothetical protein	**1.8**
SaMRSA252-1640 (5A10)	**SAR1640**	conserved hypothetical protein	**1.8**
SaMRSA252-1593 (5B4)	**bfmB**	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (metabolism)	**1.8**

SaMRSA252-2724 (7M22)	**SAR2724**	isochorismatase family protein (metabolism)	**1.7**
SaMRSA252-2656 (7I14)	**SAR2656**	conserved hypothetical protein (regulation of nitrogen utilisation)	**1.7**
SaMRSA252-2589 (7A18)	**SAR2589**	putative transporter protein	**1.7**
SaMRSA252-1783 (5D15)	**SAR1783**	putative DNA-binding protein	**1.7**
SaMRSA252-1890 (5L16)	**SAR1890**	putative exported protein	**1.7**
SaMRSA252-1488 (4J15)	**SAR1488**	putative pyridine nucleotide-disulphide oxidoreductase (electron transport)	**1.7**
SaMRSA252-1084 (4C1)	**SAR1084**	conserved hypothetical protein	**1.7**
SaMRSA252-0820 (2H4)	**SAR0820**	conserved hypothetical protein	**1.7**
SaMRSA252-1571 (5D1)	**SAR1571**	conserved hypothetical protein	**1.7**
SaMRSA252-0560 (3E9)	**SAR0560**	haloacid dehalogenase-like hydrolase (metabolism)	**1.7**
SaMRSA252-1289 (4M2)	**SAR1289**	putative exported protein	**1.7**
SaMRSA252-1171 (4H11)	**SAR1171**	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	**1.7**
SaMRSA252-0929 (3C18)	**SAR0929**	conserved hypothetical protein (DNA repair)	**1.7**
SaMRSA252-2727 (7P22)	**SAR2727**	hypothetical protein (biosynthesis)	**1.7**
SaMRSA252-1583 (5H2)	**SAR1583**	AraC family regulatory protein (regulation of transcription, DNA-dependent)	**1.7**
SaMRSA252-0756 (1I21)	**SAR0756**	aldo/keto reductase family protein (oxidoreductase activity)	**1.7**
SaMRSA252-1371 (4N12)	**SAR1371**	putative membrane protein	**1.7**
SaMRSA252-2657 (7J14)	**SAR2657**	hypothetical protein	**1.6**
SaMRSA252-0928 (3B18)	**SAR0928**	conserved hypothetical protein	**1.6**
SaMRSA252-0930	**SAR0930**	fumarylacetoacetate (FAA) hydrolase family protein (metabolism)	**1.6**

(3D18)			
SaMRSA252-2661 (7N14)	**SAR2661**	putative hydrolase	**1.6**
SaMRSA252-0994 (3K14)	**SAR0994**	putative 5'-nucleotidase (nucleotide catabolism)	**1.6**
SaMRSA252-2747 (8C1)	**icaA**	glucosaminyltransferase (transferase activity)	**1.6**
SaMRSA252-1569 (5B1)	**rluB**	ribosomal large subunit pseudouridine synthase B (RNA processing)	**1.6**
SaMRSA252-0092 (1H11)	**SAR0092**	putative hydratase (metabolism)	**1.6**
SaMRSA252-2735 (7O23)	**SAR2735**	conserved hypothetical protein	**1.6**
SaMRSA252-2558 (7B14)	**SAR2558**	conserved hypothetical protein	**1.6**
SaMRSA252-0638 (3J7)	**SAR0638**	putative membrane protein	**1.6**
SaMRSA252-2778 (8A5)	**SAR2778**	putative nickel transport protein (metal ion transport)	**1.6**
SaMRSA252-1441 (4C21)	**SAR1441**	conserved hypothetical protein	**1.6**
SaMRSA252-0582 (3C12)	**SAR0582**	hypothetical protein	**1.6**
SaMRSA252-2299 (6K18)	**SAR2299**	hypothetical protein	**1.6**
SaMRSA252-0191 (2J12)	**SAR0191**	conserved hypothetical protein	**1.5**
SaMRSA252-2434 (7H10)	**SAR2434**	hypothetical protein	**1.5**
SaMRSA252-2660 (7M14)	**SAR2660**	conserved hypothetical protein (metabolism)	**1.5**
SaMRSA252-2659 (7L14)	**SAR2659**	putative short chain dehydrogenase (metabolism; oxidoreductase activity)	**1.5**
SaMRSA252-0508 (3B3)	**SAR0508**	putative cell division protein (cell cycle)	**1.5**
SaMRSA252-0934 (3H18)	**SAR0934**	putative haloacid dehalogenase-like hydrolase (metabolism; catalytic activity)	**1.5**
SaMRSA252-0570 (3H10)	**SAR0570**	conserved hypothetical protein	**1.5**
SaMRSA252-0852	**SAR0852**	putative membrane protein	**1.4**

(2G8)			
SaMRSA252-1392 (4B15)	**SAR1392**	putative oligopeptide transporter ATPase (ATP binding; ATPase activity; nucleoside-triphosphatase activity; nucleotide binding)	**1.4**
SaMRSA252-0382 (1F23)	**SAR0382**	putative terminase small subunit (DNA packaging)	**1.4**
SaMRSA252-1388 (4G14)	**femB**	putative methicillin resistance expression factor (peptidoglycan biosynthetic process)	**1.4**
SaMRSA252-0621 (3I5)	**SAR0621**	putative hydrolase	**1.4**
SaMRSA252-2259 (6J13)	**SAR2259**	putative membrane protein	**1.4**
SaMRSA252-2512 (7L8)	**SAR2512**	putative membrane protein	**1.4**
SaMRSA252-2702 (7O19)	**SAR2702**	sensor kinase protein (ATP binding)	**1.4**
SaMRSA252-2544 (7L12)	**SAR2544**	ABC transporter ATP-binding protein (ATP binding/ATPase activity/nucleoside-triphosphatase activity/ nucleotide binding)	**1.3**

Table 4.4: Down-regulated GASM genes, normalised to BHI, using one-way ANOVA and posthoc Benjamini and Hochberg tests ($p \leq 0.05$). The corresponding ORF (Open reading frame), gene name and protein function are listed. The table is arranged according to the most down-regulated gene with the highest fold difference.

ORF	GENE	PROTEIN (FUNCTION)	FOLD
SaMRSA252-0259 (2F20)	**lrgA**	holin-like protein (export murein hydrolases)	**-9.7**
SaMRSA252-1010 (3J16)	**SAR1010**	putative membrane protein	**-9.2**
SaMRSA252-2383 (7G4)	**SAR2383**	putative exported protein	**-8.4**
SaMRSA252-0212 (2G14)	**SAR0212**	putative membrane protein (amino acid metabolism)	**-8.3**
SaMRSA252-0260 (2G20)	**lrgB**	holin-like protein (export murein hydrolases)	**-8.0**
SaMRSA252-2650 (7K13)	**isaA**	immunodominant antigen A (cellular component; extracellular region)	**-7.5**
SaMRSA252-1454 (4H22)	**SAR1454**	putative membrane protein [pseudogene] (proteolysis)	**-6.7**
SaMRSA252-2488 (7M5)	**nasE**	assimilatory nitrite reductase small subunit (electron transport; oxidoreductase activity)	**-6.3**
SaMRSA252-0114 (2M2)	**spa**	immunoglobulin G binding protein A precursor (cell wall catabolism; immunoglobulin binding)	**-6.2**
SaMRSA252-0172 (2O9)	**SAR0172**	conserved hypothetical protein	**-6.0**
SaMRSA252-2669 (7N15)	**SAR2669**	putative dihydroorotate dehydrogenase (pyrimidine base biosynthesis)	**-6.0**
SaMRSA252-2131 (6P9)	**SAR2131**	conserved hypothetical protein	**-5.9**
SaMRSA252-1060 (3L22)	**SAR1060**	putative membrane protein	**-5.9**
SaMRSA252-2504 (7L7)	**SAR2504**	extracellular solute-binding lipoprotein (transport)	**-5.9**
SaMRSA252-2329 (6I22)	**rpsC**	30S ribosomal protein S3 (translation)	**-5.5**
SaMRSA252-2487 (7L5)	**SAR2487**	tetrapyrrole (corrin/porphyrin) methylase family protein (metabolism)	**-5.5**
SaMRSA252-2331	**rpsS**	30S ribosomal protein S19 (translation)	**-5.4**

(6K22)			
SaMRSA252-2322 (6J21)	**rpsN**	30S ribosomal protein S14 (translation)	**-5.3**
SaMRSA252-2486 (7K5)	**narG**	nitrate reductase alpha chain (molybdenum ion binding; oxidoreductase activity)	**-5.3**
SaMRSA252-2328 (6P21)	**rplP**	50S ribosomal protein L16 (translation)	**-5.1**
SaMRSA252-1938 (5K22)	**SAR1938**	putative DNA-binding protein (DNA binding)	**-4.9**
SaMRSA252-2319 (6O20)	**rplR**	50S ribosomal protein L18 (translation)	**-4.9**
SaMRSA252-2324 (6L21)	**rplX**	50S ribosomal protein L24 (protein biosynthesis)	**-4.9**
SaMRSA252-1993 (6A5)	**gatC**	glutamyl-tRNA amidotransferase subunit C (regulation of translational fidelity)	**-4.8**
SaMRSA252-2508 (7P7)	**sbi**	IgG-binding protein	**-4.8**
SaMRSA252-2321 (6I21)	**rpsH**	30S ribosomal protein S8 (translation)	**-4.8**
SaMRSA252-2327 (6O21)	**rpmC**	50S ribosomal protein L29 (translation)	**-4.8**
SaMRSA252-2473 (7O3)	**SAR2473**	putative exported protein	**-4.7**
SaMRSA252-1178 (4G12)	**pyrAA**	putative carbamoyl-phosphate synthase, pyrimidine-specific, small chain- (nitrogen compound metabolic process)	**-4.5**
SaMRSA252-2438 (7D11)	**SAR2438**	putative exported protein	**-4.5**
SaMRSA252-2485 (7J5)	**narH**	nitrate reductase beta chain	**-4.4**
SaMRSA252-2489 (7N5)	**nasD; nirB; nasBC**	nitrite reductase large subunit (electron transport; oxidoreductase activity)	**-4.4**
SaMRSA252-2325 (6M21)	**rplN**	50S ribosomal protein L14 (translation)	**-4.3**
SaMRSA252-1179 (4H12)	**pyrAB**	putative carbamoyl-phosphate synthase, pyrimidine-specific, large chain- (metabolism; biosynthesis of arginine, purine base and pyrimidine base)	**-4.2**
SaMRSA252-2334 (6N22)	**rplD**	50S ribosomal protein L4 (translation)	**-4.2**

