Supplemental Table 3. Proteins Increased in Either Blood or Horizon media

Table 3A. Proteins Increased in Spores Produced on Horizon Soil Over Spores Produced on NB-CCY Medium

quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
3.05E-08	BAS0228	homogentisate 1,2-dioxygenase, putative	bat00350, bat00643	Tyrosine metabolism, Styrene degradation
0.008929	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
0.001652	BAS0331	5-methylribose kinase	bat00270	Cysteine and methionine metabolism
0.004482	BAS0498	glutamate synthase, large subunit, putative	bat00250, bat00910, bat01110	Alanine, aspartate and glutamate metabolism, Nitrogen metabolism
0.00936	BAS4521	alanine dehydrogenase	bat00250, bat00430	Alanine, aspartate and glutamate metabolism, Taurine and hypotaurine metabolism
0.010318	BAS0561	alanine dehydrogenase	bat00250, bat00430	Alanine, aspartate and glutamate metabolism, Taurine and hypotaurine metabolism
		Membrane, Wall or Surface Proteins		
0.000249	BAS0681	phosphate ABC transporter, phosphate-binding protein, putative	bat02010	
5.00E-05	BAS1049	S-layer protein, putative		Structural
0.00166	BAS1518	sodium/solute symporter family protein		
0.000623	BAS2277	N-acetylmuramoyl-L-alanine amidase		cell wall synthesis
0.00179	BAS1683	N-acetylmuramoyl-L-alanine amidase		cell wall synthesis
1.23E-05	BAS3022	ABC transporter, ATP-binding protein	bat02010	ABC-type lipoprotein export system, ATPase
1.47E-09	BAS3023	ABC transporter, permease protein, putative	bat02010	ABC-type antimicrobial peptide transport system, FtsX-like permease family, Defense mechanisms
3.10E-08	BAS4170	phosphate transport system regulatory protein PhoU, putative		
0.012047	BAS3475	phosphonate ABC transporter, phosphonate-binding protein, putative	bat02010	
5.03E-10	BAS3643	Bmp family lipoprotein		
0.023337	BAS0685	AcrB/AcrD/AcrF family transporter		
		Other Enzymes and Proteins		
4.39E-07	BAS2375	carboxyl transferase domain-containing protein		
0.001694	BAS1076	catalase		
0.00283	BAS2816	catalase		
7.93E-09	BAS1433	cytochrome b6		
0.000994	BAS2448	cytochrome P450		
0.001131	BAS3851	formamidase		
0.000891	BAS1859	intracellular serine protease		
0.000751	BAS3072	isochorismatase family protein		
0.013895	BAS1052	isocitrate lyase		
0.00011	BAS0567	neutral protease		
3.14E-07	BAS1812	NLP/P60 family protein		

0.007626	BAS2658	NLP/P60 family protein		
0.00654	BAS3884	peptide deformylase		
1.76E-05	BAS1227	phaP protein		
2.53E-06	BAS1229	phaR protein		
0.001674	BAS4071	phosphate butyryltransferase		
0.000166	BAS3484	prophage LambdaBa01 TPR domain-containing protein		
0.002585	BAS3833	prophage LambdaBa02, repressor protein		
0.049994	BAS0777	purple acid phosphatase/fibronectin domain-containing protein		
1.47E-09	BAS4293	rrf2 family protein		
0.000776	BAS1471	thermostable carboxypeptidase 1		
0.009304	BAS3687	succinyl-CoA synthetase subunit beta		
0.011512	BAS1621	alpha/beta fold family hydrolase		
0.000793	BAS3747	cell-division initiation protein DivIVA		
0.030881	BAS5182	fructose 1,6-bisphosphatase II		
		Fatty Acid Metabolism		
0.001103	BAS0832	acyl-CoA synthetase	bat00061, bat00071	Fatty acid biosynthesis, Fatty acid degradation
3.54E-07	BAS4089	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	bat00061, bat00620, bat00640, bat01110	Fatty acid biosynthesis, Pyruvate metabolism, Propanoate metabolism, Biosynthesis of secondary metabolites
1.56E-08	BAS4420	enoyl-CoA hydratase	bat00071	Fatty acid degradation
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
0.005501	BAS1177	2-oxoglutarate dehydrogenase E1 component	bat00020, bat00310, bat00380, bat01110	Citrate cycle (TCA cycle), Lysine degradation, Tryptophan metabolism, Biosynthesis of secondary metabolites
1.80E-07	BAS3348	aldehyde dehydrogenase	bat00010, bat00040, bat00053, bat00071, bat00280, bat00310, bat00330, bat00340, bat00380, bat00410, bat00561, bat00620, bat00625, bat00903, bat01110	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, Limonene and pinene degradation, Biosynthesis of secondary metabolites
0.011156	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, Biosynthesis of secondary metabolites
6.16E-08	BAS4486	malate dehydrogenase	bat00020, bat00270, bat00620, bat00630, bat00680, bat01110	Citrate cycle (TCA cycle), Cysteine and methionine metabolism, Pyruvate metabolism, Glyoxylate and dicarboxylate metabolism, Methane metabolism, Biosynthesis of secondary metabolites
0.000223	BAS4560	acetyl-CoA synthetase	bat00010, bat00620, bat00640,	Glycolysis / Gluconeogenesis, Pyruvate metabolism, Propanoate metabolism, Methane metabolism, Biosynthesis of secondary

