Supplemental Figures

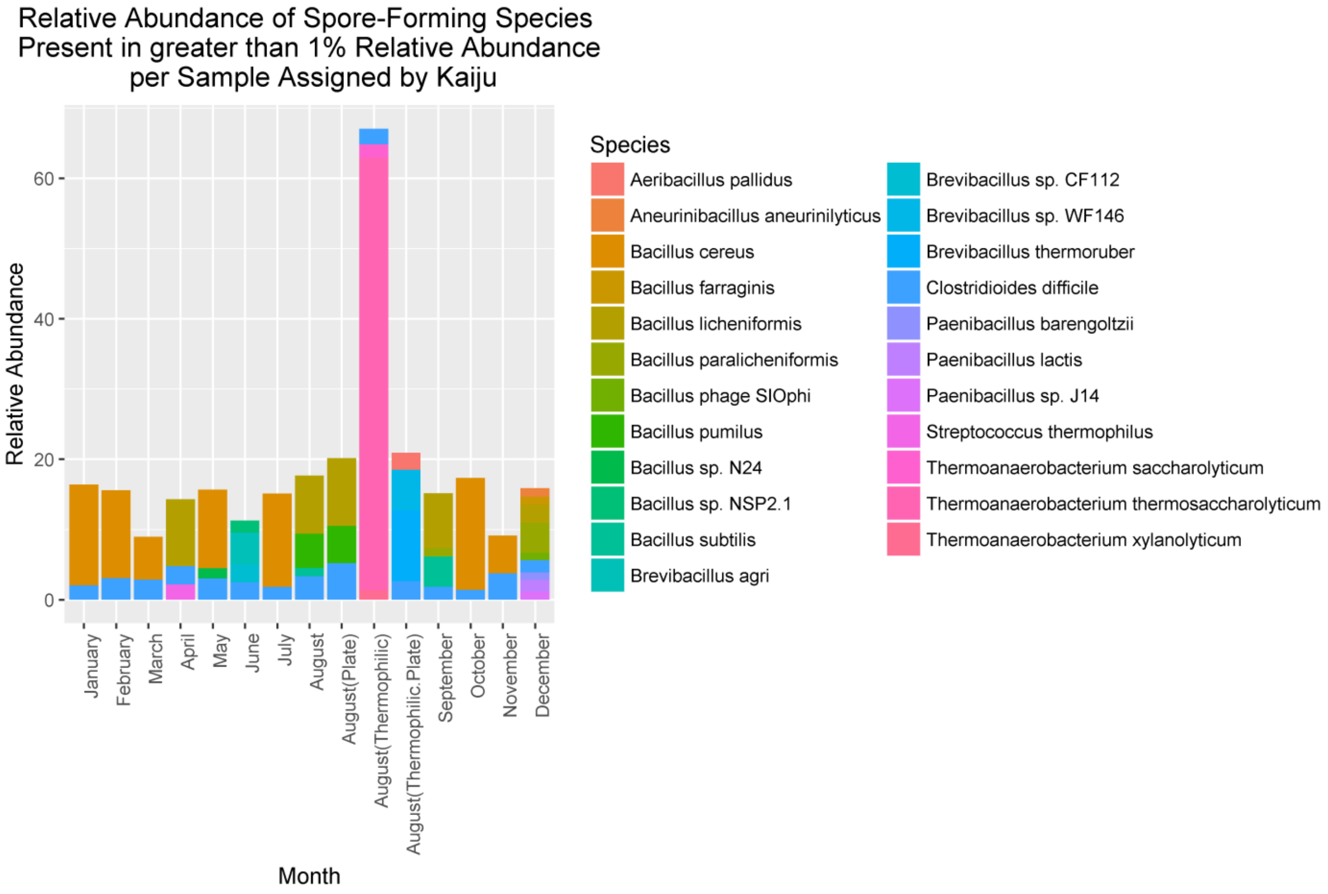

Fig S1. Kaiju species taxonomy results. Species were only included if they were present in >1% relative abundance per sample.