SaMRSA252-1361 (4L11)	**opuD1**	glycine betaine transporter 1 (transport)	**-4.2**
SaMRSA252-1132 (4C7)	**SAR1132**	hypothetical protein	**-4.1**
SaMRSA252-1450 (4D22)	**tdcB**	putative threonine dehydratase (metabolism; possible role in pyridoxine synthesis)	**-4.0**
SaMRSA252-1759 (5L12)	**rpmI**	50S ribosomal protein L35 (translation)	**-4.0**
SaMRSA252-1174 (4C12)	**pyrR**	putative pyrimidine operon regulatory protein (nucleoside metabolism)	**-4.0**
SaMRSA252-1052 (3L21)	**SAR1052**	hypothetical protein	**-4.0**
SaMRSA252-2472 (7N3)	**gltT**	putative proton/sodium-glutamate symport protein (transport)	**-3.9**
SaMRSA252-2320 (6P20)	**rplF**	50S ribosomal protein L6 (translation)	**-3.9**
SaMRSA252-1237 (1J8)	**SAR1237**	putative phosphatidate cytidylyltransferase (phospholipid biosynthesis)	**-3.9**
SaMRSA252-2333 (6M22)	**rplW**	50S ribosomal protein L23 (protein biosynthesis)	**-3.8**
SaMRSA252-2677 (7N16)	**panB**	putative 3-methyl-2-oxobutanoate hydroxymethyltransferase (pantothenate biosynthesis)	**-3.8**
SaMRSA252-0542 (3C7)	**rplK**	50S ribosomal protein L11(translation)	**-3.8**
SaMRSA252-2335 (6O22)	**rplC**	50S ribosomal protein L3 (translation)	**-3.7**
SaMRSA252-2799 (8C7)	**rnpA**	ribonuclease P protein component (tRNA processing)	**-3.7**
SaMRSA252-1404 (4F16)	**SAR1404**	ABC transporter ATP-binding protein (ATP-binding; ATPase activity; nucleoside triphosphate; nucleotide binding)	**-3.7**
SaMRSA252-1760 (5M12)	**infC**	translation initiation factor IF-3 (translational initiation)	**-3.6**
SaMRSA252-2317 (6M20)	**rpmD**	50S ribosomal protein L30 (translation)	**-3.6**
SaMRSA252-0946 (3D20)	**fabH**	putative 3-oxoacyl-[acyl-carrier-protein] synthase III (fatty acid biosynthesis)	**-3.6**
SaMRSA252-1091 (4B2)	**SAR1091**	putative membrane protein	**-3.6**
SaMRSA252-2709	**clfB**	fibrinogen and keratin-10 binding surface anchored protein (cell surface component)	**-3.6**

(7N20)			
SaMRSA252-0118 (2I3)	**sirA**	lipoprotein (iron ion transport)	**-3.5**
SaMRSA252-2132 (6I10)	**SAR2132**	putative membrane protein	**-3.5**
SaMRSA252-2676 (7M16)	**panC**	putative pantoate--beta-alanine ligase (pantothenate biosynthesis)	**-3.5**
SaMRSA252-2315 (6K20)	**secY**	preprotein translocase SecY subunit (protein secretion)	**-3.4**
SaMRSA252-2207 (6C19)	**SAR2207**	putative thymidine kinase (ATP binding; thymidine kinase activity)	**-3.4**
SaMRSA252-0545 (3F7)	**rplL**	50S ribosomal protein L7/L12 (translation)	**-3.4**
SaMRSA252-0544 (3E7)	**rplJ**	50S ribosomal protein L10 (ribosome biogenesis & assembly)	**-3.4**
SaMRSA252-2476 (7J4)	**narT**	nitrite transport protein	**-3.4**
SaMRSA252-2470 (7L3)	**SAR2470**	putative exported protein	**-3.4**
SaMRSA252-2675 (7L16)	**panD**	putative aspartate 1-decarboxylase precursor (alanine biosynthesis)	**-3.3**
SaMRSA252-0790 (2C1)	**sstD**	lipoprotein (iron ion transport)	**-3.3**
SaMRSA252-1716 (5I7)	**SAR1716**	putative single-stranded-DNA-specific exonuclease (nucleic acid binding)	**-3.3**
SaMRSA252-0406 (2M14)	**xpt**	putative xanthine phosphoribosyltransferase (nucleoside metabolism)	**-3.3**
SaMRSA252-2316 (6L20)	**rplO**	50S ribosomal protein L15 (translation)	**-3.3**
SaMRSA252-0407 (2N14)	**pbuX**	putative xanthine permease (transport)	**-3.3**
SaMRSA252-0110 (2I2)	**SAR0110**	putative Na+/Pi-cotransporter protein (transport)	**-3.2**
SaMRSA252-2484 (7I5)	**narJ**	respiratory nitrate reductase delta chain (electron transport)	**-3.2**
SaMRSA252-2215 (6C20)	**pyrG**	putative CTP synthase (pyrimidine nucleotide biosynthesis)	**-3.2**
SaMRSA252-0258 (2E20)	**lytR**	autolysin response regulator protein (regulation of transcription, DNA-dependent)	**-3.2**
SaMRSA252-1717 (5J7)	**secF**	putative protein-export membrane protein (protein transport)	**-3.2**
SaMRSA252-0173 (2P9)	**SAR0173**	putative ABC transporter ATP-binding protein (ATP binding; ATPase activity; nucleosidetriphosphate activity; nucleotide binding)	**-3.2**
SaMRSA252-2308 (6L19)	**rplQ**	50S ribosomal protein L17 (translation)	**-3.1**
SaMRSA252-1451 (4E22)	**ald2**	alanine dehydrogenase 2 (electron transport)	**-3.1**

SaMRSA252-2323 (6K21)	**rplE**	50S ribosomal protein L5 (translation)	**-3.1**
SaMRSA252-0787 (1P24)	**sstA**	FecCD transport family protein (transport)	**-3.1**
SaMRSA252-2437 (7C11)	**SAR2437**	putative transport protein	**-3.1**
SaMRSA252-0543 (3D7)	**rplA**	50S ribosomal protein L1 (translation)	**-3.1**
SaMRSA252-1715 (5P6)	**apt**	adenine phosphoribosyltransferase (nucleoside metabolism)	**-3.1**
SaMRSA252-1605 (5F5)	**accB; fabE**	biotin carboxyl carrier protein of acetyl-CoA carboxylase	**-3.0**
SaMRSA252-2386 (7B5)	**SAR2386**	putative dehydrogenase (glycerol-3-phosphate catabolism)	**-3.0**
SaMRSA252-1719 (5L7)	**tgt**	queuine tRNA-ribosyltransferase (queuosine biosynthesis; tRNA modification)	**-3.0**
SaMRSA252-1059 (3K22)	**SAR1059**	putative cytochrome ubiquinol oxidase (electron transport; oxidoreductase activity)	**-3.0**
SaMRSA252-1762 (5O12)	**thrS**	threonyl-tRNA synthetase (translation)	**-3.0**
SaMRSA252-2314 (6J20)	**adk**	adenylate kinase (nucleobase, nucleoside, nucleotide and nucleic acid metabolism)	**-3.0**
SaMRSA252-2195 (6G17)	**atpF**	putative ATP synthase subunit b (ATP synthesis coupled proton transport)	**-3.0**
SaMRSA252-1449 (4C22)	**SAR1449**	amino acid permease (amino acid transport)	**-2.9**
SaMRSA252-0781 (1J24)	**SAR0781**	putative proton-dependent oligopeptide transport protein (oligopeptide transport)	**-2.9**
SaMRSA252-2490 (7O5)	**SAR2490**	conserved hypothetical protein (possible role in cobalamin biosynthesis)	**-2.9**
SaMRSA252-0905 (3C15)	**SAR0905**	putative transporter protein	**-2.9**
SaMRSA252-1758 (5K12)	**rplT**	50S ribosomal protein L20 (protein biosynthesis)	**-2.9**
SaMRSA252-2341 (6M23)	**glcU**	glucose uptake protein (carbohydrate transport)	**-2.9**
SaMRSA252-0546 (3G7)	**SAR0546**	conserved hypothetical protein	**-2.9**
SaMRSA252-0632 (3L6)	**SAR0632**	putative membrane protein	**-2.8**
SaMRSA252-1074 (3I24)	**SAR1074**	putative ABC transport system permease protein (transport)	**-2.8**

SaMRSA252-0789 (2B1)	**sstC**	ABC transporter ATP-binding protein (ATP-binding; ATPase activity; nucleoside triphosphatase; nucleotide binding)	**-2.8**
SaMRSA252-1227 (1P6)	**SAR1227**	conserved hypothetical protein	**-2.8**
SaMRSA252-2330 (6J22)	**rplV**	50S ribosomal protein L22 (translation)	**-2.8**
SaMRSA252-0363 (1C21)	**ssb**	putative single-strand DNA-binding protein (DNA binding)	**-2.8**
SaMRSA252-1235 (1P7)	**frr**	ribosome recycling factor (translation)	**-2.8**
SaMRSA252-2194 (6F17)	**atpH**	putative ATP synthase delta chain (ATP synthesis coupled proton transport)	**-2.8**
SaMRSA252-1419 (4E18)	**SAR1419**	putative branched-chain amino acid transporter protein (aliphatic amino acid transport)	**-2.8**
SaMRSA252-1366 (4I12)	**grlB; parE**	topoisomerase IV subunit B (DNA metabolism)	**-2.8**
SaMRSA252-1836 (5H21)	**SAR1836**	putative peptidase (proteolysis)	**-2.8**
SaMRSA252-0359 (1G20)	**SAR0359**	conserved hypothetical protein	**-2.8**
SaMRSA252-0318 (1G15)	**SAR0318**	hypothetical protein	**-2.8**
SaMRSA252-0362 (1B21)	**rpsF**	30S ribosomal protein S6 (translation)	**-2.7**
SaMRSA252-0618 (3N4)	**SAR0618**	putative transport system lipoprotein (iron ion transport)	**-2.7**
SaMRSA252-0257 (2D20)	**lytS**	autolysin sensor kinase protein (cell wall organisation and biogenesis)	**-2.7**
SaMRSA252-1431 (4A20)	**SAR1431**	putative acetyltransferase (N-acetyltransferase activity)	**-2.7**
SaMRSA252-0344 (1H18)	**SAR0344**	putative Sec-independent protein translocase protein (protein transport)	**-2.7**
SaMRSA252-2318 (6N20)	**rpsE**	30S ribosomal protein S5 (translation)	**-2.7**
SaMRSA252-1604 (5E5)	**accC**	biotin carboxylase subunit of acetyl-CoA carboxylase (metabolism)	**-2.7**
SaMRSA252-0383 (1G23)	**SAR0383**	hypothetical protein	**-2.7**
SaMRSA252-2439 (7E11)	**SAR2439**	TetR family regulatory protein (regulation of transcription, DNA-dependent)	**-2.7**

