Table S1. Significantly affected genes in the presence of D-galactose in *galT* cells grown in glycerol M63 minimal medium.

Locus	Gene	MAT (w/o Gal)	MAT (w/ Gal)	MAT change*	Function
Up regulated					
b0759	*galE*	-0.18	6.66	6.84	UDP-galactose-4-epimerase
b4119	*melA*	0.80	7.24	6.44	alpha-galactosidase NAD(P)-binding
b0757	*galK*	0.75	6.37	5.62	galactokinase
b3510	*hdeA*	5.56	9.87	4.31	stress response protein acid-resistance protein
b3509	*hdeB*	4.33	8.62	4.29	acid-resistance protein
b0756	*galM*	1.92	5.29	3.37	galactose-1-epimerase (mutarotase)
b4120	*melB*	1.12	4.44	3.32	melibiose:sodium symporter
b1493	*gadB*	2.34	5.66	3.32	glutamate decarboxylase B PLP-dependent
b1492	*gadC*	0.18	3.48	3.30	predicted glutamate:gamma-aminobutyric acid antiporter
b3517	*gadA*	2.36	5.44	3.08	glutamate decarboxylase A PLP-dependent
b3511	*hdeD*	1.25	4.22	2.97	acid-resistance membrane protein
b1480	*sra*	6.82	9.74	2.92	30S ribosomal subunit protein S22
b0331	*prpB*	0.63	3.50	2.87	2-methylisocitrate lyase
b0296	*ykgM*	2.49	5.35	2.86	rpmE (L31) paralog
b1836	*yebV*	3.79	6.57	2.78	predicted protein
b4506	*ykgO*	0.73	3.49	2.76	rpmJ (L36) paralog
b0953	*rmf*	5.63	8.38	2.75	ribosome modulation factor
b2943	*galP*	0.53	3.08	2.55	D-galactose transporter
b2080	*yegP*	1.56	3.98	2.42	predicted protein
b1783	*yeaG*	0.69	3.10	2.41	conserved protein with nucleoside triphosphate hydrolase domain
b1283	*osmB*	0.00	2.34	2.34	lipoprotein
b1897	*otsB*	-0.37	1.94	2.31	trehalose-6-phosphate phosphatase biosynthetic
b1661	*cfa*	1.74	4.03	2.29	cyclopropane fatty acyl phospholipid synthase (unsaturated-phospholipid methyltransferase)
b1051	*msyB*	2.76	5.04	2.28	predicted protein
b0333	*prpC*	0.82	3.09	2.27	2-methylcitrate synthase
b4376	*osmY*	1.41	3.66	2.25	periplasmic protein
b2097	*fbaB*	3.20	5.42	2.22	fructose-bisphosphate aldolase class I
b0334	*prpD*	-0.33	1.87	2.20	2-methylcitrate dehydratase
b1004	*wrbA*	3.38	5.55	2.17	predicted flavoprotein in Trp regulation
b1482	*osmC*	1.29	3.45	2.16	osmotically inducible stress-inducible membrane protein
b1732	*katE*	1.25	3.38	2.13	hydroperoxidase HPII(III) (catalase)
b2464	*talA*	1.84	3.98	2.14	transaldolase A
b0897	*ycaC*	1.39	3.49	2.10	predicted hydrolase
b2266	*elaB*	2.17	4.21	2.04	conserved protein
b3555	*yiaG*	1.29	3.32	2.03	predicted transcriptional regulator
b0836	*yliH*	-1.25	0.70	1.95	conserved protein
b4227	*ytfQ*	1.32	3.27	1.95	predicted sugar transporter subunit: periplasmic-binding component of ABC superfamily
b1896	*otsA*	0.25	2.19	1.94	trehalose-6-phosphate synthase
b1003	*yccJ*	0.31	2.21	1.90	predicted protein
b1795	*yeaQ*	1.29	3.09	1.80	conserved inner membrane protein
b1724	*ydiZ*	1.35	3.13	1.78	predicted protein
b1259	*yciG*	-0.21	1.54	1.75	predicted protein
Down regulated					
b0928	*aspC*	5.93	3.88	-2.05	aspartate aminotransferase PLP-dependent

b0211	*mltD*	2.26	0.21	-2.05	predicted membrane-bound lytic murein transglycosylase D
b0023	*rpsT*	4.16	2.11	-2.05	30S ribosomal subunit protein S20
b3169	*nusA*	3.43	1.38	-2.05	transcription termination/antitermination L factor
