

Discretely calibrated regulatory loops controlled by ppGpp partition gene induction across the 'feast to famine' gradient in *Escherichia coli*

Matthew F. Traxler[§], Vineetha M. Zacharia, Stafford Marquardt, Sean M. Summers, Huyen-Tran Nguven, S. Elizabeth Stark, and Tyrrell Conway*

Advanced Center for Genome Technology, University of Oklahoma, Norman, OK 73019

[§] Present address: Dept. of Microbiology and Molecular Genetics, Harvard Medical School, 200 Longwood Ave., Boston MA, 02115

Email: matthew_traxler@hms.harvard.edu, Vineetha.Zacharia@UTSouthwestern.edu, staffordmarquardt@gmail.com, sean-summers@ouhsc.edu, cecelia-nguyen@ouhsc.edu, sestark@northwestern.edu

* Corresponding author: Tyrrell Conway
Department of Botany and Microbiology
The University of Oklahoma
Norman, OK 73019-0245
Voice: 405 325 1683
FAX: 405 325 3442
E-mail: tconway@ou.edu

Supplemental Table 1: Venn Diagram Gene List

Venn 2.3
>2fold lower in ΔrelAspOT, ΔrpoS
116 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspOT
dkgA	b3012	2, 5-diketo-D-gluconate reductase A	orf; Unknown	K-12_b3012_dkgA_s_at	2.062	1.357	0.679	2.854	0.099	-1.198	-1.479
rpsV	b1480	30S ribosomal subunit protein S22	structural component; Ribosomal proteins - synthesis, modification	K-12_b1480_rpsV_s_at	4.516	4.962	2.666	4.858	0.066	-1.723	-0.828
dacC	b0839	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6a)	enzyme; Murein sacculus, peptidoglycan	K-12_b0839_dacC_s_at	2.704	2.609	1.387	2.102	1.143	0.724	0.13
osmE	b1739	DNA-binding transcriptional activator	regulator; Global regulatory functions	K-12_b1739_osmE_s_at	3.273	3.143	0.736	2.589	-0.23	-0.353	-0.583
yhiE	b3512	DNA-binding transcriptional activator	orf; Unknown	K-12_b3512_yhiE_s_at	2.94	2.425	1.654	2.86	1.823	-0.115	-0.581
gadX	b3516	DNA-binding transcriptional dual regulator	putative regulator; Not classified	K-12_b3516_gadX_at	2.318	2.317	1.214	1.845	1.013	0.065	-0.022
yehV	b2127	DNA-binding transcriptional regulator	putative regulator; Not classified -/- transcriptional regulator of curl	K-12_b2127_yehV_s_at	2.171	1.975	0.693	2.69	1.142	0.413	0.131
suFA	b1684	Fe-S cluster assembly protein	orf; Unknown	K-12_b1684_suFA_s_at	1.276	1.822	0.159	2.649	0.928	0.054	-0.129
dps	b0812	Fe-binding and storage protein	regulator; Global regulatory functions	K-12_b0812_dps_s_at	3.653	3.54	0.83	2.628	-0.073	-1.337	-0.5
yedU	b1967	Hsp31 molecular chaperone	orf; Unknown	K-12_b1967_yedU_s_at	4.143	4.08	2.913	3.663	1.876	1.347	1.638
cysQ	b4214	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosph	phenotype; Central intermediary metabolism: Sulfur metabolism	K-12_b4214_cysQ_s_at	1.631	1.534	-0.266	-0.238	-0.472	-0.152	-0.275
rpoS	b2741	RNA polymerase, sigma S (sigma 38) factor	enzyme; Global regulatory functions -/- involved in the response to o	K-12_b2741_rpoS_s_at	2.752	2.798	-2.188	1.846	1.373	0.244	1.121
acnA	b1276	aconitate hydratase 1	enzyme; Energy metabolism, carbon: TCA cycle	K-12_b1276_acnA_s_at	2.167	2.14	1.165	1.621	0.96	-1.059	-0.066
astA	b1747	arginine succinyltransferase	orf; Unknown	CFT073_c2147_s_at	1.55	1.292	0.495	0.611	0.753	0.183	-0.131
bfr	b3336	bacterioferritin, iron storage and detoxification protein	carrier; Transport of small molecules: Cations	K-12_b3336_bfr_a_at	4.425	3.942	0.815	4.254	-0.205	1.557	1.44
surD	b1681	component of SurBCD complex	orf; Unknown	K-12_b1681_surD_s_at	1.237	1.297	0.033	1.507	0.625	-0.547	-0.187
suFB	b1683	component of SurBCD complex	orf; Unknown	K-12_b1683_suFB_s_at	1.794	1.952	-0.023	2.25	0.702	0.147	-0.109
suFC	b1682	component of SurBCD complex, ATP-binding component of ABC super	putative transport; Not classified	K-12_b1682_suFC_s_at	1.563	1.754	0.135	2.14	0.836	0.048	-0.012
ycaP	b0906	conserved inner membrane protein	orf; Unknown	K-12_b0906_ycaP_s_at	2.286	2.387	1.014	4.777	0.541	0.98	0.055
yeaQ	b1795	conserved inner membrane protein	orf; Unknown	K-12_b1795_yeaQ_s_at	3.716	3.492	1.061	3.01	0.994	0.807	-0.03
yqjE	b3099	conserved inner membrane protein	orf; Unknown	K-12_b3099_yqjE_s_at	3.682	2.924	1.059	2.156	0.626	1.034	0.56
psfI	b0384	conserved protein	phenotype; Central intermediary metabolism: Phosphorus compound	K-12_b0384_psfI_a_at	3.17	2.933	0.571	3.679	0.168	0.4	0.83
ybeL	b0643	conserved protein	phenotype; Not classified	K-12_b0643_ybeL_s_at	2.967	3.01	1.443	2.63	1.24	-0.837	-0.594
yhbA	b0707	conserved protein	orf; Unknown	K-12_b0707_yhbA_s_at	1.532	0.827	0.486	1.559	0.353	0.629	-0.347
ycyT	b0964	conserved protein	orf; Unknown	K-12_b0964_ycyT_s_at	1.512	1.582	0.498	1.157	1.064	0.879	0.378
ycgB	b1188	conserved protein	putative factor; Not classified	K-12_b1188_ycgB_s_at	4.447	5.094	0.926	2.493	0.965	0.489	-0.249
ydeI	b1536	conserved protein	orf; Unknown	K-12_b1536_ydeI_s_at	2.878	2.421	0.993	2.568	1.076	0.023	0.168
ynhG	b1678	conserved protein	orf; Unknown	K-12_b1678_ynhG_s_at	4.058	4.248	1.188	2.192	0.215	-0.164	-0.148
yeaH	b1784	conserved protein	orf; Unknown	K-12_b1784_yeaH_s_at	2.696	2.232	0.283	3.184	1.365	-0.435	-0.4
yedP	b1955	conserved protein	orf; Unknown	K-12_b1955_yedP_s_at	2.347	1.93	0.555	1.524	1.287	0.394	0.398
yegS	b2086	conserved protein	orf; Unknown	K-12_b2086_yegS_s_at	2.026	1.74	0.356	2.996	1.816	0.217	0.159
elaB	b2266	conserved protein	orf; Unknown	K-12_b2266_elaB_s_at	4.711	3.865	1.553	4.872	0.556	-0.245	-0.035
yfcZ	b2343	conserved protein	orf; Unknown	K-12_b2343_yfcZ_s_at	1.957	1.301	0.609	0.391	0.603	0.587	0.554
yqjC	b3097	conserved protein	orf; Unknown	K-12_b3097_yqjC_s_at	2.386	2.331	0.632	2.97	0.406	-0.482	0.244
yqjD	b3098	conserved protein	orf; Unknown	K-12_b3098_yqjD_s_at	3.284	3.195	1.099	2.504	-0.516	0.662	0.138
yqjK	b3100	conserved protein	orf; Unknown	K-12_b3100_yqjK_s_at	2.616	2.263	0.208	1.156	0.577	0.604	0.68
yhhA	b3448	conserved protein	orf; Unknown	K-12_b3448_yhhA_s_at	2.34	2.402	0.316	1.777	0.794	-0.237	-0.231
phnB	b4107	conserved protein	orf; Unknown	K-12_b4107_phnB_s_at	3.005	3.302	0.451	2.261	-0.083	0.332	-0.068
yjdI	b4126	conserved protein	orf; Unknown	K-12_b4126_yjdI_s_at	3.137	3.809	0.833	2.343	0.325	0.144	-0.128
yjHT	b4313	conserved protein	orf; Unknown	K-12_b4313_yjHT_s_at	2.875	3.038	1.567	2.227	0.921	0.923	0.749
yeaG	b1783	conserved protein with nucleoside triphosphate hydrolase domain	orf; Unknown	K-12_b1783_yeaG_s_at	4.633	4.144	0.579	3.793	2.312	-0.269	-0.55
cbpA	b1000	curved DNA-binding protein, DnaJ homologue that functions as a co-f	factor; Chaperones	K-12_b1000_cbpA_s_at	1.759	1.16	0.74	0.335	0.103	-0.037	0.541
treF	b3519	cytoplasmic trehalase	enzyme; Degradation of small molecules: Carbon compounds	K-12_b3519_treF_s_at	1.436	1.568	0.062	1.487	0.585	-0.107	-0.338
ecnB	b4411	entericidin B membrane lipoprotein	orf; Unknown	K-12_b4411_ecnB_s_at	3.398	3.49	0.244	3.907	0.305	1.291	1.674
fbaB	b2097	fructose-bisphosphate aldolase class I	orf; Unknown	K-12_b2097_fbaB_s_at	4.8	4.12	1.955	4.621	0.947	-0.457	-0.846
ybdK	b0581	gamma-glutamylcysteine ligase	orf; Unknown	K-12_b0581_ybdK_s_at	2.145	2.203	-0.016	2.284	0.9	0.369	-0.019
ggT	b3447	gamma-glutamyltranspeptidase	enzyme; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxin	K-12_b3447_ggT_s_at	1.701	1.202	-0.162	2.328	0.609	0.099	-0.524
agg	b1002	glucose-1-phosphatase/inositol phosphatase	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b1002_agg_s_at	1.2	1.086	0.081	0.757	1.138	-0.145	-0.417
ugpB	b3453	glycerol-3-phosphate transporter subunit -/- periplasmic-binding com	transport; Transport of small molecules: Carbohydrates, organic acid	K-12_b3453_ugpB_s_at	2.016	2.377	0.745	2.427	0.332	-0.76	-0.645
aidB	b4187	isovaleryl CoA dehydrogenase	putative enzyme; Not classified	K-12_b4187_aidB_s_at	1.648	1.371	0.2	1.531	0.959	0.391	0.012
osmB	b1283	lipoprotein	putative membrane; Osmotic adaptation	K-12_b1283_osmB_s_at	3.366	3.3	1.553	3.143	0.671	0.555	1.584
narU	b1469	nitrate/nitrite transporter	transport; Transport of small molecules: Anions	K-12_b1469_narU_s_at	1.426	0.863	0.276	1.429	0.701	0.721	-0.291
osmC	b1482	osmotically inducible, stress-inducible membrane protein	phenotype; Osmotic adaptation	K-12_b1482_osmC_s_at	4.519	4.311	2.846	3.913	0.983	-0.276	0.902
slp	b3506	outer membrane lipoprotein	membrane; Outer membrane constituents	K-12_b3506_slp_s_at	1.289	0.292	-0.032	-0.022	0.163	0.379	0.051
bic	b4149	outer membrane lipoprotein (lipocalin)	membrane; Macromolecule synthesis, modification: Lipoprotein	K-12_b4149_bic_s_at	2.441	2.644	-0.055	1.752	0.627	-0.283	-0.236
osmY	b4376	periplasmic protein	phenotype; Osmotic adaptation	K-12_b4376_osmY_s_at	4.39	5.016	-0.126	3.48	0.245	-0.564	0.816
treA	b1197	periplasmic trehalase	enzyme; Osmotic adaptation	K-12_b1197_treA_s_at	1.542	1.086	-0.161	1.621	0.465	-0.602	-0.753
ybeM	b0626	predicted C-N hydrolase superfamily, NAD(P)-binding amidase/nitri	putative enzyme; Not classified	K-12_b0626_ybeM_s_at	1.353	1.342	0.127	0.122	0.247	0.71	0.295
yccU	b0965	predicted CoA-binding protein with NAD(P)-binding Rossmann-fold do	orf; Unknown	O157_Ecs1049_s_at	1.78	1.622	0.199	-0.197	-2.385	-0.554	-0.194
ybhP	b0790	predicted DNase	orf; Unknown	K-12_b0790_ybhP_s_at	3.516	2.896	0.756	3.439	-0.381	0.457	-0.365
yqjG	b3102	predicted S-transferase	putative enzyme; Not classified	K-12_b3102_yqjG_s_at	2.536	2.396	0.386	2.619	0.713	0.215	-0.19

