

Supplemental Table 1. Proteins Increased in Either Soil or Laboratory media				
Table 1A. Proteins Increased in Spores Produced on Soil Over Spores Produced on Laboratory Media				
quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
2.97E-08	BAS0310	4-aminobutyrate aminotransferase	bat00250, bat00280, bat00410, bat00640, bat00650	Alanine, aspartate and glutamate metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism, Propanoate metabolism, Butanoate metabolism
5.28E-08	BAS0561	alanine dehydrogenase	bat00250, bat00430	Alanine, aspartate and glutamate metabolism, Taurine and hypotaurine metabolism
2.70E-10	BAS4521	alanine dehydrogenase	bat00250, bat00431	Alanine, aspartate and glutamate metabolism, Taurine and hypotaurine metabolism
1.21E-13	BAS5060	spermidine synthase	bat00270, bat00330, bat00410, bat00480	Cysteine and methionine metabolism, Arginine and proline metabolism, beta-Alanine metabolism, Glutathione metabolism
3.69E-13	BAS0228	homogentisate 1,2-dioxygenase, putative	bat00350, bat00643	Tyrosine metabolism, Styrene degradation
		Membrane, Wall or Surface Proteins		
8.51E-25	BAS3022	ABC transporter, ATP-binding protein	bat02010	ABC-type lipoprotein export system, ATPase
5.99E-32	BAS3023	ABC transporter, permease protein, putative	bat02010	ABC-type antimicrobial peptide transport system, FtsX-like permease family, Defense mechanisms
2.68E-10	BAS0685	AcrB/AcrD/AcrF family transporter		
8.30E-17	BAS0681	phosphate ABC transporter, phosphate-binding protein, putative	bat02010	ABC transporters
		Other Enzymes and Proteins		
1.12E-10	BAS2122	azoreductase		
1.21E-13	BAS1076	catalase		
3.93E-07	BAS2816	catalase		
2.69E-12	BAS4591	M42 family peptidase		
9.93E-08	BAS3884	peptide deformylase		
1.53E-10	BAS4071	phosphate butyryltransferase	bat00650	Butanoate metabolism (polyketide biosynthesis)
8.18E-29	BAS4170	phosphate transport system regulatory protein PhoU, putative		
8.25E-08	BAS0777	purple acid phosphatase/fibronectin domain-containing protein		
1.33E-10	BAS1763	xaa-pro aminopeptidase, putative		
2.70E-11	BAS4191	GTP cyclohydrolase		
		Fatty Acid Metabolism		
1.96E-14	BAS0832	acyl-CoA synthetase	bat00061, bat00071	Fatty acid biosynthesis, Fatty acid degradation
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
5.93E-08	BAS4068	dihydroliipoamide dehydrogenase	bat00010, bat00020, bat00260, bat00280, bat00620, bat00630	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Glycine, serine and threonine metabolism, Valine, leucine and isoleucine degradation, Pyruvate metabolism, Glyoxylate and dicarboxylate metabolism
1.08E-07	BAS1052	isocitrate lyase	bat00630	Glyoxylate and dicarboxylate metabolism
		Nucleotide Metabolism		
5.89E-07	BAS1003	endonuclease/exonuclease/phosphatase family protein		

1.02E-07	BAS0006	DNA gyrase subunit A		
		Transcription and Protein translation		
2.91E-06	BAS2027	isoleucyl-tRNA synthetase		
5.23E-09	BAS0691	transcriptional activator TenA, putative		
1.69E-27	BAS4293	rrf2 family protein - DNA-binding transcriptional regulator		
		Sporulation-Germination Proteins		
6.26E-14	BAS0047	regulatory protein SpoVG		
		Vitamin metabolism		
7.54E-10	BAS0696	glycine oxidase	bat00730	Thiamine metabolism
1.99E-14	BAS0698	thiazole synthase	bat00730	Thiamine metabolism
5.39E-11	BAS4244	alkaline phosphatase	bat00627, bat00790	Aminobenzoate degradation, Folate biosynthesis
		Hypothetical Proteins		
3.18E-14	BAS2513	hypothetical protein		
2.12E-09	BAS3081	hypothetical protein		
2.28E-10	BAS3861	hypothetical protein		

