

**Table S4.** Significantly up-regulated and down-regulated genes in nsSCV cells in the presence of a methylglyoxal concentration of 0.031% (day 55) compared to cells grown at a methylglyoxal concentration of 0.0078% ( $p < 0.05$ ,  $p_{adj} < 1^*$ ).

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>rocD</i>	Pro biosynthesis	3.6
<i>argH-argG</i>	Arg biosynthesis	3.9-4.3
<i>thrA-thrB-thrC</i>	Thr biosynthesis	3.5-3.9
<i>lysC-asd-dapA-dapB-dapD</i>	Lys biosynthesis	3.1-3.6
<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>
<b><i>ilvA</i></b>	<b>Thr metabolism</b>	<b>0.30</b>
<i>leuA-leuB-leuC-leuD</i>	Leu biosynthesis	3.4-3.7
<i>gdhA</i>	Glu metabolism	3.2
<i>hutU</i>	His metabolism	3.6
SAOUHSC_00195- <i>fadB-caiA-caiC-fadX</i>	Lipid metabolism	4.4-7.9
<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>
<i>citZ</i> , <i>pckA</i>	TCA cycle	3.1-4.2
<i>mviM</i> , SAOUHSC_02829	Oxidoreducraase	8.3
<i>ureA-ureB-ureC-ureE-ureF</i>	Urea cycle	3.3-4.6
<i>nanA</i>	Cell wall biosynthesis	3.3
<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
<b>Organic substrate transport</b>		
<b><i>potE</i></b>	<b>Amino acid transport</b>	<b>0.30</b>
<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+/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

### Inorganic ion transport and metabolism

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

### Stress response protein

<i>asp23</i>	Stress response protein	0.31
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### Membrane Protein

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
<b>SAOUHSC_01135</b>	<b>Similar to Staph_haemo; Staphylococcus haemolytic protein</b>	<b>0.29</b>
<b>SAOUHSC_01136</b>	<b>Staph_haemo; Staphylococcus haemolytic protein</b>	<b>0.29</b>
<i>hld</i>	<b>delta-hemolysin</b>	<b>0.32</b>

\* pvalue<0.05, padj <1 statistic analysis as determined by the method described in Materials and Methods.

# the ratio of the change in gene expression of nsSCV (0.03% methylglyoxal) compared to cells grown at a methylglyoxal concentration of 0.008% and determined as log<sub>2</sub>fold change.

The bold letters indicate the down regulated genes