yjdJ	b4127	predicted acyltransferase with acyl-CoA N-acyltransferase domain	orf; Unknown	K-12_b4127_yjdJ_s_at	4.053	3.979	2.933	3.829	1.085	0.658	0.277
yjgB	b4269	predicted alcohol dehydrogenase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b4269_yjgB_s_at	1.11	1.017	-0.02	1.463	1.147	-0.29	-0.738
yhcO	b3239	predicted barnase inhibitor	orf; Unknown	K-12_b3239_yhcO_s_at	2.443	2.056	-0.128	1.474	0.232	0.607	-0.305
b3000	b3000	predicted dienlactone hydrolase (pseudogene)	orf; Unknown	K-12_b3000_s_at	2.777	2.547	1.237	3.2	0.978	1.093	-0.182
ydcK	b1428	predicted enzyme	orf; Unknown	K-12_b1428_ydcK_s_at	2.328	1.664	0.739	1.866	1.232	0.739	-0.371
wrbA	b1004	predicted flavoprotein in Trp regulation	regulator; Amino acid biosynthesis: Tryptophan	K-12_b1004_wrbA_s_at	3.928	4.321	0.812	3.541	0.928	-0.549	-0.94
ybaS	b0485	predicted glutaminase	putative enzyme; Not classified	K-12_b0485_ybaS_s_at	1.561	0.848	-0.071	1.396	0.708	-0.387	-0.586
yfCG	b2302	predicted glutathione S-transferase	putative enzyme; Not classified	K-12_b2302_yfCG_s_at	2.337	2.399	0.423	3.207	0.696	0.195	-0.177
yghA	b3003	predicted glutathionylspermidine synthase, with NAD(P)-binding Ross	putative enzyme; Not classified	K-12_b3003_yghA_s_at	1.24	1.181	-0.174	1.613	1.063	0.067	-0.455
glgS	b3049	predicted glycogen synthesis protein	putative enzyme; Macromolecule synthesis, modification: Polysacchar	K-12_b3049_glgS_s_at	4.415	4.914	2.66	2.808	1.029	1.67	0.057
ycaC	b0897	predicted hydrolase	orf; Unknown	K-12_b0897_ycaC_s_at	2.975	2.323	0.3	2.817	0.918	0.07	-0.93
ysgA	b3630	predicted hydrolase	putative enzyme; Not classified	K-12_b3630_ysgA_s_at	1.548	1.34	-0.398	1.071	0.89	-0.745	-0.842
ychi	b1205	predicted inner membrane protein	orf; Unknown	K-12_b1205_ychi_s_at	2.459	2.686	0.28	1.09	0.762	0.232	-0.61
yohC	b2135	predicted inner membrane protein	orf; Unknown	K-12_b2135_yohC_s_at	5.076	4.571	2.116	3.627	1.962	1.407	0.157
yhbO	b3153	predicted intracellular protease	orf; Unknown	K-12_b3153_yhbO_s_at	2.108	1.625	-0.155	1.927	1.111	-0.316	-0.379
ybjP	b0865	predicted lipoprotein	putative enzyme; Not classified	K-12_b0865_ybjP_s_at	2.483	2.272	0.175	0.707	-0.642	-0.713	-0.714
ydcl	b1431	predicted lipoprotein	orf; Unknown	K-12_b1431_ydcl_s_at	2.327	2.507	0.533	1.901	-0.189	0.023	1.267
ybaY	b0453	predicted outer membrane lipoprotein	phenotype; Not classified	K-12_b0453_ybaY_s_at	3.132	2.687	0.024	1.641	0.316	0.154	0.102
yajO	b0419	predicted oxidoreductase, NAD(P)-binding	putative enzyme; Not classified	K-12_b0419_yajO_s_at	1.662	2.089	0.193	2.137	-0.244	-0.095	-0.134
yahK	b0325	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b0325_yahK_s_at	2.849	2.555	1.372	3.256	0.004	-0.341	-0.437
yneB	b1449	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b1449_yneB_s_at	2.511	2.268	0.669	3.117	0.67	0.622	1.22
ymA	b1725	predicted phosphotransferase/kinase	orf; Unknown	K-12_b1725_ymA_s_at	2.97	2.981	1.727	2.378	0.395	0.77	0.11
yhaO	b0329	predicted protein	orf; Unknown	K-12_b0329_yhaO_s_at	4.812	4.997	1.664	4.877	-0.46	1.794	1.28
yblM	b0806	predicted protein	orf; Unknown	K-12_b0806_yblM_s_at	2.308	3.009	1.125	3.122	0.629	0.255	-0.081
yccJ	b1003	predicted protein	orf; Unknown	K-12_b1003_yccJ_s_at	4.418	5.182	1.364	4.007	1.005	0.559	-0.594
msyB	b1051	predicted protein	phenotype; Protein, peptide secretion	K-12_b1051_msyB_s_at	4.043	4.093	0.857	4.672	0.45	-1.117	-0.864
ycG	b1259	predicted protein	orf; Unknown	K-12_b1259_ycG_s_at	2.423	2.401	0.064	3.015	1.421	-0.588	-0.539
yfND	b1586	predicted protein	orf; Unknown	K-12_b1586_yfND_s_at	2.04	2.458	0.451	2.577	-0.577	-1.214	-0.441
yocC	b1810	predicted protein	orf; Unknown	K-12_b1810_yocC_s_at	2.909	3.765	1.84	3.352	1.539	0.722	1.452
yehV	b1836	predicted protein	orf; Unknown	K-12_b1836_yehV_s_at	3.831	3.223	0.436	2.424	1.92	-0.022	0.329
yodD	b1953	predicted protein	orf; Unknown	K-12_b1953_yodD_s_at	2.788	3.252	0.087	1.7	0.906	0.327	-0.141
yegP	b2080	predicted protein	orf; Unknown	K-12_b2080_yegP_s_at	4.256	3.781	0.496	3.928	1.089	-0.251	-0.25
yehE	b2112	predicted protein	orf; Unknown	K-12_b2112_yehE_a_at	1.7	1.243	0.356	1.631	0.225	0.596	0.383
b2659	b2659	predicted protein	orf; Unknown	K-12_b2659_at	1.048	1.292	-0.001	0.66	0.833	-0.17	-0.076
ygaU	b2665	predicted protein	orf; Unknown	K-12_b2665_ygaU_s_at	3.427	2.989	0.508	3.434	0.291	0.393	1.235
ygaM	b2672	predicted protein	orf; Unknown	CFT073_c3223_ygaM_s_at	3.221	2.817	-0.009	2.399	0.484	-0.302	-0.474
yHFG	b3362	predicted protein	orf; Unknown	K-12_b3362_yHFG_s_at	2.773	2.766	0.026	2.034	0.128	0.262	0.009
yjBj	b4045	predicted stress response protein	orf; Unknown	K-12_b4045_yjBj_s_at	4.601	5.191	-0.026	3.495	0.334	0.842	1.44
yiaG	b3555	predicted transcriptional regulator	orf; Unknown	K-12_b3555_yiaG_s_at	4.68	4.799	0.153	5.188	-0.338	-0.923	-0.952
ybaT	b0486	predicted transporter	putative transport; Not classified	K-12_b0486_ybaT_s_at	1.586	0.686	0.488	1.217	1.028	0.893	0.02
yehZ	b2131	predicted transporter subunit: periplasmic-binding component of ABC	putative transport; Not classified	K-12_b2131_yehZ_s_at	3.594	3.166	0.789	5.358	1.237	-0.12	0.393
yhiO	b3494	predicted universal stress (ethanol tolerance) protein B	orf; Unknown	K-12_b3494_yhiO_s_at	2.89	3.095	0.616	1.713	0.476	0.51	-0.145
poxB	b0871	pyruvate dehydrogenase (pyruvate oxidase), thiamin-dependent, FAL	enzyme; Degradation of small molecules: Carbon compounds	K-12_b0871_poxB_s_at	1.645	1.104	-0.445	1.362	1.113	-1.006	-0.859
qor	b4051	quinolone oxidoreductase, NADPH-dependent	enzyme; Energy metabolism, carbon: Electron transport	K-12_b4051_qor_s_at	2.128	1.632	1.126	1.551	-0.491	-0.491	-0.904
boIA	b0435	regulator of penicillin binding proteins and beta lactamase transcript	putative regulator; Murein sacculus, peptidoglycan	K-12_b0435_boIA_s_at	3.239	4.214	1.313	2.267	0.782	0.677	0.314
ryjA	b4459	small RNA		K-12_b4459_ryjA_s_at	2.357	2.101	1.053	3.251	1.507	0.011	-0.288
fic	b3361	stationary-phase protein, cell division	phenotype; Cell division	K-12_b3361_fic_s_at	3.007	3.401	0.725	3.457	0.853	0.636	0.233
gabD	b2661	succinate-semialdehyde dehydrogenase I, NADP-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b2661_gabD_s_at	2.323	1.739	0.315	1.084	0.765	-0.047	-0.498
astC	b1748	succinylornithine transaminase, PLP-dependent	enzyme; Amino acid biosynthesis: Arginine	K-12_b1748_astC_s_at	1.915	2.256	0.895	2.128	1.806	0.469	0.201
sodC	b1646	superoxide dismutase, Cu, Zn	enzyme; Detoxification	K-12_b1646_sodC_s_at	3.442	4.074	1.151	3.834	0.887	0.516	0.258
thrL	b0001	thr operon leader peptide	leader; Amino acid biosynthesis: Threonine	EDL933_20001_thrL_x_at	1.379	0.949	0.129	-0.833	-0.378	0.264	-0.23
tam	b1519	trans-aconitate methyltransferase	putative enzyme; Not classified	K-12_b1519_tam_s_at	1.657	1.723	0.482	1.844	0.701	-0.23	-0.406
talA	b2464	transaldolase A	enzyme; Central intermediary metabolism: Non-oxidative branch, per	K-12_b2464_talA_s_at	2.342	1.641	-0.309	3.36	0.338	-0.612	-1.294
otsB	b1897	trehalose-6-phosphate phosphatase, biosynthetic	enzyme; Osmotic adaptation	K-12_b1897_otsB_s_at	4.085	4.373	0.444	4.642	0.592	0.192	-0.153
otsA	b1896	trehalose-6-phosphate synthase	enzyme; Osmotic adaptation	K-12_b1896_otsA_s_at	3.421	2.818	0.231	2.606	0.659	-0.337	-0.036

Venn 3.1
>2fold lower in Δ relAspOT, Δ rpoS, Δ lrp
11 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspOT
gabT	b2662	4-aminobutyrate aminotransferase, PLP-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conver	CFT073_c3210_gabT_a_at	2.736	1.322	0.661	2.972	2.21	0.965	-0.39
hdeD	b3511	acid-resistance membrane protein	orf; Unknown	K-12_b3511_hdeD_s_at	1.23	0.141	0.158	0.735	-0.109	1.212	0.049
hdeB	b3509	acid-resistance protein	orf; Unknown	K-12_b3509_hdeB_s_at	2.355	1.197	0.544	2.169	-0.046	-1.706	-2.22
gabP	b2663	gamma-aminobutyrate transporter	transport; Transport of small molecules: Carbohydrates, organic acids	K-12_b2663_gabP_s_at	1.656	0.491	0.453	1.693	0.657	0.757	-0.334
gabA	b3517	glutamate decarboxylase A, PLP-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b3517_gabA_s_at	1.417	0.333	0.38	2.096	-0.194	0.413	-0.354
gabB	b1493	glutamate decarboxylase B, PLP-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b1493_gabB_s_at	2.039	0.379	0.697	3.186	0.341	-0.13	-0.127
katE	b1732	hydroperoxidase HPII(III) (catalase)	enzyme; Detoxification	K-12_b1732_katE_s_at	2.261	0.512	0.401	2.583	1.33	-0.067	-0.302
xasA	b1492	predicted glutamate:gamma-aminobutyric acid antiporter	putative transport; Not classified	K-12_b1492_xasA_s_at	2.577	1.354	1.309	1.779	1.033	0.642	-0.009
yjgG	b3073	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent	putative enzyme; Amino acid biosynthesis: Arginine	K-12_b3073_yjgG_s_at	4.137	1.001	0.454	3.628	0.202	0.474	0.166
hdeA	b3510	stress response protein acid-resistance protein	orf; Unknown	K-12_b3510_hdeA_s_at	1.362	0.34	-0.063	2.021	-1.532	-2.181	-3.399
tktB	b2465	transketolase 2, thiamin-binding	enzyme; Central intermediary metabolism: Non-oxidative branch, per	K-12_b2465_tktB_s_at	2.782	1.748	0.292	3.461	0.855	-0.511	-0.847

Venn 2.1
>2fold lower in Δ relAspOT, Δ lrp
26 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspOT
leuA	b0074	2-isopropylmalate synthase	enzyme; Amino acid biosynthesis: Leucine	K-12_b0074_leuA_s_at	4.727	2.598	4.952	3.624	0.6	0.011	-0.162
leuB	b0073	3-isopropylmalate dehydrogenase	enzyme; Amino acid biosynthesis: Leucine	K-12_b0073_leuB_s_at	3.39	1.326	3.715	2.692	0.875	-0.84	-1.187
leuD	b0071	3-isopropylmalate isomerase subunit	enzyme; Amino acid biosynthesis: Leucine	K-12_b0071_leuD_s_at	3.084	0.596	3.02	1.306	0.074	-1.527	-1.679
leuC	b0072	3-isopropylmalate isomerase subunit, dehydratase component	enzyme; Amino acid biosynthesis: Leucine	K-12_b0072_leuC_s_at	3.51	1.084	3.501	2.279	-1.016	-1.87	-1.906
amn	b1982	AMP nucleosidase	enzyme; Salvage of nucleosides and nucleotides	K-12_b1982_amn_s_at	1.235	0.143	1.366	0.737	-1.355	-1.972	-2.65
serA	b2913	D-3-phosphoglycerate dehydrogenase	enzyme; Amino acid biosynthesis: Serine	K-12_b2913_serA_s_at	1.118	-2.173	1.205	-0.065	-2.685	-2.25	-2.682
dadA	b1189	D-amino acid dehydrogenase	enzyme; Degradation of small molecules: Amino acids	K-12_b1189_dadA_s_at	2.779	0.422	2.152	0.16	-1.703	-1.247	-1.58
add	b1623	adenosine deaminase	enzyme; Salvage of nucleosides and nucleotides	K-12_b1623_add_s_at	2.386	1.188	2.477	0.422	-0.49	-0.272	-0.232
dadX	b1190	alanine racemase 2, PLP-binding	enzyme; Degradation of small molecules: Amino acids	K-12_b1190_dadX_s_at	2.918	0.714	2.64	1.096	-0.415	-0.736	-1.344
ydiA	b1703	conserved protein	orf; Unknown	K-12_b1703_ydiA_s_at	1.161	0.084	1.204	0.43	-0.183	-1.453	-1.648

yjdB	b4109	conserved protein with nucleoside triphosphate hydrolase domain	phenotype; Not classified	K-12_b4109_yjdB_s_at	1.321	0.277	2.015	-0.494	-0.047	-0.272	-0.476
thrA	b0002	fused aspartokinase I -I- homoserine dehydrogenase I	enzyme; Amino acid biosynthesis: Threonine -I- enzyme; Amino acid	K-12_b0002_thrA_s_at	1.248	-0.289	1.082	-0.466	-1.071	-0.101	-0.464
maeB	b2463	fused malic enzyme predicted oxidoreductase -I- predicted phosphot	putative enzyme; Not classified	K-12_b2463_maeB_at	1.389	-0.002	0.892	-0.658	-0.471	0.843	0.005
glgP	b3428	glycogen phosphorylase	enzyme; Macromolecule synthesis, modification: Polysaccharides - (c	K-12_b3428_glgP_s_at	1.598	0.575	1.254	0.597	-0.353	-0.94	-1.526
glgA	b3429	glycogen synthase	enzyme; Macromolecule synthesis, modification: Polysaccharides - (c	K-12_b3429_glgA_s_at	1.928	0.726	1.855	-0.24	-0.057	-0.369	-1.155
thrB	b0003	homoserine kinase	enzyme; Amino acid biosynthesis: Threonine -I- enzyme; Amino acid	K-12_b0003_thrB_s_at	1.1	-1.199	1.003	-0.279	-0.975	-0.317	-0.673
aceA	b4015	isocitrate lyase	enzyme; Central intermediary metabolism: Glyoxylate bypass	K-12_b4015_aceA_s_at	1.309	-0.548	1.152	-0.144	-2.929	-1.298	-1.885
leuL	b0075	leu operon leader peptide	leader; Amino acid biosynthesis: Leucine	K-12_b0075_leuL_s_at	1.684	-0.611	1.62	-0.243	-1.808	-0.831	-1.935
fimA	b4314	major type 1 subunit fimbrin (pilin)	structural component; Surface structures	K-12_b4314_fimA_s_at	2.738	-2.818	2.937	-0.431	2.395	-0.2	-0.651
aceB	b4014	malate synthase A	enzyme; Central intermediary metabolism: Glyoxylate bypass	K-12_b4014_aceB_s_at	1.59	-0.33	1.687	0.781	-1.858	-1.736	-1.618
rhtB	b3824	neutral amino-acid efflux system	orf; Unknown	EDL933_Z5345_yigK_s_at	1.027	-0.029	1.758	0.981	0.339	0.633	-0.484
yfBT	b2293	predicted hydrolase or phosphatase	putative enzyme; Not classified	K-12_b2293_yfBT_s_at	2.033	1	1.645	0.785	0.325	-0.045	0.368
yilD	b0832	predicted peptide transporter subunit: membrane component of ABC	putative transport; Not classified	K-12_b0832_yilD_s_at	1.452	0.087	1.348	0.507	0.771	0.455	-0.396
yilB	b0830	predicted peptide transporter subunit: periplasmic-binding componen	putative transport; Not classified	K-12_b0830_yilB_s_at	3.55	2.546	3.587	1.789	2.148	0.143	0.406
yfD	b2579	pyruvate formate lyase subunit	putative enzyme; Energy metabolism, carbon: Anaerobic respiration	K-12_b2579_yfD_s_at	1.864	0.812	1.962	0.668	0.865	-0.591	-1.219
rybA	b4416	small RNA		K-12_b4416_rybA_s_at	2.448	1.437	1.925	-0.067	1.456	0.706	0.846

