

Supplemental Data

TABLE S1: Bacterial strains used throughout this study.

Strain	Genotype or description (species)	Source or reference
<i>E. coli</i>		
DH10 β	Cloning host	Knight Laboratory Collection
BL21 (DE3)/pLysS	Expression host	Novagen
<i>Bacillus</i>		
KMS3	<i>gerA::spec gerB::cmΩpcm::tet gerK::erm</i> ; PS832 (<i>B. subtilis</i>)	This study
ADL18	Wild type; PY79 (<i>B. subtilis</i>)	Driks Laboratory Collection
ADL831	Wild type; 569 (<i>B. cereus</i>)	Driks Laboratory Collection
RG1	Wild type; 34F2; pXO1 ⁺ pXO2 ⁻ (<i>B. anthracis</i> (Sterne))	P. Jackson
ADL2260	<i>bclA::kan</i> (<i>B. anthracis</i> (Sterne))	J. Bozue
MGM203	cotO Ω pMGM3 (<i>B. anthracis</i> (Sterne))	(21)
KMS2	<i>exsKΔ::kan</i> (<i>B. anthracis</i> (Sterne))	(15)

A

VH1a2 CTGAGGCCGCCACCATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAA
 LEAATMETGLRWLLLVAVLK
 VHy33 CTGAGGCCGCCACCATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAA
 LEAATMETGLRWLLLVAVLK
 VH1a2 GGTGTCCAGTGTGAGTCCGGTGAAGGAGTCCGAGGGAGGTCTTTCAAGCCAACGGATACC
 GVQCQSVESEGLFKPTDT
 VHy33 GGTATCCAGTGTGAGTCCGGTGAAGGAGTCCGAGGGAGGTCTTTCAAGCCAACGGATACC
 GIQCQQLSEQSGGGAAGGLVK
 VH1a2 CTGACACTCACCTGCACAGTCTCTGGATTCTCCCTCAGTAGCAATGCAATAAGCTGGGT
 LTLTCTVSGFSLSSNAISWV
 VHy33 CCTGGGGATCCCTGGAACCTGCTGCAAAGCCTCTGGATTCTCCCTCAGTAGCAGCTAC
 PGGSLLELCCKASGFSLSSSY
 VH1a2 CGCCAGGCTCCAGGGAACGGGCTGGAAATGGATCGGAGCCATTTGGTAGTAGTGGTAGCGCA
 RQAPGNGLIEWIGAISSSSA
 VHy33 TGGATATGCTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGATCGGATGCATTTAT
 WICWVRQAPGKGLEWIGCIY
 VH1a2 TACTACGCGAGCTGGCGAAAAGCCGATCCACCATCACCAGAAACCAACCTGAACACG
 YYASWAKSRSTITRNTNLNT
 VHy33 GCTGGTAGTAGTGGTAGCACTACTATGCGAGCTGGGTGAATGGCCGATTCACTCTCTCC
 AGSSSGSTYYASWVNGRFTLS
 VH1a2 GTGACTTGAAAATGACCACTGACAGCCGCGG
 VTLKMTSLTAA
 VHy33 AGAGACATCGACCAGAGCACAGGTTGCCTACAACCTGAACAGTCTGACAGCCGCGG
 RDI DQS TGLQLNSLTA A

B

Vκ GGTGGAGGAGGCTCAGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGACGCT
 GGGGSADIVMTQTPTASVEAA
 Vλ GGTGGAGGAGGCTCACAGCCTGTGCTGACTCAGTCGCCCTCTGCATCTGCTGCCCTGGGA
 GGGGSQPVL TQS P S A S A A L G
 Vκ GTGGGAGGCACAGTCCATCAAGTGCAGGCCAGTCCAGGCATTAGTAGTTACTTAGCC
 VGGTVTIKCAASQGIS SYLA
 Vλ TCCTCGCCAAGCTCACCTGCACTCTGAGCAGTGTCAAGACCTACTATATGAATGG
 S S A K L T C T L S S A H K T Y Y I E W
 Vκ TGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCATCCACTG
 WYQQQKPGQP PKLLIYRASTL
 Vλ TATCAGCAGCAGCAAGGGGAGGCCCTCGGTACTGTGATGAGCTTAAGAGTGTGGAAGC
 YQQQQQGEAPRYLMQLKSDGS
 Vκ GCATCTGGGGTCCCATCGCGTTCAAAGGCAGTGGATCTGGGCCGAGTTCCGCTCTCAGC
 ASGVPSRFKGS SGPQFALS
 Vλ TACACCAAGGGGACCGGGTCCCTGATCGCTTCTCGGGCTCCAGCTCTGGGGCTGACCGC
 YTKGTGV PDRFSSSSSGADR
 Vκ ATCAGCGACCTGGAGTGTGCCGACTGCTGCACTACTACTGTGACACTATTATTATATT
 ISDLECA D A A T Y Y C Q T Y Y Y I
 Vλ TACTTGATCATCTCCAGCGTCCAGGCTGAGGACGAAGCTGACTACATCTGTGGTGTAAC
 YLIIS SVQA E D E A D Y I C G V T
 Vκ AGTGGTAGTAGTTATGGTGCTTTCGGCGGAGGGACCGAGGTGGTTGTCAAAGGTGAATTC
 S G S S Y G A F G G G T E V V V K G E F
 Vλ GGTAGTAATGTTTATGTGTTTCGGCGGAGGGACCGAGTACCCTCACAGGTGAATTC
 GSNVYVFGGGTQLTVTGEF

