

1 **SUPPLEMENTARY MATERIAL**

2 **SUPPLEMENTARY TABLES**

3 **Table S1.** Differentially expressed genes for BPG2-4 at $P < 0.05$. Listed are only those
 4 genes that showed a fold-change of ≥ 2.0 , a Likelihood value ≥ 0.9 and an adjusted p-
 5 value ≤ 0.05 . Genes in part verified by qRT-PCR or using promoter fusions are boxed.
 6

Locus_tag	Predicted function	Fold change		
		BPG2	BPG3	BPG4
BGL_1c00060	catalase	2.1-		
BGL_1c00150	flagellar biosynthetic protein FliQ		2.4+	2.8+
BGL_1c00160	flagellar biosynthetic protein FliP		3.1+	3.6+
BGL_1c00190	flagellar motor switch protein FliM		2.2+	2.7+
BGL_1c00200	flagellar basal body-associated protein FliL	2.0+	3.4+	5.6+
BGL_1c00490	pterin-4-alpha-carbinolamine dehydratase	2.0+		
BGL_1c00500	phenylalanine-4-hydroxylase PhhA		3.2-	3.3-
BGL_1c00800	aminotransferase class I and II	2.0-	2.1-	2.6-
BGL_1c00810	lysine-arginine-ornithine-binding periplasmic protein ArgT	2.2-	2.8-	4.0-
BGL_1c00940	thiamine pyrophosphate enzyme domain protein TPP-binding			2.5-
BGL_1c01420	3-oxoacyl-(acyl carrier protein) synthase III FabH		2.8+	3.4+
BGL_1c01430	aminotransferase, DegT/DnrJ/EryC1/StrS family		2.1+	2.8+
BGL_1c01440	TPR domain protein		2.6+	3.4+
BGL_1c01520	histone-like nucleoid-structuring (H-NS) protein	8.7-		
BGL_1c01540	flagellar transcriptional activator FliH		2.5+	2.7+
BGL_1c01550	flagellar transcriptional activator FliC			2.0+
BGL_1c01560	chemotaxis protein MotA			2.1+
BGL_1c01700	flagellar biosynthetic protein FliB		3.4+	4.7+
BGL_1c01710	flagellar biosynthesis protein FliA		3.1+	4.4+
BGL_1c01720	flagellar biosynthesis protein FliF		2.5+	3.2+
BGL_1c01730	flagellar biosynthesis protein FliG			2.3+
BGL_1c01740	RNA polymerase, sigma factor FliA		2.2+	2.9+
BGL_1c01870	hypothetical protein			2.3-
BGL_1c01890	rare lipoprotein A	3.4+		
BGL_1c02030	hypothetical protein		3.2+	2.7+
BGL_1c02100	hypothetical protein		2.1+	
BGL_1c02640	ribosomal protein L14			3.1+
BGL_1c03130	thiamine-phosphate diphosphorylase	2.0-		2.5-
BGL_1c03410	ubiquinol-cytochrome c reductase, iron-sulphur subunit	2.3-		
BGL_1c03420	cytochrome b	2.8-		
BGL_1c03540	type VI secretion system inner membrane protein, DotU family	2.1-		
BGL_1c03550	type VI secretion system protein, VC_A0114 family	2.2-		
BGL_1c03560	type VI secretion system, lipoprotein VCA0113 family	2.4-		
BGL_1c03570	TPR domain protein	3.1-		
BGL_1c03580	type VI secretion system protein, VC_A0107 family	3.1-		

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_1c03590	type VI secretion protein, EvpB/VC_A0108 family	3.1-		
BGL_1c03600	type VI secretion system effector, Hcp family	3.1-		
BGL_1c03610	type VI secretion system lysozyme-like protein HsiF	2.4-		
BGL_1c03620	type VI secretion system protein, VC_A0110 family	2.5-		
BGL_1c03630	type VI secretion system protein, VC_A0111 family	2.4-		
BGL_1c03640	type VI secretion system ATPase, ClpV1 family	2.6-		
BGL_1c03650	type VI secretion-associated protein, ImpA family	2.3-		
BGL_1c03700	hypothetical protein	2.5-		
BGL_1c03750	hypothetical protein	2.2-		
BGL_1c04130	hypothetical protein	2.7-		
BGL_1c04140	glutathione S-transferase	2.9-		
BGL_1c04160	aspartate aminotransferase AspB	4.4-		
BGL_1c04170	hypothetical protein	4.2-		
BGL_1c04180	transcriptional regulator, LysR family	3.6-		
BGL_1c04230	anthranilate synthase component 1 TrpE			2.5-
BGL_1c04720	ribosomal protein L27			2.5+
BGL_1c06060	putative flavohemo protein Hmp	3.2-		
BGL_1c06190	chaperone DnaK			2.1-
BGL_1c06220	3-methyl-2-oxobutanoate hydroxymethyltransferase PanB			2.2-
BGL_1c06430	capsular polysaccharide export inner-membrane protein WcbD		2.2+	2.4+
BGL_1c06790	Protein of unknown function (DUF3318)			2.2-
BGL_1c06830	acyl-CoA dehydrogenase			2.1-
BGL_1c06860	4-hydroxybenzoate transporter PcaK	2.9+		
BGL_1c06890	cob(II)yrinic acid a,c-diamide reductase BluB	2.3-		
BGL_1c06900	transcriptional regulator, LysR family	14.0-		
BGL_1c07040	hypothetical protein	42.2-		4.9-
BGL_1c07150	rubredoxin RubA		2.0+	2.5+
BGL_1c07210	dihydroorotase-like protein PyrC			2.1-
BGL_1c07690	integrase		2.9+	2.8+
BGL_1c07900	transcriptional regulator, LysR family			13.0+
BGL_1c07910	<i>N</i> -acylhomoserine lactone synthase BpsI	2.9-		3.0+
BGL_1c07920	hypothetical protein			4.8+
BGL_1c07930	UspA domain protein			6.0+
BGL_1c07940	transcriptional regulator, LysR family			2.1+
BGL_1c07950	major facilitator superfamily MFS-1 transporter			2.4+
BGL_1c07980	autoinducer-binding transcriptional regulator, LuxR family protein	2.4-		
BGL_1c08000	thioesterase superfamily protein	2.1-		
BGL_1c08010	acyl-CoA dehydrogenase	2.5-		
BGL_1c08110	hypothetical protein	2.7-		2.4-
BGL_1c08430	hypothetical protein		29.8+	33.4+
BGL_1c08470	resolvase	2.1+		
BGL_1c08480	hypothetical protein		2.2+	2.2+
BGL_1c08690	porin Gram-negative type	2.3-		
BGL_1c08700	hypothetical protein	2.7-		
BGL_1c08710	cold-shock DNA-binding domain protein	10.1-	2.2+	2.5+

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_1c08720	DNA polymerase III, epsilon subunit	2.7-		
BGL_1c08750	transglycosylase-like protein	2.1-		
BGL_1c08830	xanthine dehydrogenase accessory protein XdhC			2.3-
BGL_1c08900	monooxygenase, FAD-binding			2.2-
BGL_1c08930	formate dehydrogenase, beta subunit			2.0-
BGL_1c08990	biodegradative arginine decarboxylase AdiA	8.9+		
BGL_1c09000	arginine/agmatine antiporter AdiC	23.5+		
BGL_1c09070	hypothetical protein		7.2+	9.9+
BGL_1c09860	ribosomal protein L32		2.1+	2.9+
BGL_1c11560	major facilitator superfamily MFS-1 transporter			2.5+
BGL_1c11780	para-aminobenzoate synthase PabB			2.1-
BGL_1c11970	HAD-superfamily hydrolase, subfamily IA, variant3	3.9+		
BGL_1c11980	major facilitator superfamily MFS-1 transporter			2.9+
BGL_1c12010	heat shock protein Hsp20		2.3-	3.4-
BGL_1c12020	heat shock protein Hsp20		2.7-	4.3-
BGL_1c12030	phosphoenolpyruvate carboxykinase	2.2+	2.1-	3.9-
BGL_1c12090	acetyl-CoA carboxylase beta subunit-like protein			2.7-
BGL_1c12100	malonate decarboxylase, gamma subunit MdcE			2.5-
BGL_1c12110	phosphoribosyl-dephospho-CoA transferase MdcG			3.0-
BGL_1c12630	MltA-interacting protein MipA family	2.2-		
BGL_1c12860	putative acyl-carrier-protein			2.1+
BGL_1c13180	hypothetical protein		3.2+	3.0+
BGL_1c13200	Rhs family protein	2.1-		
BGL_1c13390	type VI secretion system protein, Vgr family protein VgrG			2.1-
BGL_1c14040	sensor kinase protein RcsC	5.3+		
BGL_1c14340	transcriptional regulator, GntR family	2.2-		
BGL_1c14350	sodium:dicarboxylate symporter	2.4-		
BGL_1c14370	hypothetical protein	2.0-		
BGL_1c14410	hypothetical protein	2.2-	9.1+	2.5-
BGL_1c14460	hypothetical protein	4.0+		
BGL_1c14470	transcriptional regulatory protein CusR	3.6+		
BGL_1c14490	4-hydroxyphenylpyruvate dioxygenase	2.1+		
BGL_1c14710	putative mutator mutT protein	30.3-	2.7+	2.5+
BGL_1c14720	succinylglutamate desuccinylase/aspartoacylase	2.1-		
BGL_1c14740	beta-lactamase	2.1-		
BGL_1c14840	hypothetical protein		2.1+	
BGL_1c14870	Rhs element Vgr protein	2.2-		
BGL_1c14880	Rhs family protein	2.3-		
BGL_1c14890	hypothetical protein		2.0+	2.1+
BGL_1c14900	Immunity protein Imm1	2.0-		
BGL_1c15220	5-deoxy-glucuronate isomerase lolB	2.7+		
BGL_1c15230	putative amine catabolism-like protein	2.8+		
BGL_1c15240	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase lolD	3.1+		
BGL_1c15250	5-dehydro-2-deoxygluconokinase lolC	3.4+		
BGL_1c15260	sugar ABC transporter, ATP-binding protein	3.1+		

