

Supplementary Table 1: Genes differentially expressed at the basal level (± 2 -fold) in *dam* 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
argV	b2694	-	1.03	0.020	Arginine tRNA ² ; tandem quadruplicate genes
aspC	b0928	2	1.26	0.026	aspartate aminotransferase
dapA	b2478	3	1.24	0.005	dihydrodipicolinate synthase
gcvH	b2904	1	1.04	0.018	in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor
glyA	b2551	0	1.32	0.003	serine hydroxymethyltransferase
oppA	b1243	1	1.16	0.012	oligopeptide transport; periplasmic binding protein
tdh	b3616	1	1.46	0.007	threonine dehydrogenase
tnaB	b3709	1	1.48	0.031	low affinity tryptophan permease
ydgR	b1634	1	1.61	0.007	putative transport protein

Carbohydrate transport and metabolism					
Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
crr	b2417	1	1.07	0.026	PTS system, glucose-specific IIA component
deoB	b4383	1	1.05	0.041	phosphopentomutase
eno	b2779	3	1.13	0.045	enolase
fba	b2925	0	1.48	0.002	fructose-bisphosphate aldolase, class II
galK	b0757	2	1.45	0.003	galactokinase
galM	b0756	2	1.15	0.002	galactose-1-epimerase (mutarotase)
glk	b2388	2	1.07	0.000	glucokinase
glpF	b3927	2	1.58	0.035	facilitated diffusion of glycerol
glpT	b2240	0	1.25	0.010	sn-glycerol-3-phosphate permease
gnd	b2029	3	1.17	0.004	gluconate-6-phosphate dehydrogenase, decarboxylating
gpmA	b0755	0	1.09	0.019	phosphoglyceromutase 1
malE	b4034	2	2.80	0.000	periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis
malF	b4033	2	1.17	0.002	part of maltose permease, periplasmic
malG	b4032	3	1.02	0.001	part of maltose permease, inner membrane
malK	b4035	2	2.44	0.001	ATP-binding component of transport system for maltose
malP	b3417	4	1.34	0.006	maltodextrin phosphorylase
mgsA	b0963	0	1.36	0.011	methylglyoxal synthase
mtlD	b3600	0	1.30	0.030	mannitol-1-phosphate dehydrogenase
pfkA	b3916	4	1.27	0.002	6-phosphofructokinase I
pgk	b2926	3	1.44	0.002	phosphoglycerate kinase
ptsG	b1101	1	1.24	0.009	PTS system, glucose-specific IIBC component
ptsH	b2415	1	1.01	0.030	PTS system protein HPr
ptsI	b2416	2	1.15	0.024	PEP-protein phosphotransferase system enzyme I
rbsB	b3751	3	1.02	0.030	D-ribose periplasmic binding protein
talB	b0008	1	1.12	0.008	transaldolase B

Carbohydrate transport and metabolism

treB	b4240	5	2.30	0.000	PTS system enzyme II, trehalose specific
treC	b4239	1	1.19	0.015	trehalase 6-P hydrolase

Cell motility

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
	b3836	2	1.28	0.000	orf, hypothetical protein
flgB	b1073	1	1.36	0.009	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgC	b1074	1	1.62	0.006	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgD	b1075	0	1.04	0.018	flagellar biosynthesis, initiation of hook assembly
flgE	b1076	2	1.75	0.004	flagellar biosynthesis, hook protein
flgF	b1077	4	1.51	0.009	flagellar biosynthesis, cell-proximal portion of basal-body rod
flgG	b1078	1	1.59	0.005	flagellar biosynthesis, cell-distal portion of basal-body rod
flgL	b1083	1	1.17	0.023	flagellar biosynthesis; hook-filament junction protein
flgN	b1070	2	1.14	0.014	protein of flagellar biosynthesis
fliC	b1923	0	1.55	0.023	flagellar biosynthesis; flagellin, filament structural protein
fliG	b1939	3	1.12	0.002	flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction
fliL	b1944	0	1.23	0.001	flagellar biosynthesis
fliN	b1946	3	1.18	0.011	flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction
prlA	b3300	2	1.67	0.002	putative ATPase subunit of translocase
secB	b3609	3	1.08	0.007	protein export; molecular chaperone; may bind to signal sequence
secG	b3175	0	1.63	0.015	protein export - membrane protein
yajC	b0407	1	1.38	0.000	orf, hypothetical protein

