TABLE S2. *C. glutamicum* genes showing altered expression in the *gntR1* deleted strain

Gene ID	Gene Name	Δ*gntR1*/wt mRNA ratio	COG	function
cgR_2434	*gntR1*	<0.01	K	bacterial regulatory proteins, GntR family
cgR_2885		0.03	I	myo-inositol-1-phosphate synthase 5.5.1.4
cgR_6001		0.15		
cgR_1331		0.21	G	secreted sugar-binding protein
cgR_1329		0.22	G	ABC-type sugar (aldose) transport system, ATPase component
cgR_1328		0.22	K	LacI-family transcriptional regulator, probable catabolite control protein
cgR_1332		0.23	G	uncharacterized component of ribose/xylose transport systems
cgR_1330		0.25	G	ribose/xylose/arabinose/galactoside ABC-type transport system, permease component
cgR_6073		0.27		
cgR_2774		0.28		hypothetical protein
cgR_5042		0.29		hypothetical protein
cgR_1425	*ptsG*	0.29	G	phosphotransferase system, glucose-specific IIABC component 2.7.1.69
cgR_2794		0.29		hypothetical protein
cgR_0932		0.30		hypothetical protein
cgR_1038	*gapB*	0.31	G	glyceraldehyde 3-phosphate dehydrogenase B 1.2.1.12
cgR_5050		0.31		hypothetical protein
cgR_5000		0.31		hypothetical protein
cgR_2206	*rbsK2*	0.32	G	probable ribokinase protein 2.7.1.15
cgR_0687		0.32		acetyltransferase, GNAT family
cgR_5009		0.34		hypothetical protein
cgR_1511		0.35	P	siderophore-interacting protein
cgR_1384		0.36		hypothetical protein
cgR_1431	*rbsK1*	0.38	G	putative ribokinase protein 2.7.1.15
cgR_1992		0.38	QR	SAM-dependent methyltransferase
cgR_2362		0.38		hypothetical protein
cgR_0688		0.38		hypothetical protein
cgR_1432	*ccpA*	0.39	K	probable LacI-family transcriptional regulator
cgR_2692		0.39		hypothetical protein
cgR_1339	*lysE*	0.39	R	lysine efflux permease

cgR_6068		0.40		
cgR_2245		0.41		hypothetical protein
cgR_5003		0.42		hypothetical protein
cgR_2751	*pckA*	0.42	C	phosphoenolpyruvate carboxykinase 4.1.1.32
cgR_1375		0.43	K	putative TetR-family transcriptional regulator
cgR_1116		0.43	QR	short chain dehydrogenase
cgR_6003		0.43		
cgR_5037		0.43		hypothetical protein
cgR_1409	*PPCgR2*	0.43		probable phage-type integrase
cgR_6142		0.43		
cgR_0151	*ISCgR4*	0.43	L	putative transposase
cgR_2631		0.43		hypothetical protein
cgR_6002		0.43		
cgR_1969		0.44		putative membrane protein
cgR_2316		0.44		hypothetical protein
cgR_2304	*dctP2*	0.44	G	putative TRAP dicarboxylate transporter, DctP subunit
cgR_2335		0.44		hypothetical protein
cgR_0358		0.44		hypothetical protein
cgR_0134		0.44		hypothetical protein
cgR_2765		0.44		hypothetical protein
cgR_0043		0.45	P	ABC transport protein, ATP-binding subunit
cgR_5054		0.45		hypothetical protein
cgR_2436		0.45		hypothetical protein
cgR_0550		0.45		putative secreted protein
cgR_2748		0.45	M	glycosyltransferase 2.4.1.-
cgR_1429	*iunH3*	0.46	F	inosine-uridine preferring nucleoside hydrolase 3.2.2.1
cgR_6043		0.46		
cgR_1447	*ugpE*	0.46	G	sn-glycerol-3-phosphate transport system permease protein
cgR_2951		0.46		putative secreted protein
cgR_0582	*gabT*	0.47	E	probable 4-aminobutyrate aminotransferase protein 2.6.1.19
cgR_1212		0.48		putative secreted protein
cgR_2940		0.48	K	bacterial regulatory protein, TetR family
cgR_2371	*dhaS*	0.48	C	NADP-dependent aldehyde dehydrogenase 1.2.1.3
cgR_2895	*maeB*	0.48	C	malic enzyme 1.1.1.40
cgR_2374		0.48		hypothetical protein

