

Supplementary Information

Associations of indoor airborne microbiome with lung function: Evidence from a randomized, double-blind, crossover study of microbial intervention

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Table S1. Description of microbial richness in the major taxonomic class level.

Taxon	All	Sham-purification	Real-purification	<i>p</i> -Value
d_Bacteria;p_Actinobacteria;c_Actinobacteria	14 (6.75, 48)	23 (11, 55.25)	8.5 (5, 16)	5.0×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	7 (2, 11)	8.5 (3.75, 14.5)	6 (2, 7.25)	3.4×10 ⁻²
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	4.5 (1, 9)	6 (1.75, 12)	3 (0.75, 6.5)	1.4×10 ⁻²
d_Bacteria;p_Firmicutes;c_Bacilli	9 (3.75, 21.5)	12 (6, 29.75)	5 (2, 12.5)	9.0×10 ⁻²
d_Bacteria;p_Firmicutes;c_Clostridia	1.5 (0, 5)	4.5 (1.75, 7)	0.5 (0, 1.25)	2.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	17.5 (12, 36.5)	27 (15, 39.25)	15 (8.75, 22.25)	9.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	33 (23.5, 51.75)	33 (29.75, 58.25)	33.5 (18.75, 42.75)	1.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes	4 (2, 12.5)	8.5 (2, 16.5)	2 (1, 7.5)	9.1×10 ⁻²
d_Fungi;p_Ascomycota;c_Eurotiomycetes	4 (1, 12.5)	7 (2, 17.25)	2.5 (0.75, 6.25)	4.4×10 ⁻²
d_Fungi;p_Ascomycota;c_Sordariomycetes	2 (1, 8.25)	4 (1, 9)	2 (1, 4)	3.5×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes	1 (0, 4)	1 (0, 4)	1 (0, 2.5)	8.6×10 ⁻¹

Note: The data were present by median (P25, P75). The major taxonomic class was defined as microbial class with a total number of ASVs > 100 among all samples. In total, 7 bacterial classes and 4 fungal classes were identified. The *p*-value was the result of the difference between sham and real air purification using Wilcoxon signed-rank test.

Table S2. All results of associations between indoor airborne microbial richness (represented as the number of ASVs) and lung function measures.

Taxon	Lung function measures	Percentage changes (95% CIs)	p-Value
d_Bacteria;p_Actinobacteria;c_Actinobacteria	FVC	3.92 (0.43, 7.53)	3.1×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria	FEV ₁	4.6 (1.8, 7.49)	1.9×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria	FEV ₁ /FVC	0.37 (-2.33, 3.15)	7.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria	PEF	1.21 (-6.36, 9.39)	7.6×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria	FEF ₂₅₋₇₅	2.13 (-6.06, 11.03)	6.2×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria	FEF ₂₅	0.58 (-7.14, 8.94)	8.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria	FEF ₅₀	1.81 (-6.83, 11.26)	6.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria	FEF ₇₅	3.27 (-7.21, 14.92)	5.6×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	FVC	6.16 (-1.21, 14.09)	1.1×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	FEV ₁	7.83 (1.66, 14.38)	1.4×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	FEV ₁ /FVC	1.06 (-4.36, 6.8)	7.1×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	PEF	0.53 (-14.3, 17.92)	9.5×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	FEF ₂₅₋₇₅	-1.11 (-16.61, 17.27)	9.0×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	FEF ₂₅	0.23 (-14.99, 18.19)	9.8×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	FEF ₅₀	-1.99 (-18.17, 17.38)	8.3×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia	FEF ₇₅	-0.09 (-19.53, 24.04)	9.9×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	FVC	9.4 (-2.11, 22.26)	1.2×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	FEV ₁	13.23 (3.72, 23.62)	7.3×10 ⁻³
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	FEV ₁ /FVC	2.48 (-6.21, 11.98)	5.9×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	PEF	5.65 (-17.72, 35.67)	6.7×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	FEF ₂₅₋₇₅	1.12 (-22.83, 32.52)	9.4×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	FEF ₂₅	5.44 (-18.38, 36.2)	6.9×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	FEF ₅₀	-0.46 (-25.31, 32.67)	9.8×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria	FEF ₇₅	0.8 (-28.8, 42.68)	9.6×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli	FVC	7.27 (-1.56, 16.88)	1.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli	FEV ₁	11.29 (4.08, 19)	2.6×10 ⁻³
d_Bacteria;p_Firmicutes;c_Bacilli	FEV ₁ /FVC	3.28 (-3.51, 10.55)	3.6×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli	PEF	12.46 (-7.05, 36.06)	2.3×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli	FEF ₂₅₋₇₅	11.36 (-9.48, 36.99)	3.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli	FEF ₂₅	10.26 (-9.36, 34.12)	3.3×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli	FEF ₅₀	9.51 (-12.15, 36.51)	4.2×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli	FEF ₇₅	14.05 (-12.65, 48.91)	3.4×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Clostridia	FVC	4.67 (-3.15, 13.12)	2.5×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Clostridia	FEV ₁	9.39 (2.83, 16.36)	5.9×10 ⁻³
d_Bacteria;p_Firmicutes;c_Clostridia	FEV ₁ /FVC	3.69 (-2.24, 9.98)	2.3×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Clostridia	PEF	3.11 (-13.07, 22.32)	7.3×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Clostridia	FEF ₂₅₋₇₅	6.29 (-11.46, 27.61)	5.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Clostridia	FEF ₂₅	1.47 (-14.92, 21.01)	8.7×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Clostridia	FEF ₅₀	5.29 (-13.24, 27.78)	6.0×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Clostridia	FEF ₇₅	11.87 (-11.3, 41.09)	3.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	FVC	3.81 (0.34, 7.4)	3.4×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	FEV ₁	3.47 (0.61, 6.41)	2.0×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	FEV ₁ /FVC	-0.38 (-3.04, 2.35)	7.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	PEF	-1.07 (-8.43, 6.88)	7.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	FEF ₂₅₋₇₅	-2.14 (-9.92, 6.31)	6.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	FEF ₂₅	-1.8 (-9.29, 6.31)	6.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	FEF ₅₀	-2.69 (-10.86, 6.24)	5.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria	FEF ₇₅	-2.24 (-12.06, 8.67)	6.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	FVC	3.05 (0.17, 6.02)	4.1×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	FEV ₁	2.83 (0.47, 5.25)	2.2×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	FEV ₁ /FVC	-0.18 (-2.41, 2.09)	8.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	PEF	-0.25 (-6.42, 6.33)	9.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	FEF ₂₅₋₇₅	-1.15 (-7.7, 5.88)	7.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	FEF ₂₅	-0.4 (-6.72, 6.34)	9.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	FEF ₅₀	-1.37 (-8.3, 6.09)	7.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria	FEF ₇₅	-2.11 (-10.34, 6.87)	6.3×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes	FVC	19.2 (3.55, 37.21)	1.7×10 ⁻²
d_Fungi;p_Ascmycota;c_Dothideomycetes	FEV ₁	6.34 (-5.71, 19.93)	3.2×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes	FEV ₁ /FVC	-10.78 (-20.31, -0.1)	5.1×10 ⁻²
d_Fungi;p_Ascmycota;c_Dothideomycetes	PEF	-24.98 (-45.34, 2.96)	7.9×10 ⁻²
d_Fungi;p_Ascmycota;c_Dothideomycetes	FEF ₂₅₋₇₅	-13.99 (-39.39, 22.04)	4.0×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes	FEF ₂₅	-19.62 (-42.04, 11.49)	2.0×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes	FEF ₅₀	-10.57 (-38.4, 29.83)	5.6×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes	FEF ₇₅	-20.53 (-49.36, 24.72)	3.2×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	FVC	5.09 (-11.84, 25.26)	5.8×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	FEV ₁	2.36 (-11.48, 18.37)	7.5×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	FEV ₁ /FVC	-1.27 (-13.89, 13.19)	8.5×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	PEF	17.4 (-20.2, 72.71)	4.2×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	FEF ₂₅₋₇₅	-6.53 (-38.36, 41.74)	7.5×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	FEF ₂₅	4.99 (-29.38, 56.08)	8.1×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	FEF ₅₀	-6.46 (-39.88, 45.54)	7.7×10 ⁻¹
d_Fungi;p_Ascmycota;c_Eurotiomycetes	FEF ₇₅	-14.52 (-49.9, 45.82)	5.7×10 ⁻¹
d_Fungi;p_Ascmycota;c_Sordariomycetes	FVC	41.16 (5.91, 88.14)	2.1×10 ⁻²
d_Fungi;p_Ascmycota;c_Sordariomycetes	FEV ₁	27.49 (0.05, 62.47)	5.4×10 ⁻²
d_Fungi;p_Ascmycota;c_Sordariomycetes	FEV ₁ /FVC	-9.4 (-27.9, 13.84)	4.0×10 ⁻¹

d_Fungi:p_Ascomycota;c_Sordariomycetes	PEF	16.35 (-39.6, 124.11)	6.5×10 ⁻¹
d_Fungi:p_Ascomycota;c_Sordariomycetes	FEF ₂₅₋₇₅	-15 (-57.87, 71.5)	6.5×10 ⁻¹
d_Fungi:p_Ascomycota;c_Sordariomycetes	FEF ₂₅	10.35 (-43.77, 116.55)	7.8×10 ⁻¹
d_Fungi:p_Ascomycota;c_Sordariomycetes	FEF ₅₀	-11.42 (-57.97, 86.69)	7.5×10 ⁻¹
d_Fungi:p_Ascomycota;c_Sordariomycetes	FEF ₇₅	-27.29 (-70.32, 78.11)	4.9×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	FVC	-23.62 (-49.86, 16.36)	2.1×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	FEV ₁	4.78 (-26.63, 49.64)	8.0×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	FEV ₁ /FVC	27.41 (-7.44, 75.38)	1.4×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	PEF	30.01 (-48.32, 227.09)	5.8×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	FEF ₂₅₋₇₅	19.41 (-55.82, 222.72)	7.3×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	FEF ₂₅	-2.14 (-62.26, 153.72)	9.6×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	FEF ₅₀	17.78 (-59.02, 238.52)	7.6×10 ⁻¹
d_Fungi:p_Basidiomycota;c_Agaricomycetes	FEF ₇₅	50.32 (-57.8, 435.52)	5.3×10 ⁻¹

Note: The regressions were only conducted for the major taxonomic class with total number of ASVs > 100 among all samples. In total, 7 bacterial classes and 4 fungal classes were identified and analyzed. Percentage changes and 95% confidence intervals were calculated for per 100 ASVs increase. Linear mixed-effect models were adjusted for age, gender, BMI, season, PM_{2.5}, purification status (real or sham), temperature, relative humidity, and a random intercept for each participant. FVC, forced vital capacity; FEV₁, forced expiratory volume in one second; PEF, peak expiratory flow; FEF₂₅, forced expiratory flow at 25% of FVC; FEF₅₀, forced expiratory flow at 50% of FVC; FEF₇₅, forced expiratory flow at 75% of FVC; FEF₂₅₋₇₅, forced expiratory flow from 25-75% of FVC; CIs, confidence intervals.

