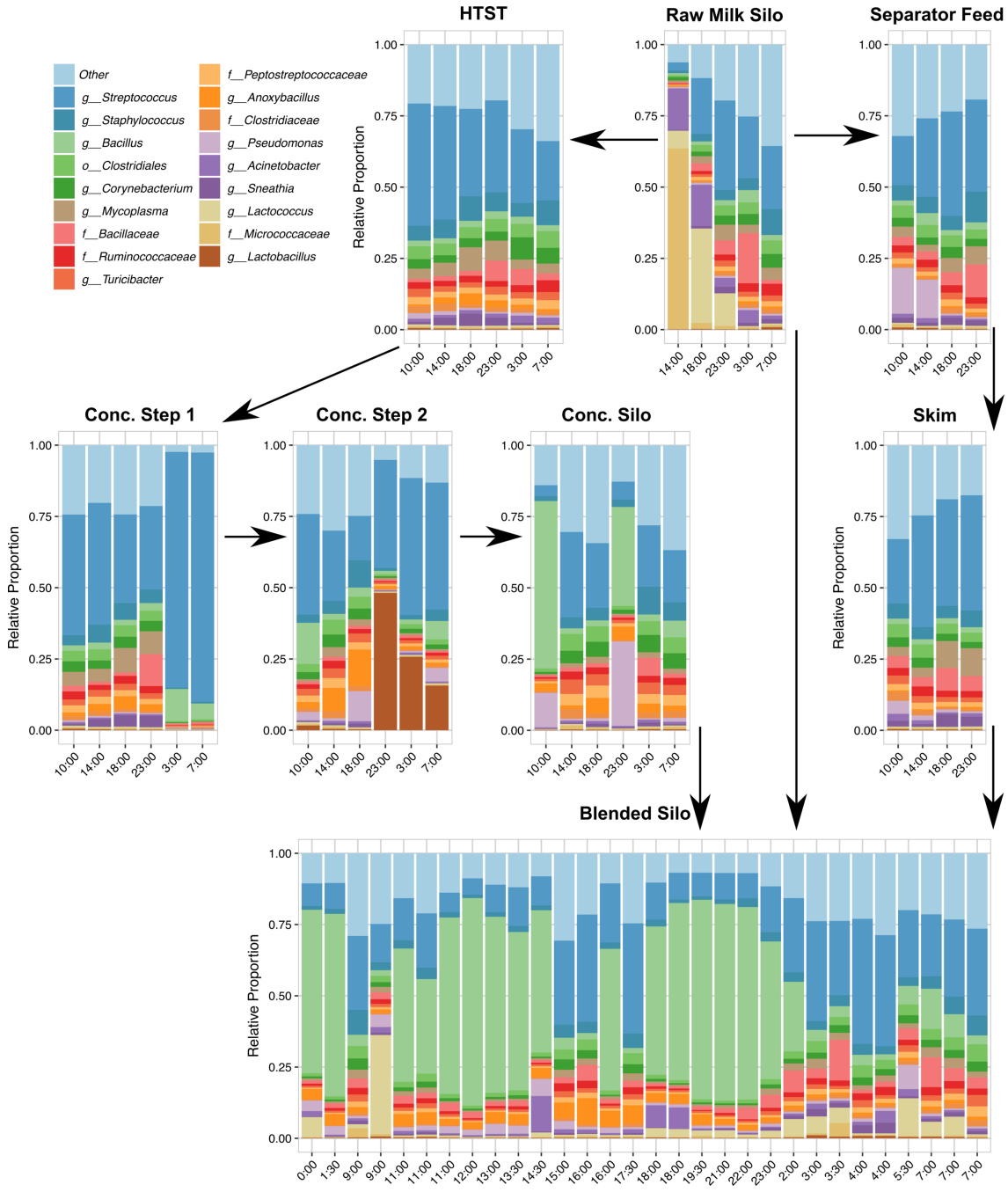

Figure S1. Dominant bacteria in milk processed on the spring sampling dates. Taxa present at greater than 0.01 average relative abundance after rarefaction to 9,000 sequences per sample are shown. Taxa present at less than 0.01 average relative abundance were grouped into the category "Other". Each bar graph is labeled with the piece of equipment from which samples were collected (see Figure 1). The time of collection is shown on the x-axis. Arrows indicate the order in which the milk was processed.

