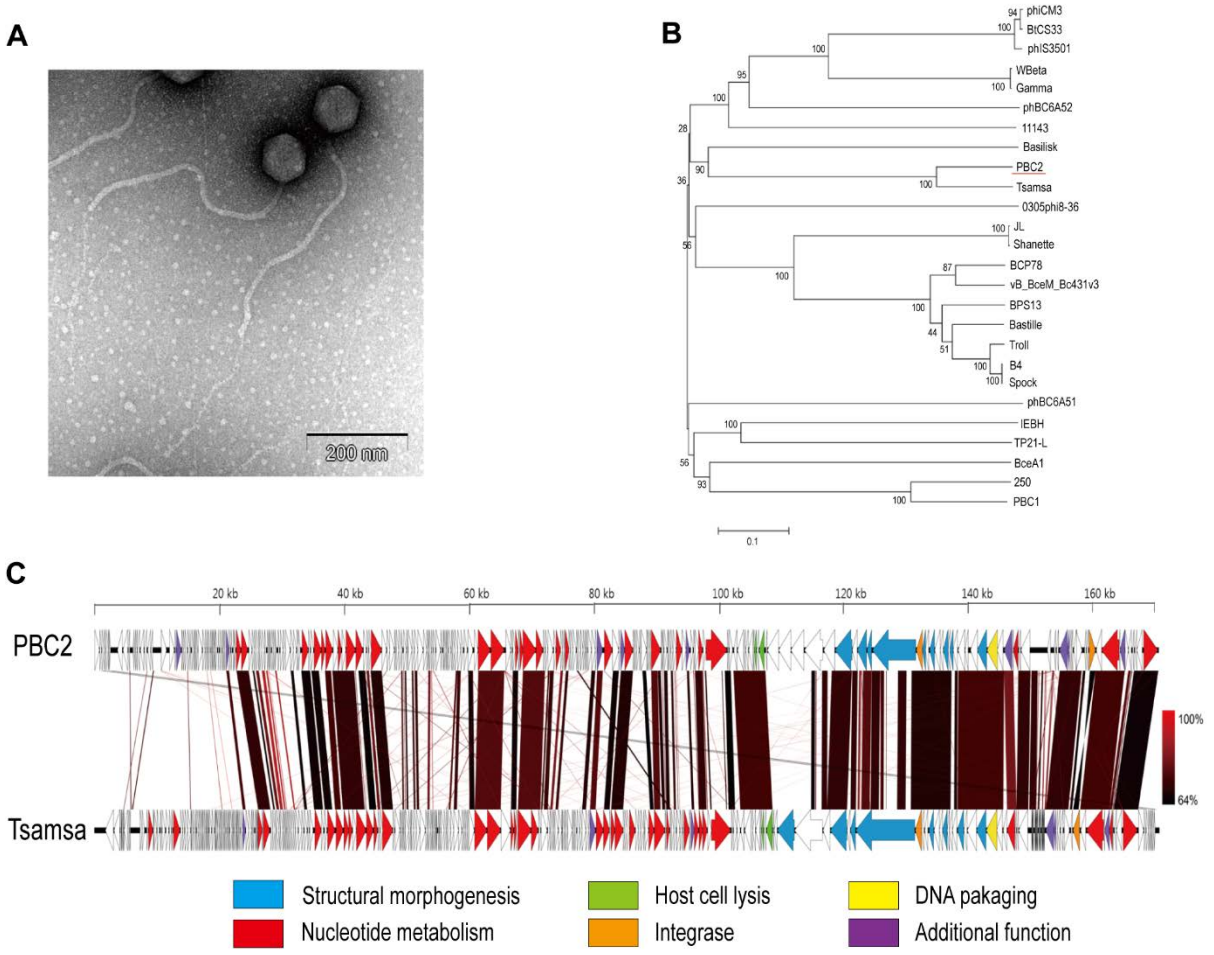

Figure S1. Isolation and genomic analysis of phage PBC2. (A) A TEM image of the PBC2 phage. (B) Phylogenetic tree of the terminase large subunits from *B. cereus* group phages. The scale bars represent the number of nucleotide substitutions per site and the numbers at the nodes indicate the bootstrap probabilities. (C) DNA-level alignment of the genomes of phage PBC2 and Tsamsa. Predicted ORFs are denoted by arrows and the color of each gene refers to the functional categories such as phage structure (blue), DNA packaging (yellow), host lysis (green), nucleotide metabolism (red), integrase (orange), and additional function (purple). The regions with at least 64% nucleotide identity are indicated by shaded bars.