SaMRSA252-0982 (3G24)	**SAR0982**	hypothetical protein	**-2.7**
SaMRSA252-2107 (6P6)	**SAR2107**	putative leukocidin F subunit (haemolysis of red blood cells)	**-2.6**
SaMRSA252-2628 (7G22)	**clpL**	putative ATP-dependent protease ATP-binding subunit ClpL (nucleotide-excision repair)	**-2.6**
SaMRSA252-1720 (5M7)	**queA**	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (queuosine biosynthesis)	**-2.6**
SaMRSA252-2680 (7I17)	**ldh2**	L-lactate dehydrogenase 2 (TCA cycle intermediate metabolism)	**-2.6**
SaMRSA252-1465 (4C24)	**asnS**	putative asparaginyl-tRNA synthetase (tRNA aminoacylation for protein translation)	**-2.6**
SaMRSA252-0216 (2C15)	**SAR0216**	putative lipoprotein	**-2.6**
SaMRSA252-2033 (6A10)	**SAR2033**	putative membrane protein	**-2.6**
SaMRSA252-2332 (6L22)	**rplB**	50S ribosomal protein L2 (translation)	**-2.6**
SaMRSA252-0174 (2I10)	**SAR0174**	putative lipoprotein	**-2.6**
SaMRSA252-2505 (7M7)	**SAR2505**	putative transport system protein	**-2.6**
SaMRSA252-1147 (4H8)	**SAR1147**	putative membrane protein	**-2.6**
SaMRSA252-2411 (7B8)	**SAR2411**	putative transport protein	**-2.6**
SaMRSA252-1905 (5K18)	**SAR1905**	serine protease (proteolysis)	**-2.6**
SaMRSA252-2344 (6P23)	**SAR2344**	putative membrane protein	**-2.6**
SaMRSA252-2430 (7D10)	**SAR2430**	putative permease (glutamate transport)	**-2.6**
SaMRSA252-1675 (5K2)	**SAR1675**	conserved hypothetical protein	**-2.5**
SaMRSA252-2231 (6C22)	**SAR2231**	putative mannose-6-phosphate isomerase (carbohydrate metabolism)	**-2.5**
SaMRSA252-2219 (6G20)	**SAR2219**	hypothetical protein	**-2.5**
SaMRSA252-0176	**SAR0176**	conserved hypothetical protein	**-2.5**

(2K10)			
SaMRSA252-0614 (3J4)	**SAR0614**	conserved hypothetical protein	**-2.5**
SaMRSA252-0220 (2G15)	**SAR0220**	putative membrane protein (glycerol metabolism)	**-2.5**
SaMRSA252-1127 (4F6)	**SAR1127**	putative exported protein	**-2.5**
SaMRSA252-0256 (2C20)	**scdA**	cell wall metabolism protein	**-2.5**
SaMRSA252-1239 (1L8)	**proS; drpA**	prolyl-tRNA synthetase (protein translation)	**-2.5**
SaMRSA252-0912 (3B16)	**mnhC**	Na+/H+ antiporter subunit	**-2.5**
SaMRSA252-1912 (5J19)	**SAR1912**	transposase (partial)	**-2.5**
SaMRSA252-2310 (6N19)	**rpsK**	30S ribosomal protein S11 (translation)	**-2.5**
SaMRSA252-2503 (7K7)	**SAR2503**	transport system membrane protein (transport)	**-2.5**
SaMRSA252-2494 (7J6)	**SAR2494**	putative membrane protein	**-2.5**
SaMRSA252-2349 (6M24)	**SAR2349**	MarR family regulatory protein (regulation of transcription, DNA-dependent)	**-2.4**
SaMRSA252-1456 (4B23)	**SAR1456**	conserved hypothetical protein	**-2.4**
SaMRSA252-0079 (1C10)	**SAR0079**	putative protein kinase (protein amino acid phosphorylation)	**-2.4**
SaMRSA252-2198 (6B18)	**atpI**	putative ATP synthase protein I	**-2.4**
SaMRSA252-1793 (5F16)	**thiI**	putative thiamine biosynthesis protein (thiamin biosynthesis)	**-2.4**
SaMRSA252-0586 (3G12)	**ung**	putative uracil-DNA glycosylase	**-2.4**
SaMRSA252-0319 (1H15)	**SAR0319**	NADH:flavin oxidoreductase / NADH oxidase family protein (electron transport; oxidoreductase activity)	**-2.4**
SaMRSA252-2192 (6D17)	**atpG**	ATP synthase gamma chain (ATP synthesis coupled proton transport)	**-2.4**
SaMRSA252-2168 (6E14)	**SAR2168**	putative helicase (ATP binding; helicase activity; nucleic acid binding)	**-2.4**
SaMRSA252-1448 (4B22)	**SAR1448**	transporter protein	**-2.4**

SaMRSA252-2209 (6E19)	**rho**	transcription termination factor (ATP synthesis coupled proton transport; transcription termination)	**-2.4**
SaMRSA252-0287 (2C24)	**SAR0287**	hypothetical protein	**-2.4**
SaMRSA252-1711 (5L6)	**hisS**	histidyl-tRNA synthetase (protein translation)	**-2.3**
SaMRSA252-1556 (4N23)	**SAR1556**	putative regulatory protein (DNA binding)	**-2.3**
SaMRSA252-0059 (1A8)	**ccrB**	site-specific recombinase (DNA recombination; regulation of transcription)	**-2.3**
SaMRSA252-2493 (7I6)	**SAR2493**	putative nitrite transporter (transport)	**-2.3**
SaMRSA252-1429 (4G19)	**SAR1429**	putative membrane protein	**-2.3**
SaMRSA252-0783 (1L24)	**SAR0783**	putative membrane protein	**-2.3**
SaMRSA252-1551 (4I23)	**SAR1551**	hypothetical phage protein	**-2.3**
SaMRSA252-1075 (3J24)	**SAR1075**	putative ABC transport system permease protein (transport)	**-2.3**
SaMRSA252-1134 (4E7)	**SAR1134**	hypothetical protein	**-2.3**
SaMRSA252-1898 (5L17)	**hsdS**	putative type I restriction modification DNA specificity protein [conserved region] (DNA modification)	**-2.3**
SaMRSA252-1600 (5A5)	**SAR1600**	putative exodeoxyribonuclease VII small subunit (DNA catabolism)	**-2.3**
SaMRSA252-0686 (3P12)	**SAR0686**	putative transposase [pseudogene] (DNA-mediated transposition)	**-2.3**
SaMRSA252-2626 (7E22)	**mvaS**	3-hydroxy-3-methylglutaryl coenzyme A synthase (acetyl CoA metabolism)	**-2.3**
SaMRSA252-0914 (3D16)	**mnhA**	Na+/H+ antiporter subunit (ATP synthesis coupled electron transport)	**-2.3**
SaMRSA252-2787 (8H5)	**SAR2787**	hypothetical protein	**-2.3**
SaMRSA252-0357 (1E20)	**SAR0357**	putative DNA-binding protein (DNA binding)	**-2.3**
SaMRSA252-0408 (2O14)	**guaB**	putative inosine-5'-monophosphate dehydrogenase (catalytic activity)	**-2.3**
SaMRSA252-0983 (3H24)	**SAR0983**	hypothetical protein	**-2.2**
SaMRSA252-0630 (3J6)	**SAR0630**	putative NADH-Ubiquinone/plastoquinone (complex I) oxidoreductase protein -	**-2.2**

		(ATP synthesis coupled transport)	
SaMRSA252-1368 (4K12)	**SAR1368**	sodium:alanine symporter family protein (Sodium ion transport)	**-2.2**
SaMRSA252-1430 (4H19)	**murG**	putative UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (carbohydrate metabolism; lipid glycosylation)	**-2.2**
SaMRSA252-1693 (5K4)	**SAR1693**	putative O-methyltransferase	**-2.2**
SaMRSA252-2313 (6I20)	**infA**	translation initiation factor IF-1 (translational initiation)	**-2.2**
SaMRSA252-0386 (1B24)	**SAR0386**	hypothetical protein	**-2.2**
SaMRSA252-0511 (3E3)	**hpt**	putative hypoxanthine phosphoribosyltransferase (nucleoside metabolism)	**-2.2**
SaMRSA252-0631 (3K6)	**SAR0631**	putative membrane protein	**-2.2**
SaMRSA252-0150 (2I7)	**adhE**	putative aldehyde-alcohol dehydrogenase (metabolism)	**-2.2**
SaMRSA252-1401 (4C16)	**SAR1401**	ABC transporter permease protein (transport)	**-2.2**
SaMRSA252-0615 (3K4)	**argS**	putative arginyl-tRNA synthetase (arginyl-tRNA aminoacylation; cysteinyl-tRNA aminoacylation)	**-2.2**
SaMRSA252-0099 (1F12)	**SAR0099**	conserved hypothetical protein (tRNA processing)	**-2.2**
SaMRSA252-0384 (1H23)	**SAR0384**	hypothetical protein	**-2.2**
SaMRSA252-1863 (5K13)	**SAR1863**	putative membrane protein	**-2.2**
SaMRSA252-1757 (5J12)	**SAR1757**	conserved hypothetical protein	**-2.2**
SaMRSA252-1111 (4F4)	**pheS**	putative phenylalanyl-tRNA synthetase alpha chain (phenylalanyl-tRNA aminoacylation)	**-2.2**
SaMRSA252-2338 (6J23)	**SAR2338**	xanthine/uracil permeases family protein (transport)	**-2.2**
SaMRSA252-1236 (1I8)	**uppS**	undecaprenyl pyrophosphate synthetase (metabolism)	**-2.2**
SaMRSA252-0393 (1H24)	**SAR0393**	hypothetical protein	**-2.2**
SaMRSA252-0652 (3O8)	**pbp4**	penicillin-binding protein 4 (proteolysis)	**-2.2**
SaMRSA252-0017 (1A3)	**purA**	putative adenylosuccinate synthetase (purine nucleotide biosynthetic process)	**-2.2**

SaMRSA252-2397 (7E6)	**SAR2397**	putative membrane protein	**-2.2**
SaMRSA252-1234 (1O7)	**pyrH**	putative uridylate kinase (amino acid biosynthesis)	**-2.2**
SaMRSA252-2651 (7L13)	**SAR2651**	putative membrane protein	**-2.2**
SaMRSA252-2197 (6A18)	**atpB**	ATP synthase subunit a (proton transport)	**-2.2**
SaMRSA252-1148 (4A9)	**SAR1148**	putative DNA-binding protein	**-2.2**
SaMRSA252-0851 (2F8)	**SAR0851**	putative exported protein	**-2.2**
SaMRSA252-0235 (2G17)	**SAR0235**	putative PTS transport system, IIBC component (phosphoenolpyruvate-dependent sugar phosphotransferase system transport)	**-2.1**
SaMRSA252-0343 (1G18)	**SAR0343**	putative Sec-independent protein translocase protein	**-2.1**
SaMRSA252-1991 (6G4)	**gatB**	glutamyl-tRNA amidotransferase subunit B (translation)	**-2.1**
SaMRSA252-0913 (3C16)	**mnhB**	Na+/H+ antiporter subunit	**-2.1**
SaMRSA252-0633 (3M6)	**SAR0633**	putative NADH-Ubiquinone/plastoquinone (complex I) oxidoreductase protein (ATP synthesis coupled electron transport)	**-2.1**
SaMRSA252-2382 (7F4)	**SAR2382**	putative transcriptional regulator (regulation of transcription, DNA-dependent)	**-2.1**
SaMRSA252-0562 (3G9)	**SAR0562**	putative deoxyadenosine kinase protein (nucleobase, nucleoside, nucleotide and nucleic acid metabolism)	**-2.1**
SaMRSA252-1992 (6H4)	**gatA**	glutamyl-tRNA amidotransferase subunit A	**-2.1**
SaMRSA252-0847 (2B8)	**nuc**	thermonuclease precursor (nucleic acid binding)	**-2.1**
SaMRSA252-2134 (6K10)	**SAR2134**	ABC transporter ATP-binding protein (ATP binding; ATPase activity; nucleoside-triphosphatase activity; nucleotide binding)	**-2.1**
SaMRSA252-1794 (5G16)	**SAR1794**	aminotransferase class-V protein (metabolism)	**-2.1**
SaMRSA252-0968 (3A23)	**pepB**	putative oligopeptidase (proteolysis)	**-2.1**
SaMRSA252-2388 (7D5)	**SAR2388**	putative exported protein	**-2.1**