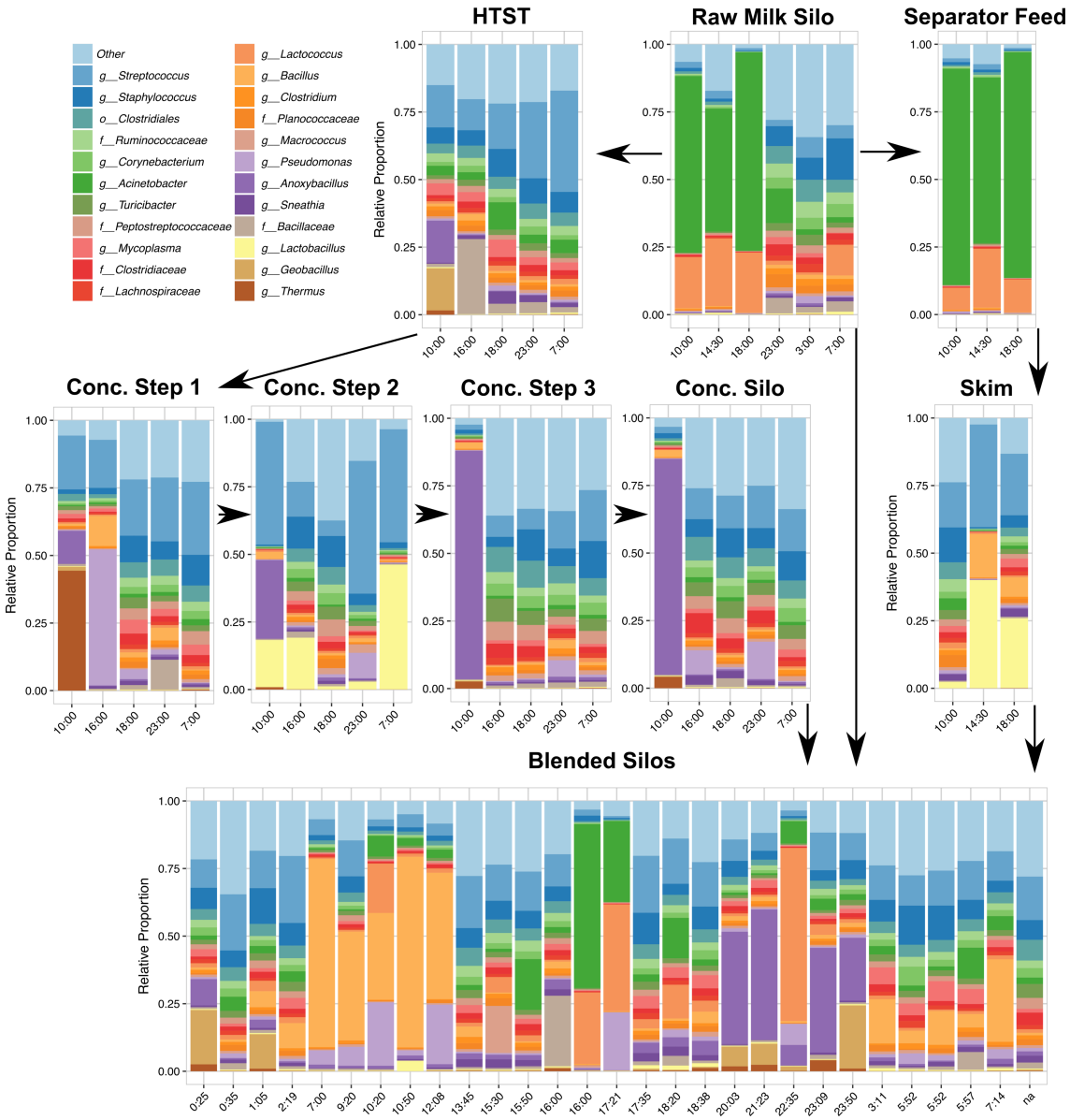

Figure S2. Dominant bacterial taxa in milk during the late summer sampling date ordered by sampling time. As shown in Figure 3, bacteria present at greater than 0.01 average proportion within the dataset after rarefaction to 9,000 sequences per sample are shown. Taxa present at less than 0.01 average relative abundance were grouped into the category "Other". Each bar graph is labeled with the piece of equipment that samples were collected from. Arrows indicate the direction that the milk moves through the facility.