			bat00680, bat01110	metabolites
0.024341	BAS4661	phosphoenolpyruvate carboxykinase	bat00010, bat00020, bat00620, bat01110	Glycolysis / Gluconeogenesis, Citrate cycle (TCA cycle), Pyruvate metabolism, Biosynthesis of secondary metabolites
		Nucleotide Metabolism		
0.046377	BAS0291	ATP-dependent DNA helicase PcrA		
0.000761	BAS2301	DEAD-box ATP dependent DNA helicase		
0.002023	BAS0006	DNA gyrase subunit A		
0.009482	BAS4202	putative metalloprotease		
0.027729	BAS0798	quinone family NAD(P)H dehydrogenase		
8.26E-06	BAS0047	regulatory protein SpoVG		
		Transcription and Protein translation		
0.011521	BAS0976	transcriptional regulator Hpr		
0.032523	BAS2027	isoleucyl-tRNA synthetase		
		Sporulation-Germination Proteins		
0.001652	BAS0041	yabG protein		
0.00129	BAS1145	spore coat protein Z		
8.38E-07	BAS1192	spore coat-associated protein		
0.004164	BAS2153	sporulation-control protein Spo0M, putative		
		Vitamin Metabolism		
0.00082	BAS0691	transcriptional activator TenA, putative	bat00730	Thiamine metabolism
0.001738	BAS0696	glycine oxidase	bat00730	Thiamine metabolism
0.00072	BAS0698	thiazole synthase	bat00730	Thiamine metabolism
0.002609	BAS4244	alkaline phosphatase	bat00627, bat00790	Aminobenzoate degradation, Folate biosynthesis
3.54E-07	BAS4089	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit		
0.000411	BAS4088	acetyl-CoA carboxylase biotin carboxylase subunit		
		Hypothetical Proteins		
0.000393	BAS2287	hypothetical protein		
0.014268	BAS4578	hypothetical protein		
0.014268	BAS4532	hypothetical protein		
0.014268	BAS3861	hypothetical protein		
0.000839	BAS3081	hypothetical protein		
0.001771	BAS4087	hypothetical protein		
0.024587	BAS4191	hypothetical protein		
0.030881	BAS3864	hypothetical protein		
0.002695	BAS2663	hypothetical protein		
0.000561	BAS2513	hypothetical protein		
0.008962	BAS5004	hypothetical protein		
0.005195	BAS2284	hypothetical protein		
0.017488	BAS2664	hypothetical protein		
0.027729	BAS4283	hypothetical protein		

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quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
2.59E-12	BAS1625	asparagine synthetase, glutamine-hydrolyzing	bat00250, bat01110	Alanine, aspartate and glutamate metabolism,
2.90E-06	BAS2268	aspartate-semialdehyde dehydrogenase	bat00260 , bat00261, bat00270, bat00300	Glycine, serine and threonine metabolism, Monobactam biosynthesis, Cysteine and methionine metabolism, Lysine biosynthesis
		Membrane, Wall or Surface Proteins		
7.13E-13	BAS0237	putative lipoprotein		Structural
3.82E-13	BAS2597	glycine betaine/L-proline ABC transporter, ATP-binding protein	bat02009	ABC transporter
9.33E-09	BAS2657	oligopeptide ABC transporter, oligopeptide-binding protein, putative	bat02010	ABC transporter
6.16E-08	BAS0607	amino acid ABC transporter, amino acid-binding protein	bat02010	ABC transporter
		Other Enzymes and Proteins		
1.42E-19	BAS0350	Rieske 2Fe-2S iron-sulfur protein, putative		
6.75E-15	BAS0405	general stress protein 26		
1.79E-08	BAS0525	SPFH domain-containing protein/band 7 family protein		
0.000301	BAS1414	GTP-binding protein EngA		
2.52E-13	BAS3707	phosphatase, putative		
2.63E-08	BAS3958	phosphoenolpyruvate-protein phosphotransferase		
0.003096	BAS0197	aldo/keto reductase family oxidoreductase		
4.09E-08	BAS2490	chitosanase		
9.04E-10	BAS0951	glyoxylase family protein		
0.001766	BAS0591	NorQ protein, putative		
1.50E-05	BAS3997	phosphopentomutase		
0.029624	BAS5128	rod shape-determining protein Mbl		
0.001766	BAS0241	S1 RNA-binding domain-containing protein		
2.93E-06	BAS0712	short chain dehydrogenase		
1.84E-13	BAS2562	spore cortex-lytic enzyme prepeptide		
3.59E-08	BAS4523	universal stress protein		
		Fatty Acid Metabolism		
0.003096	BAS1017	lipoate-protein ligase A, putative	bat00785	Lipoic acid metabolism
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
0.029624	BAS4773	gluconate 2-dehydrogenase	bat00030	Pentose phosphate pathway
6.53E-21	BAS0668	quinol oxidase, subunit I	bat00190	Oxidative phosphorylation
1.34E-23	BAS0669	quinol oxidase, subunit II	bat00190	Oxidative phosphorylation
0.029624	BAS4869	L-lactate dehydrogenase	bat00010, bat00270, bat00620, bat00640,	Glycolysis / Gluconeogenesis, Cysteine and methionine metabolism, Pyruvate metabolism, Propanoate metabolism

