Supplemental Table 2. Proteins Increased in Either Blood or Horizon media

Table 2A. Proteins Increased in Spores Produced on Horizon Soil Over Spores Produced on Blood Medium

quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
4.50E-07	BAS0310	4-aminobutyrate aminotransferase	bat00250, bat00280, bat00410, bat00640, bat00650	Alanine, aspartate and glutamate metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism to acetyl CoA, Propanoate metabolism, Butanoate metabolism
3.84E-10	BAS5060	spermidine synthase	bat00270, bat00330, bat00410, bat00480	Cysteine and methionine metabolism, Arginine and proline metabolism, beta-Alanine metabolism, Glutathione metabolism
2.30E-09	BAS5219	spermidine synthase	bat00270, bat00330, bat00410, bat00480	Cysteine and methionine metabolism, Arginine and proline metabolism, beta-Alanine metabolism, Glutathione metabolism
6.94E-07	BAS0561	alanine dehydrogenase	bat00250, bat00430	Alanine, aspartate and glutamate metabolism, Taurine and hypotaurine metabolism
5.23E-07	BAS4521	alanine dehydrogenase	bat00250, bat00430	Alanine, aspartate and glutamate metabolism, Taurine and hypotaurine metabolism
0.005627	BAS5218	agmatinase, putative	bat00330	Arginine and proline metabolism
1.40E-10	BAS3891	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase, putative	bat00300	Lysine biosynthesis
8.69E-07	BAS4068	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
		Membrane, Wall or Surface Proteins		
3.88E-14	BAS3022	ABC transporter, ATP-binding protein	bat02010	ABC-type lipoprotein export system, ATPase
4.80E-22	BAS3023	ABC transporter, permease protein, putative	bat02010	ABC-type antimicrobial peptide transport system, FtsX-like permease family, Defense mechanisms
3.78E-11	BAS0681	phosphate ABC transporter, phosphate-binding protein, putative	bat02010	ABC-2 type transport system
1.10E-06	BAS3475	phosphonate ABC transporter, phosphonate-binding protein, putative	bat02010	ABC-2 type transport system
7.47E-06	BAS0685	AcrB/AcrD/AcrF family transporter		
		Other Enzymes and Proteins		
2.84E-10	BAS2122	azoreductase		
4.71E-09	BAS1076	catalase		
0.005627	BAS2914	catalase, Mn-containing		
1.79E-09	BAS3893	CBS domain-containing protein		
0.000924	BAS1003	endonuclease/exonuclease/phosphatase family protein		
1.69E-09	BAS3851	formamidase		
1.92E-07	BAS4914	general stress protein 20U		
1.89E-07	BAS0978	HIT family protein		
9.52E-09	BAS0228	homogentisate 1,2-dioxygenase, putative		
1.68E-06	BAS1052	isocitrate lyase		
1.80E-11	BAS0850	M20/M25/M40 family peptidase		