FIGURE S1. Nucleotide and amino acid sequences of V_H and V_L germline genes

used for scFv-Ig constructs. A, V_H1a2 and V_{Hy}33 sequences. B, V_κ and V_λ sequences.

For details of scFv-Ig construction, refer to Materials and Methods.

TABLE S2. Identity of scFv-Ig⁺ intestinal isolates from Fig. 1.

scFv-Ig ⁺ Isolate	Growth conditions	16S rRNA gene sequence identity
1	LB, aerobic	<i>Bacillus pumilus</i>
2	Blood agar, aerobic	<i>Bacillus subtilis</i> , <i>Bacillus ameloliquefaciens</i> ¹
3	Phenylethanol, aerobic	<i>Bacillus pumilus</i>
4	Blood agar, aerobic	<i>Bacillus subtilis</i> subspecies
5	Blood agar, anaerobic	<i>Bacteroides uniformis</i>
6	Blood agar, anaerobic	<i>Bacteroides ovatus</i>

¹Based on the 16S rRNA gene sequence of the second isolate, we were unable to distinguish between *Bacillus subtilis* and *Bacillus ameloliquefaciens*. As a result, this isolate is designated by both names throughout the manuscript.

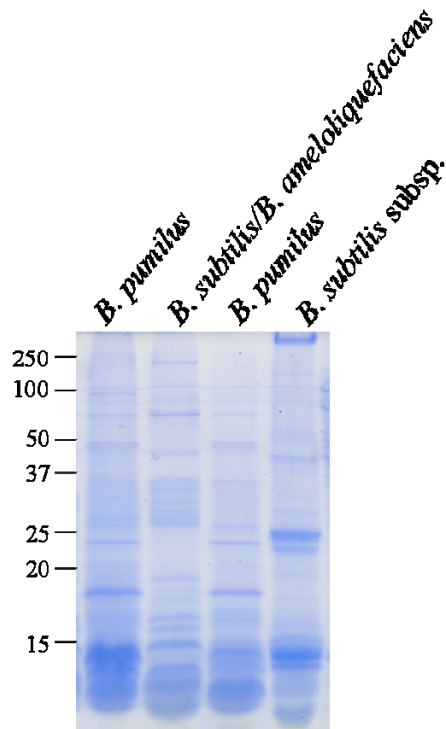


FIGURE S2. Electrophoretic analysis of extracts from intestinal *Bacillus* spores from Fig. 1F. To assess the efficiency of the spore protein extractions, lysates from the indicated intestinal *Bacillus* spores were analyzed by SDS polyacrylamide gel electrophoresis followed by Coomassie blue staining. While many proteins were extracted from spores, scFv-Ig bound to only a small number of proteins, demonstrating the specificity of scFv-Ig binding.