			bat01110	
1.72E-12	BAS1784	L-lactate dehydrogenase	bat00010, bat00270, bat00620, bat00640, bat01110	Glycolysis / Gluconeogenesis, Cysteine and methionine metabolism, Pyruvate metabolism, Propanoate metabolism
2.74E-13	BAS2111	alcohol dehydrogenase	bat00010, bat00071, bat00350, bat00625, bat00626, bat01110	Glycolysis / Gluconeogenesis, Fatty acid degradation, Tyrosine metabolism, Chloroalkane and chloroalkene degradation, Naphthalene degradation
2.90E-06	BAS2268	aspartate-semialdehyde dehydrogenase	bat00260, bat00270, bat00300, bat01110, bat01210, bat01230	Glycine, serine and threonine metabolism, Cysteine and methionine metabolism, Lysine biosynthesis, Biosynthesis of secondary metabolites, 2-Oxocarboxylic acid, biosynthesis of amino acids
1.91E-11	BAS0637	putative translaldolase	bat00030	Pentose phosphate pathway
9.22E-11	BAS2640	aldehyde dehydrogenase	bat00010, bat00040, bat00053, bat00071, bat00280, bat00310, bat00330, bat00340, bat00380, bat00410, bat00561, bat00620, bat00625, bat00903, bat01110	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, Limonene and pinene degradation,
		Nucleotide Metabolism		
0.001984	BAS0029	thymidylate kinase	bat00240	Pyrimidine metabolism
1.37E-19	BAS0254	GMP synthase	bat00230	Purine metabolism
2.09E-08	BAS3995	pyrimidine-nucleoside phosphorylase	bat00240	Pyrimidine metabolism
0.029624	BAS3676	uridylate kinase	bat00240	Pyrimidine metabolism
2.77E-05	BAS5164	uracil phosphoribosyltransferase	bat00240	Pyrimidine metabolism
		Transcription and Protein translation		
1.47E-05	BAS1408	30S ribosomal protein S1		
1.57E-08	BAS4784	glycyl-tRNA synthetase		
0.000186	BAS3670	prolyl-tRNA synthetase		
0.0001	BAS2361	metallo-beta-lactamase/rhodanese-like domain-containing protein	bat03018	RNA degradation
3.22E-09	BAS1522	metallo-beta-lactamase family protein	bat03018	RNA degradation
0.029624	BAS3683	tRNA (uracil-5-)-methyltransferase Gid		
		Sporulation-Germination Proteins		
6.82E-11	BAS4996	stage V sporulation protein AD		
0.000143	BAS0731	stage V sporulation protein R		
3.10E-07	BAS4338	GTPase ObgE - spo0B-associated GTP-binding protein		
		Vitamin metabolism		
4.22E-06	BAS5266	pyridoxal kinase	bat00750	Vitamin B6 metabolism

		Hypothetical Proteins		
0.029624	BAS4448	hypothetical protein		
0.029624	BAS4934	hypothetical protein		
2.99E-07	BAS1302	hypothetical protein		
2.09E-08	BAS3115	hypothetical protein		
1.42E-07	BAS2554	hypothetical protein		
4.98E-08	BAS1468	hypothetical protein		
2.97E-10	BAS4786	hypothetical protein		
3.61E-06	BAS0518	hypothetical protein		
1.33E-10	BAS2691	hypothetical protein		
1.72E-12	BAS1216	hypothetical protein		
4.78E-15	BAS2561	hypothetical protein		
4.78E-15	BAS3590	hypothetical protein		
4.78E-15	BAS1250	hypothetical protein		
7.32E-22	BAS0289	hypothetical protein		