

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_0136	<i>gerD</i> ; spore_germination_protein_GerD	3.83
BCE_G9241_0146	<i>glmS</i> ; glucosamine--fructose-6-phosphate_aminotransferase_isomerizing	2.40
BCE_G9241_0189	hypothetical_protein_protein	10.41
BCE_G9241_0195	hypothetical_protein_protein	5.58
BCE_G9241_0198	conserved_hypothetical_protein_protein_subfamily	2.05
BCE_G9241_0231	<i>hpcE-1</i> ; 2-hydroxyhepta-24-diene-17-dioate_isomerase	2.07
BCE_G9241_0232	<i>hmgA</i> ; homogentisate_12-dioxygenase	2.59
BCE_G9241_0347	ferrichrome_binding_protein	2.47
BCE_G9241_0348	ferrichrome_transport_permease_fhuB	4.64
BCE_G9241_0368	fatty_acid_desaturase	3.91
BCE_G9241_0370	amino_acid_ABC_transporter_periplasmic_amino_acid-binding_protein	2.14
BCE_G9241_0372	<i>glnQ</i> ; glutamine_ABC_transporter_ATP-binding_protein	2.14
BCE_G9241_0407	surface_protein	2.05
BCE_G9241_0415	cation-transporting_ATPase_E1-E2_family	8.04
BCE_G9241_0466	dihydroorotase	3.39
BCE_G9241_0467	conserved_hypothetical_protein_protein_TIGR01777	3.06
BCE_G9241_0499	<i>mrcA</i> ; penicillin-binding_protein_1A	4.03
BCE_G9241_0594	ubiquinone/menaquinone_biosynthesis_methyltransferase_UBIE	3.23
BCE_G9241_0635	hypothetical_protein_cytosolic_protein	6.67
BCE_G9241_0703	acriflavin_resistance_plasma_membrane_protein	2.68
BCE_G9241_0755	nitroreductase_family_protein_putative	4.20
BCE_G9241_0776	outer_surface_protein	5.99
BCE_G9241_0777	transcription_regulator_probable_putative	2.08
BCE_G9241_0778	PTS_system_IIA_component	6.19
BCE_G9241_0779	PTS_system_IIB_component	5.97
BCE_G9241_0780	<i>celB</i> ; PTS_system_IIC_component	5.80
BCE_G9241_0781	conserved_hypothetical_protein_protein	7.70
BCE_G9241_0782	outer_surface_protein	12.24
BCE_G9241_0785	<i>ybjZ</i> ; ABC_transporter_ATP-binding_protein	5.11
BCE_G9241_0786	ABC_transporter_ATP-binding_protein	5.32
BCE_G9241_0787	periplasmic_component_of_efflux_system	4.33
BCE_G9241_0788	hypothetical_protein_protein	3.26
BCE_G9241_0791	peptide_ABC_transporter_permease_protein_putative	2.03
BCE_G9241_0863	putative_transcriptional_regulator	2.04
BCE_G9241_0874	N-acetylmuramoyl-L-alanine_amidase	3.08
BCE_G9241_0882	sulfate_transporter	2.06
BCE_G9241_0883	hypothetical_protein_protein	2.06
BCE_G9241_0905	proline_racemase_putative	2.45
BCE_G9241_0906	<i>arcB</i> ; ornithine_cyclodeaminase	6.08
BCE_G9241_0907	hypothetical_protein_protein	9.57
BCE_G9241_1030	conserved_hypothetical_protein_protein	3.70
BCE_G9241_1031	conserved_hypothetical_protein_protein	39.89

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_1032	conserved_hypothetical_protein_protein	15.37
BCE_G9241_1037	glyoxalase_family_protein	2.35
BCE_G9241_1038	glyoxylase_family_protein	2.25
BCE_G9241_1052	<i>rep</i> ; ATP-dependent_DNA_helicase_rep	2.44
BCE_G9241_1053	ATP-dependent_DNA_helicase_rep	3.02
BCE_G9241_1092	<i>lfadD-7</i> ; ong-chain-fatty-acid--CoA_ligase	2.48
BCE_G9241_1097	dienelactone_hydrolase_domain_protein	2.05
BCE_G9241_1102	transcriptional_regulator_AraC_family_putative	4.13
BCE_G9241_1115	S-layer_homology_domain	2.52
BCE_G9241_1129	hypothetical_protein_cytosolic_protein	2.02
BCE_G9241_1174	hypothetical_protein_protein	2.13
BCE_G9241_1175	beta-ketoacyl_synthase_N-terminal_domain_protein	3.33
BCE_G9241_1189	hypothetical_protein_protein	2.54
BCE_G9241_1205	Hep_Hag_family	2.27
BCE_G9241_1228	ATP-dependent_DNA_helicase	2.03
BCE_G9241_1259	NADH_oxidase	2.01
BCE_G9241_1260	hypothetical_protein_cytosolic_protein	2.28
BCE_G9241_1261	conserved_hypothetical_protein_protein	3.49
BCE_G9241_1324	<i>maoC</i> ; enoyl-CoA_hydratase_R-specific	14.54
BCE_G9241_1325	PhaP_protein	11.38
BCE_G9241_1326	hypothetical_protein_protein	9.77
BCE_G9241_1327	transcriptional_regulator_PadR_family_putative	8.68
BCE_G9241_1328	PhaR_protein	4.73
BCE_G9241_1329	<i>fabG</i> ; 3-oxoacyl-(acyl-carrier-protein)_reductase	4.55
BCE_G9241_1330	polyhydroxyalkanoic_acid_synthase_VCA0688	5.98
BCE_G9241_1350	oligoendopeptidase_F_putative	2.24
BCE_G9241_1351	conserved_hypothetical_protein_protein	15.25
BCE_G9241_1353	sporulation_kinase	2.44