Cell wall/membrane biogenesis

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
ompA	b0957	1	1.82	0.036	outer membrane protein 3a (II*;G;d)
ompC	b2215	1	2.08	0.004	outer membrane protein 1b (Ib;c)
ompF	b0929	0	2.22	0.002	outer membrane protein 1a (Ia;b;F)
ompT	b0565	0	1.04	0.012	outer membrane protein 3b (a), protease VII
ompX	b0814	1	2.10	0.002	outer membrane protein X
pal	b0741	2	1.32	0.007	peptidoglycan-associated lipoprotein
spr	b2175	0	1.48	0.002	putative lipoprotein
tolC	b3035	3	1.13	0.003	outer membrane channel; specific tolerance to colicin E1; segregation of daughter chromosomes

Cell division					
Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
sulA	b0958	4	0.95	0.004	suppressor of lon; inhibits cell division and ftsZ ring formation

Energy production and conversion					
Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
ackA	b2296	0	1.18	0.045	acetate kinase
atpA	b3734	0	1.54	0.009	membrane-bound ATP synthase, F1 sector, alpha-subunit
atpB	b3738	1	1.01	0.007	membrane-bound ATP synthase, F0 sector, subunit a
atpC	b3731	2	1.29	0.025	membrane-bound ATP synthase, F1 sector, epsilon-subunit
atpD	b3732	3	1.69	0.004	membrane-bound ATP synthase, F1 sector, beta-subunit
atpE	b3737	3	1.45	0.002	membrane-bound ATP synthase, F0 sector, subunit c
atpF	b3736	4	1.41	0.003	membrane-bound ATP synthase, F0 sector, subunit b
atpG	b3733	1	1.45	0.006	membrane-bound ATP synthase, F1 sector, gamma-subunit
atpH	b3735	1	1.28	0.003	membrane-bound ATP synthase, F1 sector, delta-subunit
cydA	b0733	3	1.11	0.026	cytochrome d terminal oxidase, polypeptide subunit I
fdol	b3892	1	1.08	0.015	formate dehydrogenase, cytochrome B556 (FDO) subunit
frdA	b4154	2	1.11	0.002	fumarate reductase, anaerobic, flavoprotein subunit
frdB	b4153	0	1.61	0.030	fumarate reductase, anaerobic, iron-sulfur protein subunit
galT	b0758	1	1.52	0.000	galactose-1-phosphate uridylyltransferase
glcB	b2976	0	1.89	0.015	malate synthase G
glpC	b2243	1	1.10	0.000	sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit
glpK	b3926	1	1.41	0.039	glycerol kinase
lpdA	b0116	0	1.26	0.026	lipoamide dehydrogenase (NADH); component of 2-oxodehydrogenase and pyruvate complexes; L-protein of glycine cleavage complex
mdh	b3236	0	1.90	0.006	malate dehydrogenase
nuoB	b2287	0	1.29	0.009	NADH dehydrogenase I chain B
nuoH	b2282	2	1.14	0.019	NADH dehydrogenase I chain H
nuoK	b2279	1	1.04	0.004	NADH dehydrogenase I chain K
nuoL	b2278	2	1.15	0.004	NADH dehydrogenase I chain L
ppa	b4226	0	1.66	0.003	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	1.52	0.000	orf, hypothetical protein
focA	b0904	2	1.17	0.008	probable formate transporter (formate channel 1)
phnA	b4108	1	1.03	0.005	orf, hypothetical protein
sodB	b1656	1	1.29	0.018	superoxide dismutase, iron

Lipid transport and metabolism

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
accB	b3255	1	1.26	0.006	acetylCoA carboxylase, BCCP subunit; carrier of biotin
accC	b3256	1	1.22	0.002	acetyl CoA carboxylase, biotin carboxylase subunit
accD	b2316	2	1.13	0.002	acetylCoA carboxylase, carboxytransferase component, beta subunit
acpP	b1094	0	1.38	0.000	acyl carrier protein
fabB	b2323	2	1.40	0.001	3-oxoacyl-[acyl-carrier-protein] synthase I
fabF	b1095	1	1.06	0.005	3-oxoacyl-[acyl-carrier-protein] synthase II
fabI	b1288	0	1.11	0.006	enoyl-[acyl-carrier-protein] reductase (NADH)

Nucleotide transport and metabolism

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
cdd	b2143	3	1.04	0.016	cytidine/deoxycytidine deaminase
deoD	b4384	2	1.97	0.005	purine-nucleoside phosphorylase
guaB	b2508	2	1.15	0.022	IMP dehydrogenase
nupC	b2393	2	1.58	0.005	permease of transport system for 3 nucleosides
prsA	b1207	2	1.28	0.008	phosphoribosylpyrophosphate synthetase
purA	b4177	2	1.50	0.012	adenylosuccinate synthetase
udp	b3831	0	1.05	0.051	uridine phosphorylase