1.95E-12	BAS4591	M42 family peptidase		
0.000103	BAS4507	metal-dependent hydrolase		
1.89E-07	BAS3884	peptide deformylase		
4.56E-09	BAS4071	phosphate butyryltransferase		
1.41E-08	BAS3833	prophage LambdaBa02, repressor protein		
7.63E-05	BAS0777	purple acid phosphatase/fibronectin domain-containing protein		
1.07E-08	BAS5239	putative heme peroxidase		
6.44E-06	BAS2635	putative manganese-dependent inorganic pyrophosphatase		
7.70E-09	BAS0013	pyridoxal biosynthesis lyase PdxS		
1.29E-05	BAS0798	quinone family NAD(P)H dehydrogenase		
1.75E-14	BAS0047	regulatory protein SpoVG		
3.44E-08	BAS4377	ribonuclease PH		
4.80E-22	BAS4293	rrf2 family protein		
2.82E-16	BAS4177	superoxide dismutase, Mn		
6.10E-10	BAS0387	tellurium resistance protein		
2.21E-09	BAS4589	thioredoxin family protein		
0.005627	BAS4636	vrrB protein		
9.81E-10	BAS1763	xaa-pro aminopeptidase, putative		
		Fatty Acid Metabolism		
1.60E-09	BAS0832	acyl-CoA synthetase	bat00061, bat00071	Fatty acid biosynthesis, Fatty acid degradation
0.017675	BAS4420	enoyl-CoA hydratase	bat00071	Fatty acid degradation
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
8.56E-06	BAS4661	phosphoenolpyruvate carboxykinase	bat00010, bat00020, bat00620	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism
		Nucleotide Metabolism		
7.70E-09	BAS0006	DNA gyrase subunit A		
0.000128	BAS0046	endoribonuclease L-PSP, putative		
		Transcription and Protein translation		
1.42E-09	BAS3746	isoleucyl-tRNA synthetase		
2.22E-05	BAS2027	isoleucyl-tRNA synthetase		
3.15E-07	BAS0691	transcriptional activator TenA, putative		
		Sporulation-Germination Proteins		
		Vitamin metabolism		
5.04E-09	BAS0696	glycine oxidase	bat00730	Thiamine metabolism
5.23E-10	BAS0698	thiazole synthase	bat00730	Thiamine metabolism
1.47E-08	BAS4244	alkaline phosphatase	bat00627, bat00790	Aminobenzoate degradation, Folate biosynthesis
3.44E-10	BAS4021	6,7-dimethyl-8-ribityllumazine synthase	bat00740	Riboflavin metabolism
		Hypothetical Proteins		
1.19E-18	BAS2507	hypothetical protein		
2.84E-10	BAS2513	hypothetical protein		

2.58E-09	BAS0474	hypothetical protein		
4.48E-06	BAS4700	hypothetical protein		
1.89E-06	BAS3861	hypothetical protein		
8.87E-06	BAS4191	hypothetical protein		
9.44E-06	BAS3526	hypothetical protein		
7.92E-06	BAS1349	hypothetical protein		
1.61E-05	BAS1620	hypothetical protein		

Table 2B. Proteins Increased in Spores from Blood Medium Over Spores Produced in Horizon Soil

quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
3.12E-07	BAS1310	ketol-acid reductoisomerase	bat00290, bat01210, bat00770, bat01110	Valine, leucine and isoleucine biosynthesis, 2-Oxocarboxylic acid metabolism, Pantothenate and CoA biosynthesis,
0.00042	BAS1311	2-isopropylmalate synthase	bat00290, bat00620, bat01210, bat00770, bat01110	Valine, leucine and isoleucine biosynthesis, Pyruvate metabolism, 2-Oxocarboxylic acid metabolism
1.54E-13	BAS1625	asparagine synthetase, glutamine-hydrolyzing	bat00250, bat01110	Alanine, aspartate and glutamate metabolism, Biosynthesis of secondary metabolites
3.79E-08	BAS1825	homoserine dehydrogenase	bat00260, bat00270, bat00300, bat01110	Glycine, serine and threonine metabolism, Cysteine and methionine metabolism, Lysine biosynthesis, Biosynthesis of secondary metabolites
5.75E-10	BAS2095	asparagine synthetase, glutamine-hydrolyzing	bat00250, bat01110	Alanine, aspartate and glutamate metabolism, Biosynthesis of secondary metabolites
7.41E-14	BAS4067	3-methyl-2-oxobutanoate dehydrogenase, alpha subunit	bat00280, bat01110	Valine, leucine and isoleucine degradation
3.38E-17	BAS4066	3-methyl-2-oxobutanoate dehydrogenase, beta subunit	bat00280, bat01110	Valine, leucine and isoleucine degradation
6.31E-08	BAS4269	O-acetylserine lyase	bat00270	Cysteine and methionine metabolism
2.33E-08	BAS4271	putative AdoMet-dependent methyltransferase - hypothetical protein	bat00270	Cysteine and methionine metabolism
2.26E-16	BAS4879	proline dehydrogenase family protein	bat00330	Arginine and proline metabolism
1.73E-07	BAS3078	D-3-phosphoglycerate dehydrogenase, putative	bat00260, bat00680	Glycine, serine and threonine metabolism, Methane metabolism
		Membrane, Wall or Surface Proteins		
0.014311	BAS4723	ABC transporter, ATP-binding protein. ABC-type lipoprotein export system	bat02010	ABC transporters
2.17E-06	BAS0248	ABC transporter, ATP-binding protein - binding cassette domain of elongation factor 3	bat02011	ABC transporters
1.39E-12	BAS5281	ABC transporter, ATP-binding protein - binding cassette domain of elongation factor 3	bat02012	ABC transporters
0.000358	BAS2964	adhesion lipoprotein		Structural
1.60E-05	BAS0354	amino acid ABC transporter, ATP-binding protein	bat02012	ABC transporters
1.73E-08	BAS4334	bacitracin ABC transporter ATP-binding protein, ABC-2 type	bat02010	ABC-2 type transport system
0.00082	BAS3140	bacteriocin ABC transporter permease subunit, ABC-2 type transport system ATP-binding protein	bat_M00254	ABC-2 type transport system
0.037287	BAS2597	glycine betaine/L-proline ABC transporter, ATP-binding protein	bat02012	ABC transporters