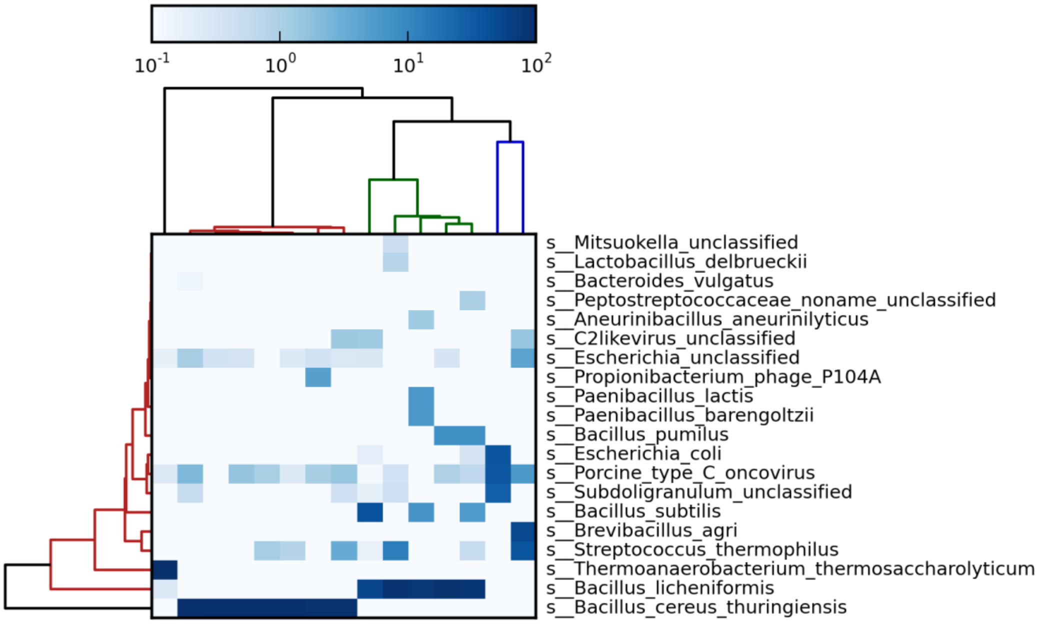

Fig S2. MetaPhlAn2 species level classification. From left to right samples are A.T, February, October, March, July, January, November, May, September, April, December, A.M.P, A.M, A.T.P, June.

