

Table S1. List of genes controlled by σ^F in transcriptome

Gene	Function	Expression ratio in transcriptome sigF/630Δerm
Sporulation		
CD0125	<i>spoIIQ</i> Stage II sporulation protein Q	0.11
CD2470	<i>gpr</i> Spore endopeptidase	0.22
CD2469	<i>spoIIP</i> Stage II sporulation protein P	0.14
CD2468	Conserved hypothetical protein	0.28
CD3564	<i>spoIIR</i> Pro-SigE endopeptidase signalling protein	0.43
CD3563	<i>sleB</i> Spore-cortex-lytic protein	0.16
CD3499	<i>spoVT</i> Stage V sporulation protein T	0.07
CD0783	<i>spoIVB'</i> Stage IV sporulation protein SpoIVB, S55 peptidase family	0.10
CD0773	<i>spoVAC</i> Stage V sporulation protein AC	0.24
CD0774	<i>spoVAD</i> Stage V sporulation protein AD	0.27
CD0775	<i>spoVAE</i> Stage V sporulation protein AE	0.32
CD2688	<i>sspA</i> Small, acid-soluble spore protein alpha	0.00
CD3249	<i>sspB</i> Small, acid-soluble spore protein alpha	0.01
CD1290	Putative small acid-soluble spore protein SASP	0.29
CD3220.1	Small acid-soluble spore protein	0.28
CD1230	<i>sigK</i> Fragment of RNA polymerase sigma-K factor SigK (Part1)	0.47
CD1613	<i>cotA</i> Spore outer coat layer protein CotA	0.13
CD0598	<i>cotCB</i> Spore-coat protein CotCB manganese catalase	0.18
CD0214	Conserved hypothetical protein	0.30
CD0213	Putative spore coat protein	0.47
CD0332	<i>bclA1</i> Putative exosporium glycoprotein	0.43
CD3230	<i>bclA2</i> Putative exosporium glycoprotein	0.16
CD3349	<i>bclA3</i> Exosporium glycoprotein BclA3	0.12
Stress		
CD1567	putative manganese catalase	0.25
CD2845	<i>rbr</i> Rubrerythrin	0.14
CD1631	<i>sodA</i> Superoxide dismutase (Mn)	0.06
CD3462	<i>mazE</i> Putative antitoxin EndoAI	0.20
CD3461	<i>mazF</i> Endoribonuclease toxin	0.31
envelopes		
CD1430	<i>pdaA</i> Putative δ -lactam-biosynthetic deacetylase	0.06
CD1291	<i>dacF</i> D-alanyl-D-alanine carboxypeptidase	0.11
CD2141	Serine-type D-Ala-D-Ala carboxypeptidase	0.30
CD2184	Putative N-acetylmuramoyl-L-alanine amidase	0.39
CD3463	<i>alr2</i> Alanine racemase 2	0.23
CD3464	Conserved hypothetical protein	0.18
CD0784	Putative N-acetylmuramoyl-L-alanine amidase	0.23
CD1229	Putative peptidoglycan glycosyltransferase	0.42
CD2664	<i>murE</i> UDP-N-acetylmuramyl-tripeptide synthetase	0.51
CD2762	<i>uppS</i> Putative undecaprenyl pyrophosphate synthetase	0.20
CD0514	<i>cwpV</i> Cell surface protein	0.61
CD0792	Putative membrane protein, DUF81 family	0.39
CD0793	Putative membrane protein, DUF81 family	0.26
CD1297	Putative membrane protein	0.31
CD1298	Conserved hypothetical protein	0.19
CD1677	Putative membrane protein	0.48
CD1940	Putative membrane protein	0.25
CD2315	Putative exported protein	0.31
CD2634	Conserved hypothetical protein	0.27
CD2635	Putative membrane protein	0.33
CD2636	Putative membrane protein	0.20
CD2686	Putative membrane protein	0.33
CD2856	Putative membrane protein	0.46
CD3551.1	Putative membrane protein	0.11

