Table S9. Complementation of the mutants inactivated for the Sigma factors of sporulation

Complementation of the *sigF* mutant

		***sigF*/630Δerm**	**complemented *sigF*/630Δerm**
CD2469	*spoIIP*	0.001	12
CD3564	*spoIIR*	0.03	9
CD3499	*spoVT*	0.004	19

Complementation of the *sigE* mutant

		***sigE*/630Δerm**	**complemented *sigE*/630Δerm**
CD1198	*spoIIIAG*	0.002	2
CD0126	*spoIIID*	0.001	0.7
CD2629	*spoIVA*	0.004	2.5
CD1230	*sigK*	0.002	0.4

Complementation of the *sigG* mutant

		***sigG*/630Δerm**	**complemented *sigG*/630Δerm**
CD2688	*sspA*	0.02	0.7
CD3249	*sspB*	0.07	1.2
CD3499	*spoVT*	0.08	0.5
CD3551.1		0.006	1.3

Complementation of the *sigK* mutant

		***sigK*/630Δerm**	**complemented *sigK*/630Δerm**
CD2401	*cotD*	0.005	0.15
CD0551	*sleC*	0.011	0.25
CD1433	*cotE*	0.01	0.15
CD1613	*cotA*	0.0005	0.05

qRT-PCR experiments were performed on two different RNA preparations for each mutant and each complemented strain. Cells were harvested after 14h of growth for the strain 630Δerm, the sigE and sigF mutants and the sigF mutant containing pMTL84121-sigF and the sigE mutant containing pMTL84121-sigE after 20h of growth for the strain 630Δerm, the sigG mutant and the sigG mutant containing pMTL84121-sigG and after 24 h of growth for the strain 630Δerm, the sigK mutant and the sigK mutant containing pMTL84121-sigK. The results presented corresponded to the mean of at least two independent experiments.