

**Table S5.** Complete data list of up-regulated and down-regulated genes (higher than log<sub>2</sub> 2-fold change) in nsSCVs cells (MG 0.031%) compared to cells grown at methylglyoxal concentration of 0.0078%.

Gene name/Gene ID	Group/Pathway	Change
<b>Metabolic pathway</b>		
<i>cysK</i> , SAOUHSC_00422	Cys biosynthesis	3.5
<i>gltB-gltD</i> , <i>rocA</i>	Glu biosynthesis	3.2
<i>gdhA</i>	Glu metabolism	3.2
<b><i>glnR</i>, <i>glnA</i></b>	<b>Glu biosynthesis</b>	<b>0.4-0.45</b>
<i>rocD</i>	Pro biosynthesis	3.6
<i>putA</i>	Pro metabolism	2.5
<i>argH-argG</i>	Arg biosynthesis	3.9-4.3
<i>arg</i> , <i>acrB-arcA</i>	Arg metabolism	2.6-2.7
<i>lysC-asd-dapA-dapB-dapD</i>	Lys biosynthesis	3.1-3.6
<b>SAOUHSC_02244</b>	<b>Lys biosynthesis</b>	<b>0.5</b>
<i>alr</i>	Ala biosynthesis	2.5
<i>ald</i>	Ala metabolism	2.5
<b><i>ald</i></b>	<b>Ala metabolism</b>	<b>0.3</b>
<i>gltD</i>	Gly biosynthesis	2.7
<i>hisC</i> , <i>hutI</i>	His metabolism	2.9-3
<i>hutU</i>	His metabolism	3.6
<i>ilvB-ilvA</i>	Iso, Val biosynthesis	2.9
SAOUHSC_01832, <i>serA</i>	Ser biosynthesis	2.3-2.5
<b><i>trpE</i>, <i>trpG</i>, <i>trpD</i>, <i>trpC</i>, <i>trpF</i>, <i>trpB</i>, <i>trpA</i></b>	<b>Tryptophan biosynthesis</b>	<b>0.29-0.31</b>
<i>thrA-thrB-thrC</i>	Thr biosynthesis	3.5-3.9
<i>tdh</i>	Thr metabolism	2.6
<b><i>ilvA</i></b>	<b>Thr metabolism</b>	<b>0.3</b>
<i>leuA-leuB-leuC-leuD</i>	Leu biosynthesis	3.4-3.7
SAOUHSC_00195- <i>fadB-caiA-caiC-fadX</i>	Lipid metabolism	4.4-7.9
<i>caiA</i> , SAOUHSC_00656, <i>lip</i>	Lipid metabolism	2.2-3
<b><i>lip</i>, <i>pnbA</i></b>	<b>Lipid metabolism</b>	<b>0.37-0.43</b>
<i>malA</i> , <i>gutB</i>	Starch and sucrose metabolism	4.4
<i>aldA</i> , <i>gap</i> , <i>acsA</i>	Glycolysis/Gluconeogenesis	4-6.3
<b><i>adhE</i>, <i>adhA</i></b>	<b>Glycolysis / Gluconeogenesis</b>	<b>0.28-0.31</b>
<b><i>plc</i>, <i>ldh</i>, <i>gapR</i>, <i>gap</i>, <i>pgk</i>, <i>tpiA</i>, <i>pgm</i></b>	<b>Glycolysis / Gluconeogenesis</b>	<b>0.33-0.37</b>
<i>citZ</i> , <i>pckA</i>	TCA cycle	3.1-4.2
<i>sdhC-sdhA-sdhB</i> ,	TCA cycle	2-2.9
<i>sucC</i> , <i>sucD</i> , <i>sucB</i> , <i>sucA</i> , <i>citC</i>	Urea cycle	3.3-4.6
<i>ureA-ureB-ureC-ureE-ureF</i>	Urea cycle	3.0
<i>ureG-ureD</i>	Urea cycle	3.0
<i>nanA</i>	Cell wall biosynthesis	3.3
<i>ddh</i> , <i>ndhF</i> , SAOUHSC_01728	Oxidoreductase	2.1-2.8
<i>arabB</i>	Ruboluse metabolism	2.5
<i>acpD</i>	Riboflavin metabolism	2.6
<b><i>pdxS</i>, <i>pdxT</i></b>	<b>Pyridoxal biosynthesis</b>	<b>0.35-0.45</b>
<b><i>nrdD</i></b>	<b>Pyrimidin metabolism</b>	<b>0.5</b>

