

Table S1 Bacterial strains, plasmids and primers used in the study

Strains and plasmids	Genetic properties/nucleotide sequence	References or purpose
<i>Bradyrhizobium diazoefficiens</i>		
USDA 110	Wild type (WT); Cm <sup>r</sup>	USDA, Beltsville, MD
JD21	<i>nodD2</i> Ω insertion; Sm <sup>r</sup> , Sp <sup>r</sup>	Jitackson and Sadowsky (2008)
Δ <i>bjaR</i> <sub>1</sub>	Mutant strain with a deletion of 365 nucleotides (nt) of <i>bjaR</i> <sub>1</sub> ( <i>blr1062</i> ) gene; Cm <sup>r</sup>	This study
Δ <i>bjaI</i>	Mutant strain with a deletion of 344 nt of <i>bjaI</i> ( <i>blr1063</i> ) gene; Cm <sup>r</sup>	This study
c-Δ <i>bjaR</i> <sub>1</sub>	Genetically complementary strain, Δ <i>bjaR</i> <sub>1</sub> mutant carrying pKS862; Cm <sup>r</sup> , Tc <sup>r</sup>	This study
W3	WT with chromosomal integration of <i>bjaI-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
W2	WT with chromosomal integration of <i>bjaR<sub>1</sub>-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
W4	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>bjaI-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
W1	Δ <i>bjaI</i> mutant with chromosomal integration of <i>bjaR<sub>1</sub>-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
WG3	WT with chromosomal integration of <i>bjaI-gusA</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
WG2	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>bjaI-gusA</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
AQ1	WT with chromosomal integration of <i>nwsA-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
AQ2	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>nwsA-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF2	WT with chromosomal integration of <i>nodD<sub>2</sub>-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF7	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>nodD<sub>2</sub>-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF8	WT with chromosomal integration of <i>nolA-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF3	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>nolA-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF10	WT with chromosomal integration of <i>nodW-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF4	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>nodW-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF1	WT with chromosomal integration of <i>nodD<sub>1</sub>-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
HF6	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>nodD<sub>1</sub>-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
YF1	WT with chromosomal integration of <i>glnB-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
YF2	Δ <i>bjaR</i> <sub>1</sub> mutant with chromosomal integration of <i>glnB-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study

YF3	WT with chromosomal integration of <i>gln II-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
YF4	ΔbjaR <sub>1</sub> mutant with chromosomal integration of <i>gln II-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
YF5	WT with chromosomal integration of <i>amtB-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
YF6	ΔbjaR <sub>1</sub> mutant with chromosomal integration of <i>amtB-lacZ</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
G1	WT with chromosomal integration of <i>nifH-gusA</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
G2	ΔbjaR <sub>1</sub> mutant with chromosomal integration of <i>nifH-gusA</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
G3	c-ΔbjaR <sub>1</sub> strain with chromosomal integration of <i>nifH-gusA</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
G4	JD21 with chromosomal integration of <i>nifH-gusA</i> ; Cm <sup>r</sup> , Km <sup>r</sup>	This study
BX2	WT carrying plasmid pZB32; Cm <sup>r</sup> , Tc <sup>r</sup>	Han et al., 2020
BX4	ΔbjaR <sub>1</sub> mutant carrying plasmid pZB32; Cm <sup>r</sup> , Tc <sup>r</sup>	This study
<i>Escherichia coli</i>		
BW23474	Δ(argF-lac)169 robA1 creC510 hsdR514 endA9 recA1 ΔuidA::pir-116	Metcalf et al., 1994
BW20767	Δ3(lac)X74RP4-2-tet: Mu-1 kan :: Tn7 integrant leu-63:: IS10 recA1 creC510 hsdR17 endA1 sbf-5 uidA (ΔMluI)::pir <sup>+</sup> thi	Metcalf et al., 1994
DH5α	supE44 ΔlacU169 (φ80lacZ ΔM15) hsdR17recA1endA1gyrA96thi-1relA	Thermo Fisher Scientific Inc.
Stellar	F-, endA1, supE44, thi-1, recA1, relA1, gyrA96, phoA, Φ80d lacZΔ M15, Δ(lacZYA-argF) U169, Δ(mrr-hsdRMS-mcrBC), ΔmcrA, λ-	Takara Biomedical Technology (Beijing) Co., Ltd.
Plasmids		
pKS800	Derivative of broad-host-range cosmid pLAFR1; IncP Tc <sup>r</sup>	Hattori et al., 2002
pVIK112	Suicide plasmid containing the vegetative origin of R6K and carrying promoterless <i>lacZYA</i> genes; Km <sup>r</sup>	Kalogeraki and Winans 1997
pVIK165	Suicide plasmid containing the vegetative origin of R6K and carrying promoterless <i>gfp</i> genes; Km <sup>r</sup>	Kalogeraki and Winans 1997
pK18mobSacB	Mobilizable suicide vector; Km <sup>r</sup>	Schäfer et al., 1994
pRK2013	ColE1 replicon carrying RK2 transfer genes; Km <sup>r</sup>	Figurski and Helinski 1979
pZB32	<i>nodY-lacZ</i> translational fusion on a broad-host-range plasmid pPP375; Tc <sup>r</sup>	Banfalvi et al., 1988
pCAM120	mTn5SSgusA20 in pUT/mini-Tn5; Sm <sup>r</sup> /Sp <sup>r</sup>	Wilson et al., 1995
pVIK166	pVIK165-derived plasmid with a replacement of <i>gusA</i> to <i>gfp</i> gene; Km <sup>r</sup>	This study

pKS862	pKS800 carrying a PCR-amplified DNA fragment using primers CΔbjaR <sub>1</sub> _for/_rev at the <i>PmeI</i> site	This study
<b>Primers</b>		
ΔbjaR <sub>1</sub> _UPfor	CGGAATTCAGCAGGAGATAGTCGATGGC	Generation of ΔbjaR <sub>1</sub> mutant using overlap PCR method
ΔbjaR <sub>1</sub> _UPrev	GATCTCCCAGGCCGACTTGGAGTGTAGAGATTGAACCATCCC	
ΔbjaR <sub>1</sub> _DNfor	GGGATGGTTCAATCTCTACACTCCAAGTCGGCCTGGGAGATC	
ΔbjaR <sub>1</sub> _DNrev	GCTCTAGACGAAACCTGTCTCGCGATG	
ΔbjaI_UPfor	CGGAATTC TGACGATGATGGCGGAGTAA	Generation of <i>B. d</i> ΔbjaI mutant using overlap PCR method
ΔbjaI_UPrev	CACCAGGTTTCCATGATCGCCGAAATGCTGCTCGAGTAC	
ΔbjaI_DNfor	GTA CTGAGCAGCATTTCCGGCGATCATGAAACCTGGTG	
ΔbjaI_DNrev	GCTCTAGA_CAGCTTGATGTTGATGCCGA	
CΔbjaR <sub>1</sub> _for	<u>ATTAAGGATCCGTTT</u> AGCAGGAGATAGTCGATGGC	Generation of genetically complemented strain <i>B. d</i> c-ΔbjaR <sub>1</sub>
CΔbjaR <sub>1</sub> _rev	<u>GAATTA CTGAGTTT</u> GACGAGCAGCATCAAGACTC	
bjaR <sub>1</sub> -lacZ_for	<u>ATTTGTGGAATTCCC</u> AGCAGGAGATAGTCGATGGC	Generation of transcriptional <i>lacZ</i> fusions in Fig. 1A and 1B
bjaR <sub>1</sub> -lacZ_rev	<u>ATATCGAGCTCTCCC</u> GGGATTGAGGTCGAGATGGA	
bjaI-lacZ_rev	<u>ATATCGAGCTCTCCC</u> GTTTCCATGATCGCGCTGAC	
gusA_for	<u>ATTTGTGGAATTCCC</u> GGGAGAGCTCGATATCGC	Amplification of <i>gusA</i> ORF as pCAM120 the DNA templet
gusA_rev	<u>AAGCTTGATAGGCC</u> TCATTGTTGCCTCCCTGC	
bjaI-gusA_for	<u>ATTTGTGGAATTCCC</u> TGACGATGATGGCGGAGTAA	Generation of <i>bjaI-gusA</i> transcriptional fusion in Fig. 1B and 1C
bjaI-gusA_rev	<u>ATATCGAGCTCTCCC</u> GTTTCCATGATCGCGCTGACC	
nifH-gusA_for	<u>ATTTGTGGAATTCCC</u> TCAGCACCATGTACCGAGTT	Generation of <i>nifH-gusA</i> transcriptional fusion in Fig. 2E
nifH-gusA_rev	<u>ATATCGAGCTCTCCC</u> GATGTAGATCTCCTGCGCCT	
nodW-lacZ_for	<u>ATTTGTGGAATTCCC</u> CTACCATTCGCGTGATCAGG	Generation of transcriptional fusions in Fig. 3A
nodW-lacZ_rev	<u>ATATCGAGCTCTCCC</u> GGCTTGCTGAGGAAATCGACC	
nodD1-lacZ_for	<u>ATTTGTGGAATTCCC</u> TGCAGTTCACCTTCCCAACG	
nodD1-lacZ_rev	<u>ATATCGAGCTCTCCC</u> CCATGCGGTCCACAATTCTG	

nwsA-lacZ_for	<u>ATTTGTGGAATTCCC</u> <b>ATCCCTGTTTCGTTCCACCT</b>	
nwsA-lacZ_rev	<u>ATATCGAGCTCTCCC</u> <b>TGCGCTGGGTGATATTTTCG</b>	
nolA-lacZ_for	<u>ATTTGTGGAATTCCC</u> <b>GACTGCCGACTTGATGCTTT</b>	
nolA-lacZ_rev	<u>ATATCGAGCTCTCCC</u> <b>GCGACTTGGACTTCTATGCG</b>	
nodD2-lacZ_for	<u>ATTTGTGGAATTCCC</u> <b>GGATGCGTCGGATATTGCTC</b>	
nodD2-lacZ_rev	<u>ATATCGAGCTCTCCC</u> <b>ATCGAATGTAAGCCGGGGTT</b>	
<hr/>		
ntrB-lacZ_for	<u>ATTTGTGGAATTCCC</u> <b>GGAAGGCGCCGATATCATC</b>	Generation of transcriptional fusions
ntrB-lacZ_rev	<u>ATATCGAGCTCTCCC</u> <b>CTCCTGAAGCATCACACGA</b>	in Fig. 4D
glnII-lacZ_for	<u>ATTTGTGGAATTCCC</u> <b>ATTGAACCAAACGCAGGCAT</b>	
glnII-lacZ_rev	<u>ATATCGAGCTCTCCC</u> <b>GGCATCATGACTTCGCACAT</b>	
glnB-lacZ_for	<u>ATTTGTGGAATTCCC</u> <b>CGGATTGAACGGGAGCAC</b>	
glnB-lacZ_rev	<u>ATATCGAGCTCTCCC</u> <b>ACGAAAATCTTGCCGTCACC</b>	
amtB-lacZ_for	<u>ATTTGTGGAATTCCC</u> <b>TAGATACCTTCCAGCTGCCC</b>	
amtB-lacZ_rev	<u>ATATCGAGCTCTCCC</u> <b>AAGACCTGCATCAAGACCGA</b>	

- (1) Nucleotide sequence in bold black indicates the sites for *EcoR* I and *Xba* I restriction enzymes.
- (2) Underlined nucleotide sequences indicate the 15 homologous bases of flanking region of restriction enzymes site for In-Fusion cloning, *Sma* I (single-underline) on the plasmid pVIK112 or pVIK166, and *Pme* I (double-underline) on the pKS800.
- (3) r, resistance toward antibiotics; Cm, chloramphenicol; Sm, streptomycin; Sp, spectinomycin; Tc, Tetracyclines; Km, kanamycin.

## Reference

Banfalvi, Z., Nieuwkoop, A., Schell, M. G., Besl, L., and Stacey, G. (1988) Regulation of *nod* gene expression in *Bradyrhizobium japonicum*. *Mol Gen Genet* 214: 420-424.