0.005732	BAS2657	oligopeptide ABC transporter, oligopeptide-binding protein, putative	bat02010	ABC-2 type transport system
1.85E-06	BAS1102	oligopeptide ABC transporter, permease protein	bat02010	ABC-2 type transport system
3.44E-10	BAS0237	putative lipoprotein		Structural
2.30E-11	BAS5128	rod shape-determining protein Mbl		Structural
0.000947	BAS1048	S-layer protein, putative		Structural
7.81E-09	BAS3642	sugar ABC transporter, ATP-binding protein	bat02010	ABC sugar transport system
9.43E-08	BAS5137	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	bat00520, bat00550	Amino sugar and nucleotide sugar metabolism, Peptidoglycan biosynthesis
0.014311	BAS4723	ABC transporter, ATP-binding protein. ABC-type lipoprotein export system	bat02010	ABC transporters
		Other Enzymes and Proteins		
2.73E-05	BAS1263	acetyltransferase		
1.60E-05	BAS2680	acetyltransferase		
1.65E-09	BAS0197	aldo/keto reductase family oxidoreductase		
1.40E-10	BAS3758	cell division protein FtsA		
3.84E-10	BAS2977	chaperone protein hscC		
4.48E-06	BAS1961	DEAD-box ATP dependent DNA helicase		
4.65E-12	BAS2195	enoyl-CoA hydratase		
1.83E-08	BAS5154	F0F1 ATP synthase subunit epsilon		
0.001737	BAS0227	fumarylacetoacetate hydrolase family protein		
0.009898	BAS0405	general stress protein 26		
3.28E-14	BAS1936	glycosyl transferase family protein		
1.17E-06	BAS3326	glyoxalase family protein		
0.000279	BAS4338	GTPase ObgE		
0.01649	BAS1414	GTP-binding protein EngA		
2.15E-11	BAS5328	GTP-dependent nucleic acid-binding protein EngD		
9.39E-06	BAS3885	HAD superfamily hydrolase		
0.002101	BAS2017	HEAT repeat-containing PBS lyase		
2.08E-06	BAS4005	lolS protein		
0.004709	BAS4593	metallo-beta-lactamase family protein		
6.45E-09	BAS2361	metallo-beta-lactamase/rhodanese-like domain-containing protein		
0.000516	BAS0557	molybdopterin oxidoreductase family protein		
2.39E-19	BAS0147	mrp protein		
1.86E-08	BAS2002	N-acetyltransferase family protein		
0.001941	BAS0591	NorQ protein, putative		
4.20E-05	BAS3556	phage integrase family site specific recombinase		
3.81E-12	BAS3863	PhoH family protein		
2.05E-07	BAS3707	phosphatase, putative		
2.12E-13	BAS3958	phosphoenolpyruvate-protein phosphotransferase		
0.000156	BAS0838	preprotein translocase subunit SecA - A diverse family of proteins involved in ATP-dependent RNA or DNA		