Table 1B. Proteins Increased in Spores from Laboratory Media Over Spores Produced in Soil

quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
0.000103	BAS1311	2-isopropylmalate synthase	bat00290, bat00620, bat01110, bat01210	Valine, leucine and isoleucine biosynthesis, Pyruvate metabolism, 2-Oxocarboxylic acid metabolism
1.38E-20	BAS1625	asparagine synthetase, glutamine-hydrolyzing	bat00250, bat01110	Alanine, aspartate and glutamate metabolism
8.73E-15	BAS2095	asparagine synthetase, glutamine-hydrolyzing	bat00250, bat01110	Alanine, aspartate and glutamate metabolism
7.69E-16	BAS4067	3-methyl-2-oxobutanoate dehydrogenase, alpha subunit		Valine, leucine and isoleucine degradation
1.56E-20	BAS4066	3-methyl-2-oxobutanoate dehydrogenase, beta subunit	bat00280, bat01110	Valine, leucine and isoleucine degradation
1.22E-12	BAS4269	O-acetylserine lyase	bat00270	Cysteine and methionine metabolism
3.07E-13	BAS4271	hypothetical protein - 100% homology to SAM-dependent methyltransferase	bat00270	Cysteine and methionine metabolism
1.31E-20	BAS4879	proline dehydrogenase family protein	bat00330, bat01110	Arginine and proline metabolism
1.13E-06	BAS1310	ketol-acid reductoisomerase	bat00290, bat00770, bat01210	Valine, leucine and isoleucine biosynthesis, Pantothenate and CoA biosynthesis, 2-Oxocarboxylic acid metabolism
5.10E-09	BAS3078	D-3-phosphoglycerate dehydrogenase, putative	bat00260, bat00680	Glycine, serine and threonine metabolism, Methane metabolism
		Membrane, Wall or Surface Proteins		
0.000287	BAS3372	hypothetical protein	bat02010	ABC transporter, 100% homology to phosphonate ABC transporter permease
9.20E-11	BAS0248	ABC transporter, ATP-binding protein	bat02010	ATP-binding cassette domain of elongation factor 3
7.44E-06	BAS3140	ABC transporter, ATP-binding protein	bat02010	ABC-type Na ⁺ transport system
2.22E-06	BAS4723	ABC transporter, ATP-binding protein	bat02010	ABC-type lipoprotein export system
3.34E-06	BAS0354	amino acid ABC transporter, ATP-binding protein	bat02010	
3.87E-17	BAS5281	ABC transporter, ATP-binding protein	bat02010	ABC transporter, 100% homology to heme ABC transporter ATP-binding protein

2.45E-13	BAS3642	sugar ABC transporter, ATP-binding protein	bat02010	
5.99E-09	BAS4334	ABC transporter, ATP-binding protein	bat02010	ABC-type lipoprotein export system
7.44E-06	BAS3140	ABC transporter, ATP-binding protein	bat02010	ABC-type Na ⁺ transport system
8.96E-09	BAS1102	oligopeptide ABC transporter, permease protein	bat02010	
1.63E-18	BAS5128	rod shape-determining protein Mbl		
7.75E-06	BAS2964	adhesion lipoprotein		
2.42E-15	BAS5038	preprotein translocase subunit SecA		
1.36E-07	BAS0838	preprotein translocase subunit SecA		
1.63E-18	BAS5128	rod shape-determining protein Mbl		
7.75E-06	BAS2964	adhesion lipoprotein		
2.42E-15	BAS5038	preprotein translocase subunit SecA		
1.36E-07	BAS0838	preprotein translocase subunit SecA		
1.60E-12	BAS5137	UDP-N-acetylglucosamine 1-carboxyvinyltransferase		
1.67E-22	BAS0525	SPFH domain-containing protein/band 7 family protein - Flotillin or reggie family		
1.86E-06	BAS1576	TPR/glycosyl transferase domain-containing protein - Glycosyltransferase involved in cell wall biosynthesis		
9.76E-11	BAS1255	hypothetical protein - 99% homology to <i>B. thuringiensis</i> putrescine importer		
		Other Enzymes and Proteins		
7.15E-08	BAS1263	acetyltransferase		
7.71E-09	BAS2680	acetyltransferase		
4.07E-11	BAS2977	chaperone protein hscC		
6.37E-05	BAS0227	fumarylacetoacetate hydrolase family protein		
1.31E-17	BAS1936	glycosyl transferase family protein		
4.24E-11	BAS3326	glyoxalase family protein		
8.46E-18	BAS5328	GTP-dependent nucleic acid-binding protein EngD		
4.39E-11	BAS3885	HAD superfamily hydrolase		
6.79E-07	BAS2017	HEAT repeat-containing PBS lyase		
7.30E-17	BAS2273	hypothetical protein - 100% homology to acetyltransferase gb AIK08488.1		
9.13E-20	BAS2829	hypothetical protein - Abhydrolase_5		
1.83E-14	BAS2803	hypothetical protein - oribabke magnesium chelatase		
3.83E-29	BAS2554	hypothetical protein - plasmid segregation protein ParM		
6.97E-17	BAS0518	hypothetical protein, putative serine protein kinase		
9.50E-11	BAS4005	lolS protein - Predicted oxidoreductase - related to aryl-alcohol dehydrogenase		
6.88E-22	BAS0147	mrp protein - ATP-binding protein involved in chromosome partitioning		
3.34E-12	BAS2002	N-acetyltransferase family protein		
7.31E-08	BAS0591	NorQ protein, putative - MoxR-like ATPase		