- Han, F., He, X.Q., Chen, W.W., Gai, H.Y., Bai, X.M., He, Y.X., Takeshima, K., Ohwada, T., Wei, M., Xie, F. 2020. Involvement of a novel TetR-like regulator (BdtR) of *Bradyrhizobium diazoefficiens* in the efflux of isoflavonoid genistein. *Mol. Plant-Microbe Interact.* 33: 1411-1423.
- Figurski, H.D., and Helinski, D.R. (1979) Replication of an origin-containing derivative of plasmid RK2 dependent on a plasmid function provided in trans. *Proc Natl Acad Sci U.S.A.* 76:1648–1652.
- Hattori, Y., Omori, H., Hanyu, M., Kaseda, N., Mishima, E., Kaneko, T., Tabata, S., and Saeki K. (2002) Ordered cosmid library of the *Mesorhizobium loti* MAFF303099 genome for systematic gene disruption and complementation analysis. *Plant Cell Physiol* 43: 1542–1557.
- Kalogeraki, V.S., Winans, S.C. (1997) Suicide plasmids containing promoterless reporter genes can simultaneously disrupt and create fusions to target genes of diverse bacteria. *Gene* 188: 69-75.
- Jitackson, S., Sadowsky, M.J. (2008) Nodulation gene regulation and quorum sensing control density-dependent suppression and restriction of nodulation in the *Bradyrhizobium japonicum*-soybean symbiosis. *Appl Environ Microbiol* 74: 3749-3756.
- Metcalf, W.W., Jiang, W., and Wanner, B.L. (1994) Use of the rep technique for allele replacement to construct new *Escherichia coli* hosts for maintenance of R6K $\lambda$  origin plasmids at different copy numbers. *Gene* 138:1-7.
- Schäfer, A., Tauch, A., Jäger, W., Kalinowski, J., Thierbach, G., Pühler, A. (1994) Small mobilizable multi-purpose cloning vectors derived from the *Escherichia coli* plasmids pK18 and pK19: selection of defined deletions in the chromosome of *Corynebacterium glutamicum*. *Gene* 145: 69-73.
- Wilson, K.J., Sessitsch, A., Corbo, J.C., Giller, K.E., Akkermans, A.D., Jefferson, R.A. (1995) beta-Glucuronidase (GUS) transposons for ecological and genetic studies of rhizobia and other gram-negative bacteria. *Microbiology* 141: 1691-1705.

Table S2 The total N content of soybean plant inoculated with different *B. diazoefficiens* strains






	N[%]	C[%]	C/N ratio	Dry weight (mg/plant)	Total N content (g/kg dry weight)
Non-inoculation	1.47 ± 0.08	42.04 ± 0.21	29.35 ± 1.51	548 ± 55	13.57 ± 0.63
wt <i>B. d</i> 110	2.79 ± 0.11	43.05 ± 0.19	15.52 ± 0.65	720 ± 43	28.74 ± 0.94
<i>B. d</i> ΔbjaR <sub>1</sub>	2.99 ± 0.05	43.51 ± 0.06	14.66 ± 0.24	661 ± 38	31.09 ± 0.79
<i>B. d</i> c-ΔbjaR <sub>1</sub>	2.91 ± 0.06	43.50 ± 0.13	15.06 ± 0.32	712 ± 18	30.53 ± 0.57
<i>B. j</i> JD21	1.55 ± 0.05	42.34 ± 0.28	28.86 ± 1.25	618 ± 27	13.77 ± 0.45

The soybean plant were divided into shoot and root parts. After drying at 60° C for at least 48 h, 50-80 mg of dry tissue was ground using ball milling. Total nitrogen and carbon content were detected by gas chromatography on an elemental analyzer (Elementar vario MACRO cube, Elementar, Germany). The data presents the mean ± SD of four soybean plant samples cultivated under low-N solution and harvested at 30 days post inoculation.

Table S3 Differentially expressed genes in the free-living  $\Delta$ bjaR<sub>1</sub> mutant compared with wild-type cells

Gene_id <sup>a</sup>	Gene name <sup>b</sup>	Description <sup>c</sup>	Ratio <sup>d</sup>	FixK <sub>2</sub> <sup>e</sup>	RpoN <sub>1+2</sub> <sup>f</sup>	NifA or RpoN <sub>1/2</sub> <sup>g</sup>	Wild-type bacteroids <sup>h</sup>
<b>Significantly down-regulated genes (408 genes)</b>							
<i>bll0031</i>	-	hypothetical protein	0.07				
<i>bll0383</i>	<i>mcpK</i>	methyl-accepting chemotaxis protein	0.21				
<i>bll0394</i>	-	two-component response regulator	0.19				
<i>bll0403</i>	-	hypothetical protein	0.07				
<i>bll0553</i>	<i>guaA</i>	glutamine amidotransferase	0.12				
<i>bll0774</i>	-	hypothetical protein	0.28				
<i>bll0818</i>	-	hypothetical protein	0.04	■			
<i>bll0896</i>	-	oxidoreductase	0.18				
<i>bll0897</i>	-	hypothetical protein	0.14				
<i>bll0965</i>	-	two-component response regulator	0.23				
<i>bll0966</i>	-	two-component hybrid sensor and regulator	0.14				■
<i>bll1044</i>	-	allophanate hydrolase	0.19				
<i>bll1209</i>	-	ABC transporter ATP-binding protein	0.10				
<i>bll1210</i>	-	ABC transporter permease	0.08				
<i>bll1211</i>	-	ABC transporter permease	0.12				
<i>bll1271</i>	<i>mdcH</i>	probable malonyl CoA-ACP transacylase	0.08				
<i>bll1272</i>	<i>mdcB</i>	triphosphoribosyl-dephospho-CoA synthase	0.21				
<i>bll1273</i>	<i>mdcG</i>	probable malonate decarboxylase	0.25				
<i>bll1274</i>	<i>mdcE</i>	malonate decarboxylase gamma subunit	0.21				
<i>bll1802</i>	-	hypothetical protein	0.27				
<i>bll1803</i>	-	hypothetical protein	0.22				
<i>bll1906</i>	-	N-acetyltransferase NrgA-like protein	0.12			■	
<i>bll2007</i>	<i>hemN1</i>	coproporphyrinogen III oxidase	0.02	■			■
<i>bll2021</i>	<i>nodD2</i>	transcriptional regulator	0.27				■
<i>bll2059</i>	<i>groEL3</i>	molecular chaperone GroEL	0.11			■	
<i>bll2060</i>	<i>groES3</i>	GroES3 chaperonin	0.12				
<i>bll2109</i>	-	transcriptional regulatory protein	0.09	■		■	■
<i>bll2329</i>	-	FAD-dependent oxidoreductase	0.12				
<i>bll2330</i>	-	hypothetical protein	0.05	■			
<i>bll2388</i>	<i>cy2</i>	cytochrome c2	0.04	■			
<i>bll2471</i>	-	hypothetical protein	0.03	■			
<i>bll2512</i>	-	transcriptional regulator	0.35				
<i>bll2514</i>	-	hypothetical protein	0.08				
<i>bll2515</i>	-	pyruvate phosphate dikinase	0.03				■
<i>bll2516</i>	-	hypothetical protein	0.02				
<i>bll2517</i>	-	acetate kinase	0.02				
<i>bll2518</i>	-	phosphoketolase	0.02				
<i>bll2590</i>	-	hypothetical protein	0.03				
<i>bll2647</i>	-	hypothetical protein	0.03				
<i>bll2661</i>	-	hypothetical protein	0.04				
<i>bll2662</i>	-	hypothetical protein	0.08	■			
<i>bll2663</i>	-	hypothetical protein	0.04				
<i>bll2664</i>	-	hypothetical protein	0.11				
<i>bll2665</i>	-	arylsulfatase	0.07				
<i>bll2757</i>	<i>fixK<sub>2</sub></i>	transcriptional regulatory protein	0.19				
<i>bll2758</i>	-	two-component response regulator	0.03				■
<i>bll2771</i>	-	hypothetical protein	0.05				

Cont.

<i>bll2778</i>	<i>glgA</i>	glycogen synthase	0.33	
<i>bll2866</i>	-	ABC transporter permease	0.20	
<i>bll2867</i>	-	ABC transporter permease	0.19	
<i>bll2868</i>	-	ABC transporter substrate-binding protein	0.23	
<i>bll2869</i>	-	ABC transporter ATP-binding protein	0.28	
<i>bll2870</i>	-	ABC transporter ATP-binding protein	0.21	
<i>bll2871</i>	-	hypothetical protein	0.27	
<i>bll3115</i>	-	hypothetical protein	0.01	
<i>bll3116</i>	-	phosphoribosylpyrophosphate synthetase	0.02	
<i>bll3117</i>	-	thymidine phosphorylase	0.02	
<i>bll3190</i>	-	ABC transporter ATP-binding protein	0.09	
<i>bll3191</i>	-	ABC transporter permease	0.10	
<i>bll3192</i>	-	ABC transporter substrate-binding protein	0.14	
<i>bll3193</i>	-	hypothetical protein	0.15	
<i>bll3238</i>	<i>hyuA</i>	hydantoinase A	0.10	
<i>bll3239</i>	-	hypothetical protein	0.07	
<i>bll3240</i>	-	hypothetical protein	0.13	
<i>bll3241</i>	-	ABC transporter ATP-binding protein	0.09	
<i>bll3242</i>	-	ABC transporter substrate-binding protein	0.12	
<i>bll3243</i>	-	ABC transporter permease	0.06	
<i>bll3244</i>	-	ABC transporter permease	0.12	
<i>bll3245</i>	-	transcriptional regulator	0.08	
<i>bll3284</i>	-	ABC transporter permease	0.20	
<i>bll3285</i>	-	ABC transporter permease	0.30	
<i>bll3286</i>	-	ABC transporter substrate-binding protein	0.39	
<i>bll3287</i>	-	ABC transporter ATP-binding protein	0.24	
<i>bll3313</i>	-	monooxygenase	0.14	
<i>bll3314</i>	-	ABC transporter permease	0.10	
<i>bll3315</i>	-	ABC transporter permease	0.14	
<i>bll3316</i>	-	ABC transporter substrate-binding protein	0.15	
<i>bll3317</i>	-	aldolase	0.10	
<i>bll3318</i>	-	ABC transporter ATP-binding protein	0.14	
<i>bll3460</i>	<i>nodN</i>	nodulation protein N	0.11	
<i>bll3461</i>	<i>pcaJ</i>	3-oxoadipate CoA-transferase subunit B	0.07	
<i>bll3462</i>	<i>pcaI</i>	acetyl-CoA--acetoacetyl-CoA transferase subunit alpha	0.08	
<i>bll3463</i>	-	hypothetical protein	0.06	
<i>bll3480</i>	-	hypothetical protein	0.07	
<i>bll3481</i>	-	hypothetical protein	0.05	
<i>bll3768</i>	-	hypothetical protein	0.18	
<i>bll3835</i>	-	hypothetical protein	0.07	
<i>bll3998</i>	-	succinate-semialdehyde dehydrogenase	0.02	
<i>bll4303</i>	-	amidase	0.30	
<i>bll4384</i>	-	substrate-binding protein	0.12	
<i>bll4412</i>	-	hypothetical protein	0.03	
<i>bll4426</i>	-	hypothetical protein	0.12	
<i>bll4571</i>	<i>nirA</i>	Putative ferredoxin--nitrite reductase	0.35	
<i>bll4618</i>	-	hypothetical protein	0.04	
<i>bll4632</i>	-	hypothetical protein	0.18	
<i>bll4634</i>	-	hypothetical protein	0.03	
<i>bll4639</i>	-	protease	0.03	



Cont.















<i>bll4640</i>	-	hypothetical protein	0.03	
<i>bll4643</i>	-	hypothetical protein	0.02	
<i>bll4644</i>	-	hypothetical protein	0.03	
<i>bll4645</i>	-	hypothetical protein	0.05	
<i>bll4648</i>	-	hypothetical protein	0.08	
<i>bll4651</i>	-	hypothetical protein	0.04	■
<i>bll4656</i>	-	hypothetical protein	0.03	
<i>bll4793</i>	-	hypothetical protein	0.15	
<i>bll4798</i>	-	glutaminase	0.38	■
<i>bll4815</i>	-	hypothetical protein	0.16	
<i>bll4816</i>	-	hypothetical protein	0.08	
<i>bll4817</i>	-	hypothetical protein	0.07	
<i>bll4818</i>	-	hypothetical protein	0.03	
<i>bll4819</i>	-	hypothetical protein	0.05	
<i>bll4820</i>	-	hypothetical protein	0.07	
<i>bll5056</i>	-	substrate-binding protein	0.36	
<i>bll5080</i>	-	AcrB/AcrD/AcrF family protein	0.06	
<i>bll5081</i>	-	multidrug resistance protein	0.07	
<i>bll5145</i>	-	mannose-6-phosphate isomerase	0.10	
<i>bll5315</i>	-	hypothetical protein	0.02	■
<i>bll5326</i>	-	hypothetical protein	0.19	
<i>bll5529</i>	-	metabolite transport protein	0.22	
<i>bll5593</i>	-	hypothetical protein	0.19	
<i>bll5655</i>	-	alcohol dehydrogenase	0.03	■
<i>bll5657</i>	-	hypothetical protein	0.06	
<i>bll5679</i>	-	hypothetical protein	0.25	
<i>bll5731</i>	-	cyanate hydratase	0.26	
<i>bll5732</i>	<i>nrtC</i>	ABC transporter ATP-binding protein	0.16	
<i>bll5733</i>	<i>nrtB</i>	nitrate ABC transporter permease	0.20	
<i>bll5734</i>	<i>nrtA</i>	ABC transporter nitrate-binding protein	0.18	■ ■ ■
<i>bll5736</i>	-	thiosulfate sulfurtransferase	0.05	
<i>bll5737</i>	-	acyl-CoA dehydrogenase	0.06	
<i>bll5738</i>	-	hypothetical protein	0.09	
<i>bll5770</i>	-	hypothetical protein	0.07	
<i>bll5771</i>	-	AcrB/AcrD/AcrF family cation efflux protein	0.05	
<i>bll5772</i>	-	hypothetical protein	0.03	
<i>bll5880</i>	-	hypothetical protein	0.09	
<i>bll5890</i>	-	monocarboxylic acid permease	0.04	
<i>bll6061</i>	<i>fixK<sub>1</sub></i>	transcriptional regulator	0.05	
<i>bll6069</i>	-	hypothetical protein	0.03	■
<i>bll6073</i>	<i>phbC</i>	poly-beta-hydroxybutyrate polymerase	0.02	■
<i>bll6154</i>	-	hypothetical protein	0.16	
<i>bll6406</i>	-	ABC transporter ATP-binding protein	0.03	
<i>bll6540</i>	-	oxidoreductase	0.06	
<i>bll6673</i>	-	hypothetical protein	0.02	
<i>bll6702</i>	-	glutathione S-transferase	0.15	■
<i>bll6709</i>	-	ATP-binding protein	0.22	
<i>bll6710</i>	-	dehydrogenase	0.18	
<i>bll6711</i>	-	dehydrogenase	0.25	
<i>bll6712</i>	-	ABC transporter permease	0.13	

Cont.






