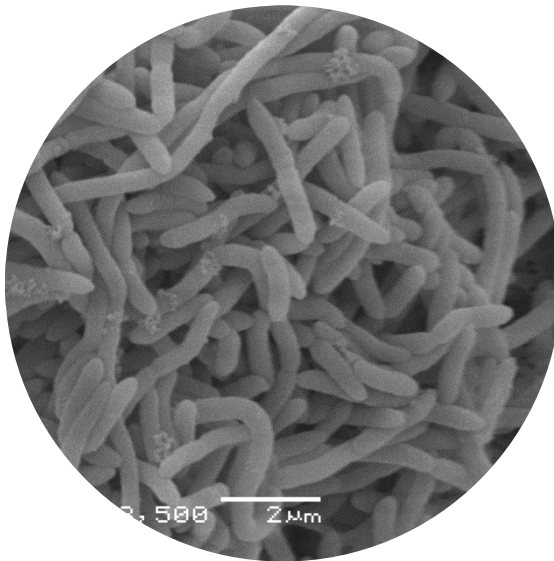


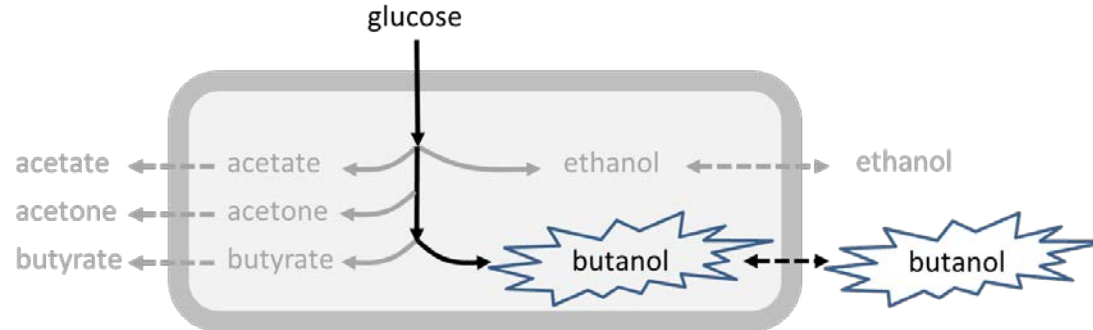
Analysis of the Transcriptional Response to Butanol Challenges during Acidogenic Continuous Culturing of *Clostridium acetobutylicum*

September 12, 2012, Servé Kengen



Butanol toxicity

- Intolerance to butanol is major factor that hampering cost-effective production



- Chaotropic effects → increase fluidity → ion leakage
- Inhibition of transport of nutrients, sugars, amino acids, ATPase activity

Tackle toxicity:

- Improving *in situ* butanol removal (DSP techniques)
- Raising the butanol tolerance
 - Classical screening for tolerant strains
 - Metabolic engineering (random/rational approaches)

➔ We need knowledge about the genes involved in butanol tolerance and their regulation.

Previous research

- 2003 Tomas et al.:** overexpression of *groESL* operon caused higher tolerance
- 2004 Tomas et al.:** transcriptional analysis of WT and mutant (0.25% and 0.75% butanol)
- 2004 Alsaker et al.:** transcriptional analysis of *spo0A* modified strains
- 2007 Borden et al.:** random genomic library approach
- 2010 Alsaker et al.:** gene expression under butanol, acetate, butyrate
- 2010 Janssen et al.:** proteomics and transcriptomics of acidogenic/solventogenic steady states
- 2010 Mao et al.:** membrane proteome of WT and butanol tolerant strain
- 2011 Grimmier et al.:** transcriptomic analysis of the acidogenic/solventogenic switch
- 2011 Mao et al.:** proteomics of WT and butanol tolerant strain
- 2012 Jia et al.:** two adjacent genes found to affect butanol tolerance (*CAC1493/1494* ortholog)
- 2012 Mann et al.:** overexpression of *groESL*, *grpE*, *htpG* improved tolerance

Previous research

2003 Tomas et al.: overexpression of groESL operon caused higher tolerance

2004 Tomas et al.: transcriptional analysis of WT and mutant (0.25% and 0.75% butanol)

2004 Alsaker et al.: transcriptional analysis of spo0A modified strains

2007 Borden et al.: random genomic library approach

2010 A

2010 Ja - Overexpression of general stress proteins encoding genes

2010 M - Overexpression of solventogenic genes / butyrate forming genes

2011 G - Repression of fatty acid biosynthesis / glycolysis / sporulation genes

2011 M - Glycerol-3-P related genes upregulated

2012 Ji - Overexpression of genes gave higher tolerance

2012 M (CAC1869/CAC0003)(CAC1493/1494)



Butanol stress response is complex.

Multiple synergistic effects are responsible for the improved solvent tolerance

New setup

COSMIC consortium (SySMo):

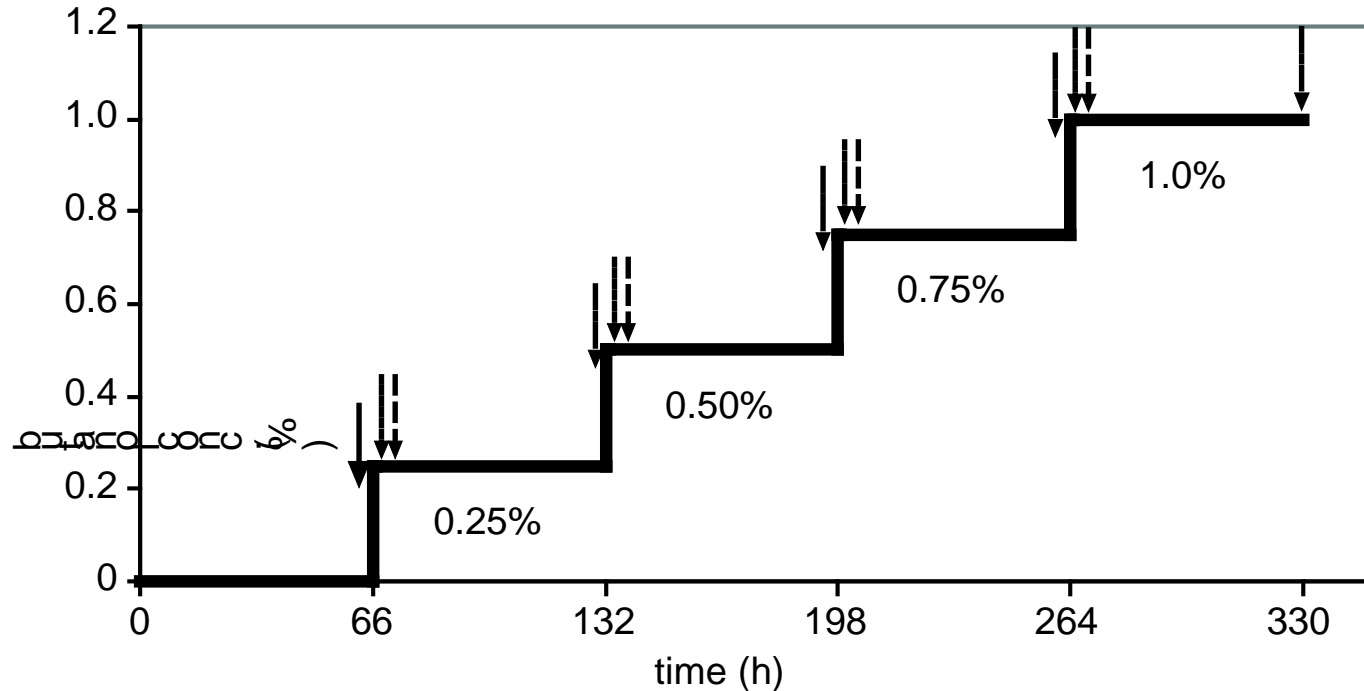
All partners used the same pH-controlled phosphate-limited chemostat system and the same *Clostridium acetobutylicum* strain ATCC824 (COSMIC strain)



pH 6.0
D= 0.075 h⁻¹
37°C
4% glucose
minimal medium
[Pi] = 0.5 mM

Enabled us to analyse the specific butanol response, with minimum background butanol formation, and uncoupled from solvent formation which occurs at low pH

