

Supplemental Table 4. Proteins Increased in Either Soil medium at 37 °C and 25 °C				
Table 4A. Proteins Increased in Spores Produced on both Soils at 37 °C over 25 °C				
quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
0.000275	BAS4270	5prime-methylthioadenosine/S-adenosylhomocysteine nucleosidase	bat00270	Cysteine and methionine metabolism
6.67E-07	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
1.55E-10	BAS0331	5-methylribose kinase	bat00270	Cysteine and methionine metabolism
1.18E-06	BAS0561	alanine dehydrogenase	bat00250, bat00430	Alanine, aspartate and glutamate metabolism, Taurine and hypotaurine metabolism
6.11E-13	BAS4102	proline dipeptidase	bat00310, bat00780	Lysine degradation, Biotin metabolism
9.62E-08	BAS4508	proline dipeptidase	bat00310, bat00780	Lysine degradation, Biotin metabolism
0.001051	BAS2268	aspartate-semialdehyde dehydrogenase	bat00260, bat00261, bat00270, bat00300	Glycine, serine and threonine metabolism, Monobactam biosynthesis, Cysteine and methionine metabolism, Lysine biosynthesis
1.02E-05	BAS5218	agmatinase, putative	bat00330	Arginine and proline metabolism
1.77E-06	BAS0498	glutamate synthase, large subunit, putative	bat00250, bat00910	Alanine, aspartate and glutamate metabolism, Nitrogen metabolism
0.04631	BAS0350	Rieske 2Fe-2S iron-sulfur protein, putative		
0.011632	BAS2145	L-lysine 2,3-aminomutase		
4.95E-08	BAS1287	D-alanine--poly(phosphoribitol) ligase subunit 1		
		Membrane, Wall or Surface Proteins		
1.70E-10	BAS1518	sodium/solute symporter family protein		
8.80E-06	BAS4853	ABC transporter, substrate-binding protein, putative		
2.65E-05	BAS4424	iron compound ABC transporter, iron compound-binding protein		
0.041817	BAS0237	putative lipoprotein		
0.011339	BAS1022	wall-associated protein, putative		
9.51E-06	BAS4346	septum site-determining protein MinD		
1.40E-05	BAS2658	NLP/P60 family protein		Cell wall-associated hydrolase
		Other Enzymes and Proteins		
0.000156	BAS5226	4-oxalocrotonate tautomerase	bat00362, bat00622	Benzoate degradation, Xylene degradation
3.49E-15	BAS0329	alkyl hydroperoxide reductase, F subunit		Oxidoreductases
1.46E-06	BAS4579	aminopeptidase, putative		Hydrolases
3.53E-07	BAS1090	ATP-dependent Clp protease, ATP-binding subunit ClpB		
1.61E-14	BAS3893	CBS domain-containing protein		
3.01E-05	BAS2490	chitosanase		
0.041817	BAS1936	glycosyl transferase family protein		
0.041817	BAS0951	glyoxylase family protein		
0.000656	BAS4214	GrpE protein		
0.002868	BAS1414	GTP-binding protein EngA		