<i>bll6713</i>	-	ABC transporter permease	0.31	
<i>bll6747</i>	-	hypothetical protein	0.08	
<i>bll6859</i>	-	hypothetical protein	0.09	
<i>bll6860</i>	-	hypothetical protein	0.05	
<i>bll6861</i>	<i>motC</i>	chemotaxis protein	0.05	
<i>bll6862</i>	<i>motB</i>	flagellar motor protein MotB	0.06	
<i>bll6863</i>	-	hypothetical protein	0.04	
<i>bll6864</i>	<i>fliF</i>	flagellar MS-ring protein	0.04	
<i>bll6870</i>	-	hypothetical protein	0.04	
<i>bll6892</i>	-	hypothetical protein	0.04	
<i>bll6893</i>	-	hypothetical protein	0.04	
<i>bll6936</i>	<i>hupH</i>	HupH protein	0.17	
<i>bll6939</i>	<i>hupD</i>	HupD protein	0.25	
<i>bll6940</i>	<i>hupC</i>	HupC protein	0.17	
<i>bll6941</i>	<i>hupL</i>	uptake hydrogenase large subunit	0.11	
<i>bll6942</i>	<i>hupS</i>	uptake hydrogenase	0.12	
<i>bll7083</i>	-	hypothetical protein	0.03	
<i>bll7086</i>	<i>hemN</i>	coproporphyrinogen III oxidase	0.02	
<i>bll7538</i>	-	hypothetical protein	0.22	
<i>bll7551</i>	-	hypothetical protein	0.02	
<i>bll7553</i>	-	hypothetical protein	0.04	
<i>bll7626</i>	-	hypothetical protein	0.11	
<i>bll7627</i>	-	hypothetical protein	0.05	
<i>bll7628</i>	-	hypothetical protein	0.05	
<i>bll7696</i>	-	transcriptional regulator	0.03	
<i>bll7787</i>	-	hypothetical protein	0.03	
<i>bll7918</i>	-	ABC transporter ATP-binding protein	0.20	
<i>bll7919</i>	-	ABC transporter permease	0.14	
<i>bll7920</i>	-	ABC transporter permease	0.15	
<i>bll7921</i>	-	ABC transporter substrate-binding protein	0.22	
<i>bll7981</i>	-	dehydrogenase	0.02	
<i>bll7982</i>	-	hypothetical protein	0.03	
<i>bll7986</i>	-	hypothetical protein	0.04	
<i>bll7987</i>	-	hypothetical protein	0.03	
<i>bll7988</i>	-	ATP-binding protein	0.04	
<i>bll7990</i>	-	hypothetical protein	0.04	
<i>bll7991</i>	-	hypothetical protein	0.03	
<i>bll7993</i>	-	hypothetical protein	0.03	
<i>bll8163</i>	<i>gtrA</i>	glycosyl transferase family protein	0.22	
<i>bll8310</i>	-	hypothetical protein	0.20	
<i>blr0219</i>	<i>hemK</i>	protoporphyrinogen oxidase	0.25	
<i>blr0314</i>	<i>nosR</i>	nitrous oxide reductase expression regulator	0.24	
<i>blr0395</i>	-	hypothetical protein	0.08	
<i>blr0397</i>	-	two-component sensor histidine kinase	0.10	
<i>blr0497</i>	-	hypothetical protein	0.03	
<i>blr0576</i>	-	methyl-accepting chemotaxis protein	0.02	
<i>blr0577</i>	-	hypothetical protein	0.04	
<i>blr0612</i>	<i>glnK</i>	nitrogen regulatory protein PII	0.11	
<i>blr0613</i>	<i>amtB</i>	ammonium transporter	0.10	
<i>blr0871</i>	-	hypothetical protein	0.32	













Cont.

<i>blr0872</i>	-	hypothetical protein	0.22	
<i>blr0972</i>	-	Amidase	0.08	
<i>blr1018</i>	-	hypothetical protein	0.17	
<i>blr1036</i>	-	ABC transporter substrate-binding protein	0.13	
<i>blr1037</i>	-	ABC transporter permease	0.12	
<i>blr1038</i>	-	ABC transporter permease	0.17	
<i>blr1039</i>	-	ABC transporter ATP-binding protein	0.17	
<i>blr1063</i>	-	autoinducer synthase	0.17	
<i>blr1190</i>	-	hypothetical protein	0.16	
<i>blr1214</i>	-	lipoprotein	0.23	
<i>blr1215</i>	-	hypothetical protein	0.09	
<i>blr1216</i>	-	ferric uptake transcriptional regulator	0.04	
<i>blr1289</i>	-	myosin-cross-reactive antigen	0.02	
<i>blr1311</i>	-	outer membrane protein	0.05	
<i>blr1357</i>	-	peptide ABC transporter ATP-binding protein	0.26	
<i>blr1404</i>	<i>clpB</i>	ATP-dependent protease ATP-binding subunit	0.22	
<i>blr1448</i>	-	ABC transporter substrate-binding protein	0.11	
<i>blr1449</i>	-	ABC transporter permease	0.11	
<i>blr1450</i>	-	ABC transporter permease	0.08	
<i>blr1451</i>	-	ABC transporter ATP-binding protein	0.10	
<i>blr1452</i>	-	ABC transporter ATP-binding protein	0.10	
<i>blr1883</i>	<i>rpoN<sub>1</sub></i>	RNA polymerase factor sigma-54	0.04	
<i>blr2011</i>	-	hypothetical protein	0.10	
<i>blr2106</i>	<i>ectC</i>	L-ectoine synthase	0.10	
<i>blr2143</i>	-	cytochrome P450-family protein	0.10	
<i>blr2144</i>	<i>CYP112</i>	cytochrome P-450 BJ-1	0.30	
<i>blr2145</i>	<i>CYP114</i>	cytochrome P-450 BJ-3	0.12	
<i>blr2146</i>	-	dehydrogenase	0.16	
<i>blr2147</i>	<i>CYP117</i>	cytochrome P-450 BJ-4	0.12	
<i>blr2148</i>	<i>fpps</i>	farnesyl diphosphate synthase	0.13	
<i>blr2222</i>	<i>dadA</i>	D-amino acid dehydrogenase small subunit	0.21	
<i>blr2341</i>	-	hypothetical protein	0.11	
<i>blr2472</i>	-	hypothetical protein	0.06	
<i>blr2611</i>	-	hypothetical protein	0.04	
<i>blr2659</i>	-	hypothetical protein	0.03	
<i>blr2666</i>	-	hypothetical protein	0.06	
<i>blr2725</i>	-	hypothetical protein	0.27	
<i>blr2726</i>	-	hypothetical protein	0.29	
<i>blr2761</i>	-	hypothetical protein	0.03	
<i>blr2762</i>	-	hypothetical protein	0.02	
<i>blr2763</i>	<i>fixN</i>	cbb3-type cytochrome c oxidase subunit I	0.02	
<i>blr2764</i>	<i>fixO</i>	cbb3-type cytochrome c oxidase subunit II	0.02	
<i>blr2766</i>	<i>fixP</i>	cbb3 oxidase subunit III	0.02	
<i>blr2767</i>	<i>fixG</i>	(Fe-S)-binding protein	0.02	
<i>blr2768</i>	<i>fixH</i>	FixH protein	0.02	
<i>blr2769</i>	<i>fixI</i>	E1-E2 type cation ATPase	0.02	
<i>blr2803</i>	<i>nrtA</i>	nitrate ABC transporter permease	0.30	
<i>blr2804</i>	<i>nrtB</i>	nitrate ABC transporter permease	0.29	
<i>blr2809</i>	<i>nasA</i>	nitrate reductase large subunit	0.31	
<i>blr2977</i>	-	hypothetical protein	0.34	







Cont.

<i>blr3124</i>	-	hypothetical protein	0.22	
<i>blr3214</i>	<i>norC</i>	nitric oxide reductase subunit C	0.24	
<i>blr3215</i>	<i>norB</i>	nitric oxide reductase subunit B	0.37	
<i>blr3291</i>	-	ABC transporter substrate-binding protein	0.30	
<i>blr3309</i>	-	ABC transporter substrate-binding protein	0.38	
<i>blr3310</i>	-	ABC transporter permease	0.16	
<i>blr3311</i>	-	ABC transporter ATP-binding protein	0.17	
<i>blr3312</i>	-	hypothetical protein	0.14	
<i>blr3321</i>	-	hypothetical protein	0.25	
<i>blr3322</i>	-	aspartate aminotransferase	0.11	
<i>blr3323</i>	<i>amaB</i>	allantoate amidohydrolase	0.15	
<i>blr3327</i>	-	N-methylhydantoinase B	0.38	
<i>blr3328</i>	-	aminotransferase	0.21	
<i>blr3329</i>	-	long-chain-fatty-acid--CoA ligase	0.26	
<i>blr3339</i>	-	ABC transporter permease	0.27	
<i>blr3340</i>	-	ABC transporter ATP-binding protein	0.30	
<i>blr3342</i>	-	ABC transporter permease	0.33	
<i>blr3343</i>	-	ABC transporter permease	0.25	
<i>blr3344</i>	-	ABC transporter ATP-binding protein	0.32	
<i>blr3345</i>	-	ABC transporter ATP-binding protein	0.26	
<i>blr3355</i>	-	ABC transporter permease	0.08	
<i>blr3357</i>	-	ABC transporter ATP-binding protein	0.13	
<i>blr3396</i>	-	major facilitator superfamily transporter	0.12	
<i>blr3397</i>	<i>nit</i>	nitrilase	0.15	
<i>blr3456</i>	-	hypothetical protein	0.05	
<i>blr3457</i>	<i>pta</i>	phosphate acetyltransferase	0.05	
<i>blr3458</i>	<i>ackA2</i>	acetate kinase	0.09	
<i>blr3459</i>	<i>fabI</i>	enoyl-(acyl carrier protein) reductase	0.10	
<i>blr3474</i>	-	Orn/Lys/Arg family decarboxylase	0.11	
<i>blr3477</i>	-	aspartate aminotransferase	0.04	
<i>blr3478</i>	-	hypothetical protein	0.05	
<i>blr3486</i>	-	hypothetical protein	0.07	
<i>blr3487</i>	-	hypothetical protein	0.07	
<i>blr3488</i>	-	hypothetical protein	0.16	
<i>blr3521</i>	-	hypothetical protein	0.04	
<i>blr3815</i>	-	cation-transporting ATPase	0.01	
<i>blr4093</i>	-	hypothetical protein	0.09	
<i>blr4094</i>	-	hypothetical protein	0.15	
<i>blr4111</i>	-	hypothetical protein	0.03	
<i>blr4112</i>	-	cation efflux system protein	0.02	
<i>blr4113</i>	-	hypothetical protein	0.02	
<i>blr4114</i>	-	hypothetical protein	0.03	
<i>blr4115</i>	<i>actP</i>	acetate permease	0.02	
<i>blr4116</i>	-	hypothetical protein	0.04	
<i>blr4169</i>	<i>glnII</i>	glutamine synthetase	0.27	
<i>blr4174</i>	-	hypothetical protein	0.03	
<i>blr4240</i>	-	hypothetical protein	0.03	
<i>blr4241</i>	-	hypothetical protein	0.03	
<i>blr4466</i>	-	transcriptional regulator	0.18	
<i>blr4467</i>	-	hypothetical protein	0.13	

Cont.