SaMRSA252-0517 (3C4)	**folK**	putative 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase- (folic acid and derivative biosynthesis)	**-2.1**
SaMRSA252-0890 (3D13)	**SAR0890**	conserved hypothetical protein	**-2.1**
SaMRSA252-0891 (3E13)	**SAR0891**	haloacid dehalogenase-like hydrolase (metabolism)	**-2.1**
SaMRSA252-1718 (5K7)	**SAR1718**	putative exported protein	**-2.1**
SaMRSA252-2106 (6O6)	**SAR2106**	phospholipase C precursor [partial]	**-2.1**
SaMRSA252-0695 (1I14)	**SAR0695**	putative membrane protein	**-2.1**
SaMRSA252-1445 (4G21)	**SAR1445**	putative membrane protein	**-2.1**
SaMRSA252-1272 (1M12)	**mutL**	DNA mismatch repair protein MutL (DNA mismatch repair)	**-2.1**
SaMRSA252-1642 (5C10)	**SAR1642**	putative glycyl-tRNA synthetase (tRNA aminoacylation for protein translation)	**-2.1**
SaMRSA252-1674 (5J2)	**SAR1674**	putative GTPase	**-2.0**
SaMRSA252-0215 (2B15)	**SAR0215**	putative sensor kinase protein (2-component signal transduction system)	**-2.0**
SaMRSA252-0490 (2P24)	**SAR0490**	tetrapyrrole (corrin/porphyrin) methylase family protein (metabolism)	**-2.0**
SaMRSA252-1374 (4A13)	**SAR1374**	putative membrane protein	**-2.0**
SaMRSA252-2529 (7M10)	**SAR2529**	sodium/hydrogen exchanger family protein (regulation of pH)	**-2.0**
SaMRSA252-2678 (7O16)	**SAR2678**	putative ketopantoate reductase (glycerol-3-phosphate catabolism)	**-2.0**
SaMRSA252-2788 (8A6)	**SAR2788**	putative exported protein	**-2.0**
SaMRSA252-0634 (3N6)	**SAR0634**	putative membrane protein (cation transport)	**-2.0**
SaMRSA252-1819 (5G19)	**SAR1819**	FtsK/SpoIIIE family protein	**-2.0**
SaMRSA252-1723 (5P7)	**SAR1723**	putative DNA-binding protein (metabolism)	**-2.0**
SaMRSA252-0761 (1N21)	**SAR0761**	putative lipoprotein	**-2.0**

SaMRSA252-2502 (7J7)	**SAR2502**	ABC transporter ATP-binding protein (ATP binding; ATPase activity; nucleoside-triphosphatase activity; nucleotide binding)	**-2.0**
SaMRSA252-0360 (1H20)	**SAR0360**	putative GTP-binding protein	**-2.0**
SaMRSA252-0801 (2F2)	**SAR0801**	putative glycosyl transferase (lipid metabolism)	**-2.0**
SaMRSA252-0469 (2K22)	**SAR0469**	putative membrane protein	**-2.0**
SaMRSA252-0760 (1M21)	**SAR0760**	putative membrane protein	**-2.0**
SaMRSA252-0947 (3E20)	**fabF**	3-oxoacyl-[acyl-carrier-protein] synthase II (fatty acid biosynthesis)	**-2.0**
SaMRSA252-1073 (3P23)	**SAR1073**	putative ABC transport ATP-binding protein (ATP binding; ATPase activity; nucleoside-triphosphtase activity; nucleotide binding)	**-2.0**
SaMRSA252-0355 (1C20)	**SAR0355**	Cys/Met metabolism PLP-dependent enzyme (amino acid metabolism)	**-2.0**
SaMRSA252-1136 (4F7)	**hla**	alpha-hemolysin precursor [pseudogene] (haemolysis of host red blood cells)	**-2.0**
SaMRSA252-0981 (3F24)	**SAR0981**	conserved hypothetical protein	**-2.0**
SaMRSA252-2193 (6E17)	**atpA**	ATP synthase alpha chain (ATP biosynthesis; ATP synthesis coupled proton transport)	**-2.0**
SaMRSA252-0307 (1D14)	**SAR0307**	putative membrane protein	**-2.0**
SaMRSA252-2385 (7A5)	**SAR2385**	putative Na+/H+ antiporter (regulation of pH; Na ion transport)	**-1.9**
SaMRSA252-2139 (6P10)	**SAR2139**	conserved hypothetical protein	**-1.9**
SaMRSA252-2580 (7G16)	**fnb**	fibronectin-binding protein precursor [conserved region] (cell adhesion)	**-1.9**
SaMRSA252-1939 (5L22)	**SAR1939**	putative response regulator (regulation of transcription, DNA-dependent)	**-1.9**
SaMRSA252-2265 (6P13)	**SAR2265**	putative membrane protein (nucleoside binding)	**-1.9**
SaMRSA252-0590 (3K1)	**SAR0590**	putative membrane protein	**-1.9**
SaMRSA252-1334 (4I8)	**nucI; nucH**	thermonuclease (nucleic acid binding)	**-1.9**
SaMRSA252-2345 (6I24)	**SAR2345**	AcrB/AcrD/AcrF family protein	**-1.9**

SaMRSA252-1820 (5H19)	**SAR1820**	conserved hypothetical protein (tRNA binding)	**-1.9**
SaMRSA252-0474 (2P22)	**SAR0474**	putative glycosyl hydrolase (carbohydrate metabolism)	**-1.9**
SaMRSA252-1282 (4O1)	**SAR1282**	conserved hypothetical protein (amino acid metabolism)	**-1.9**
SaMRSA252-1922 (5K20)	**SAR1922**	hypothetical protein	**-1.9**
SaMRSA252-2391 (7G5)	**SAR2391**	putative N-acetylmuramoyl-L-alanine amidase (peptidoglycan catabolism)	**-1.9**
SaMRSA252-1195 (1P2)	**SAR1195**	putative protein phosphatase (catalytic activity)	**-1.9**
SaMRSA252-0782 (1K24)	**SAR0782**	conserved hypothetical protein (biosynthetic process)	**-1.9**
SaMRSA252-1671 (5O1)	**SAR1671**	conserved hypothetical protein (biosynthetic process)	**-1.9**
SaMRSA252-0696 (1J14)	**SAR0696**	putative exported protein	**-1.9**
SaMRSA252-0117 (2P2)	**sirB**	putative siderophore transport system permease (transport)	**-1.9**
SaMRSA252-0485 (2K24)	**holB**	putative DNA polymerase III, delta' subunit	**-1.9**
SaMRSA252-0098 (1E12)	**SAR0098**	acetyltransferase (GNAT) family protein (n-acetyltransferase activity)	**-1.9**
SaMRSA252-0452 (2J20)	**SAR0452**	putative NADH-Ubiquinone/plastoquinone (complex I) protein (ATP synthesis coupled electron transport)	**-1.9**
SaMRSA252-2096 (6M5)	**SAR2096**	putative anti repressor (DNA binding)	**-1.9**
SaMRSA252-2495 (7K6)	**SAR2495**	hypothetical protein	**-1.9**
SaMRSA252-1253 (1J10)	**SAR1253**	conserved hypothetical protein (regulation of transcription, DNA-dependent)	**-1.9**
SaMRSA252-0617 (3M4)	**SAR0617**	putative DNA repair protein (base-excision repair)	**-1.9**
SaMRSA252-0610 (3N3)	**SAR0610**	putative acetyltransferase (N-acetyltransferase activity)	**-1.9**
SaMRSA252-1186 (1O1)	**SAR1186**	conserved hypothetical protein (transcription, DNA-dependent)	**-1.9**
SaMRSA252-2449 (7G12)	**SAR2449**	hypothetical protein	**-1.9**

SaMRSA252-2342 (6N23)	**SAR2342**	putative membrane protein	**-1.9**
SaMRSA252-0697 (1K14)	**SAR0697**	ABC transporter ATP-binding protein (ATP binding; ATPase activity; nucleoside-triphosphatase activity; nucleotide binding)	**-1.9**
SaMRSA252-0911 (3A16)	**mnhD**	Na+/H+ antiporter subunit (ATP synthesis coupled electron transport)	**-1.9**
SaMRSA252-1002 (3K15)	**SAR1002**	putative membrane protein	**-1.8**
SaMRSA252-0455 (2M20)	**SAR0455**	putative membrane protein	**-1.8**
SaMRSA252-1138 (4H7)	**SAR1138**	putative transposase (transposition, DNA-mediated)	**-1.8**
SaMRSA252-2142 (6K11)	**ilvH**	acetolactate synthase isozyme III small subunit [partial] (metabolism;amino acid binding)	**-1.8**
SaMRSA252-1217 (1N5)	**rplS**	50S ribosomal protein L19 (protein biosynthesis)	**-1.8**
SaMRSA252-2722 (7K22)	**SAR2722**	putative membrane protein (transport)	**-1.8**
SaMRSA252-2791 (8D6)	**SAR2791**	putative membrane protein (DNA binding)	**-1.8**
SaMRSA252-2674 (7K16)	**SAR2674**	conserved hypothetical protein (proteolysis)	**-1.8**
SaMRSA252-0187 (2N11)	**SAR0187**	putative branched-chain amino acid transport system carrier protein (branched-chain aliphatic amino acid transport)	**-1.8**
SaMRSA252-2187 (6G16)	**fabZ**	putative hydroxymyristoyl-(acyl carrier protein) dehydratase	**-1.8**
SaMRSA252-0765 (1J22)	**SAR0765**	conserved hypothetical protein	**-1.8**
SaMRSA252-0412 (2K15)	**SAR0412**	conserved hypothetical protein (pseudogene)	**-1.8**
SaMRSA252-2477 (7K4)	**SAR2477**	conserved hypothetical protein	**-1.8**
SaMRSA252-1634 (5C9)	**SAR1634**	putative endonuclease (DNA repair)	**-1.8**
SaMRSA252-1860 (5H24)	**SAR1860**	hypothetical protein	**-1.8**
SaMRSA252-1255	**SAR1255**	putative protease	**-1.8**