Table S3. Description of absolute abundance of the high-abundant microbial genera.

Taxon	All		Sham-purification		Real-purification		p-Value
	n ^a	Mean (Range) ^b	n ^a	Mean (Range) ^b	n ^a	Mean (Range) ^b	
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomycetes	10	0.37 (0-4.76)	6	0.36 (0-1.97)	4	0.37 (0-4.76)	7.2×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	40	17.19 (0-80.74)	21	23.43 (0-80.74)	19	10.96 (0-39.49)	3.2×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	18	1.62 (0-17.37)	13	2.1 (0-11.58)	5	1.15 (0-17.37)	9.4×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	27	13.57 (0-178.76)	17	22.57 (0-178.76)	10	4.57 (0-53.15)	7.0×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	33	14.76 (0-103.87)	18	20.54 (0-74.67)	15	8.98 (0-103.87)	5.7×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideae;g_Nocardioidea	18	2.18 (0-43.05)	10	0.87 (0-6.31)	8	3.49 (0-43.05)	3.1×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	27	24.71 (0-220.13)	16	31.64 (0-220.13)	11	17.78 (0-104.61)	4.2×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	32	45.33 (0-497.82)	17	39.95 (0-334.74)	15	50.71 (0-497.82)	2.7×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	24	33.66 (0-1395.7)	14	2.71 (0-22.01)	10	64.61 (0-1395.7)	5.4×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	20	1.91 (0-23.68)	13	3.35 (0-23.68)	7	0.48 (0-3.56)	1.8×10 ⁻²
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	39	32.98 (0-345.58)	22	42.95 (0-345.58)	17	23.01 (0-328.83)	2.0×10 ⁻²
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	17	32.51 (0-1394.95)	9	59.25 (0-1394.95)	8	5.76 (0-55.74)	9.3×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	25	2.92 (0-21.62)	14	3.9 (0-20.47)	11	1.95 (0-21.62)	1.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	24	16.55 (0-265.81)	14	10.83 (0-114.46)	10	22.27 (0-265.81)	2.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bejerinckiaceae;g_Methylobacterium	21	3.82 (0-42.63)	11	4.53 (0-42.63)	10	3.11 (0-21.72)	9.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiales;g_Hyphomicrobium	23	2.92 (0-48.44)	11	1.75 (0-14.67)	12	4.09 (0-48.44)	4.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	13	3.22 (0-38.51)	6	3.82 (0-38.51)	7	2.62 (0-26.73)	7.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	36	16.51 (0-114.24)	20	20.11 (0-114.24)	16	12.9 (0-77.05)	1.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	21	3.96 (0-114.57)	13	6.6 (0-114.57)	8	1.32 (0-10.27)	3.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	20	3.54 (0-64.69)	10	1.43 (0-12.59)	10	5.65 (0-64.69)	8.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	40	73.34 (0-885.34)	21	78.83 (0-885.34)	19	67.85 (0-377.98)	9.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodospseudomonas	23	4.86 (0-47.05)	12	3.83 (0-47.05)	11	5.9 (0-44.64)	4.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	27	3.88 (0-48.87)	18	5.5 (0-48.87)	9	2.26 (0-13.64)	1.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	28	6.87 (0-91.2)	16	7.56 (0-91.2)	12	6.18 (0-34.3)	1.0×10 ⁰
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	32	8.76 (0-68.37)	18	8.2 (0-68.37)	14	9.31 (0-66.41)	9.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	22	17.07 (0-148.61)	12	21.77 (0-148.61)	10	12.37 (0-79.11)	5.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	11	2.9 (0-71.37)	6	0.99 (0-9.39)	5	4.81 (0-71.37)	7.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	24	7.29 (0-139.56)	12	9.91 (0-139.56)	12	4.67 (0-40.99)	8.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	20	4.16 (0-36.66)	12	4.47 (0-36.66)	8	3.85 (0-24.77)	6.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	10	1.05 (0-33.95)	7	0.36 (0-3.39)	3	1.73 (0-33.95)	9.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	24	6.61 (0-80.34)	15	9.85 (0-80.34)	9	3.37 (0-22.2)	1.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	10	14.92 (0-650.37)	5	1.11 (0-14.65)	5	28.72 (0-650.37)	1.0×10 ⁰
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	13	6.84 (0-193.62)	5	8.35 (0-193.62)	8	5.34 (0-82.91)	5.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	10	9.03 (0-218.1)	5	9.73 (0-218.1)	5	8.33 (0-124.9)	7.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	10	8.31 (0-345.23)	8	1.43 (0-14.34)	2	15.19 (0-345.23)	5.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	26	3.03 (0-35.78)	15	4.93 (0-35.78)	11	1.13 (0-11.84)	6.1×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	42	109.28 (0-971.06)	22	125.64 (0-971.06)	20	92.91 (0-463.4)	6.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	34	12.16 (0-117.03)	20	10.07 (0-79.21)	14	14.25 (0-117.03)	7.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	48	101.15 (0.27-1460.66)	24	61.28 (0.27-389.26)	24	141.02 (0.56-1460.66)	9.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	39	17 (0-144.1)	20	20.6 (0-144.1)	19	13.41 (0-118.67)	4.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	11	3.97 (0-41.21)	6	4.08 (0-41.21)	5	3.86 (0-36.43)	9.2×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	24	0.36 (0-7.42)	16	0.66 (0-7.42)	8	0.05 (0-1.15)	1.5×10 ⁻²
d_Fungi;p_Ascmycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	20	0.4 (0-11.77)	12	0.23 (0-1.7)	8	0.57 (0-11.77)	1.3×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	12	0.12 (0-2.27)	7	0.21 (0-2.27)	5	0.02 (0-0.44)	6.7×10 ⁻²

d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	22	0.87 (0-20.76)	14	1.68 (0-20.76)	8	0.05 (0-1.09)	9.2×10^{-3}
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	27	0.71 (0-12.78)	14	0.79 (0-9.09)	13	0.63 (0-12.78)	3.7×10^{-2}
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	19	0.37 (0-6.58)	12	0.58 (0-6.58)	7	0.15 (0-1.39)	3.7×10^{-1}
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	22	0.58 (0-14.23)	12	0.5 (0-4.86)	10	0.65 (0-14.23)	4.5×10^{-1}
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	13	0.27 (0-7)	3	0.02 (0-0.42)	10	0.52 (0-7)	2.1×10^{-2}
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	22	3.75 (0-171.43)	8	0.05 (0-0.8)	14	7.44 (0-171.43)	3.1×10^{-2}
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	12	0.23 (0-10.79)	7	0.46 (0-10.79)	5	0.00058 (0-0.0037)	1.3×10^{-1}

Note: The high-abundant microbial genera were defined as taxonomic genera present in at least 10 dormitory air samples with average relative abundance > 0.3%. In total, 41 bacterial genera and 10 fungal genera were identified and analyzed. The *p*-Value was the result of the difference between sham and real air purification using Wilcoxon signed-rank test.

^a The number of dormitory air samples that the microbial genera existed in.

^b Absolute abundance of bacterial genera was expressed as “16S rRNA gene copies/m³”. Absolute abundance of fungal genera was expressed as “18S rRNA gene copies/m³”.

Table S4. All results of associations between indoor airborne microbial absolute abundance and lung function measures.

Taxon	Lung function measures	Percentage changes (95% CIs)	p-Value
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FVC	-0.04 (-0.95, 0.89)	9.4×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEV ₁	0.78 (0.03, 1.53)	4.6×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEV ₁ /FVC	0.54 (-0.14, 1.22)	1.3×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	PEF	2.93 (1.01, 4.89)	3.5×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₂₅₋₇₅	2.84 (0.78, 4.94)	8.0×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₂₅	2.73 (0.73, 4.76)	8.7×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₅₀	2.88 (0.69, 5.12)	1.1×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₇₅	2.78 (0.13, 5.51)	4.3×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FVC	0.4 (-0.59, 1.4)	4.3×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEV ₁	0.22 (-0.63, 1.08)	6.1×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEV ₁ /FVC	-0.31 (-1.02, 0.41)	4.0×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	PEF	-0.95 (-3.04, 1.19)	3.8×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₂₅₋₇₅	-1.26 (-3.46, 0.98)	2.7×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₂₅	-0.78 (-2.97, 1.45)	4.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₅₀	-1.56 (-3.86, 0.8)	2.0×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₇₅	-0.98 (-3.73, 1.85)	4.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FVC	0.28 (-0.53, 1.09)	5.1×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEV ₁	0.44 (-0.23, 1.11)	2.1×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEV ₁ /FVC	0.04 (-0.58, 0.66)	9.1×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	PEF	-1.2 (-2.93, 0.56)	1.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₂₅₋₇₅	0.41 (-1.49, 2.34)	6.8×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₂₅	-0.98 (-2.77, 0.84)	2.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₅₀	0.67 (-1.34, 2.72)	5.2×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₇₅	1.19 (-1.23, 3.67)	3.4×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FVC	0 (-0.69, 0.7)	9.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEV ₁	0.58 (0.02, 1.15)	4.5×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEV ₁ /FVC	0.28 (-0.23, 0.8)	2.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	PEF	1.3 (-0.16, 2.79)	8.5×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₂₅₋₇₅	0.73 (-0.86, 2.34)	3.7×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₂₅	1.36 (-0.15, 2.9)	8.1×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₅₀	0.65 (-1.03, 2.36)	4.5×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₇₅	0.57 (-1.45, 2.63)	5.8×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FVC	0.56 (-0.16, 1.29)	1.3×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEV ₁	0.25 (-0.37, 0.88)	4.3×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEV ₁ /FVC	-0.32 (-0.86, 0.23)	2.6×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	PEF	-0.71 (-2.28, 0.89)	3.9×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₂₅₋₇₅	-0.28 (-1.97, 1.44)	7.5×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₂₅	-0.47 (-2.1, 1.19)	5.8×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₅₀	-0.56 (-2.33, 1.25)	5.4×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₇₅	0.06 (-2.09, 2.25)	9.6×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	FVC	-0.18 (-0.83, 0.48)	6.0×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	FEV ₁	0.44 (-0.09, 0.97)	1.1×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	FEV ₁ /FVC	0.54 (0.04, 1.04)	3.7×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	PEF	0.65 (-0.78, 2.1)	3.8×10 ⁻¹

