Supplementary material for Zimmer *et al.* (2000) *Proc. Natl. Acad. Sci. USA* **97** (26), 14674–14679. (10.1073/pnas.250486497)

Table 2. $(R/G)_{median}$ of 99 genes over 11 experiments

UNIQID	Name		a=*glnLup* (Cy5) *vs glnLup nac* (Cy3) [NH3], 2nd PCR =>Nac control	b=*glnLup* (Cy5) *vs glnLup nac* (Cy3) [Gln], 2nd PCR =>Nac control	c=*glnLup* (Cy5) *vs glnG* (Cy3) [NH3], 1st PCR =>NtrC&Nac control	d=*glnLup* (Cy5) *vs glnG* (Cy3) [NH3], 2nd PCR =>NtrC&Nac control	e=*glnLup* (Cy5) *vs glnG* (Cy3) [Gln], 1st PCR =>NtrC&Nac control	f=*glnLup* (Cy5) *vs glnG* (Cy3) [Gln], 2nd PCR =>NtrC&Nac control	g=*glnLup nac* (Cy5) *vs glnG* (Cy3) [NH3], 1st PCR =>NtrC control	h=*glnLup nac* (Cy5) *vs glnG* (Cy3) [Gln], 2nd PCR =>NtrC control	i=Gln(Cy5) vs NH3(Cy3) [*glnG*],1st PCR =>other control	j=NH3(Cy5) vs Gln(Cy3) [glc], 1st PCR	k=NH3(Cy5) vs Gln(Cy3) [gly], 1st PCR
b0315	b0315	yahA orf, hypothetical protein	1.3	1.1	3.6	1.2	2.1	1.3	1	1.1	0.8	0.8	2.5
b0336	b0336	codB cytosine permease/transport	1.8	6.3	3.1	2.1	11.9	6	0.9	1.1	0.3	0.2	0.1
b0337	b0337	codA cytosine deaminase	1.8	3.4	2.8	2.4	7.3	3.7	0.7	1	0.4	0.3	0.1
b0450	b0450	glnK nitrogen regulatory protein P-II 2	0.9	0.7		10.3		17.2	19.6	26.1			
b0451	b0451	amtB probable ammonium transporter	0.9	1	6.2	0.9	7.9	0.9	1.3	1	1.2	0.1	0.3
b0452	b0452	tesB acyl-CoA thioesterase II	1	1	3.3	1.5	2.2	1.2	1.2	1.1	1.8	0.4	0.4
b0652	b0652	gltL ATP-binding protein of glutamate/aspartate transport system	1.1	0.8	1.5	1.2	1.7	1.3	1.5	1.4	1.1	0.8	0.9
b0653	b0653	gltK glutamate/aspartate transport system permease	1	0.9	1.6	1.1	2	1.3	1.1	1.6	0.8	1	1.1
b0654	b0654	gltJ glutamate/aspartate transport system permease	1.1	1.1	1.7	1.1	2.2		1.4	1.2	0.6	0.8	0.7
b0655	b0655	ybeJ putative periplasmic binding transport protein	1.3	1.4	3.4	0.8	6.5	1.1	1.6	1	0.9	0.8	0.7
b0809	b0809	glnQ ATP-binding component of glutamine high-affinity transport system	1.1	0.4	2.7	1.9	3.6	2	1.3	4.9	0.8	0.5	0.5
b0810	b0810	glnP glutamine high-affinity transport system; membrane component	1.2	0.6	3.5	2.1	6	2.9	2.3	6.4	1	0.4	0.5
b0811	b0811	glnH periplasmic glutamine-binding protein; permease	1	0.5	4.5	5.8	9.4	4.7	5.9	11.3	1.1	0.3	0.4
b0854	b0854	potF periplasmic putrescine-binding protein; permease protein	1.4	0.9	4.8	3.4	6.3	2.6	2.6	3.7	1.3	0.3	0.3