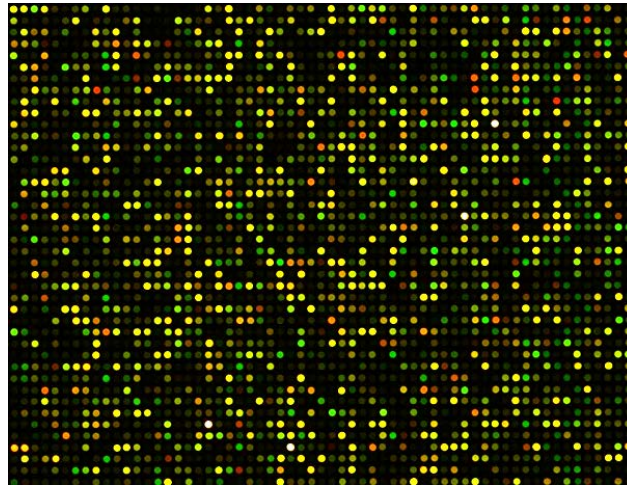
New setup



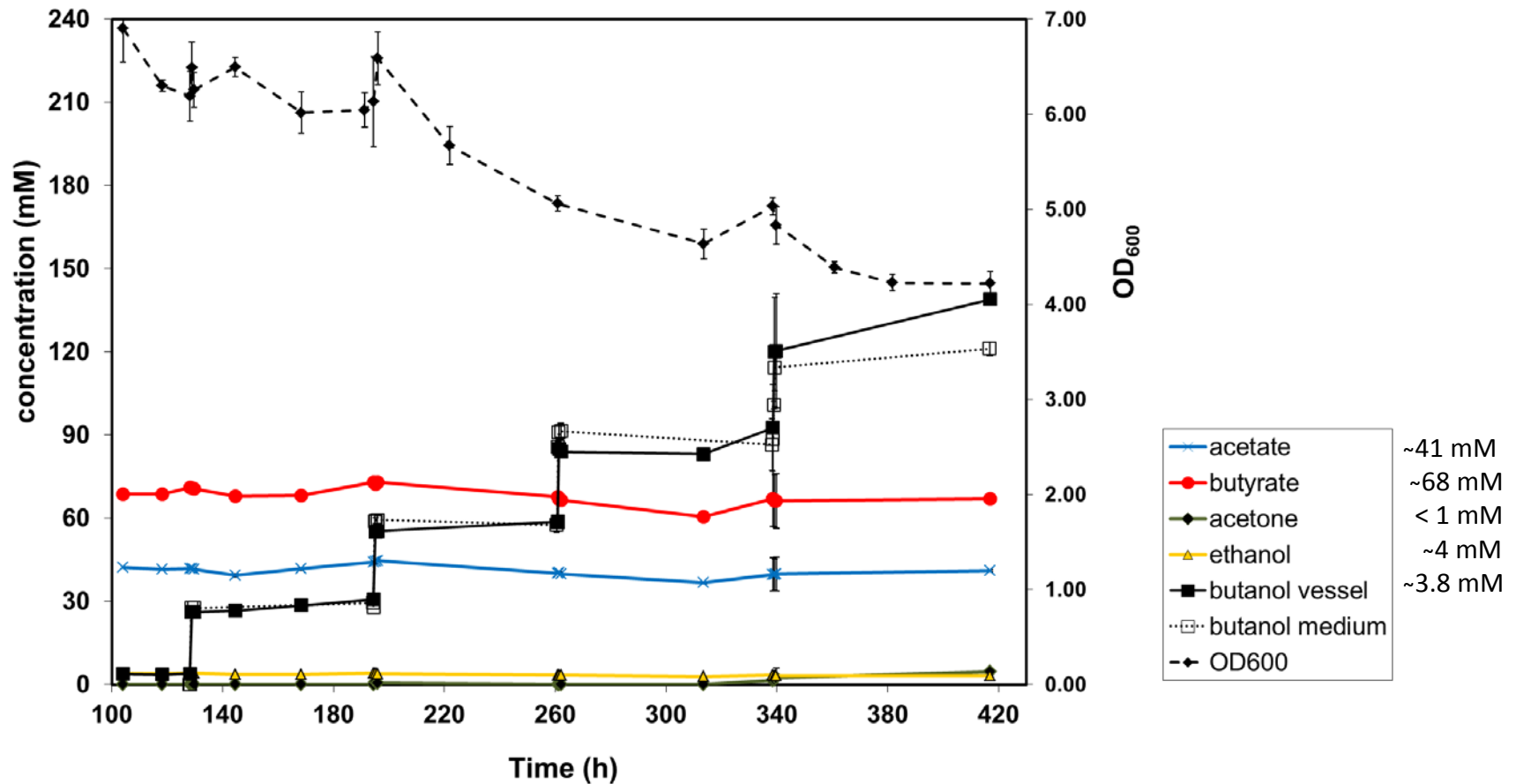
- Stepwise addition of butanol (0.25%, 0.50%, 0.75%, 1.0%)
- Samples for analysis of fermentation and RNA taken after 0.25h, 1 h and 66h
- Growth followed by OD₆₀₀ measurements

Microarrays

- Two independent biological replicates
- Common reference design (0% butanol as common reference)
- Significant up- or downregulation: expression ratio >3 or < 0.33 , respectively