d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₂₅₋₇₅	1.2 (-0.33, 2.77)	1.3×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₂₅	0.51 (-0.96, 2)	5.0×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₅₀	1.26 (-0.37, 2.92)	1.3×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₇₅	1.79 (-0.2, 3.81)	8.2×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FVC	0.62 (-0.03, 1.28)	6.6×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEV ₁	-0.21 (-0.76, 0.34)	4.5×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEV ₁ /FVC	-0.59 (-1.06, -0.13)	1.5×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	PEF	-0.53 (-1.93, 0.88)	4.6×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₂₅₋₇₅	-1.26 (-2.71, 0.22)	9.8×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₂₅	-0.8 (-2.23, 0.65)	2.8×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₅₀	-1.36 (-2.89, 0.2)	9.1×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₇₅	-1.95 (-3.77, -0.11)	4.1×10 ⁻²
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FVC	-0.28 (-0.98, 0.42)	4.3×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEV ₁	0.41 (-0.16, 0.99)	1.6×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEV ₁ /FVC	0.45 (-0.07, 0.97)	9.0×10 ⁻²
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	PEF	0.08 (-1.43, 1.62)	9.1×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₂₅₋₇₅	0.75 (-0.87, 2.39)	3.7×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₂₅	0.5 (-1.06, 2.08)	5.3×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₅₀	0.78 (-0.94, 2.52)	3.8×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₇₅	1.42 (-0.64, 3.53)	1.8×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FVC	0.45 (-0.2, 1.1)	1.8×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEV ₁	0.4 (-0.14, 0.94)	1.5×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEV ₁ /FVC	-0.1 (-0.61, 0.4)	6.9×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	PEF	0.67 (-0.76, 2.12)	3.6×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₂₅₋₇₅	-0.02 (-1.56, 1.54)	9.8×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₂₅	0.87 (-0.59, 2.35)	2.5×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₅₀	-0.22 (-1.85, 1.43)	7.9×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₇₅	-0.07 (-2.03, 1.93)	9.5×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FVC	-0.04 (-0.82, 0.74)	9.2×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEV ₁	0.32 (-0.32, 0.97)	3.3×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEV ₁ /FVC	0.21 (-0.39, 0.83)	4.9×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	PEF	0.44 (-1.26, 2.18)	6.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₂₅₋₇₅	0.63 (-1.21, 2.5)	5.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₂₅	0.47 (-1.28, 2.25)	6.0×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₅₀	0.16 (-1.8, 2.15)	8.8×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₇₅	0.82 (-1.54, 3.24)	5.0×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FVC	-0.09 (-0.96, 0.79)	8.4×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEV ₁	0.34 (-0.39, 1.06)	3.7×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEV ₁ /FVC	0.18 (-0.48, 0.84)	5.9×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	PEF	2.65 (0.86, 4.47)	4.7×10 ⁻³
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₂₅₋₇₅	0.86 (-1.16, 2.92)	4.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₂₅	2.34 (0.47, 4.25)	1.6×10 ⁻²
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₅₀	0.47 (-1.67, 2.66)	6.7×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₇₅	0.71 (-1.86, 3.35)	5.9×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FVC	0.13 (-0.49, 0.77)	6.8×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEV ₁	0.05 (-0.47, 0.57)	8.5×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEV ₁ /FVC	-0.04 (-0.53, 0.45)	8.6×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	PEF	-0.37 (-1.75, 1.02)	6.0×10 ⁻¹

d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₂₅₋₇₅	-0.18 (-1.66, 1.32)	8.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₂₅	-0.07 (-1.48, 1.36)	9.3×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₅₀	-0.19 (-1.76, 1.41)	8.1×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₇₅	-0.03 (-1.93, 1.91)	9.8×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FVC	0.2 (-0.54, 0.94)	6.0×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEV ₁	0.36 (-0.26, 0.98)	2.5×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEV ₁ /FVC	0.08 (-0.47, 0.63)	7.8×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	PEF	-0.12 (-1.71, 1.49)	8.8×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₂₅₋₇₅	0.04 (-1.66, 1.76)	9.6×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₂₅	0.36 (-1.28, 2.03)	6.7×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₅₀	0.05 (-1.74, 1.88)	9.5×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₇₅	-0.16 (-2.31, 2.03)	8.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FVC	-0.04 (-0.61, 0.54)	9.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEV ₁	0.14 (-0.33, 0.61)	5.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEV ₁ /FVC	0.15 (-0.3, 0.6)	5.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	PEF	0.72 (-0.52, 1.98)	2.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₂₅₋₇₅	0.94 (-0.41, 2.31)	1.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₂₅	0.52 (-0.76, 1.81)	4.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₅₀	0.83 (-0.61, 2.29)	2.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₇₅	0.98 (-0.79, 2.77)	2.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FVC	-0.27 (-1.05, 0.51)	4.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEV ₁	0.13 (-0.53, 0.8)	7.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEV ₁ /FVC	0.37 (-0.21, 0.94)	2.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	PEF	1.24 (-0.42, 2.93)	1.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₂₅₋₇₅	0.98 (-0.8, 2.8)	2.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₂₅	0.63 (-1.1, 2.4)	4.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₅₀	1.05 (-0.84, 2.97)	2.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₇₅	1.58 (-0.68, 3.89)	1.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FVC	0.57 (-0.16, 1.31)	1.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEV ₁	-0.27 (-0.89, 0.35)	3.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEV ₁ /FVC	-0.68 (-1.22, -0.14)	1.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	PEF	-1.07 (-2.64, 0.52)	1.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₂₅₋₇₅	-1.93 (-3.56, -0.27)	2.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₂₅	-1.7 (-3.28, -0.1)	4.0×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₅₀	-1.94 (-3.67, -0.17)	3.4×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₇₅	-2.58 (-4.63, -0.48)	1.8×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FVC	0.16 (-0.47, 0.79)	6.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEV ₁	-0.49 (-0.99, 0.01)	6.0×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEV ₁ /FVC	-0.58 (-1.06, -0.11)	1.9×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	PEF	-1.67 (-2.97, -0.36)	1.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₂₅₋₇₅	-1.56 (-2.99, -0.11)	3.8×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₂₅	-1.3 (-2.66, 0.07)	6.7×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₅₀	-1.45 (-2.98, 0.11)	7.2×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₇₅	-2.38 (-4.19, -0.53)	1.4×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FVC	0.1 (-0.65, 0.85)	8.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEV ₁	0.09 (-0.54, 0.71)	7.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEV ₁ /FVC	0.04 (-0.53, 0.62)	8.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	PEF	1.14 (-0.48, 2.79)	1.7×10 ⁻¹

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₂₅₋₇₅	0.84 (-0.91, 2.62)	3.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₂₅	0.77 (-0.9, 2.48)	3.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₅₀	0.96 (-0.89, 2.85)	3.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₇₅	0.43 (-1.79, 2.71)	7.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FVC	0.41 (-0.28, 1.1)	2.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEV ₁	0.79 (0.26, 1.33)	4.8×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEV ₁ /FVC	0.13 (-0.4, 0.66)	6.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	PEF	1.23 (-0.24, 2.72)	1.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₂₅₋₇₅	1.25 (-0.34, 2.86)	1.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₂₅	1.5 (0, 3.02)	5.3×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₅₀	1.27 (-0.42, 2.99)	1.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₇₅	0.83 (-1.23, 2.94)	4.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FVC	0.41 (-0.23, 1.05)	2.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEV ₁	0.43 (-0.09, 0.96)	1.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEV ₁ /FVC	-0.01 (-0.52, 0.5)	9.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	PEF	0.44 (-0.98, 1.89)	5.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₂₅₋₇₅	0.21 (-1.34, 1.78)	7.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₂₅	0.11 (-1.35, 1.59)	8.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₅₀	0.02 (-1.62, 1.69)	9.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₇₅	0.31 (-1.69, 2.35)	7.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FVC	0.38 (-0.38, 1.16)	3.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEV ₁	-0.14 (-0.78, 0.5)	6.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEV ₁ /FVC	-0.44 (-1.01, 0.14)	1.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	PEF	0.3 (-1.39, 2.01)	7.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₂₅₋₇₅	-0.4 (-2.19, 1.42)	6.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₂₅	-0.62 (-2.32, 1.12)	4.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₅₀	-0.32 (-2.22, 1.61)	7.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₇₅	-1.09 (-3.33, 1.21)	3.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FVC	0.38 (-0.25, 1.02)	2.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEV ₁	0.04 (-0.48, 0.57)	8.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEV ₁ /FVC	-0.28 (-0.78, 0.21)	2.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	PEF	-0.09 (-1.49, 1.33)	9.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₂₅₋₇₅	-1.21 (-2.68, 0.29)	1.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₂₅	-0.74 (-2.15, 0.7)	3.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₅₀	-1.44 (-2.99, 0.14)	7.9×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₇₅	-1.57 (-3.45, 0.36)	1.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FVC	0.29 (-0.43, 1.02)	4.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEV ₁	0.71 (0.13, 1.29)	1.9×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEV ₁ /FVC	0.18 (-0.37, 0.74)	5.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	PEF	1.78 (0.25, 3.32)	2.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₂₅₋₇₅	1.03 (-0.64, 2.74)	2.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₂₅	1.72 (0.15, 3.32)	3.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₅₀	1.14 (-0.64, 2.95)	2.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₇₅	0.64 (-1.51, 2.84)	5.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FVC	0.58 (-0.05, 1.22)	7.7×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEV ₁	0.13 (-0.4, 0.66)	6.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEV ₁ /FVC	-0.34 (-0.83, 0.15)	1.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	PEF	0.17 (-1.22, 1.58)	8.1×10 ⁻¹

