# Supplementary Materials

# A Distinct Nasal Microbiota Signature in Peritoneal Dialysis Patients

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## Table of Contents

## SI Table 1

| *Genus* | ASV | Base Mean | log2 Fold Change | Standard error | Wald stat | P value | Adj P value |
|---|---|---|---|---|---|---|---|
| *Finegoldia ASV #1* | 1f016ec26e4774c86f029301b556de28 | 24.3 | -26.4 | 2.9 | -9.0 | 3.4E-19 | 1.4E-17 |
| *Anaerococcus ASV #1* | ae7cf0f32080cf5e62b3fbd903a997af | 16.5 | -25.9 | 3.0 | -8.7 | 2.2E-18 | 4.4E-17 |
| *Lawsonella ASV #1* | b89dbfe5c74375ff3d4922b41c470740 | 49.0 | -7.3 | 2.9 | -2.5 | 1.3E-02 | 5.1E-02 |
| *Corynebacterium ASV #2* | c91b64f1467982a81922d331a310f5dc | 1172.2 | -3.7 | 1.6 | -2.2 | 2.5E-02 | 9.2E-02 |
| *Bacillus ASV #1* | 5565e52f91bc244013249656795409ca | 18.7 | 6.9 | 1.8 | 3.8 | 1.7E-04 | 7.7E-04 |
| *Staphylococcus ASV #2* | b273d7d05f0525bb87418b0138d90605 | 86.0 | 11.8 | 2.2 | 5.3 | 1.2E-07 | 6.1E-07 |
| *Porphyromonas ASV #1* | 969732ae717bf5a9282f4781499aadb4 | 10.0 | 21.4 | 3.0 | 7.2 | 6.3E-13 | 3.6E-12 |
| *Abiotrophia ASV #1* | afce1dc2c06acb90ad5d3da0fffbcd02 | 9.7 | 22.3 | 2.8 | 7.9 | 3.5E-15 | 2.4E-14 |
| *Streptococcus ASV #1* | 4481bc66d3a54f79e6abb8b557a2a104 | 19.3 | 23.2 | 2.9 | 7.9 | 2.5E-15 | 2.4E-14 |
| *Staphylococcus ASV #1* | 7b06c22a4ff85c9b2cbbf57a53462e13 | 41.9 | 23.4 | 3.0 | 7.9 | 3.6E-15 | 2.4E-14 |
| *Corynebacterium ASV #1* | 0560198302010f9b110d4ec9897e14d0 | 45.9 | 24.5 | 3.0 | 8.2 | 1.8E-16 | 2.3E-15 |

**DESeq2 Analysis of the Nasal Microbiota between the PD Group and the HC Group.** The listed amplicon sequence variant (ASV) were determined to be significantly different using an adjusted p value of 0.10. Base Mean, mean of normalized counts for all samples. Wald stat, Wald statistic. Positive log2 Fold Change is higher in the PD Group.

# SI Table 2

| *Genus* | ASV | Base Mean | log2 Fold Change | Standard error | Wald stat | P value | Adj P value |
|---|---|---|---|---|---|---|---|
| *Staphylococcus ASV #3* | 0f89ba63b47f3b624c13293cb4d56486 | 16.5 | -25.6 | 2.9 | -8.8 | 1.9E-18 | 2.0E-16 |
| *Porphyromonas ASV #1* | 969732ae717bf5a9282f4781499aadb4 | 7.4 | 21.6 | 2.9 | 7.4 | 1.1E-13 | 4.8E-12 |
| *Abiotrophia ASV #1* | afce1dc2c06acb90ad5d3da0fffbcd02 | 7.3 | 23.3 | 2.8 | 8.4 | 4.3E-17 | 3.0E-15 |
| *Corynebacterium ASV #3* | 36f00e24a741c19a5ee20f58919004ad | 12.4 | 24.0 | 2.9 | 8.2 | 1.7E-16 | 8.8E-15 |
| *Staphylococcus ASV #2* | b273d7d05f0525bb87418b0138d90605 | 65.8 | 24.8 | 2.4 | 10.2 | 1.5E-24 | 3.1E-22 |

**DESeq2 Analysis of the Nasal Microbiota between the PD Group and the KTx Group.** The listed amplicon sequence variant (ASV) were determined to be significantly different using an adjusted p value of 0.10. Base Mean, mean of normalized counts for all samples. Wald stat, Wald statistic. Positive log2 Fold Change is higher in the PD Group.