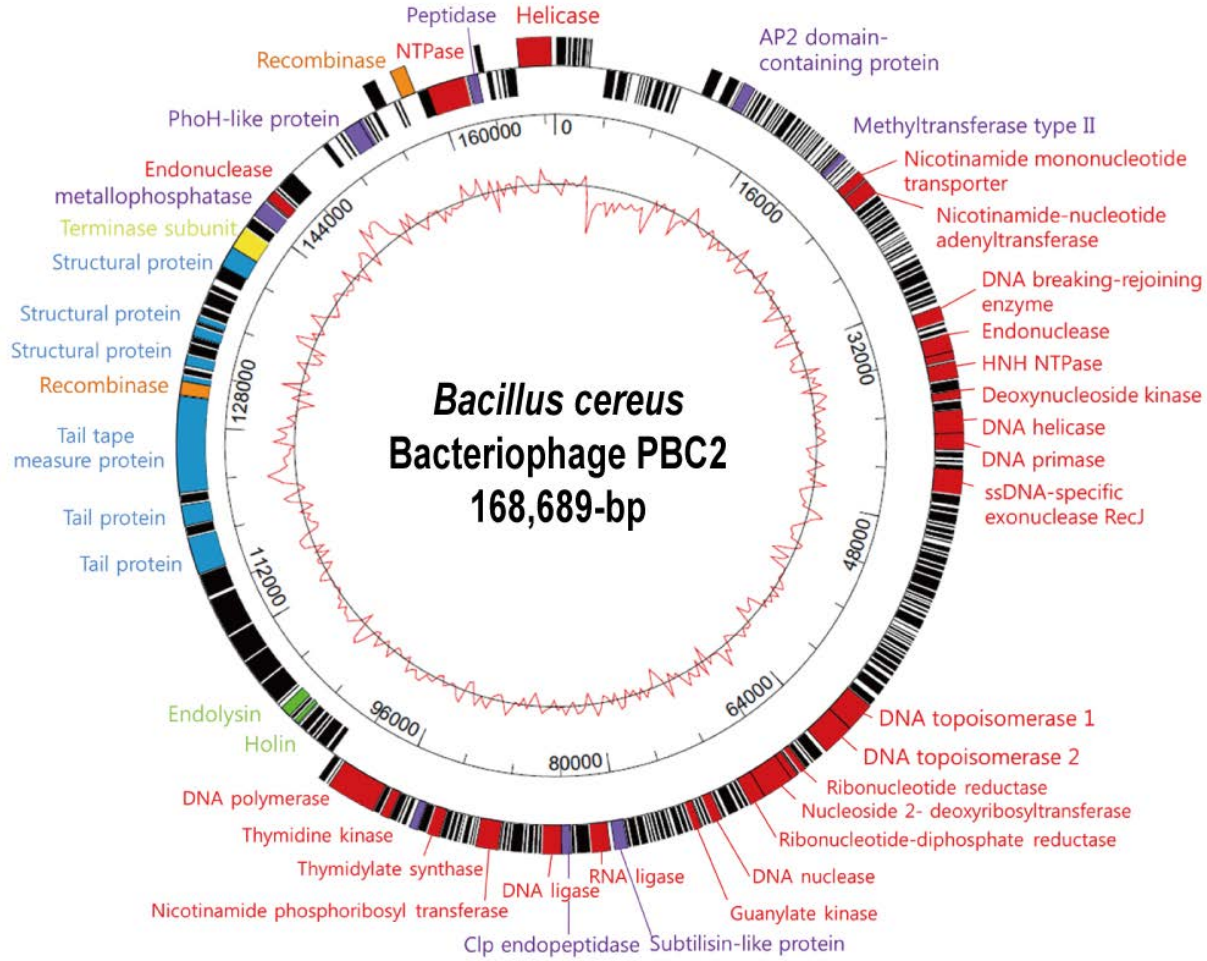

Figure S2. Genome map of PBC2. Outer circle indicates the gene coding regions by strand. The color of each gene refers to the functional categories including phage structure (blue), DNA packaging (yellow), host lysis (green), nucleotide metabolism (red), integrase (orange), and additional functions (purple). The inner circle with