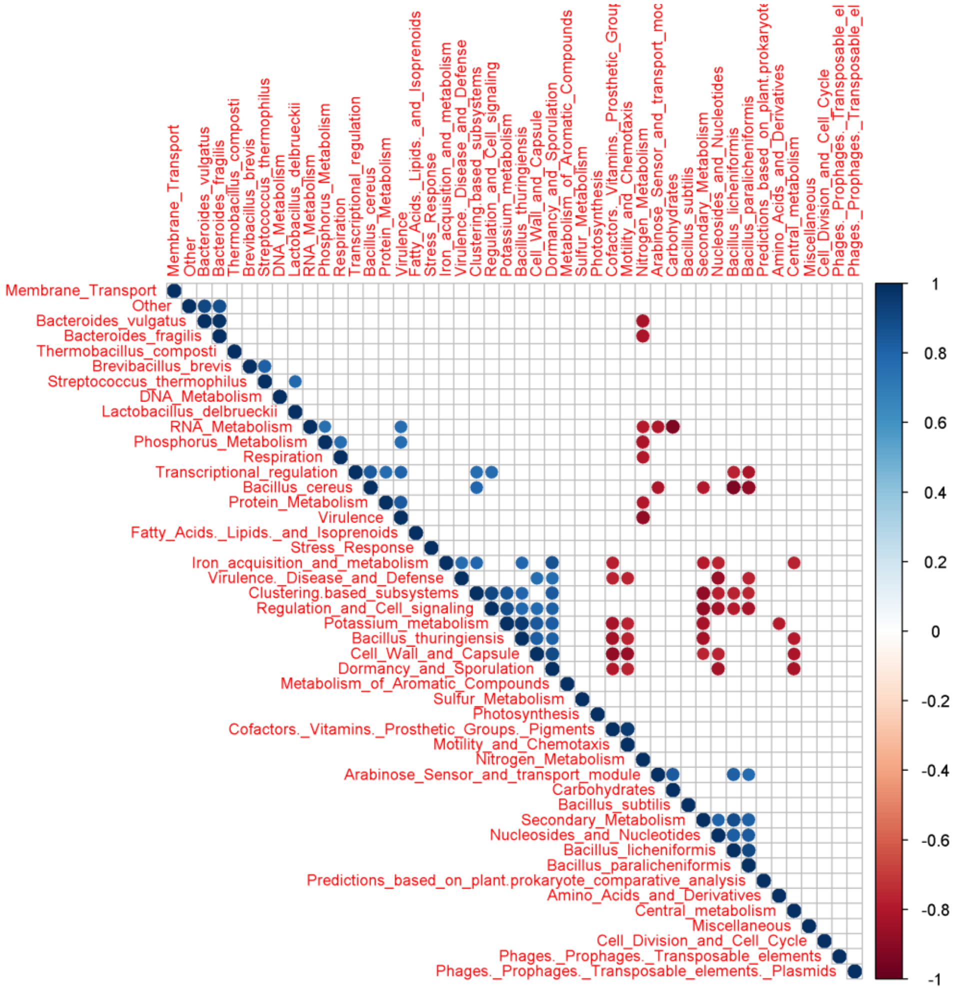

Fig S3.

Spearman correlation with Benjamini-Hochberg correction for multiple comparisons between most abundant species identified and SUPER-FOCUS L1 functional groups. Dots represent significant correlations P<= 0.05. Blue being positive correlations and red being negative correlations.

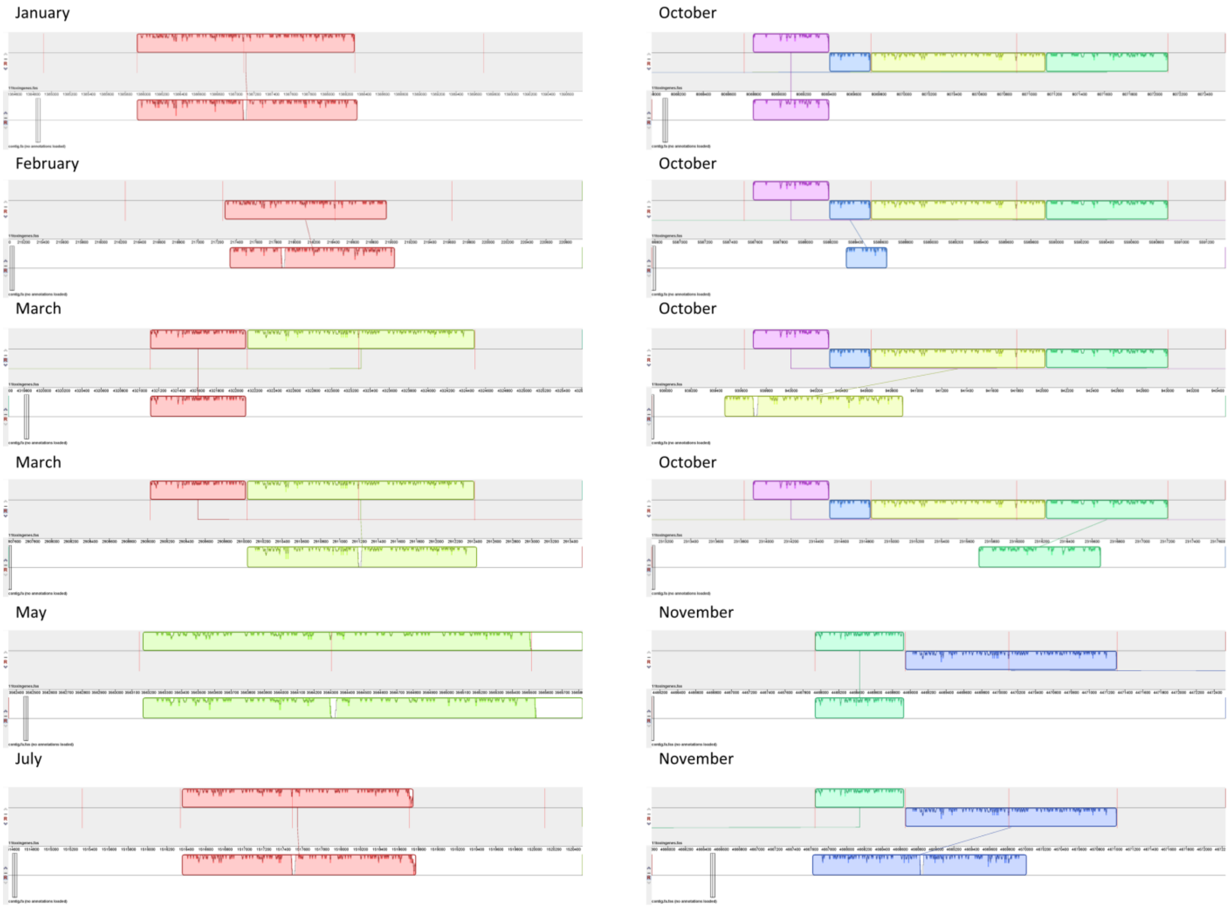

Fig S4.

