Supporting Information

Clinically Relevant Pathogens on Surfaces Display Differences in Survival and Transcriptomic Response in Relation to Probiotic and Traditional Cleaning Strategies

Jinglin Hu, Weitao Shuai, Jack T. Sumner, Anahid A. Moghadam, Erica M. Hartmann*



Supplementary Figure 1. p-values of *A. baumannii* (A) and *K. pneumoniae* (B) viable CFU counts among samples collected under two temperature/humidity conditions and four cleaning scenarios. Statistical testing was conducted using Welch's paired t-test. * p<0.05, ** p< 0.01, and ***p < 0.001.



Supplementary Figure 2. Percentages of reads mapped onto *Bacillus* spp. and either *A. baumannii* (top) or *K. pneumoniae* (bottom) genomes for samples collected from four surface cleaning scenarios.



Supplementary Figure 3. Principal components analysis on variance stabilized *K. pneumoniae* read counts. Samples were color-coded based on cleaning time.



Supplementary Figure 4. Number of differentially expressed genes for germinated *Bacillus* reads. The *Bacillus* transcriptome was compared in the presence of *A*. *baumannii* or *K. pneumoniae* using vegetative *Bacillus* without pathogen as the reference level. Comparison was also conducted between different time points.



Supplementary Figure 5. Log₂ fold change of genes associated with iron acquisition, Type VI Secretion System (T6SS), Type VI Pili, and biofilm poly-beta-1,6-N-acetyl-D-glucosamine (PGA) production in samples cleaned with Cleaner Only, Probiotic Cleaner, and Germinated *Bacillus* compared to No Cleaner samples (*A. baumannii* only). Statistically significant log₂ fold changes were determined by DESeq2 with Benjamini-Hochberg corrected p-value ≤ 0.05 . * p<0.05, ** p< 0.01, and ***p < 0.001.



Supplementary Figure 6. Log₂ fold change of genes associated with iron acquisition, Type VI Secretion System (T6SS), biofilm poly-beta-1,6-N-acetyl-D-glucosamine (PGA) production, and Type 1 Pili in samples cleaned with Cleaner Only,

Probiotic Cleaner, and Germinated *Bacillus* compared to No Cleaner samples (*K. pneumoniae* only). Statistically significant \log_2 fold changes were determined by DESeq2 with Benjamini-Hochberg corrected p-value ≤ 0.05 . Some genes have Benjamini-Hochberg corrected p-value ≤ 0.05 but \log_2 fold change < 1. * p < 0.05, ** p < 0.01, and ***p < 0.001.



Supplementary Figure 7. Expression of genes associated with siderophore and iron acquisition in vegetative *Bacillus* spp. samples in the presence of *A. baumannii* (AVEG), *K. pneumoniae* (CVEG), and in the absence of pathogen (VB).

Read counts belonging to Bacillus *spp*. were transformed using variance stabilization to enable between-sample comparisons.