<i>blr4486</i>	<i>nifR</i>	nitrogen regulation protein	0.31	
<i>blr4487</i>	<i>ntxB</i>	two-component sensor histidine kinase	0.32	
<i>blr4488</i>	<i>ntxC</i>	two-component sensor histidine kinase	0.40	
<i>blr4507</i>	-	hypothetical protein	0.04	
<i>blr4508</i>	-	hypothetical protein	0.15	
<i>blr4624</i>	-	hypothetical protein	0.13	
<i>blr4633</i>	-	hypothetical protein	0.11	
<i>blr4635</i>	<i>groEL</i>	molecular chaperone GroEL	0.03	
<i>blr4637</i>	-	HspC2 heat shock protein	0.02	
<i>blr4638</i>	-	hypothetical protein	0.02	
<i>blr4641</i>	-	hypothetical protein	0.04	
<i>blr4646</i>	-	hypothetical protein	0.03	
<i>blr4652</i>	-	hypothetical protein	0.03	
<i>blr4653</i>	<i>dnaJ</i>	DnaJ family molecular chaperone	0.02	
<i>blr4654</i>	-	hypothetical protein	0.03	
<i>blr4655</i>	<i>ppsA</i>	phosphoenolpyruvate synthase	0.03	
<i>blr4657</i>	-	beta-glucosidase	0.03	
<i>blr4658</i>	<i>glk</i>	glucokinase	0.02	
<i>blr4659</i>	-	PfkB family carbohydrate kinase	0.02	
<i>blr4660</i>	-	ABC transporter	0.03	
<i>blr4709</i>	-	hypothetical protein	0.24	
<i>blr4932</i>	-	cation efflux system protein	0.11	
<i>blr4948</i>	<i>glnB</i>	Nitrogen regulatory protein P-II 1	0.38	
<i>blr4955</i>	-	cytochrome B561	0.03	
<i>blr4988</i>	-	hypothetical protein	0.17	
<i>blr5150</i>	-	hypothetical protein	0.05	
<i>blr5575</i>	-	ABC transporter permease	0.18	
<i>blr5576</i>	-	ABC transporter permease	0.18	
<i>blr5600</i>	-	ABC transporter ATP-binding protein	0.30	
<i>blr5658</i>	-	avidin	0.05	
<i>blr5775</i>	-	thioredoxin	0.06	
<i>blr5777</i>	-	hypothetical protein	0.08	
<i>blr5778</i>	<i>fixG</i>	nitrogen fixation protein	0.08	
<i>blr5805</i>	-	transcriptional regulator	0.09	
<i>blr5829</i>	<i>flgA</i>	flagellar basal body P-ring biosynthesis protein FlgA	0.10	
<i>blr6067</i>	-	hypothetical protein	0.03	
<i>blr6070</i>	-	alcohol dehydrogenase	0.07	
<i>blr6071</i>	-	hypothetical protein	0.09	
<i>blr6074</i>	-	hypothetical protein	0.03	
<i>blr6128</i>	<i>cycB</i>	cytochrome c552	0.02	
<i>blr6145</i>	<i>dctA</i>	C4-dicarboxylate transporter DctA	0.15	 
<i>blr6148</i>	-	ABC transporter substrate-binding protein	0.21	
<i>blr6149</i>	-	ABC transporter permease	0.14	
<i>blr6150</i>	-	ABC transporter permease	0.09	
<i>blr6152</i>	-	ABC transporter ATP-binding protein	0.24	
<i>blr6402</i>	-	nitrilase	0.19	
<i>blr6541</i>	-	hypothetical protein	0.05	
<i>blr6548</i>	-	probable leucine/isoleucine/valine-binding protein precursor	0.28	
<i>blr6669</i>	-	hypothetical protein	0.14	
<i>blr6703</i>	-	hypothetical protein	0.14	

Cont.

<i>blr6887</i>	-	hypothetical protein	0.06	
<i>blr6951</i>	<i>modA</i>	molybdenum ABC transporter molybdate-binding protein	0.16	
<i>blr6996</i>	-	hypothetical protein	0.08	
<i>blr7037</i>	<i>napD</i>	periplasmic nitrate reductase	0.03	
<i>blr7038</i>	<i>napA</i>	nitrate reductase catalytic subunit	0.02	
<i>blr7039</i>	<i>napB</i>	periplasmic nitrate reductase small subunit	0.03	
<i>blr7040</i>	<i>napC</i>	cytochrome C-type protein	0.02	
<i>blr7053</i>	-	cation-transporting ATPase	0.04	
<i>blr7054</i>	-	hypothetical protein	0.03	
<i>blr7084</i>	<i>nnrR</i>	transcriptional regulator	0.03	
<i>blr7088</i>	-	hypothetical protein	0.02	
<i>blr7089</i>	<i>nirK</i>	respiratory nitrite reductase	0.02	
<i>blr7090</i>	-	periplasmic nitrate reductase	0.01	
<i>blr7228</i>	-	hypothetical protein	0.03	
<i>blr7250</i>	-	transcriptional regulator	0.22	
<i>blr7345</i>	-	hypothetical protein	0.02	
<i>blr7466</i>	-	ribonuclease	0.39	
<i>blr7616</i>	-	hypothetical protein	0.22	
<i>blr7629</i>	-	hypothetical protein	0.09	
<i>blr7630</i>	-	decarboxylase	0.07	
<i>blr7666</i>	-	transcriptional regulator	0.04	
<i>blr7780</i>	-	hypothetical protein	0.03	
<i>blr7786</i>	-	hypothetical protein	0.13	
<i>blr7872</i>	-	HlyD family secretion protein	0.02	
<i>blr7873</i>	-	ABC transporter ATP-binding protein	0.02	
<i>blr7874</i>	-	ABC transporter permease	0.02	
<i>blr7883</i>	-	hypothetical protein	0.30	
<i>blr7922</i>	-	ABC transporter substrate-binding protein	0.14	
<i>blr7961</i>	-	HspC2 heat shock protein	0.05	
<i>blr7970</i>	-	oxidoreductase	0.24	
<i>bsl0032</i>	-	hypothetical protein	0.08	
<i>bsl2070</i>	-	hypothetical protein	0.03	
<i>bsl2352</i>	-	hypothetical protein	0.05	
<i>bsl3175</i>	-	hypothetical protein	0.05	
<i>bsl3211</i>	-	hypothetical protein	0.13	
<i>bsl4625</i>	-	hypothetical protein	0.08	
<i>bsl4650</i>	-	hypothetical protein	0.08	
<i>bsl5110</i>	-	hypothetical protein	0.06	
<i>bsl5509</i>	-	hypothetical protein	0.22	
<i>bsl5624</i>	-	hypothetical protein	0.40	
<i>bsl6845</i>	-	hypothetical protein	0.07	
<i>bsl6938</i>	<i>hupF</i>	hydrogenase expression/formation protein	0.07	
<i>bsl7372</i>	-	hypothetical protein	0.06	
<i>bsl7758</i>	-	hypothetical protein	0.07	
<i>bsl7992</i>	-	hypothetical protein	0.03	
<i>bsr0033</i>	-	hypothetical protein	0.15	
<i>bsr0247</i>	-	hypothetical protein	0.04	
<i>bsr0398</i>	-	hypothetical protein	0.20	
<i>bsr2822</i>	-	hypothetical protein	0.13	
<i>bsr4175</i>	-	hypothetical protein	0.02	





Cont.

<i>bsr4619</i>	-	hypothetical protein	0.15
<i>bsr4956</i>	-	hypothetical protein	0.04
<i>bsr4957</i>	-	hypothetical protein	0.03
<i>bsr5273</i>	-	hypothetical protein	0.02
<i>bsr5776</i>	-	hypothetical protein	0.07
<i>bsr6066</i>	-	hypothetical protein	0.03
<i>bsr6520</i>	-	hypothetical protein	0.05
<i>bsr6521</i>	-	hypothetical protein	0.06
<i>bsr7036</i>	<i>napE</i>	periplasmic nitrate reductase	0.04
<i>bsr7087</i>	-	hypothetical protein	0.03
<i>bsr7705</i>	-	hypothetical protein	0.05

**Significantly up-regulated genes (123 genes)**

<i>bll0006</i>	<i>nrdF</i>	ribonucleotide-diphosphate reductase subunit beta	2.51
<i>bll0007</i>	-	ribonucleotide-diphosphate reductase subunit alpha	2.51
<i>bll0128</i>	-	hypothetical protein	2.68
<i>bll0413</i>	-	ABC transporter substrate-binding protein	2.47
<i>bll0591</i>	-	hypothetical protein	3.07
<i>bll0805</i>	-	hypothetical protein	3.62
<i>bll0913</i>	-	hypothetical protein	6.93
<i>bll0979</i>	-	hypothetical protein	3.81
<i>bll0980</i>	-	acid-CoA ligase	2.83
<i>bll0992</i>	-	peptide ABC transporter permease	3.44
<i>bll0993</i>	-	ABC transporter peptide-binding protein	4.44
<i>bll0994</i>	-	acyl-CoA synthetase	3.06
<i>bll2335</i>	-	hypothetical protein	2.92
<i>bll2948</i>	-	long-chain-fatty-acid--CoA ligase	4.25
<i>bll3050</i>	-	hypothetical protein	7.77
<i>bll3222</i>	-	ABC transporter permease	5.79
<i>bll3379</i>	-	hypothetical protein	9.00
<i>bll3381</i>	-	hypothetical protein	19.85
<i>bll3383</i>	-	ABC transporter ATP-binding protein	10.01
<i>bll4149</i>	-	glutathione peroxidase	2.79
<i>bll4166</i>	-	hypothetical protein	5.08
<i>bll4201</i>	-	hypothetical protein	4.50
<i>bll4766</i>	-	hypothetical protein	3.26
<i>bll5218</i>	-	hypothetical protein	3.66
<i>bll5219</i>	<i>hspD</i>	small heat shock protein	4.13
<i>bll5442</i>	-	oxidoreductase	2.94
<i>bll5475</i>	-	formate dehydrogenase	3.84
<i>bll5476</i>	-	formate dehydrogenase iron-sulfur subunit	4.64
<i>bll5477</i>	-	formate dehydrogenase	3.94
<i>bll5478</i>	-	formate dehydrogenase	4.34
<i>bll5551</i>	-	hypothetical protein	2.76
<i>bll5782</i>	-	sugar ABC transporter substrate-binding protein	4.98
<i>bll6058</i>	-	dicarboxylate transporter DctP	2.79
<i>bll6449</i>	-	hypothetical protein	2.94
<i>bll6478</i>	-	ABC transporter ATP-binding protein	2.79
<i>bll6479</i>	-	ABC transporter substrate-binding protein	2.97
<i>bll7322</i>	-	hypothetical protein	4.07

Cont.

<i>bll7357</i>	-	hypothetical protein	7.03		
<i>bll7411</i>		hypothetical protein	3.37		
<i>bll7414</i>	<i>fusA</i>	elongation factor G	4.00		
<i>bll7639</i>	-	alcohol dehydrogenase	2.82		
<i>bll7927</i>	-	hypothetical protein	9.49		
<i>bll7929</i>	-	ABC transporter ATP-binding protein	4.84		
<i>bll7930</i>	-	ABC transporter ATP-binding protein	3.86		
<i>bll7931</i>	-	ABC transporter permease	2.80		
<i>blr0165</i>			7.08		
<i>blr0166</i>	<i>ftsZ</i>	cell division protein FtsZ	3.81		
<i>blr0305</i>	-	hypothetical protein	3.22		
<i>blr0606</i>	<i>glnK</i>	nitrogen regulatory protein PII	3.10		
<i>blr1003</i>		hypothetical protein	2.51		
<i>blr2024</i>	<i>nodY</i>	NodY	4.39		
<i>blr2025</i>	<i>nodA</i>	Acyl transferase	3.13		
<i>blr2501</i>		hypothetical protein	4.67		
<i>blr3179</i>	-	alanine dehydrogenase	4.27		
<i>blr3183</i>	-	ABC transporter substrate-binding protein	5.57		
<i>blr3184</i>	-	ABC transporter permease	4.39		
<i>blr3186</i>	-	ABC transporter ATP-binding protein	3.56		
<i>blr3220</i>		hypothetical protein	4.64		
<i>blr3278</i>	-	hypothetical protein	2.99		
<i>blr3564</i>	-	hypothetical protein	5.40		
<i>blr3597</i>	-	hypothetical protein	1.27		
<i>blr3675</i>	-	alcohol dehydrogenase	18.39		
<i>blr3677</i>	-	monooxygenase component	38.54		
<i>blr3678</i>	-	oxidoreductase	41.17		
<i>blr3679</i>	-	monooxygenase component	58.97		
<i>blr3680</i>	-	hypothetical protein	48.68		
<i>blr3681</i>	-	hypothetical protein	47.93		
<i>blr3682</i>	-	hypothetical protein	33.25		
<i>blr3683</i>	<i>groEL</i>	molecular chaperone GroEL	28.71		
<i>blr3684</i>	-	hypothetical protein	6.35		
<i>blr3685</i>	-	transcriptional regulator	7.22		
<i>blr3686</i>	-	hypothetical protein	7.73		
<i>blr3688</i>	-	hypothetical protein	7.29		
<i>blr3745</i>	-	periplasmic mannitol-binding protein	2.71		
<i>blr3973</i>	-	NADP-dependent oxidoreductase	2.68		
<i>blr4046</i>	-	hypothetical protein	3.28		
<i>blr4068</i>		hypothetical protein	3.69		
<i>blr4312</i>		hypothetical protein	3.91		
<i>blr4554</i>	-	hypothetical protein	3.72		
<i>blr4555</i>	-	ABC transporter permease	6.64		
<i>blr4723</i>	-	hypothetical protein	2.54		
<i>blr4842</i>	-	ABC transporter substrate-binding protein	3.99		
<i>blr4884</i>	-	ABC transporter substrate-binding protein	5.54		
<i>blr5220</i>	<i>hspE</i>	small heat shock protein	2.97		
<i>blr5221</i>	<i>hspF</i>	small heat shock protein	7.10		
<i>blr5222</i>	-	hypothetical protein	6.15		
<i>blr5227</i>	<i>groEL</i>	molecular chaperone GroEL	4.92		



Cont.