BCE_G9241_1380	muramoyltetrapeptide_carboxypeptidase_putative	4.34
BCE_G9241_1390	flavodoxin	5.86
BCE_G9241_1391	conserved_hypothetical_protein_protein	6.87
BCE_G9241_1422	imidazoleglycerol-phosphate_dehydratase	2.58
BCE_G9241_1423	<i>hisH</i> ; imidazole_glycerol_phosphate_synthase_glutamine_amidotransferase_subunit	2.73
BCE_G9241_1424	phosphoribosylformimino-5-aminoimidazole_carboxamide_ribose_isomerase	2.54
BCE_G9241_1425	conserved_hypothetical_protein_protein	2.74
BCE_G9241_1426	<i>hisF</i> ; imidazoleglycerol_phosphate_synthase_cyclase_subunit	2.72
BCE_G9241_1427	phosphoribosyl-AMP_cyclohydrolase	2.12
BCE_G9241_1428	phosphoribosyl-ATP_pyrophosphohydrolase	2.05
BCE_G9241_1431	MW2224	2.64
BCE_G9241_1451	conserved_hypothetical_protein_protein	6.40
BCE_G9241_1452	phage_shock_protein_A_putative	9.83
BCE_G9241_1453	transporter_yvqF	2.19

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_1454	sensor_histidine_kinase_VC1276	2.56
BCE_G9241_1455	<i>vraR</i> ; DNA-binding response regulator LuxR family	2.52
BCE_G9241_1468	hypothetical protein membrane Spanning protein	2.29
BCE_G9241_1481	<i>deoD</i> ; purine nucleoside phosphorylase	2.23
BCE_G9241_1483	<i>npr</i> ; predicted transposase	2.03
BCE_G9241_1484	hypothetical protein protein	2.84
BCE_G9241_1485	conserved hypothetical protein protein	2.10
BCE_G9241_1497	cytochrome c-type biogenesis protein putative	2.32
BCE_G9241_1501	cell wall endopeptidase family M23/M37	3.15
BCE_G9241_1525	<i>gpsA</i> ; NAD-dependent glycerol-3-phosphate dehydrogenase superfamily	2.67
BCE_G9241_1542	cytochrome b6-f complex iron-sulfur subunit putative	3.01
BCE_G9241_1543	menaquinol-cytochrome c reductase cytochrome b subunit	3.42
BCE_G9241_1544	cytochrome b-c complex cytochrome b subunit putative	4.62
BCE_G9241_1561	<i>panC</i> ; pantoate--beta-alanine ligase	2.18
BCE_G9241_1579	spore coat protein	2.29
BCE_G9241_1593	hypothetical protein protein	8.14
BCE_G9241_1605	conserved hypothetical protein protein	3.47
BCE_G9241_1617	hypothetical protein protein	2.12
BCE_G9241_1618	hypothetical protein protein	2.51
BCE_G9241_1619	hypothetical protein protein	2.75
BCE_G9241_1647	Na ⁺ /H ⁺ antiporter	5.26
BCE_G9241_1650	conserved hypothetical protein integral membrane protein putative	2.04
BCE_G9241_1654	hypothetical protein membrane Spanning protein	4.72
BCE_G9241_1721	VanZ like family family	2.03
BCE_G9241_1722	conserved hypothetical protein protein	3.99
BCE_G9241_1723	conserved hypothetical protein protein	2.92
BCE_G9241_1724	dienelactone hydrolase family	3.91
BCE_G9241_1725	JEMB	3.83
BCE_G9241_1726	transposase putative	3.69
BCE_G9241_1727	reticulocyte binding protein	5.23
BCE_G9241_1728	collagen adhesion protein	3.20
BCE_G9241_1751	conserved hypothetical protein protein	2.45
BCE_G9241_1772	<i>fumC</i> ; fumarate hydratase class II	4.28
BCE_G9241_1774	<i>fumC</i> ; fumarate hydratase class II	4.48
BCE_G9241_1818	conserved hypothetical protein protein	2.18
BCE_G9241_1828	<i>fabH</i> ; 3-oxoacyl-(acyl-carrier-protein) synthase III subfamily	6.89
BCE_G9241_1830	<i>hflX</i> ; GTP-binding protein hflX	3.14
BCE_G9241_1899	BNR/Asp-box repeat domain protein	7.49
BCE_G9241_1951	<i>appC</i> ; cytochrome d ubiquinol oxidase subunit I	13.42
BCE_G9241_1952	<i>cydB</i> ; cytochrome d ubiquinol oxidase subunit II	17.33
BCE_G9241_1953	ABC transporter ATP-binding protein CydD	29.09
BCE_G9241_1954	ABC transporter ATP-binding protein CydC	45.53
BCE_G9241_1963	nitroreductase family protein	3.23

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_1989	transcriptional_regulator_putative	3.24
BCE_G9241_1997	MW0093_putative	3.70
BCE_G9241_1998	siderophore_biosynthesis_protein_IucC_family	4.25
BCE_G9241_2001	conserved_hypothetical_protein_protein	4.34
BCE_G9241_2002	hypothetical_protein_cytosolic_protein	5.62
BCE_G9241_2016	ABC_transporter_permease_protein_putative	5.64
BCE_G9241_2023	conserved_hypothetical_protein_protein	2.76
BCE_G9241_2024	conserved_hypothetical_protein_protein	3.58