the red line indicates the G+C content. The scale unit is a base pair.

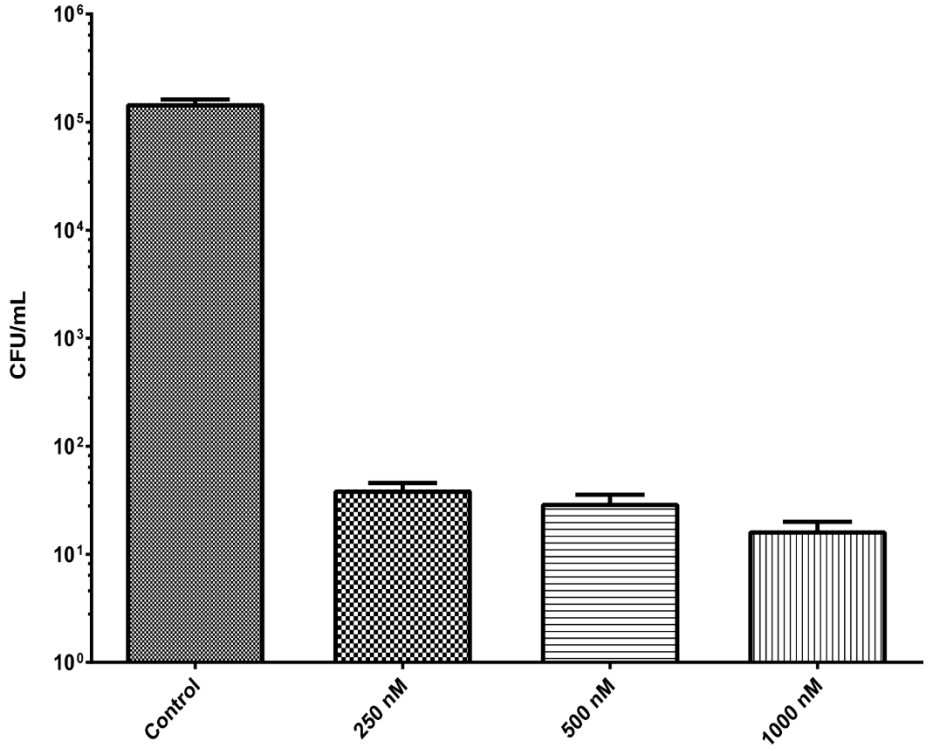

Figure S3. Antimicrobial activity of LysPBC2 against *B. cereus.* Exponentially growing *B. cereus* ATCC 13061 cells were treated with different concentrations of LysPBC2 for 1 h at 37°C. After incubation, viable cells were counted by plating on BHI agar.