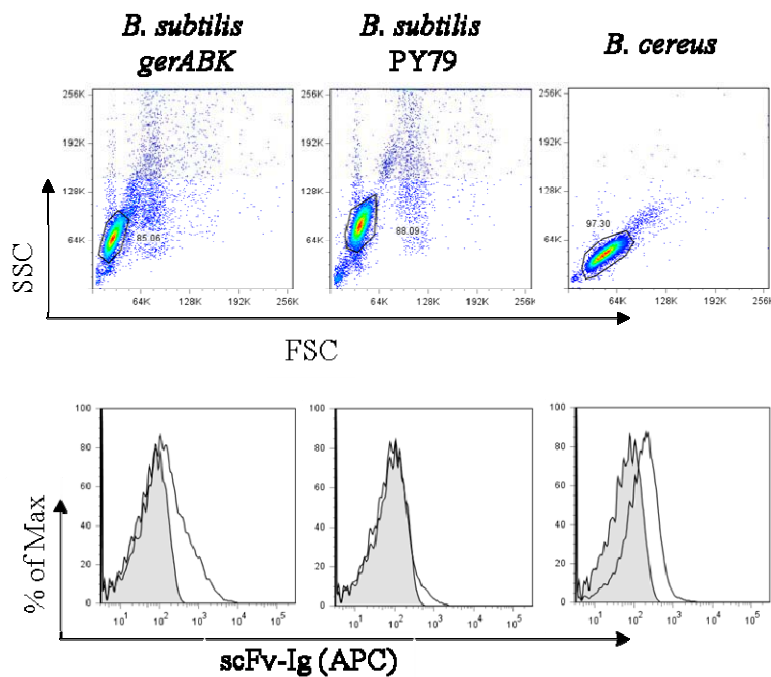


FIGURE S3. Flow cytometric analysis of *Bacillus* spores stained with scFv-Ig (related to Fig. 2). Purified spores of the indicated *Bacillus* species were stained with scFv-Ig followed by mouse anti-rabbit Fc γ and Dylight™ 649-conjugated goat Fab anti-mouse IgG. The FSC vs SSC plots are depicted in the top rows, and the scFv-Ig histograms are shown in the bottom rows. The scFv-Ig plots (unshaded histograms) were compared to staining with indirect reagents alone (shaded histograms). A limited amount of binding was observed to the surface of *B. subtilis* and *B. cereus* spores.

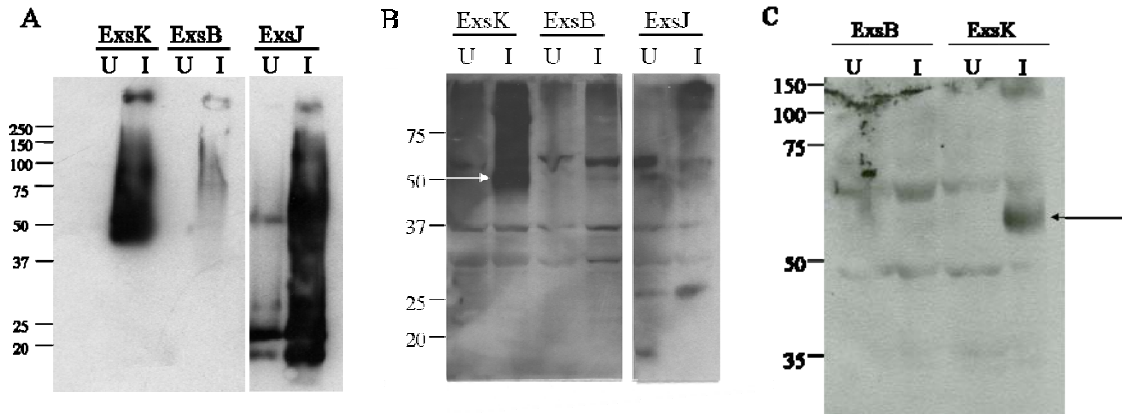


FIGURE S4. Western blot analyses of *B. anthracis* spore proteins (related to Fig. 3).

A-C, *E. coli* lysates uninduced (U) or induced (I) to produce the indicated T7-tagged *B. anthracis* protein were probed with anti-T7-HRP (A) or rabbit IgM from serum of a 6-day-old (B) or 3-week-old (C) rabbit. Arrows indicate IgM binding. These data suggest that although all four *B. anthracis* proteins were expressed, IgM bound only to ExsK.