**Organic substrate transport**

<i>dppB-dppC</i>	ABC-type Oligopeptide transport	4.5-4.7
<i>ggt</i>	Gamma-glutamyl transport	4-4.8
<i>malE</i> -SAOUHSC_00177- <i>ugpE</i>	Maltose transport	7.5-8.1
<i>msmX</i>	Multiple Sugar transport	6.8
<i>iolE</i>	Sugar phosphate transport	7.1
<i>gatC</i>	Galactitol PTS transport	3.3
<i>fruA</i>	Fructose PTS transport	3.7
<i>ulaA</i> -SAOUHSC_00311- SAOUHSC_00312	Ascorbate PTS transport	3.2
<i>alsT</i>	Na <sup>+</sup> /alanine symporter	4.8
SAOUHSC_01389	Phosphate ABC transporter substrate-binding protein	3.5
SAOUHSC_01990- SAOUHSC_01991	Amino acid ABC-type transport	3.7-4
<i>ansP</i>	Gamma-aminobutyrate transport	4.0
<i>gltS</i>	sodium/glutamate symporter	4.6
SAOUHSC_02729,SAOUHSC_02923	Amino acid ABC transport	3.6-4.1
SAOUHSC_02815	D-galactonate transport	3.8
SAOUHSC_02924	4-aminobutyrate amino transport	4.0
<i>murP</i>	N-acetylmuramic acid transport	2.0
<i>oppC-oppD-oppF-oppA</i> , SAOUHSC_00167	ABC-type Oligopeptide transporter	2-2.6
<i>uhpT</i>	Sugar phosphate antiporter	2.3
SAOUHSC_00214, SAOUHSC_00215	Galactitol transporter	2.5-2.9
<i>glpT,glpF</i>	Glycerol transport	2.5-2.9
SAOUHSC_00423, SAOUHSC_00424	Methionine transporter	2.7-2.8
SAOUHSC_00658	Mannose transport	2.3
SAOUHSC_00970	Binding protein	2.7
<i>putB</i>	Pro transporter	2.3
<i>utp</i>	Urea transporter	2.1
<i>ptsG</i>	Sugar transporter	2.5
<i>abgT</i>	p-aminobenzoyl-glutamate transporter	2.0
<i>potE</i>	<b>Amino acid transport</b>	<b>0.3</b>
SAOUHSC_02754	<b>ABC transporter ATP-binding protein</b>	<b>0.5</b>

**Inorganic ion transport**

<i>tauB-tauA</i>	ABC-type nitrate/sulfonate/bicarbonate transporter	3.1-3.5
<i>citT</i>	Di- and tricarboxylate transporters	3.5
<i>tauC</i>	nitrate/sulfonate/bicarbonate	2.6