		unwinding		
5.10E-09	BAS5038	preprotein translocase subunit SecA - A diverse family of proteins involved in ATP-dependent RNA or DNA unwinding		
3.56E-16	BAS4935	pyridine nucleotide-disulphide oxidoreductase		
9.55E-08	BAS4447	recombination and DNA strand exchange inhibitor protein		
5.23E-07	BAS0241	S1 RNA-binding domain-containing protein		
3.95E-22	BAS0525	SPFH domain-containing protein/band 7 family protein		
2.24E-13	BAS5300	superoxide dismutase, Mn		
2.24E-06	BAS0390	tellurite resistance protein, putative		
0.001941	BAS1576	TPR/glycosyl transferase domain-containing protein		
1.64E-12	BAS4523	universal stress protein		
		Fatty Acid Metabolism		
3.78E-14	BAS1019	long-chain-fatty-acid--CoA ligase	bat00061, bat00071	Fatty acid biosynthesis, Fatty acid degredation
1.23E-14	BAS4876	acetyl-CoA acetyltransferase	bat00071, bat00290, 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
2.84E-10	BAS3703	acyl-carrier-protein S-malonyltransferase	bat00061	Fatty acid biosynthesis
2.53E-08	BAS1840	acyl-CoA synthetase		
0.000253	BAS1017	lipoate-protein ligase A, putative	bat00785	Lipoic acid metabolism
1.68E-14	BAS4840	lipoyl synthase	bat00785	Lipoic acid metabolism
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
8.12E-18	BAS0481	formate acetyltransferase	bat00620, bat00640, bat00650	Pyruvate metabolism, Propanoate metabolism, Butanoate metabolism
0.002792	BAS0641	alcohol dehydrogenase, zinc-containing	bat00650	Butanoate metabolism
2.83E-14	BAS2111	alcohol dehydrogenase	bat00010, bat00071, bat00350, bat00625, bat00626	Glycolysis / Gluconeogenesis, Fatty acid degradation, Tyrosine metabolism, Chloroalkane and chloroalkene degradation, Naphthalene degradation
4.23E-09	BAS1176	dihydrolipoamide succinyltransferase	bat00020, bat00310	Citrate cycle (TCA cycle), Lysine degradation
0.005786	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
1.13E-15	BAS2376	acetoacetyl-CoA synthase	bat00010, bat00620, bat00640, bat00680, bat01110	Glycolysis / Gluconeogenesis, Pyruvate metabolism, Propanoate metabolism, Methane metabolism
0.000249	BAS2588	TPP-dependent acetoin dehydrogenase E1 alpha-subunit	bat00010, bat00020, bat00620	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism
1.04E-07	BAS2587	TPP-dependent acetoin dehydrogenase E1 beta-subunit	bat00010, bat00020,	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism