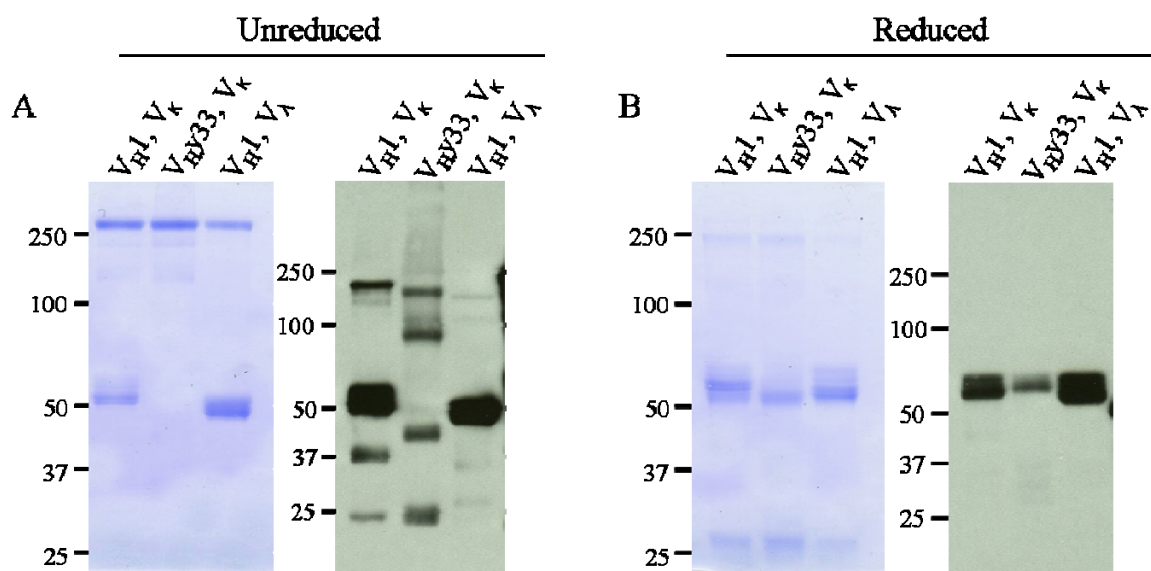


FIGURE S5. Electrophoretic analysis of scFv-Ig proteins from Fig. 4. Coomassie blue-stained SDS polyacrylamide gels (left) and western blots (right) of purified scFv-Ig proteins probed with HRP-conjugated donkey anti-rabbit IgG. Proteins were either left unreduced (A) or reduced (B) prior to gel loading to assess the purity as well as the aggregation status. V_{H1} encodes V_{Ha} ; V_{HY33} encodes V_{Hn} . These data suggest that the aggregation status of the scFv-Ig proteins does not affect binding to spores.

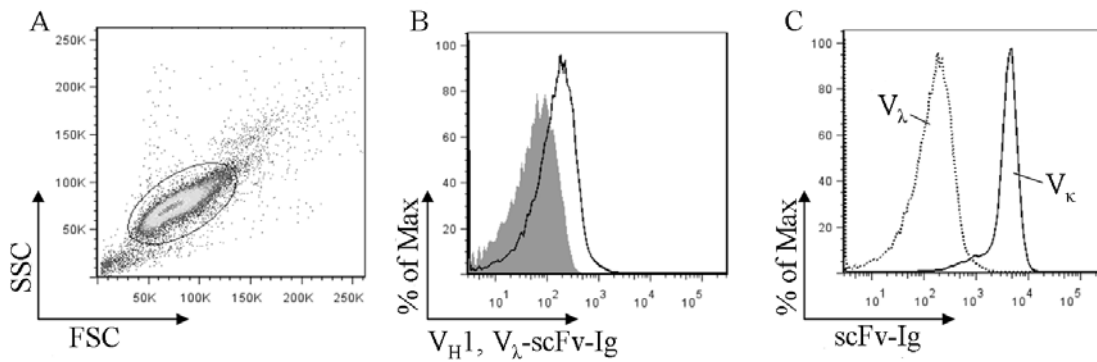


FIGURE S6. Flow cytometric analysis of *bclA* mutant *B. anthracis* spores stained with scFv-Igs from Fig. 4. *A*, FSC vs SSC dot plot spores. Gate indicates population used for staining analyses in *B* and *C*. *B*, Histograms of spores stained with V_{H1} , V_{λ} -scFv-Ig followed by mouse anti-rabbit Fc γ and FITC-conjugated goat Fab anti-mouse IgG (unshaded) or secondary antibodies alone (shaded). *C*, Histogram overlay comparing V_{H1} , V_{κ} -scFv-Ig (from Fig. 2C) and V_{H1} , V_{λ} -scFv-Ig staining (from part *B*). These data confirm that V_{H1} , V_{κ} -scFv-Ig binds more intensely to spores than does V_{H1} , V_{λ} -scFv-Ig.