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₂₅₋₇₅	-0.08 (-1.57, 1.44)	9.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₂₅	-0.1 (-1.52, 1.34)	8.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₅₀	0.02 (-1.57, 1.63)	9.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₇₅	-0.63 (-2.53, 1.3)	5.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FVC	0.63 (-0.08, 1.35)	8.8×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEV ₁	0.07 (-0.53, 0.67)	8.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEV ₁ /FVC	-0.7 (-1.24, -0.16)	1.3×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	PEF	0.03 (-1.55, 1.63)	9.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₂₅₋₇₅	-0.96 (-2.63, 0.74)	2.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₂₅	-0.56 (-2.16, 1.07)	5.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₅₀	-0.94 (-2.71, 0.87)	3.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₇₅	-1.81 (-3.91, 0.34)	1.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	FVC	0.36 (-0.24, 0.96)	2.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	FEV ₁	-0.44 (-0.92, 0.04)	7.9×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	FEV ₁ /FVC	-0.63 (-1.06, -0.2)	5.1×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	PEF	-0.58 (-1.86, 0.71)	3.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	FEF ₂₅₋₇₅	-1.58 (-2.9, -0.25)	2.2×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	FEF ₂₅	-0.73 (-2.04, 0.6)	2.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	FEF ₅₀	-1.64 (-3.03, -0.22)	2.6×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolunomas	FEF ₇₅	-2.31 (-3.97, -0.63)	8.6×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FVC	0.14 (-0.6, 0.89)	7.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEV ₁	0.13 (-0.48, 0.75)	6.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEV ₁ /FVC	-0.06 (-0.63, 0.52)	8.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	PEF	-1.28 (-2.86, 0.33)	1.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₂₅₋₇₅	-0.77 (-2.5, 0.99)	3.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₂₅	-0.94 (-2.58, 0.72)	2.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₅₀	-0.55 (-2.39, 1.32)	5.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₇₅	-0.73 (-2.94, 1.54)	5.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FVC	0.25 (-0.35, 0.86)	4.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEV ₁	-0.07 (-0.58, 0.44)	7.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEV ₁ /FVC	-0.16 (-0.62, 0.31)	5.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	PEF	-1.09 (-2.38, 0.23)	1.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₂₅₋₇₅	-0.75 (-2.15, 0.68)	3.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₂₅	-0.99 (-2.33, 0.36)	1.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₅₀	-1.03 (-2.51, 0.47)	1.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₇₅	-0.57 (-2.38, 1.28)	5.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FVC	0.83 (0.08, 1.58)	3.2×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEV ₁	-0.03 (-0.67, 0.6)	9.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEV ₁ /FVC	-0.69 (-1.22, -0.15)	1.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	PEF	-2.1 (-3.6, -0.56)	8.9×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₂₅₋₇₅	-1.79 (-3.44, -0.12)	3.9×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₂₅	-2.16 (-3.72, -0.58)	9.1×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₅₀	-1.9 (-3.64, -0.14)	3.8×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₇₅	-1.81 (-3.91, 0.35)	1.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FVC	0.39 (-0.51, 1.3)	4.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEV ₁	1.06 (0.35, 1.78)	4.5×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEV ₁ /FVC	0.45 (-0.22, 1.13)	1.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	PEF	1.68 (-0.24, 3.65)	9.1×10 ⁻²

d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₂₅₋₇₅	1.96 (-0.11, 4.08)	6.7×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₂₅	1.3 (-0.7, 3.34)	2.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₅₀	1.65 (-0.55, 3.9)	1.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₇₅	2.55 (-0.11, 5.28)	6.3×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FVC	0.06 (-0.62, 0.75)	8.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEV ₁	0.42 (-0.13, 0.98)	1.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEV ₁ /FVC	0.3 (-0.22, 0.83)	2.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	PEF	1.33 (-0.13, 2.81)	7.8×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₂₅₋₇₅	1.53 (-0.05, 3.13)	6.1×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₂₅	1.19 (-0.32, 2.72)	1.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₅₀	1.54 (-0.13, 3.24)	7.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₇₅	1.7 (-0.34, 3.79)	1.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FVC	-0.23 (-1.11, 0.66)	6.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEV ₁	-0.31 (-1.05, 0.44)	4.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEV ₁ /FVC	0.11 (-0.54, 0.77)	7.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	PEF	-0.86 (-2.73, 1.05)	3.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₂₅₋₇₅	-0.52 (-2.52, 1.52)	6.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₂₅	-0.21 (-2.17, 1.79)	8.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₅₀	-0.81 (-2.91, 1.33)	4.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₇₅	0.14 (-2.4, 2.75)	9.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FVC	0.5 (-0.21, 1.22)	1.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEV ₁	-0.07 (-0.67, 0.54)	8.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEV ₁ /FVC	-0.43 (-0.97, 0.11)	1.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	PEF	-2.01 (-3.48, -0.52)	1.0×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₂₅₋₇₅	-1.04 (-2.69, 0.64)	2.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₂₅	-1.69 (-3.22, -0.14)	3.6×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₅₀	-1.1 (-2.85, 0.68)	2.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₇₅	-1.07 (-3.18, 1.08)	3.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FVC	0 (-0.69, 0.7)	9.97×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEV ₁	-0.15 (-0.71, 0.43)	6.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEV ₁ /FVC	0.02 (-0.53, 0.57)	9.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	PEF	-1.06 (-2.54, 0.44)	1.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₂₅₋₇₅	-0.63 (-2.26, 1.02)	4.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₂₅	-0.93 (-2.45, 0.62)	2.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₅₀	-0.77 (-2.49, 0.98)	3.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₇₅	-0.34 (-2.44, 1.81)	7.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FVC	-1.18 (-2, -0.36)	6.4×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEV ₁	-0.07 (-0.73, 0.6)	8.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEV ₁ /FVC	0.56 (-0.05, 1.18)	7.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	PEF	-0.47 (-2.21, 1.31)	6.1×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₂₅₋₇₅	1.17 (-0.72, 3.09)	2.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₂₅	0.12 (-1.68, 1.95)	9.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₅₀	0.97 (-1.04, 3.02)	3.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₇₅	2.11 (-0.28, 4.55)	8.8×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FVC	0.64 (-0.19, 1.49)	1.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEV ₁	0.71 (0.02, 1.4)	4.7×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEV ₁ /FVC	-0.1 (-0.73, 0.55)	7.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	PEF	1.2 (-0.62, 3.05)	2.0×10 ⁻¹

d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₂₅₋₇₅	0.39 (-1.57, 2.38)	7.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₂₅	1.39 (-0.48, 3.3)	1.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₅₀	0.23 (-1.84, 2.35)	8.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₇₅	0.17 (-2.31, 2.71)	9.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FVC	0.8 (0.06, 1.55)	3.8×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEV ₁	0.11 (-0.52, 0.74)	7.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEV ₁ /FVC	-0.55 (-1.11, 0.02)	6.2×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	PEF	-0.04 (-1.69, 1.64)	9.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₂₅₋₇₅	-1.81 (-3.5, -0.08)	4.3×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₂₅	-0.42 (-2.1, 1.29)	6.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₅₀	-2.04 (-3.82, -0.23)	3.1×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₇₅	-2.74 (-4.86, -0.58)	1.5×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FVC	-0.23 (-1, 0.54)	5.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEV ₁	-0.26 (-0.89, 0.38)	4.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEV ₁ /FVC	-0.15 (-0.74, 0.45)	6.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	PEF	-0.45 (-2.12, 1.25)	6.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₂₅₋₇₅	-1.03 (-2.79, 0.78)	2.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₂₅	-0.23 (-1.94, 1.52)	8.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₅₀	-1.39 (-3.25, 0.51)	1.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₇₅	-1.02 (-3.27, 1.29)	3.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FVC	-3.35 (-5.7, -0.94)	8.6×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEV ₁	-2.98 (-4.89, -1.03)	4.1×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEV ₁ /FVC	0.62 (-1.4, 2.7)	5.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	PEF	-1.43 (-6.91, 4.36)	6.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₂₅₋₇₅	-2.8 (-8.58, 3.35)	3.7×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₂₅	-1.24 (-6.84, 4.71)	6.8×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₅₀	-3.05 (-9.19, 3.5)	3.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₇₅	-1.59 (-9.11, 6.55)	6.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FVC	0.16 (-0.82, 1.15)	7.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEV ₁	0 (-0.82, 0.83)	9.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEV ₁ /FVC	-0.35 (-1.08, 0.39)	3.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	PEF	-1.3 (-3.38, 0.83)	2.3×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₂₅₋₇₅	-2 (-4.18, 0.24)	8.3×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₂₅	-1.07 (-3.22, 1.14)	3.4×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₅₀	-2.28 (-4.58, 0.07)	6.0×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₇₅	-2.07 (-4.84, 0.79)	1.6×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FVC	0.3 (-0.4, 1.01)	4.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEV ₁	-0.25 (-0.83, 0.33)	4.0×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEV ₁ /FVC	-0.35 (-0.88, 0.18)	1.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	PEF	-0.72 (-2.22, 0.79)	3.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₂₅₋₇₅	-0.96 (-2.56, 0.66)	2.5×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₂₅	-0.79 (-2.33, 0.77)	3.2×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₅₀	-0.62 (-2.32, 1.12)	4.9×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₇₅	-1.22 (-3.26, 0.85)	2.5×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FVC	0.76 (-0.17, 1.69)	1.2×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEV ₁	0.65 (-0.12, 1.42)	1.0×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEV ₁ /FVC	-0.12 (-0.85, 0.61)	7.4×10 ⁻¹
d_Fungi;p_Ascmycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	PEF	0.44 (-1.61, 2.54)	6.8×10 ⁻¹

