

Table S2. Significantly up-regulated and down-regulated genes in nsSCV cells in the presence of 0.031% methylglyoxal (day 55) compared to cells grown in batch culture conditions ($p < 0.05$, $\text{padj} < 1^*$).

Gene name/Gene ID	Group/Pathway	Change#
Metabolic pathway		
<i>argB-argD</i>	Arg and Pro metabolism	3.80
<i>argH-argD</i>	Arg biosynthesis	6.10
<i>arcD-arcB-arcA</i>	Arg metabolism	3.6-4.3
<i>cysK</i> , SAOUHSC_00422	Cys biosynthesis	5.50
<i>hisH-hisZ</i>	His biosynthesis	3.70
<i>ilvD-ilvB-ilvH-ilvC-ilvA</i>	Iso and Val biosynthesis	4.2-5
<i>leuA-leuB-leuC-leuD</i>	Leu biosynthesis	4.7-4.9
<i>glbB</i>	Glu biosynthesis	3.70
<i>putA</i>	Pro metabolism	5.80
<i>thrA-thrB-thrC</i>	Thr biosynthesis	3.60
<i>ald</i>	Ala metabolism	0.26
<i>trpE-trpG-trpD-trpC-trpF-trpB-trpA</i>	Trp biosynthesis	0.14-0.18
<i>dapF</i>	Lys biosynthesis	0.23
<i>ilvA</i>	Thr metabolism	0.26
<i>aldA, pckA, acsA</i>	Glycolysis/Gluco-genesis	4.2-5.6
<i>adhE</i>	Glycolysis/Gluco-genesis	0.11
<i>plc, lip</i>	Lipid metabolism	0.2-0.26
<i>fadA-caiA-caiC-fadX</i>	Lipid metabolism	5.2-6.1
<i>azoR</i> , SAOUHSC_00320	Riboflavin metabolism	6.90
<i>ribD</i>	Riboflavin biosynthesis	0.28
<i>malA</i>	Starch and sucrose metabolism	3.90
<i>ureA-ureB-ureC</i>	Urea cycle	3.6-4
<i>pdxD-pdxT</i>	Pyridoxal biosynthesis	0.27
<i>ndh</i>	Energy production and conversion	0.14
DNA replication		
<i>dinP</i>	Similar to Nucleotidyltransferase/DNA polymerase	3.60
Ribosome		
<i>rspN</i>	Ribosome	0.21
Organic substrate transport		
<i>ggt</i>	Gamma-glutamyl transport	5.46
SAOUHSC_00424	D-methionine transport	4.30
SAOUHSC_00426	ABC transporter substrate-binding protein	4.99
<i>alsT</i>	Na ⁺ /alanine symporter	3.67
SAOUHSC_01990, SAOUHSC_1991	Amino acid ABC transporter	5.7-5.9
<i>ansP</i>	Gamma-aminobutyrate transport	5.51
SAOUHSC_02729, SAOUHSC_02923	Amino acid transporter	3.7-3.9
SAOUHSC_02924	4-aminobutyrate	5.01

<i>malE</i> , SAOUHSC_00177- SAOUHSC_00178	aminotransferase Maltose transport	6.5-7.6
SAOUHSC_00167-SAOUHSC_02833 <i>dppB-dppC</i>	Peptide ABC-type transport ABC-type oligopeptide transport	3.60 5.7-6
<i>msmX</i>	Multiple sugar transport	5.89
<i>iolE</i>	Sugar phosphate transport	6.81
SAOUHSC_03017	Similar to acetyltransferase (GNAT) domain	3.65
<i>potE</i>, <i>betT</i>	Amino acid transport	0.17- 0.27
SAOUHSC_02763,SAOUHSC_02767	ABC-type Peptide transport	0.27
Inorganic ion transport		
<i>cbiQ-cbiO</i>	ABC-type Cobalt transporter	3.7-4
<i>tauB-tauA-tauC</i>	ABC-type Nitrate/sulfonate/bicarbonate transport	5.7-6.5
<i>ceuD</i>	ABC-type Enterochelin (iron chelate) transport	3.70
<i>feoA</i>	Iron (Fe ²⁺) transport	4.70
SAOUHSC_00423	ABC-type metal ion transport	4.30
SAOUHSC_02754	ABC transporter ATP- binding protein	0.26
SAOUHSC_02765	Nickel ABC transporter permease	0.28
<i>sirC</i>	Iron complex (Iron- Siderophore) transport	0.18
Stress response gene		
<i>sodA</i>	Superoxide dismutase	0.26
<i>asp23</i>	Alkaline shock protein 23	0.20
<i>trxB</i>	Thioredoxin reductase	0.20
Membrane protein		
<i>ebh</i>	Extracellular matrix binding protein	5.30
<i>epiD-epiB-epiA</i>	Lantibiotic epidermin biosynthesis protein	3.6-6
<i>rlp</i>	RGD-containing lipoprotein	6.10
SAOUHSC_01135	Staph_haemo; Staphylococcus haemolytic protein	0.24
SAOUHSC_01136	Staph_haemo; Staphylococcus haemolytic protein	0.23
SAOUHSC_02019	Autolysin	0.26
SAOUHSC_02243	Leukocidin/hemolysin toxin family protein	0.28

* 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 compared to batch grown cells as log₂fold change

The bold letters indicate the down regulated genes