Posttranslational modification, protein turnover, chaperones

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
ahpC	b0605	1	1.12	0.011	alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides
grpE	b2614	3	1.83	0.030	phage lambda replication; host DNA synthesis; heat shock protein; protein repair

Posttranslational modification, protein turnover, chaperones

hflB	b3178	1	1.47	0.024	degrades sigma32, integral membrane peptidase, cell division protein
slyD	b3349	4	1.20	0.010	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
sspA	b3229	0	1.10	0.020	regulator of transcription; stringent starvation protein A
tig	b0436	0	1.42	0.005	trigger factor; a molecular chaperone involved in cell division
tpx	b1324	1	1.14	0.027	thiol peroxidase
yeaA	b1778	1	-1.01	0.007	orf, hypothetical protein

Replication, recombination and repair

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
hupA	b4000	0	1.04	0.015	DNA-binding protein HU-alpha (HU-2)
hupB	b0440	3	1.89	0.001	DNA-binding protein HU-beta, NS1 (HU-1)
priB	b4201	4	2.19	0.001	primosomal replication protein N
recA	b2699	1	2.02	0.000	DNA strand exchange and renaturation, DNA-dependent ATPase, DNA- and ATP-dependent coprotease
smf_1		1	-1.31	0.000	orf, fragment 1

Signal transduction mechanisms

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
crp	b3357	0	1.13	0.034	cyclic AMP receptor protein
dksA	b0145	1	1.18	0.003	dnaK suppressor protein
yebJ	b1831	1	1.16	0.008	orf, hypothetical protein
ygaG	b2687	1	1.42	0.005	orf, hypothetical protein

Secondary metabolites biosynthesis, transport and catabolism

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
fabG	b1093	1	1.18	0.001	3-oxoacyl-[acyl-carrier-protein] reductase
srlD	b2705	1	1.64	0.000	glucitol (sorbitol)-6-phosphate dehydrogenase

Transcription

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
cspA	b3556	0	1.34	0.019	cold shock protein 7.4, transcriptional activator of hns
cspB	b1557	0	1.22	0.050	cold shock protein; may affect transcription

Transcription

fliA	b1922	3	1.13	0.008	flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons
fliM	b1945	1	1.25	0.006	flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction
lexA	b4043	1	1.60	0.001	regulator for SOS(lexA) regulon
rpoA	b3295	2	2.54	0.001	RNA polymerase, alpha subunit
rpoZ	b3649	0	1.04	0.014	RNA polymerase, omega subunit
yeeD	b2012	1	1.19	0.009	orf, hypothetical protein

Translation

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
asnS	b0930	0	1.50	0.012	asparagine tRNA synthetase
efp	b4147	3	1.14	0.026	elongation factor P (EF-P)
fusA	b3340	1	1.78	0.004	GTP-binding protein chain elongation factor EF-G
glnS	b0680	4	1.10	0.003	glutamine tRNA synthetase
infB	b3168	4	1.08	0.029	protein chain initiation factor IF-2
rplA	b3984	0	2.02	0.002	50S ribosomal subunit protein L1, regulates synthesis of L1 and L11
rplB	b3317	1	2.49	0.004	50S ribosomal subunit protein L2
rplC	b3320	8	2.58	0.002	50S ribosomal subunit protein L3
rplD	b3319	1	2.68	0.002	50S ribosomal subunit protein L4, regulates expression of S10 operon
rplE	b3308	0	3.06	0.001	50S ribosomal subunit protein L5
rplF	b3305	3	2.08	0.006	50S ribosomal subunit protein L6
rplI	b4203	3	1.81	0.006	50S ribosomal subunit protein L9
rplJ	b3985	0	2.04	0.008	50S ribosomal subunit protein L10
rplK	b3983	1	1.80	0.005	50S ribosomal subunit protein L11
rplL	b3986	2	1.29	0.044	50S ribosomal subunit protein L7/L12
rplM	b3231	2	1.50	0.003	50S ribosomal subunit protein L13
rplN	b3310	1	1.64	0.003	50S ribosomal subunit protein L14
rplO	b3301	1	2.53	0.002	50S ribosomal subunit protein L15
rplP	b3313	2	2.26	0.002	50S ribosomal subunit protein L16
rplQ	b3294	5	2.21	0.013	50S ribosomal subunit protein L17
rplR	b3304	2	2.53	0.006	50S ribosomal subunit protein L18
rplS	b2606	0	1.67	0.005	50S ribosomal subunit protein L19
rplT	b1716	3	1.92	0.008	50S ribosomal subunit protein L20, and regulator
rplU	b3186	1	1.60	0.003	50S ribosomal subunit protein L21
rplV	b3315	1	2.92	0.001	50S ribosomal subunit protein L22
rplW	b3318	4	2.55	0.010	50S ribosomal subunit protein L23
rplX	b3309	2	1.83	0.005	50S ribosomal subunit protein L24
rpmA	b3185	1	1.46	0.004	50S ribosomal subunit protein L27
rpmB	b3637	3	1.91	0.009	50S ribosomal subunit protein L28
rpmC	b3312	4	2.06	0.001	50S ribosomal subunit protein L29
rpmD	b3302	2	3.07	0.004	50S ribosomal subunit protein L30
rpmF	b1089	1	1.40	0.003	50S ribosomal subunit protein L32
rpmG	b3636	0	1.88	0.037	50S ribosomal subunit protein L33

