Additional file 1:

Additional method: Microarray hybridization

The hybridization of whole-genome oligonucleotide microarrays was performed as described previously [48], using 10 µg of total RNA from *C. glutamicum* cultures for cDNA synthesis. The normalization and evaluation of the hybridization data was done with the software package EMMA 2 [49] using a signal intensity (A-value) cut-off of ≥7.0 and a signal intensity ratio (M-value) cut-off of ±0.6 (corresponding to fold changes of 1.52 and 0.66, respectively).

Comparison of gene expression in *C. glutamicum* ATCC 13032 vs. Δ*argR*

Coding sequence	Gene	Fold change[a]	Annotation
cg1580	*argC*	9.45	N-acetyl-γ-glutamyl-phosphate reductase
cg1584	*argF*	9.13	Ornithine carbamoyltransferase
cg1583	*argD*	9.06	Acetylornithine aminotransferase, AT class II
cg1581	*argJ*	8.34	Glutamate N-acetyltransferase
cg1582	*argB*	7.62	Acetylglutamate kinase
cg1586	*argG*	6.63	Argininosuccinate synthase
cg1588	*argH*	5.82	Argininosuccinate lyase
cg1813	*carB*	5.17	Carbamoyl-phosphate synthase, large chain
cg1812	*pyrF*	4.06	Orotidine-5'-phosphate decarboxylase
cg1814	*carA*	3.94	Carbamoyl-phosphate synthase, small chain
cg0536		3.81	Putative 5-dehydro-4-deoxyglucarate dehydratase
cg0535		3.39	Putative ketoglutarate semialdehyde dehydrogenase
cg0534		2.91	Putative integral membrane protein
cg3226		2.43	Putative MFS-type L-lactate permease
cg3145		2.36	Hypothetical protein
cg2636	*catA*	2.33	Catechol 1.2-dioxygenase
cg0611		2.25	Putative secreted protein
cg3227	*lldD*	2.17	Quinone dependent L-lactate dehydrogenase
cg1589		1.95	Putative secreted protein
cg0749	*spoU*	1.87	Putative tRNA/rRNA methyltransferase

cg1737	*acn*	1.82	Aconitate hydratase
cg0607		1.77	Putative secreted protein
cg3431	*rnpA*	1.74	Ribonuclease P
cg2546		1.73	Putative secondary C4-dicarboxylate transporter, TRAP-T family
cg0446	*sdhA*	1.69	Succinate dehydrogenase, subunit A
cg1695		1.67	Conserved hypothetical protein, probably HTH-type transcriptional reg.
cg0228		1.65	Two-component system, sensory histidine kinase, putative pseudogene
cg2320		1.64	Putative transcriptional regulator, ArsR-family
cg1343	*narH*	1.62	Respiratory nitrate reductase 2, beta chain
cg2235	*rplS*	1.61	50S ribosomal protein L19
cg2348		1.60	Putative secreted protein
cg1090	*ggtB*	1.58	Putative gamma-glutamyltranspeptidase
cg0445	*sdhCD*	1.57	Succinate dehydrogenase, subunit CD
cg1546	*rbsK1*	1.57	Putative ribokinase
cg2751		1.57	Xanthosine triphosphate pyrophosphatase
cg0961		1.54	Putative hydrolase, alpha/beta-fold
cg2402		1.54	Secreted protein NLP/P60 family
cg2574		1.54	Put. threonine efflux transporter, resistance to homoserine/threonine (RhtB) family
cg1680		1.53	Short-chain dehydrogenase/reductase
cg2071	*int2'*	1.53	Putative phage Integrase (N-terminal fragment)
cg0447	*sdhB*	1.52	Succinate dehydrogenase, subunit B
cg1279		0.66	Putative secreted protein
cg2199	*pbp*	0.66	Putative penicillin-binding protein
cg2824		0.66	SAM-dependent methyltransferase
cg0009		0.65	Putative membrane protein
cg0365		0.65	Putative membrane protein
cg0926		0.65	ABC-type putative iron-siderophore transporter, permease subunit
cg0119	*ureD*	0.65	Urease accessory protein UreD
cg1405		0.64	Siderophore-interacting protein
cg2777		0.63	Conserved putative membrane protein
cg2052		0.63	Putative secreted protein
cg0924		0.62	ABC-type putative iron-siderophore transporter, substrate-binding lipoprotein
cg2962		0.62	Hypothetical protein
cg0726		0.61	Putative secreted lipoprotein

cg1120	*ripA*	0.60	Putative transcriptional regulator, AraC-family
cg2950	*radA*	0.60	Putative ATP-dependent protease, involved in DNA repair
cg0767		0.58	Siderophore-interacting protein
cg2283		0.58	Conserved hypothetical protein
cg0927		0.58	ABC-type putative iron-siderophore transporter, permease subunit
cg1931		0.57	Putative secreted protein
cg1476	*thiC*	0.57	Thiamine biosynthesis protein ThiC
cg0748		0.57	ABC-type putative iron-siderophore transporter, substrate-binding lipoprotein
cg1930		0.54	Putative secreted hydrolase
cg0922		0.52	ABC-type putative iron-siderophore transporter, substrate-binding lipoprotein
cg0771	*irp1*	0.50	ABC-type putative iron-siderophore transporter, substrate-binding lipoprotein
cg4005		0.50	Putative secreted protein
cg1514		0.49	Secreted protein
cg1412	*rbsC*	0.39	ABC-type ribose transporter, permease subunit (TC 3.A.1.2.1)
cg0405		0.38	ABC-type putative iron(III) dicitrate transporter, substrate-binding lipoprotein
cg1411	*rbsA*	0.38	ABC-type ribose transporter, ATPase subunit (TC 3.A.1.2.1)
cg0471		0.37	Conserved secreted protein
cg1413	*rbsB*	0.25	ABC-type ribose transporter, substrate-binding lipoprotein (TC 3.A.1.2.1)
cg1585	*argR*	0.16	Transcriptional repressor of arginine biosynthesis, ArgR-family

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All genes that showed an alteration of transcript levels at least by a factor of ±2 in two independent transcriptome analyses (biological replicates) using DNA microarrays with fourfold genome coverage are listed.

[a] Fold change, signal intensity ratio as defined by $2^{(\text{m-value})}$.