Table S1. *B. thailandensis* genes upregulated in the presence of GS[a]

Gene ID	Common Name	Fold-change in amplified sample[b]	Fold-change in nonamplified sample[b]
BTH_I0026	Flagellar protein FliL	4.5	3.4
BTH_I0199	Flagellar motor switch protein FliG	4.1	3.9
BTH_I0203	Conserved hypothetical protein	2.7	2.2
BTH_I0241	Flagellar basal-body rod protein FlgC	3.5	4.2
BTH_I0283	Copper-translocating P-type ATPase	3.5	3.2
BTH_I0284	LemA family protein	3.7	3.1
BTH_I0286	Conserved hypothetical protein	2.9	2.8
BTH_I0287	Streptavidin, putative	4.4	3.3
BTH_I0446	Transcriptional regulator, GntR family	2.0	1.8
BTH_I0504	Conserved hypothetical protein	2.1	1.7
BTH_I0506	**Carboxymuconolactone decarboxylase family protein**	**2.4**	**2.4**
BTH_I0565	3-Hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase/isomerase family protein	2.1	1.9
BTH_I0623	Erythromycin esterase family	2.7	2.5
BTH_I0626	Phosphoribosyl transferase domain protein	2.4	1.6
BTH_I0627	Conserved hypothetical protein	2.4	2.0
BTH_I0902	Conserved hypothetical protein	4.9	3.2
BTH_I1005	Phospholipase C accessory protein, putative	2.9	2.8
BTH_I1006	Conserved hypothetical protein	3.6	3.5
BTH_I1295	**Phospho-2-dehydro-3-deoxyheptonate aldolase**	**3.7**	**3.2**
BTH_I1302	Heat-inducible transcription repressor HrcA	2.2	1.7
BTH_I1620	Pentachlorophenol 4-monooxygenase; PcpB	2.8	2.2
BTH_I1645	Conserved hypothetical protein	2.0	1.8
BTH_I1656	D-amino acid dehydrogenase, small subunit	3.6	3.7
BTH_I1657	Leucine-responsive regulatory protein	2.4	2.5
BTH_I1800	Oxygen-independent coproporphyrinogen III oxidase	2.8	3.1
BTH_I2124	Sigma 54 modulation protein, putative	4.3	3.6
BTH_I2125	Conserved hypothetical protein	3.1	3.0
BTH_I2272	Oxidoreductase, 2-nitropropane dioxygenase family	2.2	2.6
BTH_I2273	Outer membrane protein, OmpW family	2.1	2.5
BTH_I2382	Conserved hypothetical protein	4.7	5.1
BTH_I2909	**Anthranilate synthase component I**	**2.1**	**2.0**
BTH_I2910	**Anthranilate synthase component II**	**2.4**	**2.4**
BTH_I3183	Chemotaxis response regulator	2.1	1.9
BTH_I3186	Flagellar transcriptional activator FlhC	3.1	2.8
BTH_I3216	Streptogramin acetyl transferase	2.5	2.5
BTH_I3218	Oxidoreductase, FAD-binding, putative	3.0	2.6
BTH_I3337	**Phenylalanine-4-hydroxylase**	**4.5**	**4.0**
BTH_II0055	Sulfide:quinone oxidoreductase	2.4	2.1
BTH_II0059	Efflux transporter, RND family, MFP subunit, putative	2.7	3.0
BTH_II0060	ArsR family regulatory protein	2.5	2.3