Translation					
rpmH	b3703	3	1.92	0.017	50S ribosomal subunit protein L34
rpmI	b1717	2	1.85	0.003	50S ribosomal subunit protein A
rpmJ	b3299	1	1.33	0.001	50S ribosomal subunit protein L36
rpsA	b0911	2	1.63	0.000	30S ribosomal subunit protein S1
rpsB	b0169	1	2.26	0.001	30S ribosomal subunit protein S2
rpsC	b3314	4	2.56	0.003	30S ribosomal subunit protein S3
rpsD	b3296	2	2.34	0.001	30S ribosomal subunit protein S4
rpsE	b3303	0	2.94	0.002	30S ribosomal subunit protein S5
rpsF	b4200	0	2.58	0.001	30S ribosomal subunit protein S6
rpsG	b3341	2	2.61	0.002	30S ribosomal subunit protein S7, initiates assembly
rpsH	b3306	2	2.64	0.004	30S ribosomal subunit protein S8, and regulator
rpsI	b3230	0	2.01	0.005	30S ribosomal subunit protein S9
rpsJ	b3321	1	2.43	0.001	30S ribosomal subunit protein S10
rpsK	b3297	4	2.66	0.001	30S ribosomal subunit protein S11
rpsL	b3342	1	2.18	0.001	30S ribosomal subunit protein S12
rpsM	b3298	1	2.11	0.001	30S ribosomal subunit protein S13
rpsN	b3307	4	2.13	0.005	30S ribosomal subunit protein S14
rpsO	b3165	3	2.03	0.006	30S ribosomal subunit protein S15
rpsP	b2609	0	2.40	0.002	30S ribosomal subunit protein S16
rpsQ	b3311	1	1.13	0.011	30S ribosomal subunit protein S17
rpsR	b4202	1	1.87	0.005	30S ribosomal subunit protein S18
rpsS	b3316	1	1.99	0.006	30S ribosomal subunit protein S19
rpsT	b0023	0	1.38	0.010	30S ribosomal subunit protein S20
thrS	b1719	2	1.39	0.000	threonine tRNA synthetase
trmD	b2607	6	1.82	0.002	tRNA methyltransferase; tRNA (guanine-7)-methyltransferase
tsf	b0170	2	1.54	0.023	protein chain elongation factor EF-Ts
tufA	b3339	0	1.93	0.007	protein chain elongation factor EF-Tu (duplicate of tufB)
tufB	b3980	0	2.46	0.004	protein chain elongation factor EF-Tu (duplicate of tufA)
yfjA	b2608	4	1.75	0.004	orf, hypothetical protein
yjgF	b4243	4	1.45	0.025	orf, hypothetical protein

Unclassified, unknown or general function prediction only

Gene	Blattner Number	Number of GATC sites*	Signal Log Ratio	ANOVA p-value	Gene Product and Function
fliZ	b1921	2	1.22	0.002	orf, hypothetical protein
hns	b1237	0	1.24	0.002	DNA-binding protein HLP-II (HU, BH2, HD, NS); pleiotropic regulator
lamB	b4036	1	3.15	0.001	phage lambda receptor protein; maltose high-affinity receptor
malM	b4037	0	1.29	0.002	periplasmic protein of mal regulon
slyB	b1641	2	1.91	0.003	putative outer membrane protein
smp	b4387	0	1.13	0.018	orf, hypothetical protein
wzzB	b2027	1	1.06	0.006	regulator of length of O-antigen component of lipopolysaccharide chains
ybgF	b0742	2	1.12	0.016	orf, hypothetical protein
yceD	b1088	1	1.49	0.001	orf, hypothetical protein

Unclassified, unknown or general function prediction only

yeaC	b1777	1	-1.09	0.029	orf, hypothetical protein
yebF	b1847	1	1.11	0.004	orf, hypothetical protein
yebG	b1848	2	1.60	0.001	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.