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_1c15270	sugar ABC transporter, permease protein	3.9+		
BGL_1c15280	sugar ABC transporter, periplasmic sugar-binding protein	5.7+	2.8+	
BGL_1c15290	SIS domain protein	2.9+	2.2+	2.4+
BGL_1c15300	inositol 2-dehydrogenase IdhA	2.2+		
BGL_1c15710	50S ribosomal protein L35			3.1+
BGL_1c15810	L-sulfolactate dehydrogenase ComC			2.0-
BGL_1c15950	hypothetical protein			3.3+
BGL_1c16020	hypothetical protein	2.1+		
BGL_1c16240	putative exported heme utilisation-like protein	6.9-		
BGL_1c16250	hypothetical protein	130.1-		3.0-
BGL_1c16260	hypothetical protein	274.1-		3.0-
BGL_1c16270	Flp/Fap pilin component	7.1-	2.4+	2.1+
BGL_1c16280	peptidase A24A, prepilin type IV	12.0-		
BGL_1c16290	TadE-like protein	11.1-		
BGL_1c16300	flp pilus assembly CpaB	10.2-		
BGL_1c16310	putative Flp pilus assembly protein secretin CpaC	9.5-		
BGL_1c16320	putative pilus assembly protein, CpaE-like protein	10.9-		
BGL_1c16330	putative Flp pilus assembly protein ATPase CpaF	12.4-		
BGL_1c16340	flp pilus assembly protein TadB	10.8-		
BGL_1c16350	flp pilus assembly protein TadC	11.3-		
BGL_1c16360	flp pilus assembly protein TadD	10.5-		
BGL_1c16370	hypothetical protein	10.6-		
BGL_1c16380	sigma 54 specific transcriptional regulator, Fis family	7.4-		
BGL_1c16420	AMP-dependent synthase and ligase			4.0-
BGL_1c17000	death-on-curing family protein	3.0+	2.9+	2.9+
BGL_1c17290	hypothetical protein	2.6-		
BGL_1c17300	nucleoside 2-deoxyribosyltransferase	2.1-		
BGL_1c17730	hypothetical protein	2.3+		
BGL_1c17810	putative bacteriophage protein	2.6-	6.8-	6.6-
BGL_1c17820	hypothetical protein	3.2-	8.4-	8.3-
BGL_1c17830	putative bacteriophage protein	2.0-	3.8-	3.3-
BGL_1c17840	putative bacteriophage protein	2.8-	4.4-	4.9-
BGL_1c17860	phage-like tail protein		2.0-	2.2-
BGL_1c17870	hypothetical protein		2.1-	2.6-
BGL_1c17890	hypothetical protein		2.0-	2.5-
BGL_1c17900	putative bacteriophage protein		3.0-	3.1-
BGL_1c17920	putative phage baseplate assembly protein		2.3-	2.9-
BGL_1c17940	hypothetical protein		2.0-	
BGL_1c17990	lysozym	9.0-	9.0-	5.3-
BGL_1c18200	ABC-type sugar transport system, ATPase component		2.2-	2.8-
BGL_1c18220	transcriptional regulator, LacI family			2.0-
BGL_1c18230	ribokinase			2.2-
BGL_1c18240	protein kinase			2.8-
BGL_1c18600	methyl-accepting chemotaxis protein	4.0-		
BGL_1c18610	hypothetical protein		3.3+	2.5+

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_1c18690	hypothetical protein		7.7+	8.4+
BGL_1c18740	hypothetical protein			2.3+
BGL_1c18770	hypothetical protein	2.4-		
BGL_1c18780	hypothetical protein	2.4-		
BGL_1c18810	CRISPR-associated protein Cas1	2.2-		
BGL_1c18820	CRISPR-associated helicase Cas3, Yersinia-type	3.1-		
BGL_1c18830	CRISPR-associated protein, Csy1 family	8.3-	3.3-	4.2-
BGL_1c18840	CRISPR-associated protein, Csy2 family	9.5-	3.9-	5.5-
BGL_1c18850	CRISPR-associated protein, Csy3 family	7.5-	3.1-	3.7-
BGL_1c18860	CRISPR-associated protein, Csy4 family	6.7-	2.7-	3.1-
BGL_1c18870	hypothetical protein	3.2-		
BGL_1c19000	non-ribosomal peptide synthase	2.4-		
BGL_1c19170	hypothetical protein		2.8+	3.0+
BGL_1c19330	hypothetical protein	2.4-		
BGL_1c19370	phosphocarrier HPr protein	2.6+		
BGL_1c19520	major facilitator superfamily MFS-1 transporter	2.4+		
BGL_1c19540	putative gluconolactonase			2.2-
BGL_1c19770	hypothetical protein	175.0-		
BGL_1c19850	lactate utilization protein A		2.5-	2.2-
BGL_1c19900	hypothetical protein			2.5-
BGL_1c19910	short chain dehydrogenase			2.2-
BGL_1c19920	mandelate racemase	2.0+		
BGL_1c19940	peptidase, M1 family protein	6.3-		
BGL_1c20290	hypothetical protein	2.7-		
BGL_1c20300	putative esterase	3.9-		
BGL_1c20310	beta-ketoacyl synthase	2.6-		
BGL_1c20330	hypothetical protein	2.7-		
BGL_1c20340	major facilitator superfamily MFS-1 transporter	2.6-		
BGL_1c20350	4Fe-4S ferredoxin, iron-sulfur binding domain protein FdxA	2.8-		
BGL_1c20360	hypothetical protein	2.8-		
BGL_1c20370	putative GCN5-like N-acetyltransferase	3.3-		
BGL_1c20380	hypothetical protein	3.1-		
BGL_1c20390	AMP-dependent synthase and ligase	3.3-		
BGL_1c20400	hypothetical protein	2.8-		
BGL_1c20530	TonB-dependent Fe(III)-pyochelinreceptor	2.0-		
BGL_1c20760	serine metalloprotease	17.5-		
BGL_1c20770	Fungal chitosanase of glycosyl hydrolase group 75	2.1-		
BGL_1c20950	metallophosphoesterase			2.4-
BGL_1c20970	hypothetical protein		2.1+	2.1+
BGL_1c21030	YbaK/prolyl-tRNA synthase associated region	2.2-		
BGL_1c21040	linear gramicidin synthase subunit C	2.9-		
BGL_1c21050	linear gramicidin dehydrogenase LgrE	2.4-		
BGL_1c21060	hypothetical protein, acyl carrier protein-like, phosphopantetheine binding domain	2.5-		
BGL_1c21070	protein CmaB	5.3-		
BGL_1c21090	putative periplasmic substrate-binding protein			2.1-

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_1c21170	hypothetical protein	3.2+		
BGL_1c21180	hypothetical protein	3.3+		
BGL_1c21240	hypothetical protein	5.5-		
BGL_1c21470	2-dehydro-3-deoxygluconokinase KdgK			2.1-
BGL_1c21750	cystathionine beta-lyase MetC			2.5-
BGL_1c22090	phosphatidylserine decarboxylase-like protein	2.5-		
BGL_1c22110	hypothetical protein	17.6-		
BGL_1c22350	small nuclear ribonucleo protein (Sm protein)		2.1+	2.3+
BGL_1c22680	acetoin catabolism regulatory protein AcoR			2.3-
BGL_1c22710	ATP-dependent Clp protease, ATP-binding subunit ClpB			2.2-
BGL_1c23260	hypothetical protein			2.2-
BGL_1c23490	putative class-V aminotransferase			2.3-
BGL_1c23590	transport-associated protein	3.0-		
BGL_1c23640	ABC sugar transporter, ATPase protein			2.1-
BGL_1c23700	sensor histidine kinase			2.6-
BGL_1c23840	alkyl hydroperoxide reductase AhpC			2.1-
BGL_1c23870	acetylornithine deacetylase ArgE			2.0-
BGL_1c24010	ureidoglycolate hydrolase			2.5-
BGL_1c24090	CMP/dCMP deaminase, zinc-binding	12.5+		
BGL_1c24100	hypothetical protein	9.5+		
BGL_1c24220	hypothetical protein		5.0+	3.7+
BGL_1c24870	acyl-CoA-binding protein		2.2+	2.0+
BGL_1c24880	DEAD/DEAH box helicase-like protein	3.3+		2.2+
BGL_1c24890	isocitrate lyase AceA			2.0-
BGL_1c25050	anaerobic dehydrogenase			2.5-
BGL_1c25200	hypothetical protein	6.4-		
BGL_1c25310	ABC-type polar amino acid transport system periplasmic substrate-binding protein			2.6+
BGL_1c26330	phasin-like protein	2.5-		2.1+
BGL_1c26400	oligopeptidase A			2.1-
BGL_1c26420	putative transmembrane efflux protein	4.7-		
BGL_1c26430	argininosuccinate synthase ArgG	10.2-		
BGL_1c26440	putative non-ribosomal peptide synthase, acetyl-CoA ligase-like protein	8.1-		
BGL_1c26450	aldo/keto reductase	7.0-		
BGL_1c26460	adenylylsulfate kinase	5.7-		
BGL_1c26500	oxidoreductase, molybdopterin binding		7.6+	3.1-
BGL_1c26510	putative transmembrane hydrogenase cytochrome b-type subunit		18.0+	3.0-
BGL_1c26710	putative lipoprotein			2.1-
BGL_1c26720	aminotransferase, class III	3.2-		
BGL_1c26730	gamma-glutamylputrescine synthase PuuA	2.7-		
BGL_1c26740	gamma-glutamyl-gamma-aminobutyrate hydrolase PuuD	3.0-		
BGL_1c26750	hypothetical protein	2.0-		
BGL_1c26770	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase PuuC			2.0-
BGL_1c26780	protein HutG	2.1+		
BGL_1c26790	formimidoylglutamate deiminase HutF	2.7+		