4.32E-09	BAS0978	HIT family protein		protease
0.000347	BAS2106	HSP20 family protein		
5.47E-08	BAS3071	hydrogenase expression/formation protein HyeE		
3.24E-07	BAS3072	isochorismatase family protein		
0.002115	BAS1522	metallo-beta-lactamase family protein	bat03018	RNA degradation
0.009904	BAS5005	mutT/nudix family protein		
1.19E-10	BAS5310	oligoendopeptidase F, putative		Hydrolases
0.041817	BAS5178	peptide chain release factor 1		
2.19E-06	BAS3884	peptide deformylase		Hydrolases
		Fatty Acid Metabolism		
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
2.67E-08	BAS0472	PTS system, N-acetylglucosamine-specific IIBC component, putative	bat00520, bat02060	Amino sugar and nucleotide sugar metabolism, Phosphotransferase system
0.04885	BAS0637	putative transaldolase	bat00030, bat01110, bat01230	Pentose phosphate pathway, Biosynthesis of secondary metabolites, Biosynthesis of amino acids
2.40E-06	BAS1052	isocitrate lyase	bat00630	Glyoxylate and dicarboxylate metabolism
1.32E-07	BAS1177	2-oxoglutarate dehydrogenase E1 component	bat00020, bat00310, bat00380, bat01110	Citrate cycle (TCA cycle), Lysine degradation, Tryptophan metabolism, Biosynthesis of secondary metabolites
0.002839	BAS2111	alcohol dehydrogenase	bat00010, bat00071, bat00350, bat00625	Glycolysis / Gluconeogenesis, Fatty acid degradation, Tyrosine metabolism, Chloroalkane and chloroalkene degradation
1.45E-09	BAS3965	N-acetylglucosamine-6-phosphate deacetylase	bat00520, bat01110	Amino sugar and nucleotide sugar metabolism, Biosynthesis of secondary metabolites
1.32E-06	BAS4068	dihydrolipoamide dehydrogenase	bat00010, bat00020, bat00260, bat00280, bat00620, bat01110	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Glycine, serine and threonine metabolism, Valine, leucine and isoleucine degradation, Pyruvate metabolism,
2.67E-06	BAS4661	phosphoenolpyruvate carboxykinase	bat00010, bat00020, bat00620, bat01110	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism, Biosynthesis of secondary metabolites
0.011632	BAS2587	TPP-dependent acetoin dehydrogenase E1 beta-subunit	bat00010, bat00020, bat00620	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism
0.000134	BAS5238	phosphotransacetylase	bat00430, bat00620, bat00640	Taurine and hypotaurine metabolism, Pyruvate metabolism, Propanoate metabolism
3.04E-06	BAS5182	fructose 1,6-bisphosphatase II	bat00010, bat00030, bat00051, bat00680	Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Fructose and mannose metabolism, Methane metabolism
0.002868	BAS1415	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase		
2.67E-08	BAS0472	PTS system, N-acetylglucosamine-specific IIBC component, putative	bat00520, bat02060	Amino sugar and nucleotide sugar metabolism, Phosphotransferase system
		Nucleotide Metabolism		
0.011632	BAS0254	GMP synthase	bat00230	Purine metabolism
0.041817	BAS0029	thymidylate kinase	bat00240	Pyrimidine metabolism
0.003755	BAS0947	3prime-5prime exoribonuclease YhaM		
3.68E-07	BAS1270	ribonucleotide-diphosphate reductase	bat00230,	Purine metabolism, Pyrimidine metabolism

		subunit beta	bat00240	
0.003001	BAS3995	pyrimidine-nucleoside phosphorylase	bat00240	Pyrimidine metabolism
3.48E-11	BAS5007	thioredoxin reductase	bat00240, bat00450	Pyrimidine metabolism, Selenocompound metabolism
0.041817	BAS4325	quinolinate synthetase	bat00760	Nicotinate and nicotinamide metabolism
1.32E-07	BAS1372	purine nucleoside phosphorylase	bat00230, bat00240, bat00760	Purine metabolism, Pyrimidine metabolism, Nicotinate and nicotinamide metabolism
0.011632	BAS0254	GMP synthase	bat00230	Purine metabolism
		Transcription and Protein translation		
7.61E-11	BAS4454	asparaginyl-tRNA synthetase	bat00970	Aminoacyl-tRNA biosynthesis
0.016091	BAS0306	aspartyl/glutamyl-tRNA amidotransferase subunit A		
0.000656	BAS0307	aspartyl/glutamyl-tRNA amidotransferase subunit B		
1.48E-06	BAS5213	arginyl-tRNA synthetase		
0.009904	BAS4472	threonyl-tRNA synthetase		
0.000126	BAS0566	transcriptional regulator		
0.000656	BAS0078	transcriptional regulator CtsR		
5.50E-05	BAS0037	methionyl-tRNA synthetase		
2.67E-08	BAS1386	DNA-binding response regulator ResD		
7.61E-11	BAS4454	asparaginyl-tRNA synthetase	bat00970	Aminoacyl-tRNA biosynthesis
		Sporulation-Germination Proteins		
		Vitamin Metabolism		
3.07E-11	BAS0691	transcriptional activator TenA, putative	bat00730	Thiamine metabolism
1.28E-08	BAS0696	glycine oxidase	bat00730	Thiamine metabolism
1.06E-08	BAS4021	6,7-dimethyl-8-ribityllumazine synthase	bat00740	Riboflavin metabolism
		Hypothetical Proteins		
2.05E-14	BAS1349	hypothetical protein		
0.009904	BAS3115	hypothetical protein		
5.47E-08	BAS5003	hypothetical protein		
1.70E-07	BAS4700	hypothetical protein		
1.71E-06	BAS3864	hypothetical protein		
0.011632	BAS2453	hypothetical protein		
0.04631	BAS2561	hypothetical protein		
0.04631	BAS1255	hypothetical protein		
0.000981	BAS3647	hypothetical protein		
0.001073	BAS1643	hypothetical protein		
0.001073	BAS1872	hypothetical protein		
0.000696	BAS1431	hypothetical protein		
0.041817	BAS1302	hypothetical protein		
5.97E-07	BAS1148	hypothetical protein		
2.05E-14	BAS1349	hypothetical protein		
Table 4B. Proteins Increased in Spores Produced on both Soils at 25 °C over 37 °C				
quasi.fdr	Protein	Protein Class/Name	KEGG	Pathway Names or Function