(1L10)			
SaMRSA252-2542 (7J12)	**SAR2542**	putative transport protein	**-1.8**
SaMRSA252-2346 (6J24)	**fmhB**	putative peptidoglycan pentaglycine interpeptide biosynthesis protein (peptidoglycan biosynthesis)	**-1.8**
SaMRSA252-0353 (1A20)	**metE**	5-methyltetrahydropteroyltriglutamate--homocyst eine methyltransferase (methionine biosynthesis)	**-1.8**
SaMRSA252-0894 (3H13)	**dltA**	D-alanine-D-alanyl carrier protein ligase (metabolism)	**-1.8**
SaMRSA252-2789 (8B6)	**SAR2789**	putative subtilase family protease (proteolysis)	**-1.8**
SaMRSA252-0356 (1D20)	**SAR0356**	Cys/Met metabolism PLP-dependent enzyme (amino acid metabolism)	**-1.8**
SaMRSA252-1846 (5B23)	**SAR1846**	conserved hypothetical protein	**-1.8**
SaMRSA252-0846 (2A8)	**SAR0846**	putative exported protein	**-1.8**
SaMRSA252-2442 (7H11)	**tcaA**	teicoplanin resistance associated membrane protein	**-1.8**
SaMRSA252-2311 (6O19)	**rpsM**	30S ribosomal protein S13 (translation)	**-1.7**
SaMRSA252-1264 (1M11)	**SAR1264**	conserved hypothetical protein	**-1.7**
SaMRSA252-0906 (3D15)	**SAR0906**	conserved hypothetical protein	**-1.7**
SaMRSA252-0925 (3G17)	**SAR0925**	putative membrane protein	**-1.7**
SaMRSA252-1692 (5J4)	**SAR1692**	putative peptidase (proteolysis)	**-1.7**
SaMRSA252-2003 (6C6)	**SAR2003**	conserved hypothetical protein	**-1.7**
SaMRSA252-0221 (2H15)	**SAR0221**	hypothetical protein	**-1.7**
SaMRSA252-0483 (2I24)	**tmk**	putative thymidylate kinase (tTDP biosynthesis)	**-1.7**
SaMRSA252-2458 (7P1)	**SAR2458**	acetyltransferase (GNAT) family protein (N-acetyltransferase activity)	**-1.7**
SaMRSA252-1475 (4M13)	**aroA**	3-phosphoshikimate 1-carboxyvinyltransferase	**-1.7**
SaMRSA252-1599	**SAR1599**	putative geranyltranstransferase (isoprenoid biosynthesis)	**-1.7**

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SaMRSA252-2251 (6C24)	**SAR2251**	putative transposase (transposition, DNA-mediated)	**-1.7**
SaMRSA252-0524 (3B5)	**nupC**	nucleoside permease (transport)	**-1.7**
SaMRSA252-1455 (4A23)	**SAR1455**	putative exported protein	**-1.7**
SaMRSA252-0979 (3D24)	**SAR0979**	putative membrane protein	**-1.7**
SaMRSA252-1844 (5H22)	**SAR1844**	putative membrane protein	**-1.7**
SaMRSA252-1158 (4C10)	**mraY**	phospho-N-acetylmuramoyl-pentapeptide-transferase (lipid metabolism)	**-1.7**
SaMRSA252-2004 (6D6)	**SAR2004**	putative membrane protein	**-1.7**
SaMRSA252-1756 (5I12)	**SAR1756**	hypothetical protein	**-1.7**
SaMRSA252-2221 (6A21)	**SAR2221**	putative peptidase (proteolysis)	**-1.7**
SaMRSA252-0515 (3A4)	**folP**	dihydropteroate synthase (folic acid and derivative biosynthesis)	**-1.7**
SaMRSA252-1697 (5O4)	**alaS**	putative alanyl-tRNA synthetase (alanyl-t-RNA aminoacylation)	**-1.7**
SaMRSA252-0086 (1B11)	**SAR0086**	hypothetical protein	**-1.7**
SaMRSA252-2233 (6E22)	**czrA**	zinc and cobalt transport repressor protein (regulation of transcription, DNA-dependent)	**-1.7**
SaMRSA252-2774 (8E4)	**cna**	collagen adhesin precursor (collagen binding)	**-1.7**
SaMRSA252-1635 (5D9)	**SAR1635**	putative helicase (ATP binding; helicase activity; nucleic acid binding)	**-1.6**
SaMRSA252-1750 (5K11)	**hemC**	porphobilinogen deaminase (porphyrin biosynthesis)	**-1.6**
SaMRSA252-2001 (6A6)	**SAR2001**	staphopain protease (proteolysis)	**-1.6**
SaMRSA252-0943 (3A20)	**SAR0943**	conserved hypothetical protein	**-1.6**
SaMRSA252-1095 (4F2)	**SAR1095**	conserved hypothetical protein	**-1.6**
SaMRSA252-0771	**SAR0771**	conserved hypothetical protein	**-1.6**

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SaMRSA252-1913 (5K19)	**SAR1913**	hypothetical protein	**-1.6**
SaMRSA252-1110 (4E4)	**SAR1110**	SpoU rRNA Methylase family protein (RNA processing)	**-1.6**
SaMRSA252-0619 (3O4)	**SAR0619**	FecCD transport family protein (transport)	**-1.6**
SaMRSA252-2204 (6H18)	**SAR2204**	conserved hypothetical protein	**-1.6**
SaMRSA252-0988 (3M13)	**murE**	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-dia minopimelate ligase (biosynthesis)	**-1.6**
SaMRSA252-1653 (5F11)	**SAR1653**	conserved hypothetical protein (catalytic activity; Fe ion binding)	**-1.6**
SaMRSA252-0516 (3B4)	**folB**	dihydroneopterin aldolase (folic acid and derivative metabolism)	**-1.6**
SaMRSA252-1602 (5C5)	**SAR1602**	putative N utilization substance protein B (regulation of transcription, DNA-dependent)	**-1.6**
SaMRSA252-2340 (6L23)	**SAR2340**	acetyltransferase (GNAT) family protein (N-acetyltransferase activity)	**-1.6**
SaMRSA252-2441 (7G11)	**tcaB**	teicoplanin resistance associated membrane protein	**-1.6**
SaMRSA252-0766 (1K22)	**SAR0766**	glutamine amidotransferase class-I protein (catalytic activity)	**-1.6**
SaMRSA252-0456 (2N20)	**SAR0456**	putative membrane protein	**-1.6**
SaMRSA252-0636 (3P6)	**SAR0636**	putative membrane protein (pseudogene)	**-1.6**
SaMRSA252-0616 (3L4)	**SAR0616**	hypothetical protein	**-1.5**
SaMRSA252-0563 (3H9)	**SAR0563**	putative deaminase (hydrolase activity; Zn ion binding)	**-1.5**
SaMRSA252-1838 (5B22)	**SAR1838**	RNA pseudouridine synthase (RNA processing)	**-1.5**
SaMRSA252-1743 (5L10)	**valS**	valyl-tRNA synthetase (tRNA aminoacylation for protein translation)	**-1.5**
SaMRSA252-1778 (5G14)	**accA**	acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (fatty acid biosynthesis)	**-1.5**
SaMRSA252-0764 (1I22)	**SAR0764**	putative 6-pyruvoyl tetrahydropterin synthase	**-1.5**
SaMRSA252-0770 (1O22)	**SAR0770**	conserved hypothetical protein	**-1.5**

SaMRSA252-2772 (8C4)	**pcp**	pyrrolidone-carboxylate peptidase (proteolysis)	**-1.5**
SaMRSA252-1749 (5J11)	**hemD**	uroporphyrinogen III synthase (heme and porphyrin biosynthesis)	**-1.5**
SaMRSA252-0365 (1E21)	**SAR0365**	hypothetical protein	**-1.5**
SaMRSA252-0097 (1D12)	**SAR0097**	putative DNA-binding protein (regulation of transcription, DNA-dependent)	**-1.5**
SaMRSA252-2792 (8E6)	**SAR2792**	putative membrane protein	**-1.5**
SaMRSA252-1672 (5P1)	**SAR1672**	conserved hypothetical protein	**-1.5**
SaMRSA252-2170 (6G14)	**SAR2170**	D-alanine--D-alanine ligase (peptidoglycan biosynthesis)	**-1.5**
SaMRSA252-0291 (2G24)	**SAR0291**	putative membrane protein	**-1.5**
SaMRSA252-2387 (7C5)	**SAR2387**	putative membrane protein	**-1.5**
SaMRSA252-0611 (3O3)	**SAR0611**	putative phosphohydrolase (catalytic activity)	**-1.5**
SaMRSA252-0963 (3D22)	**SAR0963**	putative transposase (transposition, DNA-mediated)	**-1.5**
SaMRSA252-0529 (3G5)	**radA**	putative DNA repair protein (nucleoside-triphosphatase activity; nucleotide binding)	**-1.4**
SaMRSA252-0198 (2A13)	**SAR0198**	ABC transporter ATP-binding protein (ATP binding; ATPase activity; nucleoside-triphosphatase activity; nucleotide binding)	**-1.4**
SaMRSA252-1621 (5F7)	**SAR1621**	hypothetical protein (transport)	**-1.4**
SaMRSA252-0881 (2C12)	**SAR0881**	putative membrane protein	**-1.4**
SaMRSA252-0394 (2I13)	**SAR0394**	phosphoglycerate mutase family protein	**-1.4**
SaMRSA252-2671 (7P15)	**SAR2671**	conserved hypothetical protein	**-1.4**
SaMRSA252-1680 (5O2)	**SAR1680**	hypothetical protein	**-1.4**
SaMRSA252-0374 (1F22)	**SAR0374**	hypothetical protein	**-1.4**
SaMRSA252-0845 (2H7)	**SAR0845**	putative exported protein	**-1.3**

SaMRSA252-0967 (3H22)	**SAR0967**	hypothetical protein	**-1.3**
SaMRSA252-0959 (3H21)	**SAR0959**	putative oligopeptide transport system permease protein (pseudogene)	**-1.3**
SaMRSA252-2548 (7P12)	**SAR2548**	putative membrane protein	**-1.3**
SaMRSA252-0665 (3L10)	**SAR0665**	putative esterase	**-1.3**

APPENDIX II: MICROARRAY NORMALIZED DATA

Table 4.5: Differentially regulated ASM vs GASM genes normalised to BHI, using one-way ANOVA and posthoc Benjamini and Hochberg tests ($p \leq 0.05$).

