

Supplementary Table 2: Genes differentially expressed at the basal level (± 2 -fold) in *dam mutS* mutant *E. coli* compared to wildtype. Only genes for which ANOVA $p \leq 0.05$ are listed.

Amino acid transport and metabolism					
Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
artI	b0863	0	1.21	0.002	arginine 3rd transport system periplasmic binding protein
artQ	b0862	2	1.06	0.000	arginine 3rd transport system permease protein
ydgR	b1634	1	1.27	0.047	putative transport protein
Carbohydrate transport and metabolism					
Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
	b2097	1	1.07	0.000	orf, hypothetical protein
crr	b2417	1	1.08	0.050	PTS system, glucose-specific IIA component
fba	b2925	0	1.17	0.013	fructose-bisphosphate aldolase, class II
galK	b0757	2	1.12	0.024	galactokinase
galM	b0756	2	1.04	0.004	galactose-1-epimerase (mutarotase)
glk	b2388	2	1.43	0.000	glucokinase
gpmA	b0755	0	1.02	0.023	phosphoglyceromutase 1
malE	b4034	2	2.12	0.002	periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis
malK	b4035	2	1.60	0.018	ATP-binding component of transport system for maltose
pfkA	b3916	4	1.22	0.006	6-phosphofructokinase I
pgk	b2926	3	1.10	0.027	phosphoglycerate kinase
ptsH	b2415	1	1.17	0.035	PTS system protein HPr
ptsI	b2416	2	1.18	0.045	PEP-protein phosphotransferase system enzyme I
Cell motility					
Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
flgB	b1073	1	1.20	0.023	flagellar biosynthesis, cell-proximal portion of basal-body rod _
flgC	b1074	1	1.43	0.020	flagellar biosynthesis, cell-proximal portion of basal-body rod _
flgE	b1076	2	1.41	0.016	flagellar biosynthesis, hook protein _
fliL	b1944	0	1.02	0.005	flagellar biosynthesis
prlA	b3300	2	1.55	0.003	putative ATPase subunit of translocase

Cell wall/membrane biogenesis

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
ompA	b0957	1	1.86	0.037	outer membrane protein 3a (Il*;G;d)
ompC	b2215	1	1.39	0.050	outer membrane protein 1b (Ib;c)
ompX	b0814	1	2.41	0.001	outer membrane protein X

Energy production and conversion

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
ppa	b4226	0	1.26	0.031	inorganic pyrophosphatase

Inorganic ion transport and metabolism

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
	b2431	2	1.54	0.000	orf, hypothetical protein
focA	b0904	2	1.13	0.010	probable formate transporter (formate channel 1)

Lipid transport and metabolism

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
accB	b3255	1	1.09	0.012	acetylCoA carboxylase, BCCP subunit; carrier of biotin
accC	b3256	1	1.25	0.003	acetyl CoA carboxylase, biotin carboxylase subunit
accD	b2316	2	1.05	0.004	acetylCoA carboxylase, carboxytransferase component, beta subunit
acpP	b1094	0	1.19	0.002	acyl carrier protein
fabB	b2323	2	1.10	0.010	3-oxoacyl-[acyl-carrier-protein] synthase I

Nucleotide transport and metabolism

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
dut	b3640	3	1.07	0.000	deoxyuridinetriphosphatase
guaB	b2508	2	1.26	0.012	IMP dehydrogenase
nupC	b2393	2	1.24	0.016	permease of transport system for 3 nucleosides
prsA	b1207	2	1.01	0.053	phosphoribosylpyrophosphate synthetase

Posttranslational modification, protein turnover, chaperones

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
slyD	b3349	4	1.07	0.028	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
tig	b0436	0	1.29	0.008	trigger factor; a molecular chaperone involved in cell division
yeaA	b1778	1	-1.36	0.001	orf, hypothetical protein

Replication, recombination and repair

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
hupB	b0440	3	1.60	0.003	DNA-binding protein HU-beta, NS1 (HU-1)
priB	b4201	4	1.63	0.018	primosomal replication protein N
recA	b2699	1	1.70	0.000	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprot
smf_1		1	-1.04	0.001	orf, fragment 1

Signal transduction mechanisms

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
ygaG	b2687	1	1.47	0.010	putative 2-component transcriptional regulator

Secondary metabolites biosynthesis, transport and catabolism

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
srID	b2705	1	1.16	0.011	glucitol (sorbitol)-6-phosphate dehydrogenase

Transcription

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
rpoA	b3295	2	2.15	0.004	RNA polymerase, alpha subunit