Venn 1.1
>2fold lower in Δ lrp
2 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
ydcF	b1414	conserved protein	orf; Unknown	K-12_b1414_ydcF_s_at	1.002	-0.117	1.148	-0.688	0.005	0.263	0.868
ydjN	b1729	predicted transporter	putative enzyme; Not classified	K-12_b1729_ydjN_s_at	4.235	2.957	3.957	0.887	3.058	3.601	4.331

Venn 1.2
>2fold lower in Δ rpoS
6 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
adhP	b1478	alcohol dehydrogenase, 1-propanol preferring	enzyme; Energy metabolism, carbon: Anaerobic respiration	K-12_b1478_adhP_s_at	2.109	1.497	0.465	2.433	1.319	0.291	1.214
ybaA	b0456	conserved protein	orf; Unknown	K-12_b0456_ybaA_s_at	1.507	1.134	0.362	1.534	1.131	0.685	1.368
yqaE	b2666	predicted membrane protein	orf; Unknown	K-12_b2666_yqaE_s_at	1.994	1.407	0.16	0.6	0.237	1.195	1.05
yaiA	b0389	predicted protein	orf; Unknown	K-12_b0389_yaiA_s_at	2.306	2.505	0.191	1.058	-0.415	0.991	1.836
yqjF	b3101	predicted quinol oxidase subunit	orf; Unknown	K-12_b3101_yqjF_s_at	1.079	0.825	-0.037	1.168	1.542	1.116	0.914
hnr	b1235	response regulator of RpoS	regulator; Basic proteins - synthesis, modification	K-12_b1235_hnr_s_at	1.847	1.59	0.715	2.072	0.097	0.854	1.145

Venn 1.3
>2fold lower in Δ relAspoT
212 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
cysH	b2762	3'-phosphoadenosine 5'-phosphosulfate reductase	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2762_cysH_s_at	5.638	5.594	5.355	3.987	3.787	2.261	2.092
aroD	b1693	3-dehydroquinate dehydratase	enzyme; Amino acid biosynthesis: Chorismate	K-12_b1693_aroD_s_at	2.053	1.687	1.887	1.069	0.006	-0.574	-1.17
aroG	b0754	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalani	enzyme; Amino acid biosynthesis: Phenylalanine	K-12_b0754_aroG_s_at	1.319	0.763	1.463	1.057	-0.445	-0.379	-0.479
ydcE	b1461	4-oxalocrotonate tautomerase	orf; Unknown	K-12_b1461_ydcE_s_at	1.715	1.247	1.881	0.699	0.538	0.221	0.465
pfkB	b1723	6-phosphofructokinase II	enzyme; Energy metabolism, carbon: Glycolysis	K-12_b1723_pfkB_s_at	2.728	2.755	2.685	2.38	1.099	0.533	0.748
ybHE	b0767	6-phosphogluconolactonase	orf; Not classified	K-12_b0767_ybHE_s_at	1.223	0.934	0.316	0.281	-0.63	-1.177	-1.378
ssrS	b2911	6S regulatory RNA	RNA; Ribosomal and stable RNAs -I- modulates promoter use via inte	K-12_b2911_ssrS_s_at	1.544	1.204	1.007	0.906	-0.857	-0.167	0.131
hdhA	b1619	7-alpha-hydroxysteroid dehydrogenase, NAD-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b1619_hdhA_s_at	2.722	2.491	2.294	2.001	1.282	-0.781	-0.394
clpA	b0882	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine pro	enzyme; Degradation of proteins, peptides, glyco	K-12_b0882_clpA_s_at	2.802	2.793	2.787	1.847	0.939	-0.425	-0.209
yfFO	b2446	CPZ-55 prophage; predicted protein	orf; Unknown	K-12_b2446_yfFO_s_at	1.028	1.093	0.641	1.267	0.922	-0.283	-0.275
b2449	b2449	CPZ-55 prophage; predicted protein	orf; Unknown	K-12_b2449_at	1.541	1.35	1.576	1.117	0.257	-0.123	-0.166
yedO	b1919	D-cysteine desulfhydrase, PLP-dependent	putative enzyme; Not classified	K-12_b1919_yedO_s_at	2.239	2.123	1.832	0.889	0.904	0.312	0.402
did	b2133	D-lactate dehydrogenase, FAD-binding, NADH independent	enzyme; Energy metabolism, carbon: Aerobic respiration	K-12_b2133_did_s_at	1.255	0.579	1.267	0.796	-0.826	-1.786	-1.797
sbmC	b2009	DNA gyrase inhibitor	orf; Unknown function	K-12_b2009_sbmC_s_at	2.574	2.659	2.045	2.818	1.014	0.451	1.049
b2805	b2805	DNA-binding transcriptional activator	regulator; Degradation of small molecules: Carbon compounds	K-12_b2805_fucR_s_at	1.563	1.274	1.744	0.815	0.537	0.016	-0.443
cspD	b1040	DNA-binding transcriptional activator in two-component regulatory sy	putative regulator; Not classified	K-12_b1040_cspD_s_at	2.93	2.945	3.327	2.247	0.63	0.614	0.585
cbI	b1987	DNA-binding transcriptional activator of cysteine biosynthesis	regulator; Amino acid biosynthesis: Cysteine	K-12_b1987_cbI_s_at	2.53	2.595	2.021	1.299	1.894	0.688	0.089
iciA	b2916	DNA-binding transcriptional activator, replication initiation inhibitor	regulator; DNA - replication, repair, restriction/modification	K-12_b2916_iciA_s_at	1.041	1.126	1.148	0.269	-0.617	-0.819	-1.408
crp	b3357	DNA-binding transcriptional dual regulator	regulator; Global regulatory functions	K-12_b3357_crp_s_at	1.291	1.51	1.248	-5.177	-0.442	-0.115	-0.293
folE	b2153	GTP cyclohydrolase I	enzyme; Biosynthesis of cofactors, carriers: Folic acid	K-12_b2153_folE_s_at	1.049	0.862	1.07	0.535	-1.282	-1.864	-0.584
ybiK	b0828	L-asparaginase	orf; Not classified	K-12_b0828_ybiK_s_at	3.514	3.813	3.701	3.089	2.089	1.652	1.108
fucU	b2804	L-fucose mutarotase	phenotype; Degradation of small molecules: Carbon compounds	K-12_b2804_fucU_s_at	2.303	2.213	2.351	1.299	0.442	-0.031	0.231
sdaA	b1814	L-serine deaminase I	enzyme; Degradation of small molecules: Amino acids	K-12_b1814_sdaA_s_at	1.375	1.82	0.904	0.777	0.767	-1.031	-0.414
ceIA	b1738	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	enzyme; Transport of small molecules: Carbohydrates, oranic acids,	K-12_b1738_ceIA_s_at	2.699	2.384	2.698	1.894	1.561	1.243	1.299
ampD	b0110	N-acetyl-anhydromuramyl-L-alanine amidase	regulator; Not classified	K-12_b0110_ampD_s_at	1.37	1.695	1.689	0.594	-0.665	0.169	-1.077
nemA	b1650	N-ethylmaleimide reductase, FMN-linked	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b1650_nemA_s_at	1.078	0.58	0.883	0.85	0.921	-0.377	-0.295
nadE	b1740	NAD synthetase, NH3/glutamine-dependent	enzyme; Biosynthesis of cofactors, carriers: Pyridine nucleotide	K-12_b1740_nadE_s_at	1.018	0.584	1.324	0.465	-0.667	-2.137	-1.587
acpD	b1412	NADH-azoreductase, FMN-dependent	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b1412_acpD_s_at	1.726	1.849	2.088	1.02	0.018	-0.902	-0.759
ilvG	b4988	acetoaldehyde synthase II, large subunit (pseudogene)	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b4988_ilvG_s_at	4.511	5.36	4.624	5.511	2.614	2.801	2.503
argE	b3957	acetylornithine deacetylase	enzyme; Amino acid biosynthesis: Arginine	K-12_b3957_argE_s_at	1.307	1.171	1.225	0.792	-0.596	-1.119	-0.894
asr	b1597	acid shock-inducible periplasmic protein	phenotype; Not classified	K-12_b1597_asr_s_at	1.215	1.872	0.896	1.606	1.396	-0.615	-0.293
fadE	b0221	acyl coenzyme A dehydrogenase	putative enzyme; Not classified	K-12_b0221_fadE_s_at	1.735	1.195	1.268	1.207	0.714	1.405	0.467
cysC	b2750	adenosine 5'-phosphosulfate kinase	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2750_cysC_s_at	4.154	3.243	3.839	2.541	2.74	1.279	1.217
asd	b3433	aspartate-semialdehyde dehydrogenase, NAD(P)-binding	enzyme; Amino acid biosynthesis: Lysine	K-12_b3433_asd_s_at	1.204	0.875	1.614	0.402	-1.196	-1.933	-2.576
ushA	b0480	bifunctional UDP-sugar hydrolase and 5'-nucleotidase	enzyme; Central intermediary metabolism: Suqar-nucleotide biosynt	K-12_b0480_ushA_s_at	1.054	0.731	0.898	1.063	0.666	-0.299	-0.605
ilvE	b3770	branched-chain amino-acid aminotransferase	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3770_ilvE_s_at	3.008	3.338	3.201	0.488	-0.033	1.339	0.726
cbiA	b0598	carbon tetravalent protein	phenotype; Global regulatory functions	K-12_b0598_cbiA_s_at	1.592	1.71	0.885	1.027	1.195	0.027	0.171
ybhO	b0789	cardiolipin synthase 2	orf; Not classified	K-12_b0789_ybhO_s_at	1.465	1.378	0.465	2.309	1.658	-0.577	-0.894
yfA	b2597	cold shock protein associated with 30S ribosomal subunit	putative regulator; Not classified	K-12_b2597_yfA_s_at	2.195	1.757	1.979	0.788	0.785	0.07	-0.531
csuD	b0880	cold shock protein homolog	phenotype; Not classified	K-12_b0880_cspD_s_at	3.875	3.916	4.055	1.766	1.727	0.427	0.431
ybgE	b0735	conserved inner membrane protein	orf; Unknown	K-12_b0735_ybgE_s_at	1.294	0.632	0.809	0.149	0.031	0.464	0.105
yedI	b1958	conserved inner membrane protein	orf; Unknown	K-12_b1958_yedI_s_at	1.434	1.777	1.008	1.105	0.171	0.293	0.383
yohJ	b2141	conserved inner membrane protein	orf; Unknown	K-12_b2141_yohJ_s_at	1.231	0.653	1.457	1.561	0.837	1.055	0.058
ygbE	b2749	conserved inner membrane protein	putative enzyme; Not classified	K-12_b2749_ygbE_s_at	1.989	1.852	2.159	1.549	0.587	1.161	0.39