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_1c26810	putative acyl-CoA dehydrogenase HutD		2.0-	
BGL_1c26830	histidine utilization repressor HutC	3.6+		
BGL_1c26840	histidine ammonia-lyase HutH	3.1+		
BGL_1c26970	putative plasmid recombination enzyme		10.5+	8.5+
BGL_1c27180	bacterioferritin-associated ferredoxin			2.3+
BGL_1c27300	hypothetical protein			2.9+
BGL_1c27570	acyl-CoA dehydrogenase			2.2-
BGL_1c27800	30S ribosomal protein S15			2.6+
BGL_1c27820	carbonate dehydratase	6.9-		
BGL_1c27830	sulphate transporter	9.5-		
BGL_1c27880	hypothetical protein		2.7+	4.7+
BGL_1c28240	hypothetical protein	2.0-		
BGL_1c28280	hypothetical protein	2.0-		2.0-
BGL_1c28530	hypothetical protein	2.1-	5.7+	5.7+
BGL_1c28560	cytochrome c family protein	2.3-		
BGL_1c28570	cytochrome c553	2.3-		
BGL_1c28660	G/U mismatch-specific uracil-DNA glycosylase (EC 3.2.2.-)			2.3-
BGL_1c28670	chorismate lyase (EC 4.1.3.40)			2.3-
BGL_1c28680	molecular chaperone, HSP90 family protein			2.2-
BGL_1c28810	Domain of unknown function (DUF4399)	2.2-		
BGL_1c28970	hypothetical protein		2.5+	2.5+
BGL_1c28980	hypothetical protein	2.1-		
BGL_1c28990	hypothetical protein		2.2+	2.1+
BGL_1c29070	hypothetical protein			2.5-
BGL_1c29080	hypothetical protein			2.1+
BGL_1c29170	hypothetical protein			3.1-
BGL_1c29180	alpha,alpha-trehalose-phosphate synthase OtsA			2.7-
BGL_1c29250	hypothetical protein		2.9+	3.0+
BGL_1c29560	surface antigen (D15)	2.0-		
BGL_1c29970	hypothetical protein		2.2+	2.3+
BGL_1c30010	acetyltransferase, GNAT family			2.0-
BGL_1c30020	ABC transporter-like protein	3.1+		
BGL_1c30030	branched-chain amino acid ABC transporter, ATP-binding protein	3.1+		
BGL_1c30040	inner-membrane translocator	3.2+		
BGL_1c30050	ABC branched-chain amino acid family transporter, inner membrane protein	3.2+		
BGL_1c30100	50S ribosomal protein L33		3.1+	5.0+
BGL_1c30260	multicopper oxidase family protein			2.2-
BGL_1c30580	30S ribosomal protein S20		2.4+	3.9+
BGL_1c30670	methylated-DNA--protein-cysteinemethyl transferase Ogt			2.3-
BGL_1c30730	thioredoxin			2.1-
BGL_1c30750	pyridoxine/pyridoxamine 5'-phosphate oxidase PdxH	2.2+		
BGL_1c31020	zinc-containing alcohol dehydrogenasesuperfamilyprotein		2.2+	2.1+
BGL_1c31140	sterol desaturase family protein		2.4+	
BGL_1c31150	phospholipase/lecithinase/hemolysin-likeprotein	2.1+		
BGL_1c31330	hypothetical protein	2.3-		2.4-

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_1c31340	hypothetical protein	2.5-		2.6-
BGL_1c31350	Rhs element Vgr protein	2.7-		
BGL_1c31500	transcriptional regulator, ArgP family	18.1-		
BGL_1c31660	dTDP-glucose 4,6-dehydratase RfbB	5.5-	2.5+	
BGL_1c31940	putative cytochrome c4	2.2-		
BGL_1c31950	putative periplasmic cytochrome ccontainingprotein	2.7-		
BGL_1c32020	hypothetical protein	3.4-		
BGL_1c32050	glycerol kinase GlpK			2.0-
BGL_1c32150	tetratricopeptide TPR_2 repeat protein			2.0-
BGL_1c32640	hypothetical protein	5.3+		
BGL_1c33180	cytochrome bd ubiquinol oxidase, subunit I		2.4-	3.2-
BGL_1c33190	cytochrome d ubiquinol oxidase subunit 2		2.4-	3.4-
BGL_1c33400	hypothetical protein	2.4-		
BGL_1c33410	cytochrome c oxidase subunit 3 CtaE	2.5-		
BGL_1c33420	Protein of unknown function (DUF2970)	2.2-		
BGL_1c33430	cytochrome c oxidase assembly protein CtaG	2.4-		
BGL_1c33720	C4-dicarboxylate transport protein DctA	2.6+		
BGL_1c34000	hypothetical protein		2.5+	3.2+
BGL_1c34010	phospholipase, patatin family protein			2.0-
BGL_1c34340	beta and gamma crystallin	5.3-		
BGL_1c34500	<i>N</i> -acylglucosamine 2-epimerase family protein		2.7-	3.2-
BGL_1c34970	flagellar basal-body rod protein FlgG		2.2+	3.1+
BGL_1c34990	flagellar hook protein FlgE		2.4+	4.1+
BGL_1c35000	flagellar hook capping protein FlgD		2.4+	3.6+
BGL_1c35020	flagellar basal-body rod protein FlgB		2.4+	4.4+
BGL_1c35300	PepSY-associated TM helix family protein			2.2+
BGL_1c35340	flagellar protein FliS		2.1+	2.0+
BGL_1c35360	flagellar M-ring protein FliF		3.6+	5.3+
BGL_1c35370	flagellar motor switch protein FliG		2.1+	2.7+
BGL_1c35380	flagellar assembly protein FliH		2.5+	3.6+
BGL_1c35400	flagellar export protein FliJ		3.2+	3.8+
BGL_1c35440	NAD-dependent aldehyde dehydrogenase			2.6-
BGL_1c35870	queuosine biosynthesis protein QueD	2.0+		
BGL_1c36080	hypothetical protein	4.4-		2.2+
BGL_1c36090	hypothetical protein	5.5-	2.2+	3.1+
BGL_1c36100	major facilitator superfamily MFS-1 transporter	3.3-		
BGL_2c00060	hypothetical protein	3.0-		
BGL_2c00170	major facilitator superfamily MFS-1 transporter			2.4-
BGL_2c00180	glucarate dehydratase	2.1+		
BGL_2c00190	5-dehydro-4-deoxyglucarate dehydratase	2.6+		
BGL_2c00250	hypothetical protein	2.2-		
BGL_2c00970	putative antibiotic synthase, amino acid adenylation domain	2.3-		
BGL_2c01450	dimethyl sulfoxide reductase DmsA			2.7-
BGL_2c01470	putative alcohol dehydrogenase, cytochrome c subunit			2.5-
BGL_2c01540	D-mannonate oxidoreductase UxuB	2.4+		