Translation

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
fusA	b3340	1	1.49	0.022	GTP-binding protein chain elongation factor EF-G
rplA	b3984	0	1.41	0.015	50S ribosomal subunit protein L1, regulates synthesis of L1 and L11
rplB	b3317	1	1.84	0.021	50S ribosomal subunit protein L2
rplC	b3320	8	1.84	0.032	50S ribosomal subunit protein L3
rplD	b3319	1	1.93	0.025	50S ribosomal subunit protein L4, regulates expression of S10 operon
rplE	b3308	0	2.27	0.012	50S ribosomal subunit protein L5
rplF	b3305	3	1.70	0.023	50S ribosomal subunit protein L6
rplJ	b3985	0	1.84	0.030	50S ribosomal subunit protein L10
rplM	b3231	2	1.02	0.031	50S ribosomal subunit protein L13
rplO	b3301	1	2.42	0.004	50S ribosomal subunit protein L15
rplP	b3313	2	1.97	0.010	50S ribosomal subunit protein L16
rplR	b3304	2	2.00	0.026	50S ribosomal subunit protein L18
rplU	b3186	1	1.10	0.040	50S ribosomal subunit protein L21
rplV	b3315	1	2.46	0.007	50S ribosomal subunit protein L22
rplW	b3318	4	1.90	0.049	50S ribosomal subunit protein L23
rpmA	b3185	1	1.11	0.046	50S ribosomal subunit protein L27
rpmC	b3312	4	1.74	0.005	50S ribosomal subunit protein L29
rpmD	b3302	2	2.31	0.024	50S ribosomal subunit protein L30
rpmF	b1089	1	1.41	0.004	50S ribosomal subunit protein L32
rpmI	b1717	2	1.54	0.020	50S ribosomal subunit protein A
rpmJ	b3299	1	1.24	0.002	50S ribosomal subunit protein L36
rpsA	b0911	2	1.27	0.002	30S ribosomal subunit protein S1
rpsB	b0169	1	1.76	0.007	30S ribosomal subunit protein S2
rpsC	b3314	4	2.40	0.010	30S ribosomal subunit protein S3
rpsD	b3296	2	2.03	0.003	30S ribosomal subunit protein S4
rpsE	b3303	0	2.44	0.007	30S ribosomal subunit protein S5
rpsF	b4200	0	1.69	0.041	30S ribosomal subunit protein S6
rpsG	b3341	2	2.28	0.009	30S ribosomal subunit protein S7, initiates assembly
rpsH	b3306	2	2.03	0.022	30S ribosomal subunit protein S8, and regulator
rpsI	b3230	0	1.61	0.031	30S ribosomal subunit protein S9
rpsJ	b3321	1	1.98	0.009	30S ribosomal subunit protein S10
rpsK	b3297	4	2.24	0.007	30S ribosomal subunit protein S11
rpsL	b3342	1	1.69	0.016	30S ribosomal subunit protein S12
rpsM	b3298	1	1.78	0.004	30S ribosomal subunit protein S13
rpsN	b3307	4	1.40	0.045	30S ribosomal subunit protein S14
rpsP	b2609	0	1.73	0.052	30S ribosomal subunit protein S16
rpsQ	b3311	1	1.13	0.020	30S ribosomal subunit protein S17
rpsS	b3316	1	1.42	0.038	30S ribosomal subunit protein S19
rpsT	b0023	0	1.05	0.054	30S ribosomal subunit protein S20
thrS	b1719	2	1.16	0.002	threonine tRNA synthetase
trmD	b2607	6	1.34	0.023	tRNA methyltransferase; tRNA (guanine-7)-methyltransferase
tufA	b3339	0	1.78	0.023	protein chain elongation factor EF-Tu (duplicate of tufB)
tufB	b3980	0	2.27	0.026	protein chain elongation factor EF-Tu (duplicate of tufA)

yfjA	b2608	4	1.32	0.029	orf, hypothetical protein
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Unclassified, unknown or general function prediction only

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
b0332	b0332	3	1.03	0.001	orf, hypothetical protein
b2655	b2655	2	1.16	0.009	orf, hypothetical protein
ecs0702	b0667	0	1.41	0.003	putative RNA
glgS	b3049	2	-1.82	0.033	glycogen biosynthesis, rpoS dependent
insA_2		0	1.39	0.004	IS1 protein InsA
lamB	b4036	1	2.18	0.012	phage lambda receptor protein; maltose high-affinity receptor
pheL	b2598	1	1.03	0.002	leader peptide of chorismate mutase-P-prephenate dehydratase
slyB	b1641	2	1.59	0.021	putative outer membrane protein
yadH	b0128	2	1.06	0.002	orf, hypothetical protein
ybjX	b0877	1	1.42	0.006	putative enzyme
ycdV	b1031	0	1.79	0.000	putative ribosomal protein
yceD	b1088	1	1.35	0.002	orf, hypothetical protein
yeaC	b1777	1	-1.38	0.008	orf, hypothetical protein
yebF	b1847	1	1.40	0.001	orf, hypothetical protein
yebG	b1848	2	1.11	0.011	orf, hypothetical protein
yecR	b1904	0	1.09	0.002	orf, hypothetical protein
ydhI	b1643	2	1.00	0.001	orf, hypothetical protein
ydiH	b1685	0	1.21	0.000	orf, hypothetical protein
ygiA	b3036	1	1.48	0.000	orf, hypothetical protein
yhcE	b3217	2	1.21	0.000	orf, hypothetical protein
yi82	1	1	1.23	0.027	IS186 and IS421 hypothetical protein
yihM	b3873	1	1.08	0.004	orf, hypothetical protein
yneK	b1527	1	1.02	0.025	orf, hypothetical protein
ytfI	b4215	0	1.05	0.010	orf, hypothetical protein

***Number of GATC sites in the upstream sequence regions was determined by searching -400 bp from the start site of each gene.**