b0855	b0855	potG ATP-binding component of putrescine transport system	1.3	0.8	1.9	2.1	4	1.6	1.2	2.3	1	0.4	0.4
b0856	b0856	potH putrescine transport protein; permease	1.2	0.9	2.5	1.5	2.6	1.2	1.2	1.9	0.9	0.5	0.5
b0857	b0857	potI putrescine transport protein; permease	1.1	0.9	1.2	1.1	1.7	0.9	0.6	1.3	0.9	0.7	0.7
b0897	b0897	ycaC orf, hypothetical protein	1.7	0.5	1.9	2.6	1	0.4	0.9	0.6	4.4	0.3	0.4
b0929	b0929	ompF outer membrane protein 1a (Ia;b;F)	2.6	8.8	4.1	4.9	24.9	28.8	2.1	2.8	0.2	0.5	0.6
b1006	b1006	ycdG putative transport protein	1.1	0.6	5.1	2.6	6.5	2.4	1.5	5.9	1	0.2	0.2
b1007	b1007	b1007 orf, hypothetical protein	1	0.6	1.8	2	6.6	3.1	2.3	6.4	1	0.3	0.2
b1008	b1008	b1008 putative enzyme	1	0.7	16	2.4	16.9	3	2.4	6.1	1.5	0.3	0.1
b1009	b1009	b1009 putative acetyltransferase	1	0.7	7.1	4.4	17.1	3.5	3.3	9.3	1	0.3	0.1
b1010	b1010	b1010 orf, hypothetical protein	1	0.6	4	1.9	2.8	2.6	2.4	4.3	0.8	0.6	0.3
b1011	b1011	b1011 putative synthetase	1.2	0.6	25	5.5	32.9	3.4	2.7	8.4	1	0.2	0.1
b1012	b1012	b1012 orf, hypothetical protein	1.2	0.7	26.3	10.6	51.8	6.7	4.3	15.8	1.1	0.1	0.1
b1034	b1034	ycdX orf, hypothetical protein	1	1.1	3.6	1.1	4.9	1.1	0.9	1.1	1.1	0.7	0.6
b1035	b1035	ycdY putative oxidoreductase component	0.9	0.9	0.7	1.1	0.9	1	1.4	1.1	0.9	1.3	1.5
b1217	b1217	chaB cation transport regulator	1.1	0.9	1	1.2	1.1	0.8	1	0.9	0.9	1	1
b1218	b1218	chaC cation transport regulator	1.2	0.7	3.8	1.7	5.3	1.5	1.1	2.5	1.4	0.2	0.4
b1243	b1243	oppA oligopeptide transport; periplasmic binding protein	1.4	1.7	2	2.8	5.8	3.7	1.4	2.7	0.3	2.4	0.9
b1244	b1244	oppB oligopeptide transport permease protein	1.3	1.6	1.4	1.6	3.3	2.2	0.9	1.4	0.3	1.2	0.9
b1245	b1245	oppC homolog of Salmonella oligopeptide transport permease protein	1.2	1.4	1.3	1.2	3		0.9	1.4	0.4	1.1	1
b1246	b1246	oppD homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system	1.3	1.6	1.6	1.3	3.9	1.7	1.3	1.2	0.4	0.8	0.7
b1296	b1296	ycjJ putative amino acid/amine transport protein	1.2	1.1	3	1.2	2.7	0.9	0.8	1.1	1.8	0.5	0.4
b1384	b1384	feaR regulatory protein for 2-phenylethylamine catabolism	1.3	1.3	2.7	1.9	3.6	1.1	0.8	0.9	0.7	0.3	0.9
b1440	b1440	b1440 putative transport protein	2.5	6.1	3.8	3	7.4	4.8	0.7	0.9	1	0.4	0.3
b1441	b1441	b1441 putative ATP-binding component of a transport system	1.8	2.3	2.1	1.8	3.3	2.3	2.2	1	1.3	0.6	0.5
b1442	b1442	b1442 putative transport system permease protein	1.3	2.1	2.6	1.4	3.9	1.8	0.8	1	1.1	0.6	0.6