b3796	*argX*	1.77	-0.29	-2.06	tRNA-Arg(CCG)
b1304	*pspA*	2.19	0.13	-2.06	regulatory protein for phage-shock-protein operon
b2007	*yeeX*	5.31	3.23	-2.08	conserved protein
b1717	*rpmI*	6.20	4.11	-2.09	50S ribosomal subunit protein L35
b0434	*yajG*	4.18	2.09	-2.09	predicted lipoprotein
b0672	*leuW*	5.40	3.30	-2.10	tRNA-Leu(UAG)
b0150	*fhuA*	1.30	-0.79	-2.09	ferrichrome outer membrane transporter
b0889	*lrp*	4.78	2.68	-2.10	DNA-binding transcriptional dual regulator leucine-binding
b0748	*lysZ*	7.18	5.08	-2.10	tRNA-Lys(UUU)
b3672	*ivbL*	6.51	4.40	-2.11	ilvB operon leader peptide
b1207	*prsA*	4.19	2.08	-2.11	phosphoribosylpyrophosphate synthase
b0033	*carB*	2.36	0.24	-2.12	carbamoyl-phosphate synthase large subunit
b4142	*groS*	8.62	6.50	-2.12	Cpn10 chaperonin GroES small subunit of GroESL
b3261	*fis*	3.49	1.36	-2.13	global DNA-binding transcriptional dual regulator
b2669	*stpA*	1.66	-0.46	-2.12	DNA binding protein nucleoid-associated
b4172	*hfq*	5.10	2.98	-2.12	HF-I host factor for RNA phage Q beta replication
b0177	*ecfK*	3.75	1.61	-2.14	conserved protein
b3170	*yhbC*	2.96	0.80	-2.16	conserved protein
b2480	*bcp*	5.41	3.25	-2.16	thiol peroxidase thioredoxin-dependent
b3165	*rpsO*	4.22	2.04	-2.18	30S ribosomal subunit protein S15
b3609	*secB*	3.73	1.52	-2.21	protein export chaperone
b2463	*maeB*	3.24	1.03	-2.21	malic enzyme
b0115	*aceF*	4.09	1.87	-2.22	pyruvate dehydrogenase dihydrolipoyl transacetylase component E2
b3339	*tufA*	11.36	9.13	-2.23	protein chain elongation factor EF-Tu (duplicate of tufB)
b4418	*sraB*	4.71	2.47	-2.24	small RNA
b0071	*leuD*	5.34	3.10	-2.24	3-isopropylmalate isomerase subunit
b2323	*fabB*	7.88	5.64	-2.24	3-oxoacyl-[acyl-carrier-protein] synthase I
b2185	*rplY*	6.13	3.89	-2.24	50S ribosomal subunit protein L25
b3164	*pnp*	4.20	1.94	-2.26	polynucleotide phosphorylase/polyadenylase
b2608	*rimM*	8.13	5.85	-2.28	16S rRNA processing protein
b4203	*rplI*	2.36	0.07	-2.29	50S ribosomal subunit protein L9
b2752	*cysD*	3.91	1.61	-2.30	sulfate adenylyltransferase subunit 2
b1094	*acpP*	9.00	6.71	-2.29	acyl carrier protein (ACP)
b3299	*rpmJ*	9.73	7.43	-2.30	50S ribosomal subunit protein L36
b1602	*pntB*	3.83	1.53	-2.30	pyridine nucleotide transhydrogenase beta subunit
b0170	*tsf*	6.26	3.96	-2.30	protein chain elongation factor EF-Ts
b0746	*valZ*	8.74	6.43	-2.31	tRNA-Val(UAC)
b0721	*sdhC*	6.97	4.66	-2.31	succinate dehydrogenase membrane subunit binds cytochrome b556
b2283	*nuoG*	3.60	1.28	-2.32	NADH:ubiquinone oxidoreductase chain G
b0565	*ompT*	10.27	7.94	-2.33	DLP12 prophage outer membrane protease VII
b2693	*argY*	5.55	3.23	-2.32	tRNA-Arg(ACG)
b0114	*aceE*	4.88	2.55	-2.33	pyruvate dehydrogenase decarboxylase component E1 thiamin-binding
b2093	*gatB*	9.15	6.79	-2.36	galactitol-specific enzyme IIB component of PTS
b3255	*accB*	5.04	2.69	-2.35	acetyl CoA carboxylase BCCP subunit
b1782	*mipA*	4.44	2.07	-2.37	scaffolding protein for murein synthesizing machinery
b3065	*rpsU*	5.85	3.47	-2.38	30S ribosomal subunit protein S21
b0747	*lysY*	8.01	5.63	-2.38	tRNA-Lys(UUU)