1.32E-06	BAS3556	phage integrase family site specific recombinase		
1.66E-09	BAS3863	PhoH family protein - Predicted ribonuclease YlaK		
2.39E-11	BAS4447	recombination and DNA strand exchange inhibitor protein, Endonuclease MutS2		
5.55E-11	BAS0241	S1 RNA-binding domain-containing protein - ribonuclease with RNase H fold		
1.91E-16	BAS5300	superoxide dismutase, Mn		
1.40E-10	BAS0390	tellurite resistance protein, putative		
1.01E-15	BAS4936	tyrosyl-tRNA synthetase		
		Fatty Acid Metabolism		
1.28E-18	BAS1019	long-chain-fatty-acid-CoA ligase	bat00061, bat00071	Fatty acid biosynthesis, Fatty acid degradation
2.70E-19	BAS4840	lipoyl synthase	bat00785	Lipoic acid metabolism
3.10E-18	BAS4876	acetyl-CoA acetyltransferase	bat00071, bat00280, bat00281, bat00362, bat00592, bat00642, bat01110	Fatty acid degradation, Valine, leucine and isoleucine degradation, Geraniol degradation, Benzoate degradation, alpha-Linolenic acid metabolism, Ethylbenzene degradation, Biosynthesis of secondary metabolites
1.40E-12	BAS1840	acyl-CoA synthetase		
5.21E-14	BAS3703	acyl-carrier-protein S-malonyltransferase		
1.10E-09	BAS3349	3-ketoacyl-(acyl-carrier-protein) reductase	bat00061, bat00780	Fatty acid biosynthesis, Biotin metabolism
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
1.42E-27	BAS0481	formate acetyltransferase	bat00620, bat00640 bat00650	Pyruvate metabolism, Propanoate metabolism, Butanoate metabolism
5.33E-35	BAS0669	quinol oxidase, subunit II	bat00190	Oxidative phosphorylation
2.07E-16	BAS0668	quinol oxidase, subunit I	bat00190	Oxidative phosphorylation
9.62E-16	BAS2361	metallo-beta-lactamase/rhodanese-like domain-containing protein	bat00620	Pyruvate metabolism
0.000251	BAS4593	metallo-beta-lactamase family protein		
1.66E-18	BAS2376	acetoacetyl-CoA synthase, putative	bat00010, bat00620, bat00640, bat00680, bat01110	Glycolysis / Gluconeogenesis, Pyruvate metabolism, Propanoate metabolism, Methane metabolism, Biosynthesis of secondary metabolites
1.15E-05	BAS2586	branched-chain alpha-keto acid dehydrogenase subunit E2	bat00010, bat00020, bat00620, bat01110	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism, Biosynthesis of secondary metabolites
2.11E-15	BAS2762	malate:quinone oxidoreductase	bat00020, bat00620, bat01110	Citrate cycle (TCA cycle), Pyruvate metabolism, Biosynthesis of secondary metabolites
9.25E-12	BAS1726	acetyl-CoA hydrolase/transferase family protein	bat00020, bat00620, bat00650	Citrate cycle (TCA cycle), Pyruvate metabolism, Butanoate metabolism
3.00E-12	BAS0197	aldo/keto reductase family oxidoreductase		
0.000147	BAS2640	aldehyde dehydrogenase	bat00010, bat00040, bat00071, bat00053, bat00350, bat00625, bat00280, bat00310, bat00330, bat00340, bat00380, bat00410, bat00561, bat00620	Glycolysis / Gluconeogenesis, Pentose and glucuronate interconversions, Ascorbate and aldarate metabolism, Fatty acid degradation, Valine, leucine and isoleucine degradation, Lysine degradation, Arginine and proline metabolism, Histidine metabolism, Tryptophan metabolism, beta-Alanine metabolism, Glycerolipid metabolism, Pyruvate metabolism, Chloroalkane and chloroalkene degradation
1.25E-19	BAS2111	alcohol dehydrogenase	bat00010, bat00071,	Glycolysis / Gluconeogenesis, Fatty acid

