## Online Data Supplement

# Culture-independent Analysis of Pediatric Broncho-alveolar Lavage (BAL) Specimens

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## Supplementary Table

**Table S1** Long-form of Table 4 with taxa expanded to show each OTU. All OTUs included in the top 5 OTUs are listed, organized by genus. Some genera, e.g. *Stenotrophomonas*, had multiple different OTUs with the same designation, with species or strain not identified. These had different OTU numbers so it is assumed that they are different species or strains.

* The genus *[Prevotella]* belongs to the family *Paraprevotellaceae*.

† 21 different OTUs, detected in 61 samples, were not identified to genus level.

| **OTU** | **Identified by routine culture** | | | | **Not identified by routine culture** | | | |
|---|---|---|---|---|---|---|---|---|
| | **n samples** | | | **Mean** | **n samples** | | | **Mean** |
| | **CF** | **IC** | **nIC** | | **CF** | **IC** | **nIC** | |
| *Staphylococcus* sp. | 18 | 2 | 1 | 2127 | 4 | 14 | 16 | 1004 |
| *Staphylococcus sciuri* | - | - | - | - | 3 | 1 | 2 | 38 |
| *Streptococcus* sp. | - | 3 | 1 | 653 | 12 | 4 | 13 | 398 |
| *Streptococcus* sp. | - | 2 | - | 14 | - | - | - | - |
| *Streptococcus agalactiae* | - | - | - | - | - | - | 1 | 480 |
| *Streptococcus anginosus* | - | - | - | - | 1 | - | - | 91 |
| *Streptococcus* sp. | - | - | - | - | - | - | 1 | 1 |
| *Haemophilus* sp. | 1 | 1 | 4 | 2531 | 2 | 4 | 9 | 997 |
| *Stenotrophomonas* sp. | 11 | - | 1 | 2815 | 3 | 1 | 2 | 205 |
| *Stenotrophomonas* sp. | 4 | - | - | 499 | 2 | - | 1 | 81 |
| *Stenotrophomonas* sp. | 6 | - | - | 39 | - | - | - | - |
| *Stenotrophomonas* sp | 1 | - | - | 6 | - | - | - | - |
| *Escherichia coli* | - | 1 | - | 892 | 5 | 6 | 7 | 213 |
| *Prevotella melaninogenca* | | | | | 4 | 2 | 1 | 485 |
| *Prevotella melaninogenica* | | | | | 2 | - | 1 | 90 |

