

SI Table 1

Genus	ASV	Base Mean	log2 Fold Change	Standard error	Wald stat	P value	Adj P value
<i>Finegoldia</i> ASV #1	1f016ec26e4774c86f029301b556de28	24.3	-26.4	2.9	-9.0	3.4E-19	1.4E-17
<i>Anaerococcus</i> ASV #1	ae7cf0f32080cf5e62b3fbd903a997af	16.5	-25.9	3.0	-8.7	2.2E-18	4.4E-17
<i>Lawsonella</i> ASV #1	b89dbfe5c74375ff3d4922b41c470740	49.0	-7.3	2.9	-2.5	1.3E-02	5.1E-02
<i>Corynebacterium</i> ASV #2	c91b64f1467982a81922d331a310f5dc	1172.2	-3.7	1.6	-2.2	2.5E-02	9.2E-02
<i>Bacillus</i> ASV #1	5565e52f91bc244013249656795409ca	18.7	6.9	1.8	3.8	1.7E-04	7.7E-04
<i>Staphylococcus</i> ASV #2	b273d7d05f0525bb87418b0138d90605	86.0	11.8	2.2	5.3	1.2E-07	6.1E-07
<i>Porphyromonas</i> ASV #1	969732ae717bf5a9282f4781499aad4b4	10.0	21.4	3.0	7.2	6.3E-13	3.6E-12
<i>Abitrophia</i> ASV #1	afce1dc2c06acb90ad5d3da0fffbcd02	9.7	22.3	2.8	7.9	3.5E-15	2.4E-14
<i>Streptococcus</i> ASV #1	4481bc66d3a54f79e6abb8b557a2a104	19.3	23.2	2.9	7.9	2.5E-15	2.4E-14
<i>Staphylococcus</i> ASV #1	7b06c22a4ff85c9b2cbbf57a53462e13	41.9	23.4	3.0	7.9	3.6E-15	2.4E-14
<i>Corynebacterium</i> 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 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

<i>Genus</i>	ASV	Base Mean	log2 Fold Change	Standard error	Wald stat	P value	Adj P value
<i>Staphylococcus ASV #3</i>	0f89ba63b47f3b624c13293cb4d56486	16.5	-25.6	2.9	-8.8	1.9E-18	2.0E-16
<i>Porphyromonas ASV #1</i>	969732ae717bf5a9282f4781499aadb4	7.4	21.6	2.9	7.4	1.1E-13	4.8E-12
<i>Abitrophia ASV #1</i>	afce1dc2c06acb90ad5d3da0fffbcd02	7.3	23.3	2.8	8.4	4.3E-17	3.0E-15
<i>Corynebacterium ASV #3</i>	36f00e24a741c19a5ee20f58919004ad	12.4	24.0	2.9	8.2	1.7E-16	8.8E-15
<i>Staphylococcus ASV #2</i>	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 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

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

Genus	Age \geq 65	Age < 65	P value	Adj P value
	n = 28	n = 63		
<i>Staphylococcus</i>	0.187	0.346	0.11	0.40
<i>Finegoldia</i>	0.000	0.001	0.11	0.40
<i>Anaerococcus</i>	0.001	0.013	0.14	0.40
<i>Moraxella</i>	0.000	0.000	0.18	0.40
<i>Unspecified Neisseriaceae</i>	0.000	0.000	0.30	0.48
<i>Streptococcus</i>	0.012	0.007	0.32	0.48
<i>Corynebacterium</i>	0.124	0.139	0.56	0.72
<i>Peptoniphilus</i>	0.000	0.000	0.66	0.74
<i>Cutibacterium</i>	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	Male Sex	P value	Adj P value
	n = 50	n = 41		
	Median Abundance	Median Abundance		
<i>Peptoniphilus</i>	0.000	0.005	0.01	0.10
<i>Finegoldia</i>	0.000	0.002	0.07	0.31
<i>Anaerococcus</i>	0.002	0.017	0.19	0.51
<i>Corynebacterium</i>	0.101	0.197	0.23	0.51
<i>Cutibacterium</i>	0.002	0.007	0.38	0.64
<i>Moraxella</i>	0.000	0.000	0.43	0.64
Unspecified <i>Neisseriaceae</i>	0.000	0.000	0.90	0.91
<i>Streptococcus</i>	0.008	0.010	0.90	0.91
<i>Staphylococcus</i>	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	KTx on TMP/SMX	KTx off TMP/SMX	P value	Adj P value
	n = 12	n = 25		
	Median Abundance	Median Abundance		
<i>Finegoldia</i>	0.000	0.002	0.02	0.15
<i>Peptoniphilus</i>	0.000	0.000	0.04	0.15
<i>Anaerococcus</i>	0.0002	0.007	0.06	0.15
<i>Corynebacterium</i>	0.101	0.314	0.36	0.59
<i>Cutibacterium</i>	0.000	0.000	0.37	0.59
<i>Staphylococcus</i>	0.363	0.487	0.53	0.71
Unspecified <i>Neisseriaceae</i>	0.000	0.000	0.70	0.80
<i>Streptococcus</i>	0.002	0.005	0.84	0.84
<i>Moraxella</i>	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 7

Genus	PD Staph	PD No Staph	P value	Adj P value
	Future Peritonitis n = 6	Future Peritonitis n = 26		
	Median Abundance	Median Abundance		
Unspecified <i>Neisseriaceae</i>	0.000	0.000	0.08	0.66
<i>Staphylococcus</i>	0.521	0.240	0.38	0.73
<i>Streptococcus</i>	0.009	0.035	0.38	0.73
<i>Anaerococcus</i>	0.0002	0.022	0.39	0.73
<i>Peptoniphilus</i>	0.000	0.000	0.48	0.73
<i>Cutibacterium</i>	0.001	0.000	0.55	0.73
<i>Finegoldia</i>	0.000	0.000	0.76	0.87
<i>Corynebacterium</i>	0.101	0.098	1.00	1.00
<i>Moraxella</i>	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 currently had *Staphylococcus* peritonitis or developed *Staphylococcus* peritonitis within 10 to 12 months (last follow up).