b1443	b1443	b1443 putative transport system permease protein	1.9	2	1.6	1.8	2.6	1.8	0.9	1	0.9	0.7	0.5
b1444	b1444	b1444 putative aldehyde dehydrogenase	1.9	2.2	3.8	4.3	5.3	2.6	1.2	1.2	1.2	0.3	0.3
b1483	b1483	b1483 putative ATP-binding component of a transport system	0.9	0.9	5.3	2	4.5	1.7	1.9	2.5	1.3	0.6	0.3
b1484	b1484	b1484 putative ATP-binding component of a transport system	1.1	0.9	6.9	2.4	6.7	2.9	1.8	3.6	0.9	0.5	0.3
b1485	b1485	b1485 putative transport protein	1.1	0.9	4.9	2.1	7.2	2.1	1.5	2.9	1	0.5	0.5
b1486	b1486	b1486 putative transport system permease protein	1.1	0.9	1	1.9	1.2	2.2	2.5	3.2	0.8	1.1	0.8
b1487	b1487	b1487 putative hemin-binding lipoprotein	1	0.6	50.4	18.3	65.3	7.2	4.9	15.2	0.9	0	0.1
b1488	b1488	b1488 orf, hypothetical protein	0.8	0.8	9.7	4.7	14.6	3.1	4.1	4.9	0.8	0.1	0.1
b1492	b1492	xasA acid sensitivity protein, putative transporter	2.9	1.1	2.4	2.6	0.6	0.4	1.2	0.3	9.4	0.2	0.1
b1493	b1493	gadB glutamate decarboxylase isozyme	4.9	1.3	2.7	4.5	0.7	0.3	0.5	0.2	13.4	0.2	0
b1537	b1537	ydeJ orf, hypothetical protein	1	1.2	1	0.9	0.9	1	1.3	0.9	1.3	0.8	0.9
b1744	b1744	ydjS orf, hypothetical protein	0.9	0.8	6.9	1.6	6.3	1.3	1.4	1.9	1.2	0.3	0.3
b1745	b1745	b1745 orf, hypothetical protein	0.9	0.7	4	1.8	5.3	1.7	1.5	2.6	1.3	0.4	0.4
b1746	b1746	b1746 putative aldehyde dehydrogenase	0.9	0.7	11.5	2	7.3	1.6	1.4	2.4	1.4	0.3	0.2

UNIQID	Name		a=*glnLup* (Cy5) vs *glnLup nac* (Cy3) [NH3], 2nd PCR =>Nac control	b=*glnLup* (Cy5) vs *glnLup nac* (Cy3) [Gln], 2nd PCR =>Nac control	c=*glnLup* (Cy5) vs *glnG* (Cy3) [NH3], 1st PCR =>NtrC&Nac control	d=*glnLup* (Cy5) vs *glnG* (Cy3) [NH3], 2nd PCR =>NtrC&Nac control	e=*glnLup* (Cy5) vs *glnG* (Cy3) [Gln], 1st PCR =>NtrC&Nac control	f=*glnLup* (Cy5) vs *glnG* (Cy3) [Gln], 2nd PCR =>NtrC&Nac control	g=*glnLup nac* (Cy5) vs *glnG* (Cy3) [NH3], 1st PCR =>NtrC control	h=*glnLup nac* (Cy5) vs *glnG* (Cy3) [Gln], 2nd PCR =>NtrC control	i=Gln(Cy5) vs NH3(Cy3) [*glnG*],1st PCR =>other control	j=NH3(Cy5) vs Gln(Cy3) [glc], 1st PCR	k=NH3(Cy5) vs Gln(Cy3) [gly], 1st PCR
b1747	b1747	b1747 orf, hypothetical protein	0.8	0.8	2.3	2.9	8.2	1.8	1.8	3.6	0.8	0.3	0.2
b1748	b1748	cstC acetylornithine delta-aminotransferase	0.8	0.6	7.7	3.6	10.9	3.4	2.2	7.9	0.7	0.2	0.2
b1783	b1783	yeaG orf, hypothetical protein	1.4	0.5	4.5	4.4	2.9	1.1	1.7	2.4	3	0.6	0.3