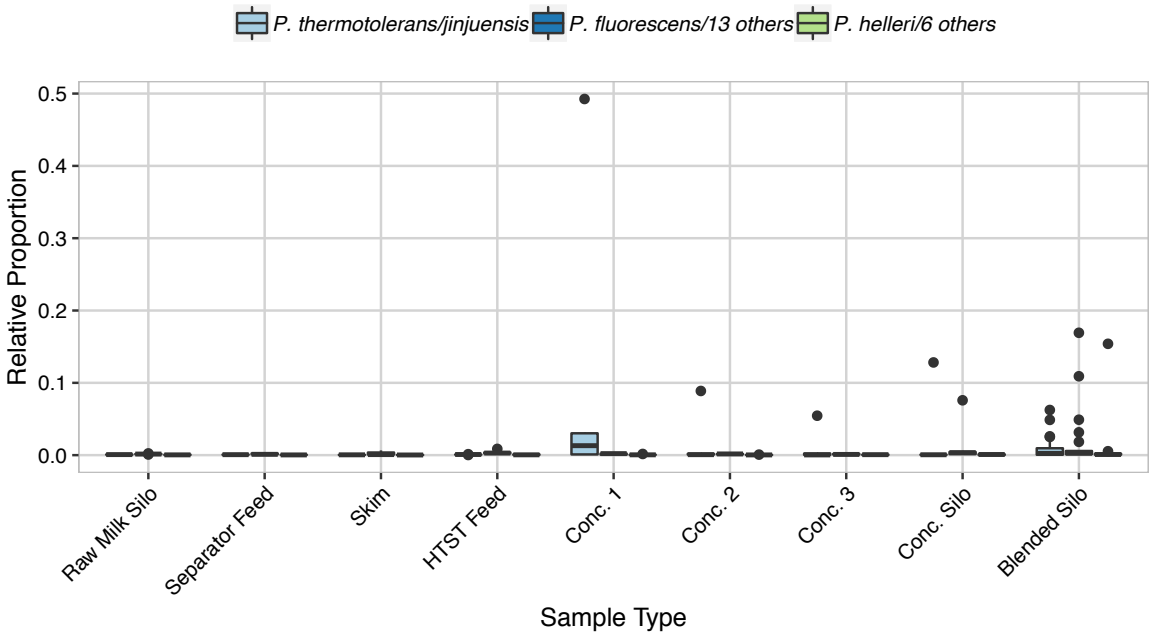

Figure S3. Proportions of the three most abundant *Pseudomonas* OTUs detected at the late summer sampling. Representative sequences from each OTU were used to search the Targeted Loci Nucleotide 16S rRNA gene sequence database using BLAST. The legend contains the number of species potentially represented by each OTU along with a representative species.