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c01560	starvation-sensing protein RspA			2.3-
BGL_2c01820	hypothetical protein		2.1+	
BGL_2c01940	hypothetical protein		3.7+	5.0+
BGL_2c01960	putative periplasmic substrate-binding protein	4.6-		
BGL_2c01980	putative monooxygenase MoxC	3.4-		
BGL_2c02100	'putative HpaB; type III secretion chaperone, CesT family'		3.4+	3.7+
BGL_2c02450	tyrocidine synthase 2	2.1-	2.3+	3.5+
BGL_2c02460	phosphopantetheine attachment site domain protein, BarA-like		2.6+	3.9+
BGL_2c02470	chlorinating enzyme, SyrB2/BarB2-like protein	2.9-		2.1+
BGL_2c02480	thioesterase type II, NRPS/PKS/S-FAS family, BarC-like	2.7-		
BGL_2c02490	putative transferase	2.2-		
BGL_2c02500	branched-chain amino acid aminotransferase IlvE	2.7-		2.0+
BGL_2c02510	thioesterase type II, NRPS/PKS/S-FAS family, BarC-like	2.2-		
BGL_2c02520	acetaldehyde dehydrogenase (acetylating)	2.2-	2.0+	
BGL_2c02530	4-hydroxy-2-oxovalerate aldolase family	2.4-		2.1+
BGL_2c02540	hypothetical protein, RmIC-like cupins superfamily			2.2+
BGL_2c02550	putative translocator protein, LysE family	2.2-		
BGL_2c02560	putative flavin reductase domain-containing protein	2.2-		
BGL_2c03190	putative alcohol dehydrogenase, zinc-binding domain protein			2.1-
BGL_2c03510	putative lipoprotein		2.2+	2.0+
BGL_2c03650	putative L-sorbose dehydrogenase	6.5-	3.6-	6.2-
BGL_2c03660	hypothetical protein	7.0-	3.1-	5.2-
BGL_2c03670	putative transcriptional regulator, LysR family	2.2-	2.2-	
BGL_2c03680	isoquinoline 1-oxidoreductase subunit alpha	2.4-	2.4-	3.1-
BGL_2c03690	isoquinoline 1-oxidoreductase subunit beta		3.3-	3.7-
BGL_2c03700	putative membrane-bound alcohol dehydrogenase, cytochrome c subunit		3.1-	4.0-
BGL_2c03710	putative XdhC-CoxI family protein		3.7-	4.6-
BGL_2c03720	putative transcriptional regulator, LysR family	2.3-		2.3-
BGL_2c03780	hypothetical protein			2.4-
BGL_2c03790	putative transcriptional regulator, LysR family	2.3-		
BGL_2c03800	putative aldo/keto reductase	3.0-	3.1-	2.9-
BGL_2c03810	branched-chain amino acid aminotransferase	2.0-	2.1-	2.3-
BGL_2c03830	Mn ²⁺ /Fe ²⁺ transporter NRAMP family	22.4-	16.6-	12.4-
BGL_2c03840	hypothetical protein	91.8-	55.8-	104.1-
BGL_2c03850	cysteine synthase CysB	69.9-	54.3-	51.5-
BGL_2c03860	putative SAM-dependent methyltransferase	128.0-	53.3-	67.4-
BGL_2c03870	carbamoyltransferase family protein	111.4-	63.7-	63.7-
BGL_2c03880	putative alpha/beta hydrolase fold protein	131.0-	60.5-	98.3-
BGL_2c03890	putative luciferase family protein	108.4-	39.2-	42.7-
BGL_2c03900	hypothetical protein	225.7-	148.4-	193.4-
BGL_2c03910	putative phytanoyl-CoA dioxygenase family protein	149.8-	50.9-	52.9-
BGL_2c03920	ABC transporter family protein, ATP-binding and transmembrane domain, <i>abc1</i>	32.5-	18.8-	22.5-
BGL_2c03930	hypothetical protein	23.8-	18.9-	26.8-
BGL_2c03940	putative non-ribosomal peptide synthase	22.8-	18.8-	25.5-
BGL_2c03950	putative aminoglycoside phosphotransferase	33.6-	21.0-	23.2-

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c03960	putative thiopurine S-methyltransferase family protein	24.8-	8.4-	17.5-
BGL_2c03970	hypothetical protein	15.7-	4.5+	5.7-
BGL_2c03980	acyl-homoserine-lactone synthase LasI	10.5-	68.3-	5.7-
BGL_2c03990	transcriptional activator protein LasR	5.9-		4.3-
BGL_2c04000	ABC transporter, ATP-binding/permease protein			2.7-
BGL_2c04010	hypothetical protein			2.5-
BGL_2c04020	putative 4Fe-4S ferredoxin, iron-sulfur binding domain protein		2.1-	2.9-
BGL_2c04050	transcriptional regulator, IclR family	2.0-	2.0-	2.1-
BGL_2c04070	methyl-accepting chemotaxis sensory transducer with Pas/Pac sensor	2.1-		
BGL_2c04090	succinate-semialdehyde dehydrogenase (NADP+)	2.4-		
BGL_2c04100	4-aminobutyrate aminotransferase	2.9-		
BGL_2c04110	transcriptional regulator, GntR family		2.3-	2.8-
BGL_2c04130	hypothetical protein	2.1-		2.0-
BGL_2c04190	hypothetical protein	2.7-		
BGL_2c04200	transposase IS3/IS911 family protein	2.6-		
BGL_2c04210	putative transposase	2.9-	2.1-	2.5-
BGL_2c04220	putative transposase	2.5-		
BGL_2c04230	putative type VI secretion system Vgr family protein	2.6-	2.5-	3.7-
BGL_2c04250	putative membrane protein	9.1-	2.8-	2.3-
BGL_2c04260	selenide, water dikinase SelD	2.6-	2.5-	2.8-
BGL_2c04280	cation diffusion facilitator family transporter		2.3-	2.4-
BGL_2c04290	putative purine nucleoside permease	4.3-	2.7-	4.1-
BGL_2c04300	putative exported protein	6.9-	3.3-	2.6-
BGL_2c04310	aspartate-proton symporter YveA	2.0-	2.0-	2.2-
BGL_2c04320	putative malate/L-lactate dehydrogenase	2.3-	2.4-	2.6-
BGL_2c04330	transcriptional regulator, LysR family		2.5-	2.9-
BGL_2c04340	alpha/beta hydrolase	2.6-	2.6-	3.3-
BGL_2c04350	RND efflux transporter, MFP subunit	3.8-	4.8-	3.6-
BGL_2c04360	RND efflux transporter, hydrophobe/amphiphile efflux-1 (HAE1) family	3.5-	3.6-	3.8-
BGL_2c04370	RND efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	2.1-	3.0-	3.3-
BGL_2c04400	hypothetical protein	2.0-	2.4-	2.2-
BGL_2c04410	acyl-CoA dehydrogenase	2.6-	2.6-	2.6-
BGL_2c04420	hypothetical protein	3.4-		
BGL_2c04450	transcriptional regulatory protein QseB	2.1-	2.7-	3.2-
BGL_2c04460	sensor protein QseC		2.2-	2.5-
BGL_2c04470	phosphoserine transaminase	2.2-	2.5-	3.2-
BGL_2c04480	two component heavy metal response transcriptional regulator, winged helix family		2.2-	2.8-
BGL_2c04490	heavy metal sensor signal transduction histidine kinase		2.6-	3.1-
BGL_2c04610	D-galactonate transporter, MFS transport family	3.5-	8.2-	7.3-
BGL_2c04620	aldehyde dehydrogenase	5.0-	8.8-	7.7-
BGL_2c04630	tryptophanyl-tRNA synthase TrpS		3.8-	4.9-
BGL_2c04640	5-dehydro-4-deoxyglucarate dehydratase	3.7-	4.3-	2.8-
BGL_2c04650	D-galactarate dehydratase GarD		5.6-	5.2-
BGL_2c04660	hypothetical protein	3.3-		3.1-

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c04670	acetyltransferase	3.8-		
BGL_2c04680	hypothetical protein, DoxX family	6.2-		
BGL_2c04710	proline racemase		2.0-	3.2-
BGL_2c04750	transcriptional regulator, AraC family	3.0-	2.1-	2.3-
BGL_2c04770	4-hydroxyphenylpyruvate dioxygenase	4.0-	6.0-	4.9-
BGL_2c04780	3-dehydroquinase dehydratase AroQ, type-II 3-dehydroquinase family		2.1-	2.3-
BGL_2c04790	shikimate 5-dehydrogenase AroE		2.6-	3.1-
BGL_2c04800	putative glucarate transporter GudP		2.1-	2.6-
BGL_2c04810	2-aminoethylphosphonate-pyruvate transaminase PhnW	8.4-	6.2-	14.3-
BGL_2c04820	2-aminoethylphosphonate ABC transport, periplasmic substrate-binding protein PhnS	4.2-	4.6-	5.2-
BGL_2c04830	2-aminoethylphosphonate ABC transport, ATP-binding protein PhnT	4.7-	2.1-	2.2-
BGL_2c04840	2-aminoethylphosphonate ABC transport, permease protein PhnU	3.9-		2.1-
BGL_2c04850	2-aminoethylphosphonate ABC transport, membrane protein PhnV	3.2-		2.4-
BGL_2c04860	phosphonoacetate hydrolase PhnA	4.1-	3.6-	6.0-
BGL_2c04870	HD phosphohydrolase-like protein	4.5-	3.0-	4.8-
BGL_2c04930	hypothetical protein		2.5+	6.0+
BGL_2c05050	serine-type carboxypeptidase			2.1-
BGL_2c05630	long-chain-fatty-acid-CoA ligase FadD	2.2-	2.2+	3.3+
BGL_2c05670	putative membrane-anchored cell surface protein	36.9-		2.5-
BGL_2c05770	hydroxylamine reductase, hybrid-cluster protein	2.8-		
BGL_2c05800	putative hydroxypyruvate isomerase			2.3-
BGL_2c05930	flavin-type monooxygenase			2.3-
BGL_2c06160	tyrosine-specific transport protein TyrP	2.5+		
BGL_2c06180	glutamate/gamma-aminobutyrate antiporter	3.0+	2.7-	
BGL_2c06390	L-serine dehydratase SdaA		2.4+	
BGL_2c06420	sarcosine oxidase subunit alpha SoxA	2.0+	2.4+	
BGL_2c06440	dihydroneopterin aldolase		2.0+	2.2-
BGL_2c06460	CsbD family protein		3.7+	3.4+
BGL_2c06600	NADH flavin oxidoreductase/NADH oxidase			2.3-
BGL_2c06700	phosphoesterase family protein	2.2-		
BGL_2c07030	alpha/beta hydrolase	2.1-		
BGL_2c07040	hypothetical protein	2.2-		
BGL_2c07100	peptidase S1 and S6, chymotrypsin/Hap			2.0-
BGL_2c07470	rhamnosyltransferase I subunit A	26.0-		
BGL_2c07480	rhamnosyltransferase I subunit B	30.7-		
BGL_2c07490	multidrug resistance protein B	18.9-		
BGL_2c07500	rhamnosyltransferase I subunit C	29.9-		
BGL_2c07510	RND efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	16.3-		
BGL_2c07520	secretion protein, HlyD family	4.0-		
BGL_2c07530	chitinase	12.5-		
BGL_2c07540	aldolase, isopropylmalate synthase-like protein	69.6-		
BGL_2c07550	hypothetical protein, haem oxygenase-like	16.4-		2.0+
BGL_2c07560	branched-chain amino acid aminotransferase IlvE	14.1-		

