Table S3. Complete data list of up-regulated and down-regulated genes (higher than log$_2$ 2-fold change) in nsSCVs formed under high stress condition (MG 0.031%) compared to cells grown in batch conditions.

Gene name/Gene ID	Group/Pathway	Change#
Metabolic pathway		
argB-argD	Arg and Pro metabolism	3.8
arcB-arcC,argJ-argC	Arg metabolism	2.2-3.3
arcD-arcB-arcA	Arg metabolism	3.6-4.3
argH-argD	Arg biosynthesis	6.1
*cysK,*SAOUHSC_00422	Cys biosynthesis	5.5
hisH-hisZ	His biosynthesis	3.7
hisF-hisA-hisB-hisC-hisD-hisG	His biosythesis	2-3.2
leuA-leuB-leuC-leuD	Leu biosynthesis	4.7-4.9
gltB	Glu biosynthesis	3.7
putA	Pro metabolism	5.8
rocD	Pro biosynthesis	2.7
thrA-thrB-thrC	Thr biosynthesis	3.6
alr	Ala metabolism	2.0
ald	**Ala metabolism**	**0.3**
trpE-trpG-trpD-trpC-trpF-trpB-trpA	**Trp biosynthesis**	**0.14-0.18**
lysC,asd-dapA-dapB-dapD	Lys biosynthesis	2.3-3.2
dapF	**Lys biosynthesis**	**0.2**
ilvA	**Thr metabolism**	**0.3**
lysA	**Lys biosynthesis**	**0.5**
gltD	Glu biosynthesis	3.3
rocA,gdhA	Glu metabolism	2.4
glnR-glnA	**Glu biosynthesis**	**0.4**
*serA,*SAOUHSC_01832	Ser metabolism	3.1
aldA, pckA,acsA	Glycolysis/Glucogenesis	4.2-5.6
gap	Glycolysis/Glucogenesis	3.4
adhE	**Glycolysis/Glucogenesis**	**0.1**
ldh1, adhA, gap-pgk-tpiA-pgm	**Glycolysis/Glucogenesis**	**0.4**
aldH,gpmA,ldh	**Glycolysis/Glucogenesis**	**0.5**
plc,lip	**Lipid metabolism**	**0.2-0.26**
pnbA	**Lipid metabolism**	**0.4**
fadA-caiA-caiC-fadX	Lipid metabolism	5.2-6.1
fadB,dhaL,lip	Lipid metabolism	2.3-2.7
malA	Starch and sucrose metabolism	3.9
gutB	Starch and sucrose metabolism	2.3
xynB	**Starch and sucrose metabolism**	**0.4**
fdhD	Formate metabolism	2.0
lacG-lacD-lacC-lacB-lacA	Galactose metabolism	2.1-3
araB	Ribulose metabolism	2.1

pfkB	Lactose metabolism	2.8
ureA-ureB-ureC	Urea cycle	3.6-4
ureE-ureF-ureG-ureD	Urea cycle	2.8-3.2
ndh	**Energy production and conversion**	**0.1**
narJ-narY-narG	**Energy production and conversion**	**0.5**
pflA, pycA, sdhB,citC-citZ	TCA cycle	2-2.2
sucC-sucD-sucB-sucA	TCA cycle	2.1-3.2
drm,nrdD	**Pyrimidine/Purine metabolism**	**0.5**
SAOUHSC_02057	Pyrimidine/Purine metabolism	2.1
ndhF,ldh, SAOUHSC_01728,SAOUHSC_02829	Oxidoreductase	2.8
murQ-murP,nanA	Cell wall biosynthesis	2.4-2.8
*azoR,*SAOUHSC_00320	Riboflavin metabolism	6.9
ribH-ribD-ribB	**Riboflavin biosynthesis**	**0.4**
ribD	**Riboflavin biosynthesis**	**0.3**
thiM-thiD-tenA	**Thiamine biosynthesis**	**0.5**
pdxD-pdxT	**Pyridoxal biosynthesis**	**0.3**
crtI	**Carotenoid biosynthesis**	**0.4**
SAOUHSC_02849	**Pyruvate metabolism**	**0.4**
Organic substrate transport		
ggt	Gamma-glutamyl transport	5.5
SAOUHSC_00424	D-methionine transport	4.3
SAOUHSC_00426	ABC transporter substrate-binding protein	5.0
alsT	Na+/alanine symporter	3.7
SAOUHSC_01990, SAOUHSC_1991	Amino acid ABC transporter	5.7-5.9
ansP	Gamma-aminobutyrate transport	5.5
SAOUHSC_02729,SAOUHSC_02923	Amino acid transporter	3.7-3.9
SAOUHSC_02924	4-aminobutyrate aminotransferase	5.0
malE, SAOUHSC_00177-SAOUHSC_00178	Maltose transport	6.5-7.6
SAOUHSC_00167-SAOUHSC_02833	Peptide ABC-type transport	3.6
dppB-dppC	ABC-type oligopeptide transport	5.7-6
msmX	Multiple sugar transport	5.9
iolE	Sugar phosphate transport	6.8
SAOUHSC_03017	Similar to acetyltransferase (GNAT) domain	3.6
SAOUHSC_00970	ABC transporter ATP-binding protein	3.5
SAOUHSC_01389	Phosphate ABC transporter substrate-binding protein	2.4
putB	Proline transport	2.6
abgT	p-aminobenzoyl-glutamate	2.6