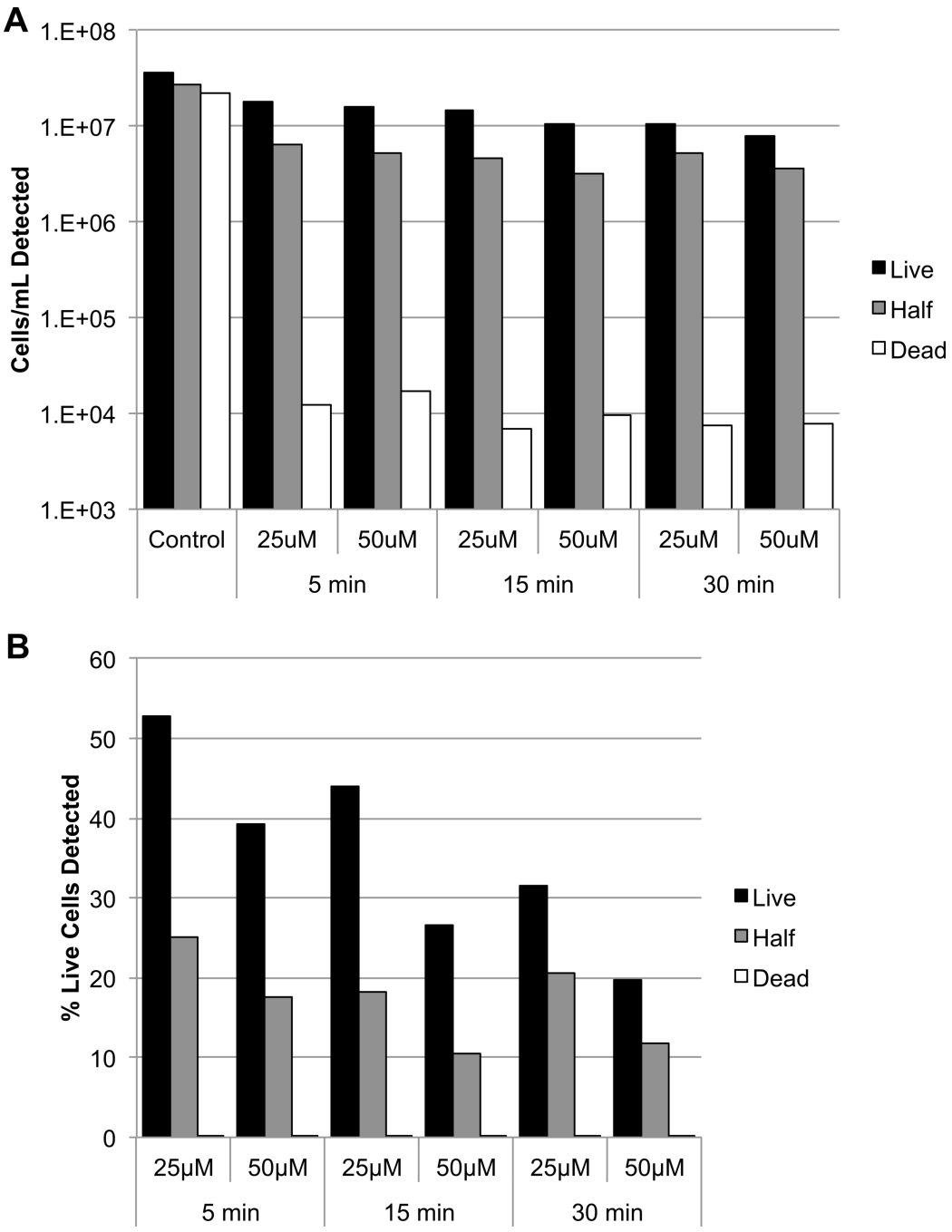

Figure S4. Evaluation of different Propidium Monoazide (PMA) treatment conditions on *Lactobacillus casei* in UHT milk. UHT milk was spiked with either 100% (10^6 cells/mL) viable exponential phase *L. casei* (Live), 50% viable *L. casei* mixed with 50% heat treated *L. casei* (Half), or 100% heat treated *L. casei* (Dead). **A)** Estimated *L. casei* cell counts determined using qPCR of bacterial DNA after incubation in 25 µM or 50 µM PMA for 5, 15 or 30 minutes. **B)** The percentage of live *L. casei* cells detected relative to the Control (untreated) group for each PMA treatment protocol described in panel A.