BCE_G9241_2031	<i>dps</i> ; non-specific_DNA-binding_protein_Dps / _iron-binding_ferritin-like_antioxidant_protein / _ferroxidase	5.02
BCE_G9241_2032	conserved_hypothetical_protein_protein	2.79
BCE_G9241_2036	flavin_monoamine_oxidase-related_protein	2.34
BCE_G9241_2060	acyl-CoA_hydrolase	2.04
BCE_G9241_2069	CBS_domain_protein	3.31
BCE_G9241_2079	conserved_hypothetical_protein_protein	4.93
BCE_G9241_2080	stomatin-like_protein	5.79
BCE_G9241_2081	hypothetical_protein_protein	5.65
BCE_G9241_2131	hypothetical_protein_conserved_protein_putative	2.60
BCE_G9241_2150	siroheme_synthase_putative	2.03
BCE_G9241_2151	transcriptional_regulator_NirR_putative	2.84
BCE_G9241_2176	bacillolysin	2.41
BCE_G9241_2200	hypothetical_protein_protein	3.96
BCE_G9241_2201	penicillin-binding_protein	28.62
BCE_G9241_2214	cytochrome_c_oxidase_Cu(A)_center_assembly_protein	2.42
BCE_G9241_2229	<i>adhP</i> ; alcohol_dehydrogenase_propanol-preferring	4.33
BCE_G9241_2230	oligopeptide_transport_system_permease_protein_oppC	3.63
BCE_G9241_2262	<i>ctfA</i> ; butyrate-acetoacetate_CoA-transferase_subunit_A	2.31
BCE_G9241_2263	coenzyme_A_transferase_beta_subunit	2.68
BCE_G9241_2264	peptidase_M20/M25/M40_family_putative	2.96
BCE_G9241_2265	beta-lysine_acetyltransferase	2.24
BCE_G9241_2268	<i>kamA</i> ; L-lysine_23-aminomutase	26.24
BCE_G9241_2269	YokU	11.83
BCE_G9241_2277	sporulation-control_protein	3.90
BCE_G9241_2283	conserved_hypothetical_protein_protein	3.18
BCE_G9241_2309	penicillin-binding_protein_1A	2.35
BCE_G9241_2314	<i>mmgE</i> ; 2-methylcitrate_dehydratase	3.06
BCE_G9241_2315	<i>prpB</i> ; methylisocitrate_lyase	2.65
BCE_G9241_2317	<i>acdA</i> ; acyl-CoA_dehydrogenase_short-chain_specific	2.59
BCE_G9241_2318	3-hydroxyisobutyrate_dehydrogenase	2.45
BCE_G9241_2319	<i>mmsA</i> ; methylmalonate-semialdehyde_dehydrogenase	3.31
BCE_G9241_2322	enol-CoA_hydratase/isomerase_family_protein	3.30
BCE_G9241_2334	<i>dhbC</i> ; isochorismate_synthase	3.48
BCE_G9241_2335	yersiniabactin_synthetase_salicylate_ligase_component	11.63
BCE_G9241_2336	<i>dhbB</i> ; isochorismatase	5.31

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_2337	reticulocyte_binding_protein	6.86
BCE_G9241_2339	drug_transporter_putative	8.91
BCE_G9241_2340	EntD/Gsp/HetI/Sfp_family_protein_putative	3.26
BCE_G9241_2344	DinB_protein	2.16
BCE_G9241_2345	alkaline_protease_A	3.96
BCE_G9241_2353	ABC_transporter_ATP-binding_protein	2.86
BCE_G9241_2354	ABC_transporter_permease_protein_probable_SP0913_putative	3.58
BCE_G9241_2387	cold_shock_protein-related_protein	2.05
BCE_G9241_2420	<i>omt</i> ; caffeoyl-CoA_O-methyltransferase	6.84
BCE_G9241_2421	tellurite_resistance_protein	3.59
BCE_G9241_2422	conserved_hypothetical_protein_protein	3.13
BCE_G9241_2460	SpoIIISA_like_protein	3.02
BCE_G9241_2461	SpoIIISA_like_protein	2.56
BCE_G9241_2464	<i>pepD-2</i> ; aminoacyl-histidine_dipeptidase	2.51
BCE_G9241_2465	hypothetical_protein_protein	2.58
BCE_G9241_2468	Patatin-like_phospholipase_family	2.00
BCE_G9241_2503	<i>crt</i> ; 3-hydroxybutyryl-CoA_dehydratase	2.64
BCE_G9241_2504	<i>pccB</i> ; propionyl-CoA_carboxylase_beta_chain	4.87
BCE_G9241_2505	<i>acs-4</i> ; acetyl-CoA_synthetase	3.82
BCE_G9241_2535	oligoendopeptidase_putative	3.13
BCE_G9241_2550	formamidase	2.87
BCE_G9241_2555	ABC_transporter_ATP-binding_protein_putative	4.92
BCE_G9241_2556	acetyltransferase	7.27
BCE_G9241_2575	conserved_hypothetical_protein_protein	2.72
BCE_G9241_2579	<i>cypA</i> ; cytochrome_P450	4.73
BCE_G9241_2580	transporter_putative	5.65
BCE_G9241_2581	streptogramin_A_acetyl_transferase	6.27
BCE_G9241_2590	macrolide_glycosyltransferase	2.07
BCE_G9241_2612	DegV_family_protein_putative	2.08
BCE_G9241_2654	outer_membrane_protein_romA	2.36
BCE_G9241_2656	YwqG-like_protein	2.95
BCE_G9241_2657	putative_esterase_family	7.09
BCE_G9241_2658	conserved_hypothetical_protein_protein	5.82
BCE_G9241_2675	conserved_hypothetical_protein_protein	2.18
BCE_G9241_2726	uridine_kinase_putative	2.21
BCE_G9241_2738	<i>rpiA</i> ; ribose_5-phosphate_isomerase	4.20
BCE_G9241_2740	hypothetical_protein_protein	17.84
BCE_G9241_2741	chitin-binding_protein_putative	18.66
