

**Table S3.** Genes targeted for microarray data validation via reporter-gene fusion studies

FC <sup>a</sup>	Gene ID	Common name	Relevant properties
<b>Genes up-regulated in GS<sup>b</sup></b>			
2.4 (2.4)	BTH_I0506	Carboxymuconolactone decarboxylase family protein	Benzoate degradation
3.7 (3.2)	BTH_I1295	Phospho-2-dehydro-3-deoxyheptonate aldolase	Chorismate biosynthesis, inhibited by tyrosine, induced by amino acids starvation
2.1, 2.4 (2.0, 2.4)	BTH_I2909, 2910	Anthranilate synthase component I, II	Tryptophan biosynthesis
4.5 (4.0)	BTH_I3337	Phenylalanine-4-hydroxylase	Catalyze conversion of Phenylalanine to tyrosine
2.1 (3.1)	BTH_II0922	Alanine dehydrogenase	Alanine metabolism
<b>Genes down-regulated in GS<sup>c</sup></b>			
2.5 (2.1)	BTH_I0157	Homoserine O-acetyltransferase	Methionine biosynthesis
2.1, 2.3 (3.1, 2.6)	BTH_I1045, 1046	Acetolactate synthase large, small subunits	Branched-chain amino acids synthesis
4.2 (3.9)	BTH_II0217	Hippurate hydrolase	Phenylalanine metabolism
<b>Genes unchanged in GS (controls)<sup>c</sup></b>			
1.0 (1.0)	BTH_I2028	translation elongation factor TS	Translation, ribosomal structure and biogenesis
1.0 (0.8)	BTH_I2199	threonine synthase	Threonine biosynthesis

<sup>a</sup>Gene expression fold-changes obtained in microarray data from three single-cell amplifications of two conditions; in parentheses are fold-change of non-amplified samples.

<sup>b</sup>The fold-changes were calculated as the gene expression levels in the presence of versus in the absence of GS.

<sup>c</sup>The fold-changes were calculated as the gene expression levels in the absence of GS versus in the presence of GS.