---

<i>blr5230</i>	<i>hspA</i>	small heat shock protein	2.94
<i>blr5233</i>	<i>hspB</i>	small heat shock protein	3.60
<i>blr5234</i>	<i>hspC</i>	small heat shock protein	3.28
<i>blr5359</i>	-	hypothetical protein	5.46
<i>blr5541</i>	-	hypothetical protein	2.74
<i>blr5564</i>	-	hypothetical protein	3.50
<i>blr5625</i>	<i>groES</i>	co-chaperonin GroES	2.70
<i>blr5626</i>	<i>groEL</i>	molecular chaperone GroEL	5.56
<i>blr5909</i>	-	hypothetical protein	3.71
<i>blr5966</i>	-	ABC transporter substrate-binding protein	2.91
<i>blr6167</i>	-	hypothetical protein	7.61
<i>blr6207</i>	<i>exaA</i>	quinoprotein ethanol dehydrogenase	3.43
<i>blr6208</i>	-	cytochrome C55X	3.33
<i>blr6418</i>	-	hypothetical protein	2.62
<i>blr6437</i>	-	gluconolactonase	5.52
<i>blr6447</i>	-	ABC transporter ATP-binding protein	3.78
<i>blr6465</i>	-	steroid monooxygenase	4.39
<i>blr6659</i>	<i>thiC</i>	thiamine biosynthesis protein ThiC	3.52
<i>blr7064</i>	-	ABC transporter substrate-binding protein	4.51
<i>blr7065</i>	-	ABC transporter permease	3.02
<i>blr7269</i>	-	acyl-CoA dehydrogenase	2.85
<i>blr7270</i>	-	acyl-CoA dehydrogenase	3.13
<i>blr7490</i>	-	hypothetical protein	2.80
<i>blr7806</i>	-	acetyl-CoA acetyltransferase	2.73
<i>blr7816</i>	-	mannitol-binding protein	3.81
<i>blr7829</i>	-	hypothetical protein	8.65
<i>blr7868</i>	-	ABC transporter substrate-binding protein	5.03
<i>bsl2596</i>	-	hypothetical protein	3.07
<i>bsl4167</i>	-	glutamine synthetase	3.91
<i>bsl4437</i>	-	hypothetical protein	3.33
<i>bsl4623</i>	-	hypothetical protein	4.24
<i>bsl5479</i>	-	hypothetical protein	5.81
<i>bsl5486</i>	-	hypothetical protein	4.26
<i>bsl6528</i>	-	hypothetical protein	8.20
<i>bsr0862</i>	-	hypothetical protein	3.12
<i>bsr7532</i>	<i>groES</i>	co-chaperonin GroES	3.13

---

<sup>a</sup> Nomenclature according to Kaneko and associates (2002).

<sup>b</sup> Gene name according to the EMBL-EBI database.

<sup>c</sup> Gene description according to GeneBank.

<sup>d</sup> Indicating the transcript ratio of genes in free-living  $\Delta bjaR_1$  mutant relative to those in wild-type cells. Genistein was added in both bacterial culture with a final concentration of 5.0  $\mu$ M for 12 h at 30°C.

<sup>e</sup> Orange colour represents 42 genes overlapped with those whose expression was decreased in the *fixK2* mutant in microoxic free-living condition and in bacteroids compared to their expression in wild-type *B. d 110* as reported by Mesa and associates (2008).

<sup>f</sup> Green colour represents 22 genes overlapped with those whose expression was decreased in nodule infected by an *rpoN*<sub>1+2</sub> double mutant as compared to those in nodules induced by wild-type *B. d 110* as reported by Pessi and associates (2007).

<sup>g</sup> Blue colour represents 20 genes overlapped with those whose expression was decreased in anaerobically grown wild-type versus *nifA* mutant cell or wild-type versus *rpoN*<sub>1/2</sub> mutant cells as reported by Hauser and associates (2007).

<sup>e</sup> Purple colour represents 32 genes overlapped with those whose expression was increased in wild-type *B. d 110* bacteroids as compared to aerobically grown wild-type *B. d 110* cells as reported by Pessi and associates (2007).

Table S4 Transcription of 58 genome-wide genes involved in nitrogen metabolism process in the free-living  $\Delta bjaR_1$  mutant compared with wild-type cells

Gene_id <sup>a</sup>	Gene name <sup>b</sup>	Description <sup>c</sup>	Ratio <sup>c</sup>	Pathway (No.) <sup>d</sup>	Branch pathway (or module)
<b>Structural protein genes</b>					
<i>bll1069</i>		probable glutamine synthetase	0.97		NH <sub>4</sub> <sup>+</sup> assimilation
<i>bll1137</i>	<i>cah</i>	carbonate dehydratase	0.88		
<i>bll2065</i>	<i>icfA</i>	carbonic anhydrase	0.72		
<i>bll4571</i>	<i>nirA</i>	putative ferredoxin--nitrite reductase	0.35 *		
<i>bll4798</i>		putative glutaminase	0.33 *		NH <sub>4</sub> <sup>+</sup> assimilation
<i>bll4863</i>		putative carbonic anhydrase	1.24		
<i>bll4865</i>		putative carbonic anhydrase	0.77		
<i>bll5091</i>		nitronate monooxygenase	1.61		
<i>bll5092</i>		nitronate monooxygenase	1.21		
<i>bll5731</i>		probable cyanate hydratase	0.28 *		
<i>bll5732</i>	<i>nrtC</i>	ABC transporter ATP-binding protein	0.18 *		Nitrate assimilation
<i>bll5733</i>	<i>nrtB</i>	nitrate ABC transporter permease protein	0.20 *	Nitrogen metabolism	Nitrate assimilation
<i>bll5734</i>	<i>nrtA</i>	ABC transporter nitrate-binding protein	0.18 *	(bja00910)	Nitrate assimilation
<i>bll6402</i>		nitrilase	0.19 *		
<i>blr0314</i>	<i>nosR</i>	nitrous oxide reductase expression regulator	0.24 *		
<i>blr0315</i>	<i>nosZ</i>	nitrous oxide reductase	0.63		Denitrification
<i>blr0500</i>	<i>cah</i>	carbonate dehydratase	1.19		
<i>blr0972</i>		amidase	0.64		
<i>blr1327</i>		nitronate monooxygenase	3.10 *		
<i>blr1330</i>		nitronate monooxygenase	1.11		
<i>blr1743</i>	<i>nifD</i>	nitrogenase molybdenum-iron protein alpha chain	0.56		nitrogen fixation
<i>blr1744</i>	<i>nifK</i>	nitrogenase molybdenum-iron protein beta chain	0.59		nitrogen fixation
<i>blr1769</i>	<i>nifH</i>	dinitrogenase reductase protein	1.23		nitrogen fixation
<i>blr2084</i>		putative glutamine synthetase	0.99		NH <sub>4</sub> <sup>+</sup> assimilation
<i>blr2803</i>	<i>nrtA</i>	ABC transporter nitrate-binding protein	0.30 *		Nitrate assimilation
<i>blr2804</i>	<i>nrtB</i>	nitrate ABC transporter permease protein	0.29 *		Nitrate assimilation
<i>blr2805</i>	<i>nrtC</i>	nitrate ABC transporter ATP-binding protein	0.40 *		Nitrate assimilation
<i>blr2806</i>		nitrite extrusion protein	0.69		Nitrate assimilation
<i>blr2808</i>		putative nitrite reductase	0.41		
<i>blr2809</i>	<i>nasA</i>	nitrate reductase large subunit	0.31 *		Assimilatory nitrate reduction
<i>blr3214</i>	<i>norC</i>	nitric oxide reductase subunit C	0.24 *		Denitrification
<i>blr3215</i>	<i>norB</i>	nitric oxide reductase subunit B	0.37 *		Denitrification
<i>blr3397</i>	<i>nit</i>	nitrilase	0.15 *		
<i>blr4169</i>	<i>glnII</i>	glutamine synthetase	0.28 *		NH <sub>4</sub> <sup>+</sup> assimilation
<i>blr4835</i>	<i>glnA</i>	glutamine synthetase I	0.95		NH <sub>4</sub> <sup>+</sup> assimilation

Cont.					
<i>blr4949</i>	<i>glnA</i>	glutamine synthetase I	2.04		NH <sub>4</sub> <sup>+</sup> assimilation
<i>blr6144</i>	<i>amiF</i>	putative aliphatic amidase	1.49		
<i>blr7037</i>	<i>napD</i>	periplasmic nitrate reductase	0.03 *		Denitrification
<i>blr7038</i>	<i>napA</i>	periplasmic nitrate reductase large subunit precursor	0.02 *	Nitrogen metabolism (bja00910)	Denitrification
<i>blr7039</i>	<i>napB</i>	periplasmic nitrate reductase small subunit precursor	0.03 *		Denitrification
<i>blr7040</i>	<i>napC</i>	cytochrome C-type protein	0.02 *		Denitrification
<i>blr7089</i>	<i>nirK</i>	respiratory nitrite reductase	0.02 *		Denitrification
<i>blr7743</i>	<i>gltB</i>	glutamate synthase large subunit	0.69		
<i>blr7744</i>	<i>gltD</i>	glutamate synthase small subunit	0.67		
<i>blr7995</i>		glutamate dehydrogenase	1.17		
<i>bsr7036</i>	<i>napE</i>	periplasmic nitrate reductase protein	0.04 *		
<b>Regulatory protein genes</b>					
<i>bll0916</i>	<i>glnD</i>	[protein-PII] uridylyltransferase	1.15		
<i>blr0606</i>	<i>glnK</i>	nitrogen regulatory protein P-II 2	3.39 *		
<i>blr0612</i>	<i>glnK</i>	nitrogen regulatory protein P-II 2	0.12 *		
<i>blr0613</i>	<i>amtB</i>	ammonium transporter	0.10 *		
<i>blr0723</i>	<i>rpoN2</i>	RNA polymerase sigma-54 factor	0.47		
<i>blr1883</i>	<i>rpoN1</i>	RNA polymerase sigma-54 factor	0.04 *		
<i>blr2037</i>	<i>nifA</i>	nif-specific regulatory protein	1.42		
<i>blr4486</i>	<i>nifR</i>	nitrogen regulation protein	0.31 *		
<i>blr4487</i>	<i>ntxB</i>	two-component sensor histidine kinase	0.31 *		
<i>blr4488</i>	<i>ntxC</i>	two-component response regulator	0.40 *		
<i>blr4489</i>	<i>ntxY</i>	two-component sensor histidine kinase	0.73		
<i>blr4490</i>	<i>ntxX</i>	two-component response regulator	0.78		
<i>blr4948</i>	<i>glnB</i>	nitrogen regulatory protein P-II 1	0.38 *		
<i>blr7084</i>	<i>nnrR</i>	transcriptional regulatory protein	0.03 *		

<sup>a</sup> Nomenclature according to Kaneko and associate (2002).

<sup>b</sup> Gene name according to the EMBL-EBI database.

<sup>c</sup> Gene description according to GeneBank.

<sup>d</sup> Indicating the transcript ratio of genes in  $\Delta$ bjaR<sub>1</sub> mutant relative to those in wild-type cells freely grown in YEM medium in the presence of 5.0  $\mu$ M genistein for 12h at 28 °C.

<sup>e</sup> Pathway according to KEGG DataBase (<https://www.genome.jp/pathway/bja00910>)

\* Indicating the ratio value with statistical significance, ratio  $\geq 2.5$  or  $\leq 0.4$  for up-or down-regulated genes.