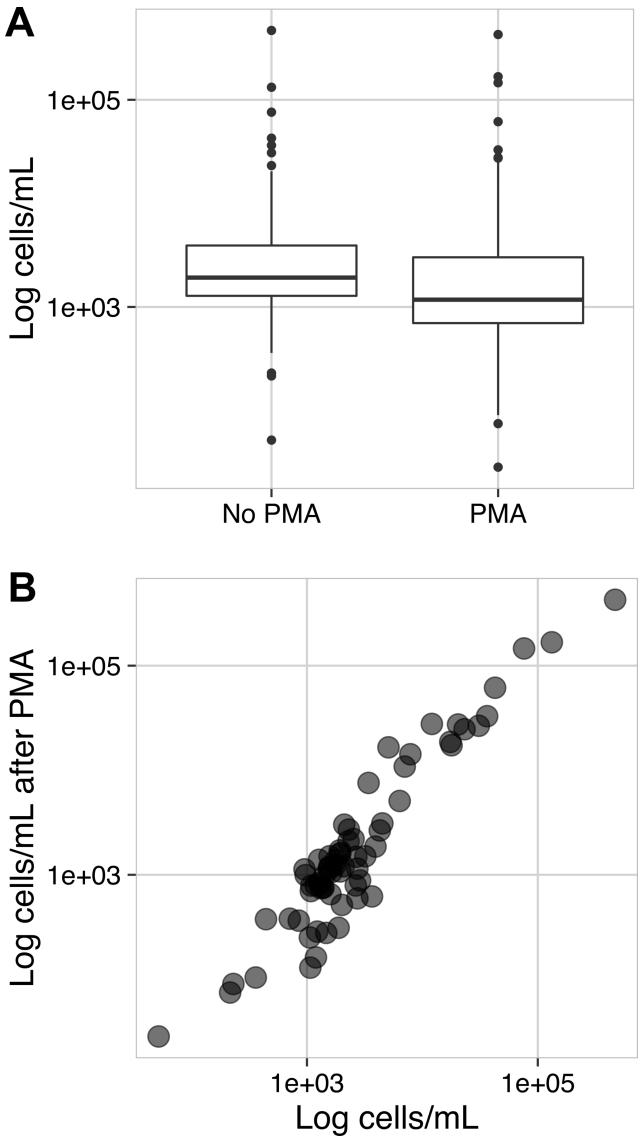

Figure S5. Effects of PMA treatment on bacterial cell counts in milk. A total of 69 samples are shown including the pre- and post-pasteurization steps (raw milk silo, separator feed, skim and cream from separator, HTST feed tank, three concentration steps, concentration silo and blended silo) from the late summer sampling date. Bacterial cell counts were estimated by qPCR for one untreated 30 mL aliquot and one 30 mL aliquot treated with 25µM PMA for 5 minutes. **A)** Boxplot of the distribution of estimated bacterial cell counts for each milk sample with and without PMA treatment. **B)** Relationship between estimated bacterial cell counts for PMA treated and untreated aliquots of each milk sample.