BTH_II0062	ABC transporter, ATP-binding protein	2.5	3.1
BTH_II0065	CreA protein, putative	3.2	2.7
BTH_II0069	Cation efflux family protein	2.4	2.7
BTH_II0363	Conserved hypothetical protein	2.1	1.5
BTH_II0417	Phosphate acetyl/butyryltransferase family protein	4.7	5.5
BTH_II0418	Poly-beta-hydroxybutyrate polymerase	2.7	2.5
BTH_II0419	ATP synthase F1, beta subunit	3.1	2.8
BTH_II0425	ATP synthase F0, B subunit	2.1	2.2
BTH_II0428	Alcohol dehydrogenase, zinc-containing	2.3	2.6
BTH_II0430	Conserved hypothetical protein	2.2	2.3
BTH_II0440	RND efflux system, outer membrane protein	3.6	3.5
BTH_II0444	ABC transporter, permease protein	3.6	3.3
BTH_II0445	ABC transporter, ATP-binding protein	3.0	3.0
BTH_II0446	Membrane protein	3.4	3.2
BTH_II0453	Osmotically inducible protein Y domain protein	2.5	3.0
BTH_II0455	Conserved hypothetical protein	2.3	2.6
BTH_II0456	Conserved hypothetical protein	3.5	4.5
BTH_II0457	Cytochrome c family protein	2.3	2.3
BTH_II0458	Conserved hypothetical protein	3.3	3.7
BTH_II0538	Rubrerythrin	3.3	2.5
BTH_II0787	Predicted ATP-dependent protease	2.8	2.2
BTH_II0917	Conserved hypothetical protein	2.0	2.0
BTH_II0919	Glutamine-dependent NAD+ synthetase	4.9	5.5
BTH_II0920	CBS domain protein	3.3	3.2
BTH_II0922	**Alanine dehydrogenase**	**2.1**	**3.1**
BTH_II0923	Hypothetical protein	4.3	3.1
BTH_II0924	Heat shock protein, family	2.4	2.5
BTH_II0939	1,4-Alpha-glucan branching enzyme	2.9	2.5
BTH_II0944	Mulitcopper oxidase domain protein	2.4	2.4
BTH_II0945	Nitric oxide reductase	2.1	2.4
BTH_II0971	Aspartyl/Asparaginyl beta-hydroxylase family	2.6	2.3
BTH_II1008	Response regulator	2.2	2.1
BTH_II1298	ATP-dependent metalloprotease, FtsH family	2.3	2.3
BTH_II1309	Cation-transporting P-ATPase PacL	2.3	2.7
BTH_II1310	Conserved hypothetical protein	2.4	1.8
BTH_II1312	Conserved hypothetical protein	3.7	4.0
BTH_II1313	Uncharacterized conserved protein	4.1	3.5
BTH_II1314	Uncharacterized conserved protein	2.3	2.3
BTH_II1315	Conserved hypothetical protein	2.6	2.5
BTH_II1316	Hypothetical protein	2.1	2.3
BTH_II1317	Hypothetical protein	2.3	1.9
BTH_II1318	Polyglutamate synthase	2.5	1.7
BTH_II1371	Protein of unknown function (DUF355) superfamily	2.1	2.4
BTH_II1372	Hypothetical protein	2.7	3.1

BTH_II1448	Conserved hypothetical protein	3.2	2.8
BTH_II1483	Conserved hypothetical protein	3.1	3.3
BTH_II1516	Conserved hypothetical protein	2.2	2.4
BTH_II1565	Alcohol dehydrogenase, zinc-containing	3.4	3.2
BTH_II1567	Universal stress family protein	3.8	3.6
BTH_II1568	Universal stress family protein	4.1	3.3
BTH_II1569	Universal stress family protein	3.1	2.7
BTH_II1571	Conserved hypothetical protein	2.3	2.1
BTH_II1572	Conserved hypothetical protein	3.1	3.4
BTH_II1574	Conserved hypothetical protein	3.0	3.3
BTH_II1653	Conserved hypothetical protein	2.2	2.9
BTH_II1698	Enoyl-(acyl-carrier-protein) reductase	2.4	2.1
BTH_II1776	Hypothetical protein	3.3	2.7
BTH_II1778	Cytochrome c	3.1	2.8
BTH_II1779	Cytochrome c family protein	2.8	2.5
BTH_II1903	Coenzyme A transferase	4.0	2.7
BTH_II2121	Iron-sulfur cluster-binding protein, Rieske family	2.3	1.4
BTH_II2311	C4-type zinc finger protein, DksA/TraR family	2.1	2.2
BTH_II2314	Conserved hypothetical protein	2.5	2.5
BTH_II2315	Conserved hypothetical protein	4.7	4.2
BTH_II2316	Sulfate permease family protein	2.8	2.6
BTH_II2317	CBS domain protein	3.9	3.9
BTH_II2318	Conserved hypothetical protein	2.9	2.8
BTH_II2322	Polysaccharide deacetylase family protein	2.0	1.8
BTH_II2357	Glutamine ABC transporter, periplasmic glutamine-binding protein	2.2	1.9

[a]Genes in bold were chosen for reporter-gene fusion studies to validate the microarray data.
[b]Fold-change values were averaged over three different two-color microarray slides with *P*-values ≤ 0.05. Numbers in grey indicate that the fold-change values from the non-amplified sample are below 2.0 for comparison.