ORF	GENE	FOLD ASM	FOLD GASM
SaMRSA252-0013 (1E2)	**SAR0013**	0.46468106	0.8918642
SaMRSA252-0016 (1H2)	**dnaC**	0.53992015	0.8762845
SaMRSA252-0022 (1F3)	**yycJ**	0.729247	1.4204
SaMRSA252-0024 (1H3)	**SAR0024**	0.874725	1.7696714
SaMRSA252-0048 (1F6)	**SAR0048**	6.287764	1.814429
SaMRSA252-0101 (1H12)	**SAR0101**	1.1625729	0.6440747
SaMRSA252-0109 (2P1)	**SAR0109**	1.2635933	0.7634881
SaMRSA252-0110 (2I2)	**SAR0110**	1.5920168	0.3095714
SaMRSA252-0111 (2J2)	**SAR0111**	2.8357062	0.3729886
SaMRSA252-0112 (2K2)	**SAR0112**	0.61468023	0.13412818
SaMRSA252-0113 (2L2)	**lldP1**	1.7183038	0.8133743
SaMRSA252-0150 (2I7)	**adhE**	1.3430483	0.45129952
SaMRSA252-0151 (2J7)	**capA**	8.371157	2.1304312
SaMRSA252-0152 (2K7)	**capB**	15.33862	3.465002
SaMRSA252-0153 (2L7)	**capC**	64.001526	8.281368
SaMRSA252-0154 (2M7)	**capD**	33.27507	4.371519
SaMRSA252-0155 (2N7)	**capE**	24.455772	3.5634563
SaMRSA252-0156 (2O7)	**capF**	14.19307	2.9339175
SaMRSA252-0158 (2I8)	**cap8H**	9.755827	2.175777
SaMRSA252-0163 (2N8)	**capM**	6.9461827	1.7309104
SaMRSA252-0164 (2O8)	**capN**	6.1501455	1.7297816
SaMRSA252-0187 (2N11)	**SAR0187**	1.1260557	0.54936343
SaMRSA252-0191 (2J12)	**SAR0191**	14.18649	1.5319127
SaMRSA252-0192 (2K12)	**SAR0192**	11.392867	1.1757923
SaMRSA252-0193 (2L12)	**SAR0193**	12.702764	1.4399105
SaMRSA252-0194 (2M12)	**SAR0194**	10.818244	1.2772143
SaMRSA252-0204 (2G13)	**SAR0204**	2.7809114	0.9627453
SaMRSA252-0206 (2A14)	**SAR0206**	2.3606691	1.1021621
SaMRSA252-0207 (2B14)	**SAR0207**	3.5640159	1.3266948
SaMRSA252-0208 (2C14)	**SAR0208**	5.8903646	1.3699492
SaMRSA252-0209 (2D14)	**SAR0209**	3.2597508	1.1438533
SaMRSA252-0210 (2E14)	**SAR0210**	4.1923976	1.0522432
SaMRSA252-0211 (2F14)	**SAR0211**	6.3751216	1.1716555
SaMRSA252-0212 (2G14)	**SAR0212**	0.32571846	0.12021539
SaMRSA252-0213 (2H14)	**uhpT**	2.4304507	0.9366067
SaMRSA252-0215 (2B15)	**SAR0215**	1.1194017	0.48859078
SaMRSA252-0216	**SAR0216**	1.3707523	0.3855865

(2C15)			
SaMRSA252-0218 (2E15)	**SAR0218**	2.9170387	0.25630042
SaMRSA252-0219 (2F15)	**SAR0219**	1.8668467	0.1562219
SaMRSA252-0220 (2G15)	**SAR0220**	1.3579767	0.3952986
SaMRSA252-0221 (2H15)	**SAR0221**	0.95297754	0.5812597
SaMRSA252-0222 (2A16)	**coa**	2.5444415	0.87432736
SaMRSA252-0222v (2B16)	**coa**	2.300444	0.7413258
SaMRSA252-0235 (2G17)	**SAR0235**	1.3265718	0.4652363
SaMRSA252-0251 (2F19)	**SAR0251**	0.44368398	0.5944115
SaMRSA252-0276 (2G22)	**SAR0276**	0.96288073	0.5861894
SaMRSA252-0277 (2H22)	**SAR0277**	2.3515658	1.0785847
SaMRSA252-0287 (2C24)	**SAR0287**	1.0098027	0.42515013
SaMRSA252-0291 (2G24)	**SAR0291**	1.2181065	0.67379504
SaMRSA252-0293 (1A13)	**SAR0293**	1.4962282	0.86213666
SaMRSA252-0294 (1B13)	**SAR0294**	1.6146489	0.856953
SaMRSA252-0295 (1C13)	**SAR0295**	1.4573473	0.99920726
SaMRSA252-0305 (1B14)	**SAR0305**	4.6145506	2.0549307
SaMRSA252-0306 (1C14)	**SAR0306**	4.2110868	1.6459296
SaMRSA252-0307 (1D14)	**SAR0307**	0.86055624	0.5120401
SaMRSA252-0308 (1E14)	**SAR0308**	2.1710634	0.8401185
SaMRSA252-0309 (1F14)	**SAR0309**	2.6541984	0.8357773
SaMRSA252-0310 (1G14)	**SAR0310**	1.6844846	0.73628896
SaMRSA252-0312 (1A15)	**SAR0312**	4.833047	1.3346497
SaMRSA252-0313 (1B15)	**SAR0313**	2.104855	0.9634332
SaMRSA252-0314 (1C15)	**SAR0314**	1.6627566	0.8750828
SaMRSA252-0317 (1F15)	**geh**	1.8109337	0.9805433
SaMRSA252-0318 (1G15)	**SAR0318**	0.7792553	0.36207578
SaMRSA252-0319 (1H15)	**SAR0319**	0.8426718	0.41777495
SaMRSA252-0325 (1F16)	**SAR0325**	1.5491469	0.7274927
SaMRSA252-0330 (1C17)	**SAR0330**	0.7637386	1.1472974
SaMRSA252-0333	**glpT**	3.478413	1.1045313

(1F17)			
SaMRSA252-0334 (1G17)	**SAR0334**	2.7958033	7.5052075
SaMRSA252-0335 (1H17)	**SAR0335**	0.977215	3.6095557
SaMRSA252-0336 (1A18)	**SAR0336**	1.0571787	2.821556
SaMRSA252-0378 (1B23)	**SAR0378**	1.86775	8.969302
SaMRSA252-0379 (1C23)	**SAR0379**	0.860358	3.7094965
SaMRSA252-0380 (1D23)	**SAR0380**	0.94656414	2.0422332
SaMRSA252-0381 (1E23)	**SAR0381**	0.93379253	2.073526
SaMRSA252-0382 (1F23)	**SAR0382**	0.9475221	1.3964286
SaMRSA252-0390 (1E24)	**SAR0390**	2.7000778	0.6112165
SaMRSA252-0392 (1G24)	**SAR0392**	2.3658993	0.69770944
SaMRSA252-0400 (2O13)	**SAR0400**	2.0147393	6.542723
SaMRSA252-0419 (2I16)	**SAR0419**	1.1223867	2.7930872
SaMRSA252-0426 (2P16)	**SAR0426**	1.0509486	0.31987083
SaMRSA252-0450 (2P19)	**SAR0450**	0.6034885	0.98016745
SaMRSA252-0454 (2L20)	**SAR0454**	0.4030579	1.0825
SaMRSA252-0468 (2J22)	**SAR0468**	1.0756818	0.7147368
SaMRSA252-0469 (2K22)	**SAR0469**	1.0397065	0.5024951
SaMRSA252-0506 (3H2)	**SAR0506**	0.56996506	1.1402757
SaMRSA252-0507 (3A3)	**SAR0507**	0.7301069	1.1886168
SaMRSA252-0508 (3B3)	**SAR0508**	0.74043894	1.5028244
SaMRSA252-0517 (3C4)	**folK**	0.73597705	0.47621188
SaMRSA252-0559 (3D9)	**SAR0559**	1.0344523	2.0505857
SaMRSA252-0565 (3B10)	**SAR0565**	0.87295514	3.1392572
SaMRSA252-0569 (3G10)	**SAR0569**	1.1602532	2.2392614
SaMRSA252-0572 (3B11)	**SAR0572**	0.8244016	1.4366922
SaMRSA252-0574 (3D11)	**SAR0574**	2.5007913	1.2052732
SaMRSA252-0583 (3D12)	**SAR0583**	0.95329225	1.7891588
SaMRSA252-0584 (3E12)	**SAR0584**	1.0583587	3.3078778
SaMRSA252-0590 (3K1)	**SAR0590**	0.95498496	0.5169464
SaMRSA252-0598 (3K2)	**mvaK2**	1.7587502	0.9208038
SaMRSA252-0609 (3M3)	**SAR0609**	3.304547	1.3392518
SaMRSA252-0616 (3L4)	**SAR0616**	1.1040673	0.6487962
SaMRSA252-0618 (3N4)	**SAR0618**	0.5560844	0.36583415
SaMRSA252-0626 (3N5)	**SAR0626**	1.4602909	0.653484
SaMRSA252-0629 (3I6)	**SAR0629**	3.417953	1.0389584
SaMRSA252-0630 (3J6)	**SAR0630**	2.4843543	0.44590223
SaMRSA252-0631 (3K6)	**SAR0631**	1.8996552	0.45092213

SaMRSA252-0632 (3L6)	**SAR0632**	1.5209657	0.35138708
SaMRSA252-0633 (3M6)	**SAR0633**	1.4893664	0.46969733
SaMRSA252-0634 (3N6)	**SAR0634**	1.5399393	0.49455386
SaMRSA252-0635 (3O6)	**SAR0635**	1.2378716	0.663227
SaMRSA252-0636 (3P6)	**SAR0636**	1.2435576	0.6400808
SaMRSA252-0663 (3J10)	**SAR0663**	0.89870083	2.6295123
SaMRSA252-0667 (3N10)	**SAR0667**	0.9990628	3.3208873
SaMRSA252-0675 (3N11)	**SAR0675**	3.621745	0.8221818
SaMRSA252-0680 (3J12)	**SAR0680**	0.6512578	1.2809916
SaMRSA252-0681 (3K12)	**SAR0681**	0.47230715	1.1786345
SaMRSA252-0682 (3L12)	**SAR0682**	1.0270505	2.265806
SaMRSA252-0699 (1M14)	**SAR0699**	0.9939254	1.4632269
SaMRSA252-0704 (1P14)	**SAR0704**	0.72204727	1.2806602
SaMRSA252-0707 (1K15)	**SAR0707**	1.2780637	3.666898
SaMRSA252-0715 (1P15)	**SAR0715**	0.70893186	1.4935954
SaMRSA252-0734 (1K18)	**SAR0734**	2.1742618	1.2069931
SaMRSA252-0752 (1M20)	**SAR0752**	0.25659445	0.59146357
SaMRSA252-0763 (1P21)	**SAR0763**	1.3698791	0.69622207
SaMRSA252-0764 (1I22)	**SAR0764**	1.6964288	0.65571976
SaMRSA252-0765 (1J22)	**SAR0765**	1.2290485	0.5534975
SaMRSA252-0772 (1I23)	**SAR0772**	0.73885334	1.4307061
SaMRSA252-0776 (1M23)	**SAR0776**	2.0287447	0.98375595
SaMRSA252-0799 (2D2)	**SAR0799**	0.4613194	0.69853044
SaMRSA252-0802 (2G2)	**SAR0802**	0.9659037	2.0883722
SaMRSA252-0803 (2H2)	**SAR0803**	0.51797	0.8881307
SaMRSA252-0807 (2D3)	**secA**	0.849651	2.288079
SaMRSA252-0811 (2H3)	**SAR0811**	0.72314346	1.0061675
SaMRSA252-0815 (2D4)	**lgt**	0.7778712	1.1221565
SaMRSA252-0821 (2A5)	**SAR0821**	3.3691092	1.9238251
SaMRSA252-0825 (2E5)	**SAR0825**	3.502403	1.4250748
SaMRSA252-0837 (2A7)	**smpB**	1.8648777	1.0639266
SaMRSA252-0840 (2D7)	**SAR0840**	3.0290346	1.0678478
SaMRSA252-0841 (2E7)	**SAR0841**	3.0662901	0.9958238
SaMRSA252-0849 (2D8)	**SAR0849**	2.6591408	0.8699937
SaMRSA252-0850 (2E8)	**SAR0850**	3.3150826	0.9235972
SaMRSA252-0882 (2D12)	**SAR0882**	3.0982707	0.9202519
SaMRSA252-0898 (3D14)	**SAR0898**	0.5002504	1.5868772
SaMRSA252-0901 (3G14)	**SAR0901**	0.8342097	2.4178452
SaMRSA252-0906 (3D15)	**SAR0906**	0.27218154	0.57793075
SaMRSA252-0921 (3C17)	**glpQ**	7.206343	2.2777202
SaMRSA252-0930	**SAR0930**	0.6580122	1.624189