## SI Table 3

| *Genus* | ASV | Base Mean | log2 Fold Change | Standard error | Wald stat | P value | Adj P value |
|---|---|---|---|---|---|---|---|
| *Anaerococcus ASV #1* | ae7cf0f32080cf5e62b3fbd903a997af | 12.0 | -25.4 | 3.0 | -8.5 | 2.8E-17 | 2.2E-15 |
| *Corynebacterium ASV #4* | 9f6c00ff9e1f455f42f211770d60dec0 | 11.2 | -25.3 | 3.0 | -8.4 | 3.6E-17 | 2.2E-15 |
| *Staphylococcus ASV #3* | 0f89ba63b47f3b624c13293cb4d56486 | 12.5 | 21.6 | 3.0 | 7.2 | 7.4E-13 | 2.8E-11 |
| *Staphylococcus ASV #1* | 7b06c22a4ff85c9b2cbbf57a53462e13 | 11.8 | 22.9 | 3.0 | 7.6 | 2.8E-14 | 1.3E-12 |
| *Corynebacterium ASV #1* | 0560198302010f9b110d4ec9897e14d0 | 237.4 | 27.1 | 3.0 | 9.0 | 2.2E-19 | 4.1E-17 |

**DESeq2 Analysis of the Nasal Microbiota between the KTx Group and the HC Group.** The listed amplicon sequence variant (ASV) were determined to be significantly different using an adjusted p value of 0.10. Base Mean, mean of normalized counts for all samples. Wald stat, Wald statistic. Positive log2 Fold Change is higher in the KTx Group.

# SI Table 4

| | Age >=65<br>n = 28 | Age < 65<br>n = 63 | | |
|---|---|---|---|---|
| Genus | Median Abundance | Median Abundance | P value | Adj P value |
| *Staphylococcus* | 0.187 | 0.346 | 0.11 | 0.40 |
| *Finegoldia* | 0.000 | 0.001 | 0.11 | 0.40 |
| *Anaerococcus* | 0.001 | 0.013 | 0.14 | 0.40 |
| *Moraxella* | 0.000 | 0.000 | 0.18 | 0.40 |
| *Unspecified Neisseriaceae* | 0.000 | 0.000 | 0.30 | 0.48 |
| *Streptococcus* | 0.012 | 0.007 | 0.32 | 0.48 |
| *Corynebacterium* | 0.124 | 0.139 | 0.56 | 0.72 |
| *Peptoniphilus* | 0.000 | 0.000 | 0.66 | 0.74 |
| *Cutibacterium* | 0.003 | 0.002 | 0.81 | 0.81 |

**Comparison of Nasal Microbiota Based on Patient's Age at the Genus Level.** P value was calculated between groups using Wilcoxon rank sum test. Adjusted p value (Adj P value) was calculated using Benjamini-Hochberg adjustment.

# SI Table 5

| Genus | Female Sex<br>n = 50<br>Median Abundance | Male Sex<br>n = 41<br>Median Abundance | P value | Adj P value |
|---|---|---|---|---|
| *Peptoniphilus* | 0.000 | 0.005 | 0.01 | 0.10 |
| *Finegoldia* | 0.000 | 0.002 | 0.07 | 0.31 |
| *Anaerococcus* | 0.002 | 0.017 | 0.19 | 0.51 |
| *Corynebacterium* | 0.101 | 0.197 | 0.23 | 0.51 |
| *Cutibacterium* | 0.002 | 0.007 | 0.38 | 0.64 |
| *Moraxella* | 0.000 | 0.000 | 0.43 | 0.64 |
| Unspecified *Neisseriaceae* | 0.000 | 0.000 | 0.90 | 0.91 |
| *Streptococcus* | 0.008 | 0.010 | 0.90 | 0.91 |
| *Staphylococcus* | 0.285 | 0.250 | 0.91 | 0.91 |

**Comparison of Nasal Microbiota Based on Patient's Sex at the Genus Level.** P value was calculated between groups using Wilcoxon rank sum test. Adjusted p value (Adj P value) was calculated using Benjamini-Hochberg adjustment.

## SI Table 6

| Genus | Abx Hx 1 year (n = 63) median abundance | No Abx Hx 1 year (n = 28) median abundance | P value | Adj P Value |
|---|---|---|---|---|
| *Moraxella* | 0.000 | 0.000 | 0.002 | 0.02 |
| *Peptoniphilus* | 0.000 | 0.007 | 0.01 | 0.04 |
| *Cutibacterium* | 0.000 | 0.009 | 0.01 | 0.04 |
| *Streptococcus* | 0.010 | 0.003 | 0.05 | 0.10 |
| Unspecified *Neisseriaceae* | 0.000 | 0.002 | 0.06 | 0.10 |
| *Staphylococcus* | 0.275 | 0.211 | 0.07 | 0.10 |
| *Corynebacterium* | 0.097 | 0.382 | 0.08 | 0.10 |
| *Finegoldia* | 0.000 | 0.001 | 0.18 | 0.20 |
| *Anaerococcus* | 0.006 | 0.014 | 0.60 | 0.60 |

**Comparison of Nasal Microbiota Based on Antibiotic Usage within the Past Year at the Genus Level.** P value was calculated between groups using Wilcoxon rank sum test. Adjusted p value (Adj P value) was calculated using Benjamini-Hochberg adjustment. Abx, antibiotic; Hx, history.