	ID		Pathways	(if found in KEGG)
		Amino Acid Metabolism		
1.14E-14	BAS5060	spermidine synthase	bat00270, bat00330, bat00410, bat00480	Cysteine and methionine metabolism, Arginine and proline metabolism, beta- Alanine metabolism, Glutathione metabolism
0.04631	BAS0160	glucosamine--fructose-6-phosphate aminotransferase	bat00250, bat00520	Alanine, aspartate and glutamate metabolism, Amino sugar and nucleotide sugar metabolism
0.041817	BAS1310	ketol-acid reductoisomerase	bat00290, bat00770	Valine, leucine and isoleucine biosynthesis, Pantothenate and CoA biosynthesis
0.000514	BAS1673	asparagine synthetase AsnA	bat00250, bat00460	Alanine, aspartate and glutamate metabolism, Cyanoamino acid metabolism
0.04631	BAS1825	homoserine dehydrogenase	bat00260, bat00270, bat00300	Glycine, serine and threonine metabolism, Cysteine and methionine metabolism, Lysine biosynthesis
0.00231	BAS4687	S-ribosylhomocysteinase	bat00270	Cysteine and methionine metabolism
		Membrane, Wall or Surface Proteins		
3.71E-09	BAS0685	AcrB/AcrD/AcrF family transporter		Multidrug efflux pump
1.83E-08	BAS3475	phosphonate ABC transporter, phosphonate-binding protein, putative	bat02010	phosphonate uptake
0.000696	BAS3671	membrane-associated zinc metalloprotease, putative		regulating intramembrane proteolysis (RIP)
1.85E-18	BAS2277	N-acetylmuramoyl-L-alanine amidase		peptidoglycan aminohydrolase
0.041817	BAS3463	N-acetylmuramoyl-L-alanine amidase		peptidoglycan aminohydrolase
8.85E-17	BAS1683	N-acetylmuramoyl-L-alanine amidase		peptidoglycan aminohydrolase
0.041817	BAS3725	cation transporter E1-E2 family ATPase		
0.010528	BAS1048	S-layer protein, putative		
		Other Enzymes and Proteins		
1.80E-06	BAS0777	purple acid phosphatase/fibronectin domain-containing protein		
3.24E-10	BAS3629	recombinase A		
7.61E-11	BAS3875	transglutaminase		
0.002559	BAS4199	GTP-binding protein Era		
3.00E-07	BAS2816	catalase		
3.54E-09	BAS2615	glycosyl hydrolase family protein		
0.041817	BAS3627	phosphodiesterase		
0.000165	BAS1045	M48 family peptidase		
0.000514	BAS4163	metallo-beta-lactamase family protein		
3.05E-09	BAS1621	alpha/beta fold family hydrolase		
0.000141	BAS0460	prophage LambdaBa04, glycosyl hydrolase family protein 25, putative		
0.04631	BAS0288	SPFH domain-containing protein/band 7 family protein		
0.000656	BAS4636	vrrB protein		
		Fatty Acid Metabolism		
0.010808	BAS2195	enoyl-CoA hydratase	bat00071	Fatty acid degradation
		Glycolysis-Pyruvate metabolism- TCA cycle-Oxidative phosphorylation		
		Nucleotide Metabolism		
1.26E-05	BAS1003	endonuclease/exonuclease/phosphatase family protein		

0.001073	BAS5015	excinuclease ABC subunit A		
0.002839	BAS2215	DinB family DNA polymerase		
6.95E-13	BAS2301	DEAD-box ATP dependent DNA helicase		
		Transcription and Protein translation		
9.31E-07	BAS3769	S-adenosyl-methyltransferase MraW		
1.26E-05	BAS4053	ribosomal-protein-alanine acetyltransferase, putative		
		Sporulation-Germination Proteins		
1.05E-07	BAS1145	spore coat protein Z		
6.90E-12	BAS1141	spore coat protein Z		
0.001073	BAS4076	stage 0 sporulation protein A		
0.002839	BAS0768	cotJA protein		
9.76E-11	BAS3653	dipicolinate synthase subunit B		
1.79E-13	BAS0041	yabG protein		sporulation peptidase YabG
		Vitamin metabolism		
		Hypothetical Proteins		
1.93E-22	BAS0342	hypothetical protein		
1.46E-16	BAS2264	hypothetical protein		
1.95E-13	BAS2663	hypothetical protein		
1.85E-18	BAS3081	hypothetical protein		
8.85E-17	BAS0474	hypothetical protein		
0.000215	BAS4426	hypothetical protein		
7.10E-06	BAS3526	hypothetical protein		
4.27E-08	BAS2284	hypothetical protein		
6.66E-09	BAS2377	hypothetical protein		
1.61E-14	BAS3375	hypothetical protein		