Table S5 Differentially expressed proteins in the free-living  $\Delta$ bjar<sub>1</sub> mutant (OD<sub>600</sub>=1.2) compared with those in the wild-type cells

Protein Accession <sup>a</sup>	Gene ID <sup>b</sup>	Gene name <sup>c</sup>	Description <sup>d</sup>	Ratio <sup>e</sup>
<b>Significantly down-regulated proteins (207 proteins)</b>				
Q89XV9	<i>bll0196</i>		ABC transporter substrate-binding protein	0.49
Q89XI2	<i>bll0332</i>		unknown protein	0.52
Q89XI1	<i>bll0333</i>		probable alcohol dehydrogenase precursor	0.66
Q89X75	<i>bll0439</i>	<i>atpC</i>	ATP synthase epsilon chain	0.50
Q89X16	<i>bll0506</i>		hypothetical protein	0.61
Q89WS5	<i>bll0603</i>		putative oxidoreductase protein	0.66
H7C6K3	<i>bll0768</i>	<i>irr</i>	iron response regulator	0.59
Q89WB9	<i>bll0773</i>		hypothetical glutathione S-transferase like protein	0.64
Q89WB8	<i>bll0774</i>		unknown protein	0.52
Q89W93	<i>bll0800</i>		hypothetical protein	0.66
Q89W32	<i>bll0861</i>	<i>dinP</i>	DNA-damage-inducible protein	0.44
Q89W30	<i>bll0863</i>		unknown protein	0.56
Q89W04	<i>bll0889</i>		putative transport protein	0.62
Q89VV4	<i>bll0941</i>	<i>bla</i>	beta-lactamase L2 precursor	0.66
Q89VT8	<i>bll0957</i>		hypothetical protein	0.47
Q89VM1	<i>bll1024</i>		hypothetical protein	0.60
Q89V92	<i>bll1155</i>		hypothetical protein	0.37
P08262	<i>bll1200</i>	<i>hemA</i>	5-aminolevulinic acid synthase	0.64
Q89UJ7	<i>bll1419</i>	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	0.50
Q89UI1	<i>bll1436</i>	<i>ctpG</i>	pilus assembly protein	0.46
Q89UI0	<i>bll1437</i>	<i>ctpF</i>	pilus assembly protein	0.56
Q89U26	<i>bll1593</i>		unknown protein	0.48
H7C6T9	<i>bll1791</i>		hypothetical protein	0.47
H7C7S9	<i>bll2045</i>		unknown protein	0.49
H7C6Q0	<i>bll2065</i>	<i>icfA</i>	carbonic anhydrase	0.48
Q89SV9	<i>bll2291</i>		unknown protein	0.40
Q89SV6	<i>bll2294</i>	<i>papA</i>	putative alkaline protease	0.24
Q89SF5	<i>bll2445</i>		oxidoreductase	0.65
Q89SD7	<i>bll2463</i>		hypothetical protein	0.65
Q89S87	<i>bll2518</i>		hypothetical protein	0.55
Q89RW5	<i>bll2647</i>		hypothetical protein	0.40
Q89RK6	<i>bll2757</i>	<i>fixK<sub>2</sub></i>	transcriptional regulatory protein	0.29
Q89RA4	<i>bll2868</i>		ABC transporter substrate-binding protein	0.64
Q89R99	<i>bll2873</i>		ABC transporter ATP-binding protein	0.60
Q89QQ9	<i>bll3065</i>		hypothetical aldolase class II protein	0.65
Q89QL2	<i>bll3112</i>		probable glucosyl transferase	0.48
Q89QK9	<i>bll3115</i>		hypothetical protein	0.33
Q89Q44	<i>bll3286</i>		ABC transporter substrate-binding protein	0.66
Q89Q43	<i>bll3287</i>		ABC transporter ATP-binding protein	0.62
Q89Q14	<i>bll3316</i>		ABC transporter substrate-binding protein	0.57
Q89PW5	<i>bll3365</i>		unknown protein	0.51
Q89N54	<i>bll3988</i>		unknown protein	0.61
Q89MX0	<i>bll4072</i>	<i>dnaC</i>	replicative DNA helicase	0.52
Q89MB9	<i>bll4274</i>	<i>nrpE</i>	ribonucleoside-diphosphate reductase 2 alpha chain	0.59
Q89MA9	<i>bll4284</i>		putative acetyl hydrolase	0.39
Q89M09	<i>bll4384</i>		probable substrate-binding protein	0.57
Q89LU9	<i>bll4444</i>		hypothetical protein	0.41
Q89L40	<i>bll4708</i>		probable ATP-binding protein	0.21
Q89KW6	<i>bll4784</i>		aldehyde dehydrogenase	0.66
Q89KN9	<i>bll4865</i>		putative carbonic anhydrase	0.60
Q89KM6	<i>bll4879</i>		hypothetical protein	0.62
Q89KM5	<i>bll4880</i>		hypothetical protein	0.57
Q89KM4	<i>bll4881</i>		hypothetical protein	0.66
Q89KF7	<i>bll4950</i>		probable L-asparaginase	0.55
Q89KA0	<i>bll5009</i>		putative deoxycytidine triphosphate deaminase	0.64
Q89K74	<i>bll5036</i>	<i>mucS</i>	transcriptional regulatory protein	0.43
Q89K71	<i>bll5040</i>		unknown protein	0.56
Q89K70	<i>bll5041</i>		unknown protein	0.32
Q89K69	<i>bll5042</i>		unknown protein	0.54
Q89K62	<i>bll5049</i>		AttM/AiiB family protein	0.47
Q89K11	<i>bll5108</i>		oxidoreductase	0.52
Q89JW4	<i>bll5155</i>		hypothetical protein	0.53
Q89JE6	<i>bll5337</i>		unknown protein	0.28
Q89JA8	<i>bll5375</i>	<i>rplQ</i>	50S ribosomal protein L17	0.60
Q89J41	<i>bll5443</i>		hypothetical protein	0.43
Q89J06	<i>bll5478</i>		similar to formate dehydrogenase	0.59
Q89IY0	<i>bll5504</i>		putative polyvinyl-alcohol dehydrogenase	0.56
Q89IP1	<i>bll5593</i>		unknown protein	0.47
Q89IH9	<i>bll5655</i>		alcohol dehydrogenase	0.42
Q89IH8	<i>bll5656</i>		hypothetical protein	0.64
Q89I94	<i>bll5745</i>		unknown protein	0.49
Q89I84	<i>bll5755</i>	<i>recA</i>	RecA protein	0.64
Q89I32	<i>bll5807</i>		hypothetical protein	0.56

Cont.

Q89HZ6	<i>bl15843</i>		hypothetical protein	0.63
Q89HZ3	<i>bl15846</i>		hypothetical protein	0.53
Q89HQ5	<i>bl15935</i>		hypothetical protein	0.62
Q89HC1	<i>bl16073</i>	<i>phbC</i>	probable poly-beta-hydroxybutyrate polymerase	0.55
Q89H54	<i>bl16141</i>		hypothetical protein	0.61
Q89G96	<i>bl16449</i>		hypothetical protein	0.32
Q89G41	<i>bl16506</i>		serine protease DO-like precursor	0.55
Q89F13	<i>bl16888</i>		putative porin	0.49
Q89F02	<i>bl16899</i>		ABC transporter substrate-binding protein	0.56
Q89ER5	<i>bl17007</i>		putative oxidoreductase	0.61
Q89ER1	<i>bl17011</i>		ABC transporter aliphatic-sulfonate-binding protein	0.35
Q89EN7	<i>bl17035</i>		transcriptional regulatory protein	0.63
Q89EK2	<i>bl17073</i>	<i>exbB</i>	biopolymer transport protein	0.59
H7C6P0	<i>bl17075</i>		hypothetical protein	0.54
Q89E88	<i>bl17199</i>		putative N-ethylmeline chlorohydrolase	0.65
Q89E87	<i>bl17200</i>		probable substrate-binding protein	0.54
Q89E80	<i>bl17207</i>		probable N-Carbamoyl-D-Amino-Acid Amidohydrolase	0.42
Q89E68	<i>bl17219</i>		unknown protein	0.65
Q89DY3	<i>bl17304</i>		unknown protein	0.62
Q89DX7	<i>bl17310</i>		probable ArcA2 arginine deiminase	0.12
Q89DM5	<i>bl17414</i>		probable Elongation factor G	0.54
Q89D17	<i>bl17452</i>	<i>ribH</i>	6,7-dimethyl-8-ribityllumazine synthase	0.51
Q89DA1	<i>bl17538</i>		hypothetical protein	0.49
Q89D88	<i>bl17553</i>		unknown protein	0.61
Q89CL4	<i>bl17783</i>		hypothetical protein	0.38
Q89CI6	<i>bl17811</i>		hypothetical protein	0.54
Q89C77	<i>bl17920</i>		ABC transporter permease protein	0.50
Q89C59	<i>bl17938</i>		hypothetical protein	0.53
Q89C29	<i>bl17969</i>		putative dihydrodipicolinate synthase	0.62
Q89BQ5	<i>bl18093</i>		unknown protein	0.58
Q89BJ6	<i>bl18152</i>		hypothetical protein	0.55
Q89BJ5	<i>bl18153</i>		hypothetical protein	0.46
Q89Y98	<i>blr0056</i>		unknown protein	0.56
Q89Y06	<i>blr0149</i>	<i>cyoA</i>	cytochrome O ubiquinol oxidase subunit II	0.41
Q89Y05	<i>blr0150</i>	<i>cyoB</i>	cytochrome O ubiquinol oxidase subunit I	0.35
Q89XJ7	<i>blr0314</i>	<i>nosR</i>	nitrous oxide reductase expression regulator	0.56
H7C6L4	<i>blr0515</i>	<i>sdhB</i>	succinate dehydrogenase iron-sulfur protein subunit	0.61
Q89WV7	<i>blr0571</i>		hypothetical protein	0.52
Q89WQ7	<i>blr0621</i>		hypothetical protein	0.56
Q89WE1	<i>blr0749</i>		hypothetical protein	0.61
Q89WA5	<i>blr0787</i>		hypothetical protein	0.37
Q89W22	<i>blr0871</i>		unknown protein	0.42
Q89W21	<i>blr0872</i>		unknown protein	0.26
Q89VS3	<i>blr0972</i>		amidase	0.15
Q89VP2	<i>blr1003</i>		hypothetical protein	0.60
Q89UX0	<i>blr1289</i>		hypothetical protein	0.38
Q89UK8	<i>blr1408</i>		hypothetical protein	0.46
Q89UD5	<i>blr1482</i>		ABC transporter sulfate-binding protein	0.60
Q89UC1	<i>blr1496</i>		unknown protein	0.39
Q89UA9	<i>blr1508</i>		HlyB/MsbA family ABC transporter	0.65
Q89UA1	<i>blr1516</i>	<i>acrB</i>	RND multidrug efflux transporter	0.56
Q89U55	<i>blr1564</i>		unknown protein	0.51
H7C6T3	<i>blr1830</i>		unknown protein	0.64
H7C7V3	<i>blr1896</i>		transcriptional regulatory protein	0.59
Q89TC4	<i>blr2114</i>		hypothetical protein	0.41
Q89T28	<i>blr2222</i>	<i>dadA</i>	D-amino acid dehydrogenase, small subunit	0.54
Q89T10	<i>blr2240</i>		hypothetical protein	0.62
Q89SW0	<i>blr2290</i>		unknown protein	0.18
Q89SH6	<i>blr2424</i>		transcriptional regulatory protein	0.58
Q89SB7	<i>blr2488</i>		unknown protein	0.46
Q89RG7	<i>blr2805</i>	<i>nrtC</i>	nitrate ABC transporter ATP-binding protein	0.63
Q89R38	<i>blr2934</i>	<i>ragC</i>	probable cation efflux protein	0.62
Q89QY8	<i>blr2984</i>		unknown protein	0.23
Q89QY7	<i>blr2985</i>		two-component hybrid sensor and regulator	0.30
Q89QY6	<i>blr2986</i>		two-component hybrid sensor and regulator	0.36
Q89QK0	<i>blr3124</i>		unknown protein	0.21
P45399	<i>blr3125</i>	<i>cycH</i>	cytochrome C-type biogenesis protein	0.65
Q89Q56	<i>blr3274</i>		hypothetical protein	0.60
Q89Q39	<i>blr3291</i>		ABC transporter substrate-binding protein	0.53
Q89Q18	<i>blr3312</i>		hypothetical protein	0.52
Q89PQ2	<i>blr3428</i>		organic hydroperoxide resistance protein	0.59
Q89ND4	<i>blr3908</i>		hypothetical protein	0.64
Q89NB2	<i>blr3930</i>		aminotransferase	0.54
Q89NB1	<i>blr3931</i>		probable substrate-binding protein	0.57
Q89N86	<i>blr3956</i>		enoyl-CoA hydratase	0.64
Q89MY9	<i>blr4053</i>		hypothetical protein	0.40
Q89MU8	<i>blr4094</i>		unknown protein	0.19

Cont.

