Table 1S. Oligonucleotide primers used in this study.

Name	Sequence[a]
BA00465'Kpn	TATTAGGTACCGGTATCCTCTGGATG
BA00463'Bam	TAGATGGATCCTTTCTGAATCTAG
BA00463'Bam2	ATCCGTAGGATCCAACGAGATAGATC
BA00465'Nde	TTCATTTCACATATGAACGTAACGAAAC
BA18775'EcoRI	TAAACGAATTCCTTTCTATATTATC
BA18773'Bam	CAGTTGGATCCGAAATTCCATTACAC
BA18773'Bam2	GAAAGGGATCCTAATGTGTACTTCCT
BA18775'Nhe	TGAATGGCTAGCGTAAAAAGGAAGTAC
BA11875'ScaII	CTTTGTCCGCGGAAGAAAAGGCATAACAG
BA18773'SalI	ATATAGTCGACTTATTATACTTCCATGC
BA18775'SalI	GGCGAAGTCGACTGGCTGGTTTTATG
BA18773'Xho	CATCGAACTCGAGATAAAACGAATTAATG
BA24165'Kpn	AGAGAGGTACCGATTTGTTATGAATATG
BA24163'Bam	TCCCCGGATCCTGAAATGTACGTATG
BA24165'Nde	GAAGTAAAACCATATGGAATTAGTGAAATTGG
BAYisi5'Eco	TAATTGAATTCGCATCCGTAAGAAAAAAAC
BAYisi3'Bam	TACAAGGATCCTTTCGTTTTTAAAATAAAC
BAYisi5'Nde	CGATTCATATGTTTGAGCAAGCG
BAYisI3'SalI	ATCGCGTCGACAAACATTGAAATCGGCTC
BAYisI3'Sal2	CCATAGTCGACAGCAAAATAAATCATTTTTTCAC

a) Regions underlined denote the restriction site.

Legend to Supplementary Figures

Figure 1S: MALDI TOF analysis of the BAYisI protein isolated from *E. coli*. The sequence of one possible protein resulting from the frameshift repair is shown with the His-tag sequence at the N-terminal end. The predicted molecular weight of this protein is also shown.

Figure 2S: Phosphorelay dephosphorylation assay. Purified Spo0E-like proteins of *B. anthracis* were tested for their ability to dephosphorylate KinA (0.2µM) or Spo0F (2.5µM). BA1877, BA0046, BA2416 and BAYisI were added at 5µM final concentration. The reactions were initiated by the addition of ATP. Aliquots were withdrawn at the indicated times. The position of the phosphorylated KinA and Spo0F proteins is indicated by the arrows. The asterisk denotes a dimer form of Spo0F.

Figure 3S: Quantitation of residual phosphorylated Spo0A in the phosphorelay reactions in the presence of the *B. anthracis* Spo0E-like proteins. The 0' and 5' time points of the reaction shown in Figure 3 were quantitated using the ImageQuant software (Molecular Dynamics/Amersham). The phosphorylation level was measured in pixel and expressed as a percentage of the phosphorylation level of Spo0A in the corresponding time point of the control reaction carried out without the phosphatase.