BCE_G9241_2762	Butirosin_biosynthesis_protein_BtrG	2.19
BCE_G9241_2788	conserved_hypothetical_protein_protein	3.67
BCE_G9241_2789	conserved_hypothetical_protein_protein	2.82
BCE_G9241_2800	cell_wall-associated_hydrolase	3.71
BCE_G9241_2801	mandelate_racemase/muconate_lactonizing_enzyme_family_protein	4.47
BCE_G9241_2812	X-pro_dipeptidyl-peptidase_putative	2.16

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_2857	hypothetical_protein_protein	6.04
BCE_G9241_2871	hypothetical_protein_protein	16.98
BCE_G9241_2897	PTS_system_IIC_component_putative	2.14
BCE_G9241_2902	hypothetical_protein_protein	2.81
BCE_G9241_2903	transcriptional_regulator_putative	2.81
BCE_G9241_2904	hypothetical_protein_protein	2.78
BCE_G9241_2905	hypothetical_protein_protein	3.13
BCE_G9241_2936	fructose-bisphosphate_aldolase	2.42
BCE_G9241_2939	glyoxalase_family_protein_superfamily	2.00
BCE_G9241_2941	antibiotic_biosynthesis_monooxygenase_domain_protein	3.64
BCE_G9241_2971	<i>moxR</i> ; ATPase_MoxR_family	3.60
BCE_G9241_2972	hypothetical_protein_secreted_protein	3.31
BCE_G9241_2973	hypothetical_protein_membrane_Spanning_protein	3.16
BCE_G9241_2986	<i>phnA</i> ; alkylphosphonate_utilization_operon_protein_PhnA	6.06
BCE_G9241_2987	sulfate_permease_family_protein_VCA0077	8.76
BCE_G9241_2988	transcriptional_regulator_arsR_family	4.33
BCE_G9241_3046	short-chain-specific_acyl-CoA_dehydrogenase	3.44
BCE_G9241_3047	EpiH/GdmH-related_protein	3.11
BCE_G9241_3048	acetyltransferase_GNAT_family	2.22
BCE_G9241_3060	metal-dependent_hydrolase	2.02
BCE_G9241_3100	hydrolase_isochorismatase_family	2.14
BCE_G9241_3150	transposase_(IS4_family)_domain_protein	2.25
BCE_G9241_3151	conserved_hypothetical_protein_protein	2.41
BCE_G9241_3170	NADPH-cytochrome_P450_reductase	2.07
BCE_G9241_3187	putative_phosphohydrolases_Icc_family	2.53
BCE_G9241_3188	penicillin-binding_protein	2.23
BCE_G9241_3201	permease_putative	4.69
BCE_G9241_3208	MccC_family_protein	2.19
BCE_G9241_3211	conserved_hypothetical_protein_protein	2.44
BCE_G9241_3212	<i>serA</i> ; D-isomer_specific_2-hydroxyacid_dehydrogenase_family_protein	2.68
BCE_G9241_3213	<i>serC</i> ; phosphoserine_aminotransferase	2.14
BCE_G9241_3220	penicillin_G_acylase_putative	2.49
BCE_G9241_3227	internalin	2.36
BCE_G9241_3236	6-aminohexanoate-dimer_hydrolase	3.10
BCE_G9241_3249	SWIM_zinc_finger_family	2.26
BCE_G9241_3252	conserved_hypothetical_protein_protein	4.71
BCE_G9241_3278	conserved_hypothetical_protein_protein	2.25
BCE_G9241_3280	conserved_hypothetical_protein_protein	2.83
BCE_G9241_3309	collagen-like_triple_helix_repeat_protein	2.06
BCE_G9241_3317	conserved_hypothetical_protein_protein	2.05
BCE_G9241_3318	ATP_synthase_protein_I	2.55
BCE_G9241_3323	dTDP-glucose_46-dehydratase_putative	2.05
BCE_G9241_3325	CDP-4-dehydro-6-deoxy-D-gulose_4-reductase	2.01

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_3395	AiiA-like_enzyme	2.06
BCE_G9241_3399	alcohol dehydrogenase zinc-containing	2.92
BCE_G9241_3412	ferrichrome ABC transporter permease protein	2.35
BCE_G9241_3425	acetyltransferase GNAT family	2.01
BCE_G9241_3460	hy	3.33
BCE_G9241_3477	hypothetical protein protein	2.43
BCE_G9241_3491	reticulocyte binding protein	2.67
BCE_G9241_3496	D-alanyl-D-alanine carboxypeptidase	2.50
BCE_G9241_3500	<i>dhaS</i> ; aldehyde dehydrogenase family protein	4.28
BCE_G9241_3504	integral membrane protein	2.21
BCE_G9241_3543	ABC transporter permease protein putative	2.43
BCE_G9241_3544	ABC transporter ATP-binding protein	2.62
BCE_G9241_3554	<i>nrdG</i> ; anaerobic_ribonucleoside-triphosphate reductase activating protein	10.01
BCE_G9241_3555	anaerobic_ribonucleoside-triphosphate reductase putative	8.06
BCE_G9241_3572	conserved hypothetical protein protein	2.47
BCE_G9241_3573	spore_coat_protein_L-related_protein	2.63
BCE_G9241_3580	<i>fadA-2</i> ; 3-ketoacyl-CoA thiolase	2.02
BCE_G9241_3589	CsbD-like family	12.74
BCE_G9241_3597	phospholipase/carboxylesterase family protein	2.77
BCE_G9241_3598	glyoxalase family protein putative	3.21
BCE_G9241_3599	<i>opuE</i> ; sodium/proline symporter	2.08