cgR_1445		0.48		hypothetical protein
cgR_0531		0.48		hypothetical protein
cgR_5048		0.48	P	hypothetical protein
cgR_6158		0.48		
cgR_1430		0.49	GEPR	permease of the major facilitator superfamily
cgR_6150		0.49		
cgR_0729		0.49		hypothetical protein
cgR_1250	*lipP*	0.49	I	lipase 3.1.1.3
cgR_2211	*aceB*	0.50	C	malate synthase 2.3.3.9
cgR_0163	*merA2*	0.50	C	mercuric reductase 1.16.1.1
cgR_5036		0.50		hypothetical protein
cgR_2660		0.50		putative secreted protein
cgR_2544		0.51		hypothetical protein
cgR_6135		0.51		
cgR_2152		0.51		hypothetical protein
cgR_2370		0.51		AraC-type regulator
cgR_1882	*PPCgR6*	0.51	M	hypothetical protein
cgR_1293		0.51		hypothetical protein
cgR_2578		0.51		hypothetical protein
cgR_2075		0.51		putative membrane protein
cgR_2798		0.51	S	hypothetical protein
cgR_2797		0.51		hypothetical protein
cgR_1741		0.52		hypothetical protein
cgR_6067		0.52		
cgR_6114		0.52		
cgR_0430		0.52		hypothetical protein
cgR_2990		0.52		hypothetical protein
cgR_2285	*benA*	0.52	PR	benzoate 1,2-dioxygenase alpha subunit (aromatic ring hydroxylation dioxygenase A)
cgR_5049		0.53		hypothetical protein
cgR_1410	*ISCg11b*	0.53	L	transposase
cgR_0583	*gabD2*	0.53	C	putative succinate-semialdehyde dehydrogenase (NADP+) 1.2.1.16

cgR_2212	*aceA*	0.53	C	isocitrate lyase 4.1.3.1
cgR_0535	*res1*	0.53	L	resolvase family recombinase
cgR_2389		0.53		hypothetical protein
cgR_6046		0.54		
cgR_0604		0.54	C	acetyl-CoA transferase
cgR_2693		0.54		hypothetical protein
cgR_0002		0.54		hypothetical protein
cgR_0335	*brnF*	0.54	E	branched chain amino acid exporter, large subunit
cgR_0554		0.55		hypothetical protein
cgR_2319		0.55	R	putative membrane protein
cgR_5025		0.55		hypothetical protein
cgR_0084	*phoH1*	0.55	T	ATPase related to phosphate starvation-inducible protein
cgR_6033		0.56		
cgR_0052		0.56		hypothetical protein
cgR_1858		0.56	O	predicted ATPase with chaperone activity
cgR_6127		0.56		
cgR_0063		0.56		hypothetical protein
cgR_2315		0.57		hypothetical protein
cgR_0477		0.57		hypothetical protein
cgR_0067		0.57		hypothetical protein
cgR_1031		0.57	E	ABC-type branched-chain amino acid transport systems, secreted component
cgR_0911		0.57	F	putative cytidine deaminase
cgR_2837		0.57		permease of the major facilitator superfamily
cgR_0349	*madM*	0.57		malonate transporter MadM subunit
cgR_0968		0.57		hypothetical protein
cgR_0157		0.58	K	Iron dependent repressor
cgR_1821		0.58	EP	ABC-type peptide transport system, permease component
cgR_5060		0.58		hypothetical protein
cgR_0336	*brnE*	0.58		branched chain amino acid exporter, small subunit
cgR_0317		0.58		hypothetical protein
cgR_2686		0.58	C	aldehyde dehydrogenase 1.2.1.3
cgR_2224		0.59		hypothetical protein
cgR_2461		0.59		hypothetical protein
cgR_0012		0.59		helix-turn-helix protein, CopG family
cgR_1412		0.59		hypothetical protein

cgR_2724	*hmp*	0.59	C	flavohemoprotein 1.5.1.34
cgR_6042		0.59		
cgR_6134		0.59		
cgR_2259		0.60	EP	ABC-type dipeptide/oligopeptide/nickel transport system, secreted component
cgR_0385		0.60	E	putative phosphatase
cgR_1029		0.60		hypothetical protein
cgR_0585		0.60	P	cation-transporting ATPase 3.6.1.-
cgR_0803		0.60		hypothetical protein
cgR_0118	*ISCgR1*	0.60	L	putative transposase
cgR_1055		0.60	Q	ABC-type multidrug/protein/lipid transport system, ATPase component
cgR_0150	*ISCgR4*	0.60		putative transposase
cgR_1993	*gip*	0.60	G	putative hydroxypyruvate isomerase protein 5.3.1.22
cgR_5051		0.61		putative secreted protein
cgR_6152		0.61		
cgR_6153		0.61		
cgR_1393		0.61		hypothetical protein
cgR_5039		0.61		hypothetical protein
cgR_1352		0.61	P	ABC-type nitrate/sulfonate/taurine/bicarbonate transport system, ATPase component (N-terminal fragment)
cgR_0309		0.62	Q	putative ABC transporter transmembrane subunit
cgR_0338		0.62	K	hypothetical protein
cgR_1820		0.62	EP	ABC-type peptide transport system, permease component
cgR_6133		0.63		
cgR_6012		0.63		
cgR_0584		0.63	E	permease for amino acids and related compounds, family
cgR_0917		0.63		hypothetical protein
cgR_5053		0.63		hypothetical protein
cgR_2961		0.63	R	hypothetical protein
cgR_1918		0.63	S	putative antirepressor
cgR_1270	*mog*	0.63	H	putative molybdopterin biosynthesis MOG protein
cgR_2421		0.63		hypothetical protein
cgR_0171	*ISCgR7*	0.63	L	putative transposase
cgR_0815	*prpB1*	0.63	G	probable methylisocitric acid lyase 4.1.3.30
cgR_5058		0.64		hypothetical protein