(3D18)			
SaMRSA252-0931 (3E18)	**SAR0931**	1.7321172	0.6826681
SaMRSA252-0933 (3G18)	**SAR0933**	0.65305185	1.2815228
SaMRSA252-0934 (3H18)	**SAR0934**	0.54043883	1.5027121
SaMRSA252-0970 (3C23)	**SAR0970**	1.3282714	3.1005714
SaMRSA252-0975 (3H23)	**SAR0975**	0.77873516	1.4699986
SaMRSA252-0986 (3K13)	**SAR0986**	0.8763961	1.9587433
SaMRSA252-0992 (3I14)	**SAR0992**	0.7407757	0.4742173
SaMRSA252-1049 (3I21)	**SAR1049**	4.5883822	14.640269
SaMRSA252-1050 (3J21)	**SAR1050**	5.746336	19.28062
SaMRSA252-1051 (3K21)	**SAR1051**	4.555158	19.083761
SaMRSA252-1054 (3N21)	**SAR1054**	1.3044372	2.387946
SaMRSA252-1066 (3I23)	**SAR1066**	0.54897743	1.9485464
SaMRSA252-1079 (3N24)	**SAR1079**	0.35845894	2.7937887
SaMRSA252-1081 (3P24)	**SAR1081**	0.8043508	2.5910513
SaMRSA252-1084 (4C1)	**SAR1084**	1.1008649	1.6977886
SaMRSA252-1085 (4D1)	**SAR1085**	1.019481	2.363324
SaMRSA252-1086 (4E1)	**SAR1086**	0.83376646	2.1141768
SaMRSA252-1117 (4D5)	**SAR1117**	0.7898956	1.3995013
SaMRSA252-1138 (4H7)	**SAR1138**	0.79489857	0.544595
SaMRSA252-1144 (4F8)	**SAR1144**	1.4886609	0.73445994
SaMRSA252-1146 (4G8)	**SAR1146**	0.5942711	2.1793044
SaMRSA252-1151 (4D9)	**SAR1151**	1.2556902	2.7030556
SaMRSA252-1153 (4F9)	**SAR1153**	1.443294	4.6624227
SaMRSA252-1158 (4C10)	**mraY**	1.1389228	0.5946273
SaMRSA252-1168 (4E11)	**SAR1168**	0.7266735	1.5569783
SaMRSA252-1171 (4H11)	**SAR1171**	0.79100555	1.6801589
SaMRSA252-1174 (4C12)	**pyrR**	0.41208595	0.25032
SaMRSA252-1188 (1I2)	**priA**	0.88479745	1.620783
SaMRSA252-1197 (1J3)	**SAR1197**	0.8874229	2.4730105
SaMRSA252-1198 (1K3)	**SAR1198**	0.7461038	2.1706061
SaMRSA252-1203 (1P3)	**recG**	0.9336269	2.1120212
SaMRSA252-1225 (1N6)	**SAR1225**	0.71119165	0.2748725
SaMRSA252-1226 (1O6)	**topA**	1.0556458	0.6988616
SaMRSA252-1245 (1J9)	**infB**	0.5765104	1.0528471
SaMRSA252-1254 (1K10)	**SAR1254**	1.1771258	0.61312836
SaMRSA252-1261 (1J11)	**recA**	1.0044913	1.9427842
SaMRSA252-1265 (1N11)	**SAR1265**	1.0115081	5.920014
SaMRSA252-1266 (1O11)	**SAR1266**	0.48103064	5.258159
SaMRSA252-1267 (1P11)	**SAR1267**	0.6225463	1.3832681

SaMRSA252-1279 (4L1)	**SAR1279**	0.71481746	2.6435697
SaMRSA252-1284 (4I2)	**glnA**	0.9863276	0.51340914
SaMRSA252-1288 (4L2)	**SAR1288**	1.3689644	3.9565003
SaMRSA252-1312 (4I5)	**SAR1312**	1.4834946	4.456924
SaMRSA252-1317 (4N5)	**SAR1317**	1.4164617	4.440857
SaMRSA252-1326 (4I7)	**SAR1326**	0.92047817	3.5565271
SaMRSA252-1328 (4K7)	**SAR1328**	0.717452	1.3543725
SaMRSA252-1333 (4P7)	**SAR1333**	0.92974025	2.6899016
SaMRSA252-1338 (4M8)	**SAR1338**	1.6314249	0.5167573
SaMRSA252-1339 (4N8)	**thrC**	1.4996514	0.53818935
SaMRSA252-1341 (4P8)	**SAR1341**	0.64291674	1.1728145
SaMRSA252-1350 (4I10)	**SAR1350**	0.65999645	2.0569696
SaMRSA252-1361 (4L11)	**opuD1**	0.54965353	0.2408207
SaMRSA252-1363 (4N11)	**SAR1363**	1.3653331	2.2387235
SaMRSA252-1366 (4I12)	**grlB**	0.5918387	0.36008093
SaMRSA252-1368 (4K12)	**SAR1368**	0.7084515	0.44590306
SaMRSA252-1369 (4L12)	**SAR1369**	0.68764013	1.1949857
SaMRSA252-1371 (4N12)	**SAR1371**	0.87031615	1.6584486
SaMRSA252-1378 (4E13)	**SAR1378**	1.1249583	0.7057574
SaMRSA252-1380 (4G13)	**trpE**	1.215179	0.65280706
SaMRSA252-1396 (4F15)	**SAR1396**	0.50359505	1.134806
SaMRSA252-1399 (4A16)	**SAR1399**	1.753862	0.7480826
SaMRSA252-1400 (4B16)	**SAR1400**	1.4686277	0.6577418
SaMRSA252-1404 (4F16)	**SAR1404**	0.48823446	0.27051452
SaMRSA252-1415 (4A18)	**SAR1415**	1.0856936	4.550116
SaMRSA252-1416 (4B18)	**SAR1416**	0.8790099	2.4055398
SaMRSA252-1417 (4C18)	**SAR1417**	1.0661075	3.2639074
SaMRSA252-1418 (4D18)	**SAR1418**	0.9088879	2.8502138
SaMRSA252-1422 (4H18)	**SAR1422**	0.80868304	1.9379743
SaMRSA252-1423 (4A19)	**SAR1423**	1.3804976	3.6474955
SaMRSA252-1429 (4G19)	**SAR1429**	0.7309806	0.4303688
SaMRSA252-1431 (4A20)	**SAR1431**	0.70230114	0.3671887
SaMRSA252-1439 (4A21)	**dfrB**	1.963855	1.0251838
SaMRSA252-1440 (4B21)	**thyA**	2.3273325	0.8517861
SaMRSA252-1455 (4A23)	**SAR1455**	0.9027445	0.5917137
SaMRSA252-1456 (4B23)	**SAR1456**	0.67489475	0.41342312

SaMRSA252-1459 (4E23)	**SAR1459**	0.84245485	2.3415577
SaMRSA252-1466 (4D24)	**SAR1466**	0.61238414	1.3489516
SaMRSA252-1492 (4N15)	**SAR1492**	0.86510223	6.9110475
SaMRSA252-1543 (4I22)	**SAR1543**	0.63325864	0.2946172
SaMRSA252-1569 (5B1)	**rluB**	0.86726534	1.6020694
SaMRSA252-1571 (5D1)	**SAR1571**	0.9645274	1.6899518
SaMRSA252-1572 (5E1)	**SAR1572**	0.7804171	1.4855555
SaMRSA252-1573 (5F1)	**xerD**	1.2613442	3.8113089
SaMRSA252-1574 (5G1)	**fur**	1.2087466	3.735957
SaMRSA252-1589 (5F3)	**gnd**	0.6342126	2.2477493
SaMRSA252-1593 (5B4)	**bfmB**	0.7846024	1.7506498
SaMRSA252-1602 (5C5)	**SAR1602**	0.44708532	0.63315284
SaMRSA252-1610 (5C6)	**SAR1610**	1.4491228	3.864697
SaMRSA252-1611 (5D6)	**SAR1611**	0.7194571	2.2899566
SaMRSA252-1631 (5H8)	**zur**	0.74645513	1.3812275
SaMRSA252-1633 (5B9)	**mreA**	0.8142331	2.4687715
SaMRSA252-1640 (5A10)	**SAR1640**	0.84926766	1.7522871
SaMRSA252-1641 (5B10)	**SAR1641**	1.1069362	2.159852
SaMRSA252-1643 (5D10)	**SAR1643**	1.3235724	2.8229802
SaMRSA252-1644 (5E10)	**era**	1.1566461	2.312268
SaMRSA252-1645 (5F10)	**cdd**	1.8053241	3.516316
SaMRSA252-1693 (5K4)	**SAR1693**	0.76160365	0.44848996
SaMRSA252-1706 (5O5)	**SAR1706**	0.64109766	2.2770884
SaMRSA252-1707 (5P5)	**SAR1707**	1.00899	1.9465007
SaMRSA252-1712 (5M6)	**SAR1712**	0.73226786	0.44855282
SaMRSA252-1716 (5I7)	**SAR1716**	0.61630803	0.3027052
SaMRSA252-1717 (5J7)	**secF**	0.90324104	0.31227684
SaMRSA252-1732 (5I9)	**SAR1732**	0.67024153	1.086254
SaMRSA252-1769 (5F13)	**polA**	1.4180975	2.3993483
SaMRSA252-1776 (5E14)	**pyk**	0.41749287	0.70586896
SaMRSA252-1777 (5F14)	**pfkA**	0.33913073	0.63316107
SaMRSA252-1782 (5C15)	**SAR1782**	1.049404	2.0009587
SaMRSA252-1783 (5D15)	**SAR1783**	0.69296366	1.7152853
SaMRSA252-1833 (5E21)	**SAR1833**	0.6206138	1.096078
SaMRSA252-1837 (5A22)	**SAR1837**	3.324786	1.8899668
SaMRSA252-1858 (5F24)	**SAR1858**	0.80688614	2.758749
SaMRSA252-1863 (5K13)	**SAR1863**	0.7190963	0.45633465
SaMRSA252-1890 (5L16)	**SAR1890**	0.8495076	1.7078474
SaMRSA252-1891 (5M16)	**SAR1891**	1.1671354	2.3818016