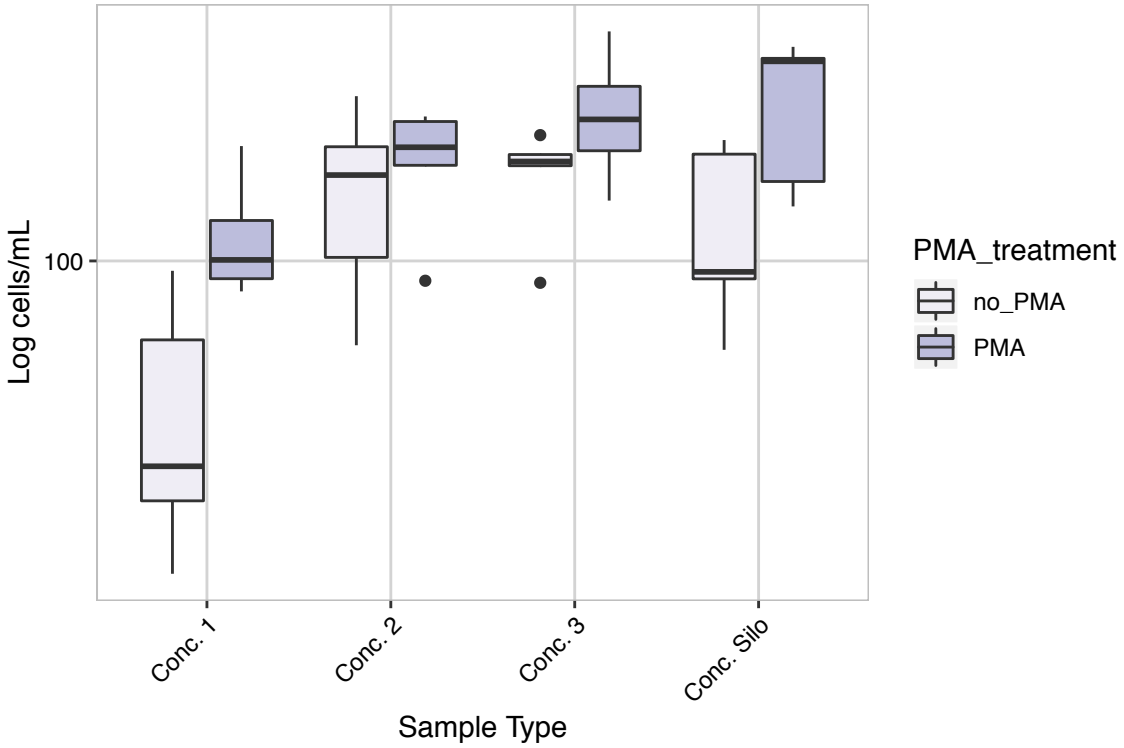

Figure S6. Estimated numbers of *Turicibacter* spp. cells/mL of milk. qPCR was used to estimate *Turicibacter* cell the numbers.