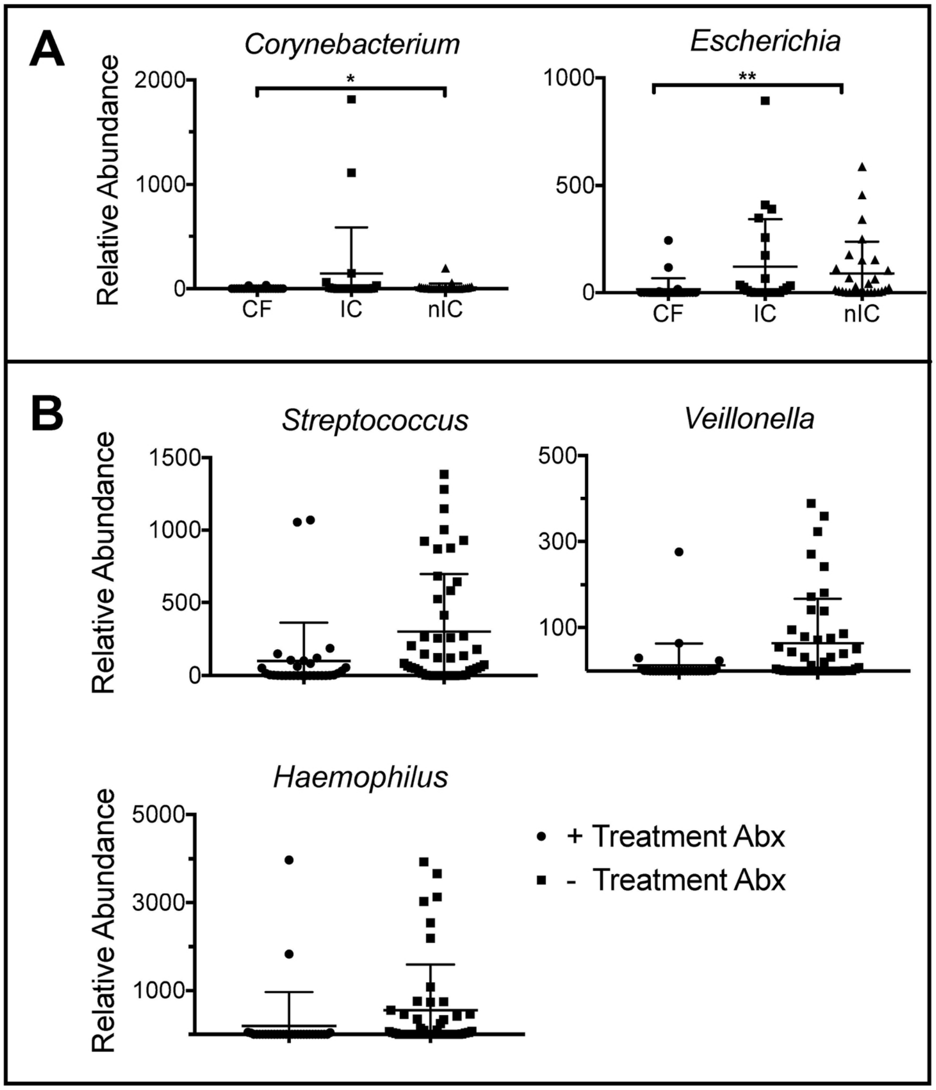
| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| *Prevotella nanceiensis* | | | | | 1 | 2 | - | 143 |
| *Prevotella* sp. | | | | | 1 | - | 1 | 127 |
| *Prevotella* sp. | | | | | - | 1 | - | 422 |
| [*Prevotella*] sp. * | | | | | - | - | 3 | 600 |
| [*Prevotella*] sp. * | | | | | 1 | - | - | 21 |
| *Neisseria subflava* | | | | | 2 | 2 | 7 | 581 |
| *Neisseria cinerea* | | | | | - | - | 1 | 502 |
| *Actinobacillus parahaemolyticus* | | | | | 2 | 3 | 7 | 490 |
| *Veillonella dispar* | | | | | 3 | 3 | 5 | 132 |
| *Veillonella dispar* | | | | | 1 | - | - | 190 |
| *Pseudomonas* sp. | 4 | - | - | 1695 | 2 | 1 | 2 | 772 |
| *Enterococcus* sp. | | | | | 2 | 1 | 5 | 261 |
| *Methylobacterium* sp. | | | | | 2 | 5 | 1 | 240 |
| *Fusobacterium* sp. | | | | | 1 | 3 | 2 | 505 |
| *Moraxella* sp. | | | | | 1 | 2 | 3 | 334 |
| *Brevibacillus* sp. | | | | | 1 | 4 | 1 | 138 |
| *Sphingomonas* sp. | | | | | 2 | 4 | - | 111 |
| *Acinetobacter rhizosphaerae* | | | | | - | 2 | 1 | 1286 |
| *Acinetobacter* sp. | | | | | 1 | - | 1 | 70 |
| *Delftia* sp. | - | - | 1 | 851 | 1 | 1 | 2 | 775 |
| *Corynebacterium* sp. | | | | | - | 2 | 1 | 974 |
| *Corynebacterium* sp. | | | | | 1 | - | - | 1 |
| *Corynebacterium* sp. | | | | | - | 1 | - | 1 |
| *Rothia mucilaginosa* | | | | | 4 | - | 1 | 89 |
| *Granulicatella* sp. | | | | | 2 | - | 2 | 731 |
| *Capnocytophaga ochracea* | | | | | - | 1 | 1 | 339 |
| *Capnocytophaga* sp. | | | | | - | - | 2 | 148 |
| *Achromobacter* sp. | 1 | - | 1 | 2049 | - | - | 1 | 1275 |
| *Parvimonas* sp. | | | | | 1 | 2 | - | 636 |
| *Parvimonas* sp. | | | | | 1 | - | - | 303 |
| *Pantoea agglomerans* | | | | | - | - | 2 | 1962 |
| *Legionella* sp. | | | | | 1 | 1 | - | 403 |
| *Porphyromonas endodontalis* | | | | | - | - | 1 | 560 |
| *Porphyromonas* sp. | | | | | 1 | - | - | 63 |
| *Campylobacter* sp. | | | | | - | 1 | 1 | 293 |
| *Aggregatibacter* sp. | | | | | - | 1 | 1 | 261 |
| WAL_1855D | | | | | 2 | - | - | 219 |
| *Meiothermus* sp. | | | | | - | 2 | - | 129 |
| *Leptotrichia* sp. | | | | | - | - | 1 | 127 |
| *Leptotrichia* sp. | | | | | 1 | - | - | 1 |
| *Proteus* sp. | 1 | - | - | 2338 | - | - | 1 | 38 |
| *Nocardia* sp. | - | 1 | - | 936 | - | - | - | - |