Results – chemostat culturing



No significant changes in fermentation pattern

Culture remains in acidogenic phase

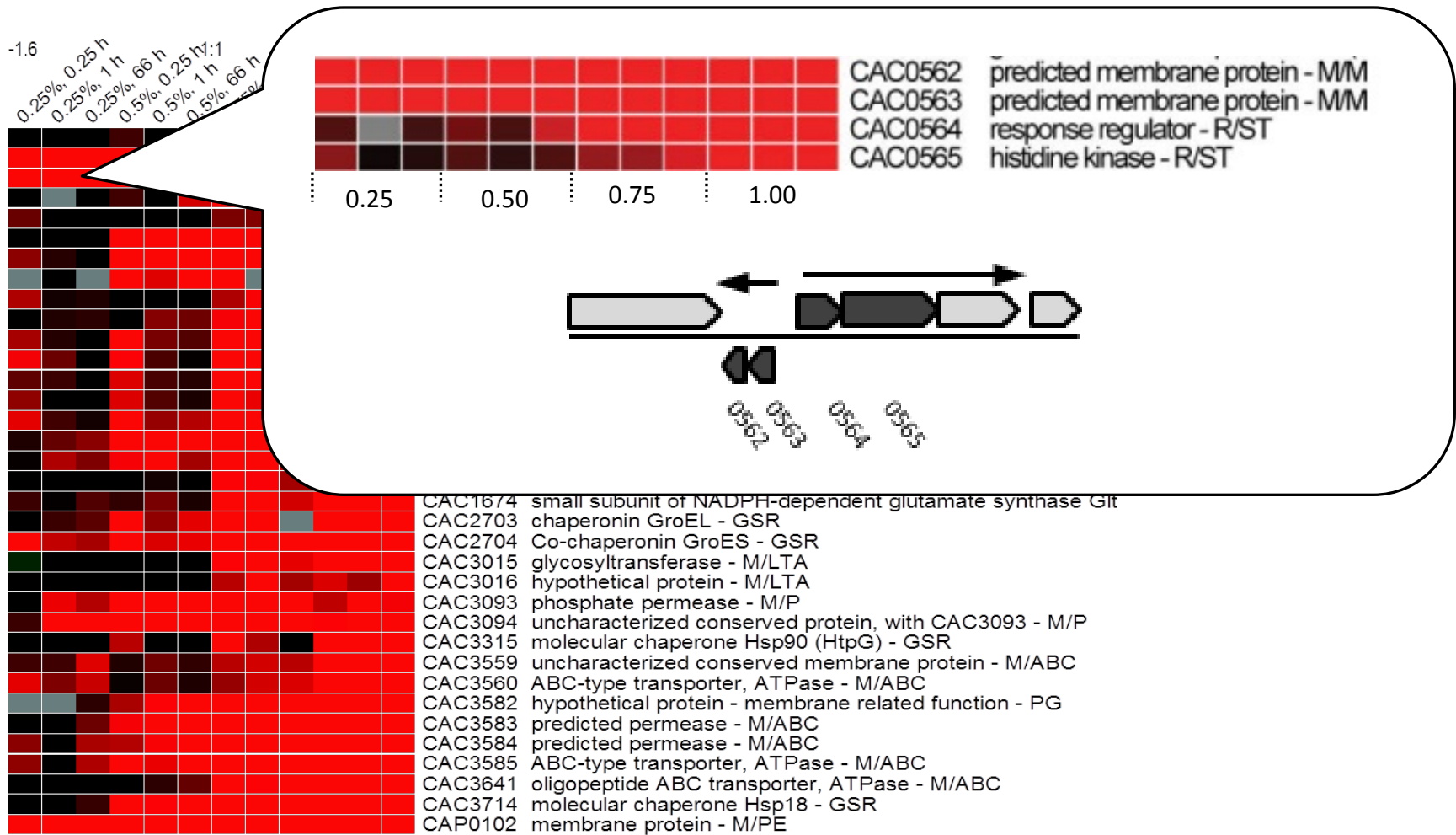
OD₆₀₀ decreases → ATP used for dealing with stress

Results – transcriptome analysis

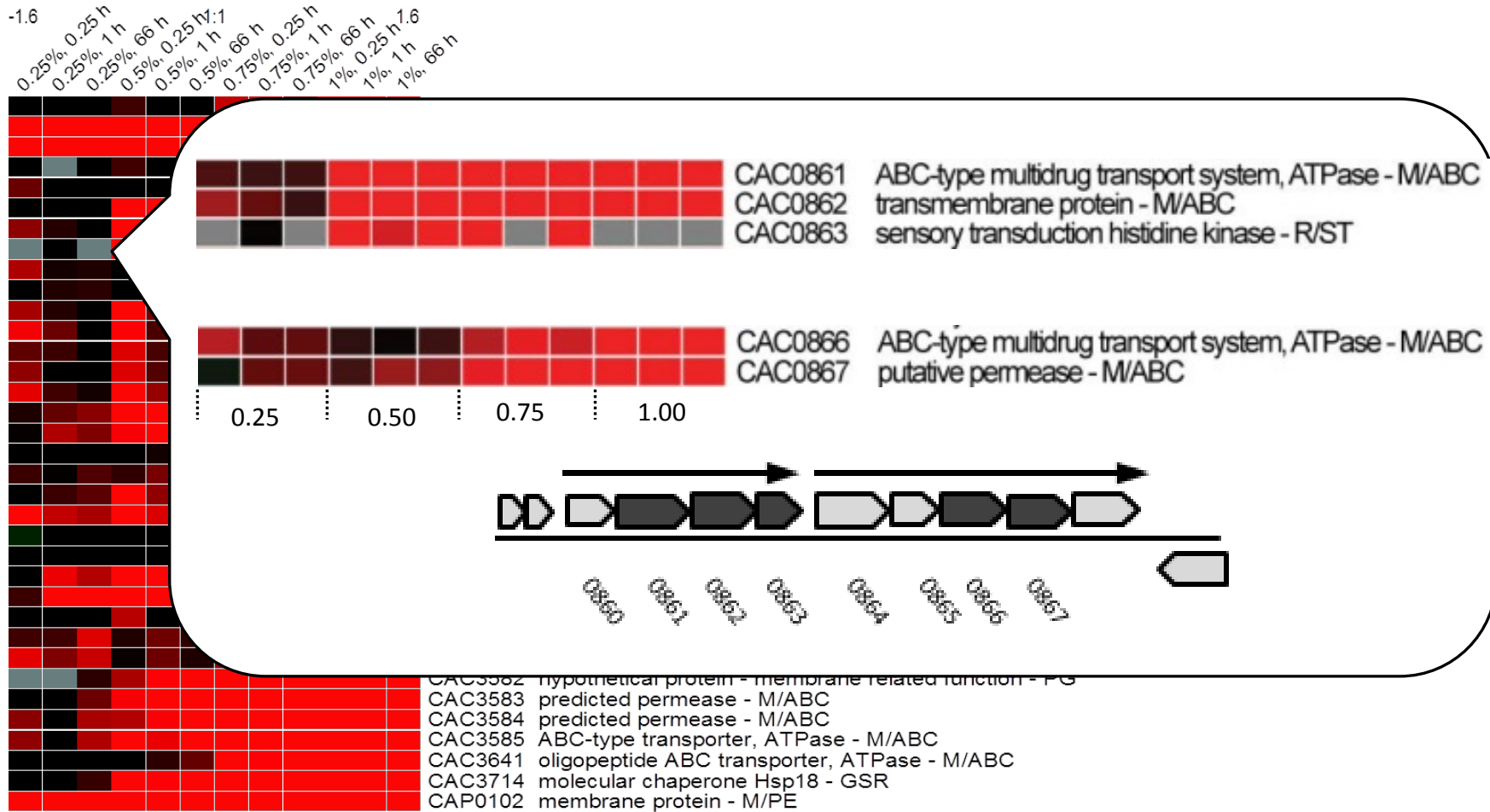
- 132 genes (35 up; 97 down) considered significantly up- or downregulated
- Only 13 were located on het pSOL1 plasmid (1 up; 12 repressed)
- Spread over the genome; often clustered in putative transcriptional units (Paredes)
- Genes grouped according to function:

functional group		upregulated genes	repressed genes
membrane associated	M	20	36
general stress response	GSR	8	
regulation	R	4	4
glutamate/glutamine metabolism	GG	2	-
hypothetical proteins	HP	-	14
hydrolases	H	-	11
oxidoreductases	OR	-	7
cofactor synthesis	CF	-	6
carbohydrate metabolism	C	-	5
defense mechanism	D	-	5
peptidoglycan	PG	1	3
bacterial cyclic lipopeptide metabolism	BCL	-	2
sporulation	S	-	2
nucleotide metabolism	N	-	1
polyketide metabolism	PK	-	1