ydgC	b1607	conserved inner membrane protein associated with alga	Unknown	K-12_b1607_ydgC_s_at	2.211	2.025	2.625	1.576	1.231	0.961	1.025
ybgI	b0710	conserved metal-binding protein	Unknown	K-12_b0710_ybgI_s_at	1.089	1.134	1.375	0.673	-0.24	-0.267	-0.937
yecA	b1908	conserved metal-binding protein	Unknown	K-12_b1908_yecA_s_at	2.184	2.559	2.853	2.121	0.185	0.508	0.96
yaeH	b0163	conserved protein	Unknown	K-12_b0163_yaeH_s_at	1.87	1.47	1.647	1.133	0.975	-0.44	-0.348
yibA	b0515	conserved protein	Unknown	K-12_b0515_yibA_s_at	1.341	1.28	1.454	0.31	-0.43	-0.927	-0.634
yblI	b0803	conserved protein	Unknown	K-12_b0803_yblI_s_at	1.163	1.263	0.245	0.975	0.395	-0.139	-0.368
yilH	b0836	conserved protein	Unknown	K-12_b0836_yilH_s_at	4.304	4.011	4.131	2.805	1.87	0.251	-0.113
yblJ	b0844	conserved protein	Unknown	K-12_b0844_yblJ_s_at	1.415	0.959	1.882	0.773	0.616	0.25	-0.06
ycbK	b0926	conserved protein	Unknown	K-12_b0926_ycbK_s_at	1.567	1.666	1.923	1.96	-0.321	0.722	0.15
yceH	b1067	conserved protein	Unknown	K-12_b1067_yceH_s_at	1.647	1.209	1.564	0.492	0.897	0.354	-0.403
ycfP	b1108	conserved protein	Unknown	K-12_b1108_ycfP_s_at	1.586	1.753	1.179	1.721	-0.706	-0.167	-0.189
yciF	b1258	conserved protein	Unknown	K-12_b1258_yciF_s_at	1.175	1.13	0.237	1.954	1.215	-0.002	-0.044
yihQ	b1664	conserved protein	Unknown	K-12_b1664_yihQ_s_at	1.615	1.69	1.249	1.374	0.505	-0.591	0.021
yeeO	b1792	conserved protein	Unknown	K-12_b1792_yeeO_s_at	1.579	1.694	1.131	-0.229	-0.235	-0.836	-0.32
yeeX	b2007	conserved protein	Unknown	K-12_b2007_yeeX_s_at	1.367	1.449	1.376	0.535	0.311	-0.874	0.025
yfbU	b2294	conserved protein	Unknown	K-12_b2294_yfbU_s_at	1.525	1.064	1.079	-0.253	-1.93	-0.81	0.003
yggE	b2922	conserved protein	Unknown	K-12_b2922_yggE_s_at	1.12	0.572	0.6	1.942	-0.603	-0.637	-0.103
ysmG	b3284	conserved protein	Unknown	K-12_b3284_ysmG_s_at	1.198	1.426	1.247	0.722	-0.096	0.014	0.198
yihD	b3858	conserved protein	Unknown	K-12_b3858_yihD_s_at	1.074	0.737	1.393	0.924	-0.033	-1.034	-1.077
yilS	b3922	conserved protein	Unknown	K-12_b3922_yilS_s_at	2.483	2.736	2.645	2.749	1.88	0.829	0.152
yjeI	b4144	conserved protein	Unknown	K-12_b4144_yjeI_s_at	1.089	0.949	1.266	-0.01	0.122	0.398	-0.52
yjFO	b4189	conserved protein	Unknown	K-12_b4189_yjFO_s_at	1.579	1.901	0.785	1.357	1.232	0.406	0.461
yaeP	b4406	conserved protein	Unknown	K-12_b4406_yaeP_s_at	2.228	2.044	2.196	1.435	0.974	-0.232	0.021
erfK	b1990	conserved protein with NAD(P)-binding	Unknown	K-12_b1990_erfK_s_at	2.006	2.279	1.343	2.189	1.115	1.06	0.955
phoH	b1020	conserved protein with nucleoside triphosphate hydrolase domain	Unknown	K-12_b1020_phoH_s_at	4.143	4.418	4.164	2.271	1.347	0.024	0.617
csaG	b1042	cryptic curlin major subunit	Unknown	K-12_b1042_csaG_s_at	3.245	2.999	3.543	1.847	-0.177	0.972	0.549
csaB	b1041	curlin nucleator protein, minor subunit in curlin complex	Unknown	K-12_b1041_csaB_s_at	1.417	1.514	1.736	1.606	0.236	0.435	0.012
cfa	b1661	cytochrome fatty acyl phospholipid synthase (unsaturated-phospholipid synthase)	Unknown	K-12_b1661_cfa_s_at	2.865	2.382	2.527	1.312	-0.08	-0.014	0.991
cysK	b2414	cysteine synthase A, O-acetylserine sulfhydrylase A subunit	Unknown	K-12_b2414_cysK_s_at	3.913	3.79	3.622	2.643	3.113	3.33	2.795
cysM	b2421	cysteine synthase B (O-acetylserine sulfhydrylase B)	Unknown	K-12_b2421_cysM_s_at	2.914	2.701	3.09	3.3	1.383	1.741	1.329
flhY	b1920	cystine transporter subunit -1- periplasmic-binding component of ABC transporter	Unknown	K-12_b1920_flhY_s_at	2.737	2.491	2.292	1.224	1.269	0.283	0.149
cydA	b0733	cytochrome d terminal oxidase, subunit I	Unknown	K-12_b0733_cydA_s_at	1.041	0.779	1.131	-0.269	-0.716	-0.672	-0.568
cydB	b0734	cytochrome d terminal oxidase, subunit II	Unknown	K-12_b0734_cydB_s_at	1.618	1.694	1.631	0.341	0.129	-0.206	0.37
nlpA	b3661	cytoplasmic membrane lipoprotein-28	Unknown	K-12_b3661_nlpA_s_at	3.5	3.38	2.995	0.854	0.93	2.193	0.891
ilvD	b3771	dihydroxyacid dehydratase	Unknown	K-12_b3771_ilvD_s_at	3.483	3.512	3.329	1.73	0.076	1.607	1.354
ymfI	b1143	e14 prophage; predicted protein	Unknown	K-12_b1143_ymfI_s_at	1.681	1.044	1.785	-0.017	-0.243	-0.819	-0.451
focA	b0904	formate transporter	Unknown	K-12_b0904_focA_s_at	1.432	1.659	0.91	0.54	-0.023	-0.263	-0.659
putA	b1014	fused DNA-binding transcriptional regulator -1- proline dehydrogenase	Unknown	K-12_b1014_putA_s_at	1.912	1.27	1.543	1.355	0.286	-0.092	-0.367
yfcX	b2341	fused enoyl-CoA hydratase and epimerase -1- 3-hydroxyacyl-CoA lyase	Unknown	K-12_b2341_yfcX_s_at	1.386	1.11	1.663	2.226	1.751	-0.525	-0.548
fruA	b2167	fused fructose-specific PTS enzymes: IIB component -1- IIC component	Unknown	K-12_b2167_fruA_s_at	1.218	1.249	1.35	1.745	1.796	0.623	0.06
trpC	b1262	fused indole-3-glycerol phosphate synthetase -1- N-(5-phosphoribosyl)-L-tryptophan synthase	Unknown	K-12_b1262_trpC_s_at	1.198	1.636	1.53	1.622	0.205	-0.679	-0.402
yliA	b0829	fused predicted peptide transport subunits of ABC superfamily: ATP-binding subunit	Unknown	K-12_b0829_yliA_s_at	3.064	2.831	3.151	1.893	1.835	0.035	0.868
glgC	b3430	glucose-1-phosphate adenylyltransferase	Unknown	K-12_b3430_glgC_s_at	2.02	1.03	2.085	0.474	0.363	-1.72	-1.685
glgB	b3431	glucose-1-phosphate transporter subunit -1- periplasmic-binding protein	Unknown	K-12_b3431_glgB_s_at	1.181	0.954	1.216	1.157	-0.403	-1.193	-0.501
gdhA	b1761	glutamate dehydrogenase, NADP-specific	Unknown	K-12_b1761_gdhA_s_at	1.299	0.82	1.188	-0.988	-0.09	0.075	-0.175
grxB	b1064	glutaredoxin 2 (Grx2)	Unknown	K-12_b1064_grxB_s_at	1.756	1.178	1.65	0.733	-1.336	-1.491	-1.284
gst	b1635	glutathione S-transferase	Unknown	K-12_b1635_gst_s_at	2.709	2.448	2.684	1.082	0.113	0.158	1.155
ilvL	b3766	ilvG operon leader peptide	Unknown	K-12_b3766_ilvL_s_at	1.338	2.041	1.478	0.579	0.169	0.625	-0.974
yccA	b0970	inner membrane protein	Unknown	K-12_b0970_yccA_s_at	2.298	1.682	2.27	-0.026	0.407	0.713	1.298
ilvC	b3774	ketol-acid reductoisomerase, NAD(P)-binding	Unknown	K-12_b3774_ilvC_s_at	1.208	0.576	1.699	0.158	-0.085	-0.393	0.23
argT	b2310	lysine/arginine/ornithine transporter subunit -1- periplasmic-binding protein	Unknown	K-12_b2310_argT_s_at	1.323	0.512	1.225	0.879	0.285	0.32	0.264
glcB	b2976	malate synthase G	Unknown	K-12_b2976_glcB_s_at	1.069	0.76	0.886	1.555	0.601	-0.56	-0.664
yggB	b2924	mechanosensitive channel	Unknown	K-12_b2924_yggB_s_at	1.263	2.052	2.306	3.045	1.147	0.143	0.737
msrA	b4219	methionine sulfoxide reductase A	Unknown	K-12_b4219_msrA_s_at	1.952	2.164	1.791	0.99	0.449	-0.609	-1.181
moaB	b0782	molybdopterin biosynthesis protein B	Unknown	K-12_b0782_moaB_s_at	1.17	0.245	1.352	-0.585	-0.706	-0.847	-0.929
tesA	b0494	multifunctional acyl-CoA thioesterase I and protease I and lysophospholipase	Unknown	K-12_b0494_tesA_s_at	1.353	1.301	1.614	-0.131	-0.013	-0.152	-0.661
ycjI	b1326	murein peptide amidase A	Unknown	K-12_b1326_ycjI_s_at	1.187	1.138	1.34	1.327	0.255	0.27	-0.256
napA	b2206	nitrate reductase, periplasmic, large subunit	Unknown	K-12_b2206_napA_s_at	1.028	0.591	1.379	1.249	2.334	0.134	-0.479
napB	b2203	nitrate reductase, small, cytochrome C550 subunit, periplasmic	Unknown	K-12_b2203_napB_s_at	1.076	0.732	1.453	0.77	1.014	0.146	-0.153
nuoP	b2964	nucleoside transporter	Unknown	K-12_b2964_nuoP_s_at	1.026	0.602	0.877	0.954	0.134	-0.164	-0.400
csaG	b1037	outer membrane lipoprotein	Unknown	K-12_b1037_csaG_s_at	1.978	1.712	2.169	1.437	0.068	-0.115	0.386
slxB	b1641	outer membrane lipoprotein	Unknown	K-12_b1641_slxB_s_at	1.009	1.055	0.662	0.15	-0.325	-0.075	-0.098
pepT	b1127	peptidase T	Unknown	K-12_b1127_pepT_s_at	2.445	2.134	1.632	1.879	0.72	0.324	-0.734
pgsA	b1912	phosphatidylglycerophosphate synthetase	Unknown	K-12_b1912_pgsA_s_at	1.109	0.286	1.173	-0.629	0.338	0.603	-0.143
ppsA	b1702	phosphoenolpyruvate synthase	Unknown	K-12_b1702_ppsA_s_at	1.418	0.706	1.646	-0.507	-1.518	-1.974	-1.286
csuE	b1039	predicted transport protein	Unknown	K-12_b1039_csuE_s_at	1.882	1.574	2.648	2.318	0.344	0.302	-0.148
yjiR	b4263	predicted ATPase	Unknown	K-12_b4263_yjiR_s_at	1.072	0.876	0.303	1.644	0.653	-0.168	-0.12
yaeV	b0219	predicted C-N hydrolase family amidase, NAD(P)-binding	Unknown	K-12_b0219_yaeV_s_at	1.104	1.518	0.641	1.004	0.818	-0.048	-0.204
yeeT	b1799	predicted DNA-binding transcriptional regulator	Unknown	K-12_b1799_yeeT_s_at	1.718	1.156	1.197	1.608	0.657	0.181	-0.246
yghU	b2989	predicted S-transferase	Unknown	K-12_b2989_yghU_s_at	1.692	0.96	1.528	2.435	0.758	-0.159	-0.792
yhhY	b3441	predicted acetyltransferase	Unknown	K-12_b3441_yhhY_s_at	1.318	1.962	1.438	0.494	-0.447	0.132	-0.914
yccX	b0968	predicted acylphosphatase	Unknown	K-12_b0968_yccX_s_at	2.247	2.521	2.007	2.319	0.728	0.128	-0.428
ynaC	b1448	predicted acyltransferase with acyl-CoA N-acyltransferase domain	Unknown	K-12_b1448_ynaC_s_at	1.541	1.163	1.537	1.166	0.384	-0.171	-0.679
eiaA	b2267	predicted acyltransferase with acyl-CoA N-acyltransferase domain	Unknown	K-12_b2267_eiaA_s_at	1.184	1.077	1.509	1.729	-0.996	0.157	-0.169
yneI	b1525	predicted aldehyde dehydrogenase	Unknown	K-12_b1525_yneI_s_at	1.37	1.114	1.538	0.887	0.744	-0.314	-0.077
ycbB	b0925	predicted carboxypeptidase	Unknown	K-12_b0925_ycbB_s_at	1.686	1.831	0.87	0.909	0.217	0.112	0.36
ytfB	b4206	predicted cell envelope opacity-associated protein	Unknown	K-12_b4206_ytfB_s_at	1.442	1.939	1.591	1.207	0.864	-0.243	0.04
ybiC	b0801	predicted dehydrogenase	Unknown	K-12_b0801_ybiC_s_at	1.7	0.803	1.929	0.833	0.272	0.329	0.029
yddV	b1490	predicted diguanylate cyclase	Unknown	K-12_b1490_yddV_s_at	1.289	1.005	0.494	0.597	0.207	-0.167	0.061
yciI	b1251	predicted enzyme	Unknown	K-12_b1251_yciI_s_at	1.859	1.209	1.855	0.138	0.31	-0.939	-1.375
yfcF	b2301	predicted enzyme	Unknown	K-12_b2301_yfcF_s_at	1.326	0.693	0.355	1.105	0.694	0.419	-0.307
ybgJ	b0712	predicted enzyme subunit	Unknown	K-12_b0712_ybgJ_s_at	1.089	0.874	1.151	-0.321	-0.31	-0.381	-0.816
ybgK	b0712	predicted enzyme subunit	Unknown	K-12_b0712_ybgK_s_at	1.11	1.396	1.022	1.196	-1.495	-0.328	-1.017
yelG	b2154	predicted esterase	Unknown	K-12_b2154_yelG_s_at	1.187	0.538	1.24	0.035	-0.242	0.048	-0.564
yliJ	b0838	predicted glutathione S-transferase	Unknown	K-12_b0838_yliJ_s_at	2.538	2.088	2.469	1.551	0.279	-0.333	-0.805
yibF	b3592	predicted glutathione S-transferase	Unknown	K-12_b3592_yibF_s_at	1.623	1.067	0.838	0.399	-0.375	0.385	-0.862
btuE	b1710	predicted glutathione peroxidase	Unknown	K-12_b1710_btuE_s_at	1.012	0.597	0.061	1.799	-0.379	-0.993	-0.445
b2999	b2999	predicted hydrolase (pseudogene)	Unknown	K-12_b2999_s_at	1.05	0.98	0.81	1.246	0.123	-0.104	-0.078
ybhL	b0786	predicted inner membrane protein	Unknown	K-12_b0786_ybhL_s_at	1.373	1.228	0.481	0.395	0.06	0.429	0.014