d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₂₅₋₇₅	1.51 (-0.7, 3.76)	1.9×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₂₅	0.46 (-1.65, 2.61)	6.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₅₀	2.09 (-0.24, 4.47)	8.3×10 ⁻²
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₇₅	0.91 (-1.91, 3.82)	5.3×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FVC	0.41 (-0.5, 1.32)	3.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEV ₁	0.38 (-0.36, 1.13)	3.2×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEV ₁ /FVC	-0.05 (-0.77, 0.67)	8.9×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	PEF	0.36 (-1.64, 2.41)	7.3×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₂₅₋₇₅	1.6 (-0.57, 3.8)	1.5×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₂₅	0.44 (-1.61, 2.53)	6.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₅₀	1.9 (-0.39, 4.25)	1.1×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₇₅	1.46 (-1.32, 4.33)	3.1×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FVC	0.41 (-0.78, 1.62)	5.1×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEV ₁	0.71 (-0.28, 1.7)	1.7×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEV ₁ /FVC	0.13 (-0.78, 1.04)	7.9×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	PEF	0.12 (-2.46, 2.78)	9.3×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₂₅₋₇₅	0.75 (-2.02, 3.6)	6.0×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₂₅	0.03 (-2.63, 2.77)	9.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₅₀	0.59 (-2.35, 3.61)	7.0×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₇₅	1.26 (-2.26, 4.91)	4.9×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FVC	0.26 (-0.67, 1.2)	5.9×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEV ₁	0.38 (-0.4, 1.16)	3.5×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEV ₁ /FVC	0.13 (-0.57, 0.84)	7.2×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	PEF	0.47 (-1.54, 2.53)	6.5×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₂₅₋₇₅	0.92 (-1.23, 3.13)	4.1×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₂₅	0.72 (-1.36, 2.84)	5.0×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₅₀	0.96 (-1.33, 3.3)	4.2×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₇₅	0.65 (-2.09, 3.46)	6.5×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FVC	-0.11 (-0.95, 0.74)	8.0×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEV ₁	0.3 (-0.4, 1.01)	4.0×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEV ₁ /FVC	0.4 (-0.24, 1.05)	2.3×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	PEF	2.54 (0.75, 4.37)	6.7×10 ⁻³
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₂₅₋₇₅	1.48 (-0.49, 3.5)	1.5×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₂₅	1.75 (-0.13, 3.67)	7.2×10 ⁻²
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₅₀	1.89 (-0.2, 4.03)	8.1×10 ⁻²
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₇₅	0.93 (-1.61, 3.52)	4.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FVC	0.45 (-0.51, 1.42)	3.6×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEV ₁	-0.12 (-0.93, 0.69)	7.7×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEV ₁ /FVC	-0.44 (-1.17, 0.29)	2.4×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	PEF	0.01 (-2.08, 2.15)	9.9×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₂₅₋₇₅	-1.07 (-3.27, 1.18)	3.5×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₂₅	-0.44 (-2.58, 1.75)	6.9×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₅₀	-1.06 (-3.4, 1.34)	3.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₇₅	-1.3 (-4.11, 1.59)	3.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FVC	0.4 (-0.68, 1.49)	4.7×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEV ₁	0.85 (-0.05, 1.76)	6.9×10 ⁻²
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEV ₁ /FVC	0.37 (-0.42, 1.17)	3.6×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	PEF	2.43 (0.16, 4.76)	3.9×10 ⁻²

d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₂₅₋₇₅	1.39 (-1.08, 3.92)	2.8×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₂₅	2.87 (0.52, 5.28)	1.9×10 ⁻²
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₅₀	1.1 (-1.5, 3.76)	4.1×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₇₅	1.12 (-1.98, 4.32)	4.8×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FVC	-1.24 (-2.5, 0.05)	6.3×10 ⁻²
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEV ₁	-0.71 (-1.78, 0.38)	2.0×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEV ₁ /FVC	0.39 (-0.59, 1.38)	4.4×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	PEF	-0.98 (-3.75, 1.86)	4.9×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₂₅₋₇₅	-0.14 (-3.12, 2.93)	9.3×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₂₅	-1.24 (-4.08, 1.68)	4.0×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₅₀	-0.61 (-3.75, 2.63)	7.1×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₇₅	1.36 (-2.45, 5.33)	4.9×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FVC	-0.15 (-1.14, 0.85)	7.7×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEV ₁	0.63 (-0.18, 1.44)	1.3×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEV ₁ /FVC	0.82 (0.06, 1.59)	3.8×10 ⁻²
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	PEF	-0.45 (-2.6, 1.75)	6.9×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₂₅₋₇₅	1.36 (-1, 3.78)	2.6×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₂₅	-0.14 (-2.35, 2.13)	9.1×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₅₀	1.58 (-0.93, 4.15)	2.2×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₇₅	2.18 (-0.84, 5.3)	1.6×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FVC	1.37 (-0.19, 2.96)	9.0×10 ⁻²
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEV ₁	0.99 (-0.35, 2.35)	1.5×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEV ₁ /FVC	-0.43 (-1.57, 0.73)	4.7×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	PEF	-0.99 (-4.29, 2.42)	5.7×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₂₅₋₇₅	-1.54 (-5.02, 2.06)	4.0×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₂₅	-1.49 (-4.89, 2.04)	4.1×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₅₀	-2.05 (-5.69, 1.73)	2.9×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₇₅	-1.58 (-5.94, 2.97)	4.9×10 ⁻¹

Note: The regressions were only conducted for the high-abundant taxonomic genera present in at least 10 dormitory air samples with an average relative abundance > 0.3%. In total, 41 bacterial genera and 10 fungal genera were identified and analyzed. Percentage changes and 95% confidence intervals were calculated for per unit increase in the transformed absolute abundance ($\log_{10}(\text{absolute abundance} * 10^5 + 1)$). Linear mixed-effect models were adjusted for age, gender, BMI, season, PM_{2.5}, purification status (real or sham), temperature, relative humidity, and a random intercept for each participant. FVC, forced vital capacity; FEV₁, forced expiratory volume in one second; PEF, peak expiratory flow; FEF₂₅, forced expiratory flow at 25% of FVC; FEF₅₀, forced expiratory flow at 50% of FVC; FEF₇₅, forced expiratory flow at 75% of FVC; FEF₂₅₋₇₅, forced expiratory flow from 25-75% of FVC; CIs, confidence intervals.

Table S5. All results of associations between indoor airborne microbial relative abundance and lung function measures.

Taxon	Lung function measures	Percentage changes (95% CIs)	p-Value
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FVC	0.17 (-1.52, 1.88)	8.46×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEV ₁	1.57 (0.2, 2.95)	2.81×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEV ₁ /FVC	0.91 (-0.37, 2.21)	1.67×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	PEF	5.41 (1.8, 9.15)	4.04×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₂₅₋₇₅	5.21 (1.34, 9.23)	9.61×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₂₅	5.03 (1.3, 8.9)	9.52×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₅₀	5.48 (1.35, 9.78)	1.06×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	FEF ₇₅	4.84 (-0.18, 10.11)	6.24×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FVC	0.67 (-1.02, 2.4)	4.40×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEV ₁	0.93 (-0.5, 2.38)	2.06×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEV ₁ /FVC	-0.2 (-1.43, 1.04)	7.49×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	PEF	-0.76 (-4.33, 2.95)	6.85×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₂₅₋₇₅	-1.01 (-4.78, 2.91)	6.10×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₂₅	-0.47 (-4.19, 3.4)	8.10×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₅₀	-1.33 (-5.29, 2.79)	5.21×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Corynebacteriales;f_Corynebacteriaceae;g_Corynebacterium	FEF ₇₅	-0.52 (-5.24, 4.43)	8.33×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FVC	0.19 (-1.51, 1.92)	8.28×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEV ₁	0.91 (-0.5, 2.34)	2.10×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEV ₁ /FVC	0.35 (-0.94, 1.66)	5.94×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	PEF	-1.45 (-5.06, 2.29)	4.43×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₂₅₋₇₅	1.95 (-2.01, 6.06)	3.42×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₂₅	-1.08 (-4.8, 2.8)	5.82×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₅₀	2.59 (-1.6, 6.95)	2.33×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Frankiales;f_Geodermatophilaceae;g_Geodermatophilus	FEF ₇₅	3.79 (-1.29, 9.12)	1.50×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FVC	0.04 (-1.15, 1.24)	9.48×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEV ₁	1.34 (0.41, 2.28)	6.26×10 ⁻³
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEV ₁ /FVC	0.73 (-0.16, 1.62)	1.12×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	PEF	3.3 (0.81, 5.85)	1.09×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₂₅₋₇₅	2.59 (-0.13, 5.37)	6.57×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₂₅	3.32 (0.75, 5.94)	1.30×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₅₀	2.47 (-0.42, 5.45)	9.81×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Kocuria	FEF ₇₅	2.43 (-1.08, 6.05)	1.80×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FVC	0.94 (-0.39, 2.3)	1.72×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEV ₁	0.76 (-0.38, 1.91)	1.95×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEV ₁ /FVC	-0.36 (-1.36, 0.65)	4.84×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	PEF	-0.5 (-3.39, 2.47)	7.38×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₂₅₋₇₅	0.17 (-2.92, 3.36)	9.14×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₂₅	-0.13 (-3.12, 2.96)	9.35×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₅₀	-0.28 (-3.54, 3.08)	8.68×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_Micrococcaceae;g_Micrococcus	FEF ₇₅	0.71 (-3.2, 4.79)	7.26×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	FVC	-0.31 (-1.6, 0.99)	6.37×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	FEV ₁	0.85 (-0.21, 1.92)	1.21×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	FEV ₁ /FVC	0.98 (-0.01, 1.98)	5.55×10 ⁻²
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioidaceae;g_Nocardioides	PEF	1.44 (-1.39, 4.35)	3.25×10 ⁻¹