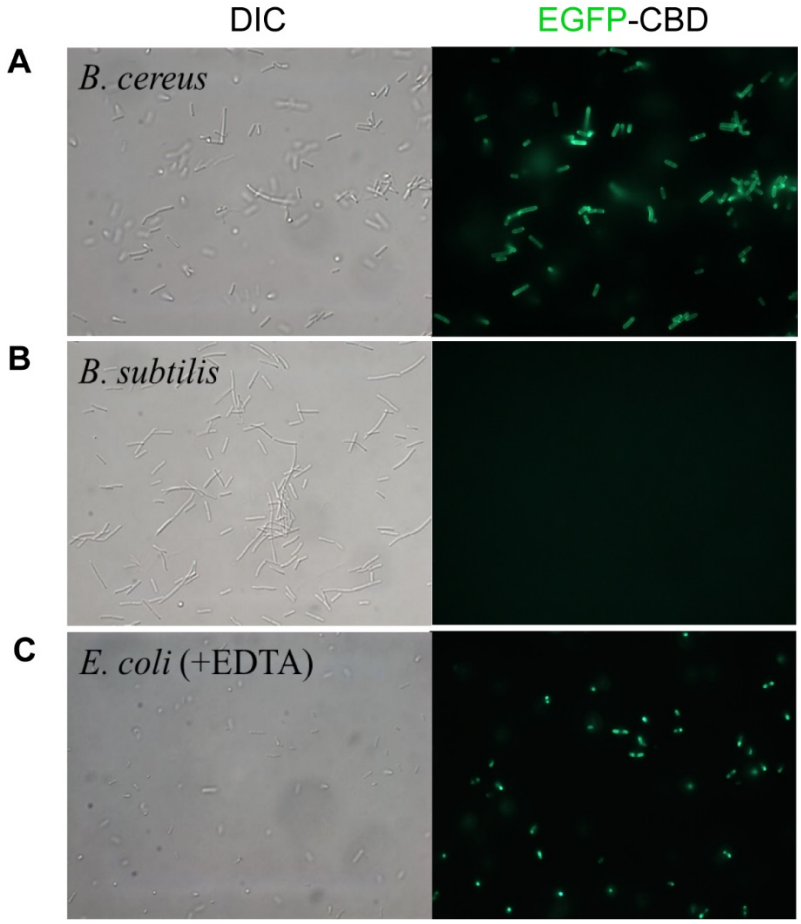

Figure S4. Cell binding activity of EGFP-fused LysPBC2_CBD. Fluorscent microscopy images of binding of EGFP-CBD proteins to *B. cereus* ATCC 14579 (A), *B. subtilis* ATCC 6051 (B) and EDTA-treated *E. coli* MG1655 cells (C).