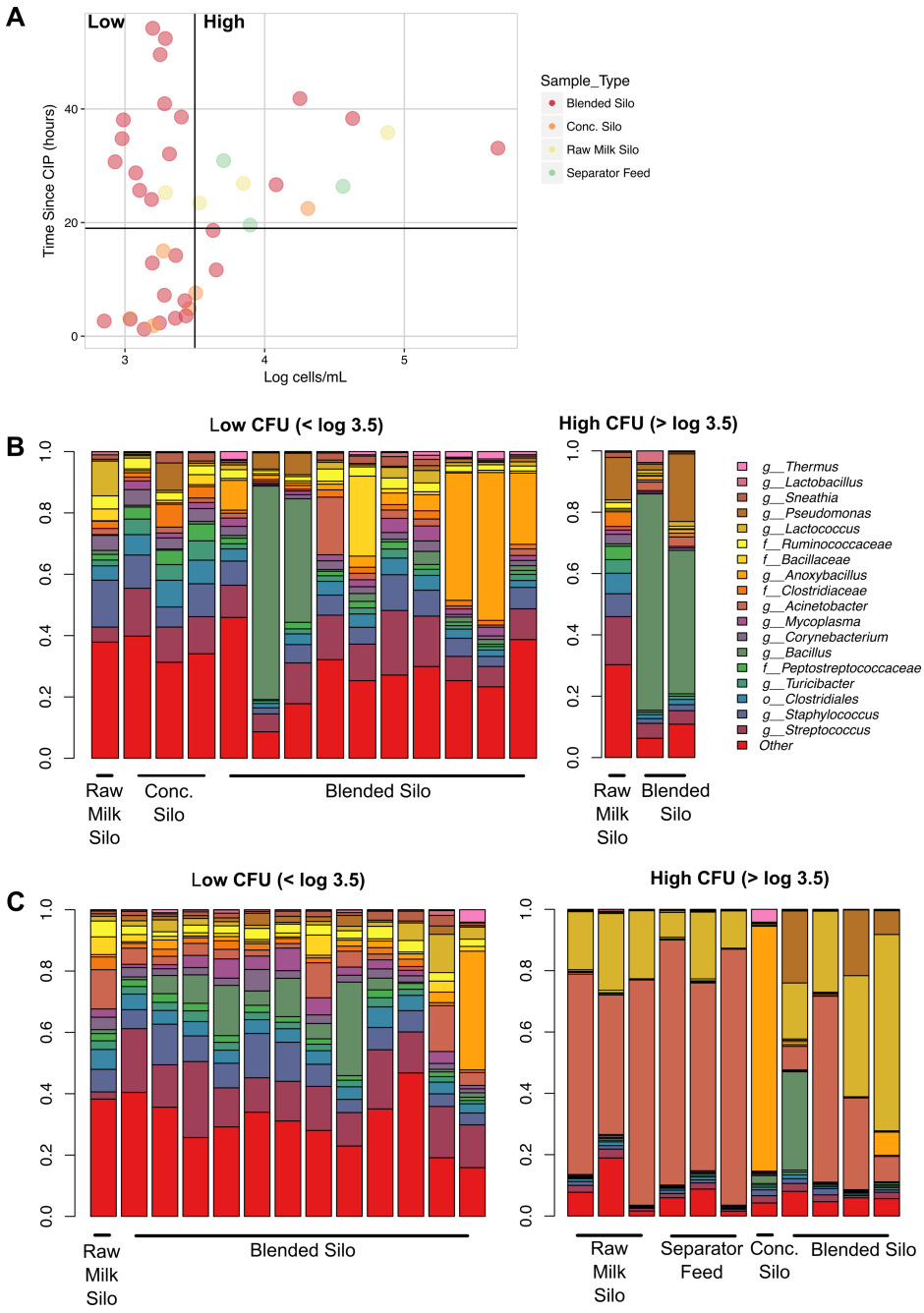

Figure S7. Potential growth of specific bacterial taxa in a subset of silos with extended time since CIP. Milk samples collected from silos in the summer that were not PMA treated. **A)** Estimated total bacterial cell counts compared to the number of hours since clean in place (CIP) for each milk sample. A vertical line at 3,200 cells/mL and a horizontal line at 19 h since CIP delineate the cut-off for low and high bacterial loads the in silos. **B)** Microbial community structure of individual milk samples collected from silos with less than 19 h since CIP. **C)** Microbial community structure of milk samples collected from silos with greater than 19 hours since CIP and low (left panel) or high (right panel) bacterial loads.

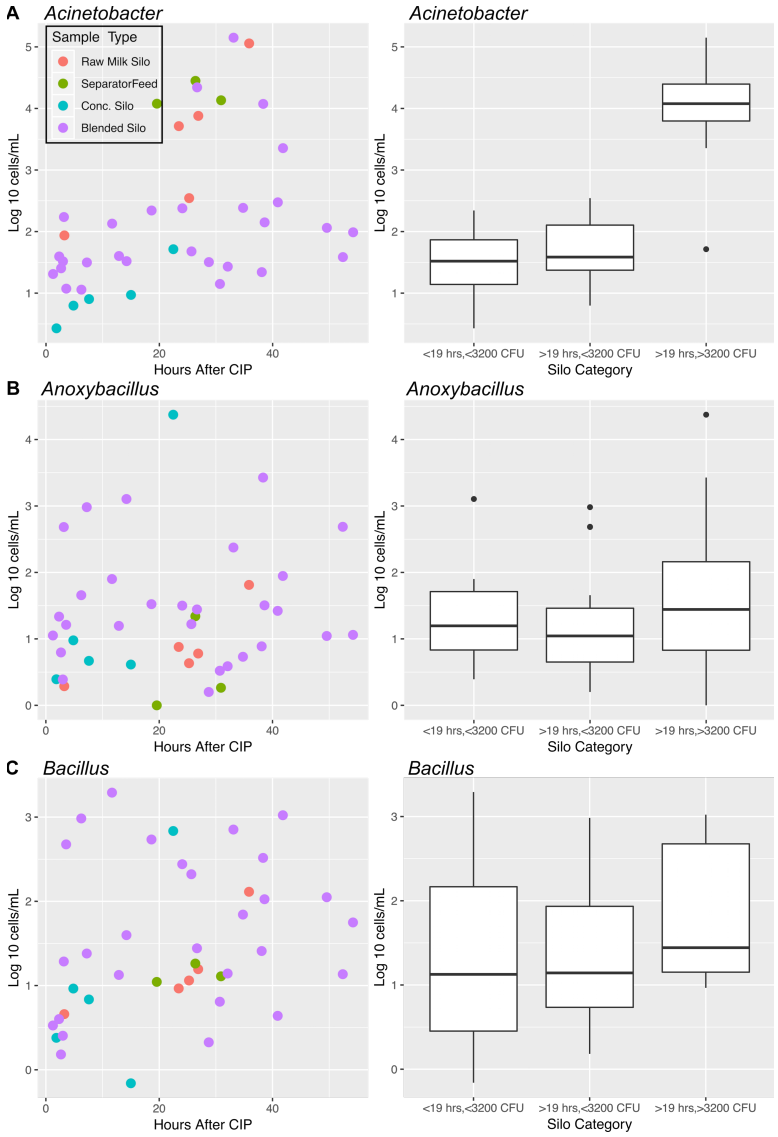

Figure S8. Estimated numbers of potential spoilage organisms relative to time since CIP. The numbers of bacterial cells potentially associated with *Acinetobacter* (**A**), *Anoxybacillus* (**B**) and *Bacillus* (**C**) were estimated for each sample by multiplying the relative abundance of each genus by total bacterial cell numbers determined by qPCR.