

Table S4. List of genes controlled by σ K in transcriptome

Gene	Function	Expression ratio in transcriptome sigK/630Aerm
Sporulation		
CD1230	Fragment of RNA polymerase sigma-K factor SigK (Part1)	0.05
CD3569	Sporulation-specific protease, YabG-like protein	0.22
CD1613	<i>cotA</i> Spore outer coat layer protein CotA	0.05
CD2399	Conserved hypothetical protein	0.01
CD2400	<i>cotJB2</i> Spore coat peptide assembly protein CotJB 2	0.01
CD2401	<i>cotD</i> Spore coat protein CotD manganese catalase	0.01
CD0596	Conserved hypothetical protein	0.02
CD0597	<i>cotJB1</i> Spore coat peptide assembly protein	0.02
CD0598	<i>cotCB</i> Spore-coat protein CotCB manganese catalase	0.01
CD1433	<i>cotE</i> Spore coat protein CotE peroxiredoxin/chitinase	0.03
CD2968	<i>dpaA</i> Dipicolinate synthase subunit A	0.08
CD2967	<i>spoVFB</i> Dipicolinate synthase subunit B	0.09
CD0551	<i>sleC</i> Spore cortex-lytic enzyme pre-pro-form	0.14
CD0332	<i>bclA1</i> Putative exosporium glycoprotein	0.08
CD3230	<i>bclA2</i> Putative exosporium glycoprotein	0.04
CD3349	<i>bclA3</i> Exosporium glycoprotein BclA3	0.02
Enveloppes		
CD0514	<i>cwpV</i> Cell surface protein	0.20
CD1898	Cell wall hydrolase, N-acetylmuramic acid L-alanine amidase	0.12
CD1897	Conserved hypothetical protein	0.13
CD2184	Putative N-acetylmuramoyl-L-alanine amidase (cell wall hydrolase)	0.13
CD2664	<i>murE</i> UDP-N-acetylmuramyl-tripeptide synthetase	0.42
CD3007	Putative L,D-transpeptidases	0.48
CD2537	Putative membrane-associated 5'-nucleotidase/phosphoesterase	0.22
CD2458	Transporter, Major Facilitator Superfamily (MFS)	0.39
CD2459	Putative glucokinase, ROK family	0.41
CD0902	Putative cation efflux protein	0.17
CD1517	<i>feoB</i> Ferrous iron transport protein B	0.05
CD1518	<i>feoA</i> Ferrous iron transport protein	0.05
CD1904	ABC-type transport system, permease	0.13
CD2720	Putative transporter	0.16
CD1927	<i>ytIC</i> Fragment of ABC transporter component, ATP-binding	0.08
CD1891	Fragment of ABC-type transport system, substrate-binding protein	0.08
CD2346	Putative membrane protein	0.24
CD2144	Putative membrane protein	0.12
CD1824	P-type calcium transport ATPase	2.69
CD0147	Putative transporter	2.25
Metabolism		
CD3350	Putative glycosyl transferase, family 2	0.09
CD3032	Putative pyridoxal phosphate-dependent transferase	0.11
CD1951	putative Acyl-CoA N-acyltransferase	0.19
CD0119	<i>glmM</i> Phosphoglucosamine mutase	0.49
CD0120	<i>glmS</i> Glucosamine--fructose-6-phosphate aminotransferase	0.52
CD0995	<i>serA</i> Putative D-3-phosphoglycerate dehydrogenase	6.49
CD0996	Conserved hypothetical protein	3.08
CD2480	Putative hydrolase	2.03
Miscellaenous		
CD0749	Putative DNA helicase, UvrD/REP type	0.05
CD1845	Putative membrane protein Tn1549-like, CTn5-Orf1	0.17
CD1846	Putative conjugative transposon protein Tn1549-like, CTn5-Orf2	0.20
CD0564	putative ATP-dependent protease, Lon family	0.39
CD0309	Putative hydrolase, HAD superfamily, subfamily IB	0.38
Regulator		
CD2048	Transcriptional regulator, RpiR family	2.05
Proteins of unknown function		
CD0196	Fragment of conserved hypothetical protein, DUF111 family (part 2	0.18
CD0896	Conserved hypothetical protein	0.02
CD1063.1	Conserved hypothetical protein	0.21
CD1063.2	Conserved hypothetical protein	0.04
CD1063.3	Conserved hypothetical protein	0.04
CD1065	Conserved hypothetical protein	0.30
CD1067	Conserved hypothetical protein	0.03

CD1133	Conserved hypothetical protein	0.16
CD1581	Conserved hypothetical protein	0.01
CD2055	Conserved hypothetical protein	0.33
CD2409	Conserved hypothetical protein	0.11
CD3580	Conserved hypothetical protein	0.12
CD3613	Conserved hypothetical protein	0.04
CD3620	Conserved hypothetical protein	0.04
CD1286	Conserved hypothetical protein	2.17
CD1831.1	Conserved hypothetical protein	2.36

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