Q89MP1	<i>blr4151</i>		hypothetical protein	0.65
Q89M29	<i>blr4364</i>		putative haloacid dehalogenase	0.61
Q89LN8	<i>blr4505</i>		hypothetical protein	0.48
Q89L93	<i>blr4655</i>	<i>ppsA</i>	Phosphoenolpyruvate synthase	0.40
Q89L47	<i>blr4701</i>		putative outer-membrane immunogenic protein precursor	0.42
Q89KU7	<i>blr4803</i>		two-component hybrid sensor and regulator	0.61
Q89KS4	<i>blr4829</i>		unknown protein	0.48
Q89KN3	<i>blr4872</i>		unknown protein	0.41
Q89K15	<i>blr5104</i>	<i>smf</i>	DNA processing protein	0.54
Q89JZ4	<i>blr5125</i>		hypothetical protein	0.64
Q89JU6	<i>blr5173</i>		hypothetical protein	0.61
Q89JH5	<i>blr5308</i>		anti-oxidant protein	0.64
Q89J53	<i>blr5431</i>		hypothetical protein	0.62
Q89IX1	<i>blr5513</i>		hypothetical protein	0.65
Q89IR1	<i>blr5573</i>		ABC transporter ATP-binding protein	0.59
Q89IR0	<i>blr5574</i>		ABC transporter substrate-binding protein	0.66
Q89IG4	<i>blr5675</i>		ABC transporter substrate-binding protein	0.39
Q89HZ2	<i>blr5847</i>		hypothetical protein	0.59
Q89HC0	<i>blr6074</i>		hypothetical protein	0.34
Q89H51	<i>blr6144</i>		putative aliphatic amidase	0.41
Q89H37	<i>blr6158</i>		ABC transporter substrate-binding protein	0.60
Q89GY6	<i>blr6209</i>		unknown protein	0.65
Q89GY5	<i>blr6210</i>		hypothetical protein	0.63
Q89GL4	<i>blr6331</i>	<i>bkdA1</i>	2-oxoisovalerate dehydrogenase alpha subunit	0.53
Q89GL3	<i>blr6332</i>	<i>bkdA2</i>	2-oxoisovalerate dehydrogenase beta subunit	0.55
Q89GL2	<i>blr6333</i>	<i>bkdB</i>	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase	0.57
Q89GL1	<i>blr6334</i>	<i>lpdA</i>	dihydrolipoamide dehydrogenase	0.53
Q89G29	<i>blr6518</i>		hypothetical protein	0.60
Q89G25	<i>blr6523</i>		putative iron transport protein	0.66
Q89FP4	<i>blr6655</i>	<i>thiO</i>	thiamine biosynthesis oxidoreductase	0.53
Q89FP0	<i>blr6659</i>	<i>thiC</i>	thiamine biosynthesis protein	0.59
Q89EW0	<i>blr6960</i>		arylesterase	0.59
Q89ER6	<i>blr7006</i>		probable carboxypeptidase G2	0.57
Q89EL0	<i>blr7063</i>		probable 2-ketogluconate reductase	0.33
H7C6N5	<i>blr7077</i>	<i>hmuT</i>	hemin ABC transporter hemin-binding protein	0.51
H7C7W5	<i>blr7078</i>	<i>hmuU</i>	hemin ABC transporter permease protein	0.39
Q93SH7	<i>blr7079</i>	<i>hmuV</i>	hemin ABC transporter ATP-binding protein	0.24
H7C6M6	<i>blr7084</i>	<i>nnrR</i>	transcriptional regulatory protein	0.45
Q89EF5	<i>blr7130</i>		two-component response regulator	0.40
Q89E78	<i>blr7209</i>		probable glutamine amidotransferase	0.60
Q89DV5	<i>blr7332</i>		putative inosine-5'-monophosphate dehydrogenase protein	0.54
Q89DU3	<i>blr7345</i>		unknown protein	0.41
Q89DH3	<i>blr7466</i>		ribonuclease	0.41
Q89DF5	<i>blr7484</i>		hypothetical zinc protease	0.57
Q45233	<i>blr7544</i>	<i>cycA</i>	cytochrome c550	0.64
Q89D27	<i>blr7618</i>		hypothetical protein	0.44
Q89CQ8	<i>blr7738</i>		hypothetical protein	0.49
Q89CH0	<i>blr7827</i>		ABC transporter substrate-binding protein	0.46
Q89CC5	<i>blr7872</i>		HlyD family secretion protein	0.54
Q89BR1	<i>blr8087</i>		unknown protein	0.58
Q89BR0	<i>blr8088</i>		hypothetical protein	0.60
Q89DC2	<i>bsr7517</i>		hypothetical protein	0.61
Q89L22	<i>bsr4726</i>		unknown protein	0.51
Q89G27	<i>bsr6520</i>		hypothetical protein	0.31
Q89FP3	<i>bsr6656</i>		thiamin biosynthesis protein homolog	0.49
Q89ES4	<i>bsr6998</i>		hypothetical protein	0.48
Q89EH5	<i>bsr7110</i>		hypothetical protein	0.58
Q89DU0	<i>bsr7348</i>		unknown protein	0.56

### Significantly up-reguated proteins (131 proteins)

Q89Y34	<i>blI0121</i>		transcriptional regulatory protein	1.63
Q89Y12	<i>blI0143</i>		putative enoyl-CoA hydratase	1.77
Q89XD3	<i>blI0381</i>		ABC transporter substrate-binding protein	1.67
Q89WT0	<i>blI0598</i>		hypothetical protein	3.04
Q89WA2	<i>blI0790</i>		probable transcriptional regulator	10.17
Q89VU1	<i>blI0954</i>		hypothetical protein	1.51
Q89VQ1	<i>blI0994</i>		probable acid-CoA ligase	1.55
Q89VQ0	<i>blI0995</i>		maleylacetate reductase	1.57
Q89V80	<i>blI1167</i>	<i>sipS</i>	signal peptidase	4.49
Q89UH0	<i>blI1447</i>	<i>rhlE</i>	dead-box ATP-dependent RNA helicase	1.94
Q89UF2	<i>blI1465</i>		hypothetical protein	1.62
P15939	<i>blI1715</i>	<i>nodV</i>	two component regulator	1.52
Q89SU1	<i>blI2309</i>	<i>mobA</i>	molybdopterin-guanine dinucleotide biosynthesis protein A	2.15
Q89SR5	<i>blI2335</i>		hypothetical protein	3.44
Q89SL9	<i>blI2381</i>		probable glycosyl transferase	1.60
Q89SL5	<i>blI2385</i>		hypothetical protein	1.84
Q89SE6	<i>blI2454</i>		probable transcriptional regulator	1.81

Cont.

Q89SB1	<i>bll2494</i>		hypothetical protein	1.95
Q89S74	<i>bll2532</i>	<i>ispB</i>	octaprenyl-diphosphate synthase	1.67
Q89RZ1	<i>bll2621</i>		hypothetical protein	2.20
Q89RY5	<i>bll2627</i>		hypothetical protein	2.17
Q89RX2	<i>bll2640</i>		major facilitator superfamily transporter	1.53
Q89RT4	<i>bll2678</i>		putative D-lactate dehydrogenase (cytochrome) protein	2.57
Q89RI7	<i>bll2785</i>		probable transcriptional regulator	1.91
Q89RI6	<i>bll2786</i>		transcriptional regulatory protein	1.63
Q89R57	<i>bll2915</i>		hypothetical oxidoreductase	2.47
Q89QW8	<i>bll3006</i>		hypothetical protein	2.45
Q89QL7	<i>bll3107</i>		unknown protein	1.54
Q89QI2	<i>bll3146</i>		hypothetical protein	1.90
Q89QH8	<i>bll3150</i>		putative Oxalate:formate antiporter	1.95
Q89Q62	<i>bll3268</i>	<i>cobK</i>	precorrin-6x reductase	1.61
Q89PU3	<i>bll3387</i>		unknown protein	1.91
Q89PR9	<i>bll3411</i>	<i>iorA</i>	indolepyruvate ferredoxin oxidoreductase alpha subunit	2.05
Q89PQ7	<i>bll3423</i>		ABC transporter ATP-binding protein	1.60
Q89P78	<i>bll3605</i>		hypothetical protein	1.65
Q89P72	<i>bll3611</i>		hypothetical protein	1.52
Q89NE0	<i>bll3902</i>		AcrB/AcrD/AcrF family protein	2.09
Q89ME1	<i>bll4252</i>		putative hydrolase	1.79
Q89M39	<i>bll4354</i>		hypothetical protein	1.54
Q89LR4	<i>bll4479</i>		probable cytochrome C4	3.06
Q89LJ6	<i>bll4548</i>		hypothetical protein	1.68
Q89KC4	<i>bll4983</i>		hypothetical protein	2.74
Q89K00	<i>bll5119</i>		transcriptional regulator	1.76
Q89JS4	<i>bll5198</i>		unknown protein	2.91
Q89JI2	<i>bll5301</i>		two-component response regulator	2.59
Q89JC9	<i>bll5354</i>		probable transmembrane protein	1.59
Q89J71	<i>bll5413</i>		2-hydroxyacid dehydrogenase	1.85
Q89IK5	<i>bll5629</i>		hypothetical protein	1.51
Q89II7	<i>bll5647</i>		putative adenylate cyclase	1.56
Q89IE5	<i>bll5694</i>		hypothetical protein	1.57
Q89I99	<i>bll5740</i>		hypothetical protein	2.52
Q89I56	<i>bll5783</i>		ABC transporter permease protein	1.52
Q89HP7	<i>bll5943</i>		unknown protein	1.50
Q89HN2	<i>bll5958</i>		hypothetical protein	1.82
Q89H41	<i>bll6154</i>		unknown protein	2.39
Q89H12	<i>bll6183</i>		hypothetical protein	1.60
Q89GQ1	<i>bll6294</i>		unknown protein	7.09
Q89GD8	<i>bll6407</i>		ABC transporter substrate-binding protein	2.22
Q89GC0	<i>bll6425</i>		putative oxidoreductase	1.82
Q89G68	<i>bll6477</i>		ABC transporter ATP-binding protein	1.63
Q89G67	<i>bll6478</i>		ABC transporter ATP-binding protein	1.60
Q89G66	<i>bll6479</i>		ABC transporter substrate-binding protein	1.59
Q89G43	<i>bll6504</i>		tRNA delta(2)-isopentenylpyrophosphate	2.04
Q89FV3	<i>bll6596</i>	<i>ftsZ</i>	cell division protein	1.62
Q89FB0	<i>bll6791</i>		putative acyl-CoA dehydrogenase	1.62
Q89ED3	<i>bll7154</i>	<i>tolR</i>	tolR protein	1.65
Q89E27	<i>bll7260</i>	<i>lrp</i>	leucine-responsive transcriptional regulatory protein	2.08
Q89DC6	<i>bll7513</i>		hypothetical protein	1.63
Q89CC2	<i>bll7875</i>		hypothetical protein	1.65
Q89C89	<i>bll7908</i>		hypothetical protein	1.67
Q89C69	<i>bll7928</i>		putative fatty-acid--CoA ligase	1.81
Q89C68	<i>bll7929</i>		ABC transporter ATP-binding protein	1.83
Q89C67	<i>bll7930</i>		ABC transporter ATP-binding protein	1.62
Q89C66	<i>bll7931</i>		ABC transporter permease protein	2.01
Q89BX9	<i>bll8019</i>		unknown protein	1.81
Q89BI4	<i>bll8168</i>		Na <sup>+</sup> /H <sup>+</sup> antiporter	1.52
Q89XJ6	<i>blr0315</i>	<i>nosZ</i>	nitrous oxide reductase	1.52
Q89WS0	<i>blr0608</i>		similar to ammonium transporter	1.81
Q89W79	<i>blr0814</i>		transcriptional regulatory protein	1.73
Q89VX6	<i>blr0919</i>		ABC transporter ATP-binding protein	2.07
Q89VR4	<i>blr0981</i>		acyl-CoA dehydrogenase	1.97
Q89V52	<i>blr1206</i>		unknown protein	4.13
Q89V20	<i>blr1238</i>		hypothetical protein	2.17
Q89UU5	<i>blr1314</i>		penicillin tolerance protein	1.50
Q89UE0	<i>blr1477</i>		probable trifunctional enzyme subunit	1.96
P94323	<i>blr1632</i>	<i>nodM</i>	putative glucosamine synthase	6.91
Q9AMZ0	<i>blr2025</i>	<i>nodA</i>	acyl transferase	2.36
Q89SL8	<i>blr2382</i>	<i>lspL</i>	UDP-glucuronic acid epimerase	1.58
Q89SE5	<i>blr2455</i>		isocitrate lyase	1.55
Q89SD4	<i>blr2466</i>		hypothetical protein	1.74
Q89SA4	<i>blr2501</i>		hypothetical protein	2.10
Q89QE5	<i>blr3183</i>		ABC transporter substrate-binding protein	1.59
Q89QE1	<i>blr3187</i>		ABC transporter ATP-binding protein	1.71
Q89QB0	<i>blr3220</i>		hypothetical protein	2.00

Cont.