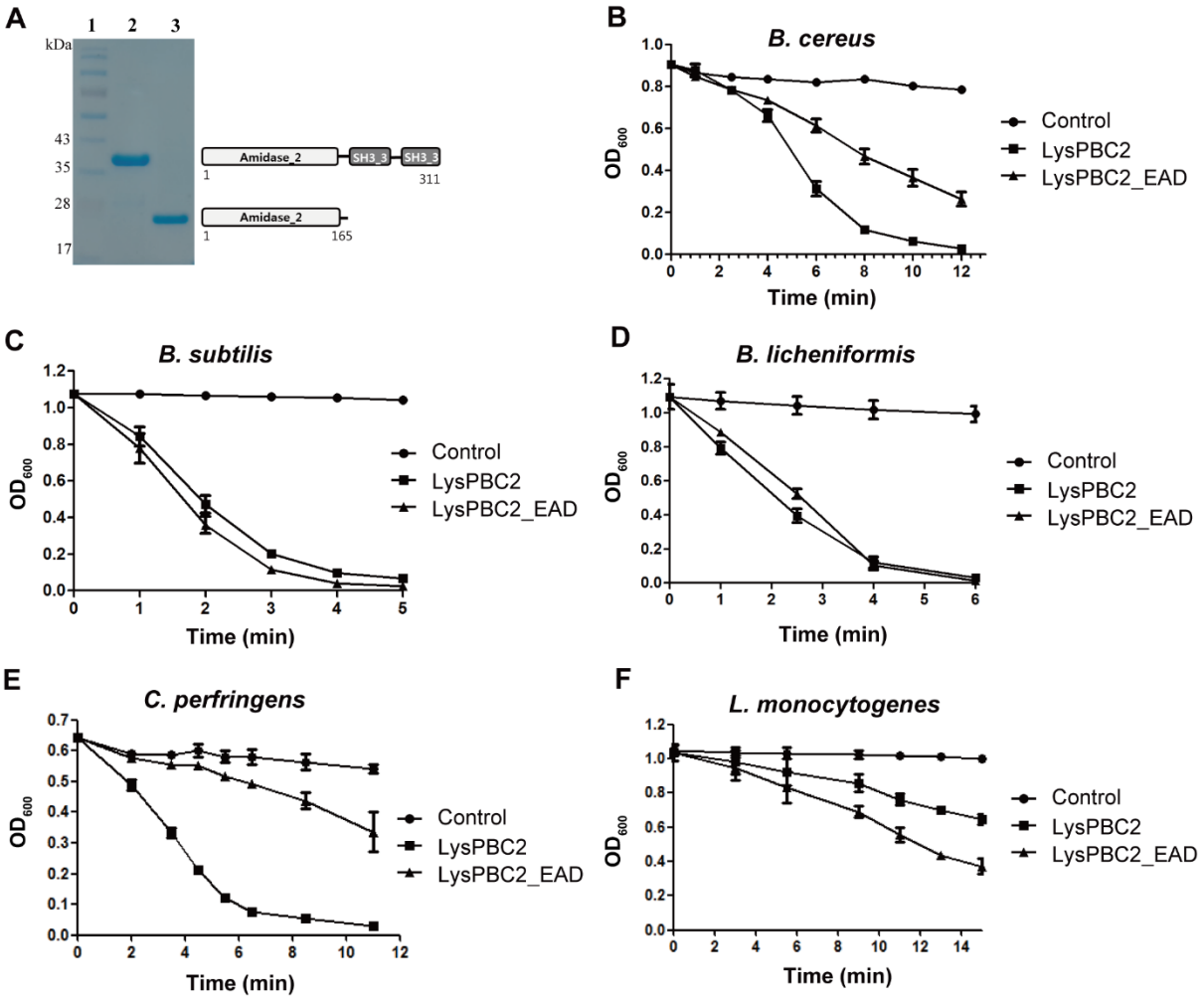

Figure S5. Lytic activities of LysPBC2 and LysPBC2_EAD. (A) Analysis of Ni-NTA purified proteins on a SDS-PAGE gel (Lane 1, size marker; lane 2, LysPBC2; lane 3, LysPBC2_EAD). Corresponding diagrams were shown on the right. Equimolar concentrations (0.4 μM) of LysPBC2 and LysPBC2_EAD were added to the suspension of *B. cereus* ATCC 13061 (B), *B. subtilis* ATCC 6051 (C), *B. licheniformis* JCM 2505 (D), *C. perfringens* ATCC 13124 (E), *L. monocytogenes* Scott A (F), and the decrease in turbidity was monitored.