| | | | | | | |
|---|---|---|---|---|---|---|
| *Nocardia* sp. | | | 1 | - | - | 22 |
| *Chryseobacterium* sp. | | | - | - | 1 | 2126 |
| *Bacteroides* sp. | | | - | - | 1 | 1163 |
| *Abiotrophia* sp. | | | - | - | 1 | 397 |
| *Mycoplasma* sp. | | | - | - | 1 | 365 |
| *Dialister* sp. | | | - | - | 1 | 232 |
| *Lautropia* sp. | | | - | - | 1 | 152 |
| *Jeotgalicoccus* sp. | | | - | 1 | - | 93 |
| *Janthinobacterium* sp. | | | - | 1 | - | 88 |
| *Sporosarcina* sp. | | | - | - | 1 | 75 |
| *Paracoccus* sp. | | | - | 1 | - | 63 |
| *Geobacillus* sp. | | | - | 1 | - | 52 |
| *Bacillus endophyticus* | | | - | - | 1 | 46 |
| *Cloacibacterium* sp. | | | 1 | - | - | 26 |
| *Enterobacter* sp. | | | - | - | 1 | 14 |
| *Serratia marcescens* | | | - | 1 | - | 7 |
| *Sphingobium* sp. | | | 1 | - | - | 1 |
| *Devosia* sp. | | | 1 | - | - | 1 |
| *Bradyrhizobium* sp. | | | 1 | - | - | 1 |
| *Finegoldia* sp. | | | 1 | - | - | 1 |
| unidentified † | | | 20 | 21 | 20 | 331 |

## Supplementary Figure Legends

**Figure S1. (A)** Genus abundance, by OTU read count, in each diagnostic group. Following multivariate analysis, relative abundance of *Corynebacterium* and *Escherichia* are significantly lower in the CF group compared to the nIC group ($p=0.03$ and 0.001,respectively). **(B)** Genus abundance separated by use of treatment antibiotics. Following multivariate analysis, relative abundance of the genera shown are significantly lower ($p<0.05$) in the samples exposed to treatment antibiotics within 7 days of sampling.

**Figure S2. (A)** Pearson correlation analysis of correlation of OTU abundance with prevalence. In all diagnosis groups, abundance is positively correlated with prevalence, with significant Pearson correlation coefficients with r values of 0.55-0.62 ($p<0.0001$ in all diagnoses). **(B)** Defining core taxa: 30% and 50% prevalence are marked with dashed lines. The 2.5% and 97.5% confidence limits of a chi-squared distribution are marked. OTUs falling outside of these limits are non-randomly dispersed. Dots representing non-randomly dispersed OTUs present in ≥30% but <50% of samples are solid grey, and open circles represent OTUs present in ≥50% of samples. Black dots are not included in any core.



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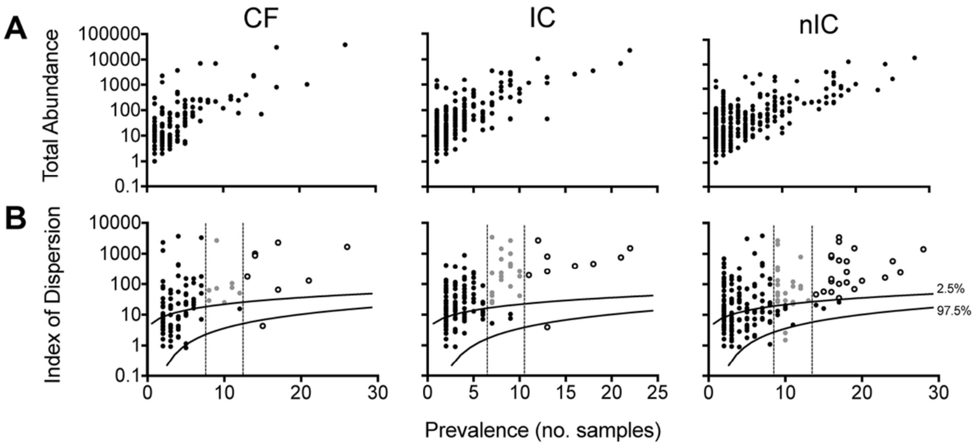
155x169mm (300 x 300 DPI)



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103x48mm (300 x 300 DPI)