			bat00620	
7.29E-10	BAS2762	malate:quinone oxidoreductase	bat00020, bat00620	Citrate cycle (TCA cycle), Pyruvate metabolism
8.17E-07	BAS1726	acetyl-CoA hydrolase/transferase family protein	bat00020, bat00620, bat00650	Citrate cycle (TCA cycle), Pyruvate metabolism, Butanoate metabolism
2.74E-06	BAS3622	2-oxoglutarate ferredoxin oxidoreductase subunit beta	bat00020	Citrate cycle (TCA cycle)
5.43E-05	BAS2586	branched-chain alpha-keto acid dehydrogenase subunit E2	bat00010, bat00020, bat00620,	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism,
7.90E-06	BAS4773	gluconate 2-dehydrogenase	bat00030	Pentose phosphate pathway
2.75E-09	BAS3997	phosphopentomutase	bat00030	Pentose phosphate pathway
2.16E-05	BAS0668	quinol oxidase, subunit I	bat00190	Oxidative phosphorylation
2.19E-15	BAS0669	quinol oxidase, subunit II	bat00190	Oxidative phosphorylation
1.09E-11	BAS4789	UTP-glucose-1-phosphate uridylyltransferase		bat00040, bat00052
0.006241	BAS4869	L-lactate dehydrogenase	bat00010, bat00270, bat00620, bat00640	Glycolysis / Gluconeogenesis, Cysteine and methionine metabolism, Pyruvate metabolism, Propanoate metabolism
		Nucleotide Metabolism		
0.01649	BAS3995	pyrimidine-nucleoside phosphorylase	bat00240	Pyrimidine metabolism
0.000317	BAS0029	thymidylate kinase	bat00240	Pyrimidine metabolism
0.014311	BAS3398	anaerobic ribonucleoside triphosphate reductase	bat00230, bat00240	Purine metabolism, Pyrimidine metabolism
3.26E-12	BAS3676	uridylate kinase	bat00240	Pyrimidine metabolism
0.000287	BAS5164	uracil phosphoribosyltransferase	bat00240	Pyrimidine metabolism
		Transcription and Protein translation		
1.36E-09	BAS1408	30S ribosomal protein S1		
3.76E-07	BAS5325	30S ribosomal protein S18		
4.58E-07	BAS4472	threonyl-tRNA synthetase		
2.30E-11	BAS3683	tRNA (uracil-5-)-methyltransferase Gid		
2.70E-05	BAS4291	tRNA-specific 2-thiouridylase MnmA		
4.15E-10	BAS4936	tyrosyl-tRNA synthetase		
8.09E-11	BAS0306	aspartyl/glutamyl-tRNA amidotransferase subunit A		
2.18E-12	BAS0307	aspartyl/glutamyl-tRNA amidotransferase subunit B		
3.02E-05	BAS4784	glycyl-tRNA synthetase		
0.003028	BAS3670	prolyl-tRNA synthetase		
1.34E-05	BAS1014	LacI family sugar-binding transcriptional regulator		
0.000108	BAS4013	LacI family sugar-binding transcriptional regulator		
		Sporulation-Germination Proteins		
3.44E-08	BAS5185	stage 0 sporulation protein F		
2.17E-05	BAS5332	stage 0 sporulation protein J		
0.00017	BAS0731	stage V sporulation protein R		
1.20E-08	BAS3654	dipicolinate synthase subunit A		
		Vitamin Biosynthesis		
5.07E-08	BAS4023	biotin synthase	bat00780	biotin synthesis

6.40E-06	BAS4027	dithiobiotin synthetase	bat00780	biotin synthesis
1.82E-05	BAS4328	cysteine desulfurase	bat00730	Thiamine metabolism
7.99E-06	BAS5266	pyridoxal kinase	bat00750	Vitamin B6 metabolism
		Hypothetical Proteins		
0.045607	BAS0289	hypothetical protein		
0.000825	BAS4934	hypothetical protein		
0.006198	BAS2158	hypothetical protein		
0.001051	BAS3372	hypothetical protein		
0.000895	BAS1250	hypothetical protein		
0.004285	BAS2691	hypothetical protein		
0.001175	BAS0997	hypothetical protein		
6.40E-07	BAS3810	hypothetical protein		
0.000365	BAS1377	hypothetical protein		
2.67E-05	BAS2950	hypothetical protein		
0.000378	BAS4448	hypothetical protein		
2.33E-07	BAS1468	hypothetical protein		
4.23E-09	BAS2803	hypothetical protein		
2.16E-05	BAS3307	hypothetical protein		
5.98E-05	BAS1927	hypothetical protein		
4.87E-06	BAS0915	hypothetical protein		
1.24E-05	BAS0394	hypothetical protein		
4.67E-06	BAS3621	hypothetical protein		
5.69E-07	BAS0084	hypothetical protein		
1.36E-09	BAS3590	hypothetical protein		
3.75E-14	BAS2273	hypothetical protein		
1.75E-14	BAS2829	hypothetical protein		
4.67E-17	BAS0518	hypothetical protein		
1.45E-20	BAS2554	hypothetical protein		