Table S2. *B. thailandensis* genes down-regulated in the presence of GS[a]

Gene ID	Common Name	Fold-change in amplified sample[b]	Fold-change in nonamplified sample[b]
BTH_I0121	Uncharacterized domain 1, putative	2.0	1.7
BTH_I0155	AmpG-related permease	2.4	1.9
BTH_I0157	**Homoserine O-acetyltransferase**	**2.5**	**2.1**
BTH_I0428	Cytochrome c oxidase assembly protein ctaG, putative	2.5	2.4
BTH_I0474	Ribose-phosphate pyrophosphokinase	2.2	2.5
BTH_I0690	Possible solute binding protein of ABC transporter system	3.1	4.1
BTH_I0691	Transcriptional regulator, putative	2.1	2.9
BTH_I0868	Lipoprotein, putative	2.2	2.2
BTH_I0944	Membrane protein, putative	3.1	2.1
BTH_I1045	**Acetolactate synthase, large subunit, biosynthetic type**	**2.1**	**3.1**
BTH_I1046	**Acetolactate synthase, small subunit**	**2.3**	**2.6**
BTH_I1061	NADH dehydrogenase I, A subunit	2.6	2.6
BTH_I1164	3-Dehydroquinate dehydratase, type II	2.1	1.7
BTH_I1874	Iron-sulfur cluster assembly transcription factor IscR	2.5	2.1
BTH_I2027	Ribosomal protein S2	2.0	2.1
BTH_I2118	Trigger factor	2.1	2.4
BTH_I2248	Transcription accessory protein, TEX	2.1	2.8
BTH_I2558	Transcriptional regulator, MarR family	2.1	3.1
BTH_I3046	Ribosomal protein L36	2.0	2.1
BTH_I3049	Ribosomal protein L15	2.2	2.1
BTH_I3058	Ribosomal protein L14	2.6	2.2
BTH_I3067	Ribosomal protein L4/L1 family	2.0	2.7
BTH_I3073	Ribosomal protein S12	2.3	2.7
BTH_I3110	NADP-dependent malic enzyme	2.2	2.6
BTH_I3195	Ribosomal protein S21-related protein	2.4	2.2
BTH_I3307	ATP synthase F1, epsilon subunit	2.0	2.1
BTH_I3328	Branched-chain amino acid ABC transporter, permease protein	2.0	2.7
BTH_II0217	**Hippurate hydolase**	**4.2**	**3.9**
BTH_II0694	Polysaccharide biosynthesis family protein	2.0	1.8
BTH_II1002	Cold-shock domain family protein-related protein	2.9	2.7
BTH_II1164	Acetylpolyamine aminohydrolase	2.5	2.1
BTH_II1428	Conserved hypothetical protein	2.2	2.0
BTH_II2243	4-Hydroxy-3-methylbut-2-enyl diphosphate reductase	2.0	2.1
BTH_II2252	Carbon starvation protein A	2.6	2.8
BTH_II2336	Toluene tolerance, Ttg2 superfamily	2.2	2.0

[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.