Mauve *B. cereus* toxin genes alignment (3 toxin genes) 7 sets of contigs. Toxin genes on top row, CytK, Nhe L2 Nhe L1, contigs on bottom rows. Samples that align to more than one contig have multiple images. March and November have cytK gene on different contig to two NHE genes, so 2 alignments shown. October has 4 alignments shown as genes are at the edge of contigs.

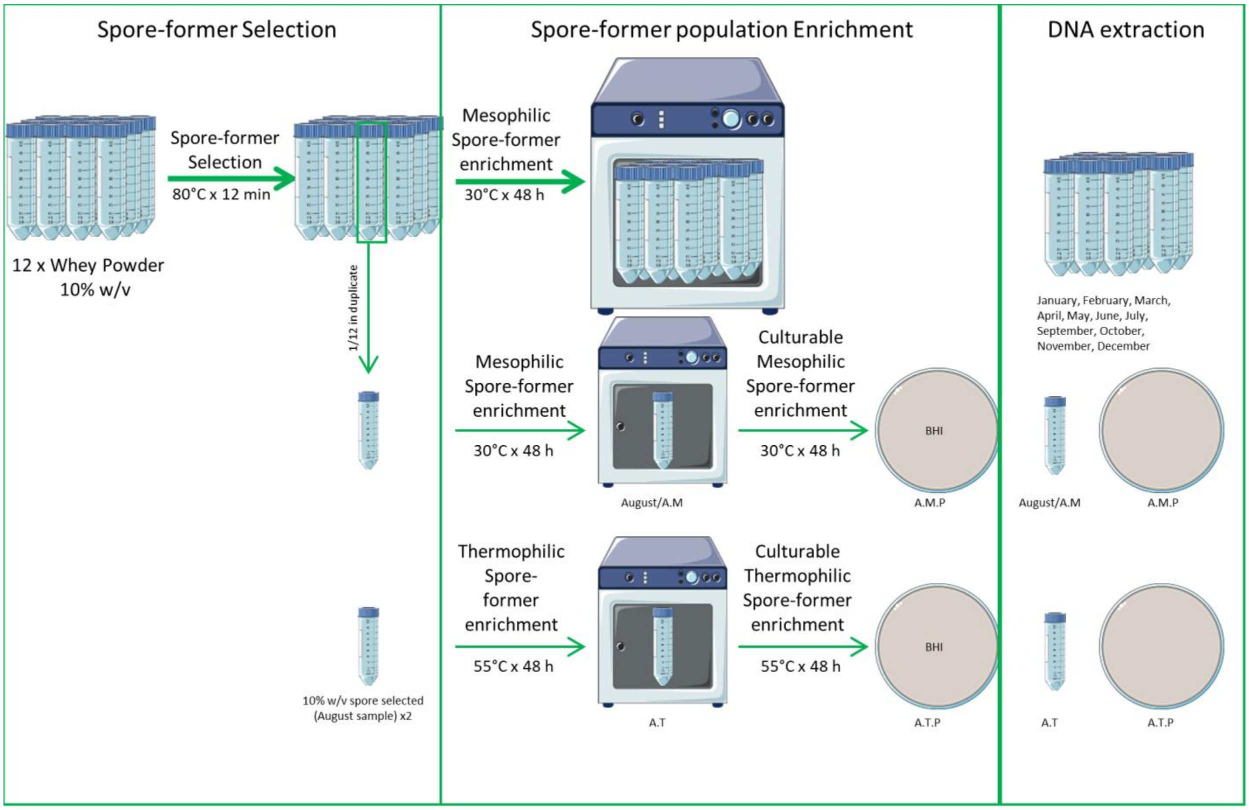

Fig S5.

Detailed Schematic of spore selection and enrichment protocols followed by DNA extraction. The schematic shows how each sample was treated for spore-former selection and mesophilic spore-former enrichment prior to DNA extraction. In addition one sample was also subject to thermophilic spore-former enrichment (A.T), BHI culturable mesophilic spore-former enrichment (A.M.P) and BHI culturable thermophilic spore-former enrichment (A.T.P).