

Table S2. List of genes controlled by σ^E in transcriptome

Gene	Function	Expression ratio in transcriptome sigE/630Δerm
Sporulation		
CD0124	<i>spoIID</i> peptidoglycane hydrolase SpoIID	0.24
CD1192	<i>spoIIIAA</i> ATP-binding stage III sporulation protein	0.05
CD1193	<i>spoIIIB</i> Stage III sporulation protein AB	0.05
CD1194	<i>spoIIIC</i> Stage III sporulation protein AC	0.03
CD1195	<i>spoIIID</i> Stage III sporulation protein AD	0.07
CD1196	<i>spoIIIE</i> Stage III sporulation protein AE	0.09
CD1197	<i>spoIIIF</i> Stage III sporulation protein AF	0.08
CD1198	<i>spoIIIG</i> Stage III sporulation protein AG	0.02
CD1199	<i>spoIIIAH</i> Stage III sporulation ratchet engulfment protein	0.05
CD0126	<i>spoIIID</i> Transcriptional regulator SpoIIID	0.04
CD2629	<i>spoIVA</i> Stage IV sporulation protein A	0.02
CD0783	<i>spoIVB</i> Stage IV sporulation protein SpoIVB, S55 peptidase family	0.12
CD3567	<i>sipl</i> Functional homolog to SpoIVD	0.05
CD2442	<i>spoIV</i> Stage IV sporulation protein YqfD-like	0.14
CD2443	Conserved hypothetical protein YqfC-like	0.05
CD2967	<i>spoVFB</i> Dipicolinate synthase subunit B	0.29
CD2968	<i>dpaA</i> Dipicolinate synthase subunit A	0.30
CD1230	<i>sigK</i> Fragment of RNA polymerase sigma-K factor SigK (Part1)	0.13
CD0782	Putative sporulation protein YunB	0.32
CD1168	Putative membrane protein, BDBH YIbJ involved in spore cortex formation	0.18
CD1613	<i>cotA</i> Spore outer coat layer protein CotA	0.10
CD1511	<i>cotB</i> Spore outer coat layer protein CotB	0.05
CD0598	<i>cotCB</i> Spore-coat protein CotCB manganese catalase	0.18
CD2399	Conserved hypothetical protein	0.14
CD2400	<i>cotJB2</i> Spore coat peptide assembly protein CotJB 2	0.10
CD2401	<i>cotD</i> Spore coat protein CotD manganese catalase	0.11
CD1433	<i>cotE</i> Spore coat protein CotE peroxiredoxin/chitinase	0.14
CD0213	Putative spore coat protein	0.42
CD0214	Conserved hypothetical protein	0.23
CD0551	<i>sleC</i> Spore cortex-lytic enzyme pre-pro-form	0.15
CD0332	<i>bclA1</i> Putative exosporium glycoprotein	0.21
CD3230	<i>bclA2</i> Putative exosporium glycoprotein	0.12
CD3349	<i>bclA3</i> Exosporium glycoprotein BclA3	0.01
CD3542	<i>spmA</i> Spore maturation protein A	0.16
CD3541	<i>spmB</i> Spore maturation protein B	0.11
CD0106	<i>cwlD</i> Germination-specific N-acetylmuramoyl-L-alanine amidase, Autolysin	0.14
CD2246	<i>cspC</i> Subtilisin-like serine germination related protease	0.16
CD2247	<i>cspBA</i> Subtilisin-like serine germination related protease	0.11
CD3249	<i>sspB</i> Small, acid-soluble spore protein alpha	0.04
CD1320	Putative peptidase, M16 family	0.25
CD1321	Putative sporulation protein	0.23
CD1322	<i>dapG</i> Aspartokinase 1	0.32
CD1068	Putative polysaccharide biosynthesis/sporulation protein	0.23
CD2639	Putative cytotoxic factor	0.21
CD2640	<i>nrdR</i> Transcriptional regulator, repressor NrdR family	0.23
CD2641	Putative sporulation protein	0.13
CD2439	Putative diacylglycerol kinase/undecaprenol kinase	0.45
CD3455	Putative carboxy-terminal protease, homolog of CtpB	0.25
CD3493	Putative membrane protein	0.18
CD3494	Putative spore protein	0.20
CD1234	Putative phage protein, skin element	0.22
stress		
CD1631	<i>sodA</i> Superoxide dismutase (Mn)	0.21
CD3461	<i>mazF</i> Endoribonuclease toxin	0.11
CD3462	<i>mazE</i> Putative antitoxin EndoAI	0.05
CD2865	Putative bacterioferritin	0.19
envelopes		
CD2664	<i>murE</i> UDP-N-acetylmuramyl-tripeptide synthetase	0.45
CD3463	<i>alr2</i> Alanine racemase 2	0.05
CD3464	Conserved hypothetical protein	0.04
CD2761	Putative N-acetylmuramoyl-L-alanine amidase	0.40
CD3007	Putative L,D-transpeptidases	0.37