b2403	*valY*	7.89	5.50	-2.39	tRNA-Val(UAC)
b0474	*adk*	5.08	2.69	-2.39	adenylate kinase
b4036	*lamB*	3.27	0.87	-2.40	maltose outer membrane porin (maltoporin)
b2285	*nuoE*	5.52	3.12	-2.40	NADH:ubiquinone oxidoreductase chain E
b3936	*rpmE*	5.28	2.86	-2.42	50S ribosomal subunit protein L31
b3341	*rpsG*	9.94	7.52	-2.42	30S ribosomal subunit protein S7

b3707	*tnaC*	3.38	0.95	-2.43	tryptophanase leader peptide
b2935	*tktA*	4.37	1.94	-2.43	transketolase 1 thiamin-binding
b2607	*trmD*	7.99	5.55	-2.44	tRNA (guanine-1-)-methyltransferase
b0178	*hlpA*	5.66	3.22	-2.44	periplasmic chaperone
b2402	*valX*	2.56	0.11	-2.45	tRNA-Val(UAC)
b1093	*b1093*	5.22	2.75	-2.47	3-oxoacyl-[acyl-carrier-protein] reductase
b2284	*nuoF*	4.04	1.57	-2.47	NADH:ubiquinone oxidoreductase chain F
b3260	*dusB*	2.97	0.49	-2.48	tRNA-dihydrouridine synthase B
b3460	*livJ*	8.59	6.10	-2.49	leucine/isoleucine/valine transporter subunit
b1761	*gdhA*	4.62	2.12	-2.50	glutamate dehydrogenase NADP-specific
b0337	*codA*	2.92	0.42	-2.50	cytosine deaminase
b2599	*pheA*	6.05	3.53	-2.52	chorismate mutase; prephenate dehydratase
b4034	*malE*	3.54	1.00	-2.54	maltose transporter subunit
b3976	*thrU*	6.41	3.85	-2.56	tRNA-Thr(UGU)
b3766	*ilvL*	5.65	3.08	-2.57	ilvG operon leader peptide
b3739	*atpI*	4.31	1.73	-2.58	ATP synthase membrane-bound accesory subunit
b3980	*tufB*	11.31	8.72	-2.59	protein chain elongation factor EF-Tu (duplicate of tufA)
b1713	*pheT*	4.89	2.30	-2.59	phenylalanine tRNA synthetase beta subunit
b3433	*asd*	4.76	2.14	-2.62	aspartate-semialdehyde dehydrogenase NAD(P)-binding
b1237	*hns*	6.84	4.21	-2.63	global DNA-binding transcriptional dual regulator H-NS
b4000	*hupA*	8.39	5.76	-2.63	HU DNA-binding transcriptional regulator alpha subunit
b3230	*rpsI*	6.00	3.37	-2.63	30S ribosomal subunit protein S9
b1089	*rpmF*	4.16	1.52	-2.64	50S ribosomal subunit protein L32
b3321	*rpsJ*	9.80	7.15	-2.65	30S ribosomal subunit protein S10
b1452	*yncE*	3.47	0.82	-2.65	conserved protein
b2609	*rpsP*	7.58	4.94	-2.64	30S ribosomal subunit protein S16
b4414	*tff*	6.59	3.94	-2.65	small RNA
b3308	*rplE*	9.96	7.32	-2.64	50S ribosomal subunit protein L5
b2288	*nuoA*	5.34	2.69	-2.65	NADH:ubiquinone oxidoreductase membrane subunit A
b3294	*rplQ*	5.94	3.28	-2.66	50S ribosomal subunit protein L17
b3636	*rpmG*	8.03	5.35	-2.68	50S ribosomal subunit protein L33
b2286	*nuoC*	4.57	1.89	-2.68	NADH:ubiquinone oxidoreductase chain CD
b0407	*yajC*	4.85	2.14	-2.71	SecYEG protein translocase auxillary subunit
b3310	*rplN*	9.80	7.08	-2.72	50S ribosomal subunit protein L14
b3296	*rpsD*	9.69	6.95	-2.74	30S ribosomal subunit protein S4
b2287	*nuoB*	5.26	2.51	-2.75	NADH:ubiquinone oxidoreductase chain B
b3342	*rpsL*	9.40	6.65	-2.75	30S ribosomal subunit protein S12
b3670	*ilvN*	2.34	-0.42	-2.76	acetolactate synthase I small subunit
b2243	*glpC*	2.44	-0.33	-2.77	sn-glycerol-3-phosphate dehydrogenase (anaerobic) small subunit
b0763	*modA*	6.36	3.59	-2.77	molybdate transporter subunit
b2414	*cysK*	8.45	5.68	-2.77	cysteine synthase A O-acetylserine sulfhydrolase A subunit