ymgE	b1195	predicted inner membrane protein	orf; Unknown	K-12_b1195_ymgE_s_at	1.213	1.412	0.384	2.983	1.033	0.536	0.092
ydiK	b1688	predicted inner membrane protein	orf; Unknown	K-12_b1688_ydiK_s_at	2.098	2.261	1.865	0.738	1.533	0.516	0.716
yfdC	b2347	predicted inner membrane protein	putative transport; Not classified	K-12_b2347_yfdC_s_at	1.07	0.91	0.441	2.69	0.51	0.175	-0.06
yphA	b2543	predicted inner membrane protein	orf; Unknown	K-12_b2543_yphA_s_at	1.312	1.017	0.396	1.49	0.869	1.018	-0.166
b2670	b2670	predicted inner membrane protein	orf; Unknown	CT073_b2670_yphA_s_at	2.408	2.31	2.821	0.81	0.512	0.378	0.301
yhaH	b3103	predicted inner membrane protein	putative carrier; Not classified	K-12_b3103_yhaH_s_at	1.365	1.506	0.467	1.156	0.262	0.048	-0.213
ycgM	b1180	predicted isomerase/hydrolase	putative enzyme; Not classified	K-12_b1180_ycgM_s_at	2.825	2.588	2.962	1.056	1.206	0.882	1.245
yclW	b1287	predicted oxidoreductase	putative enzyme; Not classified	K-12_b1287_yclW_s_at	2.69	2.145	2.712	1.757	1.423	0.669	0.53
yjdJ	b1765	predicted oxidoreductase	orf; Unknown	K-12_b1765_yjdJ_s_at	1.167	1.263	1.598	0.499	0.63	0.196	-0.256
mvjM	b1068	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain	putative factor; Not classified	K-12_b1068_mvjM_s_at	1.448	1.518	1.365	0.987	1.072	-0.477	-0.162
tas	b2834	predicted oxidoreductase, NAD(P)(H)-dependent aldo-keto reductase	orf; Unknown	K-12_b2834_tas_s_at	1.303	1.355	1.302	1.637	0.792	-0.654	0.133
yhdH	b3253	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b3253_yhdH_s_at	1.322	1.262	0.957	1.393	-0.625	-0.895	-1.649
yqfA	b2899	predicted oxidoreductase, inner membrane subunit	putative enzyme; Not classified	K-12_b2899_yqfA_s_at	2.808	2.807	2.986	2.881	1.466	1.685	1.309
ydgD	b1598	predicted peptidase	orf; Unknown	O157_Ec2304_ydgD_s_at	1.644	1.674	0.762	2.131	0.883	-0.137	0.34
tlidD	b3244	predicted peptidase	phenotype; Not classified	K-12_b3244_tlidD_s_at	1.026	1.349	0.605	0.922	-0.232	-0.674	-0.246
yliC	b0831	predicted peptide transporter subunit: membrane component of ABC	putative transport; Not classified	K-12_b0831_yliC_s_at	2.779	1.928	2.864	1.516	1.869	0.826	0.336
yjbA	b4030	predicted phosphate starvation inducible protein	orf; Unknown	K-12_b4030_yjbA_s_at	4.062	4.9	4.068	1.407	1.787	1.391	0.122
yaiB	b0382	predicted protein	orf; Unknown	K-12_b0382_yaiB_s_at	3.421	3.49	3.736	3.186	2.396	1.263	1.146
ybeH	b0625	predicted protein	orf; Unknown	K-12_b0625_ybeH_s_at	2.041	1.888	1.276	2.202	1.213	1.305	0.473
ybfA	b0699	predicted protein	orf; Unknown	K-12_b0699_ybfA_s_at	2.492	2.397	2.71	1.768	1.377	0.381	0.612
yceF	b1087	predicted protein	orf; Unknown	K-12_b1087_yceF_s_at	2.548	2.17	2.301	1.446	1.134	0.815	0.672
ycfL	b1104	predicted protein	orf; Unknown	K-12_b1104_ycfL_s_at	1.17	0.9	0.908	0.158	-1.147	-0.86	-0.554
ycgJ	b1177	predicted protein	orf; Unknown	K-12_b1177_ycgJ_s_at	1.119	1.153	1.442	1.048	-0.125	-0.244	-0.283
ydiH	b1685	predicted protein	orf; Unknown	K-12_b1685_ydiH_s_at	1.677	1.879	2.254	1.576	-0.281	-0.721	-0.031
ydiZ	b1724	predicted protein	orf; Unknown	K-12_b1724_ydiZ_s_at	4.776	4.9	3.946	5.859	1.574	0.152	0.572
yodG	b1957	predicted protein	orf; Unknown	K-12_b1957_yodG_s_at	2.974	3.684	2.184	4.524	1.086	1.337	0.766
yfgG	b2504	predicted protein	orf; Unknown	K-12_b2504_yfgG_s_at	1.052	0.887	0.947	-0.043	-1.267	0.226	-0.505
yfIL	b2602	predicted protein	orf; Unknown	K-12_b2602_yfIL_s_at	1.188	1.535	1.046	2.277	0.446	0.09	-0.51
ygeA	b2840	predicted racemase	putative transport; Drug/analog sensitivity	K-12_b2840_ygeA_s_at	1.135	1.775	1.401	1.912	0.723	0.38	-0.145
yedY	b1971	predicted reductase	putative enzyme; Not classified	K-12_b1971_yedY_s_at	1.676	1.383	0.993	1.628	0.884	0.508	0.436
ypdB	b2381	predicted response regulator in two-component system with ypdA	putative regulator; Not classified	K-12_b2381_ypdB_s_at	1.008	1.018	0.659	1.076	0.182	-0.288	-0.712
yjdC	b4135	predicted transcriptional regulator	orf; Unknown	K-12_b4135_yjdC_s_at	1.664	1.637	1.172	1.658	-0.029	-0.988	-1.47
ybhK	b0780	predicted transferase with NAD(P)-binding Rossmann-fold domain	putative structure; Not classified	K-12_b0780_ybhK_s_at	1.288	1.521	1.273	0.36	0.514	0.601	0.103
ybiB	b0800	predicted transferase/phosphorylase	putative enzyme; Not classified	K-12_b0800_ybiB_s_at	2.033	2.251	1.765	0.66	-0.756	-0.369	0.08
csfJ	b1038	predicted transport protein	structural component; Surface structures	K-12_b1038_csfJ_s_at	3.039	2.964	3.488	2.646	0.282	0.518	0.787
yhiE	b3523	predicted transporter subunit: ATP-binding component of ABC superfamily	putative transport; Not classified	K-12_b3523_yhiE_s_at	1.646	0.96	1.464	0.422	-0.053	1.073	-0.739
yecC	b1917	predicted transporter subunit: membrane component of ABC superfamily	putative transport; Not classified	K-12_b1917_yecC_s_at	2.068	1.602	1.603	0.438	0.632	0.412	0.606
yecS	b1918	predicted transporter subunit: membrane component of ABC superfamily	putative transport; Not classified	K-12_b1918_yecS_s_at	2.466	1.704	1.995	0.292	0.428	0.519	0.722
yagT	b0286	predicted xanthine dehydrogenase, 2Fe-2S subunit	putative enzyme; Not classified	K-12_b0286_yagT_s_at	1.18	1.732	0.57	2.277	1.054	0.116	-0.137
yfdZ	b2379	predicted aminotransferase, PLP-dependent	putative enzyme; Not classified	K-12_b2379_yfdZ_s_at	1.812	2.146	1.533	1.065	0.52	0.105	-0.194
ycfF	b1103	purine nucleoside phosphoramidase	orf; Unknown	K-12_b1103_ycfF_s_at	1.491	0.828	0.872	0.487	-1.114	-0.941	-0.239
potF	b0854	putrescine transporter subunit: periplasmic-binding component of ABC superfamily	transport; Transport of small molecules: Amino acids, amines	K-12_b0854_potF_s_at	1.295	0.539	0.51	1.365	-0.737	-1.84	-2.301
pdxJ	b2564	pyridoxine 5'-phosphate synthase	enzyme; Biosynthesis of cofactors, carriers: Pyridoxine	K-12_b2564_pdxJ_s_at	1.448	0.813	1.625	0.973	-0.171	-0.657	-0.258
pykA	b1854	pyruvate kinase II	enzyme; Energy metabolism, carbon: Glycolysis	K-12_b1854_pykA_s_at	1.395	1.122	1.005	0.316	0.815	1.348	-1.082
ygiN	b3029	quinol monooxygenase	orf; Unknown	K-12_b3029_ygiN_s_at	1.085	0.713	1.359	0.238	-0.314	-0.56	-0.557
yjIA	b0881	regulatory protein for CtpA substrate specificity	orf; Unknown	K-12_b0881_yjIA_s_at	1.704	2.005	1.842	1.828	0.141	-0.498	-0.975
rydB	b4430	regulatory sRNA		K-12_b4430_rydB_at	1.188	2.034	1.683	2.425	1.39	-0.019	-0.133
csrC	b4457	regulatory sRNA		K-12_b4457_csrC_at	2.796	3.483	2.756	2.347	-0.237	-1.214	-1.437
ribC	b1662	riboflavin synthase, alpha subunit	enzyme; Biosynthesis of cofactors, carriers: Riboflavin	K-12_b1662_ribC_s_at	1.139	0.837	0.967	-0.152	0.38	-0.433	-0.174
rimJ	b1066	ribosomal-protein-S5-alanine N-acetyltransferase	enzyme; Ribosomes - maturation and modification	K-12_b1066_rimJ_s_at	1.372	1.938	1.256	0.802	-0.182	-1.219	-0.617
rmf	b0953	ribosome modulation factor	factor; Ribosomes - maturation and modification	LT2_STM1066_rmf_s_at	5.376	5.3	5.489	5.034	2.327	-0.877	-0.588
surS	b1680	selenocysteine lyase, PLP-dependent	orf; Unknown	K-12_b1680_surS_s_at	1.481	1.602	0.678	2.14	0.54	0.416	-0.031
degQ	b3234	serine endoprotease, periplasmic	enzyme; Degradation of proteins, peptides, glyco	K-12_b3234_degQ_s_at	1.291	1.461	1.171	1.96	0.45	-0.44	-0.416
ryeA	b4432	small RNA		K-12_b4432_ryeA_at	1.765	1.273	2.656	0.12	0.646	-0.134	-0.882
tkel	b4441	small RNA		K-12_b4441_tkel_at	1.117	0.701	0.872	1.269	-0.835	-1.555	-1.079
ygiJ	b3089	sodium:serine/threonine symporter	putative transport; Not classified	K-12_b3089_ygiJ_s_at	1.49	0.855	1.389	1.152	-1.188	0.136	-0.076
csiE	b2535	stationary phase inducible protein	orf; Unknown	K-12_b2535_csiE_s_at	1.053	1.732	0.342	1.181	1.596	0.246	-0.331
rsd	b3995	stationary phase protein, binds sigma 70 RNA polymerase subunit	putative regulator; Not classified	K-12_b3995_rsd_s_at	1.735	1.89	1.939	0.626	-1.427	-0.841	-1.044
ydaA	b1333	stress-induced protein	orf; Unknown	K-12_b1333_ydaA_s_at	3.464	3.606	3.536	2.864	1.574	0.606	1.034
yitT	b3923	stress-induced protein	putative regulator; Not classified	K-12_b3923_yitT_s_at	2.87	3.043	2.883	0.979	1.442	0.17	0.668
ynaF	b1376	stress-induced protein, ATP-binding protein	putative structure; Not classified	K-12_b1376_ynaF_s_at	2.911	3.085	2.021	1.47	1	1.282	1.152
cysN	b2751	sulfate adenylyltransferase, subunit 1	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2751_cysN_s_at	6.392	5.69	5.901	3.994	4.288	3.303	2.948
cysD	b2752	sulfate adenylyltransferase, subunit 2	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2752_cysD_s_at	6.739	6.841	6.479	5.492	4.318	4.379	3.545
cysA	b2422	sulfate/thiosulfate transporter subunit -1- ATP-binding component of f	transport; Transport of small molecules: Anions	K-12_b2422_cysA_s_at	4.784	4.231	4.435	3.971	3.152	3.11	3.218
cysW	b2423	sulfate/thiosulfate transporter subunit -1- membrane component of A	transport; Transport of small molecules: Anions	K-12_b2423_cysW_s_at	4.951	4.883	4.897	4.027	3.165	3.545	3.739
cysU	b2424	sulfate/thiosulfate transporter subunit -1- membrane component of A	transport; Transport of small molecules: Anions	K-12_b2424_cysU_s_at	4.773	4.93	4.652	3.575	2.781	3.409	3.296
cysJ	b2764	sulfite reductase, alpha subunit, flavoprotein	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2764_cysJ_s_at	5.858	5.983	5.657	4.928	4.51	3.402	3.114
cysI	b2763	sulfite reductase, beta subunit, NAD(P)-binding, heme-binding	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2763_cysI_s_at	5.38	5.063	4.949	3.314	3.5	2.073	2.189
garR	b3125	tarttronate semialdehyde reductase	putative enzyme; Not classified	K-12_b3125_garR_s_at	1.253	0.893	1.023	2.362	1.07	0.632	-0.125
taub	b0366	taurine transporter subunit -1- ATP-binding component of ABC superfamily	transport; Transport of small molecules: Amino acids, amines	K-12_b0366_taub_s_at	1.197	1.178	1.257	1.359	1.528	0.601	0.172
cysP	b2425	thiosulfate transporter subunit -1- periplasmic-binding component of f	transport; Transport of small molecules: Anions	K-12_b2425_cysP_s_at	5.822	6.303	5.38	3.442	3.666	3.514	3.701
ilvA	b3772	threonine deaminase	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3772_ilvA_s_at	3.372	2.882	3.259	1.347	0.825	1.05	0.77
deoA	b4382	thymidine phosphorylase	enzyme; Salvage of nucleosides and nucleotides	K-12_b4382_deoA_s_at	1.309	0.523	0.442	0.257	0.085	-0.704	-0.714
trpA	b1260	tryptophan synthase, alpha subunit	enzyme; Amino acid biosynthesis: Tryptophan	K-12_b1260_trpA_s_at	1.82	1.7	2.092	1.083	-0.31	-0.805	-1.094
trpB	b1261	tryptophan synthase, beta subunit	enzyme; Amino acid biosynthesis: Tryptophan	K-12_b1261_trpB_s_at	1.189	1.45	1.523	0.23	-0.241	-0.901	-1.173
uspA	b3495	universal stress global response regulator	putative regulator; Adaptations, atypical conditions	K-12_b3495_uspA_s_at	1.379	1.296	0.995	-2.398	-3.681	-0.994	-0.757
udp	b3831	uridine phosphorylase	enzyme; Salvage of nucleosides and nucleotides	K-12_b3831_udp_s_at	1.207	0.355	0.613	0.305	0.067	-0.063	-0.944
ybgR	b0752	zinc efflux system	putative transport; Not classified	CTF073_c0827_s_at	2.068	2.447	1.802	0.793	0.482	0.709	-0.04
ygiE	b3040	zinc transporter	orf; Unknown	K-12_b3040_ygiE_s_at	2.132	2.132	2.005	0.801	0.061	0.296	0.534

Venn: Unaffected
121 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspOT
cysH	b2762	3'-phosphoadenosine 5'-phosphosulfate reductase	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2762_cysH_s_at	5.638	5.594	5.355	3.987	3.787	2.261	2.092
aroD	b1693	3-dehydroquinate dehydratase	enzyme; Amino acid biosynthesis: Chorismate	K-12_b1693_aroD_s_at	2.053	1.687	1.887	1.069	0.006	-0.574	-1.17
aroG	b0754	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalanine	enzyme; Amino acid biosynthesis: Phenylalanine	K-12_b0754_aroG_s_at	1.319	0.763	1.463	1.057	-0.445	-0.379	-0.479
ydcE	b1461	4-oxalocrotonate tautomerase	orf; Unknown	K-12_b1461_ydcE_s_at	1.715	1.247	1.881	0.699	0.538	0.221	0.465