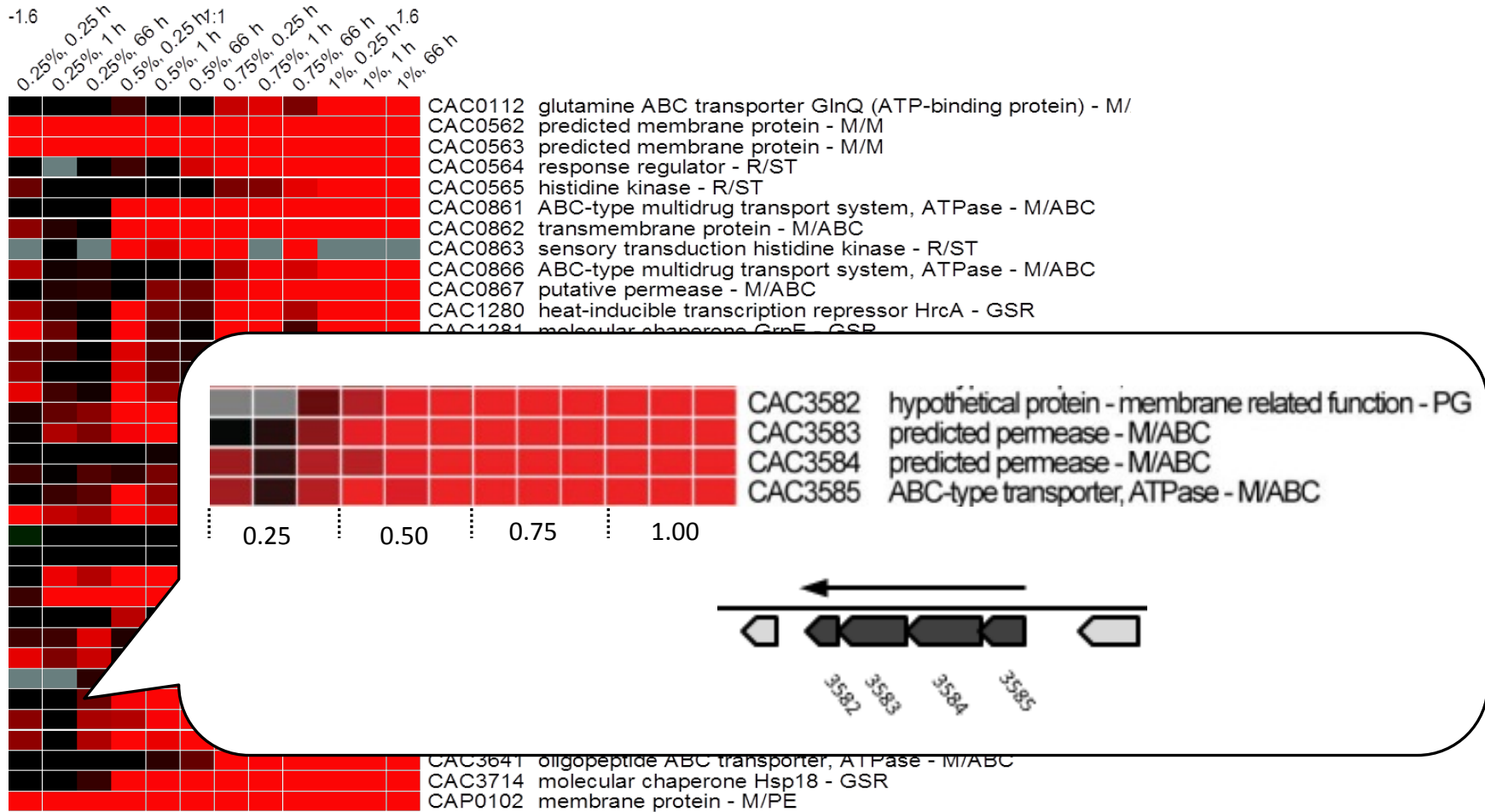
Results – transcriptome - upregulated genes



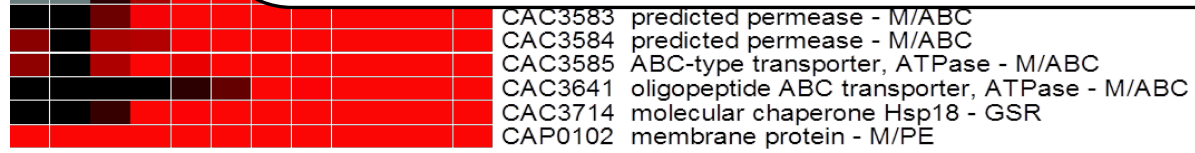
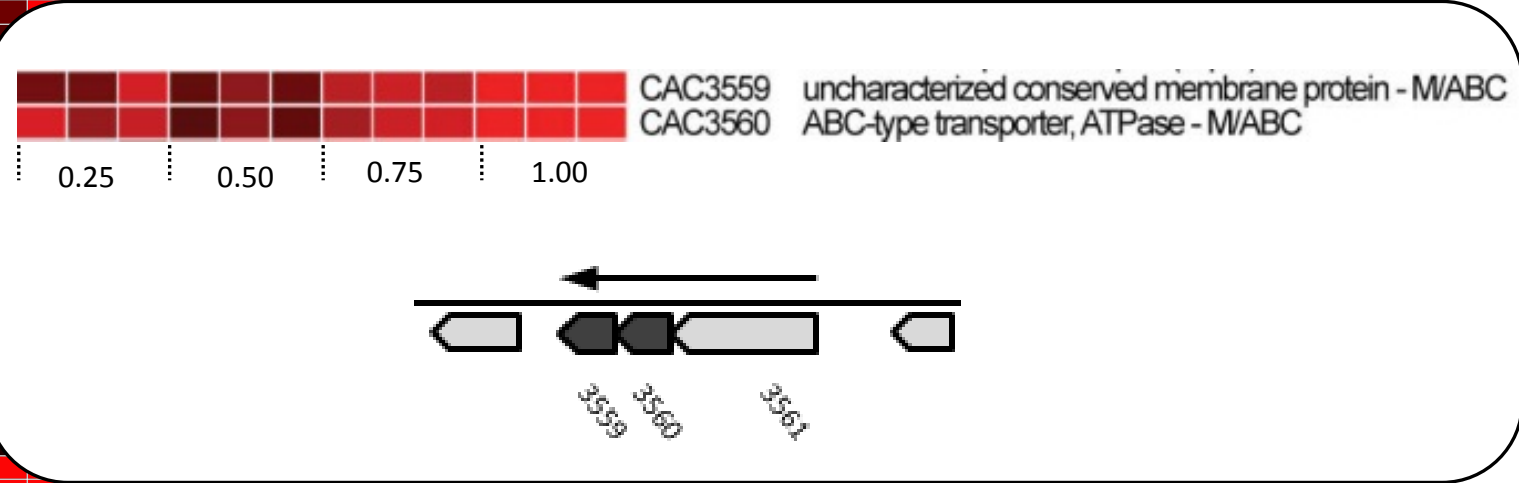
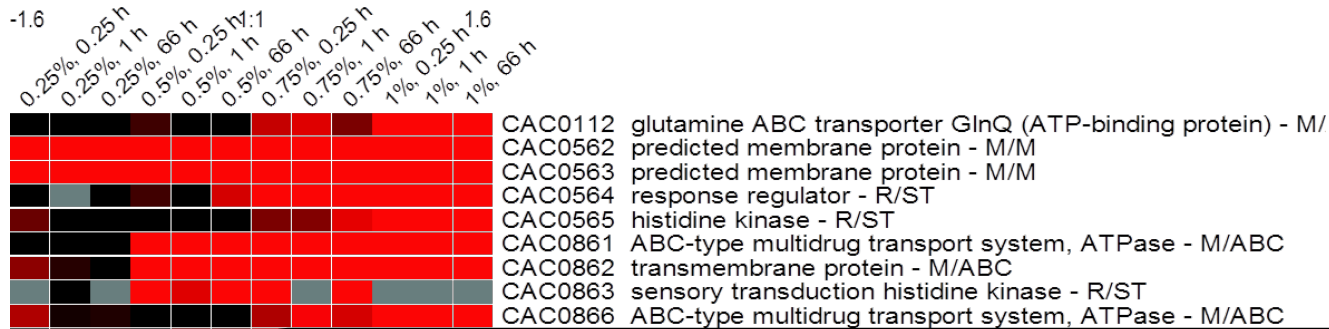
Results – transcriptome - upregulated genes