b1784	b1784	yeaH orf, hypothetical protein	1.2	0.6	4.1	3.1	2.5	0.9	1.2	1.7	2.4	0.4	0.3
b1932	b1932	yedL orf, hypothetical protein	3	3.6	5.2	7.5	4.6	3.3	1.2	0.8	0.8	0.1	0.2
b1987	b1987	cbl transcriptional regulator cys regulon; accessory regulatory circuit affecting cysM	3.1	2.3	29.6	9.9	19.3	2.4	0.7	1	0.7	0.1	0.1
b1988	b1988	nac nitrogen assimilation control protein	15.5	25	48.2	25.4	56.2	22.7	0.7	0.8	1	0	0
b2000	b2000	flu outer membrane fluffing protein, similar to adhesin	1	1.4	1.1	4.2	1.1	1.3	0.8	1	0.9	2.3	0.7
b2306	b2306	hisP ATP-binding component of histidine transport	1	0.6	3.2	1.8	8.4	2	1.7	4.3	0.7	0.7	0.5
b2307	b2307	hisM histidine transport, membrane protein M	1	0.9	1.8	1.6	5.3	1.8	1.5	2.6	0.6	0.5	0.5
b2308	b2308	hisQ histidine transport system permease protein	0.9	0.8	2.1	2.2	3.1	1.4	1.3	1.9	0.6	0.6	0.4
b2309	b2309	hisJ histidine-binding periplasmic protein of high-affinity histidine transport system	0.8	0.6	4.1	2.5	7.4	5.2	2.7	6.7	0.5	0.4	0.4
b2310	b2310	argT lysine-, arginine-, ornithine-binding periplasmic protein	1.1	0.6	10.5	5.5	18.1	12	6.9	26.3	0.5	0.2	0.3
b2393	b2393	nupC permease of transport system for 3 nucleosides	2	2.9	3.9	3.5	5.3	2.6	0.8	1.2	0.6	0.8	0.3
b2661	b2661	gabD succinate-semialdehyde dehydrogenase, NADP-dependent activity	1.7	1.5	2.6	2	1.9	1.4	1	0.8	1.4	0.7	0.8
b2662	b2662	gabT 4-aminobutyrate aminotransferase activity	1.3	1.2	4.3	1.5	2.6	1.1	0.9	0.8	1.4	0.3	0.5
b2663	b2663	gabP transport permease protein of gamma-aminobutyrate	2	2	5.2	2.7	2.9	1.4	0.8	0.8	1.1	0.4	0.5
b2664	b2664	ygaE putative transcriptional regulator	1.2	1	2.2	1.6	1.2	0.8	1	0.8	1.7	0.4	0.6
b2875	b2875	b2875 putative synthases	1.1	0.5	4.8	1.7	7.4	1.8	1.2	4.9	1.1	0.4	0.3
b2876	b2876	b2876 orf, hypothetical protein	1	0.9	3.2		3.1	1.2	1	2	0.5	0.6	0.8
b2882	b2882	ygfO putative transport protein	1	0.9	0.9	1	0.7	0.9	0.9	1	1.4	0.8	1.2
b2883	b2883	ygfP orf, hypothetical protein	1.2	1.3	5.1	2.3	4.2	1.4	1.3	1.1	1.2	0.4	0.3
b2884	b2884	ygfQ orf, hypothetical protein	1.2	1.2	1.4	1	1.3	1	0.9	1	1	0.8	1.1
b2885	b2885	ygfR putative oxidoreductase	1	1.1	1.7	1	1.2	1	1	1.1	1	0.7	0.8
b3073	b3073	ygjG probable ornithine aminotransferase	1.4	0.8	4.8	4.9	3.6	1.8	1.6	1.7	2.2	0.2	0.2
b3225	b3225	nanA N-acetylneuraminate lyase (aldolase); catabolism of sialic acid; not K-12?	1.1	1.4	2.9	1.1	1.5	1.2	0.9	0.9	0.9	0.6	1