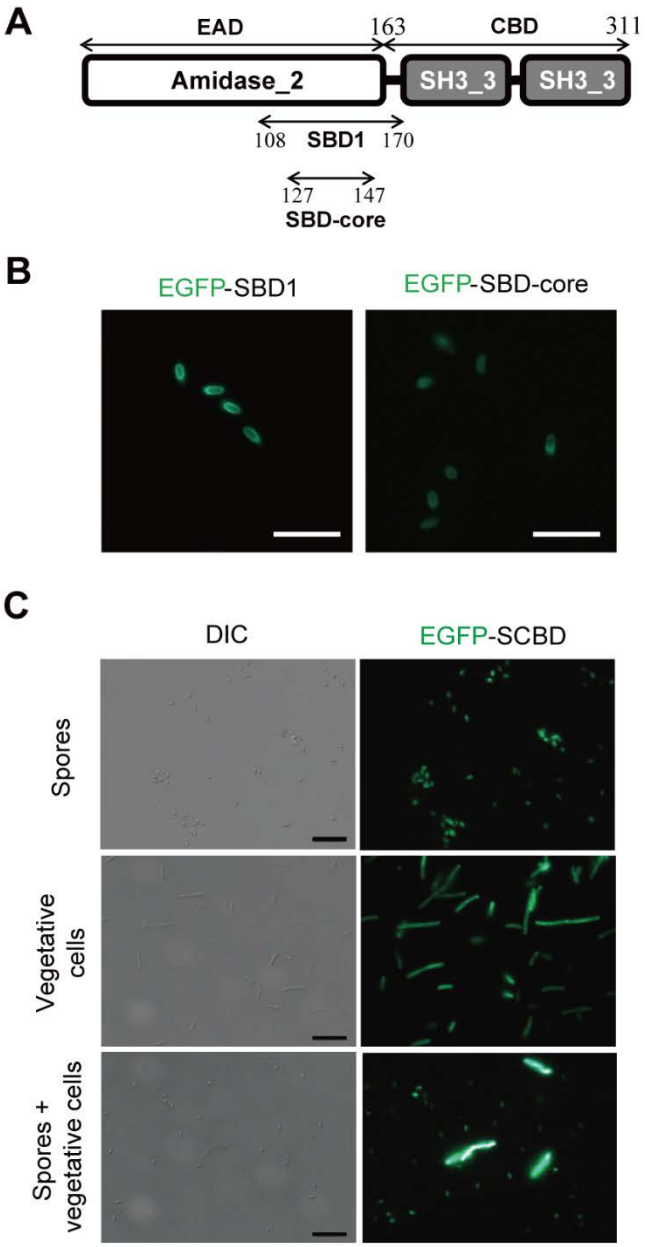

Figure S6. Comparison of spore binding activity between SBD1 and SBD-core and confirmation of SCBD for binding both spores and vegetative cells. (A) Schematic representation of SBD constructs used in this study. (B) Fluorescent images of *B. cereus* spores labeled with 1 μM of the EGFP-SBD1 (left) and EGFP-SBD-core (right), respectively. Scale bars = 10 μm. (C) EGFP-tagged SCBD fusion protein showed binding activity to both *B. cereus* spores and vegetative cells in mixed samples. Scale bars = 5 μm.