cgR_1136		0.64	MG	short chain dehydrogenase
cgR_2136		0.64		hypothetical protein
cgR_0085		0.64		hypothetical protein
cgR_0046		0.64	G	probable ABC transport protein, ATP-binding component
cgR_1759		0.64		hypothetical protein
cgR_2857		0.64	E	putative regulatory protein
cgR_5002		0.64		membrane protein
cgR_1822		0.64	R	ATPase component of peptide ABC-type transport system, contains duplicated ATPase domains
cgR_0778	*prpB2*	0.64	G	probable methylisocitric acid lyase 4.1.3.30
cgR_2562		0.64		putative membrane protein
cgR_6126		0.64		
cgR_6013		0.65		
cgR_2901		0.65		putative membrane protein
cgR_1446	*ugpA*	0.65	G	sn-glycerol-3-phosphate transport system permease protein
cgR_6100		0.65		
cgR_1418		0.65		putative membrane protein
cgR_0350	*madL*	0.65		malonate transporter MadL subunit
cgR_1819		0.65	EP	ABC-type peptide transport system, secreted component
cgR_2253		0.65		putative secreted or membrane protein
cgR_0170	*mcrC*	0.65		putative protein mcrC
cgR_2284	*catA1*	0.65	Q	catechol 1,2-dioxygenase 1.13.11.1
cgR_0044		0.65	G	probable solute-binding lipoprotein, signal peptide
cgR_1376		0.65		hypothetical protein
cgR_0558		0.65		hypothetical protein
cgR_2469	*sucC*	0.66	C	succinyl-CoA synthetase beta chain 6.2.1.5
cgR_0737		0.66	L	polymerase involved in DNA repair
cgR_1949		0.66		putative hemagglutinin-related protein
cgR_2400	*pncA*	0.66	Q	nicotinamidase/pyrazinamidase 3.5.1.-
cgR_0564		0.66		putative membrane protein
cgR_2355		0.66		hypothetical protein
cgR_1233	*cydA*	1.50	C	cytochrome d ubiquinol oxidase subunit I 1.10.3.-
cgR_1863		1.52	P	ABC-type cobalamin/Fe3+-siderophores transport system, secreted component
cgR_5017		1.52		hypothetical protein
cgR_2263		1.53	K	bacterial regulatory proteins, TetR family

cgR_2942	*tcbF*	1.53	C	maleylacetate reductasetase 1.3.1.32
cgR_6137		1.53		
cgR_1691		1.53	R	putative NADH-dependent FMN reductase 1.5.1.29
cgR_2646		1.54	GEPR	permease of the major facilitator superfamilyynebacterium glutamicum]
cgR_0924		1.55	P	ABC-type cobalamin/Fe3+-siderophores transport system
cgR_2170		1.55	Q	putative beta (1-->2) glucan export composite transmembrane/ATP-binding protein
cgR_2208		1.55	S	uncharacterized iron-regulated membrane protein
cgR_1717		1.55	P	predicted iron-dependent peroxidase, secreted protein
cgR_1039	*pth1*	1.57	J	probable peptidyl-tRNA hydrolase protein 3.1.1.29
cgR_2894		1.58	G	putative arabinose efflux permease
cgR_0672		1.58	S	secreted protein
cgR_1514		1.58	Q	uncharacterized protein, possibly involved in aromatic compounds catabolism
cgR_1625	*tal*	1.59	G	transaldolase 2.2.1.2
cgR_2946		1.61	G	sugar phosphate isomerase/epimerase
cgR_1589		1.61	S	putative membrane protein
cgR_1627	*opcA*	1.62	S	putative subunit of glucose-6-P dehydrogenase
cgR_1231	*cydD*	1.63	Q	ABC-type multidrug/protein/lipid transport system, ATPase component
cgR_0492		1.67	GEPR	putative integral membrane transport protein
cgR_1232	*cydB*	1.68	C	cytochrome d terminal oxidase polypeptide subunit 1.10.3.-
cgR_2547	*ptsS*	1.69	G	enzyme II sucrose protein 2.7.1.69
cgR_1626	*zwf*	1.70	G	glucose-6-phosphate 1-dehydrogenase 1.1.1.49
cgR_0145		1.71	K	putative transcription regulator
cgR_2802		1.73	S	putative carboxymuconolactone decarboxylase subunit
cgR_0493		1.73	G	sugar phosphate isomerases/epimerases
cgR_2732		1.73	PH	putative iron-siderophore uptake system transmembr
cgR_1230	*cydC*	1.76	Q	ABC-type multidrug/protein/lipid transport system, ATPase component
cgR_0144		1.76	R	hypothetical protein
cgR_2388	*betT*	1.76	M	high-affinity choline transport protein
cgR_5055		1.77		hypothetical protein
cgR_2799		1.78	Q	putative aryldialkylphosphatase