d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₂₅₋₇₅	2.44 (-0.61, 5.59)	1.22×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₂₅	1.27 (-1.63, 4.26)	3.98×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₅₀	2.64 (-0.61, 5.99)	1.16×10 ⁻¹
d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Propionibacteriales;f_Nocardioideaceae;g_Nocardioide	FEF ₇₅	3.25 (-0.69, 7.36)	1.11×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FVC	0.88 (-0.36, 2.14)	1.67×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEV ₁	-0.47 (-1.5, 0.57)	3.77×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEV ₁ /FVC	-0.88 (-1.75, 0)	5.38×10 ⁻²
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	PEF	-0.39 (-3, 2.29)	7.74×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₂₅₋₇₅	-1.72 (-4.43, 1.07)	2.27×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₂₅	-1.04 (-3.72, 1.71)	4.55×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₅₀	-1.89 (-4.74, 1.05)	2.08×10 ⁻¹
d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Flavobacteriales;f_Weeksellaceae;g_Cloacibacterium	FEF ₇₅	-2.84 (-6.19, 0.63)	1.10×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FVC	-0.42 (-1.59, 0.76)	4.87×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEV ₁	0.86 (-0.1, 1.82)	8.41×10 ⁻²
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEV ₁ /FVC	0.9 (0.02, 1.79)	4.80×10 ⁻²
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	PEF	0.25 (-2.31, 2.87)	8.51×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₂₅₋₇₅	1.5 (-1.25, 4.32)	2.92×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₂₅	1.08 (-1.54, 3.78)	4.26×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₅₀	1.58 (-1.34, 4.58)	2.96×10 ⁻¹
d_Bacteria;p_Cyanobacteria;c_Oxyphotobacteria;o_Chloroplast;f_Chloroplast;g_Chloroplast	FEF ₇₅	2.6 (-0.92, 6.26)	1.53×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FVC	0.5 (-0.67, 1.68)	4.06×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEV ₁	0.66 (-0.29, 1.63)	1.80×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEV ₁ /FVC	0.05 (-0.86, 0.97)	9.10×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	PEF	1.65 (-0.92, 4.27)	2.14×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₂₅₋₇₅	0.47 (-2.3, 3.31)	7.45×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₂₅	2 (-0.61, 4.69)	1.39×10 ⁻¹
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₅₀	0 (-2.93, 3.01)	1.00×10 ⁰
d_Bacteria;p_Deinococcus-Thermus;c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	FEF ₇₅	0.66 (-2.88, 4.33)	7.20×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FVC	-0.34 (-1.86, 1.21)	6.70×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEV ₁	0.74 (-0.52, 2.02)	2.53×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEV ₁ /FVC	0.69 (-0.5, 1.9)	2.60×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	PEF	1.82 (-1.54, 5.29)	2.96×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₂₅₋₇₅	2.13 (-1.49, 5.87)	2.56×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₂₅	1.74 (-1.69, 5.3)	3.28×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₅₀	1.28 (-2.57, 5.28)	5.23×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Abyssicoccus	FEF ₇₅	2.35 (-2.32, 7.24)	3.33×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FVC	-0.18 (-1.55, 1.21)	8.03×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEV ₁	0.89 (-0.23, 2.02)	1.25×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEV ₁ /FVC	0.54 (-0.51, 1.6)	3.16×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	PEF	4.7 (1.87, 7.6)	1.55×10 ⁻³
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₂₅₋₇₅	1.82 (-1.39, 5.12)	2.73×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₂₅	4.35 (1.42, 7.37)	4.62×10 ⁻³
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₅₀	1.17 (-2.23, 4.69)	5.05×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	FEF ₇₅	1.45 (-2.65, 5.72)	4.95×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FVC	-0.05 (-1.24, 1.15)	9.32×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEV ₁	-0.17 (-1.15, 0.83)	7.39×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEV ₁ /FVC	-0.06 (-0.99, 0.87)	8.93×10 ⁻¹

d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	PEF	-0.46 (-3.05, 2.2)	7.32×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₂₅₋₇₅	-0.26 (-3.06, 2.61)	8.57×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₂₅	0.06 (-2.6, 2.8)	9.63×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₅₀	-0.17 (-3.14, 2.9)	9.13×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	FEF ₇₅	-0.36 (-3.93, 3.35)	8.47×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FVC	0.51 (-0.97, 2.01)	5.03×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEV ₁	1.26 (0.01, 2.52)	5.11×10 ⁻²
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEV ₁ /FVC	0.35 (-0.73, 1.45)	5.28×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	PEF	1.14 (-2.02, 4.39)	4.86×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₂₅₋₇₅	0.96 (-2.4, 4.43)	5.81×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₂₅	1.8 (-1.47, 5.19)	2.87×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₅₀	1.12 (-2.43, 4.79)	5.43×10 ⁻¹
d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	FEF ₇₅	0.38 (-3.83, 4.77)	8.64×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FVC	-0.12 (-1.15, 0.92)	8.27×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEV ₁	0.41 (-0.43, 1.26)	3.41×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEV ₁ /FVC	0.43 (-0.39, 1.25)	3.09×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	PEF	1.58 (-0.67, 3.88)	1.74×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₂₅₋₇₅	1.93 (-0.52, 4.44)	1.28×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₂₅	1.31 (-1, 3.67)	2.72×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₅₀	1.66 (-0.95, 4.34)	2.18×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	FEF ₇₅	2.12 (-1.07, 5.42)	2.00×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FVC	-0.31 (-1.82, 1.23)	6.95×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEV ₁	0.42 (-0.87, 1.72)	5.31×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEV ₁ /FVC	0.65 (-0.48, 1.8)	2.65×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	PEF	2.04 (-1.23, 5.41)	2.28×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₂₅₋₇₅	1.41 (-2.09, 5.03)	4.37×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₂₅	0.89 (-2.49, 4.38)	6.12×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₅₀	1.63 (-2.08, 5.47)	3.96×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Methylobacterium	FEF ₇₅	2.48 (-1.98, 7.14)	2.83×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FVC	1.12 (-0.31, 2.58)	1.30×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEV ₁	-0.49 (-1.69, 0.73)	4.30×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEV ₁ /FVC	-1.36 (-2.4, -0.32)	1.25×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	PEF	-2.05 (-5.06, 1.06)	1.97×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₂₅₋₇₅	-3.92 (-7.01, -0.72)	1.90×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₂₅	-3.27 (-6.27, -0.18)	4.16×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₅₀	-3.78 (-7.07, -0.36)	3.33×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	FEF ₇₅	-5.58 (-9.42, -1.57)	8.18×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FVC	0.35 (-0.9, 1.62)	5.87×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEV ₁	-0.95 (-1.93, 0.05)	6.76×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEV ₁ /FVC	-1.19 (-2.13, -0.25)	1.50×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	PEF	-3.14 (-5.67, -0.54)	2.08×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₂₅₋₇₅	-3.04 (-5.82, -0.18)	4.08×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₂₅	-2.46 (-5.11, 0.27)	8.14×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₅₀	-2.8 (-5.78, 0.28)	7.81×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas	FEF ₇₅	-4.82 (-8.29, -1.21)	1.11×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FVC	0.37 (-0.98, 1.75)	5.95×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEV ₁	0.43 (-0.7, 1.57)	4.61×10 ⁻¹

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEV ₁ /FVC	0.12 (-0.92, 1.16)	8.26×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	PEF	2.09 (-0.87, 5.13)	1.72×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₂₅₋₇₅	1.9 (-1.27, 5.18)	2.46×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₂₅	1.35 (-1.69, 4.49)	3.91×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₅₀	2.43 (-0.93, 5.91)	1.61×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Allorhizobium	FEF ₇₅	0.98 (-3.05, 5.17)	6.40×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FVC	0.73 (-0.59, 2.07)	2.83×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEV ₁	1.62 (0.6, 2.65)	2.80×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEV ₁ /FVC	0.35 (-0.67, 1.39)	5.01×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	PEF	2.96 (0.12, 5.87)	4.46×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₂₅₋₇₅	3 (-0.06, 6.16)	5.88×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₂₅	3.51 (0.62, 6.48)	1.96×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₅₀	3.12 (-0.15, 6.49)	6.59×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiales_Incertae_Sedis;g_Phreatobacter	FEF ₇₅	2.05 (-1.94, 6.2)	3.23×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FVC	0.62 (-0.65, 1.89)	3.44×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEV ₁	0.86 (-0.17, 1.9)	1.08×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEV ₁ /FVC	0.13 (-0.87, 1.13)	8.07×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	PEF	1.33 (-1.46, 4.2)	3.55×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₂₅₋₇₅	1.05 (-1.98, 4.17)	5.04×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₂₅	0.69 (-2.17, 3.63)	6.41×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₅₀	0.72 (-2.48, 4.03)	6.64×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium	FEF ₇₅	1.3 (-2.59, 5.36)	5.19×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FVC	0.77 (-0.45, 2.01)	2.23×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEV ₁	0.06 (-0.97, 1.11)	9.07×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEV ₁ /FVC	-0.61 (-1.53, 0.31)	1.96×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	PEF	0.85 (-1.84, 3.6)	5.42×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₂₅₋₇₅	-0.21 (-3.06, 2.72)	8.85×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₂₅	-0.64 (-3.37, 2.16)	6.52×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₅₀	-0.11 (-3.13, 3)	9.43×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Pseudolabrys	FEF ₇₅	-1.37 (-4.93, 2.31)	4.61×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FVC	0.88 (-0.35, 2.14)	1.67×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEV ₁	0.07 (-0.96, 1.11)	8.98×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEV ₁ /FVC	-0.71 (-1.67, 0.26)	1.57×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	PEF	-0.37 (-3.11, 2.45)	7.97×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₂₅₋₇₅	-2.33 (-5.19, 0.61)	1.24×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₂₅	-1.66 (-4.4, 1.16)	2.51×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₅₀	-2.72 (-5.72, 0.39)	8.99×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Rhodopseudomonas	FEF ₇₅	-3.12 (-6.75, 0.65)	1.08×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FVC	0.51 (-0.8, 1.84)	4.52×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEV ₁	1.47 (0.43, 2.52)	7.12×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEV ₁ /FVC	0.5 (-0.49, 1.51)	3.27×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	PEF	4 (1.26, 6.82)	5.22×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₂₅₋₇₅	2.85 (-0.18, 5.97)	6.93×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₂₅	3.83 (0.99, 6.74)	9.63×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₅₀	3.13 (-0.08, 6.44)	5.99×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	FEF ₇₅	2.11 (-1.8, 6.17)	2.98×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FVC	1.04 (-0.19, 2.29)	1.04×10 ⁻¹