BAYisI (predicted MW 9,255.35)
MGSSHHHHHHSSGLVPRGSHMFEQAIEKKREKMIYFAERYGMTSQKTVDCSQELDRLLNVIWHVHTDVHPNQTLDTHTQ

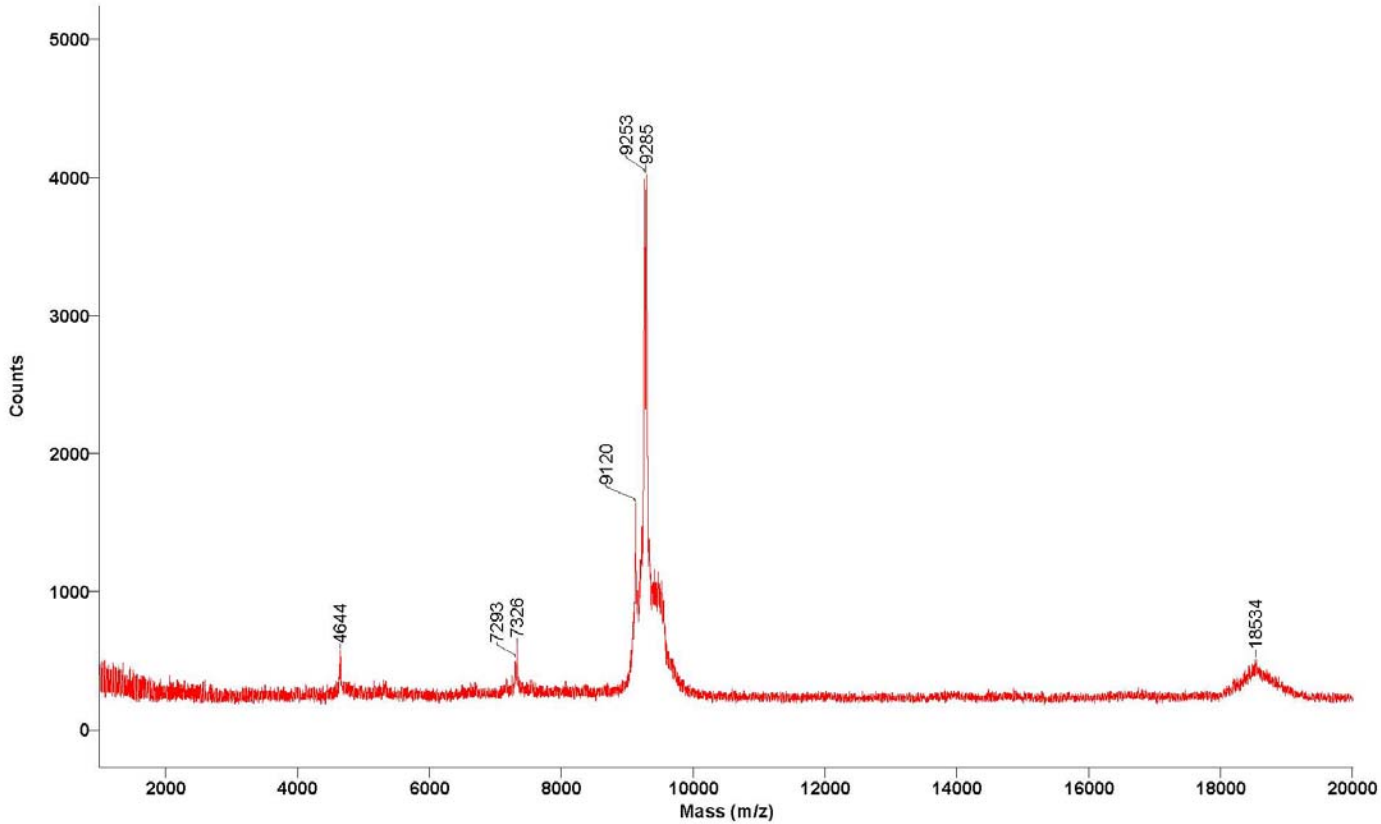

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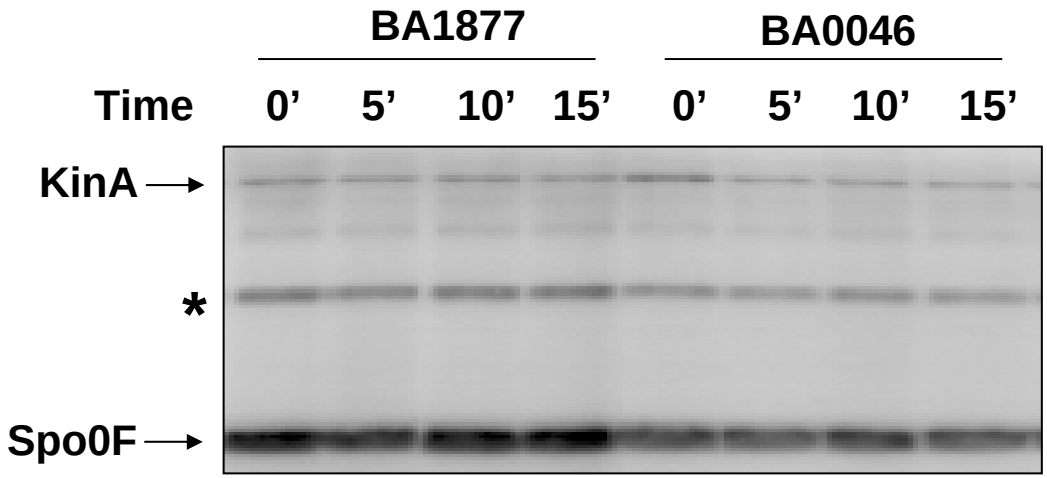
Fig.1S