BCE_G9241_3603	<i>carD</i> ; CarD-like transcriptional regulator	4.78
BCE_G9241_3604	<i>hutG</i> ; formiminoglutamase	4.47
BCE_G9241_3605	<i>hutI</i> ; imidazolonepropionase	7.65
BCE_G9241_3606	<i>hutU</i> ; urocanate hydratase	6.26
BCE_G9241_3623	CcdC protein	3.12
BCE_G9241_3624	cytochrome c-type biogenesis protein putative	4.39
BCE_G9241_3664	N-acetylmuramoyl-L-alanine amidase	3.13
BCE_G9241_3672	<i>pXOI-18</i> ; DNA integration/recombination/inversion protein	3.85
BCE_G9241_3673	hypothetical protein membrane Spanning protein	2.06
BCE_G9241_3695	copper-translocating P-type ATPase	4.61
BCE_G9241_3696	<i>pacS</i> ; cation-transporting ATPase P-type	6.80
BCE_G9241_3700	IroE protein	2.78
BCE_G9241_3736	phosphoglycerol transferase	8.40
BCE_G9241_3797	YlxP-like protein	2.01
BCE_G9241_3814	<i>codY</i> ; transcriptional regulator CodY	3.59
BCE_G9241_3815	<i>hslU</i> ; heat shock protein HslVU ATPase subunit HslU	3.05
BCE_G9241_3816	<i>clpQ</i> ; heat shock protein HslV	2.50
BCE_G9241_3820	MW1132	4.23
BCE_G9241_3834	<i>fabG</i> ; 3-oxoacyl-(acyl-carrier-protein) reductase	2.40
BCE_G9241_3866	hypothetical protein membrane Spanning protein	2.60
BCE_G9241_3931	cytochrome c oxidase subunit III	3.72
BCE_G9241_3932	<i>qoxA</i> ; quinol oxidase subunit I	3.77

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_3933	cytochrome_c_oxidase_polypeptide_II	3.06
BCE_G9241_3935	<i>ctaA</i> ; cytochrome oxidase assembly protein	2.02
BCE_G9241_3996	<i>metE</i> ; 5-methyltetrahydropteroyltrimethylglutamate--_homocysteine_S-methyltransferase	3.11
BCE_G9241_4002	conserved_hypothetical_protein_protein	9.65
BCE_G9241_4042	conserved_hypothetical_protein_protein	3.36
BCE_G9241_4043	conserved_hypothetical_protein_protein	6.54
BCE_G9241_4108	alpha/beta hydrolase	2.12
BCE_G9241_4117	<i>ribD</i> ; riboflavin_biosynthesis_protein_RibD	3.31
BCE_G9241_4118	<i>ribE</i> ; riboflavin_synthase_alpha_subunit	4.17
BCE_G9241_4119	<i>ribBA</i> ; 34-dihydroxy-2-butanone_4-phosphate_synthase/GTP_cyclohydrolase_II	4.95
BCE_G9241_4120	<i>ribH</i> ; 6, 7-dimethyl-8-ribityllumazine_synthase	6.71
BCE_G9241_4128	conserved_hypothetical_protein_protein	2.13
BCE_G9241_4133	transcriptional_regulator_MarR_family_putative	2.56
BCE_G9241_4173	MutT/nudix_family_protein	2.04
BCE_G9241_4195	cell wall surface anchor family protein putative	2.48
BCE_G9241_4196	transposase_IS4_family_putative	4.52
BCE_G9241_4249	hypothetical_protein_protein	3.06
BCE_G9241_4250	conserved_hypothetical_protein_protein	9.61
BCE_G9241_4260	conserved_hypothetical_protein_protein	2.79
BCE_G9241_4273	transposase (IS4 family) domain protein	2.07
BCE_G9241_4308	superoxide_dismutase	2.20
BCE_G9241_4387	hypothetical_protein_membrane_Spanning_protein	2.03
BCE_G9241_4388	conserved_hypothetical_protein_protein	2.75
BCE_G9241_4389	spore_germination_protein_xc_precursor_bacillus	3.70
BCE_G9241_4393	transposase	2.38
BCE_G9241_4400	transposase_X	7.66
BCE_G9241_4406	<i>npr</i> ; predicted_transposase	3.34
BCE_G9241_4508	<i>mreC</i> ; rod_shape-determining_protein_MreC	2.45
BCE_G9241_4531	hypothetical_protein_protein	6.45
BCE_G9241_4532	conserved_hypothetical_protein_protein	7.75
BCE_G9241_4671	maoC_family_protein	2.31
BCE_G9241_4695	<i>pepQ</i> ; proline_dipeptidase	2.08
BCE_G9241_4707	<i>ald</i> ; alanine_dehydrogenase	2.03
BCE_G9241_4709	universal_stress_protein_family	5.84
BCE_G9241_4714	conserved_hypothetical_protein_protein	2.41
BCE_G9241_4715	cysteine-rich_protein	3.14
BCE_G9241_4729	<i>acs-6</i> ; acetyl-CoA_synthetase	4.67
BCE_G9241_4753	<i>acuC</i> ; acetoin_utilization_protein_AcuC	5.25
BCE_G9241_4754	hydrolase_alpha/beta_fold_family_putative	3.42
BCE_G9241_4782	nicotinate_phosphoribosyltransferase	2.22
BCE_G9241_4800	transcriptional_regulator_DeoR_family-related_protein	5.08
BCE_G9241_4810	<i>carD</i> ; CarD-like_transcriptional_regulator	2.70

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO ₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_4836	Na ⁺ /H ⁺ _antiporter_putative	5.99
BCE_G9241_4837	TrkA_C-terminal_domain_protein	3.23