Q89Q98	<i>blr3232</i>		ABC transporter ATP-binding protein	2.61
Q89PX3	<i>blr3357</i>		ABC transporter ATP-binding protein	1.85
Q89PU1	<i>blr3389</i>		probable ABC transporter substrate-binding protein	2.50
Q89PQ1	<i>blr3429</i>		hypothetical protein	1.73
Q89PD0	<i>blr3552</i>		putative glutamate-1-semialdehyde 2,1-aminomutase	1.58
Q89P85	<i>blr3598</i>		unknown protein	1.92
Q89P83	<i>blr3600</i>		hypothetical protein	2.55
Q89P82	<i>blr3601</i>		hypothetical protein	1.79
Q89P06	<i>blr3677</i>		putative monooxygenase component	1.66
Q89P05	<i>blr3678</i>		putative oxidoreductase	1.88
Q89P00	<i>blr3683</i>		chaperonin GroEL	1.56
Q89NF6	<i>blr3884</i>		putative dihydrodipicolinate synthase	1.66
Q89NC2	<i>blr3920</i>		ABC transporter permease protein	1.64
Q89MD6	<i>blr4257</i>		putative hydrolase	1.76
Q89LI7	<i>blr4557</i>		ABC transporter ATP-binding protein	2.29
Q89LG9	<i>blr4575</i>		hypothetical protein	2.46
Q89LE1	<i>blr4603</i>	<i>recG</i>	ATP-dependent DNA helicase	1.68
Q89L61	<i>blr4687</i>	<i>asd</i>	aspartate-semialdehyde dehydrogenase	3.34
Q89L49	<i>blr4699</i>		putative outer-membrane protein precursor	6.40
H7C6L5	<i>blr4775</i>		two-component response regulator	4.16
Q89KD6	<i>blr4971</i>		hypothetical protein	1.57
H7C7Z2	<i>blr5235</i>	<i>degP</i>	serine protease	2.13
Q89JP7	<i>blr5236</i>		unknown protein	2.52
Q89JN1	<i>blr5252</i>		probable polysaccharide deacetylase	1.64
Q89HE6	<i>blr6045</i>		hypothetical protein	1.68
Q89GZ9	<i>blr6195</i>		hypothetical protein	1.58
Q89GK5	<i>blr6340</i>	<i>hycC</i>	probable hydrogenlyase component	1.55
Q89EH1	<i>blr7114</i>	<i>purE</i>	phosphoribosylaminoimidazole carboxylase catalytic subunit	2.45
Q89E17	<i>blr7270</i>		probable acyl-CoA dehydrogenase	1.81
Q89DE3	<i>blr7496</i>		nitrogen fixation protein	1.52
Q89D91	<i>blr7549</i>		hypothetical protein	1.51
Q89CE1	<i>blr7856</i>		hypothetical protein	1.83
Q89CE0	<i>blr7857</i>		putative 3-hydroxybutyryl-CoA dehydratase	1.51
Q89CB2	<i>blr7885</i>		oxidoreductase	1.51
Q89BJ3	<i>blr8155</i>		hypothetical protein	2.44
Q89VK5	<i>bsr1040</i>		hypothetical protein	1.55
Q89L82	<i>bsr4666</i>		unknown protein	1.64

<sup>a</sup> Nomenclature according to UniProt.

<sup>b</sup> Nomenclature according to Kaneko and associate (2002).

<sup>c</sup> Gene name according to the EMBL-EBI database.

<sup>d</sup> Gene description according to GeneBank.

<sup>e</sup> Indicating the abundance ratio of proteins in  $\Delta$ bjaR<sub>1</sub> mutant relative to wild-type cells freely grown in YEM medium at OD<sub>600</sub> of 1.2.



Table S6 50 differentially expressed genes and their protein products at both the transcriptional and translational level in the free-living *ΔbjaR*<sub>1</sub> mutant (OD<sub>600</sub>=1.2) compared with wild-type cells

Gene ID <sup>a</sup>	Protein accession <sup>b</sup>	Gene name <sup>c</sup>	Description <sup>d</sup>	Ratio <sup>e</sup>	
				Transcriptome	Proteome*
<b>Significantly up-regulated</b>					
<i>bll0994</i>	Q89VQ1	-	Acyl-CoA synthetase	3.36	1.55
<i>bll2335</i>	Q89SR5	-	Hypothetical protein	3.27	3.44
<i>bll6478</i>	Q89G67	-	ABC transporter ATP-binding protein	3.18	1.60
<i>bll6479</i>	Q89G66	-	ABC transporter substrate-binding protein	3.30	1.59
<i>bll7929</i>	Q89C68	-	ABC transporter ATP-binding protein	4.60	1.83
<i>bll7930</i>	Q89C67	-	ABC transporter ATP-binding protein	3.90	1.62
<i>bll7931</i>	Q89C66	-	ABC transporter permease	3.19	2.01
<i>blr2025</i>	Q9AMZ0	<i>nodA</i>	Acyl transferase	3.45	2.36
<i>blr2501</i>	Q89SA4	-	Hypothetical protein	4.47	2.10
<i>blr3183</i>	Q89QE5	-	ABC transporter substrate-binding protein	5.13	1.59
<i>blr3220</i>	Q89QB0	-	Hypothetical protein	4.45	2.00
<i>blr3677</i>	Q89P06	-	Monooxygenase component	73.93	1.66
<i>blr3678</i>	Q89P05	-	Oxidoreductase	85.44	1.88
<i>blr3683</i>	Q89P00	<i>groEL</i>	Molecular chaperone GroEL	41.01	1.56
<i>blr7270</i>	Q89E17	-	Acyl-CoA dehydrogenase	3.41	1.81
<b>Significantly down-regulated</b>					
<i>bll0774</i>	Q89WB8	-	Hypothetical protein	0.27	0.52
<i>bll2518</i>	Q89S87	-	Phosphoketolase	0.01	0.55
<i>bll2647</i>	Q89RW5	-	Hypothetical protein	0.02	0.40
<i>bll2757</i>	Q89RK6	<i>fixK<sub>2</sub></i>	Transcriptional regulatory protein	0.15	0.29
<i>bll2868</i>	Q89RA4	-	ABC transporter substrate-binding protein	0.24	0.64
<i>bll3115</i>	Q89QK9	-	Hypothetical protein	0.00	0.33
<i>bll3286</i>	Q89Q44	-	ABC transporter substrate-binding protein	0.33	0.66
<i>bll3287</i>	Q89Q43	-	ABC transporter ATP-binding protein	0.24	0.62
<i>bll3316</i>	Q89Q14	-	ABC transporter substrate-binding protein	0.16	0.57
<i>bll4384</i>	Q89M09	-	Substrate-binding protein	0.14	0.57
<i>bll5593</i>	Q89IP1	-	Hypothetical protein	0.21	0.47
<i>bll5655</i>	Q89IH9	-	Alcohol dehydrogenase	0.01	0.42
<i>bll6073</i>	Q89HC1	<i>phbC</i>	Poly-beta-hydroxybutyrate polymerase	0.01	0.55
<i>bll7538</i>	Q89DA1	-	Hypothetical protein	0.22	0.49
<i>bll7553</i>	Q89D88	-	Hypothetical protein	0.03	0.61
<i>bll7920</i>	Q89C77	-	ABC transporter permease	0.17	0.50
<i>blr0314</i>	Q89XJ7	<i>nosR</i>	Nitrous oxide reductase expression regulator	0.24	0.56
<i>blr0871</i>	Q89W22	-	Hypothetical protein	0.29	0.42
<i>blr0872</i>	Q89W21	-	Hypothetical protein	0.23	0.26
<i>blr0972</i>	Q89VS3	-	Amidase	0.08	0.15
<i>blr1289</i>	Q89UX0	-	Myosin-cross-reactive antigen	0.01	0.38
<i>blr2222</i>	Q89T28	<i>dadA</i>	D-amino acid dehydrogenase small subunit	0.22	0.54
<i>blr2805</i>	Q89RG7	<i>nrtC</i>	Nitrate ABC transporter permease	0.41	0.63
<i>blr3124</i>	Q89QK0	-	Hypothetical protein	0.23	0.21
<i>blr3291</i>	Q89Q39	-	ABC transporter substrate-binding protein	0.30	0.53
<i>blr3312</i>	Q89Q18	-	Hypothetical protein	0.15	0.52
<i>blr4094</i>	Q89MU8	-	Hypothetical protein	0.15	0.19
<i>blr4655</i>	Q89L93	<i>ppsA</i>	Phosphoenolpyruvate synthase	0.02	0.40
<i>blr4829</i>	Q89KS4	-	Hypothetical protein	0.40	0.48
<i>blr6074</i>	Q89HC0	-	Hypothetical protein	0.01	0.34
<i>blr7084</i>	H7C6M6	<i>nnrR</i>	Transcriptional regulatory protein	0.03	0.45
<i>blr7345</i>	Q89DU3	-	Hypothetical protein	0.01	0.41
<i>blr7466</i>	Q89DH3	-	Ribonuclease	0.39	0.41
<i>blr7872</i>	Q89CC5	-	HlyD family secretion protein	0.01	0.54
<i>bsr6520</i>	Q89G27	-	Hypothetical protein	0.04	0.31

<sup>a</sup> Nomenclature according to Kaneko et al (2002).

<sup>b</sup> Protein accession according to the UniProt database.

<sup>c</sup> Gene name according to the EMBL-EBI database.

<sup>d</sup> Gene description according to GeneBank.

<sup>e</sup> Indicating the ratio of transcript (or abundance) of genes (or protein) in the free-living *ΔbjaR*<sub>1</sub> mutant compared to those in the wild-type cells in the presence of 5.0 μM genistein. The used threshold ratio value for up- or down-reg in the transcriptome analysis was  $\geq 2.5$  or  $\leq 0.4$ , in the proteome analysis being  $\geq 1.5$  or  $\leq 0.67$ , respectively.

\* indicating the data at the high cell-density (OD<sub>600</sub>=1.2)

Table S7 Symbiotic properties of *B diazoefficiens*-infected soybean (William82) plant cultivated in the solution containing varying external N compounds

Nitrogen Levels	Inoculating strain (per plant)	Nodule number	Nodule biomass	ARA	Nodule specific activity	Root volume	Plant biomass
		(n=30)	(mg/per plant) (n=30)	( $\mu$ mole/h/plant) (n=9)	( $\mu$ moles ARA /h/g dry weight nodu (n=9)	(cm <sup>3</sup> /plant) (n=9)	( mg/plant dry weight) (n=26)
Low nitrogen	wt <i>B. d</i> 110	15 ± 1	15.2 ± 2.2	0.13 ± 0.05	9.0 ± 4.3	0.61 ± 0.20	427 ± 29
	<i>B. d</i> $\Delta$ bjar <sub>1</sub>	18 ± 1	11.0 ± 0.7 *	0.20 ± 0.04 *	18.0 ± 3.0*	0.96 ± 0.13*	353 ± 20*
	<i>B. d</i> c- $\Delta$ bjar <sub>1</sub>	15 ± 1	11.3 ± 2.0	0.08 ± 0.03	7.8 ± 3.0	0.37 ± 0.02	391 ± 38
Low nitrogen + 20 mM NH <sub>4</sub> Cl	wt <i>B. d</i> 110	13 ± 1	8.5 ± 0.9	0.11 ± 0.06	11.7 ± 5.8	0.51 ± 0.09	459 ± 17
	<i>B. d</i> $\Delta$ bjar <sub>1</sub>	14 ± 1	10.5 ± 2.4	0.25 ± 0.07*	25.2 ± 7.7*	0.81 ± 0.27*	489 ± 54
	<i>B. d</i> c- $\Delta$ bjar <sub>1</sub>	13 ± 1	9.7 ± 1.9	0.08 ± 0.05	7.6 ± 4.4	0.54 ± 0.14	435 ± 69
Low nitrogen +20 mM NaNO <sub>3</sub>	wt <i>B. d</i> 110	7 ± 1	2.4 ± 0.6	0.007 ± 0.003	2.9 ± 1.7	0.68 ± 0.13	488 ± 33
	<i>B. d</i> $\Delta$ bjar <sub>1</sub>	4 ± 1	3.9 ± 1.2	0.003 ± 0.002	0.8 ± 0.3 *	0.48 ± 0.09*	591 ± 47*
	<i>B. d</i> c- $\Delta$ bjar <sub>1</sub>	4 ± 2	1.5 ± 0.8	0.008 ± 0.004	5.3 ± 2.1	0.68 ± 0.16	437 ± 25
Low nitrogen + 20 mM NaNO <sub>2</sub>	wt <i>B. d</i> 110	3 ± 1	1.5 ± 0.3	0.001 ± 0.000	0.7 ± 0.4	0.28 ± 0.07	378 ± 22
	<i>B. d</i> $\Delta$ bjar <sub>1</sub>	6 ± 1	1.6 ± 0.2	0.007 ± 0.001*	2.4 ± 0.1*	0.40 ± 0.07*	369 ± 17
	<i>B. d</i> c- $\Delta$ bjar <sub>1</sub>	2 ± 0	1.3 ± 0.3	0.001 ± 0.000	1.2 ± 0.6	0.38 ± 0.08	303 ± 19

(1) Biomass, dry weight; ARA, acetylene reduction activity.

(2) \* Indicating the significant difference from other strains within the same level nitrogen treatment (P-value <0.05).

(3) Values in the table represent mean ± SE from three independent experiments. n, number of plants used.