	transporter	
SAOUHSC_00658	Mannose PTS transpoter	2.3
lacE	Galactose PTS transport	2.7
glpF, glpT	Glycerol transpot	2.3-3.3
SAOUHSC_02848	Glucose PTS transpoter	3.3
oppC-oppD-oppF-oppA-dppA	ABC-type Oligopeptide transport	2.2-2.7
uhpT	Sugar phosphate antiport	2.6
treP	Trehalose PTS transpot	2.6
utp	Urea transporter	3.0
potE, betT	**Amino acid transport**	**0.17-0.27**
SAOUHSC_02763,SAOUHSC_02767	**ABC-type Peptide transport**	**0.3**
potE	**Amino acid transporter**	**0.3**
lldP	**Lactate transporter**	**0.3**
SAOUHSC_02764, _02766	**Peptide ABC-type transport**	**0.3**
mltA/mltF	**Mannitol PTS transporter**	**0.3**
Inorganic ion transport		
cbiQ-cbiO	ABC-type Cobalt transporter	3.7-4
tauB-tauA-tauC	ABC-type Nitrate/sulfonate/bicarbonate transport	5.7-6.5
ceuD	ABC-type Enterochelin (iron chelat) transport	3.7
feoA	Iron (Fe2+) transport	4.7
SAOUHSC_00423	ABC-type metal ion transport	4.3
SAOUHSC_02754	**ABC transporter ATP-binding protein**	**0.3**
SAOUHSC_02765	**Nickel ABC transporter permease**	**0.3**
sirC	**Iron complex (Iron-Siderophore) transport**	**0.2**
cbiO	ABC-type Cobalt transport	3.3
fepG	ABC-type Enterobactin transport	2.0
fecB	ABC-type Fe3+-citrate transport	3.1
fepB	ABC-type Fe3+-hydroxamate transport	2.5
ceuA	ABC-type Enterochelin transport	2.7
natB	Na+ efflux pump	2.1
SAOUHSC_02137	Sodium-dependent transporter	2.5
cbiQ-cbiO	**ABC-type Cobalt transporter**	**0.4**
focA	**Formate/nitrite transporter**	**0.5**
nhaC	**Na+/H+ antiporter**	**0.4**
narK	**Nitrate/nitrite transporter**	**0.4**

Ribosome		
rspN	**Ribosome**	**0.2**
DNA replication		
dinP	Similar to Nucleotidyltransferase/DNA polymerase	3.6
SAOUHSC_00049	**Similar to superfamily I DNA and RNA helicases and helicase subunits**	**0.5**
SAOUHSC_00624	**Integrase/recombinase**	**0.5**
Transcription/Regulatory protein		
SAOUHSC_00296	ROK family protein (repressors, open reading frames, and kinases)	**2.1**
malR	Maltose operon transcriptional repressor	3.2
rpiR	Transcriptional regulators	2.9
marR	MarR family transcriptional regulator	3.5
agr	**Accessory regulator-like protein**	**0.4**
gntR	**GntR family transcriptional regulator**	**0.4**
lrgB	**Antiholin-like protein LrgB**	**0.4**
gapR	**Glycolytic operon regulator**	**0.3**
rsbW	**Serine-protein kinase RsbW (anti sigma factor)**	**0.5**
rsbV	**STAS domain-containing protein (Sulphate Transporter and Anti-Sigma)**	**0.5**
blgG	**Similar to Transcriptional antiterminator BlgG**	**0.4**
Translation		
SAOUHSC_00031	**Similar to tRNA-dihydrouridine synthase**	**0.3**
SAOUHSC_00039	**Similar to tRNA-dihydrouridine synthase**	**0.4**
Stress response gene		
sodA	**Superoxide dismutase**	**0.3**
asp23	**Alkaline shock protein 23**	**0.2**
trxB	**Thioredoxin reductase**	**0.2**
Bacteriophage		
SAOUHSC_01539	Terminase small subunit	3.6
Capsule biosynthesis		
cap5B-cap8C-cap5D-cap5E-cap8F-cap5H	**Capsule biosynthesis**	**0.3-0.42**
Membrane protein/Chaperon		
ebh	Extracellular matrix binding protein	5.3

epiD-epiB-epiA	Lantibiotic epidermin biosynthesis protein	3.6-6
rlp	RGD-containing lipoprotein	6.1
SAOUHSC_00069	Protein A	2.5
lytN	Cell wall hydrolase	3.5
chp	Chemotaxis-inhibiting protein CHIPS	2.9
epiC	Epidermin biosynthesis protein EpiC	3.4
drp35	Lactonase Drp35	2.0
clpB	ATP-dependent Clp protease ATP-binding subunit ClpB	2.3
SAOUHSC_01949	Intracellular serine protease	3.0
SAOUHSC_01135	**Staph_haemo; Staphylococcus haemolytic protein**	**0.2**
SAOUHSC_01136	**Staph_haemo; Staphylococcus haemolytic protein**	**0.2**
SAOUHSC_02019	**Autolysin**	**0.3**
SAOUHSC_02243	**Leukocidin/hemolysin toxin family protein**	**0.3**
emp	**Extracellular matrix and plasma binding protein**	**0.4**
SAOUHSC_02821	**Membrane spanning protein**	**0.4**
SAOUHSC_02167	**Similar to CompInhib_SCIN; Staphylococcal complement inhibitor SCIN**	**0.4**
sak	**Staphylokinase**	**0.3**
SAOUHSC_02241	**Similar to Leukocidin**	**0.3**
hld	**Delta-hemolysin**	**0.4**
sbi	**Immunoglobulin G-binding protein Sbi**	**0.4**
clpC	**Chaperon ATP-dependent Clp protease ATP-binding subunit ClpC**	**0.4**

the ratio of the change in gene expression of nsSCV compared to batch grown cells as $\log_2$fold change

The bold letters indicate the down regulated genes