Supplementary Table 1. Oligonucleotides used in this study

Name	**Sequence 5'-3'**	**Enzyme**
mazEFpSE100 F	AAATTTGGATCCGGAGGGAATAATGACTCCCGCGCGTGACCG	BamHI
mazFpSE100 F	AAATTTGGATCCGGAGGGAATAGTGCGGCGCGGCGATATCTA	BamHI
mazFpSE100 R	AAATTTCTGCAGCGTGCCGAAGCAGGTGGTCA	PstI
phd/docpMind F	AAATTTGGATCCGGAGGGAATAATGCCGTCGCTGAACATCGA	BamHI
docpMind F	AAATTTGGATCCGGAGGGAATAGTGACCGAGTACCTCGACCG	BamHI
docpMind R	AAATTTACTAGTGGCCGCGCTACCAAAGTTCA	SpeI
mazRT-PCR1 F	GCGCTGCAGGAGACGTTCCA	
mazRT-PCR2 F	TGACCGAGTACGCCGACATC	
mazRT-PCR3 R	AAGCTGGAGCGGGGAACTGT	
docRT-PCR1 F	TGGCAATGGCATCCAACATG	
docRT-PCR2 F	ACCTGTCGCTGAAGAAGGTTC	
docRT-PCR3 R	TGGAATCCAGGTCGCAGTCA	
docRT-PCR4 R	CCTGCTCTGAAGGTTGACGA	
mazF RACE1 R	TCC CAG AAA AAC CAG GAG TG	
mazE RACE2 R	CGT CGA CGA AAG CTT GAT CT	
doc RACE1 R	ACA CCG TTG ATG TGC AGA AA	
phd RACE2 R	GTT GAG CTC AGC CGA ACG	
mazElac F	AAATTTGGATCCTTCGCCGAATACACCACGAT	BamHI
mazElac R	AAATTTGGTACCCGAAATTCGGGTGCATTCAC	Asp718
phdlac F	AAATTTAGTACTAAGCTGGACGAGGAGGTTGC	ScaI
phdlac R	AAATTTAGTACTGAACTTCTTCAGCGACAGGT	ScaI
mazEFKOLF F	AAATTTACTAGTCCTCATCGTCGATGTCGTGT	SpeI
mazEFKOLF R	CAGGAGTGATGTCGGCGTACTCGGTCA	
mazEFKORF F	CGACATCACTCCTGGTTTTTCTGGGAA	
mazEFKORF R	AAATTTACTAGTTACCACGATGGGCGGATTGT	SpeI
phd/docKOLF F	AAATTTACTAGTGTGCGATGTCGACCGACAGT	SpeI
phd/docKOLF R	AAATTTGAATTCGAACTTCTTCAGCGACAGGT	EcoRI
phd/docKORF F	AAATTTCTGCAGTGACTGCGACCTGGATTCCA	PstI
phd/docKORF R	AAATTTACTAGTTCGTGATGGATGCGACGTAT	SpeI
3'mcspUC R	GTTTTCCCAGTCACGACGTT	
5'mcspUC F	CACACAGGAAACAGCTATGA	
MSMEG_1277 F	GAAGCCGAGATGGAACAGAT	
MSMEG_1277	GTTGAGCTCAGCCGAACG	

R		
MSMEG_1279 F	AATGCCTCGTTGGTCTTGTC	
MSMEG_1279 R	TAGTGCACTTCGTCGTCACC	
MSMEG_1280 F	GGAGACCACCATCAGGAAGA	
MSMEG_1280 R	GATCTCGGCGTACTGGAGTC	
MSMEG_1281 F	GCGGGATATCGACTCCAGTA	
MSMEG_1281 R	TTGTTGTAAGCGGCTTTGTG	
MSMEG_1282 F	ATACCCATGGATTTGCGATT	
MSMEG_1282 R	CGGTAGAGCTGCTGTTCCTC	

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Supplementary Table 2. Specific growth rates (h^{-1})[a] of TA deletion strains

Growth medium	**Wild-type**	**RF100**	**RF101**	**RF105**
LBT	0.27 (±0.009)	0.27 (±0.008)	0.25 (±0.007)	0.25 (±0.012)
HdB	0.27 (±0.011)	0.26 (±0.010)	0.24 (±0.020)	0.25 (±0.015)
Carbon Limited HdB	0.25 (±0.020)	0.23 (±0.009)	0.26 (±0.006)	0.18 (±0.028)
Nitrogen Limited HdB	0.23 (±0.010)	0.20 (±0.015)	0.19 (±0.014)	0.18 (±0.004)
Phosphate Limited HdB	0.23 (±0.018)	0.23 (±0.006)	0.20 (±0.004)	0.21 (±0.024)

[a] The specific growth rate constant (h^{-1}) for the log phase of growth is reported. Results are shown as mean ± SD for three biological replicates.

Supplementary Table 3. Differentially regulated genes from day 1 microarray analysis.