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c07570	hypothetical protein, <i>N</i> -acetylglucosaminyl phosphatidylinositol de- <i>N</i> -acetylase-like	9.2-		
BGL_2c07580	phenazine biosynthesis-like protein	10.9-		
BGL_2c07590	phosphoribosyl glycinamide synthase	5.9-		
BGL_2c07600	tetracycline resistance protein TetA	3.9-		
BGL_2c07900	hypothetical protein		2.9+	3.2+
BGL_2c07940	hypothetical protein			2.1-
BGL_2c08030	3-hydroxybutyrate dehydrogenase BdhA			3.2-
BGL_2c08040	enoyl-CoA hydratase			3.1-
BGL_2c08060	DNA binding protein	4.3-		
BGL_2c08120	glycoside hydrolase-like protein	10.7-		
BGL_2c08160	penicillin-binding protein, 1A family; Pbp-1a; PBP1a		2.0-	2.7-
BGL_2c08180	putative chitinase	2.5-		
BGL_2c08450	hypothetical protein		2.4+	2.5+
BGL_2c08490	transcriptional regulator, LacI family	3.8-		
BGL_2c08880	hypothetical protein	2.4+		
BGL_2c08910	threonine ammonia-lyase, biosynthetic	2.4+		2.4+
BGL_2c08980	hypothetical protein		2.5+	2.2+
BGL_2c09000	PepSY and peptidase M4 protein	2.4-		
BGL_2c09010	TonB-dependent siderophore receptor	3.3-		
BGL_2c09060	hypothetical protein		2.1+	
BGL_2c09510	putative exported protein		2.7+	3.3+
BGL_2c09540	methyl-accepting chemotaxis sensory transducer	2.2-		
BGL_2c09820	allophanate hydrolase	3.0+		
BGL_2c09830	transcriptional regulator, LysR family	2.5+		
BGL_2c09850	<i>N</i> -hexanoyl homoserine lactone synthase RhII/TofI	4.1-		
BGL_2c09860	hypothetical protein	25.1-		
BGL_2c09870	<i>N</i> -octanoyl homoserine lactone synthase RhIR/TofR	5.6+		
BGL_2c09990	amidase		2.0-	2.6-
BGL_2c10110	hydrolase, epoxide hydrolase-like		2.0-	
BGL_2c10120	metal-dependent hydrolase	2.0+		
BGL_2c10130	short chain dehydrogenase	2.4+		
BGL_2c10140	flavin-containing monooxygenase	2.5+		
BGL_2c10150	transcriptional regulator, LysR family	2.3-		
BGL_2c10160	hypothetical protein	2.4-		
BGL_2c10170	hypothetical protein	4.0+		
BGL_2c10520	2-dehydropantoate 2-reductase PanE			2.0-
BGL_2c10540	putative cyanate transport protein CynX, MFS family	2.1-		
BGL_2c10630	hypothetical protein			2.3-
BGL_2c10640	hypothetical protein		2.1-	3.6-
BGL_2c10650	hypothetical protein			2.6-
BGL_2c10660	hypothetical protein			2.5-
BGL_2c10690	transcriptional regulator, LysR family			2.2-
BGL_2c10910	oxalyl-CoA decarboxylase Oxc			2.9-
BGL_2c10920	formyl-CoA oxalate CoA-transferase Frc			2.9-
BGL_2c10940	hypothetical protein			2.8-

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c10950	hypothetical protein			2.7-
BGL_2c11060	alpha-L-arabinofuranosidase B	4.5-		
BGL_2c11280	TRAP dicarboxylate transporter, DctP subunit	2.0+		
BGL_2c11580	hypothetical protein, transglutaminase-like			2.1-
BGL_2c11690	channel protein, hemolysin III family protein	2.2+		
BGL_2c11830	putative periplasmic substrate-binding protein	2.6+		
BGL_2c11950	thermostable hemolysin	2.3-	2.3+	3.3+
BGL_2c11990	flavin-dependent oxidoreductase-like protein			2.8+
BGL_2c12190	quinoprotein glucose dehydrogenase Gcd	4.5-		
BGL_2c12340	putative exported protein	3.1+		
BGL_2c12350	alpha/beta hydrolase	3.0+		
BGL_2c12360	putative glyoxalase (dioxxygenase domain)	2.9+		
BGL_2c12370	uncharacterized Rieske-protein, [2Fe-2S] center	2.4+		
BGL_2c12380	monooxygenase FAD-binding, aromatic-ring hydroxylase-like	2.6+		
BGL_2c12390	MFS general substrate transporter	2.1+		
BGL_2c12400	putative cyclase	2.0+		
BGL_2c12420	putative fumarylacetoacetate hydrolase			2.2-
BGL_2c12620	putative mandelate racemase	2.3+		
BGL_2c12640	D-galactonate transporter, MFS transport family	2.2+		
BGL_2c12870	thiamine pyrophosphate enzyme-like TPP binding region			2.2-
BGL_2c12970	putative hippurate hydrolase		2.3-	3.9-
BGL_2c13840	hypothetical protein			2.0-
BGL_2c13850	hypothetical protein			2.5-
BGL_2c13860	hypothetical protein			2.3-
BGL_2c13870	30S ribosomal protein S21			2.1-
BGL_2c13890	cold shock-like protein CspA	2.7+	5.7+	3.7+
BGL_2c13950	putative signal peptide protein	2.1-		
BGL_2c13960	tetratricopeptide TPR_2	2.4-		
BGL_2c13970	putative lipoprotein	2.7-		
BGL_2c13980	putative transmembrane protein	2.5-		
BGL_2c13990	hypothetical transmembrane protein	2.3-		
BGL_2c14000	glycosyl transferase, group 1	2.6-		
BGL_2c14010	putative transmembrane protein	2.7-		
BGL_2c14020	hypothetical protein	2.3-		
BGL_2c14110	hypothetical protein		2.4+	2.1+
BGL_2c14120	putative transcriptional regulator, GntR family protein	2.6-		2.0+
BGL_2c14140	alkylhydroperoxidase AhpD-like protein	3.0-		
BGL_2c14150	acyl-CoA synthases (AMP-forming)/AMP-acid ligase II-like protein	2.7-		
BGL_2c14160	phenylacetate-CoA oxygenase, PaaA subunit	3.2-		
BGL_2c14250	anthranilate synthase component 1 TrpE	2.4-		
BGL_2c14530	hypothetical protein	2.1+		
BGL_2c14540	putative lipoprotein	2.1+		
BGL_2c14550	putative lipoprotein			2.1-
BGL_2c14690	hypothetical protein		2.8+	2.6+
BGL_2c14880	hypothetical protein	11.8-		

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c14890	hypothetical protein	6.6-		
BGL_2c14900	TonB-dependent siderophore receptor			4.0+
BGL_2c15120	methyl-accepting chemotaxis sensory transducer	3.6-		
BGL_2c15150	glyoxalase/bleomycin resistance protein/dioxygenase			2.3-
BGL_2c15220	hypothetical protein		6.0+	6.1+
BGL_2c15240	NADH oxidoreductase containing a GroES-like domain			2.3-
BGL_2c15420	Protein of unknown function (DUF3304)		2.8+	2.3+
BGL_2c15550	hypothetical protein	5.3-		
BGL_2c15730	ABC transporter-like protein	2.9+		
BGL_2c15830	hypothetical protein	3.2-		
BGL_2c15840	hypothetical protein	4.0-		
BGL_2c15850	mandelate racemase	3.9-		
BGL_2c16310	GCN5-like N-acetyltransferase			2.3-
BGL_2c16320	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding			2.0-
BGL_2c16410	drug resistance transporter, EmrB/QacA subfamily	305.1-		
BGL_2c16420	secretion protein, HlyD family	368.3-		
BGL_2c16430	RND efflux system, outer membrane lipoprotein, NodT family	313.9-		
BGL_2c16450	polyketide cyclase/dehydrase	74.8-		
BGL_2c16460	putative non-ribosomal peptide synthase	98.5-		
BGL_2c16470	hypothetical protein	214.4-		
BGL_2c16480	hypothetical protein, RmIC-like cupins superfamily	327.6-	2.2-	
BGL_2c16490	hypothetical protein	397.5-		
BGL_2c16500	transcriptional regulator, AraC family	19.8-		
BGL_2c16510	transcriptional regulator, LuxR family	4.1-		2.1+
BGL_2c16800	nitrite reductase NAD(P)H small subunit	2.3-		2.8-
BGL_2c16810	nitrite reductase NAD(P)H large subunit	2.1-	2.5-	3.1-
BGL_2c17020	hypothetical protein	2.1-		
BGL_2c17290	hypothetical protein			2.1-
BGL_2c17410	hypothetical protein		6.1+	
BGL_2c17420	hypothetical protein		6.5+	2.0-
BGL_2c17470	drug resistance transporter, EmrB/QacA family	5.1-	2.0+	
BGL_2c17500	transcriptional regulator, LysR family	2.0-		
BGL_2c17680	glutamate-1-semialdehyde 2,1-aminomutase HemL	2.3-		
BGL_2c17690	hypothetical protein	6.7-		
BGL_2c17700	putative non-ribosomal peptide synthase	2.9-		
BGL_2c18200	succinate dehydrogenase cytochrome b556 subunit		2.1+	2.5+
BGL_2c18330	FAD/FMN-containing dehydrogenases	2.1+		
BGL_2c18550	putative mutt/nudix hydrolase	2.2-		
BGL_2c18660	lipase LipA	2.5-		2.3-
BGL_2c18690	hypothetical protein		2.3+	2.6+
BGL_2c18700	hypothetical protein	2.1-		
BGL_2c18890	transcriptional regulator, GntR family	2.1-		
BGL_2c18910	PPE-repeat protein	4.7-		
BGL_2c18920	hypothetical protein	2.4-		
BGL_2c18940	hypothetical protein	6.0-		