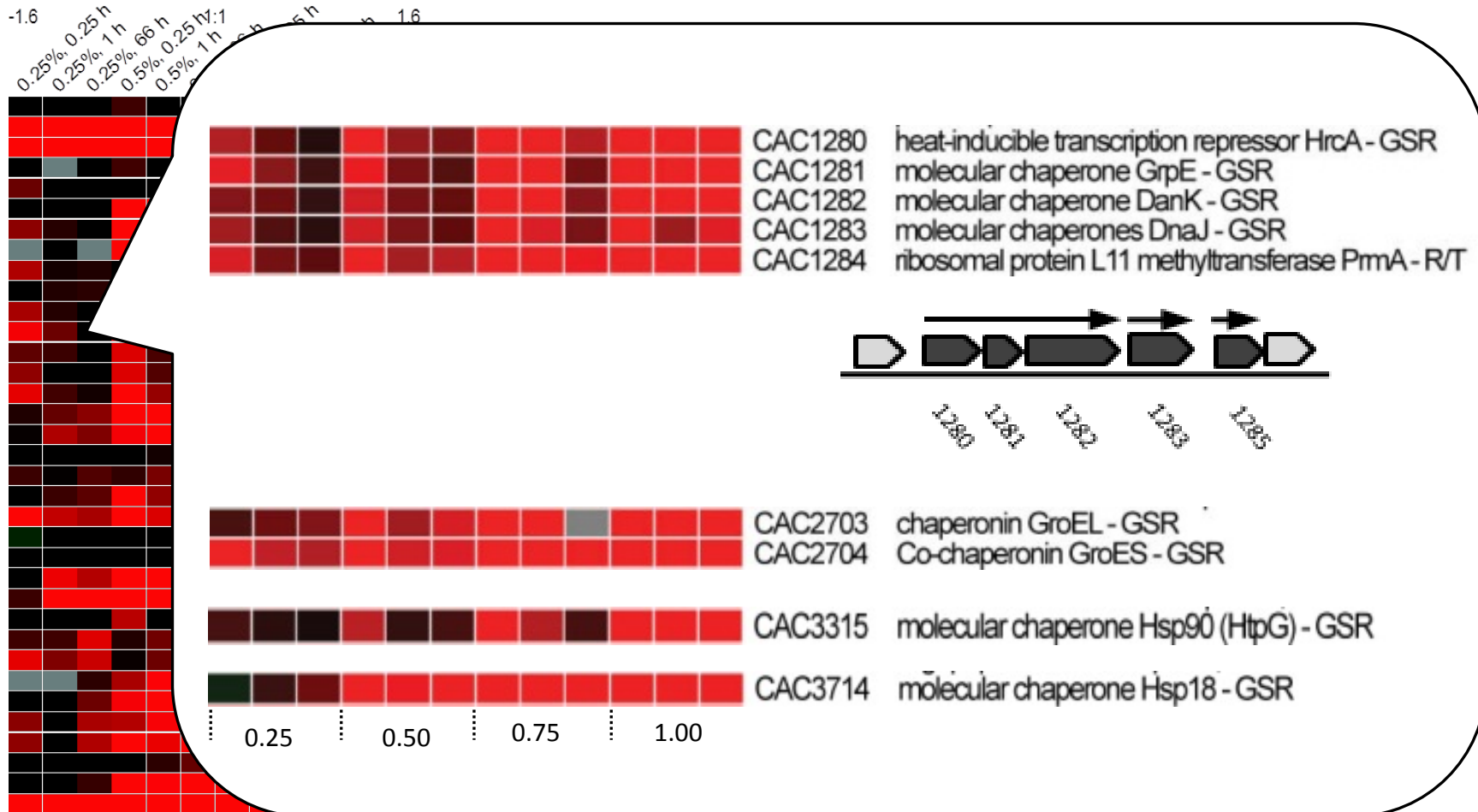
Results – transcriptome - upregulated genes



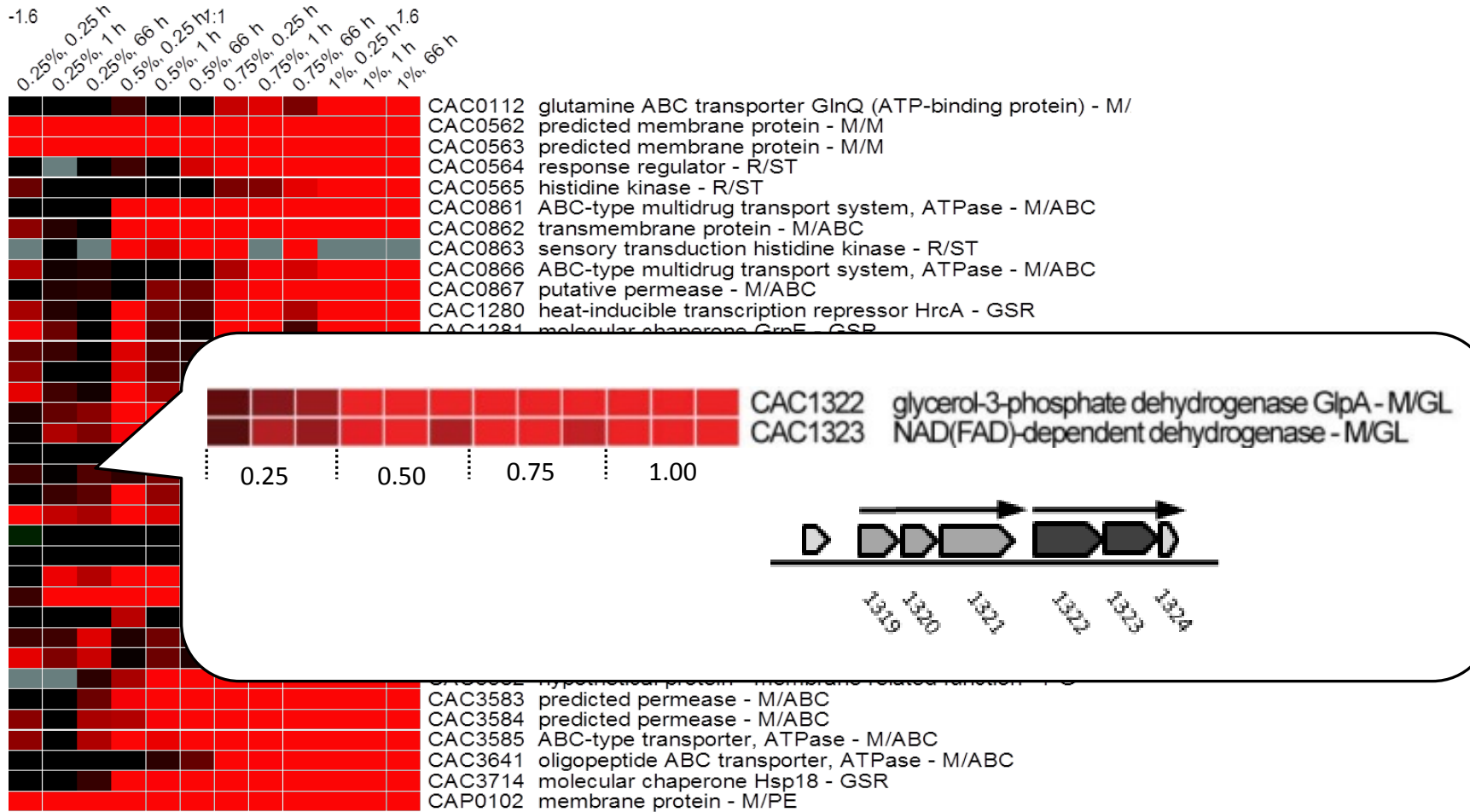
Results – transcriptome - upregulated genes



