

Supplemental data

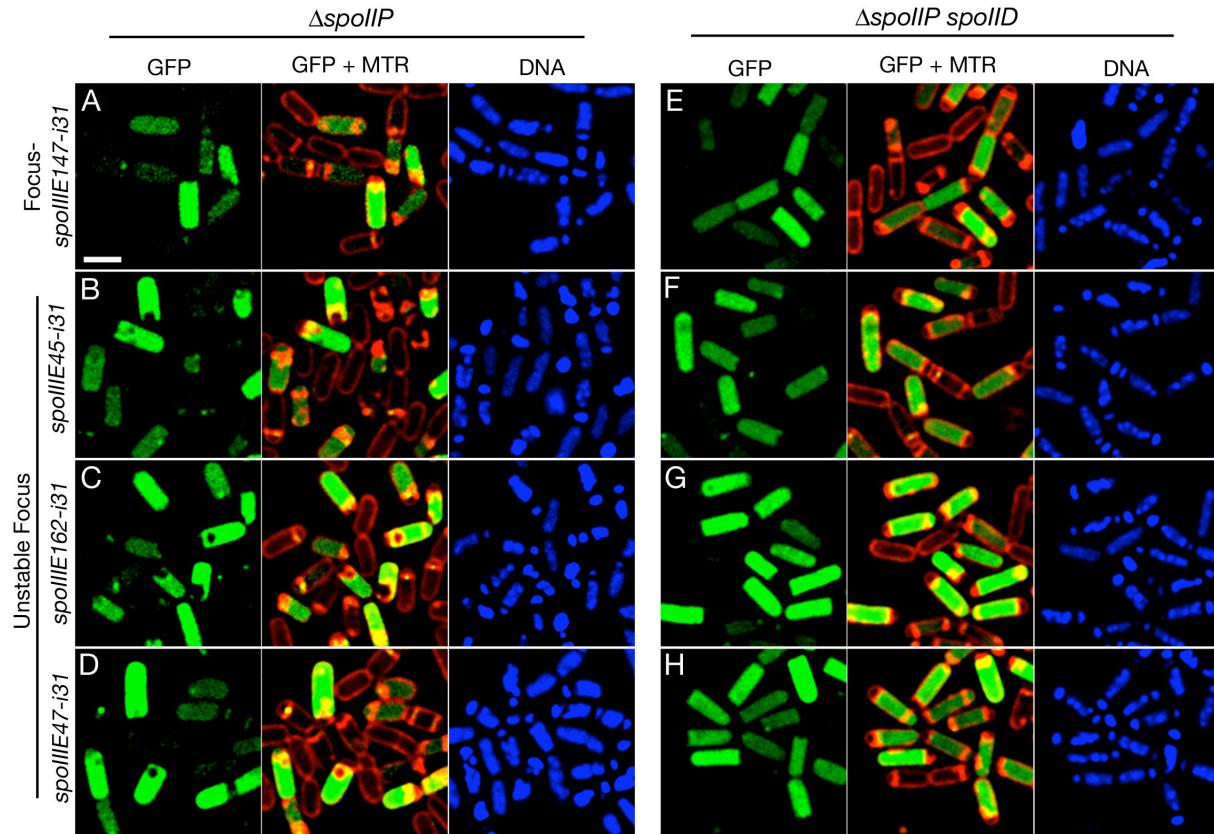


Figure S1: Engulfment mutants rescue the GFP diffusion defect in SpoIIIIE assembly mutants. Images were collected at t_3 , with membranes stained with Mitotracker Red and DNA with DAPI (blue). (A) Focus defective insertion *spoIIIIE147-i31* in *spoIIIP* (KP6149). (B) Unstable focus insertion *spoIIIIE45-i31* in *spoIIIP* (KP6151). (C) Unstable focus insertion *spoIIIIE162-i31* in *spoIIIP* (KP6152). (D) Unstable focus insertion *spoIIIIE47-i31* in *spoIIIP* (KP6153). (E) Focus defective *spoIIIIE147-i31* in *spoIIIP spoIID* (KP6176). (F) Unstable focus insertion *spoIIIIE45-i31* in *spoIIIP spoIID* (KP6177). (G) Unstable focus insertion *spoIIIIE162-i31* in *spoIIIP spoIID* (KP6178). (H) Unstable focus insertion *spoIIIIE47-i31* in *spoIIIP spoIID* (KP6179). For each of these mutant proteins at t_3 , the *spoIIIP* mutation improved the ability of the protein to block GFP diffusion (by about 50%), while introducing both *spoIIIP* and *spoIID* mutations almost completely rescued the diffusion defect (by about 97%, Table S1). Thus, septal peptidoglycan is sufficient to prevent GFP diffusion in *SpoIIIIE* mutants that are completely or partially defective in focus assembly. Scale bar in A is 2 μ m.