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c18980	pseudomonalysin	10.9-		
BGL_2c19200	acyltransferase		2.4+	2.5+
BGL_2c19430	methyl-accepting chemotaxis sensory transducer	5.2-		
BGL_2c19440	hypothetical protein	5.3-		
BGL_2c20210	hypothetical protein	2.9-		
BGL_2c20220	putative phospholipase D / transphosphatidylase	9.1-		
BGL_2c20230	hypothetical protein	108.5-		
BGL_2c20240	hypothetical protein	28.5-		
BGL_2c20250	hypothetical protein	27.7-	2.0+	
BGL_2c20260	RNA polymerase sigma factor 70	24.0-	2.0+	
BGL_2c20280	hypothetical protein	10.5-		
BGL_2c20290	hypothetical protein	33.1-		2.1-
BGL_2c20300	hypothetical protein	43.6-		
BGL_2c20310	hypothetical protein	7.4-		
BGL_2c20320	2-aminoethylphosphonate-pyruvate transaminase PhnW	3.7-		
BGL_2c20330	O-acetylhomoserine/O-acetylserine sulfhydrylase	4.4-		
BGL_2c20340	fatty acid desaturase type 1	4.3-		
BGL_2c20350	glutamine amidotransferase type 1	4.4-		
BGL_2c20370	glucose-methanol-choline oxidoreductase	3.3-		
BGL_2c20530	transcriptional regulator, LysR family	2.3-		
BGL_2c20610	hypothetical protein	3.7-		
BGL_2c20620	ABC transporter, substrate binding protein	3.0-		
BGL_2c20630	ABC transporter, permease protein	2.7-		
BGL_2c20660	putative acetylpolymine aminohydrolase AphA	2.2-		
BGL_2c20670	putative glycoside hydrolase	7.7-		
BGL_2c20920	glycoside hydrolase family 28	2.7+		
BGL_2c21180	glutamine ABC transporter substrate binding protein			2.3-
BGL_2c21190	glutamine ABC transporter permease protein			2.6-
BGL_2c21770	alpha amylase	2.3-		2.8-
BGL_2c21940	glycosyl transferase			2.1-
BGL_2c22020	putative transposase of IS4/5 family (DUF4096)	2.1-		
BGL_2c22460	type VI secretion system Vgr family protein	2.4-		
BGL_2c22490	spermidine/putrescine ABC transporter periplasmic spermidine/putrescine-binding protein	2.8-		
BGL_2c22500	spermidine/putrescine ABC transporter permease protein	3.7-		
BGL_2c22570	putative glucose uptake permease	2.1-		2.0-
BGL_2c22580	hypothetical protein	5.0-		
BGL_2c22590	putative translation initiation inhibitor	5.8-		
BGL_2c22600	asparagine synthase, glutamine-hydrolyzing AsnB	6.2-		
BGL_2c22610	3-phosphoshikimate 1-carboxyvinyltransferase AroA	7.7-		
BGL_2c22620	3-phosphoshikimate 1-carboxyvinyltransferase AroA	7.6-		
BGL_2c22750	aldehyde dehydrogenase			2.3-
BGL_2c22830	hypothetical protein		2.8+	2.3+
BGL_2c23140	ribose transport system permease protein RbsC			2.0-
BGL_2c23230	hypothetical protein	2.5+	2.2+	2.3+
BGL_2c23260	putative lipoprotein	137.3-		3.0-

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c23270	hypothetical membrane protein	43.8-		
BGL_2c23280	nitrate reductase alpha subunit	2.5+		
BGL_2c23410	thiaminase I precursor	21.9-		
BGL_2c23420	phosphomethylpyrimidine kinase ThiD	21.8-		
BGL_2c23430	methyltransferase type 11	21.6-		
BGL_2c23440	thymidylate synthase ThyA	22.2-		
BGL_2c23450	nucleoside 2-deoxyribosyltransferase	22.9-		
BGL_2c23460	MutT/Nudix hydrolase	21.0-		
BGL_2c23470	phosphoethanolamine N-methyltransferase	157.8-		
BGL_2c23480	gamma-butyrobetaine 2-oxoglutarate dioxygenase	104.7-		
BGL_2c23570	hypothetical protein	3.8+		
BGL_2c23940	response regulator receiver protein	71.3-		
BGL_2c23990	acyl-CoA <i>N</i> -acyltransferase			2.3-
BGL_2c24060	fimbrial biogenesis outer membrane usher protein			2.3-
BGL_2c24070	pili assembly chaperone			2.3-
BGL_2c24110	glyoxalase/bleomycin resistance protein/dioxygenase			2.9-
BGL_2c24130	amylase- α -1,6-glucosidase family			2.2-
BGL_2c24160	sensor histidine kinase	2.2+		
BGL_2c24570	hypothetical protein	2.7-	2.8+	2.6+
BGL_2c24900	putative NmrA-like family protein	3.9+		
BGL_2c24910	maleylacetoacetate isomerase MaiA	3.1+		
BGL_2c24930	homogentisate 1,2-dioxygenase HmgA	3.2+		
BGL_2c24950	putative insertion element protein	9.3-		
BGL_2c24960	hypothetical protein, CoA-dependent acyltransferase	10.7-		
BGL_2c24990	putative PAS/PAC sensor signal transduction histidine kinase	2.2-		
BGL_2c25000	putative haem oxygenase-like protein	2.1-		
BGL_2c25210	putative xanthine dehydrogenase YagR molybdenum-binding subunit			2.0-
BGL_2c25430	putative exported protein	2.2-		
BGL_2c25640	putative membrane protein	2.3+		
BGL_2c25680	putative membrane protein DUF1295	2.3-		
BGL_2c25690	cyclopropane-fatty-acyl-phospholipid synthase (cyclopropane fatty acid synthase)	2.7-		2.7-
BGL_2c25700	lipocalin-like protein	2.5-		3.0-
BGL_2c25750	major facilitator superfamily MFS-1 transporter	3.3-		
BGL_2c25760	MlrC domain protein	3.0-		
BGL_2c25770	hypothetical protein	2.9-		
BGL_2c25840	putative flavin-containing monooxygenase	2.0+		
BGL_2c25850	putative short-chain dehydrogenase/reductase SDR	2.8+		
BGL_2c25860	hypothetical protein	2.2+		
BGL_2c26140	hypothetical protein		2.1+	2.2+
BGL_2c26180	putative NAD(P)H dehydrogenase (quinone)	2.3-	2.0+	
BGL_2c26190	putative GCN5-like N-acetyltransferase (GNAT)	3.7-	2.6+	
BGL_2c26210	putative alginate lyase 2	2.9-		
BGL_2c26310	putative glycoside hydrolase family 3 domain protein	2.2-		
BGL_2c26400	hypothetical protein			2.2-
BGL_2c26450	putative prokaryotic membrane lipoprotein			2.0-

Locus_tag	Predicted function	Fold change		
		BGPG2	BGPG3	BGPG4
BGL_2c26570	putative sugar transporter, major facilitator superfamily (MFS-1) transporter		2.5+	3.6+
BGL_2c26610	putative membrane protein			2.3-
BGL_2c26760	hypothetical protein		3.0+	2.8+
BGL_2c26870	hypothetical protein		2.0+	2.5+
BGL_2c26920	hypothetical protein		3.1+	2.2+
BGL_2c27190	hypothetical protein	3.4-		
BGL_2c27200	putative glutathione-dependent formaldehyde-activating enzyme, GFA	3.1-		
BGL_2c27210	putative membrane protein	2.4-		
BGL_2c27220	transcriptional regulator, LysR family	2.1-		
BGL_2c27580	arginine biosynthesis bifunctional protein ArgJ	2.5-		
BGL_2c27610	putative enoyl-CoA hydratase	4.4-		
BGL_2c27620	putative asparagine synthase (glutamine-hydrolyzing)	4.2-		
BGL_2c27630	glutamate 5-kinase	4.0-		
BGL_2c27640	putative transcriptional regulator, LuxR family	41.5-		
BGL_2c27760	putative methyl-accepting chemotaxis sensory transducer		2.5+	2.3+
BGL_2c27900	5-oxoprolinase (ATP-hydrolyzing)	3.8+		
BGL_2c27990	putative gluconolactonase			2.4+
BGL_2c28040	hypothetical protein		2.5+	2.3+
BGL_2c28120	putative natural resistance-associated macrophage protein			3.7+
BGL_2c28180	putative lysine-arginine-ornithine-binding periplasmic protein	2.5+		
BGL_2c28530	phenylacetic acid degradation-like protein	2.3-		
BGL_2c28540	putative alpha-methylacyl-CoA racemase			2.7-
BGL_2c28550	putative AcnD-accessory protein PrpF			2.4-
BGL_2c28560	Fe/S-dependent 2-methylisocitrate dehydratase AcnD family			2.5-
BGL_2c28610	putative diguanylate cyclase/phosphodiesterase with PAS sensor	2.4-		
BGL_2c28620	hypothetical protein	4.5-		
BGL_2c28640	transcriptional regulator, IclR family	2.1-		
BGL_2c28730	outer membrane porin, OprD family		2.4-	2.5-
BGL_2c28750	amino acid/peptide transporter family		2.0-	2.5-
BGL_2c28900	hypothetical protein	153.8-		
BGL_2c28920	hypothetical protein	2.6+	2.0-	
BGL_2c28930	carbon starvation protein CstA	2.5+		
BGL_2c28940	hypothetical protein	2.2+		2.0-
BGL_2c28960	porin Gram-negative type			2.1-
BGL_2c29020	coenzyme PQQ synthesis protein C			2.1-
BGL_2c29030	coenzyme PQQ synthesis protein B			2.1-
BGL_2c29440	putative membrane protein		2.0-	2.7-
BGL_2c29450	aminotransferase class-III	2.6-	3.1-	4.7-
BGL_2c29460	putative peptidase C45, acyl-coenzyme A 6-aminopenicillanic acid acyl-transferase	2.0-	2.4-	2.3-