b3268	b3268	yhdW putative periplasmic binding transport protein	1.1	0.8	1	9.2	1.4	4.4	2.9	6.7	1	1.5	1
b3269	b3269	yhdX putative transport system permease protein	1.1	1	3	1.5	1.7	1.1	0.8	1.3	1.1	0.6	0.7
b3270	b3270	yhdY putative transport system permease protein	1.1	0.8	1	1.1	1.2	0.9	0.9	1.2	1.7	0.8	0.8
b3271	b3271	yhdZ putative ATP-binding component of a transport system	0.9	0.9	4.4	1.7	4.2	1.5	1.8	1.7	1.3	0.4	0.5
b3509	b3509	hdeB orf, hypothetical protein	4.6	1.1	2.5	5.4	1.2	0.5	1.4	0.6	7.2	0.1	0.1
b3510	b3510	hdeA orf, hypothetical protein	4.8	1	2.8	6.7	1.6	0.6	1.7	0.6	5.6	0.2	0.1
b3511	b3511	hdeD orf, hypothetical protein	1.5	1.2	1.7	2.8	0.9	0.8	1.1	0.7	4.7	0.2	0.4
b3512	b3512	yhiE orf, hypothetical protein	3.1		3.1	3.2	1		0.7	0.4	8.6	0.1	0
b3517	b3517	gadA glutamate decarboxylase isozyme	5.9	1.5	2.6	5.2	0.6	0.3	0.9	0.2	10.3	0.1	0
b3540	b3540	dppF putative ATP-binding component of dipeptide transport system	1.8	2	3.3	2.4	5	2.8	1.1	1.4	0.5	0.6	0.3
b3541	b3541	dppD putative ATP-binding component of dipeptide transport system	1.5	2.2	3.1	1.8	3.9	2.5	0.8	1.3	0.4	0.7	0.5
b3542	b3542	dppC dipeptide transport system permease protein 2	1.6	1.9	2.7	2.1	2.6	2.3	1	1.2	0.5	0.7	0.5
b3543	b3543	dppB dipeptide transport system permease protein 1	1.4	2.6	3.5	1.9	4.4	2.4	0.6	1.2	0.3	0.8	0.7
b3544	b3544	dppA dipeptide transport protein	3.3	5.9	5.5	8.4	10.4	9.6	1.7	2.5	0.5	1.3	0.5
b3868	b3868	glnG response regulator for gln (sensor glnL) (nitrogen regulator I, NRI)	0.9	0.7	2.5	1.7	1.2	1.3	1.1	1.7	1.7	0.5	0.3
b3869	b3869	glnL histidine protein kinase sensor for GlnG regulator (nitrogen regulator II, NRII)	0.9	0.9	3.4	2.6	1.4	1.6	2.7	2.1	2	0.5	0.2
b3870	b3870	glnA glutamine synthetase	1.2	1.1	11.6	9.3	24.4	13.1	5.2	16.7	0.5	0.5	0.2
b4031	b4031	xylE xylose-proton symport	1.1	1	2.7	1.1	1.4	0.9	1.1	0.9	3.3	0.3	0.7
b4207	b4207	fklB FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase)	1.3	1.7	1.6	2.1	3.5	1.8	0.9	1.2	0.7	0.6	0.5
b4208	b4208	cycA transport of D-alanine, D-serine, and glycine	2.5	3.1	5.2	2.8	7.9	3	1	1	0.8	0.2	0.3

Operons were identified by the following criteria: The mRNA level for at least one gene in the operon was at least 2.5-fold higher in the *glnL* (Up) strain than the *glnG* strain on ammonia for arrays printed with at least one set of PCR products. See *Materials and Methods* for details.