## SI Table 7

| Genus | KTx on TMP/SMX<br>n = 12<br>Median Abundance | KTx off TMP/SMX<br>n = 25<br>Median Abundance | P value | Adj P value |
|---|---|---|---|---|
| *Finegoldia* | 0.000 | 0.002 | 0.02 | 0.15 |
| *Peptoniphilus* | 0.000 | 0.000 | 0.04 | 0.15 |
| *Anaerococcus* | 0.0002 | 0.007 | 0.06 | 0.15 |
| *Corynebacterium* | 0.101 | 0.314 | 0.36 | 0.59 |
| *Cutibacterium* | 0.000 | 0.000 | 0.37 | 0.59 |
| *Staphylococcus* | 0.363 | 0.487 | 0.53 | 0.71 |
| Unspecified *Neisseriaceae* | 0.000 | 0.000 | 0.70 | 0.80 |
| *Streptococcus* | 0.002 | 0.005 | 0.84 | 0.84 |
| *Moraxella* | 0.000 | 0.000 | NA | NA |

**Comparison of Nasal Microbiota Based on Trimethoprim/Sulfamethoxazole usage in the Kidney Transplant Recipients at the Genus Level.** P value was calculated between groups using Wilcoxon rank sum test. Adjusted p value (Adj P value) was calculated using Benjamini-Hochberg adjustment. P values with NA were unable to be calculated because the abundances were 0 in both groups. KTx, Kidney Transplant; TMP/SMX, trimethoprim/sulfamethoxazole.

## SI Table 8

| Genus | PD Staph Future Peritonitis n = 6 Median Abundance | PD No Staph Future Peritonitis n = 26 Median Abundance | P value | Adj P value |
|---|---|---|---|---|
| Unspecified *Neisseriaceae* | 0.000 | 0.000 | 0.08 | 0.66 |
| *Staphylococcus* | 0.521 | 0.240 | 0.38 | 0.73 |
| *Streptococcus* | 0.009 | 0.035 | 0.38 | 0.73 |
| *Anaerococcus* | 0.0002 | 0.022 | 0.39 | 0.73 |
| *Peptoniphilus* | 0.000 | 0.000 | 0.48 | 0.73 |
| *Cutibacterium* | 0.001 | 0.000 | 0.55 | 0.73 |
| *Finegoldia* | 0.000 | 0.000 | 0.76 | 0.87 |
| *Corynebacterium* | 0.101 | 0.098 | 1.00 | 1.00 |
| *Moraxella* | 0.000 | 0.000 | NA | NA |

**Comparison of Nasal Microbiota Based on PD patients who developed *Staphylococcus* peritonitis status and PD patients who did not develop *Staphylococcus* peritonitis at the Genus Level.** P value was calculated between groups using Wilcoxon rank sum test. Adjusted p value (Adj P value) was calculated using Benjamini-Hochberg adjustment. P values with NA were unable to be calculated because the abundances were 0 in both groups. PD Staph peritonitis cohort was defined as PD patients who concurrently had *Staphylococcus* peritonitis or developed *Staphylococcus* peritonitis withn 10 to 12 months (last follow up).

## SI Table 9

| Genus | PD Patients History of Peritonitis (n = 10) median abundance | PD Patients No History of Peritonitis (n = 22) median abundance | P value | Adj P Value |
|---|---|---|---|---|
| *Finegoldia* | 0.000 | 0.001 | 0.005 | 0.04 |
| *NeisseriaceaeUnspecified* | 0.000 | 0.000 | 0.06 | 0.24 |
| *Peptoniphilus* | 0.000 | 0.000 | 0.10 | 0.26 |
| *Cutibacterium* | 0.000 | 0.002 | 0.14 | 0.28 |
| *Corynebacterium* | 0.047 | 0.141 | 0.32 | 0.51 |
| *Staphylococcus* | 0.428 | 0.240 | 0.48 | 0.64 |
| *Anaerococcus* | 0.020 | 0.013 | 0.76 | 0.86 |
| *Streptococcus* | 0.018 | 0.027 | 0.95 | 0.95 |
| *Moraxella* | 0.000 | 0.000 | NA | NA |

**Comparison of Nasal Microbiota Based on PD patients who had a history of peritonitis and PD patients who did not have a history of peritonitis at the Genus Level.** P value was calculated between groups using Wilcoxon rank sum test. Adjusted p value (Adj P value) was calculated using Benjamini-Hochberg adjustment. P values with NA were unable to be calculated because the abundances were 0 in both groups.