b3403	*pck*	5.68	2.90	-2.78	phosphoenolpyruvate carboxykinase
b3340	*fusA*	9.91	7.13	-2.78	protein chain elongation factor EF-G GTP-binding
b4314	*b4314*	5.15	2.35	-2.80	major type 1 subunit fimbrin (pilin)
b3986	*rplL*	7.69	4.86	-2.83	50S ribosomal subunit protein L7/L12
b0741	*pal*	6.38	3.53	-2.85	peptidoglycan-associated outer membrane lipoprotein
b0811	*glnH*	6.72	3.85	-2.87	glutamine transporter subunit
b3295	*rpoA*	9.04	6.17	-2.87	RNA polymerase alpha subunit
b3870	*glnA*	4.42	1.54	-2.88	glutamine synthetase
b1714	*pheS*	4.96	2.08	-2.88	phenylalanine tRNA synthetase alpha subunit
b3311	*rpsQ*	7.01	4.12	-2.89	30S ribosomal subunit protein S17
b3301	*rplO*	8.12	5.23	-2.89	50S ribosomal subunit protein L15
b1243	*oppA*	5.39	2.49	-2.90	oligopeptide transporter subunit
b0004	*thrC*	3.85	0.93	-2.92	threonine synthase
b0074	*leuA*	6.18	3.26	-2.92	2-isopropylmalate synthase
b4246	*pyrL*	4.17	1.24	-2.93	pyrBI operon leader peptide
b3300	*secY*	8.32	5.38	-2.94	preprotein translocase membrane subunit
b3309	*rplX*	9.74	6.79	-2.95	50S ribosomal subunit protein L24

b0911	*rpsA*	8.17	5.18	-2.99	30S ribosomal subunit protein S1
b3767	*ilvG_1*	3.86	0.85	-3.01	acetolactate synthase II large subunit N-ter fragment (pseudogene)
b0072	*leuC*	5.87	2.86	-3.01	3-isopropylmalate isomerase subunit dehydratase component
b3985	*rplJ*	8.55	5.53	-3.02	50S ribosomal subunit protein L10
b3983	*rplK*	9.22	6.19	-3.03	50S ribosomal subunit protein L11
b3320	*rplC*	9.07	6.05	-3.02	50S ribosomal subunit protein L3
b3303	*rpsE*	8.03	5.00	-3.03	30S ribosomal subunit protein S5
b3297	*rpsK*	9.35	6.30	-3.05	30S ribosomal subunit protein S11
b3307	*rpsN*	8.61	5.55	-3.06	30S ribosomal subunit protein S14
b3458	*livK*	3.90	0.80	-3.10	leucine transporter subunit
b1779	*gapA*	9.27	6.15	-3.12	glyceraldehyde-3-phosphate dehydrogenase A
b3306	*rpsH*	8.48	5.34	-3.14	30S ribosomal subunit protein S8
b0440	*hupB*	5.81	2.64	-3.17	HU DNA-binding transcriptional regulator beta subunit
b3231	*rplM*	8.95	5.77	-3.18	50S ribosomal subunit protein L13
b0003	*thrB*	3.62	0.42	-3.20	homoserine kinase
b3637	*rpmB*	8.71	5.51	-3.20	50S ribosomal subunit protein L28
b0429	*cyoD*	5.32	2.11	-3.21	cytochrome o ubiquinol oxidase subunit IV
b0436	*tig*	4.98	1.73	-3.25	peptidyl-prolyl cis/trans isomerase (trigger factor)
b3984	*rplA*	8.20	4.95	-3.25	50S ribosomal subunit protein L1
b0169	*rpsB*	7.62	4.37	-3.25	30S ribosomal subunit protein S2
b3298	*rpsM*	9.21	5.95	-3.26	30S ribosomal subunit protein S13
b3316	*rpsS*	8.08	4.79	-3.29	30S ribosomal subunit protein S19
b3313	*rplP*	7.53	4.23	-3.30	50S ribosomal subunit protein L16
b0430	*cyoC*	4.48	1.17	-3.31	cytochrome o ubiquinol oxidase subunit III
b3305	*rplF*	8.04	4.72	-3.32	50S ribosomal subunit protein L6
b2241	*glpA*	1.87	-1.46	-3.33	sn-glycerol-3-phosphate dehydrogenase large subunit
b2242	*glpB*	2.47	-0.86	-3.33	sn-glycerol-3-phosphate dehydrogenase membrane anchor subunit
b3314	*rpsC*	7.47	4.13	-3.34	30S ribosomal subunit protein S3
b3302	*rpmD*	7.65	4.31	-3.34	50S ribosomal subunit protein L30