BCE_G9241_4838	DNA_integration/recombination/inversion_protein	2.31
BCE_G9241_4913	conserved_hypothetical_protein_protein	6.49
BCE_G9241_4921	cell_surface_protein	2.73
BCE_G9241_4922	hypothetical_protein_protein	2.08
BCE_G9241_4923	conserved_hypothetical_protein_protein	4.13
BCE_G9241_4956	hypothetical_protein_protein	4.38
BCE_G9241_4957	hypothetical_protein_protein	3.31
BCE_G9241_5024	transcriptional_regulator_DeoR_family	2.35
BCE_G9241_5067	DNA-binding_protein	2.07
BCE_G9241_5069	cell_wall_endopeptidase_family_M23/M37	2.41
BCE_G9241_5102	<i>acd-7</i> ; acyl-CoA_dehydrogenase	7.44
BCE_G9241_5103	hypothetical_protein_protein	9.48
BCE_G9241_5104	<i>atoB-4</i> ; acetyl-CoA_acetyltransferase	9.05
BCE_G9241_5105	<i>hbd-1</i> ; putative_3-hydroxyacyl-CoA_dehydrogenase_FadB	12.11
BCE_G9241_5106	hypothetical_protein_protein	7.34
BCE_G9241_5108	hypothetical_protein_protein	4.17
BCE_G9241_5109	D-alanyl-D-alanine_carboxypeptidase_putative	2.48
BCE_G9241_5133	DedA_family_protein_putative	3.06
BCE_G9241_5166	IG_hypothetical_protein_16995	3.02
BCE_G9241_5196	hypothetical_protein_protein	3.32
BCE_G9241_5199	iron_compound_ABC_transporter_ATP-binding_protein	4.24
BCE_G9241_5200	iron_compound_ABC_transporter_permease_protein	3.81
BCE_G9241_5201	iron_compound_ABC_transporter_permease_protein	4.52
BCE_G9241_5202	iron(III)_ABC_transporter_periplasmic_binding_protein_putative	4.03
BCE_G9241_5231	<i>crh</i> ; phosphocarrier_protein_Hpr	2.14
BCE_G9241_5236	integral_membrane_protein	2.11
BCE_G9241_5273	ribosomal_subunit_interface_protein	2.47
BCE_G9241_5355	integral_membrane_protein	4.25
BCE_G9241_5423	phosphoglycerate_transporter_protein	7.31
BCE_G9241_5459	<i>alkK-2</i> ; medium-chain_acyl-CoA_ligase	4.33
BCE_G9241_5469	NADH-ubiquinone_oxidoreductase_NQO10_subunit_(NQO10)_putative	2.10
BCE_G9241_5470	<i>nuoI</i> ; NADH-ubiquinone_oxidoreductase_NQO9_subunit_(NQO9)	2.78
BCE_G9241_5515	transcriptional_regulator_tetR_family	2.12
BCE_G9241_5516	<i>acdA</i> ; acyl-CoA_dehydrogenase_short-chain_specific	2.44
BCE_G9241_5531	collagen_adhesin_protein	2.88
BCE_G9241_5563	<i>fhuB</i> ; ferrichrome_transport_permease_fhuB	2.80
BCE_G9241_5623	acriflavin_resistance_plasma_membrane_protein	3.04
BCE_G9241_CNI_0001	transposase_(IS4_family)_domain_protein	2.03
BCE_G9241_CNI_0048	<i>pXOI-80</i> ; peptidase_M23/M37_family	2.05
BCE_G9241_CNI_0049	reticulocyte_binding_protein	2.85
BCE_G9241_CNI_0053	conserved_hypothetical_protein_protein	2.42

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_CNI_0054	transposase_(IS4_family)_domain_protein	2.29
BCE_G9241_CNI_0055	acetyltransferase GNAT_family_family	2.06
BCE_G9241_CNI_0123	transcriptional_regulator GntR_family	2.08
BCE_G9241_CNI_0125	conserved_hypothetical_protein_protein	8.91
BCE_G9241_CNI_0139	main_capsid_protein_Gp34-like_protein	2.32
BCE_G9241_CNI_0141	protein_gp8	2.63
BCE_G9241_CNI_0142	gp9_putative	2.41
BCE_G9241_CNI_0143	conserved_hypothetical_protein_protein	2.76
BCE_G9241_CNI_0144	major_capsid_protein_gpP	3.20
BCE_G9241_CNI_0145	gp14_-like_protein	3.25
BCE_G9241_CNI_0152	major_capsid_protein_gpP	3.21
BCE_G9241_CNI_0154	protein_gp15	3.19
BCE_G9241_CNI_0155	<i>carB</i> ; carbamoyl-phosphate_synthase_large_subunit_domain_protein	3.15
BCE_G9241_CNI_0166	conserved_hypothetical_protein_protein	3.21
BCE_G9241_CNI_0215	peptidase_M23/M37_family_putative	2.19
BCE_G9241_CNI_0216	glutaredoxin-like_protein NrdH-related_protein	2.68
BCE_G9241_CNI_0217	conserved_hypothetical_protein_protein	2.75
BCE_G9241_CNI_0218	conserved_hypothetical_protein_protein	2.96
BCE_G9241_CNI_0219	hypothetical_protein_protein	3.07
BCE_G9241_CNI_0220	hypothetical_protein_protein	3.11
BCE_G9241_CNI_0222	conserved_hypothetical_protein_protein	2.84
BCE_G9241_CNI_0223	hypothetical_protein_protein	3.04
BCE_G9241_CNI_0224	conserved_hypothetical_protein_protein	2.85
BCE_G9241_CNI_0225	hypothetical_protein_protein	2.50
BCE_G9241_CNI_0248	transposase_for_insertion_sequence_element_is231e	2.06
BCE_G9241_CNI_0261	adhesin_protein	3.69
BCE_G9241_CNI_0265	acetyltransferase	2.55