Locus	Gene Name	Functional Category	Fold Change	*p*-value
Downregulated				
MSMEG_1283	Probable ribbon-helix-helix transcriptions factor, family protein	Regulatory functions	0.0983	$8.6x10^{-6}$
MSMEG_1284	PIN domain protein	Unknown function	0.147	$9.8x10^{-4}$
MSMEG_1278	Death-on-curing protein	Mobile and extrachromosomal element functions	0.248	0.0042
MSMEG_4447	Conserved hypothetical protein	Hypothetical proteins	0.263	0.0088
MSMEG_4448	Transcriptional modulator of MazE	Cellular processes	0.361	0.011
MSMEG_3771	Arginine repressor (*argR*)	Amino acid biosynthesis	0.479	0.0089
MSMEG_1999	Hypothetical protein	Hypothetical proteins	0.491	0.011
Upregulated				
MSMEG_1279	Conserved hypothetical protein	Hypothetical protein	65.85	0.041
MSMEG_1275	HNH nuclease, putative	DNA metabolism	12.92	0.0048
MSMEG_1280	Hypothetical cytosolic protein	Energy metabolism	11.74	$5.4x10^{-4}$
MSMEG_1281	Conserved hypothetical protein	Hypothetical proteins	5.82	0.0019
MSMEG_4451	Probable monooxygenase	Biosynthesis of cofactors, prosthetic groups, and carriers	3.81	0.027
MSMEG_1282	Hypothetical cytosolic protein	Energy metabolism	2.65	0.0031
MSMEG_4831	Transcriptional regulator, TetR family protein	Regulatory functions	2.56	0.048
MSMEG_0418	Succinate dehydrogenase flavoprotein subunit	Energy metabolism	2.49	0.019
MSMEG_5165	Integral membrane protein	Cell envelope	2.30	0.020
MSMEG_5166	Na^+/solute symporter	Transport and binding	2.14	0.0047
MSMEG_5021	Alcohol dehydrogenase, zinc-containing	Energy metabolism	2.10	0.014
MSMEG_5022	Flavin-containing monooxygenase FMO	Energy metabolism	2.08	0.017

Supplementary Table 4. Differentially regulated genes from day 5 microarray analysis.

Locus	Gene Name	Functional Category	Fold Change	p-value
Upregulated				
MSMEG_1280	Hypothetical cytosolic protein	Energy metabolism	17.36	0.045
MSMEG_6236	Two-component system, regulatory protein	Regulatory functions	6.06	0.046
MSMEG_1275	HNH nuclease, putative	DNA metabolism	5.49	0.042
Downregulated				
MSMEG_1770	Conserved hypothetical protein	Hypothetical proteins	0.223	1.5x10^{-4}
MSMEG_1771	Methylase, putative	Unknown function	0.229	0.0013
MSMEG_1076	Conserved hypothetical protein	Hypothetical proteins	0.276	6.1x10^{-5}
MSMEG_3439	Hypothetical protein	Hypothetical proteins	0.282	6.6x10^{-4}
MSMEG_0795	ABC transporter ATP-binding protein	Transport and binding	0.282	0.0053
MSMEG_6212	Hemerythrin HHE cation binding domain subfamily protein, putative	Unknown function	0.295	0.0014
MSMEG_3776	N-acetyl-gamma-glutamyl-phosphate reductase	Amino acid biosynthesis	0.322	0.0041
MSMEG_1919	Transcription factor WhiB	Unknown function	0.323	4.1x10^{-4}
MSMEG_2755	Conserved hypothetical protein	Hypothetical proteins	0.334	0.0061
MSMEG_5388	Conserved hypothetical protein	Hypothetical proteins	0.345	0.0014
MSMEG_2016	Molybdate ABC transporter, periplasmic molybdate-binding protein (*modA*)	Transport and binding	0.346	0.013
MSMEG_1790	Conserved hypothetical protein	Hypothetical proteins	0.352	4.5x10^{-4}
MSMEG_0732	Chaperone ClpB	Cellular processes	0.355	0.010
MSMEG_5011	Hypothetical protein	Hypothetical proteins	0.359	0.0065
MSMEG_0230	Conserved hypothetical protein	Hypothetical proteins	0.364	0.023
MSMEG_5039	Siderophore-interacting protein	Unclassified	0.368	0.0042
MSMEG_5352	Conserved hypothetical protein	Hypothetical proteins	0.370	0.0061
MSMEG_2927	ABC transporter, permease protein OpuCB	Unclassified	0.371	0.011
MSMEG_6456	Conserved hypothetical protein	Hypothetical proteins	0.374	0.0044
MSMEG_5010	Conserved hypothetical protein	Hypothetical proteins	0.377	0.013
MSMEG_3068	Hypothetical protein	Hypothetical proteins	0.377	0.017
MSMEG_3613	Conserved hypothetical protein	Hypothetical proteins	0.382	0.021
MSMEG_1788	Conserved hypothetical protein	Hypothetical proteins	0.384	0.0056
MSMEG_2422	Acylphosphatase	Fatty acid and phospholipid metabolism	0.385	0.0044
MSMEG_5328	Conserved hypothetical protein	Hypothetical proteins	0.392	0.0037
MSMEG_6092	Lsr2 protein	Cellular processes	0.393	0.0029
MSMEG_1773	Conserved hypothetical protein	Hypothetical proteins	0.397	0.0051