SaMRSA252-1914 (5L19)	**SAR1914**	0.7735187	2.578354
SaMRSA252-1954 (5K24)	**SAR1954**	1.0411499	2.4540284
SaMRSA252-1963 (6D1)	**SAR1963**	0.743763	1.8899945
SaMRSA252-1964 (6E1)	**SAR1964**	0.8790183	3.0797398
SaMRSA252-1995 (6C5)	**SAR1995**	0.6552535	0.9611286
SaMRSA252-2010 (6B7)	**SAR2010**	2.5700839	0.86652184
SaMRSA252-2105 (6N6)	**int**	1.0930096	0.5389688
SaMRSA252-2106 (6O6)	**SAR2106**	0.8057229	0.48091838
SaMRSA252-2107 (6P6)	**SAR2107**	0.6458813	0.37886417
SaMRSA252-2108 (6I7)	**SAR2108**	1.1123862	0.44509915
SaMRSA252-2109 (6J7)	**SAR2109**	7.311793	1.160173
SaMRSA252-2119 (6L8)	**SAR2119**	2.775482	1.1478336
SaMRSA252-2121 (6N8)	**SAR2121**	1.1763545	2.724482
SaMRSA252-2128 (6M9)	**scrB**	1.0422435	1.8565555
SaMRSA252-2134 (6K10)	**SAR2134**	0.9495356	0.47409657
SaMRSA252-2153 (6N12)	**rsbW**	1.7983415	0.9171606
SaMRSA252-2184 (6D16)	**SAR2184**	2.7816274	0.7249816
SaMRSA252-2186 (6F16)	**SAR2186**	1.0739685	0.67882186
SaMRSA252-2188 (6H16)	**murA1**	1.2030783	0.5489191
SaMRSA252-2189 (6A17)	**SAR2189**	2.112052	1.0028553
SaMRSA252-2193 (6E17)	**atpA**	1.0871086	0.5119499
SaMRSA252-2194 (6F17)	**atpH**	0.7847439	0.35843208
SaMRSA252-2195 (6G17)	**atpF**	0.8050963	0.33882532
SaMRSA252-2198 (6B18)	**atpI**	0.9674913	0.41433123
SaMRSA252-2207 (6C19)	**SAR2207**	0.5110102	0.29248273
SaMRSA252-2213 (6A20)	**SAR2213**	0.4585006	0.76013404
SaMRSA252-2231 (6C22)	**SAR2231**	0.83040357	0.39282966
SaMRSA252-2233 (6E22)	**czrA**	2.4657042	0.60327
SaMRSA252-2245 (6G23)	**SAR2245**	2.1910203	0.6484807
SaMRSA252-2261 (6L13)	**SAR2261**	0.63114166	1.1607786
SaMRSA252-2263 (6N13)	**SAR2263**	1.1017318	2.8574197
SaMRSA252-2274 (6I15)	**SAR2274**	5.088405	2.1119266
SaMRSA252-2276 (6K15)	**opuD2**	2.788676	0.7115176
SaMRSA252-2279 (6N15)	**SAR2279**	1.8664368	4.0450864
SaMRSA252-2290 (6I17)	**SAR2290**	1.1485374	4.646416
SaMRSA252-2291 (6J17)	**SAR2291**	1.1662822	3.490584
SaMRSA252-2294 (6M17)	**SAR2294**	0.97685623	1.9172401

SaMRSA252-2296 (6O17)	**SAR2296**	1.1458637	15.48309
SaMRSA252-2297 (6P17)	**SAR2297**	0.46112514	22.774578
SaMRSA252-2299 (6K18)	**SAR2299**	0.8810989	1.5501517
SaMRSA252-2302 (6N18)	**SAR2302**	0.67431206	1.1052182
SaMRSA252-2330 (6J22)	**rplV**	0.82074946	0.35631707
SaMRSA252-2331 (6K22)	**rpsS**	0.49862272	0.18463457
SaMRSA252-2334 (6N22)	**rplD**	0.52386343	0.23684348
SaMRSA252-2337 (6I23)	**SAR2337**	1.0551952	2.3573105
SaMRSA252-2342 (6N23)	**SAR2342**	0.807362	0.5379894
SaMRSA252-2345 (6I24)	**SAR2345**	0.78560483	0.518235
SaMRSA252-2348 (6L24)	**SAR2348**	1.0615394	0.66864866
SaMRSA252-2356 (7D1)	**mobB**	0.9715027	2.928149
SaMRSA252-2359 (7G1)	**moaB**	1.1857909	3.578227
SaMRSA252-2361 (7A2)	**modC**	0.4991859	1.015381
SaMRSA252-2368 (7H2)	**SAR2368**	0.5682429	1.4254922
SaMRSA252-2369 (7A3)	**SAR2369**	0.42601746	2.006894
SaMRSA252-2371 (7C3)	**SAR2371**	1.2349043	3.0050142
SaMRSA252-2372 (7D3)	**ureA**	1.4874339	5.084831
SaMRSA252-2373 (7E3)	**ureB**	1.1750546	3.6501412
SaMRSA252-2374 (7F3)	**ureC**	1.3346074	3.5829763
SaMRSA252-2375 (7G3)	**ureE**	1.248785	3.1727018
SaMRSA252-2376 (7H3)	**ureF**	1.1946504	3.565164
SaMRSA252-2378 (7B4)	**ureD**	1.6539929	3.9222908
SaMRSA252-2379 (7C4)	**sarR**	0.6328243	2.0333102
SaMRSA252-2383 (7G4)	**SAR2383**	1.1446447	0.11971289
SaMRSA252-2385 (7A5)	**SAR2385**	1.6605369	0.51399887
SaMRSA252-2386 (7B5)	**SAR2386**	1.8012245	0.33154294
SaMRSA252-2387 (7C5)	**SAR2387**	1.4735298	0.6789819
SaMRSA252-2388 (7D5)	**SAR2388**	5.1713166	0.4759401
SaMRSA252-2396 (7D6)	**SAR2396**	1.6043496	3.2498379
SaMRSA252-2408 (7G7)	**SAR2408**	1.3095633	4.6447163
SaMRSA252-2420 (7B9)	**SAR2420**	7.1340647	2.501297
SaMRSA252-2434 (7H10)	**SAR2434**	0.82898635	1.5258524
SaMRSA252-2437 (7C11)	**SAR2437**	0.21577725	0.32191244
SaMRSA252-2444 (7B12)	**SAR2444**	2.491324	0.75838596
SaMRSA252-2451 (7I1)	**SAR2451**	0.82690036	2.081786
SaMRSA252-2472 (7N3)	**gltT**	0.6426751	0.25345513
SaMRSA252-2499 (7O6)	**SAR2499**	0.4724116	0.9743131
SaMRSA252-2500 (7P6)	**SAR2500**	0.42976326	0.94612026
SaMRSA252-2502 (7J7)	**SAR2502**	0.24529848	0.49952772
SaMRSA252-2503 (7K7)	**SAR2503**	0.21657951	0.40434593
SaMRSA252-2505 (7M7)	**SAR2505**	0.79907435	0.38875312
SaMRSA252-2522 (7N9)	**SAR2522**	1.0092856	2.3575854
SaMRSA252-2525 (7I10)	**SAR2525**	1.3237295	0.5373617
SaMRSA252-2528 (7L10)	**SAR2528**	1.7695054	1.02556

SaMRSA252-2539 (7O11)	**SAR2539**	0.7304307	2.3149438
SaMRSA252-2541 (7I12)	**SAR2541**	2.7962556	0.90368533
SaMRSA252-2542 (7J12)	**SAR2542**	0.9553454	0.5648206
SaMRSA252-2543 (7K12)	**SAR2543**	4.524537	0.98055327
SaMRSA252-2544 (7L12)	**SAR2544**	4.664336	1.3443356
SaMRSA252-2545 (7M12)	**SAR2545**	1.2099801	3.473688
SaMRSA252-2558 (7B14)	**SAR2558**	5.0922637	1.5767926
SaMRSA252-2559 (7C14)	**SAR2559**	6.7962766	1.6534109
SaMRSA252-2560 (7D14)	**SAR2560**	2.449029	0.9524388
SaMRSA252-2581 (7A17)	**SAR2581**	0.443871	1.2403115
SaMRSA252-2582 (7B17)	**gntP**	1.0354517	3.4062111
SaMRSA252-2583 (7C17)	**gntK**	1.1503041	3.7177267
SaMRSA252-2602 (7F19)	**SAR2602**	2.2497084	6.4499145
SaMRSA252-2618 (7E21)	**glcB**	0.42885956	1.8258067
SaMRSA252-2619 (7F21)	**SAR2619**	2.0832233	5.474948
SaMRSA252-2621 (7H21)	**SAR2621**	0.48751	5.2753344
SaMRSA252-2628 (7G22)	**clpL**	3.051173	0.37976193
SaMRSA252-2642 (7D24)	**crtN**	2.4902616	0.9802656
SaMRSA252-2645 (7F24)	**SAR2645**	4.6075287	0.8679969
SaMRSA252-2646 (7G24)	**SAR2646**	5.0779963	0.90271217
SaMRSA252-2647 (7H24)	**SAR2647**	5.569378	1.1717324
SaMRSA252-2648 (7I13)	**ssaA**	2.6725557	0.67489415
SaMRSA252-2650 (7K13)	**isaA**	1.6765643	0.13408762
SaMRSA252-2652 (7M13)	**SAR2652**	1.2931871	0.8769187
SaMRSA252-2668 (7M15)	**SAR2668**	4.876903	1.2021116
SaMRSA252-2669 (7N15)	**SAR2669**	0.4247543	0.1672614
SaMRSA252-2677 (7N16)	**panB**	0.60450274	0.2645785
SaMRSA252-2697 (7J19)	**SAR2697**	1.3697807	10.199416
SaMRSA252-2698 (7K19)	**cysJ**	1.0429815	8.20725
SaMRSA252-2699 (7L19)	**SAR2699**	0.7421925	1.6867834
SaMRSA252-2702 (7O19)	**SAR2702**	0.80438316	1.3696302
SaMRSA252-2703 (7P19)	**SAR2703**	0.6852052	1.2815194

SaMRSA252-2715 (7L21)	**SAR2715**	1.0546552	2.456144
SaMRSA252-2717 (7N21)	**isaB**	1.0285083	5.8660045
SaMRSA252-2726 (7O22)	**SAR2726**	2.1442962	1.2162427
SaMRSA252-2738 (7J24)	**SAR2738**	1.3490214	0.7138139
SaMRSA252-2739 (7K24)	**SAR2739**	3.0483608	1.119441
SaMRSA252-2740 (7L24)	**SAR2740**	2.3899858	0.6242509
SaMRSA252-2746 (8B1)	**icaR**	0.6319445	2.7494178
SaMRSA252-2747 (8C1)	**icaA**	4.3389544	1.60808
SaMRSA252-2748 (8D1)	**icaD**	3.0044913	1.3838906
SaMRSA252-2771 (8B4)	**SAR2771**	0.786412	4.1485305
SaMRSA252-2781 (8D5)	**vraD**	2.384115	0.7347819
SaMRSA252-2782 (8E5)	**vraE**	1.9555877	0.7751254
SaMRSA252-2784 (8G5)	**SAR2784**	1.2459375	0.600313
SaMRSA252-2789 (8B6)	**SAR2789**	0.880191	0.5669668
SaMRSA252-2791 (8D6)	**SAR2791**	0.83504206	0.54594046