b0598	*cstA*	5.35	1.93	-3.42	carbon starvation protein
b0032	*carA*	4.19	0.74	-3.45	carbamoyl phosphate synthetase small subunit
b3312	*rpmC*	5.48	2.02	-3.46	50S ribosomal subunit protein L29
b4243	*yjgF*	5.64	2.18	-3.46	ketoacid-binding protein
b3304	*rplR*	7.24	3.76	-3.48	50S ribosomal subunit protein L18
b3318	*rplW*	9.12	5.64	-3.48	50S ribosomal subunit protein L23
b0073	*leuB*	6.18	2.68	-3.50	3-isopropylmalate dehydrogenase
b0929	*ompF*	12.38	8.87	-3.51	outer membrane porin 1a (IabF)
b3317	*rplB*	7.97	4.46	-3.51	50S ribosomal subunit protein L2
b3671	*ilvB*	4.00	0.44	-3.56	acetolactate synthase I large subunit
b1088	*yceD*	7.77	4.18	-3.59	conserved protein
b3315	*rplV*	8.13	4.51	-3.62	50S ribosomal subunit protein L22
b2518	*ndk*	5.83	2.18	-3.65	multifunctional nucleoside diphosphate kinase
b3732	*atpD*	5.71	2.03	-3.68	F1 sector of membrane-bound ATP synthase beta subunit
b2175	*spr*	6.17	2.48	-3.69	predicted peptidase outer membrane lipoprotein
b3319	*rplD*	8.14	4.37	-3.77	50S ribosomal subunit protein L4
b1603	*pntA*	5.88	2.09	-3.79	pyridine nucleotide transhydrogenase alpha subunit
b4202	*rpsR*	6.77	2.95	-3.82	30S ribosomal subunit protein S18
b0431	*cyoB*	5.38	1.52	-3.86	cytochrome o ubiquinol oxidase subunit I
b3977	*tyrU*	7.76	3.89	-3.87	tRNA-Tyr(GUA)
b3738	*atpB*	7.45	3.52	-3.93	F0 sector of membrane-bound ATP synthase subunit a
b4201	*priB*	8.05	4.10	-3.95	primosomal protein N
b0002	*thrA*	5.23	1.27	-3.96	fused aspartokinase I and homoserine dehydrogenase I
b4200	*rpsF*	7.34	3.35	-3.99	30S ribosomal subunit protein S6
b2498	*upp*	4.45	0.43	-4.02	uracil phosphoribosyltransferase
b3979	*thrT*	7.68	3.40	-4.28	tRNA-Thr(GGU)
b3737	*atpE*	8.68	4.40	-4.28	F0 sector of membrane-bound ATP synthase subunit c
b3733	*atpG*	6.70	2.29	-4.41	F1 sector of membrane-bound ATP synthase gamma subunit

b3544	*dppA*	7.73	3.27	-4.46	dipeptide transporter
b3978	*glyT*	7.31	2.73	-4.58	tRNA-Gly(UCC)
b0432	*cyoA*	6.19	1.60	-4.59	cytochrome o ubiquinol oxidase subunit II
b3736	*atpF*	8.28	3.66	-4.62	F0 sector of membrane-bound ATP synthase subunit b
b0553	*nmpC*	9.43	4.76	-4.67	DLP12 prophage truncated outer membrane porin (pseudogene)
b3734	*atpA*	7.46	2.74	-4.72	F1 sector of membrane-bound ATP synthase alpha subunit
b3735	*atpH*	8.47	3.73	-4.74	F1 sector of membrane-bound ATP synthase delta subunit
b3774	*ilvC*	8.12	3.14	-4.98	ketol-acid reductoisomerase NAD(P)-binding
b2239	*glpQ*	4.67	-1.14	-5.81	periplasmic glycerophosphodiester phosphodiesterase
b4244	*pyrI*	7.19	0.94	-6.25	aspartate carbamoyltransferase regulatory subunit
b2240	*glpT*	6.13	-0.40	-6.53	sn-glycerol-3-phosphate transporter
b3426	*glpD*	6.79	0.20	-6.59	sn-glycerol-3-phosphate dehydrogenase aerobic FAD/NAD(P)-binding
b4245	*pyrB*	7.88	1.18	-6.70	aspartate carbamoyltransferase catalytic subunit
b3927	*glpF*	8.81	0.19	-8.62	glycerol facilitator
b3926	*glpK*	9.60	0.72	-8.88	glycerol kinase

* Genes with two times standard deviations of MAT score changes (natural log) were selected from DNA tiling arrays.