BCE_G9241_CNI_0284	membrane_protein	2.01
BCE_G9241_CNI_0314	transposase_(IS4_family)_domain_protein	2.10
BCE_G9241_pBC218_0008	conserved_hypothetical_protein_protein	8.62
BCE_G9241_pBC218_0010	hypothetical_protein_protein	47.05
BCE_G9241_pBC218_0011	hypothetical_protein_protein	50.77
BCE_G9241_pBC218_0012	<i>pXO2-42</i> ; S-layer_protein/_peptidoglycan_endo-beta-N-acetylglucosaminidase	28.56
BCE_G9241_pBC218_0013	periplasmic_component_of_efflux_system	11.27
BCE_G9241_pBC218_0015	phosphoglycerate_transporter_protein	2.92
BCE_G9241_pBC218_0017	ABC_transporter_ATP-binding_protein	2.73
BCE_G9241_pBC218_0018	<i>ybjZ</i> ; ABC_transporter_ATP-binding_protein	2.64
BCE_G9241_pBC218_0020	DNA-binding_response_regulator_VicR	2.09
BCE_G9241_pBC218_0021	sensory_box_histidine_kinase_VicK_putative	2.00
BCE_G9241_pBC218_0024	protease_HhoA	7.46
BCE_G9241_pBC218_0025	hypothetical_protein_protein	53.30
BCE_G9241_pBC218_0026	protective_antigen	40.13
BCE_G9241_pBC218_0027	lethal_factor_precursor	30.70

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_pBC218_0030	transposase	2.09
BCE_G9241_pBC218_0031	transposase IS3 family interruption	3.06
BCE_G9241_pBC218_0033	transposase IS3 family interruption	3.29
BCE_G9241_pBC218_0034	pVS1 resolvase	6.11
BCE_G9241_pBC218_0035	collagen triple helix repeat protein putative	2.02
BCE_G9241_pBC218_0037	IS861 transposase OrfB putative	2.06
BCE_G9241_pBC218_0038	transposase	2.54
BCE_G9241_pBC218_0039	enterotoxin_B	42.88
BCE_G9241_pBC218_0040	non-hemolytic enterotoxin lytic component L1	75.72
BCE_G9241_pBC218_0042	non-hemolytic enterotoxin lytic component L2 putative	24.70
BCE_G9241_pBC218_0043	S-layer homology domain protein	41.00
BCE_G9241_pBC218_0044	serine protease DO	2.29
BCE_G9241_pBC218_0045	<i>pXO1-109</i> ; transcriptional regulator <i>arsR</i> family	54.40
BCE_G9241_pBC218_0046	membrane protein putative	77.91
BCE_G9241_pBC218_0047	probable electron transfer protein Rv1937 putative	89.28
BCE_G9241_pBC218_0048	<i>cysK</i> ; cysteine synthase A	50.40
BCE_G9241_pBC218_0049	<i>pXO2-61</i> ; trans-acting positive regulator (Atx_A)	2.52
BCE_G9241_pBC218_0051	transposase	2.10
BCE_G9241_pBC218_0055	<i>yngK-1</i> ; YngK protein	6.87
BCE_G9241_pBC218_0057	pXO1_ORF14-like protein	25.96
BCE_G9241_pBC218_0058	collagen adhesion protein	2.56
BCE_G9241_pBC218_0059	polysaccharide translocase protein putative	39.13
BCE_G9241_pBC218_0060	CMP-sialic acid synthetase putative	40.68
BCE_G9241_pBC218_0061	UDP-N-acetylglucosamine 2-epimerase putative	44.33
BCE_G9241_pBC218_0062	sialic acid synthase putative	18.34
BCE_G9241_pBC218_0063	glycosyl transferase putative	77.14
BCE_G9241_pBC218_0064	<i>galU</i> ; UTP-glucose-1-phosphate uridylyltransferase	42.26
BCE_G9241_pBC218_0065	exopolysaccharide biosynthesis protein	57.93
BCE_G9241_pBC218_0066	<i>wzz</i> ; chain length determinant protein	39.44
BCE_G9241_pBC218_0067	transcriptional regulator LytR family	21.08
BCE_G9241_pBC218_0068	hypothetical protein protein	8.71
BCE_G9241_pBC218_0069	polysaccharide capsule synthesis protein	22.30
BCE_G9241_pBC218_0070	hypothetical protein protein	13.21
BCE_G9241_pBC218_0071	glycosyl transferase WecB/TagA/CpsF family	11.79
BCE_G9241_pBC218_0072	<i>wzy</i> ; polysaccharide polymerase	9.07
BCE_G9241_pBC218_0073	glycosyl transferase group 2 family protein	15.82
BCE_G9241_pBC218_0075	first of two overlapping orfs with similarity to IS3 genes	10.51
BCE_G9241_pBC218_0076	transposase	10.37
BCE_G9241_pBC218_0079	transposase (IS4 family)	7.00
BCE_G9241_pBC218_0080	MAEBL putative	2.23
BCE_G9241_pBC218_0081	<i>dnaX</i> ; DNA polymerase III gamma and tau subunits	7.30
BCE_G9241_pBC218_0082	<i>tnpB</i> ; transposase_all7245	11.06
BCE_G9241_pBC218_0084	DNA polymerase III gamma and tau subunits putative	2.25
BCE_G9241_pBC218_0085	restriction endonuclease family	2.88

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_pBC218_0086	SEC-C_motif_domain_protein	2.05
BCE_G9241_pBC218_0088	hypothetical_protein_protein	4.36
BCE_G9241_pBC218_0089	conserved_hypothetical_protein_protein	2.02