cgR_1624	*tkt*	1.82	G	transketolase 2.2.1.1
cgR_2896	*gntK*	1.83	G	putative gluconate kinase 2.7.1.12
cgR_2801		1.86	E	putative aminotransferase 2.6.1.-
cgR_2647		1.87	P	Na+/phosphate symporter
cgR_1528		1.99	GEPR	permease of the major facilitator superfamily
cgR_0440	*galU2*	2.01	M	putative UTP-glucose-1-phosphate uridylyltransferase 2.7.7.9
cgR_2800		2.04	GEPR	putative transmembrane transport protein
cgR_2948	*idhA2*	2.08	R	myo-inositol 2-dehydrogenase 1.1.1.18
cgR_2730	*fepB2*	2.10	P	ferrienterobactin-binding periplasmic protein precursor
cgR_1628	*devB*	2.14	G	putative 6-phosphogluconolactonase 3.1.1.31
cgR_1623	*ctaB*	2.16	H	polyprenyltransferase (cytochrome oxidase assembly factor) 2.5.1.-
cgR_2209		2.27	R	predicted Na+-dependent transporter
cgR_2102		2.30	GEPR	permease of the major facilitator superfamily
cgR_2731		2.39	PH	ferric enterobactin transport protein
cgR_2947	*idhA1*	2.40	R	myo-inositol 2-dehydrogenase 1.1.1.18
cgR_2451		2.40	C	Na+/H+-dicarboxylate symporter family
cgR_2806	*gntP*	2.79	GE	gluconate permease
cgR_2945		3.14	R	predicted dehydrogenase
cgR_1513	*gnd*	3.65	G	6-phosphogluconate dehydrogenase 1.1.1.44
cgR_2497	*dctA*	4.17	C	Na+/H+-dicarboxylate symporter
cgR_2220	*dctM1*	5.06	S	putative C4-dicarboxylate transport system (permease large protein)
cgR_2608	*bglG2*	5.48	K	beta-glucoside operon antiterminator
cgR_2222	*dctP1*	7.77	G	putative C4-dicarboxylate-binding protein
cgR_2221	*dctX*	8.33	S	putative C4-dicarboxylate transport system (permease small protein)
cgR_2609	*bglA2*	8.73	G	beta-glucosidase 3.2.1.21
cgR_2454		9.01	G	sugar phosphate isomerase/epimerase
cgR_2610	*bglF2*	9.40	G	PTS system beta-glucoside-specific enzyme IIABC component 2.7.1.69
cgR_2456		10.67	R	putative lipopolysaccharide biosynthesis protein
cgR_0402	*bglS*	10.72	G	putative beta-glucosidase 3.2.1.21

cgR_2455		11.43	R	predicted dehydrogenase or related protein
cgR_2457		12.11	G	putative sugar phosphate isomerase epimerase
cgR_2459		13.15	G	putative glucuronide permease
cgR_2727	*bglG*	17.97	K	transcriptional antiterminator
cgR_2728	*bglA*	20.13	G	beta-glucosidase 3.2.1.86
cgR_2729	*bglF*	33.49	G	PTS system beta-glucoside-specific enzyme IIABC component 2.7.1.69
cgR_2397	*gntV*	60.60	P	putative gluconokinase 2.7.1.12

The mRNA ratios shown represent mean values from three independent microarray experiments. The table includes those genes which showed more than 1.5-fold change mRNA level in Δ*gntR1* versus wild type. The genes are ordered according to the mRNA ratio of this comparison.