Table S1: GFP diffusion in engulfment mutant backgrounds

<i>spoIIIIE</i> mutant	Percent sporangia with GFP confined to mother cell			
			+ <i>spoIIP::tet</i>	+ <i>spoIIP::tet, spoIID::Tn917</i>
wild type	<i>t</i> ₂	100	99	99
	<i>t</i> ₃	100	98	98
<i>spoIIIIE36</i>	<i>t</i> ₂	97	97	99
	<i>t</i> ₃	100	98	98
Δ <i>spoIIIIE</i>	<i>t</i> ₂	0	62	97
	<i>t</i> ₃	0	48	95
Focus – <i>spoIIIIE147-i31</i>	<i>t</i> ₂	37	68	93
	<i>t</i> ₃	7	46	95
Unstable Focus <i>spoIIIIE45-i31</i>	<i>t</i> ₂	69	81	97
	<i>t</i> ₃	55	74	98
Unstable Focus <i>spoIIIIE162-i31</i>	<i>t</i> ₂	67	91	98
	<i>t</i> ₃	35	73	97
Unstable Focus <i>spoIIIIE47- i31</i>	<i>t</i> ₂	40	73	96
	<i>t</i> ₃	18	56	97

An average of 297 sporangia was scored for each strain at each time point.

Table S2: Strains used in this study

Strain	Genotype	Source
KP92	<i>spoIII</i> E36	Wu and Errington, 1994
KP141	Δ <i>spoIII</i> E::spc	Pogliano <i>et al.</i> 1997
KP514	<i>cotE-gfpQkan</i> , <i>spoIIP::tet</i>	This study
KP723	<i>spoIII</i> E36, <i>cotE-gfpQkan</i>	Sharp and Pogliano, 1999
KP725	<i>spoIII</i> E::spec, <i>cotE-gfpQkan</i>	Sharp and Pogliano, 1999
KP6149	<i>amyE::spoIII</i> E147-i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i>	This study
KP6151	<i>amyE::spoIII</i> E45-i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i>	This study
KP6152	<i>amyE::spoIII</i> E162-i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i>	This study
KP6153	<i>amyE::spoIII</i> E47-i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i>	This study
KP6174	<i>spoIII</i> E36, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i>	This study
KP6175	<i>spoIII</i> E::spec, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i>	This study
KP6176	<i>amyE::spoIII</i> E147-i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i> , <i>spoIID::Tn917Qmls</i>	This study
KP6177	<i>amyE::spoIII</i> E45-i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i> , <i>spoIID::Tn917Qmls</i>	This study
KP6178	<i>amyE::spoIII</i> E162-i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i> , <i>spoIID::Tn917Qmls</i>	This study
KP6179	<i>amyE::spoIII</i> E47- i31-' <i>spoIII</i> E-gfpQcat, Δ <i>spoIII</i> E::spc, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i> , <i>spoIID::Tn917Qmls</i>	This study
KP6180	<i>cotE-gfpQkan</i> , <i>spoIIP::tet</i> , <i>spoIID::Tn917Qmls</i>	This study
KP6181	<i>spoIII</i> E36, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i> , <i>spoIID::Tn917Qmls</i>	This study
KP6182	Δ <i>spoIII</i> E::spec, <i>cotE-gfpQkan</i> , <i>spoIIP::tet</i> , <i>spoIID::Tn917Qmls</i>	This study