Results – transcriptome - upregulated genes

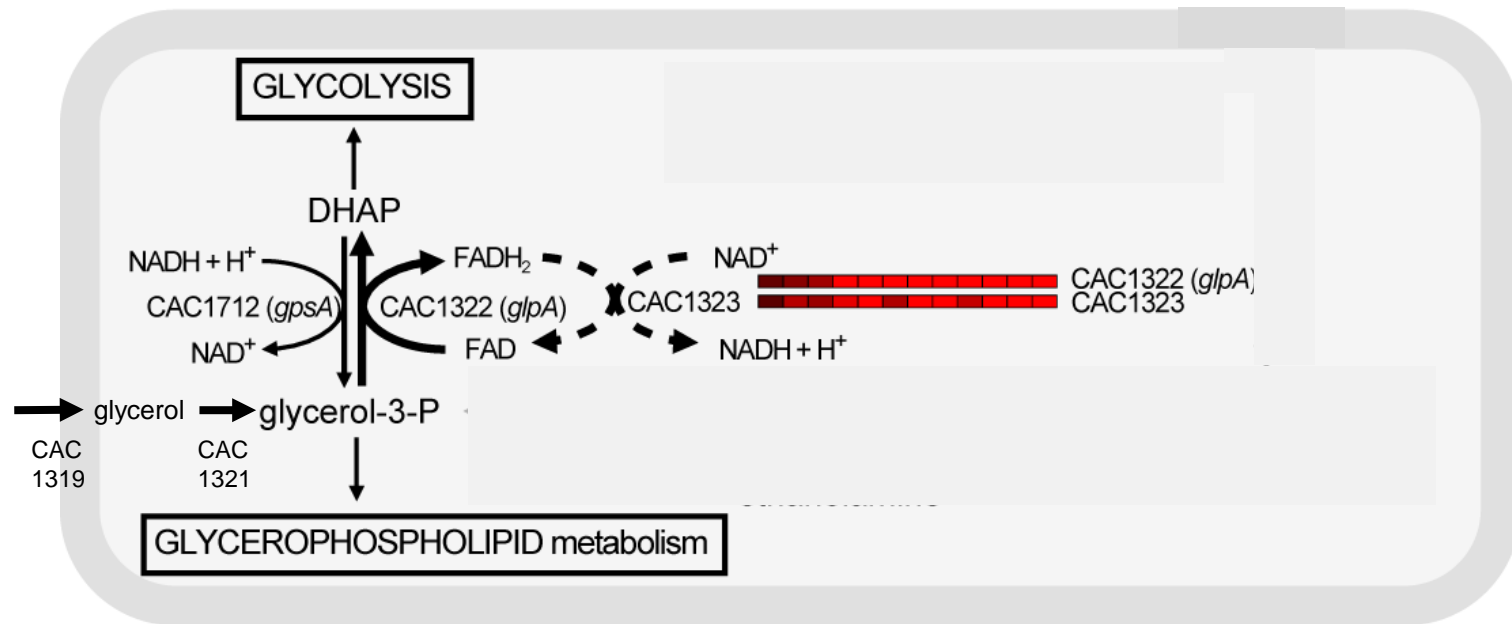


Results – transcriptome - upregulated genes



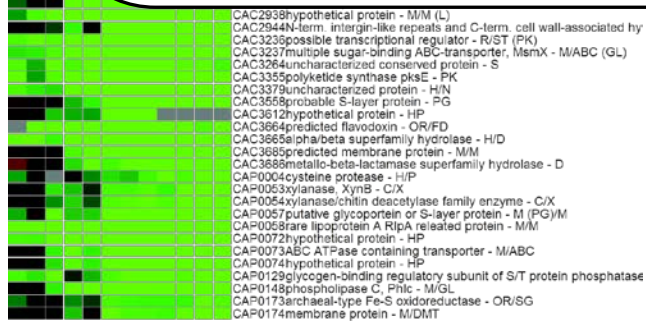
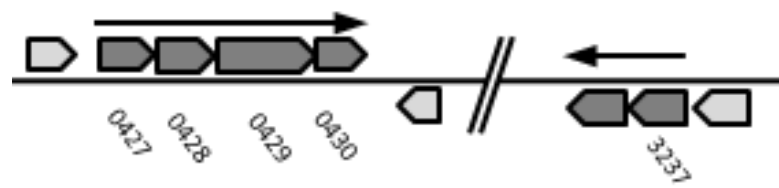
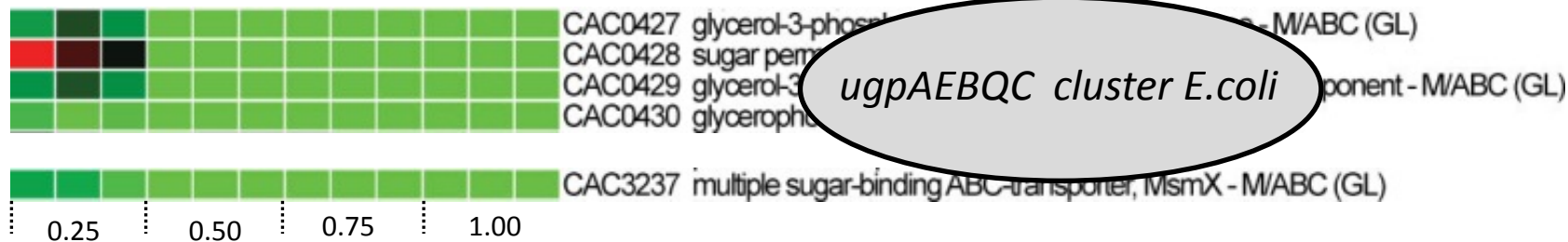
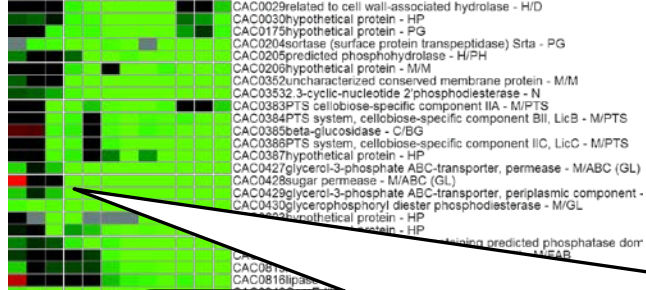
Results – transcriptome – Glycerol-3-P metabolism