			bat00350, bat00625	degradation, Tyrosine metabolism, Chloroalkane and chloroalkene degradation
8.54E-06	BAS0641	alcohol dehydrogenase, zinc-containing		
5.94E-07	BAS3622	2-oxoglutarate ferredoxin oxidoreductase subunit beta	bat00020	Citrate cycle (TCA cycle)
0.000103	BAS1311	2-isopropylmalate synthase	bat00290, bat00620	Valine, leucine and isoleucine biosynthesis, Pyruvate metabolism
9.78E-06	BAS2585	dihydrolipoamide dehydrogenase	bat00010, bat00020, bat00260, bat00280, bat00620, bat00630	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Glycine, serine and threonine metabolism, Valine, leucine and isoleucine degradation, Pyruvate metabolism, Glyoxylate and dicarboxylate metabolism
5.31E-12	BAS1176	dihydrolipoamide succinyltransferase	bat00020, bat00310	Citrate cycle (TCA cycle), Lysine degradation
3.50E-08	BAS4773	gluconate 2-dehydrogenase	bat00030	Pentose phosphate pathway
4.57E-05	BAS4869	L-lactate dehydrogenase	bat00010, bat00270, bat00620, bat00640	Glycolysis / Gluconeogenesis, Cysteine and methionine metabolism, Pyruvate metabolism, Propanoate metabolism
1.30E-07	BAS0557	molybdopterin oxidoreductase family protein	bat00630, bat00680	Glyoxylate and dicarboxylate metabolism, Methane metabolism
5.81E-05	BAS2588	TPP-dependent acetoin dehydrogenase E1 alpha-subunit	bat00010, bat00020, bat00620	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism
		Nucleotide Metabolism		
8.70E-06	BAS3398	anaerobic ribonucleoside triphosphate reductase	bat00230, bat00240	Purine metabolism, Pyrimidine metabolism
1.75E-19	BAS4935	pyridine nucleotide-disulphide oxidoreductase	bat00230, bat00240	Purine metabolism, Pyrimidine metabolism
3.62E-05	BAS4482	DNA polymerase I	bat00230, bat00240	Purine metabolism, Pyrimidine metabolism
8.53E-16	BAS3676	uridylate kinase		
		Transcription and Protein translation		
5.18E-12	BAS5325	30S ribosomal protein S18	bat03010	Protein translation
1.01E-15	BAS4936	tyrosyl-tRNA synthetase	bat00970	Protein translation
2.42E-15	BAS5038	preprotein translocase subunit SecA	bat03060	Protein export
1.36E-07	BAS0838	preprotein translocase subunit SecA	bat03060	Protein export
2.43E-08	BAS1014	LacI family sugar-binding transcriptional regulator		
9.40E-08	BAS4013	LacI family sugar-binding transcriptional regulator		
4.50E-17	BAS3683	tRNA (uracil-5-)-methyltransferase Gid		
1.14E-10	BAS4291	tRNA-specific 2-thiouridylase MnmA		
3.14E-07	BAS3670	prolyl-tRNA synthetase		
		Sporulation-Germination Proteins		
2.08E-11	BAS5185	stage 0 sporulation protein F		
1.09E-08	BAS5332	stage 0 sporulation protein J		
4.08E-07	BAS0731	stage V sporulation protein R		
4.84E-09	BAS3654	dipicolinate synthase subunit A		
		Vitamin metabolism		
8.28E-13	BAS4023	biotin synthase	bat00780	Biotin metabolism
4.39E-11	BAS4027	dithiobiotin synthetase	bat00780	Biotin metabolism
3.84E-06	BAS4328	cysteine desulfurase	bat00730	Thiamine metabolism
2.51E-12	BAS5266	pyridoxal kinase	bat00750	Vitamin B6 metabolism
		Hypothetical Proteins		

3.36E-11	BAS3810	hypothetical protein		
4.93E-10	BAS3621	hypothetical protein		
6.91E-07	BAS2158	hypothetical protein		
2.21E-06	BAS1216	hypothetical protein		
1.85E-13	BAS3590	hypothetical protein		
4.92E-06	BAS3176	hypothetical protein		
3.07E-13	BAS4271	hypothetical protein		
4.85E-07	BAS4934	hypothetical protein		
3.42E-07	BAS0915	hypothetical protein		
2.59E-06	BAS0394	hypothetical protein		
1.43E-07	BAS3307	hypothetical protein		
7.39E-08	BAS1377	hypothetical protein		
4.60E-06	BAS1927	hypothetical protein		
3.26E-06	BAS0997	hypothetical protein		
5.63E-06	BAS2950	hypothetical protein		