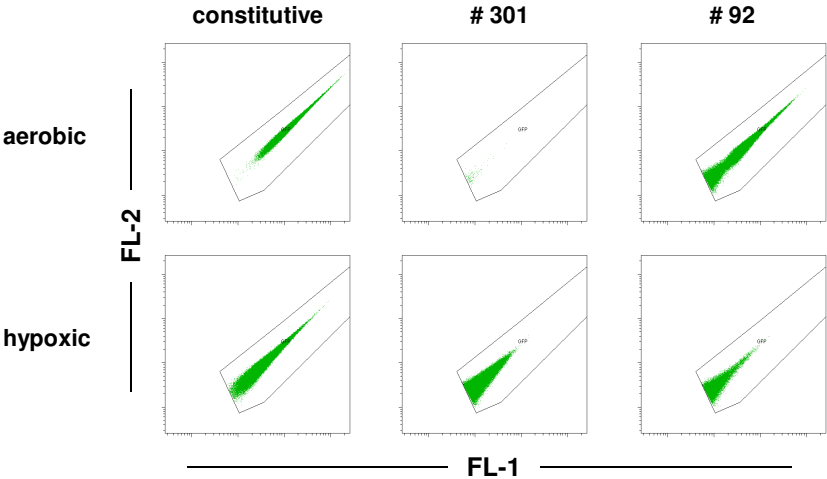


Suppl. Fig 1



Suppl. Figure 1. Expression level of the GFP reporter comparing aerobic and hypoxic growth *in vitro*. All class I clones were grown under aerobic and hypoxic conditions followed by flow cytometric analyses of the reporter gene expression. Examples are shown for constitutive expression, strong differential induction under hypoxic conditions (clone # 301) and equal induction under aerobic conditions and after oxygen deprivation (clone # 92).

Suppl. Table I. Metabolic pathways to which genes driven by class I and II promoters are annotated.

class I

Clone no.	gene	function	Metabolic pathways
4	ydiH	putative cytoplasmic protein	no EC
48	glpT	sn-glycerol-3-phosphate transporter	no EC
92	bcsG	membrane protein; endoglucanase	no EC
134	mltD	membrane-bound lytic murein transglycosylase D	no EC
154	mdh	malate dehydrogenase	A / B / C / D / E
156	mtfA	Mlc titration factor A	no EC
172	frdA	fumarate reductase flavoprotein subunit	A / E / F / G / H / I
185	pfkA	similar to E.coli 6-phosphofructokinase I	J / K / L / M / N
212	pflE	putative pyruvate formate lyase activating enzyme	O
271	nirB	nitrite reductase large subunit	P
301	glpA	sn-glycerol-3-phosphate dehydrogenase subunit A	Q
310	ybaL	putative cation::proton antiport protein	no EC

A) Citrate cycle

B) Pyruvate metabolism

C) Glyoxylate & dicarboxylate metabolism

D) Carbon fixation

E) Reductive carboxylate cycle

F) Oxidative phosphorylation

G) Benzoate degradation via CoA

H) Butanoate metabolism ligation

I) Two-component system

J) Glycolysis / Gluconeogenesis

K) Pentose phosphate pathway

L) Fructose and mannose metabolism

M) Galactose metabolism

N) Biosynthesis of phenylpropanoids

O) Anaerobic glucose metabolism

P) Nitrogen metabolism

Q) Glycerophospholipid metabolism

R) Methionine metabolism

S) One carbon pool by folate

T) Aminoacyl-tRNA biosynthesis

U) Aminosugars metabolism

V) Phosphotransferase system (PTS)

class II

Clone no.	gene	function	Metabolic pathways
28	cpxP	rescue from transitory stress	no EC
49	rpoH	transcription of heat shock proteins induced by cytoplasmic stress	no EC
50	fmt	methionyl-tRNA formyltransferase	R / S / T
53	mtfA	Mlc titration factor A	no EC
98	ibpA	heat shock protein	no EC
208	stm1129	N-acetylmannosamine-6-phosphate 2-epimerase	U
213	stbB	putative fimbrial chaperone	no EC
219	cof	putative hydrolase	no EC
233	yjeT	putative inner membrane protein	no EC
272	ptsG	glucose-specific PTS system IIBC components	J / V
291	stm1672	putative cytoplasmic protein	no EC

Suppl. Table II. Genes of *S. Typhimurium* in which the *tusp* motif matches to the promoter region.

gene	Function
<i>miaE</i>	tRNA-(ms[2]io[6]A)-hydroxylase
<i>cspA</i>	cold shock protein (beta-ribbon, CspA family)
<i>yehE</i>	outer membrane protein
<i>cspE</i>	cold shock protein (beta-ribbon, CspA family)
<i>fadB</i>	multifunctional fatty acid oxidation complex subunit alpha
<i>pepQ</i>	proline dipeptidase
<i>yifB</i>	ATP-dependent protease; magnesium chelatase family protein
<i>ilvL</i>	IlvG operon leader peptide
<i>yjeA</i>	EF-P-lysine aminoacylase
<i>pqaA</i>	PhoPQ-regulated protein
<i>rmf</i>	ribosome modulation factor
<i>tig</i>	trigger factor
<i>yjfl</i>	cytoplasmic protein
<i>ggt</i>	gamma-glutamyltranspeptidase
STM1941	putative inner membrane protein
STM2360	diaminopimelate decarboxylase
STM2361	similar to <i>E. coli</i> response regulator of atornithine decarboxylase antizyme (sensor ATOS)
STM1633	periplasmic binding transport protein
STM0276	putative cytoplasmic protein
STM1089	Pathogenicity island encoded protein: SPI5
STM2699	Fels-2 prophage protein
STM1551.1n	
STM3980	putative outer membrane protein
STM1669	Invasin-like protein; intimin
STM1833	UPF0266 membrane protein <i>yobD</i>
STM1239	Putative cytoplasmic protein