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEV ₁	0.39 (-0.64, 1.42)	4.63×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEV ₁ /FVC	-0.48 (-1.43, 0.48)	3.26×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	PEF	0.91 (-1.8, 3.69)	5.17×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₂₅₋₇₅	0.53 (-2.37, 3.52)	7.23×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₂₅	0.32 (-2.44, 3.16)	8.22×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₅₀	0.79 (-2.29, 3.98)	6.19×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	FEF ₇₅	-0.41 (-4.08, 3.4)	8.31×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FVC	1.22 (-0.08, 2.54)	7.04×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEV ₁	0.21 (-0.87, 1.3)	7.04×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEV ₁ /FVC	-1.32 (-2.31, -0.31)	1.21×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	PEF	0.24 (-2.63, 3.19)	8.75×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₂₅₋₇₅	-1.82 (-4.84, 1.3)	2.54×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₂₅	-0.91 (-3.8, 2.08)	5.49×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₅₀	-1.73 (-4.94, 1.59)	3.07×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	FEF ₇₅	-3.54 (-7.32, 0.4)	8.15×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	FVC	0.68 (-0.46, 1.82)	2.47×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	FEV ₁	-0.83 (-1.73, 0.07)	7.61×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	FEV ₁ /FVC	-1.15 (-1.95, -0.34)	6.59×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	PEF	-1.15 (-3.52, 1.28)	3.52×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	FEF ₂₅₋₇₅	-2.92 (-5.34, -0.43)	2.40×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	FEF ₂₅	-1.43 (-3.86, 1.06)	2.60×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	FEF ₅₀	-3 (-5.57, -0.37)	2.84×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_Tolomonas	FEF ₇₅	-4.17 (-7.19, -1.05)	1.07×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FVC	0.26 (-1.14, 1.68)	7.16×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEV ₁	0.26 (-0.9, 1.43)	6.68×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEV ₁ /FVC	-0.11 (-1.2, 0.98)	8.38×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	PEF	-2.32 (-5.26, 0.71)	1.37×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₂₅₋₇₅	-1.24 (-4.47, 2.1)	4.65×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₂₅	-1.71 (-4.76, 1.44)	2.86×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₅₀	-0.89 (-4.33, 2.68)	6.22×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Acidovorax	FEF ₇₅	-1.13 (-5.27, 3.19)	6.03×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FVC	0.47 (-0.71, 1.67)	4.40×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEV ₁	-0.28 (-1.26, 0.71)	5.77×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEV ₁ /FVC	-0.46 (-1.36, 0.46)	3.28×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	PEF	-1.93 (-4.43, 0.62)	1.41×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₂₅₋₇₅	-1.58 (-4.27, 1.19)	2.66×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₂₅	-1.82 (-4.38, 0.81)	1.78×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₅₀	-2.08 (-4.91, 0.83)	1.64×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Aquabacterium	FEF ₇₅	-1.59 (-5.04, 1.99)	3.82×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FVC	1.65 (0.14, 3.19)	3.51×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEV ₁	-0.35 (-1.62, 0.94)	5.94×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEV ₁ /FVC	-1.54 (-2.59, -0.47)	5.79×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	PEF	-4.57 (-7.48, -1.56)	4.01×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₂₅₋₇₅	-4.34 (-7.49, -1.07)	1.11×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₂₅	-4.72 (-7.73, -1.61)	4.09×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₅₀	-4.66 (-7.97, -1.23)	9.43×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Hydrogenophaga	FEF ₇₅	-4.46 (-8.49, -0.26)	4.02×10 ⁻²

d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FVC	0.79 (-1.13, 2.75)	4.24×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEV ₁	2.37 (0.84, 3.92)	3.28×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEV ₁ /FVC	1.14 (-0.31, 2.61)	1.28×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	PEF	4.3 (0.14, 8.63)	4.60×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₂₅₋₇₅	5.03 (0.54, 9.72)	3.05×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₂₅	3.49 (-0.81, 7.98)	1.17×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₅₀	4.44 (-0.33, 9.43)	7.19×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Massilia	FEF ₇₅	6.2 (0.41, 12.33)	3.84×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FVC	-0.04 (-1.31, 1.25)	9.53×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEV ₁	0.85 (-0.18, 1.9)	1.12×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEV ₁ /FVC	0.71 (-0.26, 1.69)	1.56×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	PEF	2.61 (-0.12, 5.42)	6.52×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₂₅₋₇₅	3.42 (0.48, 6.46)	2.51×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₂₅	2.55 (-0.27, 5.44)	8.05×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₅₀	3.38 (0.25, 6.61)	3.73×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Ralstonia	FEF ₇₅	3.94 (0.11, 7.91)	4.68×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FVC	-0.57 (-2.24, 1.13)	5.11×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEV ₁	-0.51 (-1.92, 0.92)	4.84×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEV ₁ /FVC	0.38 (-0.87, 1.64)	5.59×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	PEF	-1.19 (-4.73, 2.48)	5.22×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₂₅₋₇₅	-0.15 (-3.96, 3.82)	9.41×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₂₅	0.2 (-3.53, 4.07)	9.19×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₅₀	-0.76 (-4.75, 3.4)	7.17×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Burkholderiaceae;g_Tepidimonas	FEF ₇₅	1.25 (-3.61, 6.36)	6.22×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FVC	1.08 (-0.21, 2.4)	1.07×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEV ₁	-0.04 (-1.11, 1.06)	9.50×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEV ₁ /FVC	-0.93 (-1.91, 0.06)	6.86×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	PEF	-3.96 (-6.54, -1.32)	4.66×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₂₅₋₇₅	-2.26 (-5.21, 0.77)	1.47×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₂₅	-3.35 (-6.04, -0.59)	2.06×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₅₀	-2.22 (-5.35, 1.03)	1.82×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Dechloromonas	FEF ₇₅	-2.79 (-6.55, 1.12)	1.63×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FVC	-0.09 (-1.43, 1.27)	8.97×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEV ₁	-0.29 (-1.39, 0.82)	6.09×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEV ₁ /FVC	0.15 (-0.91, 1.22)	7.80×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	PEF	-1.93 (-4.77, 0.99)	1.97×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₂₅₋₇₅	-0.81 (-3.95, 2.42)	6.20×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₂₅	-1.58 (-4.51, 1.44)	3.05×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₅₀	-0.99 (-4.31, 2.44)	5.69×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Betaproteobacteriales;f_Rhodocyclaceae;g_Zoogloea	FEF ₇₅	0.03 (-4.03, 4.27)	9.87×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FVC	-1.45 (-2.87, -0.01)	5.32×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEV ₁	-0.39 (-1.59, 0.83)	5.31×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEV ₁ /FVC	0.93 (-0.21, 2.08)	1.15×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	PEF	-0.97 (-4.12, 2.28)	5.57×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₂₅₋₇₅	1.85 (-1.62, 5.44)	3.04×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₂₅	0.1 (-3.16, 3.47)	9.53×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₅₀	1.4 (-2.27, 5.22)	4.62×10 ⁻¹

d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	FEF ₇₅	4.34 (-0.17, 9.06)	6.32×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FVC	1.53 (-0.14, 3.22)	7.65×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEV ₁	1.87 (0.53, 3.24)	8.09×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEV ₁ /FVC	-0.08 (-1.34, 1.21)	9.07×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	PEF	3.42 (-0.2, 7.17)	6.79×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₂₅₋₇₅	1.56 (-2.34, 5.61)	4.40×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₂₅	3.65 (-0.08, 7.53)	5.89×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₅₀	1.42 (-2.71, 5.71)	5.09×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Oceanospirillales;f_Halomonadaceae;g_Halomonas	FEF ₇₅	0.84 (-4.07, 6)	7.42×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FVC	1.37 (0.12, 2.64)	3.47×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEV ₁	0.2 (-0.86, 1.27)	7.13×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEV ₁ /FVC	-0.9 (-1.83, 0.03)	6.09×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	PEF	0.8 (-1.93, 3.61)	5.72×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₂₅₋₇₅	-2.27 (-5.07, 0.61)	1.25×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₂₅	-0.03 (-2.82, 2.85)	9.85×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₅₀	-2.54 (-5.49, 0.5)	1.05×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	FEF ₇₅	-4.09 (-7.53, -0.52)	2.75×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FVC	-0.57 (-1.98, 0.86)	4.36×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEV ₁	-0.19 (-1.38, 1.02)	7.61×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEV ₁ /FVC	0.05 (-1.04, 1.14)	9.33×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	PEF	0.51 (-2.57, 3.69)	7.49×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₂₅₋₇₅	-0.73 (-4, 2.65)	6.69×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₂₅	0.87 (-2.31, 4.15)	5.98×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₅₀	-1.33 (-4.77, 2.23)	4.61×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	FEF ₇₅	-0.65 (-4.8, 3.68)	7.65×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FVC	-5.37 (-8.58, -2.06)	2.55×10 ⁻³
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEV ₁	-2.96 (-5.77, -0.07)	4.94×10 ⁻²
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEV ₁ /FVC	2.43 (-0.48, 5.43)	1.07×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	PEF	2.2 (-5.83, 10.91)	6.04×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₂₅₋₇₅	2.19 (-6.48, 11.66)	6.34×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₂₅	3.24 (-5.01, 12.19)	4.56×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₅₀	2.75 (-6.5, 12.91)	5.74×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	FEF ₇₅	3.91 (-7.34, 16.52)	5.14×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FVC	0.22 (-1.5, 1.98)	8.02×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEV ₁	0.71 (-0.73, 2.17)	3.41×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEV ₁ /FVC	-0.06 (-1.36, 1.26)	9.28×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	PEF	-0.05 (-3.76, 3.81)	9.80×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₂₅₋₇₅	-1.46 (-5.37, 2.61)	4.78×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₂₅	0.36 (-3.48, 4.35)	8.58×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₅₀	-1.84 (-5.95, 2.44)	3.96×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Vibrionales;f_Vibrionaceae;g_Vibrio	FEF ₇₅	-1.38 (-6.3, 3.81)	5.97×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FVC	0.59 (-0.75, 1.95)	3.90×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEV ₁	-0.52 (-1.62, 0.59)	3.62×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEV ₁ /FVC	-0.7 (-1.7, 0.3)	1.74×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	PEF	-1.48 (-4.29, 1.42)	3.17×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₂₅₋₇₅	-1.9 (-4.89, 1.19)	2.29×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₂₅	-1.63 (-4.52, 1.34)	2.82×10 ⁻¹