	transport	
<i>fecB</i>	Fe3+-citrate transporter	2.5
<i>pstG</i>	Glucose transport	2.6
<i>feoA</i>	Fe2+ transport	3.9
<i>cbiQ, cbiO</i>	Cobalt transport	2.4-2.6
<i>ptsC, pstA</i>	Phosphate transporter	2.2-2.7
<i>sirC</i>	<b>Iron-Siderophore transport</b>	<b>0.4</b>
<i>focA</i>	<b>Formate/nitrite transport</b>	<b>0.4</b>
<i>cbiQ</i>	<b>Cobalt transport</b>	<b>0.5</b>
SAOUHSC_01022	<b>Cobalt transport</b>	<b>0.5</b>
<i>lldP</i>	<b>Lactate transport</b>	<b>0.5</b>
<b>Transcription/Regulatory protein</b>		
<i>blgG</i>	Similar to Transcriptional antiterminator	3.3
<i>malR</i>	Maltose operon transcriptional repressor	3.6
<i>lytT</i>	Similar to Response regulator of the LytR/AlgR family	3.7
<i>marR</i>	Similar to MarR; Transcriptional regulators	4.1
SAOUHSC_00992	MarR family transcriptional regulator	2.8
SAOUHSC_00296	ROK family protein (repressors, open reading frames, and kinases)	2.3
SAOUHSC_02057	dUTP pyrophosphatase	2.0
<i>agrB</i>	<b>Accessory gene regulator protein B</b>	<b>0.4</b>
<i>agrD</i>	<b>Similar to Staphylococcal AgrD protein</b>	<b>0.4</b>
<i>argC</i>	<b>Accessory gene regulator protein C</b>	<b>0.4</b>
<i>argA</i>	<b>Accessory gene regulator protein A</b>	<b>0.4</b>
<b>Translation</b>		
SAOUHSC_02836	Similar to sortase and related acyltransferases	0.4
<b>Stress response protein</b>		
<i>asp23</i>	<b>Stress response protein</b>	<b>0.3</b>
<i>trxB</i>	<b>Similar to thioredoxin reductase</b>	<b>0.4</b>
<b>Bacteriophage</b>		
SAOUHSC_01528	bacteriophage L54aIlg-like domain-containing protein	2.7
SAOUHSC_01533	Similar to gp6; Head-Tail Connector Protein gp6 of Bacteriophage HK97 and similar proteins	2.5
SAOUHSC_01539	terminase small subunit	3.1
SAOUHSC_01580	phi PVL ORF 30-like protein	2.5

SAOUHSC_02027	SLT orf 129-like protein	3.6
SAOUHSC_02061	phi PVL orf 50-like protein	2.8
SAOUHSC_02084	phage repressor protein	2.2
SAOUHSC_02186	phi PVL orf 12-like protein	2.2
SAOUHSC_02187	HK97 family phage protein	2.9
SAOUHSC_02191	phi PVL orf 12-like protein	2.2
SAOUHSC_02207	phi PVL/orf 52-like protein	3.2
SAOUHSC_02213	phi ETA orf 25-like protein	2.5
<b>Membrane Protein</b>		
SAOUHSC_00069	Protein A	3.6
<i>ebh</i>	Extracellular matrix binding protein	3.6
<i>rlp</i>	RGD-containing lipoprotein (lipoprotein containing Arg-Gly-Asp)	4.8
SA_tandem_lipo	Staphylococcus tandem lipoproteins	2.1
<i>epiA</i>	lantibiotic epidermin biosynthesis protein EpiB	2.3
<i>chp</i>	chemotaxis-inhibiting protein CHIPS	3.4
<i>drp35</i>	lactonase Drp35	2.6
<i>lytN</i>	cell wall hydrolase	2.8
<i>sspB</i>	Cysteine protease	2.1
<i>sspA</i>	Glutamyl endopeptidase	2.4
<i>chp</i>	chemotaxis-inhibiting protein CHIPS	3.4
<i>lytN</i>	cell wall hydrolase	2.8
<b>SAOUHSC_01135</b>	<b>Similar to Staph_haemo; Staphylococcus haemolytic protein</b>	<b>0.3</b>
<b>SAOUHSC_01136</b>	<b>Staph_haemo; Staphylococcus haemolytic protein</b>	<b>0.3</b>
<i>hld</i>	<b>delta-hemolysin</b>	<b>0.3</b>
<b>SAOUHSC_02167</b>	<b>Similar to CompInhib_SCIN; Staphylococcal complement inhibitor SCIN</b>	<b>0.5</b>
<i>sak</i>	<b>Staphylokinase</b>	<b>0.4</b>
<i>sbi</i>	<b>Immunoglobulin G-binding protein Sbi</b>	<b>0.4</b>

# the change in gene expression meant log<sub>2</sub>fold change  
The bold letters indicate the down regulated genes

