**Table S1**: Summary of results obtained from 16S rRNA gene amplicon sequencing of 24 wipes collected from 8 locations over 3 flight sampling sessions. Half of each processed wipe was treated with PMA in order to characterize intact/viable bacteria and the other half left untreated to characterize the total bacterial community (both intact/viable and dead/ruptured).

|  |  |  |
| --- | --- | --- |
| Summary |  Non- PMA treated |  PMA treated |
| Total reads |  5,434,563 |  4,900,415 |
| # ASVs |  515 |  403 |
| Phyla |  (9) Actinobacteria Bacteroidetes Deinococcus-Thermus Firmicutes Fusobacteria Planctomycetes Proteobacteria Tenericutes Unidentified  |  (7) Actinobacteria Bacteroidetes Chloroflexi Firmicutes Planctomycetes Proteobacteria Unidentified |
| Top 5 Family (total counts)  |  *Enterobacteriaceae* *Methylobacteriaceae* *Staphylococcaceae* *Paenibacillaceae* *Corynebacteriaceae* |  *Enterobacteriaceae* *Methylobacteriaceae* *Staphylococcaceae* *Paenibacillaceae* *Moraxellaceae* |
| Top 5 genera (total counts) |  *Methylobacterium* *Staphylococcus* *Paenibacillus* *Corynebacterium* *Streptococcus* |  *Methylobacterium* *Staphylococcus* *Paenibacillus* *Acinetobacter* *Streptococcus* |
| # of taxa summarized to the genus level  |   109  |   76 |