d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₅₀	-1.22 (-4.43, 2.11)	4.71×10 ⁻¹
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	FEF ₇₅	-2.41 (-6.21, 1.53)	2.30×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FVC	1.27 (0.09, 2.45)	3.78×10 ⁻²
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEV ₁	0.89 (-0.09, 1.87)	7.96×10 ⁻²
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEV ₁ /FVC	-0.38 (-1.29, 0.55)	4.26×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	PEF	0.19 (-2.42, 2.86)	8.91×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₂₅₋₇₅	1.21 (-1.6, 4.11)	4.04×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₂₅	0.42 (-2.26, 3.17)	7.63×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₅₀	1.91 (-1.08, 4.98)	2.17×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Capnodiales;f_Mycosphaerellaceae;g_Mycosphaerella	FEF ₇₅	0.27 (-3.31, 3.97)	8.86×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FVC	0.71 (-0.49, 1.93)	2.50×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEV ₁	0.63 (-0.36, 1.63)	2.17×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEV ₁ /FVC	-0.14 (-1.1, 0.82)	7.68×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	PEF	0.86 (-1.81, 3.6)	5.34×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₂₅₋₇₅	2.13 (-0.74, 5.09)	1.52×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₂₅	1.01 (-1.72, 3.82)	4.74×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₅₀	2.48 (-0.58, 5.63)	1.17×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Didymellaceae;g_Calophoma	FEF ₇₅	1.81 (-1.9, 5.65)	3.47×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FVC	0.54 (-1.09, 2.19)	5.21×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEV ₁	0.89 (-0.45, 2.26)	1.98×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEV ₁ /FVC	0.15 (-1.09, 1.41)	8.14×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	PEF	0.19 (-3.33, 3.83)	9.19×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₂₅₋₇₅	0.73 (-3.06, 4.66)	7.12×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₂₅	0.04 (-3.57, 3.79)	9.81×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₅₀	0.57 (-3.43, 4.73)	7.85×10 ⁻¹
d_Fungi;p_Ascomycota;c_Dothideomycetes;o_Pleosporales;f_Pleosporaceae;g_Alternaria	FEF ₇₅	1.33 (-3.49, 6.39)	5.97×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FVC	0.39 (-0.79, 1.59)	5.18×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEV ₁	0.47 (-0.5, 1.46)	3.47×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEV ₁ /FVC	0.1 (-0.81, 1.01)	8.36×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	PEF	1.01 (-1.57, 3.65)	4.50×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₂₅₋₇₅	1.14 (-1.63, 3.98)	4.26×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₂₅	1.13 (-1.52, 3.85)	4.09×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₅₀	1.26 (-1.67, 4.28)	4.06×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Aspergillus	FEF ₇₅	0.58 (-2.93, 4.22)	7.49×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FVC	-0.06 (-1.12, 1.02)	9.18×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEV ₁	0.49 (-0.39, 1.39)	2.80×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEV ₁ /FVC	0.54 (-0.28, 1.37)	1.99×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	PEF	3.57 (1.31, 5.89)	2.57×10 ⁻³
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₂₅₋₇₅	2.05 (-0.45, 4.62)	1.13×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₂₅	2.64 (0.26, 5.07)	3.24×10 ⁻²
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₅₀	2.61 (-0.05, 5.34)	5.82×10 ⁻²
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Aspergillaceae;g_Penicillium	FEF ₇₅	1.3 (-1.91, 4.62)	4.34×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FVC	0.55 (-0.7, 1.81)	3.91×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEV ₁	-0.46 (-1.51, 0.6)	3.93×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEV ₁ /FVC	-0.82 (-1.74, 0.12)	8.97×10 ⁻²
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	PEF	-1.29 (-3.93, 1.43)	3.52×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₂₅₋₇₅	-2.28 (-5.05, 0.57)	1.19×10 ⁻¹

d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₂₅	-1.67 (-4.37, 1.11)	2.40×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₅₀	-2.29 (-5.23, 0.74)	1.40×10 ⁻¹
d_Fungi;p_Ascomycota;c_Eurotiomycetes;o_Eurotiales;f_Trichocomaceae;g_Talaromyces	FEF ₇₅	-2.38 (-5.92, 1.3)	2.06×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FVC	0.37 (-1.02, 1.78)	6.08×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEV ₁	0.75 (-0.42, 1.93)	2.16×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEV ₁ /FVC	0.36 (-0.68, 1.4)	5.01×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	PEF	2.78 (-0.19, 5.83)	7.05×10 ⁻²
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₂₅₋₇₅	1.43 (-1.78, 4.73)	3.89×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₂₅	3.32 (0.26, 6.48)	3.62×10 ⁻²
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₅₀	1.04 (-2.33, 4.53)	5.51×10 ⁻¹
d_Fungi;p_Ascomycota;c_Sordariomycetes;o_Hypocreales;f_Nectriaceae;g_Gibberella	FEF ₇₅	1.05 (-2.98, 5.24)	6.16×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FVC	-1.62 (-3.26, 0.06)	6.22×10 ⁻²
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEV ₁	-1.3 (-2.67, 0.1)	7.22×10 ⁻²
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEV ₁ /FVC	0.21 (-1.06, 1.51)	7.44×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	PEF	-2.39 (-5.91, 1.26)	2.00×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₂₅₋₇₅	-1.16 (-4.98, 2.82)	5.64×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₂₅	-2.78 (-6.38, 0.96)	1.47×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₅₀	-1.83 (-5.84, 2.35)	3.88×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Agaricomycetes;o_Atheliales;f_Atheliaceae;g_Tylospora	FEF ₇₅	0.71 (-4.22, 5.89)	7.82×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FVC	-0.1 (-1.56, 1.38)	8.96×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEV ₁	0.97 (-0.23, 2.19)	1.18×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEV ₁ /FVC	1.1 (-0.02, 2.23)	5.71×10 ⁻²
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	PEF	-0.9 (-4.03, 2.33)	5.81×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₂₅₋₇₅	1.8 (-1.65, 5.38)	3.13×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₂₅	-0.24 (-3.49, 3.11)	8.87×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₅₀	2.05 (-1.62, 5.85)	2.81×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Malasseziomycetes;o_Malasseziales;f_Malasseziaceae;g_Malassezia	FEF ₇₅	3.04 (-1.38, 7.65)	1.84×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FVC	2.08 (-0.41, 4.63)	1.07×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEV ₁	0.89 (-1.24, 3.07)	4.18×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEV ₁ /FVC	-1.23 (-3.01, 0.58)	1.86×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	PEF	-2.8 (-7.87, 2.55)	3.02×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₂₅₋₇₅	-4.16 (-9.44, 1.43)	1.45×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₂₅	-3.76 (-8.95, 1.72)	1.78×10 ⁻¹
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₅₀	-5.12 (-10.61, 0.71)	8.69×10 ⁻²
d_Fungi;p_Basidiomycota;c_Wallemiomycetes;o_Wallemiales;f_Wallemiaceae;g_Wallemia	FEF ₇₅	-4.57 (-11.16, 2.51)	2.03×10 ⁻¹

Note: The regressions were only conducted for the high-abundant taxonomic genera present in at least 10 dormitory air samples with an average relative abundance > 0.3%. In total, 41 bacterial genera and 10 fungal genera were identified and analyzed. Percentage changes and 95% confidence intervals were calculated for per unit increase in the transformed relative abundance ($\log_{10}(\text{relative abundance} * 10^5 + 1)$). Linear mixed-effect models were adjusted for age, gender, BMI, season, PM_{2.5}, purification status (real or sham), temperature, relative humidity, and a random intercept for each participant. FVC, forced vital capacity; FEV₁, forced expiratory volume in one second; PEF, peak expiratory flow; FEF₂₅, forced expiratory flow at 25% of FVC; FEF₅₀, forced expiratory flow at 50% of FVC; FEF₇₅, forced expiratory flow at 75% of FVC; FEF₂₅₋₇₅, forced expiratory flow from 25-75% of FVC; CIs, confidence intervals.

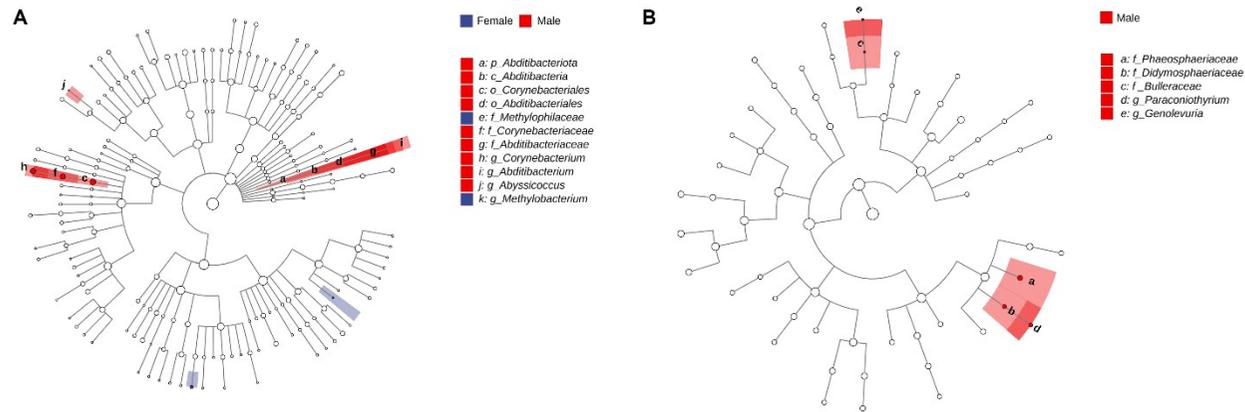


Fig. S1. Linear discriminant analysis (LDA) effect size (LEfSe) analysis on indoor airborne microbiome between the female and male dormitories. The cladogram of airborne bacterial (A) and fungal (B) community from LEfSe analysis. Differentially enriched taxa were identified according to at LDA score cutoff at 2. The blue circle represents significantly enriched taxa in female dormitories; the red circle represents significantly enriched taxa in male dormitories; and the white circle represents taxa with no significant differences between the two groups. The central circle represents the root of the tree (bacteria or fungi), and each ring represents the next lower taxonomic level (from phylum to genus).