Glycero(phospho)lipid metabolism



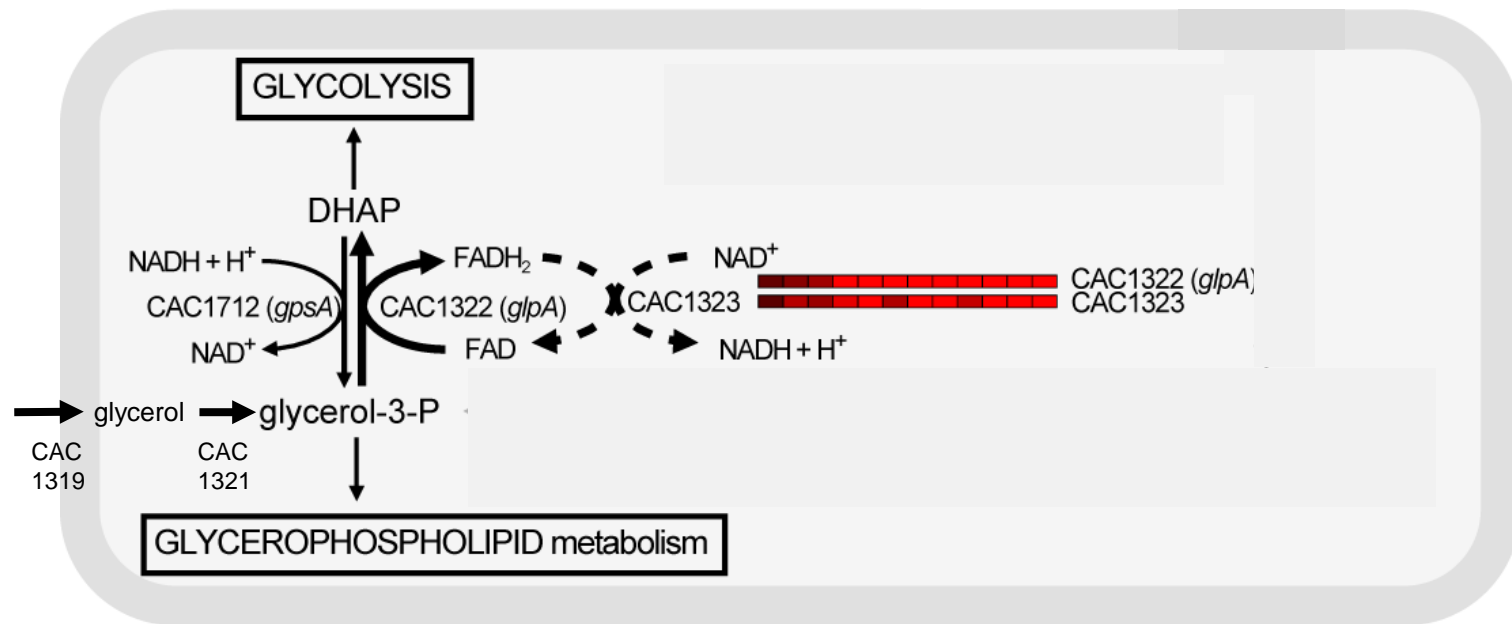
Results – transcriptome - repressed genes

-1.5
0.25h
0.5h
0.75h
1h
1.25h
1.5h
1.75h
2h
2.25h
2.5h
2.75h
3h
3.25h
3.5h
3.75h
4h
4.25h
4.5h
4.75h
5h
5.25h
5.5h
5.75h
6h
6.25h
6.5h
6.75h
7h
7.25h
7.5h
7.75h
8h
8.25h
8.5h
8.75h
9h
9.25h
9.5h
9.75h
10h



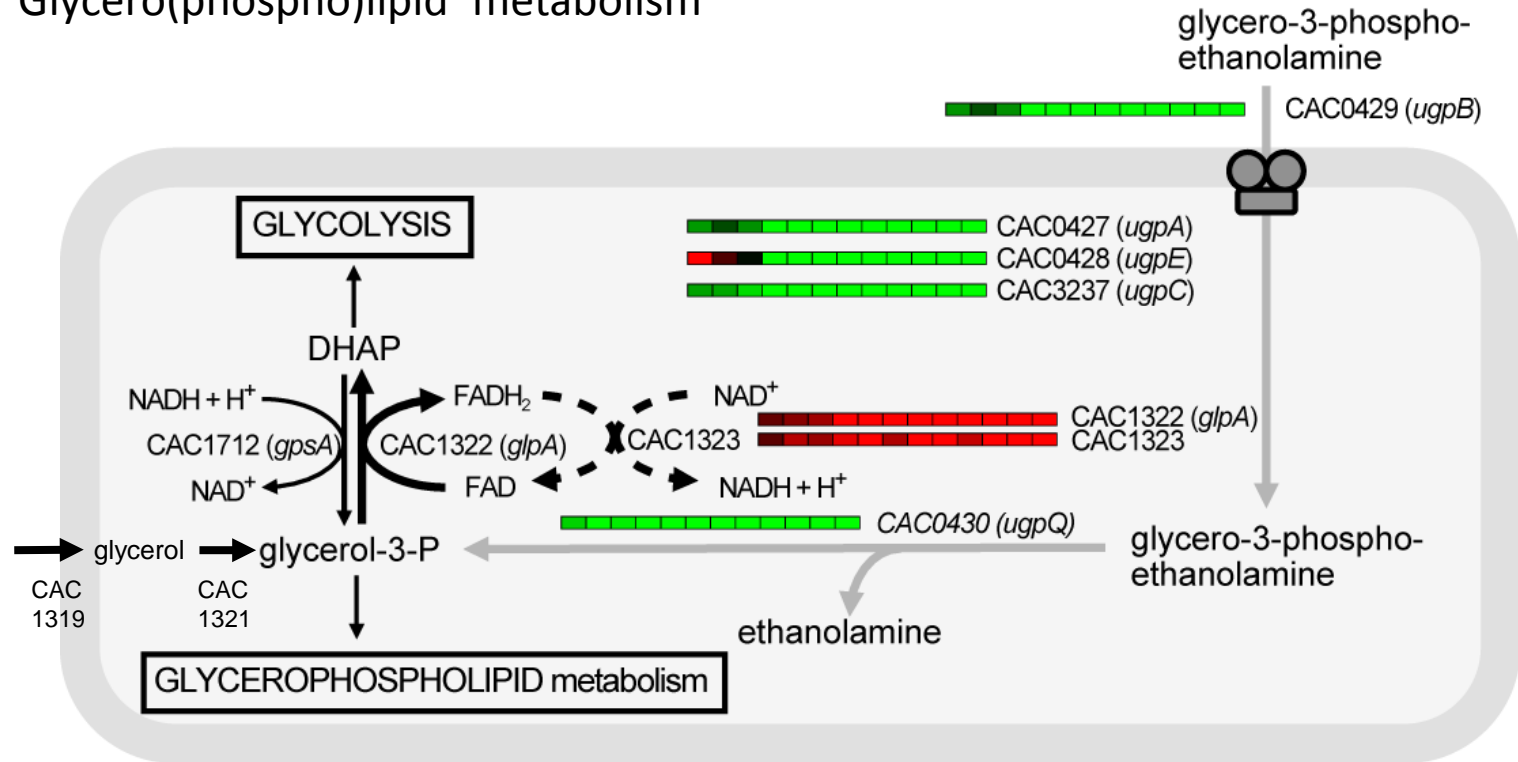
Results – transcriptome – Glycerol-3-P metabolism