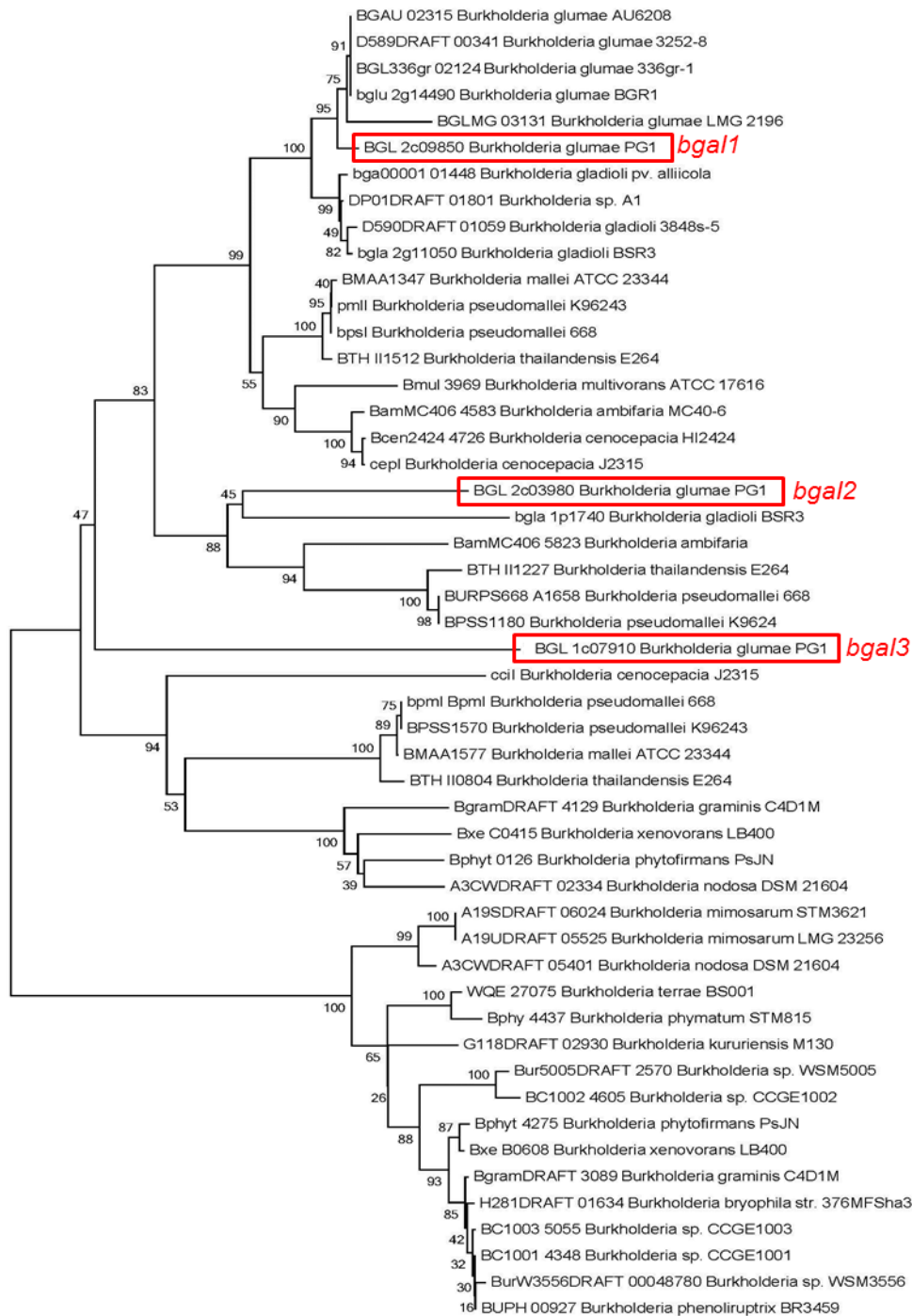
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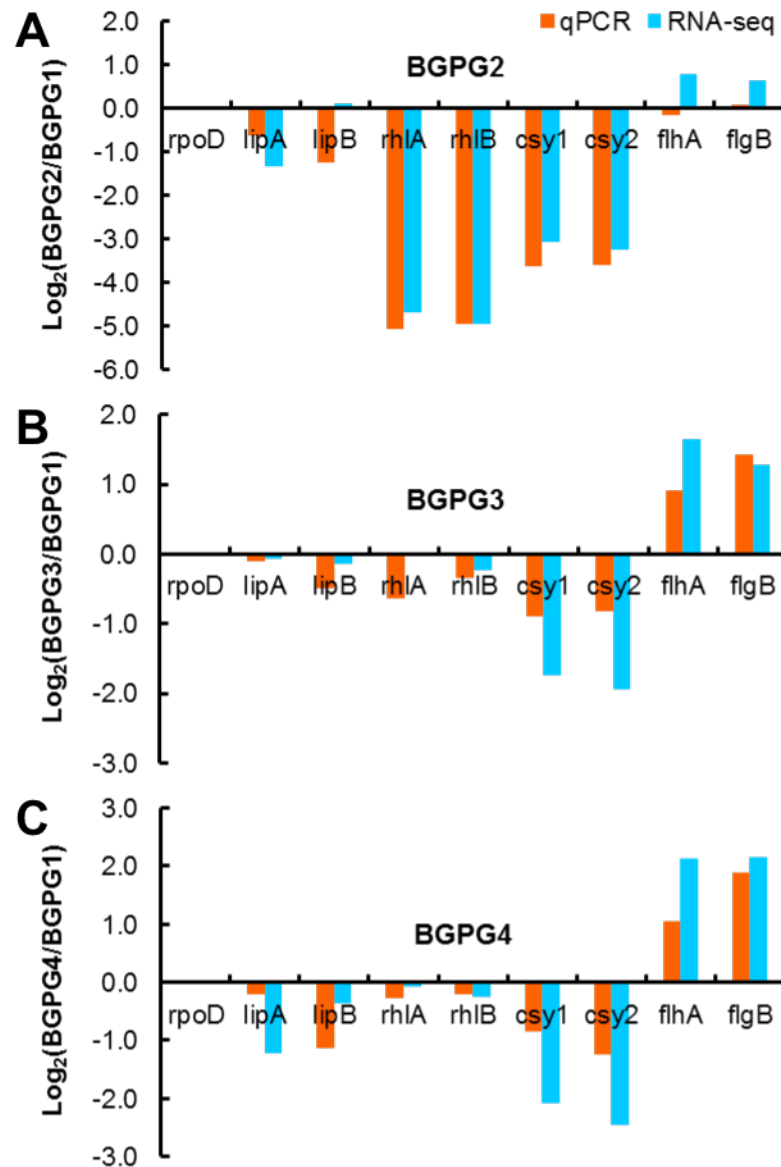
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SUPPLEMENTARY FIGURES



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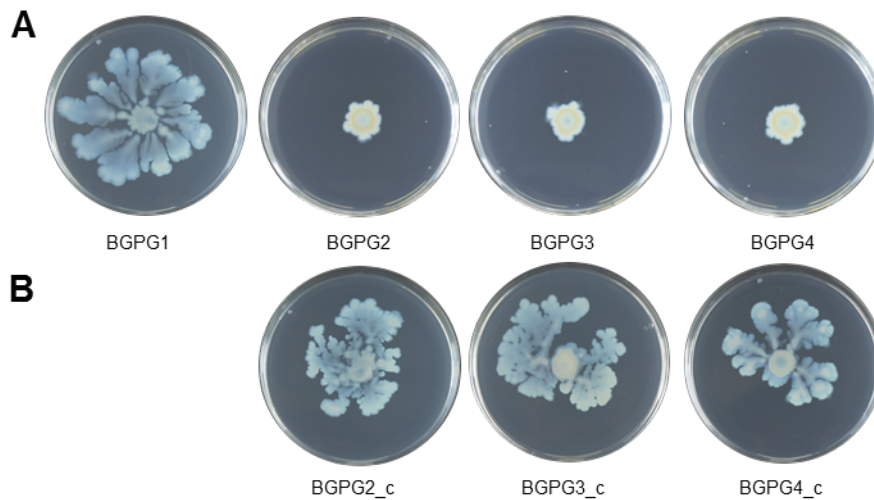
12 **Figure S1.** Phylogenetic analyses of AHL synthases between *B. glumae* PG1 and the
 13 selected *Burkholderia* strains based on amino acid sequences. The genetic tree was
 14 established using neighbor-joining method with the MUSCLE program in the MEGA
 15 software package, the percentage of bootstrap resamplings is indicated at the different
 16 nodes.



