

Table S10. List of genes controlled by SpoIIID in transcriptome

Gene	Function	Expression ratio in transcriptome <i>spoIIID</i>/630Δerm
sporulation		
CD1214	<i>spo0A</i> Stage 0 sporulation protein A	0.47
CD2644	<i>spoIIGA</i> Sigma-E factor processing peptidase	2.36
CD2643	<i>sigE</i> RNA polymerase sigma-E factor	1.85
CD2642	<i>sigG</i> RNA polymerase sigma-G factor	2.72
CD3490	<i>spoIIE</i> Phosphoprotein phosphatase	3.14
CD3563	<i>sleB</i> Spore-cortex-lytic protein	1.94
CD0125	<i>spoIIQ</i> Stage II sporulation protein Q	3.02
CD1192	<i>spoIIIAA</i> Stage III sporulation protein AA	3.85
CD1193	<i>spoIIIAB</i> Stage III sporulation protein AB	3.81
CD1194	<i>spoIIIAC</i> Stage III sporulation protein AC	4.91
CD1195	<i>spoIIIAD</i> Stage III sporulation protein AD	3.44
CD1196	<i>spoIIIAE</i> Stage III sporulation protein AE	2.42
CD1197	<i>spoIIIAF</i> Stage III sporulation protein AF	3.63
CD1198	<i>spoIIIAG</i> Stage III sporulation protein AG	7.75
CD1199	<i>spoIIIAH</i> Stage III sporulation protein AH	3.31
CD2629	<i>spoIVA</i> Stage IV sporulation protein A	3.54
CD3567	<i>sipL</i> SpoIVA-Interacting protein, coat localization	3.06
CD3541	<i>spmB</i> Spore maturation protein B	2.04
CD1511	<i>cotB</i> Spore outer coat layer protein CotB	3.54
CD2688	<i>sspA</i> Small, acid-soluble spore protein alpha	13.45
CD3249	<i>sspB</i> Small, acid-soluble spore protein alpha	11.62
CD3499	<i>spoVT</i> Stage V sporulation protein T	2.26
CD3349	<i>bclA3</i> Exosporium glycoprotein BclA3	0.19
stress		
CD1631	<i>sodA</i> Spore coat protein, superoxide dismutase	2.87
CD2865	Putative bacterioferritin	2.20
envelopes		
CD0147	Putative transporter	20.56
CD1416	Putative membrane protein	2.24
CD1928	Putative membrane protein	3.05
CD2445	Transmembrane signaling protein, TspO	2.37
CD2737	Putative nitrilase/cyanide hydratase	2.25
CD2738	Putative cytosine permease	2.14
CD2833	Putative calcium-transporting ATPase	2.25
CD2800	Putative membrane protein	2.60
CD3073	Putative membrane protein	2.19
CD2664	<i>murE</i> UDP-N-acetylmuramyl-tripeptide synthetase	1.93
CD0090	<i>prlA</i> Preprotein translocase SecY subunit	0.44
metabolism		
CD0740	Putative PLP-dependent aminotransferase	2.17
CD0777	Putative membrane protein	1.96
CD0778	Conserved hypothetical protein	2.15
CD0779	Putative amidohydrolase, M20D peptidase family	2.13
CD0780	Conserved hypothetical protein, DUF1177 family	2.46
CD0994	Putative serine-pyruvate aminotransferase	1.91
CD0995	<i>serA</i> Putative D-3-phosphoglycerate dehydrogenase	2.95
CD0996	Conserved hypothetical protein	2.22
CD1319	Putative polysaccharide deacetylase	3.24
CD1697	<i>ribH</i> 6,7-dimethyl-8-ribityllumazine synthase	15.04
CD1698	<i>ribBA</i> Riboflavin biosynthesis protein ribBA	5.68
CD1699	<i>ribE</i> Riboflavin synthase alpha subunit	3.84
CD1700	<i>ribD</i> Riboflavin biosynthesis protein ribD	3.88
CD1749	Putative 2-hydroxyacyl-CoA dehydratase	1.94
CD1750	Putative CoA enzyme activase	2.20

CD1767	<i>gapB</i>	Glyceraldehyde-3-phosphate dehydrogenase	2.70
CD2387		α -hydroxy acid dehydrogenase, FMN-dependent	2.02
CD2819		Putative amino acid racemase	2.25
CD2864		Putative hydrolase	4.00
CD3236		Putative membrane protein	1.89
CD3238		Putative component of proline reductase <i>prdE</i> -like	1.96
CD3241	<i>prdB</i>	Proline reductase (selenocysteine)	2.07
CD3243		Conserved hypothetical protein	2.19
CD3244	<i>prdA</i>	D-proline reductase proprotein <i>prdA</i>	2.09
CD3248		Polysaccharide deacetylase	2.27
CD3257		Putative polysaccharide deacetylase	2.13
CD3258		Iron hydrogenase	2.26
CD3489		Putative oligoendopeptidase F, peptidase M3B family	2.29
CD2323		Putative sugar-phosphate dehydrogenase	0.53
CD2324		Putative sugar-phosphate dehydrogenase	0.44
CD2325	<i>gatC</i>	PTS system, galactitol-specific IIC component	0.47
CD2326		PTS system, lactose/cellobiose specific IIB compo	0.47
CD2327	<i>gatA</i>	PTS system, galactitol-specific IIA component	0.48
CD2600	<i>cstA</i>	Carbon starvation protein, CstA	0.42
regulators			
CD2214	<i>sinR</i>	Transcriptional regulator, HTH-type	8.23
CD2215		Transcriptional regulator, HTH-type	8.22
miscellaenous			
CD0356	<i>xis</i>	Excisionase Tn916-like, CTn1-Orf2	2.45
CD3235	<i>ssb</i>	Single-stranded DNA-binding protein	3.63
CD2517.1		Putative phage protein	0.25
proteins of unknown function			
CD0311		Conserved hypothetical protein	4.12
CD1063		Conserved hypothetical protein	2.95
CD1463		Conserved hypothetical protein	2.41
CD1726		Conserved hypothetical protein	3.87
CD1941		Conserved hypothetical protein	2.38
CD2046		Conserved hypothetical protein	2.25
CD2098		Conserved hypothetical protein	2.09
CD2112		Conserved hypothetical protein	2.76
CD2245.1		Conserved hypothetical protein	3.35
CD2366		Conserved hypothetical protein	2.76
CD2369		Conserved hypothetical protein	2.70
CD2375		Conserved hypothetical protein	5.09
CD2409		Conserved hypothetical protein	2.28
CD2752		Conserved hypothetical protein	2.30
CD2808		Conserved hypothetical protein	3.04
CD2809		Conserved hypothetical protein	2.52
CD3457		Conserved hypothetical protein	2.62
CD3610		Conserved hypothetical protein	2.13
CD3618		Conserved hypothetical protein	2.31
CD1067		Conserved hypothetical protein	0.03
CD2216		Conserved hypothetical protein	0.39

RNA was extracted from strain 630 Δ erm strain and the *spoIIID* mutant after 15 h of growth in a sporulation medium. A gene is considered differentially expressed between the 630 Δ erm strain and the *spoIIID* mutant when the P value is <0.05 using the statistical analysis described in Materials and Methods