pfkB	b1723	6-phosphofructokinase II	enzyme; Energy metabolism, carbon: Glycolysis	K-12_b1723_pfkB_s_at	2.728	2.755	2.685	2.38	1.099	0.533	0.748
ybhE	b0767	6-phosphogluconolactonase	orf; Not classified	K-12_b0767_ybhE_s_at	1.223	0.934	0.316	0.281	-0.63	-1.177	-1.378
ssrS	b2911	6S regulatory RNA	RNA; Ribosomal and stable RNAs -I- modulates promoter use via inte	K-12_b2911_ssrS_s_at	1.544	1.204	1.007	0.906	-0.857	-0.167	0.131
hdhA	b1619	7-alpha-hydroxysteroid dehydrogenase, NAD-dependent	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b1619_hdhA_s_at	2.722	2.491	2.294	2.001	1.282	-0.781	-0.394
clpA	b0882	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine pro	enzyme; Degradation of proteins, peptides, glyco	K-12_b0882_clpA_s_at	2.802	2.793	2.787	1.847	0.938	-0.425	-0.209
yfFO	b2446	CPZ-55 prophage; predicted protein	orf; Unknown	K-12_b2446_yfFO_s_at	1.028	1.093	0.641	1.267	0.922	-0.283	-0.275
b2449	b2449	CPZ-55 prophage; predicted protein	orf; Unknown	K-12_b2449_at	1.541	1.35	1.576	1.117	0.257	-0.123	-0.166
yedO	b1919	D-cysteine desulfhydrase, PLP-dependent	putative enzyme; Not classified	K-12_b1919_yedO_a_at	2.239	2.123	1.832	0.889	0.904	0.312	0.402
did	b2133	D-lactate dehydrogenase, FAD-binding, NADH independent	enzyme; Energy metabolism, carbon: Aerobic respiration	K-12_b2133_did_s_at	1.255	0.579	1.267	0.796	-0.826	-1.786	-1.797
sbmC	b2009	DNA gyrase inhibitor	orf; Unknown function	K-12_b2009_sbmC_s_at	2.574	2.659	2.045	2.818	1.014	0.451	1.049
fucR	b2805	DNA-binding transcriptional activator	regulator; Degradation of small molecules: Carbon compounds	K-12_b2805_fucR_s_at	1.563	1.274	1.744	0.815	0.537	0.016	-0.443
csuD	b1040	DNA-binding transcriptional activator in two-component regulatory sy	putative regulator; Not classified	K-12_b1040_csuD_s_at	2.93	2.945	3.327	2.247	0.63	0.614	0.585
cbi	b1987	DNA-binding transcriptional activator of cysteine biosynthesis	regulator; Amino acid biosynthesis: Cysteine	K-12_b1987_cbi_s_at	2.53	2.595	2.021	1.299	1.894	0.688	0.089
icia	b2916	DNA-binding transcriptional activator, replication initiation inhibitor	regulator; DNA - replication, repair, restriction/modification	K-12_b2916_icia_s_at	1.041	1.126	1.148	0.269	-0.617	-0.819	-1.408
crp	b3357	DNA-binding transcriptional dual regulator	regulator; Global regulatory functions	K-12_b3357_crp_s_at	1.291	1.51	1.248	-5.177	-0.442	-0.115	-0.293
folE	b2153	GTP cyclohydrolase I	enzyme; Biosynthesis of cofactors, carriers: Folic acid	K-12_b2153_folE_s_at	1.049	0.862	1.07	0.535	-1.282	-1.864	-0.584
ybiK	b0828	L-asparaginase	orf; Not classified	K-12_b0828_ybiK_s_at	3.514	3.813	3.701	3.089	2.089	1.652	1.108
fucU	b2804	L-fucose mutarotase	phenotype; Degradation of small molecules: Carbon compounds	K-12_b2804_fucU_s_at	2.303	2.213	2.351	1.299	0.442	-0.031	0.231
sdaA	b1814	L-serine deaminase I	enzyme; Degradation of small molecules: Amino acids	K-12_b1814_sdaA_s_at	1.375	1.82	0.904	0.777	0.767	-1.031	-0.414
cea	b1738	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS	enzyme; Transport of small molecules: Carbohydrates, organic acids,	K-12_b1738_cea_s_at	2.699	2.384	2.698	1.894	1.561	1.243	1.299
ampD	b0110	N-acetyl-anhydromuramyl-L-alanine amidase	regulator; Not classified	K-12_b0110_ampD_s_at	1.37	1.695	1.689	0.594	-0.665	0.169	-1.077
nemA	b1650	N-ethylmaleimide reductase, FMN-linked	enzyme; Central intermediary metabolism: Pool, multipurpose conver	K-12_b1650_nemA_s_at	1.078	0.58	0.883	0.85	0.921	-0.377	-0.295
nadE	b1740	NAD synthetase, NH3/glutamine-dependent	enzyme; Biosynthesis of cofactors, carriers: Pyridine nucleotide	K-12_b1740_nadE_s_at	1.018	0.584	1.324	0.465	-0.667	-2.137	-1.587
acdP	b1412	NADH-azoreductase, FMN-dependent	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b1412_acdP_s_at	1.726	1.849	2.088	1.102	0.018	-0.902	-0.759
ilvG	b4488	acetylalate synthase II, large subunit (pseudogene)	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b4488_ilvG_s_at	4.511	5.26	4.624	3.891	2.614	2.801	2.503
argE	b3957	acetylornithine decarboxylase	enzyme; Amino acid biosynthesis: Arginine	K-12_b3957_argE_s_at	1.307	1.171	1.226	0.792	-0.596	-1.119	-1.223
asr	b1597	acid shock-inducible periplasmic protein	phenotype; Not classified	K-12_b1597_asr_s_at	1.215	1.872	0.896	1.606	1.396	-0.615	-0.293
fadE	b0221	acyl coenzyme A dehydrogenase	putative enzyme; Not classified	K-12_b0221_fadE_s_at	1.715	1.985	1.268	0.714	1.405	-0.465	-0.348
cysC	b2750	adenosine 5'-phosphosulfate kinase	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2750_cysC_s_at	4.154	3.243	3.895	3.279	2.541	1.217	1.217
asd	b3433	aspartate-semialdehyde dehydrogenase, NAD(P)-binding	enzyme; Amino acid biosynthesis: Lysine	K-12_b3433_asd_s_at	1.204	0.875	1.614	0.402	-1.196	-1.933	-2.576
ushA	b0480	bifunctional UDP-sugar hydrolase and 5'-nucleotidase	enzyme; Central intermediary metabolism: Sugar-nucleotide biosynt	K-12_b0480_ushA_s_at	1.054	0.731	0.898	1.063	0.666	-0.299	-0.605
ilvE	b3770	branched-chain amino-acid aminotransferase	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3770_ilvE_s_at	3.008	3.338	3.201	3.399	-0.033	1.339	0.726
cstA	b0598	carbon starvation protein	phenotype; Global regulatory functions	K-12_b0598_cstA_s_at	1.505	1.592	1.71	1.195	0.885	1.027	0.171
ybhO	b0789	cardiolipin synthase 2	orf; Not classified	K-12_b0789_ybhO_s_at	1.465	1.378	0.48	2.309	1.658	-0.577	-0.894
yfA	b2597	cold shock protein associated with 30S ribosomal subunit	putative regulator; Not classified	K-12_b2597_yfA_s_at	2.195	1.757	1.979	0.788	0.785	0.07	-0.531
csuD	b0880	cold shock protein homolog	phenotype; Not classified	K-12_b0880_csuD_s_at	3.875	3.916	4.055	1.766	1.727	0.427	0.431
ybgE	b0735	conserved inner membrane protein	orf; Unknown	K-12_b0735_ybgE_s_at	1.294	0.632	0.809	0.149	0.031	0.464	0.105
yedI	b1958	conserved inner membrane protein	orf; Unknown	K-12_b1958_yedI_s_at	1.434	1.777	1.008	1.105	0.171	0.293	0.383
yohJ	b2141	conserved inner membrane protein	orf; Unknown	K-12_b2141_yohJ_s_at	1.231	0.653	1.457	1.561	0.837	1.055	0.058
ygbE	b2749	conserved inner membrane protein	putative enzyme; Not classified	K-12_b2749_ygbE_s_at	1.989	1.852	2.159	1.549	0.587	1.161	0.39
ydgC	b1607	conserved inner membrane protein associated with alginate biosynt	orf; Unknown	K-12_b1607_ydgC_s_at	2.211	2.025	2.625	1.576	1.231	0.961	1.025
ybgI	b0710	conserved metal-binding protein	orf; Unknown	K-12_b0710_ybgI_s_at	2.089	1.134	1.375	0.673	-0.24	-0.267	-0.937
yecA	b1908	conserved metal-binding protein	K-12_b1908_yecA_s_at	1.184	2.559	2.853	2.121	0.185	0.508	0.936	
yaeH	b0163	conserved protein	putative structure; Not classified	K-12_b0163_yaeH_s_at	1.87	1.647	1.133	0.975	-0.44	-0.348	
yfBA	b0515	conserved protein	orf; Unknown	K-12_b0515_yfBA_s_at	1.341	1.28	1.454	0.31	-0.43	-0.927	-0.634
ybiI	b0803	conserved protein	orf; Unknown	K-12_b0803_ybiI_s_at	1.163	1.263	0.245	0.975	0.395	-0.139	-0.368
yliH	b0836	conserved protein	putative factor; Not classified	K-12_b0836_yliH_s_at	4.304	4.011	4.131	2.805	1.87	0.251	-0.113
ybiJ	b0844	conserved protein	orf; Unknown	K-12_b0844_ybiJ_s_at	1.415	0.959	1.882	0.773	0.616	0.25	-0.06
ycbK	b0926	conserved protein	orf; Unknown	K-12_b0926_ycbK_s_at	1.567	1.666	1.923	1.96	-0.321	0.722	0.15
yceH	b1067	conserved protein	orf; Unknown	K-12_b1067_yceH_s_at	1.647	1.209	1.564	0.492	0.897	0.354	-0.403
yfCP	b1108	conserved protein	orf; Unknown	K-12_b1108_yfCP_s_at	1.586	1.753	1.179	-0.706	-0.167	-0.189	
yciF	b1258	conserved protein	putative structure; Not classified	K-12_b1258_yciF_s_at	1.175	1.13	0.237	1.954	1.215	-0.002	-0.044
ydhQ	b1664	conserved protein	putative enzyme; Not classified	K-12_b1664_ydhQ_s_at	1.615	1.69	1.249	1.374	0.505	-0.591	0.021
yeeO	b1792	conserved protein	orf; Unknown	K-12_b1792_yeeO_s_at	1.579	1.694	1.131	-0.229	-0.235	-0.836	-0.32
yeeX	b2007	conserved protein	phenotype; Not classified	K-12_b2007_yeeX_s_at	1.367	1.449	1.376	0.535	0.311	-0.874	0.025
yfbU	b2294	conserved protein	orf; Unknown	K-12_b2294_yfbU_s_at	1.525	1.064	1.079	-0.253	-1.93	-0.81	0.003
yggE	b2922	conserved protein	phenotype; Not classified	K-12_b2922_yggE_s_at	1.12	0.572	0.6	1.942	-0.603	-0.637	-0.103
smg	b3284	conserved protein	orf; Unknown	K-12_b3284_smg_s_at	1.198	1.426	1.247	0.722	-0.096	0.014	0.198
yihD	b3858	conserved protein	orf; Unknown	K-12_b3858_yihD_s_at	1.074	0.737	1.393	0.924	-0.033	-1.034	-1.077
yjiS	b3922	conserved protein	orf; Unknown	K-12_b3922_yjiS_s_at	2.483	2.736	2.645	2.749	1.488	0.829	0.152
yjiE	b4144	conserved protein	orf; Unknown	K-12_b4144_yjiE_s_at	1.089	0.949	1.266	-0.01	0.122	0.398	-0.52
yjiO	b4189	conserved protein	orf; Unknown	K-12_b4189_yjiO_s_at	1.579	1.901	0.785	1.357	1.232	0.406	0.461
yaeP	b4406	conserved protein	K-12_b4406_yaeP_s_at	2.228	2.044	2.196	1.435	0.974	-0.232	0.021	
erfK	b1990	conserved protein with NAD(P)-binding Rossmann-fold domain	orf; Unknown	K-12_b1990_erfK_s_at	2.006	2.279	1.343	2.189	1.115	1.06	0.955
phoH	b1020	conserved protein with nucleoside triphosphate hydrolase domain	regulator; Central intermediary metabolism: Phosphorus compounds	K-12_b1020_phoH_s_at	4.143	4.418	4.164	2.271	1.347	0.024	0.617
csuA	b1042	cryptic curlin major subunit	regulator; Surface structures	K-12_b1042_csuA_s_at	3.245	2.999	3.543	1.847	-0.177	0.972	0.549
csuB	b1041	curlin nuclear protein, minor subunit in curli complex	structural component; Surface structures	K-12_b1041_csuB_s_at	1.417	1.514	1.730	1.606	0.236	0.435	0.012
cfa	b1661	cyclopropane fatty acyl phospholipid synthase (unsaturated-phosphol	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b1661_cfa_s_at	2.865	2.382	2.527	1.312	0.08	-0.014	0.991
cysK	b2414	cysteine synthase A, O-acetylserine sulphydrase A subunit	enzyme; Amino acid biosynthesis: Cysteine	K-12_b2414_cysK_s_at	3.913	3.79	3.622	2.643	2.089	3.113	2.796
cysM	b2421	cysteine synthase B (O-acetylserine sulphydrase B)	enzyme; Amino acid biosynthesis: Cysteine	K-12_b2421_cysM_s_at	2.914	2.701	3.09	3.3	1.383	1.741	1.329
fliY	b1920	cystine transporter subunit -I- periplasmic-binding component of ABC	putative transport; Not classified	K-12_b1920_fliY_s_at	2.737	2.491	2.292	1.224	1.269	0.283	0.149
cydA	b0733	cytochrome d terminal oxidase, subunit I	enzyme; Energy metabolism, carbon: Electron transport	K-12_b0733_cydA_s_at	1.041	0.779	1.131	-0.269	-0.716	-0.672	-0.568
cydB	b0734	cytochrome d terminal oxidase, subunit II	enzyme; Energy metabolism, carbon: Electron transport	K-12_b0734_cydB_s_at	1.618	1.694	1.631	0.341	0.129	-0.206	0.37
yliA	b3661	cytoplasmic membrane lipoprotein-28	membrane; Macromolecule synthesis, modification: Lipoprotein	K-12_b3661_yliA_s_at	3.35	3.831	2.955	0.854	0.933	2.193	0.891
ilvD	b3771	dihydroxyacid dehydratase	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3771_ilvD_s_at	3.483	3.512	3.329	1.73	0.076	-1.72	1.354
ymfI	b1143	e14 prophage; predicted protein	orf; Unknown	K-12_b1143_ymfI_s_at	1.681	1.044	1.785	-0.017	-0.243	-0.819	-0.451
focA	b0904	formate transporter	putative transport; Degratation of small molecules: Carbon compou	K-12_b0904_focA_s_at	1.432	1.659	0.91	0.54	-0.023	-0.263	-0.669
putA	b1014	fused DNA-binding transcriptional regulator -I- proline dehydrogenase	enzyme; Degradation of small molecules: Amino acids	K-12_b1014_putA_s_at	1.912	1.27	1.543	1.355	0.286	-0.092	-0.367
yfCX	b2341	fused enoyl-CoA hydratase and epimerase and isomerase -I- 3-hydro	putative enzyme; Not classified	K-12_b2341_yfCX_s_at	1.386	1.11	1.163	2.226	1.751	-0.525	-0.548
rfaC	b2167	fused fructose-specific PTS enzymes: IIBcomponent -I- IIC componer	regulator; Degradation of small molecules: Carbon compounds	K-12_b2167_rfaC_s_at	1.218	1.249	1.35	1.796	0.623	0.016	
trpC	b1262	fused indole-3-glycerolphosphate synthetase -I- N-(5-phosphoribosyl	enzyme; Amino acid biosynthesis: Tryptophan	K-12_b1262_trpC_s_at	1.198	1.636	1.153	1.622	0.205	-0.679	-0.402
yliA	b0829	fused nucleotide peptide transport subunits of ABC superfamily: ATP-b	putative transport; Not classified	K-12_b0829_yliA_s_at	2.612	2.831	2.155	1.893	1.835	0.035	0.868
glgC	b3430	glucose-1-phosphate adenylyltransferase	enzyme; Macromolecule synthesis, modification: Polysaccharides - (c	K-12_b3430_glgC_s_at	2.02	1.03	2.085	0.474	0.363	-1.72	-1.685
glhI	b0655	glutamate and aspartate transporter subunit -I- periplasmic-binding c	putative transport; Not classified	K-12_b0655_glhI_s_at	1.181	0.954	1.216	-0.157	-0.403	-1.193	-0.501
gdhA	b1761	glutamate dehydrogenase, NADP-specific	enzyme; Amino acid biosynthesis: Glutamate	K-12_b1761_gdhA_s_at	1.299	0.82	1.188	-0.988	-0.09	0.075	-0.175
grxB	b1064	glutaredoxin 2 (Grx2)	carrier; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxin,	K-12_b1064_grxB_s_at	1.756	1.178	1.65	0.733	-1.336	-1.491	-1.284
gstB	b1635	glutathione S-transferase	enzyme; Biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxin	K-12_b1635_gst_s_at	2.709	2.448	2.684	1.082	0.113	0.158	1.155
ilvL	b3766	ilvG operon leader peptide	leader; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3766_ilvL_s_at	1.338	2.041	1.878	0.579	0.169	0.625	-0.974
yccA	b0970	inner membrane protein	putative transport; Not classified	K-12_b0970_yccA_s_at	2.298	1.682	2.27	-0.026	0.407	0.713	1.298

