

Table S1. Genes with transcript levels significantly different in JNR7/87[pPL100] and JNR7/87[pLS1RGFP] cells after long-term induction.

Functional category	TIGR4 (No)	Gene product (gene)	Ratio ¹	P-value
Fatty acid and phospholipid metabolism	Sp0416	transcriptional regulator, MarR family (<i>fabR</i>)	0.402	2.60E-04
	Sp0417	3-oxoacyl- (acyl-carrier-protein) synthase III (<i>fabH</i>)	0.395	4.48E-03
	Sp0420	malonyl CoA-acyl carrier protein transacylase (<i>fabD</i>)	1.897	5.19E-04
	Sp0421	3-oxoacyl- [acyl-carrier protein] reductase (<i>fabG</i>)	1.898	8.40E-03
	Sp0423	acetyl-CoA carboxylase, biotin carboxyl carrier protein (<i>accB</i>)	2.022	2.29E-03
	Sp0424	hydroxymyristoyl- (acyl-carrier-protein) dehydratase (<i>fabZ</i>)	2.209	2.43E-05
	Sp0425	acetyl-CoA carboxylase, biotin carboxylase (<i>accC</i>)	2.162	9.53E-06
	Sp0426	acetyl-CoA carboxylase, carboxyl transferase, β subunit (<i>accD</i>)	2.027	1.24E-05
	Sp0427	acetyl-CoA carboxylase, carboxyl transferase, α subunit (<i>accA</i>)	1.962	7.90E-04
	Sp2222	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (<i>pgsA</i>)	0.549	8.77E-04
	Regulatory	Sp1226 ²	sensory box sensor histidine kinase (<i>yycG</i>)	7.056
Sp1227 ²		DNA-binding response regulator (<i>yycF</i>)	5.131	7.72E-08
Sp1799		sugar-binding transcriptional regulator, LacI family	0.353	5.66E-03
Transport	Sp1527	Oligopeptide ABC transporter, oligopeptide-binding protein AliB (<i>aliB</i>)	3.479	1.47E-05
	Sp1587	oxalate:formate antiporter	1.832	8.23E-04
	Sp1602	phnA protein (<i>phnA</i>)	0.574	5.30E-03
	Sp1640	manganese ABC transporter, permease protein (<i>psaC</i>)	2.042	1.97E-04
	Sp1884	trehalose PTS system, IIABC components	0.373	5.07E-03
	Sp2022 ²	PTS system, IIC component	2.132	2.99E-05
	Sp2219	ABC transporter permease protein	0.579	2.42E-02
	Sp2220	ABC transporter, ATP-binding protein	0.464	3.16E-03
	Sp2221	ABC transporter, ATP-binding protein	0.437	5.78E-03
	Cell envelop	Sp0107 ²	LysM domain protein	3.592
Sp0641 ²		serine protease, subtilase family	2.142	5.08E-03
Sp0965 ²		endo- β -N-acetylglucosaminidase (<i>lytB</i>)	8.544	5.43E-09
Sp2021		glycosyl hydrolase, family 1 (<i>bgI2</i>)	2.175	1.90E-06
Sp2063		LysM domain protein	7.941	5.60E-08
Sp2216 ²		putative cell wall hydrolase (<i>pcsB</i>)	2.613	1.35E-07
Sp2218		rod shape-determining protein MreC (<i>mreC</i>)	0.364	1.13E-04
Purine and pyrimidine biosynthesis		Sp0044	phosphoribosylaminoimidazole-succinocarboxamide synthase (<i>purC</i>)	2.180
	Sp0049	vanZ protein, putative (<i>vanZ</i>)	1.812	2.09E-04
	Sp0964	dihydroorotate dehydrogenase B (<i>pyrDb</i>)	1.892	5.80E-06
	Sp1275	carbamoyl-phosphate synthase, large subunit (<i>carB</i>)	1.784	6.04E-04
	Sp1276	carbamoyl-phosphate synthase, small subunit (<i>carA</i>)	1.700	2.87E-02
	Sp1277	aspartate carbamoyltransferase (<i>pyrB</i>)	2.012	4.30E-05
	Heat shock and stress	Sp0515 ²	heat-inducible transcription repressor HrcA (<i>hrcA</i>)	2.151
Sp0516 ²		heat shock protein GrpE (<i>grpE</i>)	2.245	3.72E-03
Sp0517 ²		dnaK protein (<i>dnaK</i>)	3.734	4.02E-03
Sp1906 ²		chaperonin, 60 kDa (<i>groEL</i>)	2.196	3.99E-03

Protein synthesis and degradation	Sp1029	RNA methyltransferase, TrmA family	2.428	4.84E-03
	Sp1343	prolyl oligopeptidase family protein	2.055	5.01E-05
	Sp2223 ²	conserved hypothetical protein	0.555	1.07E-02
	Sp2224 ²	peptidase, M16 family	0.424	6.39E-04
	Sp2225 ²	putative protease	0.281	1.07E-04
Central intermediary metabolism	Sp0918	spermidine synthase (<i>speE</i>)	2.561	7.02E-04
	Sp0919	conserved hypothetical protein	2.043	1.13E-04
	Sp0920	carboxynorspermidine decarboxylase (<i>nspC</i>)	3.047	3.17E-06
Energy metabolism	Sp1190	tagatose 1,6-diphosphate aldolase (<i>lacD</i>)	2.543	4.20E-05
	Sp1191	tagatose-6-phosphate kinase (<i>lacC</i>)	2.186	3.60E-04
	Sp1192	galactose-6-phosphate isomerase, LacB subunit (<i>lacB</i>)	2.581	5.86E-06
	Sp1853	galactokinase (<i>galK</i>)	2.215	2.50E-06
	Sp1883	dextran glucosidase DexS, putative	0.412	8.09E-03
Biosynthesis of cofactors	Sp0177	riboflavin synthase, alpha subunit (<i>ribE</i>)	2.664	1.96E-04
Hypothetical	Sp0125	hypothetical protein	1.906	4.35E-06
	Sp0171	ROK family protein	1.916	3.14E-03
	Sp0917	pilin gene inverting-related protein	1.881	5.46E-06
	Sp0922	carbon-nitrogen hydrolase family protein	2.774	2.12E-04
	Sp1093	hypothetical protein	2.711	6.19E-03
	Sp1601	conserved hypothetical protein	0.629	2.59E-02
	Sp1739	KH domain protein	0.494	3.47E-04
	Sp2061 ²	conserved hypothetical protein	2.469	4.13E-04

¹Genes with >1.75 fold expression changes between in JNR7/87 [pPL100] and JNR7/87[pLS1RGFP] were selected.

²Genes also detected by Ng *et al.* by depletion of YycF (32).