## **Supplementary Information**

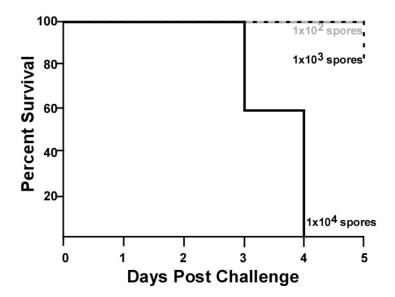
Supplementary Table 1: Data collection and refinement statistics for crystallography

| Data collection                 |                           |
|---------------------------------|---------------------------|
| Wavelength (Å)                  | 1.00                      |
| Resolution range (Å)            | 89.14-3.15 (3.37 – 3.15)  |
| Space group                     | P 6 <sub>4</sub> 2 2      |
| Unit cell (Å)                   | 84.85 x 84.85 x 178.27    |
| , ,                             | 04.03 X 04.03 X 1/0.2/    |
| Unit cell (°)                   | $90 \times 90 \times 120$ |
| Unique reflections (Total)      | 7129 (91460)              |
| Multiplicity                    | 12.8 (13.1)               |
| Completeness (%)                | 100.00 (100.00)           |
| Mean I/sigma (I/σ)              | 12.9 (2.1)                |
| R <sub>sym</sub> <sup>#</sup>   | 0.052 (0.712)             |
| Refinement                      |                           |
| R <sub>work</sub> <sup>++</sup> | 0.2755 (0.3508)           |
| R <sub>free</sub>               | 0.3260 (0.3619)           |
| No. of atoms                    | 1874                      |
| No. of hemes                    | 2                         |
| No. of waters                   | 0                         |
| No. of protein residues         | 215                       |
| R.m.s.d., bonds (Å)             | 0.004                     |
| R.m.s.d., angles (°)            | 0.98                      |
| Ramachandran favored (%)        | 96                        |
| Ramachandran outliers (%)       | 0                         |
| B-factor (Å <sup>2</sup> )      |                           |
| Average                         | 111.6                     |
| Macromolecules                  | 112.1                     |
| Ligands                         | 100.7                     |
| PDB code                        | 4YMP                      |
|                                 | •                         |

Statistics for the highest-resolution shell are shown in parentheses.

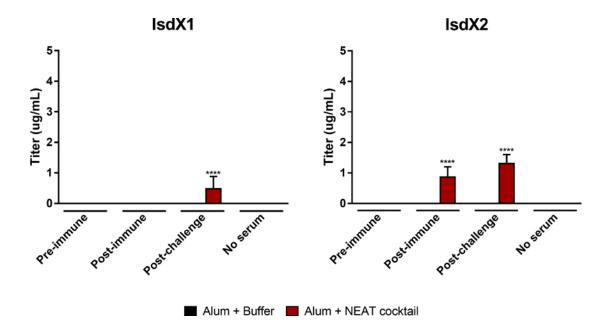
 $<sup>^{\#}</sup>R_{\text{sym}} = \sum \sum_{i} |I_{i} - (I)| / \sum \sum_{i} I_{i}$ 

 $<sup>^{++}</sup>R_{\mathrm{work}} = \Sigma ||F_{\mathrm{obs}}| - |F_{\mathit{calc}}|| / \Sigma |F_{\mathrm{obs}}|$ , where  $R_{\mathrm{free}}$  was computed identically except all reflections belonged to a test set consisting of a 5% random selection of the data.



## Supplementary Figure 1. Measurement of the LD<sub>50</sub> of *B. anthracis* Sterne for A/J mice.

Three groups of mice (n = 5) were subcutaneously challenged either with 1 X  $10^2$ , 1 X  $10^3$  or 1 X  $10^4$  spores and the LD<sub>50</sub> was determined using the Reed-Muench method using the higher dose at day five.



Supplementary Figure 2. Reactivity of the serum from mice vaccinated with the NEAT domains and Alum. Pre-immune, post-vaccine and post-challenge serum from mice vaccinated either with Alum,  $Hal_N$ , or the NEAT cocktail were evaluated for the presence of anti-NEAT antibodies using ELISA with purified NEAT domains from each NEAT protein: IsdX1, Hal, BslK, IsdC and IsdX2. The asterisks represent Tukey's multiple comparison test comparing the post-immune or post-challenge response to the pre-immune and no-serum response; \*\*\*\* p < 0.0001