Glycero(phospho)lipid metabolism



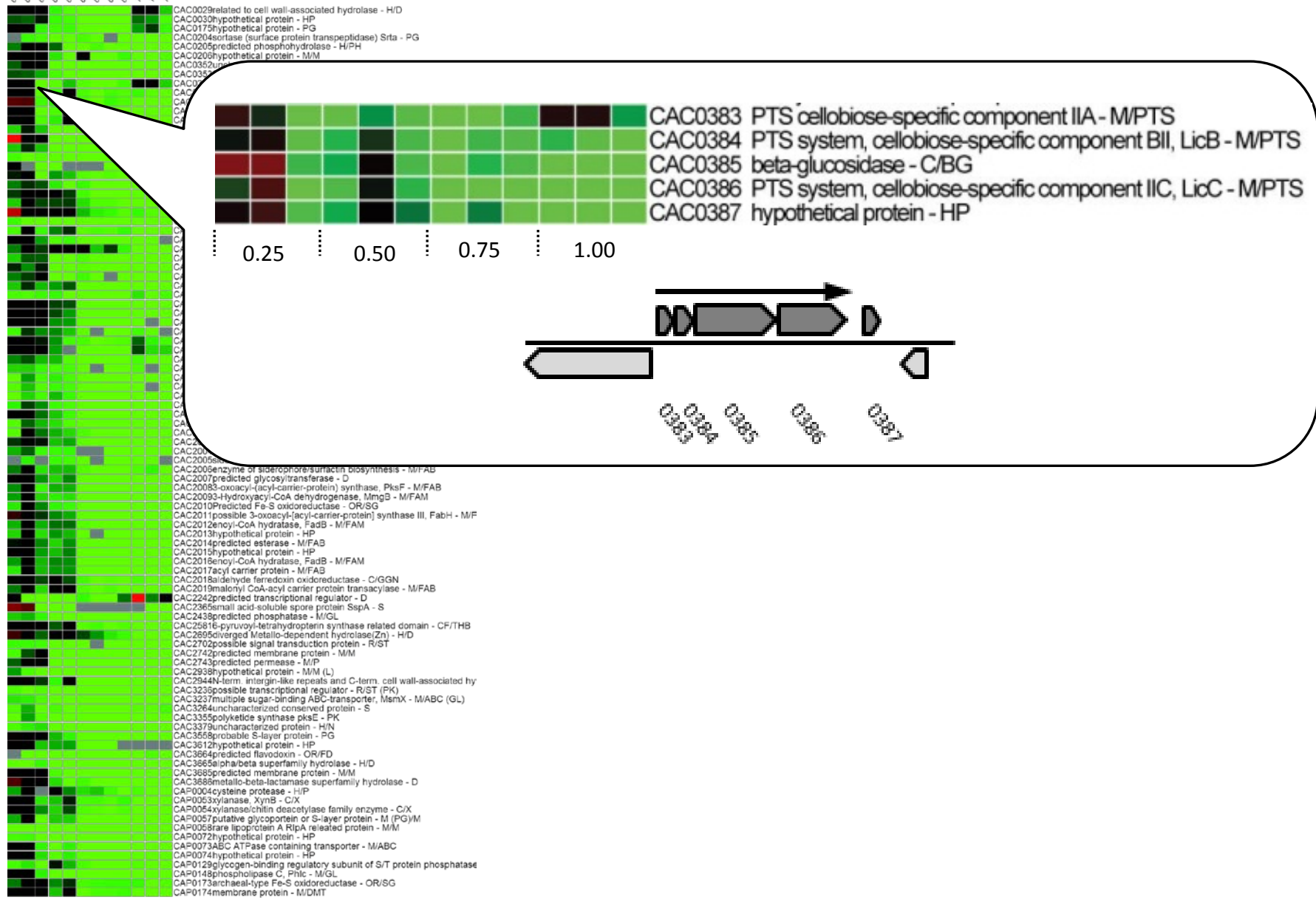
Results – transcriptome – Glycerol-3-P metabolism

Glycero(phospho)lipid metabolism



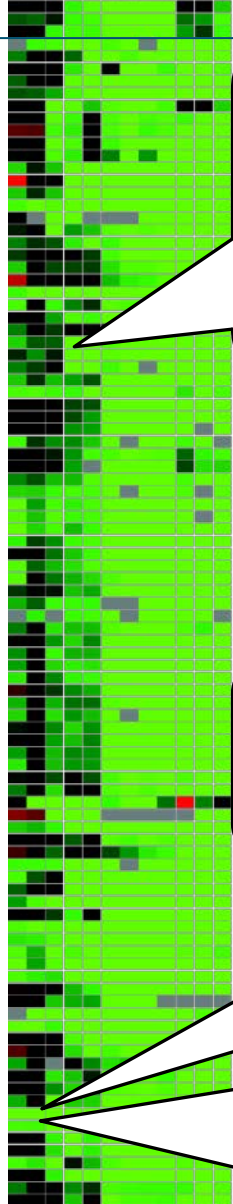
Results – transcriptome - repressed genes

-1.5 0.25h 0.5h 0.75h 1h 1.25h 1.5h 1.75h 2h 2.25h 2.5h 2.75h 3h 3.25h 3.5h 3.75h 4h 4.25h 4.5h 4.75h 5h 5.25h 5.5h 5.75h 6h 6.25h 6.5h 6.75h 7h 7.25h 7.5h 7.75h 8h 8.25h 8.5h 8.75h 9h 9.25h 9.5h 9.75h 10h 10.25h 10.5h 10.75h 11h 11.25h 11.5h 11.75h 12h 12.25h 12.5h 12.75h 13h 13.25h 13.5h 13.75h 14h 14.25h 14.5h 14.75h 15h 15.25h 15.5h 15.75h 16h



Results – transcriptome - repressed genes

-1.5
0.25% 0.25h
0.25% 1h
0.25% 8h
0.25% 17h
0.5% 1h
0.5% 8h
0.5% 17h
1% 0.25h
1% 1h
1% 8h
1% 17h



CAC0029 related to cell wall-associated hydrolase - H/D
 CAC0030 hypothetical protein - HP
 CAC1702 hypothetical protein - HP
 CAC1703 methyl-accepting chemotaxis protein - R/ST
 CAC1704 hypothetical protein - HP

0.25 0.50 0.75 1.00

1702 1703 1704

CAP0057 putative glycoprotein or S-layer protein - M (PG)/M
 CAP0058 rare lipoprotein A RlpA related protein - MM

0.25 0.50 0.75 1.00

CAP0072 hypothetical protein - HP
 CAP0073 ABC ATPase containing transporter - M/ABC
 CAP0074 hypothetical protein - HP

0.25 0.50 0.75 1.00

P0072 P0073 P0074

Results – transcriptome – non affected genes

- No significant changes in the glycolytic or solvent genes
- No class IV hsp genes (clp- lon-family proteases, htrA)
- Genes previously shown to increase tolerance were not diff. expressed
 - CAC1869, CAC0003, CAC0977, CAC1463, CAC2495, (Borden *et al.* 2007)
 - CAC1493, CAC1494 (Jia *et al.* 2012)

Results -papers

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A transcriptional study of acidogenic chemostat cells of *Clostridium acetobutylicum* – Cellular behavior in adaptation to *n*-butanol

Katrin M. Schwarz^{a,b}, Wouter Kuit^{a,b}, Christina Grimmeler^c, Armin Ehrenreich^{c,d}, Servé W.M. Kengen^{a,*}

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A transcriptional study of acidogenic chemostat cells of *Clostridium acetobutylicum*—Solvent stress caused by a transient *n*-butanol pulse

Holger Janssen^a, Christina Grimmeler^b, Armin Ehrenreich^{b,c}, Hubert Bahl^a, Ralf-Jörg Fischer^{a,*}

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