MSMEG_5904	Conserved domain protein	Hypothetical proteins	0.398	0.0088
MSMEG_0394	Hypothetical protein	Hypothetical proteins	0.401	0.0083
MSMEG_4479	Conserved hypothetical protein	Hypothetical proteins	0.402	0.011
MSMEG_1561	LysR-family protein transcriptional regulator	Regulatory functions	0.405	0.022
MSMEG_1410	Carveol dehydrogenase	Energy metabolism	0.410	0.011
MSMEG_2038	Monooxygenase, flavin-binding family protein	Central intermediary metabolism	0.411	0.0068
MSMEG_2975	Metallo-beta-lactamase family protein	Unknown function	0.411	0.024
MSMEG_2687	Carveol dehydrogenase	Energy metabolism	0.417	0.017
MSMEG_4752	Conserved hypothetical protein	Hypothetical proteins	0.424	0.0090
MSMEG_5720	Putative 3-hydroxyacyl-CoA dehydrogenase	Unclassified	0.428	0.032
MSMEG_1777	UsfY protein	Unclassified	0.429	0.010
MSMEG_3600	Hypothetical protein	Hypothetical proteins	0.430	0.022
MSMEG_4184	dtdp-glucose-46-dehydratase	Cell envelope	0.430	0.016
MSMEG_0434	Aminoglycoside 2’-N-acetyltransferase (AAC(2’)-Id)	Central intermediary metabolism	0.430	0.021
MSMEG_3863	Pyridoxamine 5’-phosphate oxidase family protein	Unknown function	0.442	0.0082
MSMEG_3685	Conserved hypothetical protein	Hypothetical proteins	0.448	0.0048
MSMEG_3918	Hypothetical protein	Hypothetical proteins	0.448	0.015
MSMEG_3004	Conserved hypothetical protein TIGR00026	Hypothetical proteins	0.448	0.042
MSMEG_5081	Conserved hypothetical protein	Hypothetical proteins	0.451	0.010
MSMEG_1808	Fe-S metabolism associated SufE	DNA metabolism	0.453	0.015
MSMEG_6739	Hypothetical protein	Hypothetical proteins	0.457	0.031
MSMEG_4765	Transcriptional regulator, MerR family protein	Regulatory functions	0.458	0.028
MSMEG_0309	Aldehyde dehydrogenase family protein	Energy metabolism	0.460	0.018
MSMEG_2688	Antibiotic biosynthesis monooxygenase domain protein	Cellular processes	0.465	0.010
MSMEG_4361	Conserved hypothetical protein	Hypothetical proteins	0.466	0.0073
MSMEG_0358	Ribonucleoside-diphosphate reductase, beta subunit	Purines, pyrimidines, nucleosides, and nucleotides	0.468	0.0067
MSMEG_2451	HAD-superfamily protein hydrolase, subfamily protein IIA	Unknown function	0.469	0.042
MSMEG_6410	Rieske 2Fe-2S family protein	Energy metabolism	0.472	0.013
MSMEG_3371	Short-chain dehydrogenase/reductase SDR	Central intermediary metabolism	0.472	0.026

	(region contains premature stop and/or frameshift)			
MSMEG_1789	Conserved hypothetical protein	Hypothetical proteins	0.473	0.0029
MSMEG_4476	Hypothetical protein	Hypothetical proteins	0.478	0.0066
MSMEG_2026	Short chain dehydrogenase	Energy metabolism	0.480	0.027
MSMEG_0558	Conserved hypothetical protein	Hypothetical proteins	0.484	0.020
MSMEG_3542	Conserved hypothetical protein	Hypothetical proteins	0.484	0.010
MSMEG_2754	Conserved hypothetical protein	Hypothetical proteins	0.488	0.013
MSMEG_5292	Hypothetical protein	Hypothetical proteins	0.489	0.0085
MSMEG_1414	Amidinotransferase	Unclassified	0.489	0.048
MSMEG_4920	Acetyl-CoA aceyltransferase	Fatty acid and phospholipid metabolism	0.491	0.015
MSMEG_3156	Conserved hypothetical protein	Hypothetical proteins	0.494	0.032
MSMEG_0119	Conserved hypothetical protein	Hypothetical proteins	0.497	0.034
MSMEG_4921	Methylmalonyl-CoA epimerase (*mce*)	Energy metabolism	0.499	0.033
MSMEG_4904	Rhomboid family protein	Unknown function	0.500	0.040