CD2184	N-acetylmuramoyl-L-alanine amidase	0.21
CD2761	Putative N-acetylmuramoyl-L-alanine amidase	0.40
CD0514	<i>cwpV</i> Cell surface protein	0.63
CD2445	Putative transmembrane signaling protein, TspO/MBR family	0.07
CD1845	Putative membrane protein Tn1549-like, CTn5-Orf1	0.14
CD1928	Putative membrane protein	0.14
CD1929	Putative membrane protein	0.27
CD2800	Putative membrane protein	0.11
CD1416	Putative membrane protein	0.20
CD0314	Putative membrane protein	0.15
CD1940	Putative membrane protein	0.08
CD3551.1	Putative membrane protein	0.31
CD0131	Putative membrane protein	0.18
CD1301	Putative membrane protein	0.33
CD2144	Putative membrane protein	0.46
CD2465	Putative amino acid/polyamine transporter	0.20
CD0902	Putative cation efflux protein	0.29
CD2833	Putative calcium-transporting ATPase	0.22
CD0760	Putative Ca ²⁺ /Na ⁺ antiporter	0.20
CD3483	Putative zinc/iron permease	0.34
metabolism		
CD3635	Conserved hypothetical protein	0.29
CD3636	Putative membrane protein	0.42
CD3637	Putative NADPH-dependent FMN reductase	0.27
CD3638	Conserved hypothetical protein	0.21
CD3251	Putative dehydrogenase	0.25
CD3258	Iron hydrogenase	0.08
CD2428	Putative flavodoxin/ferredoxin oxidoreductase beta subunit	0.38
CD2429	Putative flavodoxin/ferredoxin oxidoreductase alpha subunit	0.31
CD2429.1	Putative 4Fe-4S ferredoxin, iron-sulfur binding domain protein, delta subunit	0.27
CD2000	<i>isp</i> Intracellular serine protease	0.18
CD3652	Putative peptidase, M1 family	0.12
CD1085	Putative membrane protein	0.26
CD1086	Putative peptidase, M20D family	0.26
CD3521	Putative peptidase T, M20B family	0.33
CD1746	<i>gltC</i> Sodium/glutamate symporter	0.20
CD1555	Putative amino acid permease	0.22
CD1259	<i>brnQ-1</i> Branched chain amino acid transport system carrier protein	0.39
CD1904	ABC-type transport system, permease	0.26
CD1891	Fragment of ABC-type transport system, substrate-binding protein (Part 1)	0.26
CD1927	<i>ytIC</i> putative ABC transporter component, ATP-binding	0.30
CD1319	Putative polysaccharide deacetylase	0.06
CD3248	Polysaccharide deacetylase	0.09
CD3257	Putative polysaccharide deacetylase	0.11
CD3032	Putative pyridoxal phosphate-dependent transferase	0.32
CD0982	<i>ubiA</i> Putative UbiA prenyltransferase	0.39
CD2537	Putative membrane-associated 5'-nucleotidase/phosphoesterase	0.15
miscellaneous		
CD0749	Putative DNA helicase, UvrD/REP type	0.32
CD3235	<i>ssb</i> Single-stranded DNA-binding protein	0.03
CD1167	<i>recV</i> Tyrosine DNA recombinase, XerC/XerD family	0.26
CD1846	Putative conjugative transposon protein Tn1549-like, CTn5-Orf2	0.15
CD2864	Putative hydrolase	0.08
CD3298	Putative ATP/GTP-binding protein	0.19
CD1486	Putative ribosome recycling factor	0.26
regulator		
CD0757	Putative diguanylate kinase signaling protein	0.45
CD1616	Putative diguanylate kinase signaling protein	0.37
CD2637	Two-component sensor histidine kinase	0.30
Proteins of unknown function		
CD0129	Conserved hypothetical protein, DUF1256 family	0.15
CD0196	Fragment of conserved hypothetical protein, DUF111 family (part 2)	0.18
CD0311	Conserved hypothetical protein	0.02
CD0896	Conserved hypothetical protein	0.05
CD1063	Conserved hypothetical protein	0.11
CD1063.2	Conserved hypothetical protein	0.01
CD1063.3	Conserved hypothetical protein	0.01

CD1063.1	Conserved hypothetical protein	0.17
CD1065	Conserved hypothetical protein	0.06
CD1066	Conserved hypothetical protein	0.16
CD1067	Conserved hypothetical protein	0.00
CD1133	Conserved hypothetical protein	0.12
CD1581	Conserved hypothetical protein	0.01
CD1726	Conserved hypothetical protein	0.05
CD1880	Conserved hypothetical protein	0.21
CD1884	Conserved hypothetical protein	0.11
CD1930	Conserved hypothetical protein	0.27
CD2121	Conserved hypothetical protein	0.23
CD2374	Conserved hypothetical protein	0.23
CD2816	Conserved hypothetical protein	0.11
CD3234	Conserved hypothetical protein	0.09
CD3457	Conserved hypothetical protein	0.05
CD3465	Conserved hypothetical protein	0.40
CD3522	Conserved hypothetical protein	0.09
CD3580	Conserved hypothetical protein	0.11
CD3620	Conserved hypothetical protein, similar to YmaF	0.34

A gene is considered differentially expressed between the 630 Δ erm strain and the *sigE* 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.