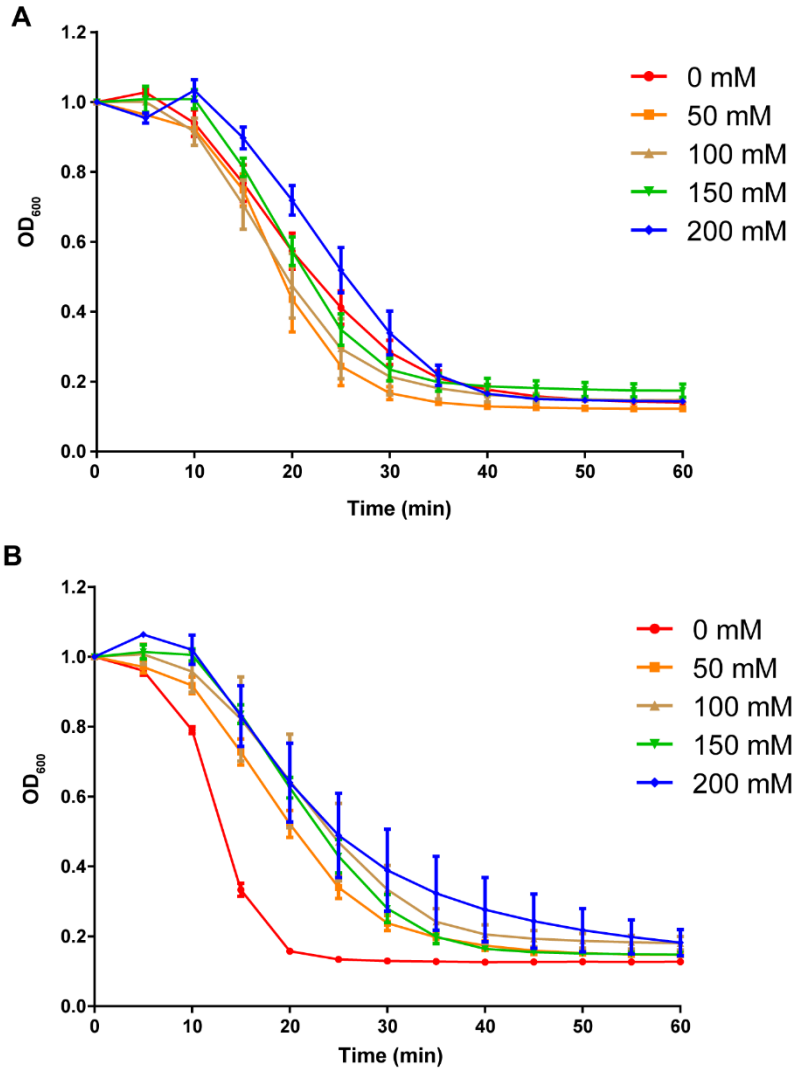

Figure S7. The effects of NaCl concentrations on lytic activity of LysPBC2 and its mutant (K129E). The lytic activities of WT (A) and K129E mutant (B) of LysPBC2 were measured using turbidity reduction assay with buffers containing different concentrations of NaCl. The error bars mean ±SD from triplicate assays.

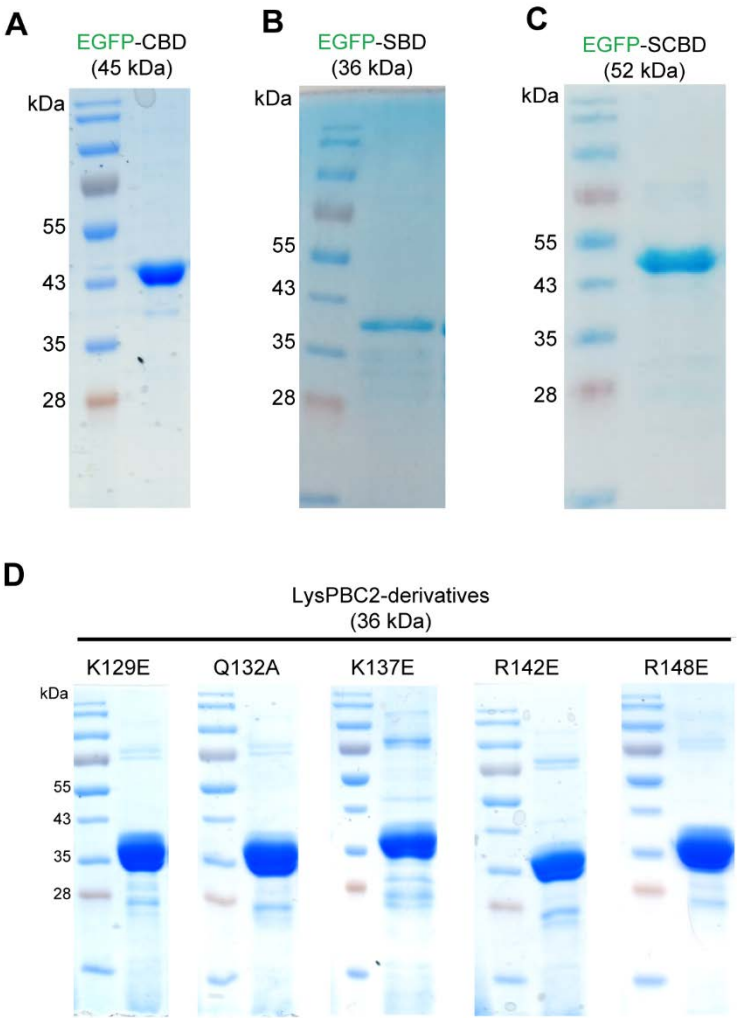

Figure S8. SDS-PAGE profiles of proteins used in this study.