ilvC	b3774	ketol-acid reductoisomerase, NAD(P)-binding	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3774_ilvC_s_at	1.208	0.576	1.699	0.158	0.158	-0.085	-0.393
argT	b2310	lysine/arginine/ornithine transporter subunit -1- periplasmic-binding c	transport; Transport of small molecules: Amino acids, amines	K-12_b2310_argT_s_at	1.323	0.512	1.225	0.879	0.285	0.32	0.264
glcB	b2976	malate synthase G	enzyme; Central intermediary metabolism: Glyoxylate bypass	K-12_b2976_glcB_a_at	1.069	0.76	0.886	1.555	0.601	-0.56	-0.664
yggB	b2924	mechanosensitive channel	putative transport; Not classified	K-12_b2924_yggB_s_at	2.961	2.052	2.306	3.045	1.147	0.143	0.737
msrA	b4219	methionine sulfoxide reductase A	enzyme; Proteins - translation and modification	K-12_b4219_msrA_s_at	1.952	2.164	1.791	0.99	0.449	-0.609	-1.181
moaB	b0782	molybdopterin biosynthesis protein B	enzyme; Biosynthesis of cofactors, carriers: Molybdopterin	K-12_b0782_moaB_s_at	1.17	0.245	1.352	-0.585	-0.706	-0.847	-0.929
tesA	b0494	multifunctional acyl-CoA thioesterase I and protease I and lysophosphol	enzyme; Fatty acid and phosphatidic acid biosynthesis	K-12_b0494_tesA_s_at	1.353	1.301	1.614	-0.131	-0.013	-0.152	-0.661
ycjI	b1326	murein peptide amidase A	putative enzyme; Not classified	K-12_b1326_ycjI_s_at	1.187	1.138	1.34	1.327	0.255	0.27	-0.256
napA	b2206	nitrate reductase, periplasmic, large subunit	putative enzyme; Energy metabolism, carbon: Anaerobic respiration	K-12_b2206_napA_s_at	1.028	0.591	1.379	1.249	2.334	0.134	-0.479
napB	b2203	nitrate reductase, small, cytochrome C550 subunit, periplasmic	carrier; Energy metabolism, carbon: Electron transport	K-12_b2203_napB_s_at	1.076	0.732	1.453	0.77	1.014	0.146	-0.153
nupG	b2964	nucleoside transporter	transport; Transport of small molecules: Nucleosides, purines, pyrimi	K-12_b2964_nupG_s_at	1.026	0.602	0.877	0.954	0.134	-0.164	-0.404
csqG	b1037	outer membrane lipoprotein	structural component; Surface structures	K-12_b1037_csqG_s_at	1.978	1.712	2.169	1.437	0.068	-0.115	0.386
shyB	b1641	outer membrane lipoprotein	putative membrane; Not classified	K-12_b1641_shyB_s_at	1.009	1.055	0.662	0.15	0.325	-0.075	-0.098
pepT	b1127	peptidase T	putative enzyme; Not classified	K-12_b1127_pepT_s_at	2.445	2.134	1.632	1.879	0.72	0.324	-0.734
pgsA	b1912	phosphatidylglycerophosphate synthetase	enzyme; Macromolecule synthesis, modification: Phospholipids	K-12_b1912_pgsA_s_at	1.109	0.286	1.173	-0.629	0.338	0.603	-0.143
ppsA	b1702	phosphoenolpyruvate synthase	enzyme; Central intermediary metabolism: Gluconeogenesis	K-12_b1702_ppsA_s_at	1.418	0.706	1.646	-0.507	-1.518	-1.974	-1.286
csqE	b1039	predicted transport protein	structural component; Surface structures	K-12_b1039_csqE_s_at	1.882	1.574	2.648	2.318	0.344	0.302	-0.148
yjgR	b4263	predicted ATPase	or; Unknown	K-12_b4263_yjgR_s_at	1.072	0.876	0.303	1.644	0.653	-0.168	-0.12
yafV	b0219	predicted C-N hydrolase family amidase, NAD(P)-binding	putative enzyme; Not classified	K-12_b0219_yafV_s_at	1.104	1.518	0.641	1.004	0.818	-0.048	-0.204
yeaT	b1799	predicted DNA-binding transcriptional regulator	putative regulator; Not classified	K-12_b1799_yeaT_s_at	1.718	1.156	1.197	1.608	0.657	0.181	-0.246
yghJ	b2989	predicted S-transferase	or; Unknown	K-12_b2989_yghJ_s_at	1.692	0.96	1.528	2.435	0.758	-0.159	-0.792
yhhY	b3441	predicted acetyltransferase	or; Unknown	K-12_b3441_yhhY_s_at	1.318	1.962	1.438	0.494	-0.447	0.132	-0.914
ycxX	b0968	predicted acylphosphatase	or; Unknown	K-12_b0968_ycxX_s_at	2.247	2.521	2.007	2.319	0.728	0.128	-0.428
yncA	b1448	predicted acyltransferase with acyl-CoA N-acyltransferase domain	putative transport; Drug/analog sensitivity	K-12_b1448_yncA_s_at	1.541	1.163	1.537	1.166	0.384	-0.171	-0.679
elaA	b2267	predicted acyltransferase with acyl-CoA N-acyltransferase domain	or; Unknown	K-12_b2267_elaA_s_at	1.134	1.087	1.509	1.729	-0.996	0.157	-0.169
yneI	b1525	predicted aldehyde dehydrogenase	putative enzyme; Not classified	K-12_b1525_yneI_s_at	1.37	1.114	1.538	0.887	0.744	-0.314	-0.357
ycbB	b0925	predicted carboxypeptidase	putative enzyme; Not classified	K-12_b0925_ycbB_s_at	1.686	1.831	0.87	0.909	0.217	0.112	0.36
yjTB	b2066	predicted cell envelope opacity-associated protein	or; Unknown	K-12_b2066_yjTB_s_at	1.442	1.207	1.59	1.865	0.29	-0.243	0.04
ybcC	b0801	predicted dehydrogenase	putative enzyme; Not classified	K-12_b0801_ybcC_s_at	1.7	0.803	1.929	0.833	0.272	0.329	0.029
yddV	b1490	predicted diguanilate cyclase	or; Unknown	K-12_b1490_yddV_s_at	1.289	1.005	0.494	0.597	0.207	-0.167	0.061
yciI	b1251	predicted enzyme	or; Unknown	K-12_b1251_yciI_s_at	1.859	1.209	1.855	0.138	0.31	-0.939	-1.375
yfcF	b2301	predicted enzyme	or; Unknown	K-12_b2301_yfcF_s_at	1.326	0.693	0.355	1.105	0.694	0.419	-0.307
ybgJ	b0711	predicted enzyme subunit	putative enzyme; Not classified	K-12_b0711_ybgJ_s_at	1.089	0.874	1.151	0.231	-0.31	-0.381	-0.816
ybgK	b0712	predicted enzyme subunit	putative enzyme; Not classified	K-12_b0712_ybgK_s_at	1.11	1.396	1.022	0.196	-1.495	-0.328	-1.017
yegG	b2154	predicted esterase	or; Not classified	K-12_b2154_yegG_s_at	1.187	0.538	1.24	0.035	-0.242	0.048	-0.564
yjiJ	b0838	predicted glutathione S-transferase	putative enzyme; Not classified	K-12_b0838_yjiJ_s_at	2.538	2.088	2.469	1.551	0.279	-0.633	-0.805
yifB	b3592	predicted glutathione S-transferase	putative enzyme; Not classified	K-12_b3592_yifB_s_at	1.623	1.067	0.388	0.399	-0.375	0.385	-0.862
btuE	b1710	predicted glutathione peroxidase	transport; Transport of small molecules: Other	K-12_b1710_btuE_s_at	1.012	0.597	0.061	1.799	-0.379	-0.993	-0.445
b2999	b2999	predicted hydrolase (pseudogene)	or; Unknown	K-12_b2999_s_at	1.05	0.98	0.181	1.246	0.123	-0.104	-0.078
ybhL	b0786	predicted inner membrane protein	or; Unknown	K-12_b0786_ybhL_s_at	1.373	1.228	0.841	0.395	0.06	0.429	0.014
ymgE	b1195	predicted inner membrane protein	or; Unknown	K-12_b1195_ymgE_s_at	1.213	1.412	0.384	2.983	1.033	0.536	0.092
ydiK	b1688	predicted inner membrane protein	or; Unknown	K-12_b1688_ydiK_s_at	2.098	2.261	1.865	0.738	1.533	0.516	0.716
ydcF	b2347	predicted inner membrane protein	putative transport; Not classified	K-12_b2347_ydcF_s_at	1.07	0.91	0.441	2.69	0.51	0.175	-0.06
yphA	b2543	predicted inner membrane protein	or; Unknown	K-12_b2543_yphA_s_at	1.312	1.017	0.396	1.49	0.869	1.018	-0.166
b2670	b2670	predicted inner membrane protein	or; Unknown	CF7073_c3221_ygaW_s_at	2.408	2.31	2.821	1.941	0.512	0.378	0.301
yhaH	b3103	predicted inner membrane protein	putative carrier; Not classified	K-12_b3103_yhaH_s_at	1.365	1.506	0.467	1.156	0.262	0.048	-0.213
ycgM	b1180	predicted isomerase/hydrolase	putative enzyme; Not classified	K-12_b1180_ycgM_s_at	2.825	2.588	2.962	1.056	1.206	0.882	1.245
yciW	b1287	predicted oxidoreductase	putative enzyme; Not classified	K-12_b1287_yciW_s_at	2.69	2.145	2.712	1.757	1.423	0.669	0.53
ydjA	b1765	predicted oxidoreductase	or; Unknown	K-12_b1765_ydjA_s_at	1.167	1.263	1.598	0.499	0.63	0.196	-0.256
mmvM	b1068	predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain	putative factor; Not classified	K-12_b1068_mmvM_s_at	1.448	1.518	1.365	0.987	1.072	-0.477	-0.162
tas	b2834	predicted oxidoreductase, NAD(P)(H)-dependent aldo-keto reductase	or; Unknown	K-12_b2834_tas_s_at	1.303	1.355	1.302	1.637	0.792	-0.654	0.133
yghD	b3253	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	putative enzyme; Not classified	K-12_b3253_yghD_s_at	1.322	1.262	0.957	1.393	-0.625	-0.895	-1.649
yqfA	b2899	predicted oxidoreductase, inner membrane subunit	putative enzyme; Not classified	K-12_b2899_yqfA_s_at	2.808	2.807	2.986	2.881	1.466	1.685	1.309
ydgD	b1598	predicted peptidase	or; Unknown	O157_Ecs2304_s_at	1.644	1.674	0.762	2.131	0.883	-0.137	0.34
tdlD	b3244	predicted peptidase	phenotype; Not classified	K-12_b3244_tdlD_s_at	1.026	1.349	0.605	0.922	-0.232	-0.674	-0.246
yliC	b0831	predicted peptide transporter subunit: membrane component of ABC	putative transport; Not classified	K-12_b0831_yliC_s_at	2.779	1.928	2.864	1.516	1.869	0.826	0.336
yjba	b4030	predicted phosphate starvation inducible protein	or; Unknown	K-12_b4030_yjba_s_at	4.062	4.9	4.068	1.407	1.787	1.391	0.122
yaiB	b0382	predicted protein	or; Unknown	K-12_b0382_yaiB_s_at	3.421	3.49	3.736	3.186	2.396	1.263	1.146
ybeH	b0625	predicted protein	or; Unknown	K-12_b0625_ybeH_s_at	2.041	1.888	1.276	2.202	1.213	1.305	0.473
ybfA	b0699	predicted protein	or; Unknown	K-12_b0699_ybfA_s_at	2.492	2.397	2.768	1.377	1.637	0.381	0.612
yceF	b1087	predicted protein	or; Unknown	K-12_b1087_yceF_s_at	2.548	2.17	2.301	1.446	1.134	0.815	0.672
ycfL	b1104	predicted protein	or; Unknown	K-12_b1104_ycfL_s_at	1.17	0.9	0.908	0.158	-1.147	-0.86	-0.554
ycgJ	b1177	predicted protein	or; Unknown	K-12_b1177_ycgJ_s_at	1.119	1.153	1.442	1.048	-0.125	-0.244	-0.283
ydiH	b1685	predicted protein	or; Unknown	K-12_b1685_ydiH_s_at	1.677	1.879	2.254	1.576	-0.281	-0.721	-0.031
ydiZ	b1724	predicted protein	or; Unknown	K-12_b1724_ydiZ_s_at	4.776	4.9	3.946	5.859	1.574	0.152	0.572
ydcC	b1957	predicted protein	or; Unknown	K-12_b1957_ydcC_s_at	2.974	3.684	2.184	4.524	1.086	1.337	0.766
yfgG	b2504	predicted protein	or; Unknown	K-12_b2504_yfgG_s_at	1.052	0.887	0.947	-0.043	1.267	0.226	-0.505
yfiL	b2602	predicted protein	or; Unknown	K-12_b2602_yfiL_s_at	1.188	1.535	0.451	2.277	0.446	0.09	-0.51
ygeA	b2840	predicted racemase	putative transport; Drug/analog sensitivity	K-12_b2840_ygeA_s_at	1.135	1.775	1.401	1.912	0.723	0.38	-0.145
yedY	b1971	predicted reductase	putative enzyme; Not classified	K-12_b1971_yedY_s_at	1.676	1.383	0.993	1.628	0.884	0.508	0.436
ypdB	b2381	predicted response regulator in two-component system withYpdA	putative regulator; Not classified	K-12_b2381_ypdB_s_at	1.008	1.018	0.659	1.076	0.182	-0.288	-0.712
yjdc	b4135	predicted transcriptional regulator	or; Unknown	K-12_b4135_yjdc_s_at	1.664	1.637	1.172	1.658	-0.029	-0.988	-1.47
ybhK	b0780	predicted transferase with NAD(P)-binding Rossmann-fold domain	putative structure; Not classified	K-12_b0780_ybhK_s_at	1.288	1.521	1.273	0.36	0.514	0.601	0.103
ybiB	b0800	predicted transferase/phosphorylase	putative enzyme; Not classified	K-12_b0800_ybiB_s_at	1.023	2.251	1.765	0.66	-0.756	-0.369	0.08
csqF	b1038	predicted transport protein	structural component; Surface structures	K-12_b1038_csqF_s_at	3.039	2.964	3.488	2.646	0.28	0.518	0.787
yjhE	b3523	predicted transporter	putative transport; Not classified	K-12_b3523_yjhE_s_at	1.646	0.96	1.464	0.422	-0.053	1.073	-0.739
yecC	b1917	predicted transporter subunit: ATP-binding component of ABC superfa	putative transport; Not classified	K-12_b1917_yecC_s_at	2.068	1.602	1.603	0.438	0.632	0.412	0.606
yecS	b1918	predicted transporter subunit: membrane component of ABC superfa	putative transport; Not classified	K-12_b1918_yecS_s_at	2.466	1.704	1.995	0.292	0.428	0.519	0.722
yagT	b0286	predicted xanthine dehydrogenase, 2Fe-2S subunit	putative enzyme; Not classified	K-12_b0286_yagT_s_at	1.18	1.732	0.57	2.277	1.054	0.116	-0.137
yfdZ	b2379	predicted aminotransferase, PLP-dependent	putative enzyme; Not classified	K-12_b2379_yfdZ_s_at	1.812	2.146	1.533	1.065	0.52	0.105	-0.194
ycfF	b1103	purine nucleoside phosphoramidase	or; Unknown	K-12_b1103_ycfF_s_at	1.491	0.828	0.872	0.487	-1.114	-0.941	-0.239
pydF	b2564	pyridoxine transporter subunit: periplasmic-binding component of ABC	transport; Transport of small molecules: Amino acids, amines	K-12_b2564_pydF_s_at	1.295	0.51	0.51	-0.365	0.51	-1.84	-2.301
pdxJ	b2564	pyridoxine 5'-phosphate synthase	enzyme; Biosynthesis of cofactors, carriers: Pyridoxine	K-12_b2564_pdxJ_s_at	1.448	0.813	1.625	0.973	-0.171	-0.657	-0.258
pykA	b1854	pyruvate kinase II	enzyme; Energy metabolism, carbon: Glycolysis	K-12_b1854_pykA_s_at	1.395	1.122	1.005	0.316	0.815	-1.348	-1.082
ygiN	b3029	quinol monooxygenase	or; Unknown	K-12_b3029_ygiN_s_at	1.085	0.713	1.359	0.238	-0.314	-0.56	-0.557
yjiA	b0881	regulatory protein for ClpA substrate specificity	or; Unknown	K-12_b0881_yjiA_s_at	1.704	2.005	1.842	1.828	0.141	-0.498	-0.975
rydB	b4430	regulatory sRNA	or; Unknown	K-12_b4430_rydB_s_at	1.188	2.034	1.683	2.425	1.39	-0.019	-0.133
csrC	b4457	regulatory sRNA	or; Unknown	K-12_b4457_csrC_s_at	2.796	3.483	2.756	2.347	-0.237	-1.214	-1.437
ribC	b1662	riboflavin synthase, alpha subunit	enzyme; Biosynthesis of cofactors, carriers: Riboflavin	K-12_b1662_ribC_s_at	1.139	0.837	0.967	-0.152	0.38	-0.433	-0.174