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18 **Figure S2.** Validation of RNA-seq data by quantitative RT-PCR in the transition from
 19 exponential to stationary growth phase. **(A)** Fold change differences of BGPG2 to
 20 BGPG1. **(B)** Fold change differences of BGPG3 to BGPG1. **(C)** Fold change differences
 21 of BGPG4 to BGPG1. Orange bars indicate the fold change differences from qRT-PCR;
 22 blue bars indicate the fold change differences from RNA-seq analyses. The *rhlA* and *rhlB*
 23 (BGL_2c07470-80) are involved in rhamnolipid biosynthesis, the *csy1* and *csy2* genes
 24 (BGL_1c18830-40) are part of a CrispR/CAS system and the *flhA1* (BGL_1c01710) and
 25 *flgB* (BGL_1c35020) genes are involved in the built up of the bacterial flagella.

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28 **Figure S3.** Complementation of the swarming phenotype of the three AHL synthase
29 mutants. **(A)** Reduced swarming phenotypes of BGPG2, BGPG3, and BGPG4
30 compared to wild-type BGPG1 on agar plates containing 0.45% Eiken agar. Plates were
31 inoculated with 1×10^7 cells and incubated for 3 days at 28°C. **(B)** Complemented strains
32 of BGPG2-4 designated BGPG2_c, BGPG3_c, BGPG4_c and expressing *bga1-3*,
33 respectively, in *trans* on the plasmid pBBR1MCS-2 could restore the swarming
34 phenotype. Therefore, 1×10^7 cells were inoculated on swarming agar plates containing
35 0.45% Eiken and were incubated for 3 days at 28°C.

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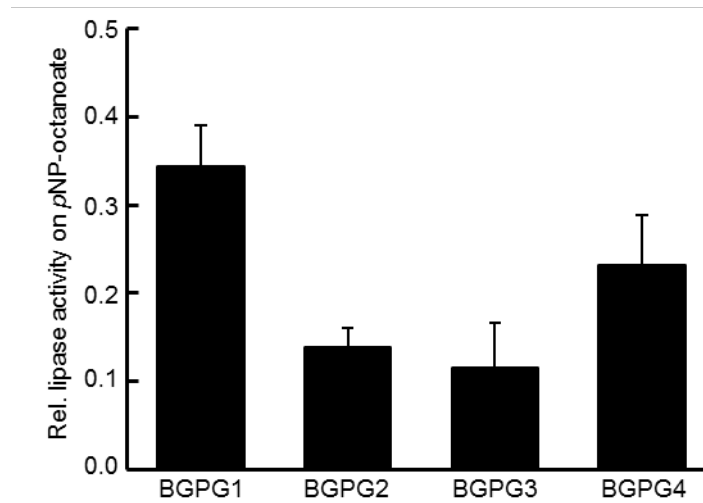
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46 **Figure S4.** Relative lipolytic activities measured in cell supernatants of *B. glumae* using
47 pNP-octanoate (C8, 0.1 mM) as a substrate according to the previously described
48 method with little modification (1). Tests were performed by incubating 40 μ l of
49 supernatant with 25 μ l of 1 mM octanoate and 435 μ l of 0.1 M phosphate buffer (pH 8.0)
50 at 37°C for up to 20 min. Solution was centrifuged at 13,000 rpm and 2°C for 5 min after
51 adding 1 ml ethanol. Extinction of the supernatant was measured at 405 nm. The
52 relative lipase activity was calculated as the ratio of OD_{405}/OD_{600} . Data are mean values
53 of at least three measurements. Bars indicate the standard deviations. Cell
54 supernatants were collected from 26 hour-old stationary phase cells.

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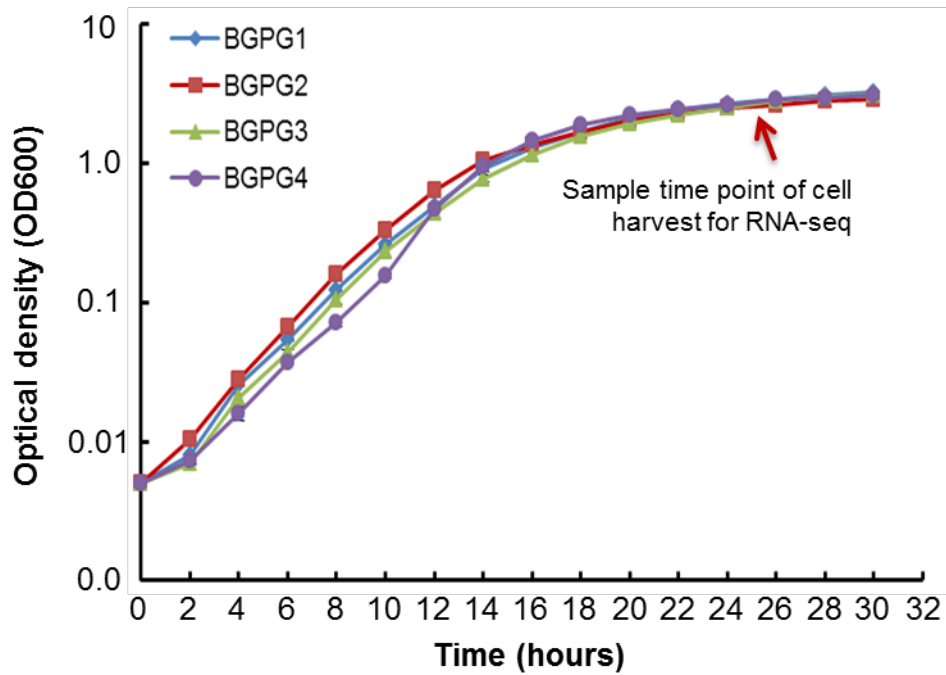
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64 **Figure S5.** Growth curve of wild-type strain BGPG1 and three AHL synthase mutants
65 BGPG2-4 over a period of 30 h (semi-log plot). The sampling point of the twelve
66 transcriptome samples is indicated with a red arrow.

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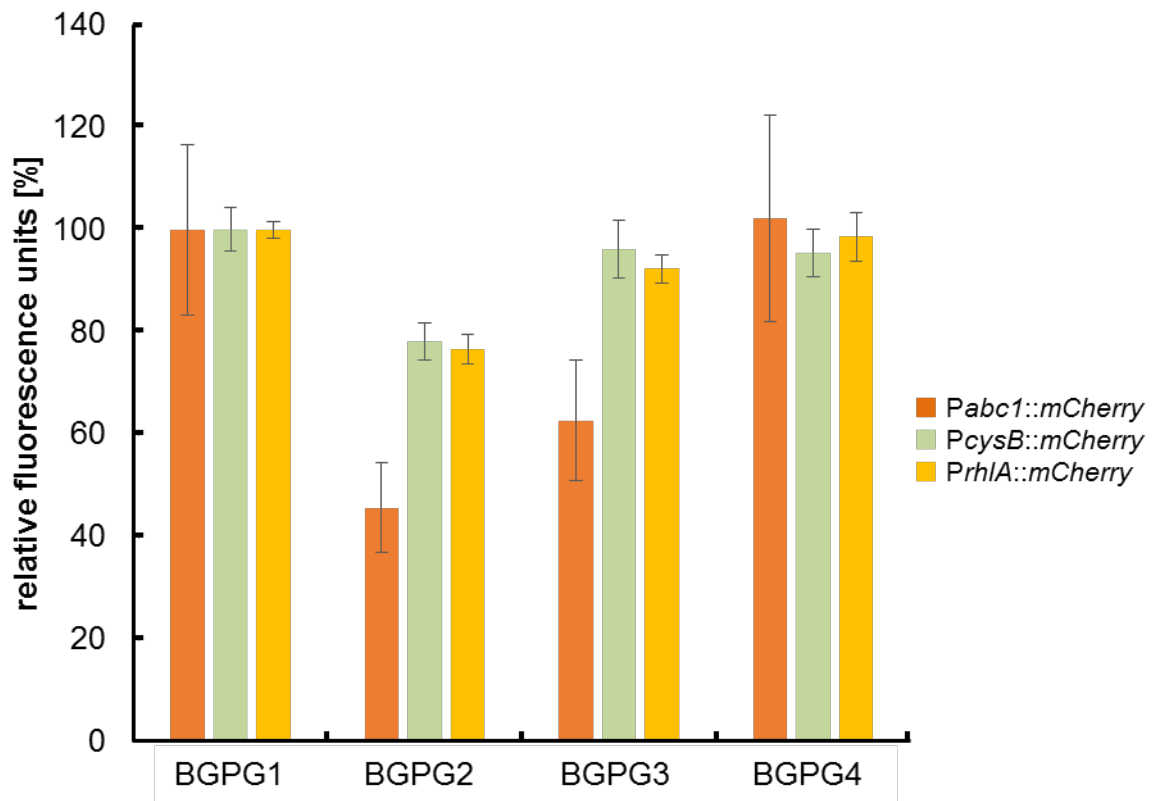
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81 **Figure S6.** Relative fluorescence of BGPG1 and the QS mutants BGPG2-4 carrying the
 82 *Pabc1::mCherry*; *PcysB::mCherry*; and *PrhIA::mCherry* promoter fusions in the vector
 83 pBBR1MCS-2. Data indicate the relative expression of the respective promoter fusions
 84 in BGPG2-4 mutants vs. the wild-type BGPG1. Samples were grown at 30°C for 48 h.
 85 Data are mean values from at least three independent cultures. Bars indicate the simple
 86 standard deviations and are a result of three measurements.

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SUPPLEMENTARY REFERENCES

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