CD1707		Putative C4-dicarboxylate anaerobic carrier, DcuC family	0.29
CD2107		Xanthine/uracil/thiamine/ascorbate permease family protein	0.37
CD1891		Fragment of ABC-type transport system, substrate-binding pr	0.40
CD2102		Putative Na(+)/H(+) antiporter	0.49
CD2465		Putative amino acid/polyamine transporter	0.36
metabolism			
CD0684		Putative ATP-dependent peptidase, M41 family	0.29
CD1319		Putative polysaccharide deacetylase	0.37
CD0580	<i>gapN</i>	Glyceraldehyde-3-phosphate dehydrogenase (NADP(+)) (GAP)	0.36
CD1543		putative FMN-dependent NADH-azoreductase	0.16
CD2431		Putative nitrite/sulphite reductase	0.23
CD2661		Putative peptidase, M16 family	0.47
CD2660		Putative peptidase, M16 family	0.48
CD0047	<i>ispD</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	0.48
CD0048	<i>ispF</i>	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	0.50
CD3595		Aminopeptidase	0.55
CD1707		Putative C4-dicarboxylate anaerobic carrier, DcuC family	0.29
CD3521		Putative peptidase T, M20B family	0.38
CD2537		Membrane-associated 5'-nucleotidase/phosphoesterase	0.42
CD0649		Putative peptidase, S9 family	3.80
CD0650		Putative peptidase, S9 family	5.21
CD0651		Putative permease	4.65
CD1599	<i>thiD</i>	Phosphomethylpyrimidine kinase	2.36
CD1600	<i>thiM</i>	Hydroxyethylthiazole kinase	2.23
CD1601	<i>thiE</i>	Thiamine-phosphate pyrophosphorylase	1.83
CD1700	<i>ribD</i>	Riboflavin biosynthesis protein ribD [Includes: Diaminohydro]	3.74
CD1699	<i>ribE</i>	Riboflavin synthase alpha subunit	2.31
CD1908	<i>eutS</i>	Ethanolamine carboxysome structural protein	3.60
CD1909	<i>eutP</i>	Ethanolamine utilization protein	2.69
CD1910	<i>eutV</i>	Two-component response regulator, Ethanolamine specific	2.22
CD1911	<i>eutW</i>	Two-component sensor histidine kinase, Ethanolamine specifi	2.15
CD0108	<i>nrdD</i>	Anaerobic ribonucleoside triphosphate reductase	1.95
CD0109	<i>nrdG</i>	Anaerobic ribonucleoside-triphosphate reductase-activating p	1.77
miscellaneous			
CD1486		Putative ribosome recycling factor	0.10
CD0761		Putative ATP-dependent RNA helicase	0.46
CD3220		Putative methyltransferase	0.39
CD1323	<i>tepA</i>	Protein export-enhancing factor	0.38
regulators			
CD0648		Transcriptional regulator, GntR family	2.79
CD2928		Conserved hypothetical protein	2.15
CD2927		Transcriptional regulator, Phage-type	2.33
Proteins of unknown function			
CD0311		Conserved hypothetical protein	0.32
CD0347		Conserved hypothetical protein	0.35
CD0348		Fragment of conserved hypothetical protein (Part 2)	0.35
CD0543		Conserved hypothetical protein	0.38
CD0896		Conserved hypothetical protein	0.21
CD1067		Conserved hypothetical protein	0.07
CD1301.1		Conserved hypothetical protein	0.28
CD1354		Conserved hypothetical protein	0.22
CD1463		Conserved hypothetical protein	0.06
CD1581		Conserved hypothetical protein	0.03
CD1880		Conserved hypothetical protein	0.07
CD2112		Conserved hypothetical protein	0.03
CD2245.1		Conserved hypothetical protein	0.10
CD2375		Conserved hypothetical protein	0.14
CD2687		Conserved hypothetical protein	0.36
CD2808		Conserved hypothetical protein	0.05

CD2809	Conserved hypothetical protein, DUF1540 family	0.05
CD2816	Conserved hypothetical protein	0.43
CD3620	Conserved hypothetical protein	0.35
CD3271	Conserved hypothetical protein	2.11
CD2067	Conserved hypothetical protein	2.05

A gene is considered differentially expressed between the 630 Δ erm strain and the *sigF* mutant when the P value is <0.05 using the statistical analysis described in Materials and Methods. We did not include genes with a fold-change < 2-fold. However, some genes with a fold-change less than 2-fold were included when they appeared to be in the same transcription units with regulated genes for which the fold-change was ≥ 2 or when they were regulated by other sigma factors of sporulation.