rimJ	b1066	ribosomal-protein-S5-alanine N-acetyltransferase	enzyme; Ribosomes - maturation and modification	K-12_b1066_rimJ_s_at	1.372	1.938	1.256	0.802	-0.182	-1.219	-0.617
rmf	b0953	ribosome modulation factor	factor; Ribosomes - maturation and modification	LT2_STM1066_rmf_s_at	5.376	5.3	5.489	5.034	2.327	-0.877	-0.588
suFS	b1680	selenocysteine lyase, PLP-dependent	orf; Unknown	K-12_b1680_suFS_s_at	1.481	1.602	0.678	2.14	0.54	0.416	-0.031
degQ	b3234	serine endoprotease, periplasmic	enzyme; Degradation of proteins, peptides, glyco	K-12_b3234_degQ_s_at	1.291	1.461	1.171	1.96	0.45	-0.44	-0.416
ryeA	b4432	small RNA		K-12_b4432_ryeA_s_at	1.765	1.273	2.656	0.12	0.646	-0.134	-0.882
tkel	b4441	small RNA		K-12_b4441_tkel_s_at	1.117	0.701	0.872	1.269	-0.835	-1.555	-1.079
ygiU	b3089	sodium:serine/threonine symporter	putative transport; Not classified	K-12_b3089_ygiU_s_at	1.49	0.855	1.389	1.152	-1.188	0.136	-0.076
csiE	b2535	stationary phase inducible protein	orf; Unknown	K-12_b2535_csiE_s_at	1.053	1.732	0.342	1.181	1.596	0.246	-0.331
rsd	b3995	stationary phase protein, binds sigma 70 RNA polymerase subunit	putative regulator; Not classified	K-12_b3995_rsd_s_at	1.735	1.89	1.939	0.626	-1.427	-0.841	-1.044
ydaA	b1333	stress-induced protein	orf; Unknown	K-12_b1333_ydaA_s_at	3.464	3.606	3.536	2.864	1.574	0.606	1.034
yit	b3923	stress-induced protein	putative regulator; Not classified	K-12_b3923_yit_s_at	2.87	3.043	2.883	0.979	1.442	0.17	0.668
ynaF	b1376	stress-induced protein, ATP-binding protein	putative structure; Not classified	K-12_b1376_ynaF_s_at	2.911	3.085	2.021	1.47	1	1.282	1.152
cysN	b2751	sulfate adenylyltransferase, subunit 1	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2751_cysN_s_at	6.392	5.69	5.901	3.994	4.288	3.303	2.948
cysD	b2752	sulfate adenylyltransferase, subunit 2	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2752_cysD_s_at	6.739	6.841	6.479	5.492	4.318	4.379	3.545
cysA	b2422	sulfate/thiosulfate transporter subunit -1- ATP-binding component of	transport; Transport of small molecules: Anions	K-12_b2422_cysA_s_at	4.784	4.231	4.435	3.971	3.152	3.11	3.218
cysW	b2423	sulfate/thiosulfate transporter subunit -1- membrane component of	transport; Transport of small molecules: Anions	K-12_b2423_cysW_x_at	4.951	4.883	4.897	4.027	3.165	3.545	3.739
cysU	b2424	sulfate/thiosulfate transporter subunit -1- membrane component of	transport; Transport of small molecules: Anions	K-12_b2424_cysU_s_at	4.773	4.93	4.652	3.575	2.781	3.409	3.296
cysJ	b2764	sulfite reductase, alpha subunit, flavoprotein	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2764_cysJ_s_at	5.858	5.983	5.657	4.928	4.51	3.402	3.114
cysI	b2763	sulfite reductase, beta subunit, NAD(P)-binding, heme-binding	enzyme; Central intermediary metabolism: Sulfur metabolism	K-12_b2763_cysI_s_at	5.38	5.063	4.949	3.314	3.5	2.073	2.189
garR	b3125	tartronate semialdehyde reductase	putative enzyme; Not classified	K-12_b3125_garR_s_at	1.253	0.893	1.023	2.362	1.07	0.632	-0.125
tauB	b0366	taurine transporter subunit -1- ATP-binding component of ABC super	transport; Transport of small molecules: Amino acids, amines	K-12_b0366_tauB_s_at	1.197	1.178	1.257	1.359	1.528	0.601	0.172
cysP	b2425	thiosulfate transporter subunit -1- periplasmic-binding component of	transport; Transport of small molecules: Anions	K-12_b2425_cysP_s_at	5.822	6.303	5.38	3.442	3.666	3.514	3.701
ilvA	b3772	threonine deaminase	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3772_ilvA_s_at	3.372	2.882	3.259	1.347	0.825	1.05	0.77
deoA	b4382	thymidine phosphorylase	enzyme; Salvage of nucleosides and nucleotides	K-12_b4382_deoA_s_at	1.309	0.523	0.442	0.257	0.085	-0.704	-0.714
trpA	b1260	tryptophan synthase, alpha subunit	enzyme; Amino acid biosynthesis: Tryptophan	K-12_b1260_trpA_s_at	1.82	1.7	2.092	1.083	-0.31	-0.805	-1.094
trpB	b1261	tryptophan synthase, beta subunit	enzyme; Amino acid biosynthesis: Tryptophan	K-12_b1261_trpB_s_at	1.189	1.45	1.523	0.23	-0.241	-0.901	-1.173
uspA	b3495	universal stress global response regulator	putative regulator; Adaptations, atypical conditions	K-12_b3495_uspA_s_at	1.379	1.296	0.995	-2.398	-3.681	-0.994	-0.757
udp	b3831	uridine phosphorylase	enzyme; Salvage of nucleosides and nucleotides	K-12_b3831_udp_s_at	1.207	0.355	0.613	0.305	0.067	-0.063	-0.944
ygeR	b0752	zinc efflux system	putative transport; Not classified	CFT073_c0827_s_at	2.068	2.447	1.802	0.793	0.482	0.709	-0.04
ygiE	b3040	zinc transporter	orf; Unknown	K-12_b3040_ygiE_s_at	2.132	2.132	2.005	0.801	0.061	0.296	0.534

Venn: Other
>2fold higher in Δ relAspoT only
17 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
cycA	b4208	D-alanine/D-serine/glycine transporter	transport; Transport of small molecules: Amino acids, amines	K-12_b4208_cycA_s_at	1.001	0.602	1.003	0.334	0.716	1.621	2.03
umuD	b1183	DNA polymerase V, subunit D	putative enzyme; DNA - replication, repair, restriction/modification	K-12_b1183_umuD_s_at	1.045	0.646	0.587	0.639	0.356	0.896	2.462
narP	b2193	DNA-binding response regulator in two-component regulatory system	regulator; Energy metabolism, carbon: Anaerobic respiration	K-12_b2193_narP_s_at	1.113	1.4	1.127	1.848	1.365	2.108	2.304
relB	b1564	Qin prophage; bifunctional antitoxin of the RelE-RelB toxin-antitoxin s	regulator; Global regulatory functions	K-12_b1564_relB_s_at	1.765	2.748	2.101	2.46	0.879	3.314	3.25
hokD	b1562	Qin prophage; small toxic polypeptide	factor; Cell killing -1- component of addiction module (incomplete)	K-12_b1562_hokD_s_at	3.075	3.327	3.168	1.799	1.502	3.514	4.238
relE	b1563	Qin prophage; toxin of the RelE-RelB toxin-antitoxin system	orf; Unknown	K-12_b1563_relE_s_at	2.26	2.457	2.169	1.388	1.714	2.616	3.312
rmr	b4179	exoribonuclease R, RNase R	putative enzyme; Not classified	K-12_b4179_rmr_s_at	1.526	2.232	1.358	-0.343	0.617	2.556	2.666
ygiT	b3021	predicted DNA-binding transcriptional regulator	orf; Unknown	K-12_b3021_ygiT_s_at	2.04	2.656	2.324	2.032	2.178	4.01	4.399
ymB	b1726	predicted inner membrane protein	orf; Unknown	K-12_b1726_ymB_s_at	1.014	1.043	1.069	0.489	0.56	1.487	2.237
yeeE	b2013	predicted inner membrane protein	putative transport; Not classified	K-12_b2013_yeeE_s_at	3.937	4.277	3.607	2.205	3.813	5.553	5.332
ykiA	b0392	predicted protein	orf; Unknown	K-12_b0392_ykiA_a_at	1.126	1.926	0.297	0.145	0.046	1.023	2.302
ycbW	b0946	predicted protein	orf; Unknown	K-12_b0946_ycbW_s_at	1.262	1.086	1.46	0.576	1.08	1.43	2.434
yceP	b1060	predicted protein	orf; Unknown	K-12_b1060_yceP_s_at	2.229	3.153	1.617	0.394	0.705	2.44	3.238
yctR	b1112	predicted protein	orf; Unknown	K-12_b1112_yctR_s_at	1.872	2.281	1.899	1.866	1.406	2.779	3.358
ydcD	b1457	predicted protein	orf; Unknown	O157_EC0244_s_at	1.307	1.644	1.91	2.362	0.376	2.337	2.816
ydhR	b1667	predicted protein	orf; Unknown	K-12_b1667_ydhR_s_at	1.228	0.927	1.193	-0.064	0.658	1.395	2.683
yejG	b2181	predicted protein	orf; Unknown	K-12_b2181_yejG_s_at	1.127	0.652	0.696	0.553	1.406	1.54	2.45

Venn: Other
>2fold higher in Δ lrp only
5 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
ybcM	b0546	DLP12 prophage; predicted DNA-binding transcriptional regulator	putative regulator; Not classified	K-12_b0546_ybcM_at	2.187	3.33	2.28	1.743	1.033	0.608	1.729
ydiV	b1707	conserved protein	orf; Unknown	K-12_b1707_ydiV_s_at	1.327	2.358	1.847	0.985	0.565	0.589	1.44
dinJ	b0226	predicted antitoxin of YafQ-DinJ toxin-antitoxin system	phenotype; Not classified	K-12_b0226_dinJ_s_at	1.732	2.874	2.2	2.836	0.566	2.265	1.94
yabQ	b0057	predicted protein	orf; Unknown	K-12_b0057_yabQ_at	1.325	2.469	1.984	0.855	0.282	0.69	0.774
ybiJ	b0802	predicted protein	orf; Unknown	K-12_b0802_ybiJ_s_at	2.026	3.311	2.394	0.563	0.75	0.444	1.055

Venn: Other
>2fold lower in Δ relAspoT, higher in Δ lrp
6 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
ilvM	b3769	acetylactate synthase II, small subunit	enzyme; Amino acid biosynthesis: Isoleucine, Valine	K-12_b3769_ilvM_s_at	4.628	5.766	5.117	3.981	2.399	3.505	2.379
ygiW	b3024	conserved protein	orf; Unknown	K-12_b3024_ygiW_s_at	1.616	3.051	1.149	3.242	0.776	-0.118	0.152
ycgZ	b1164	predicted protein	orf; Unknown	K-12_b1164_ycgZ_x_at	3.687	5.257	3.247	5.104	0.404	1.355	1.694
ymgA	b1165	predicted protein	orf; Unknown	K-12_b1165_ymgA_at	4.631	5.881	4.132	6.089	0.765	1.302	1.666
ymgC	b1167	predicted protein	orf; Unknown	K-12_b1167_ymgC_at	1.795	3.145	0.84	1.014	0.349	0.374	0.195
yhjX	b3547	predicted transporter	putative transport; Drug/analog sensitivity	K-12_b3547_yhjX_s_at	1.758	4.818	1.045	-0.036	2.251	-0.088	-0.788

Venn: Other
>2fold higher in both Δ relAspoT and Δ lrp
1 gene

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
ygiU	b3022	predicted cyanide hydratase	orf; Unknown	K-12_b3022_ygiU_at	2.184	3.299	2.196	0.93	1.13	4.031	4.616

Venn: Other
>2fold higher in Δ relAspoT, Δ lrp, and Δ rpoS
1 gene

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION	PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
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ynaE	b1375	Rac prophage; predicted DNA-binding transcriptional regulator	orf; Unknown	K-12_b1544_ydfK_s_at	2.002	3.048	3.187	2.278	0.257	1.765	3.666
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Venn: Other
>2fold higher in Δ rpoS, lower in Δ relAspoT and Δ lrp
2 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION
fimC	b4316	chaperone, periplasmic	factor; Surface structures
fimI	b4315	fimbrial protein involved in type 1 pilus biosynthesis	structural component; Surface structures

PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
K-12_b4316_fimC_s_at	1.472	-1.821	2.844	0.645	2.626	0.643	0.258
K-12_b4315_fimI_s_at	1.725	-2.317	2.745	0.482	2.398	0.455	-0.04

Venn: Other
>2fold higher in Δ lrp, lower in Δ rpoS
1 gene

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION
yhiP	b3496	predicted transporter	putative transport; Not classified

PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
K-12_b3496_yhiP_s_at	1.337	2.657	0.176	0.422	0.7	1.599	1.952

Venn: Other
>2fold higher in Δ lrp, lower in Δ rpoS, lower in Δ relAspoT
3 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION
ybgS	b0753	conserved protein	putative regulator; Not classified
ymgB	b1166	predicted protein	orf; Unknown
yjfy	b4199	predicted protein	orf; Unknown

PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
K-12_b0753_ybgS_s_at	2.62	3.658	0.948	1.505	1.086	-0.52	-0.407
K-12_b1166_ymgB_x_at	4.66	5.928	3.6	3.806	0.341	0.339	1.523
K-12_b4199_yjfy_s_at	2.466	3.675	0.712	4.135	1.213	0.267	0.053

Venn: Other
>2fold higher in Δ relAspoT, lower in Δ rpoS
2 genes

GENE	LOCUS_TAG	GENE_PRODUCT	FUNCTION
yebF	b1847	predicted protein	orf; Unknown
yjgH	b4248	predicted mRNA endoribonuclease	orf; Unknown

PROBESETS	WT	lrp	rpoS	crp	dksA	relA	relAspoT
K-12_b1847_yebF_s_at	2.024	1.654	0.259	1.017	-0.122	1.975	3.857
K-12_b4248_yjgH_s_at	1.751	1.429	0.284	1.47	-0.181	0.497	5.955