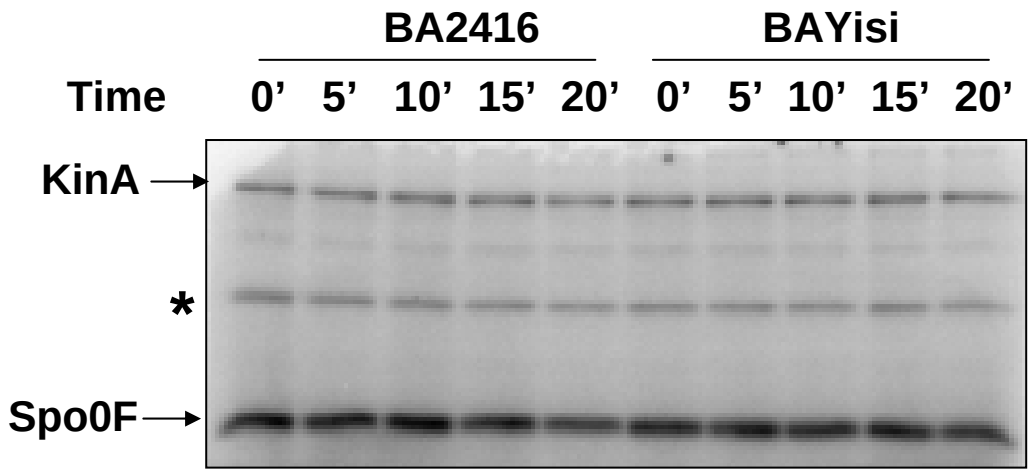


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Fig.2S

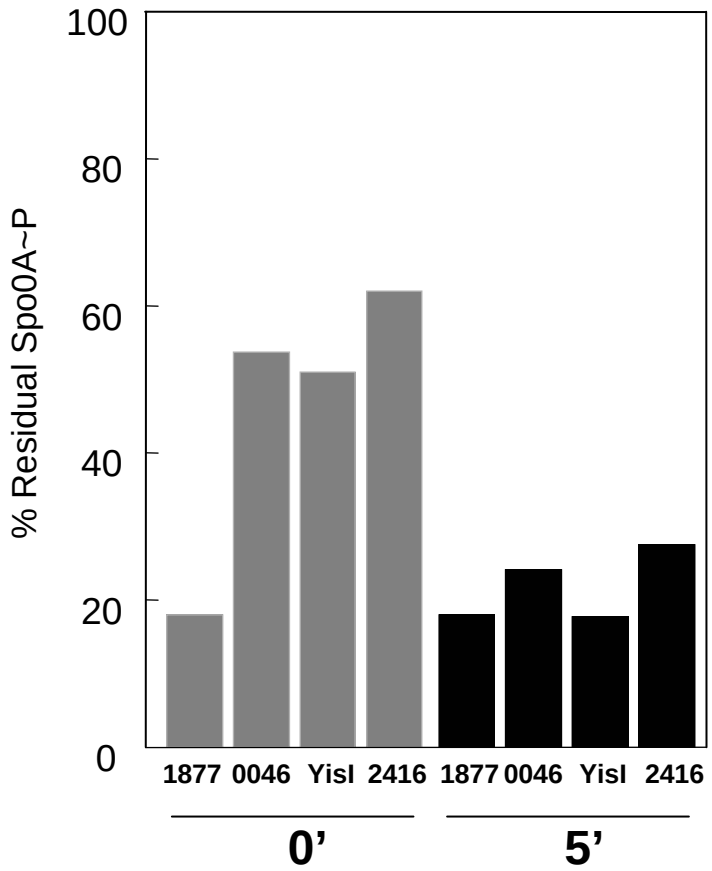

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Fig.3S