BCE_G9241_pBC218_0096	conserved_hypothetical_protein_protein_subfamily	3.71
BCE_G9241_pBC218_0097	hypothetical_protein_cytosolic_protein	3.30
BCE_G9241_pBC218_0098	hypothetical_protein_protein	2.88
BCE_G9241_pBC218_0099	hypothetical_protein_protein	2.45
BCE_G9241_pBC218_0104	geranylgeranyl_hydrogenase_BchP_putative	7.68
BCE_G9241_pBC218_0106	metallo-beta-lactamase_superfamily_protein	2.84
BCE_G9241_pBC218_0107	hypothetical_protein_protein	6.12
BCE_G9241_pBC218_0108	hypothetical_protein_protein	2.68
BCE_G9241_pBC218_0119	lipoprotein_NLP/P60_family	28.54
BCE_G9241_pBC218_0120	membrane_protein_putative	22.39
BCE_G9241_pBC218_0121	hypothetical_protein_protein	6.17
BCE_G9241_pBC218_0122	conserved_hypothetical_protein_protein	3.10
BCE_G9241_pBC218_0126	pXO1_ORF16-like_protein	2.76
BCE_G9241_pBC218_0128	<i>gnd</i> ; 6-phosphogluconate_dehydrogenase_decarboxylating	2.64
BCE_G9241_pBC218_0132	pXO1_ORF14-like_protein	2.03
BCE_G9241_pBC218_0133	hypothetical_protein_protein	3.20
BCE_G9241_pBC218_0134	hypothetical_protein_protein	3.44
BCE_G9241_pBC218_0135	<i>pXOI-42</i> ; conjugation_protein_TraG/TraD_family	11.36
BCE_G9241_pBC218_0136	hypothetical_protein_protein	7.68
BCE_G9241_pBC218_0141	DNA_primase	2.77
BCE_G9241_pBC218_0142	<i>tnpB</i> ; transposase_all7245	2.16
BCE_G9241_pBC218_0147	surface_adhesion_protein_putative	3.12
BCE_G9241_pBC218_0150	<i>pXOI-23</i> ; group II intron reverse transcriptase_maturase	3.43
BCE_G9241_pBC218_0154	conserved_hypothetical_protein_protein	2.76
BCE_G9241_pBC218_0155	conserved_hypothetical_protein_protein	2.68
BCE_G9241_pBC218_0174	conserved_hypothetical_protein_protein	16.54
BCE_G9241_pBC218_0175	hypothetical_protein_protein	2.32
BCE_G9241_pBClin29_0001	phage_putative_tail_component_N-terminal_domain_protein	3.52
BCE_G9241_pBClin29_0002	prophage_LambdaBa01_minor_structural_protein	2.90
BCE_G9241_pBClin29_0003	hypothetical_protein_protein	2.63
BCE_G9241_pBClin29_0004	XpaF1_protein	2.73
BCE_G9241_pBClin29_0028	transposase-like_protein_B	2.84
BCE_G9241_pBClin29_0029	phage_protein-related_protein	3.15
BCE_G9241_pBClin29_0036	IstB-like_ATP_binding_protein_family	2.29
BCE_G9241_pBClin29_0037	hypothetical_protein_protein	2.53
BCE_G9241_pBClin29_0038	phage_protein	2.70
BCE_G9241_pBCXO1_0008	conserved_hypothetical_protein_protein	2.71
BCE_G9241_pBCXO1_0023	conserved_hypothetical_protein_protein	2.16
BCE_G9241_pBCXO1_0030	conserved_hypothetical_protein_protein	2.54
BCE_G9241_pBCXO1_0045	transposase_(IS4_family)	2.05
BCE_G9241_pBCXO1_0061	conserved_hypothetical_protein_protein	2.77

Table S5. Genes with increased expression in <i>B. cereus</i> G9241 in CO₂ (MGM + 0.8% bicarbonate)		
SEQUENCE ID	GENE INFO	Fold difference
BCE_G9241_pBCXO1_0063	conserved_hypothetical_protein_protein	2.40
BCE_G9241_pBCXO1_0102	conserved_hypothetical_protein_protein	2.09
BCE_G9241_pBCXO1_0103	conserved_hypothetical_protein_protein	4.64
BCE_G9241_pBCXO1_0104	conserved_hypothetical_protein_protein	3.39
BCE_G9241_pBCXO1_0105	S-layer_homology_domain_protein	12.59
BCE_G9241_pBCXO1_0106	PAP2_superfamily_domain_protein	9.54
BCE_G9241_pBCXO1_0108	glycosyl_transferase_group_2_family_protein_domain_protein	172.58
BCE_G9241_pBCXO1_0109	<i>galU</i> ; UTP-glucose-1-phosphate_uridylyltransferase	226.82
BCE_G9241_pBCXO1_0110	UDP-glucose/GDP-mannose_dehydrogenase_family_NAD_binding_domain_family	123.46
BCE_G9241_pBCXO1_0114	IS861_transposase_OrfB	2.78
BCE_G9241_pBCXO1_0115	conserved_hypothetical_protein_protein	8.68
BCE_G9241_pBCXO1_0116	conserved_hypothetical_protein_protein	25.80
BCE_G9241_pBCXO1_0117	conserved_hypothetical_protein_protein	53.08
BCE_G9241_pBCXO1_0118	conserved_hypothetical_protein_protein	40.10
BCE_G9241_pBCXO1_0119	<i>cya</i> ; calmodulin-sensitive_adenylate_cyclase	10.58
BCE_G9241_pBCXO1_0120	<i>apt</i> ; adenine_phosphoribosyltransferase	27.10
BCE_G9241_pBCXO1_0121	<i>apt</i> ; adenine_phosphoribosyltransferase	26.53
BCE_G9241_pBCXO1_0126	conserved_hypothetical_protein_protein	5.61
BCE_G9241_pBCXO1_0128	conserved_hypothetical_protein_protein	2.03