Online Supplement
Differences of the Nasal Microbiome and Mycobiome by Clinical Characteristics of COPD Patients

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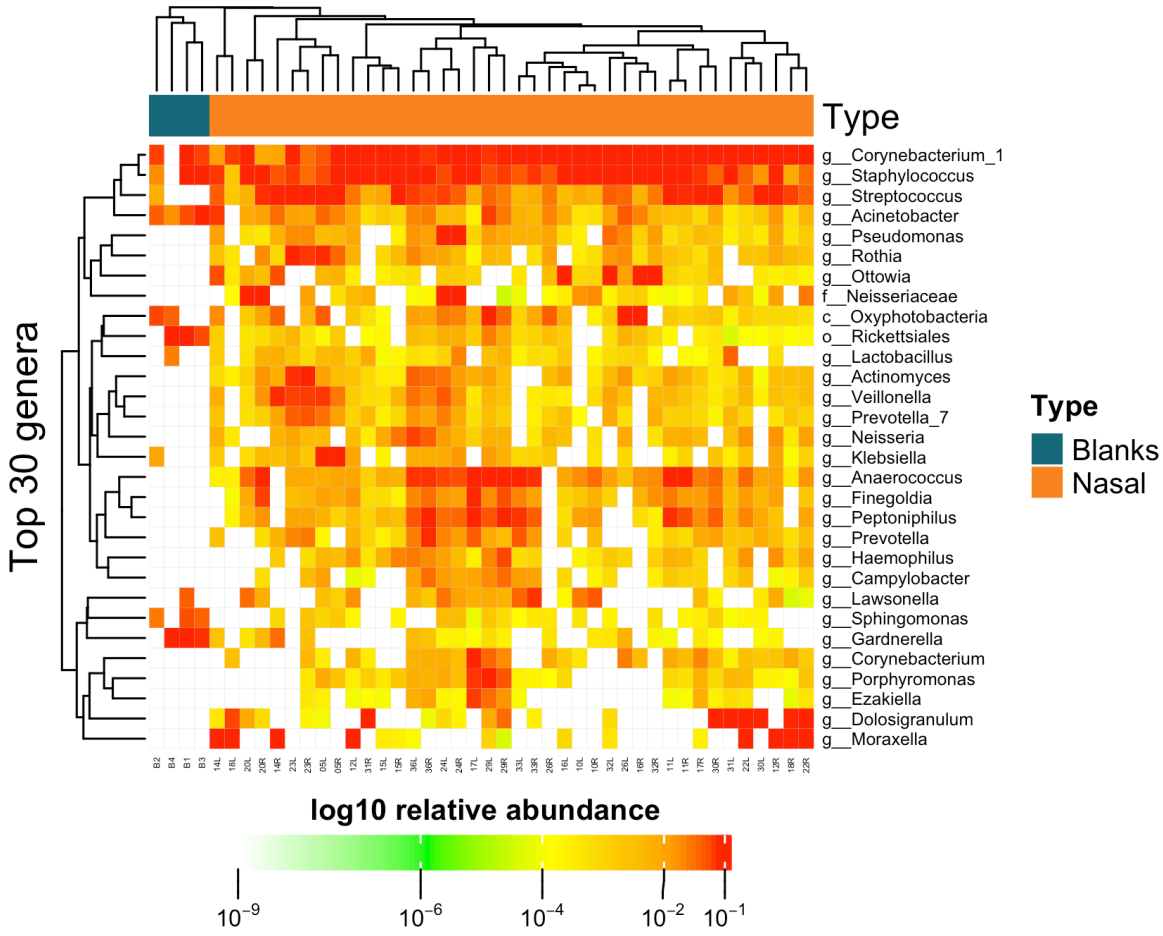
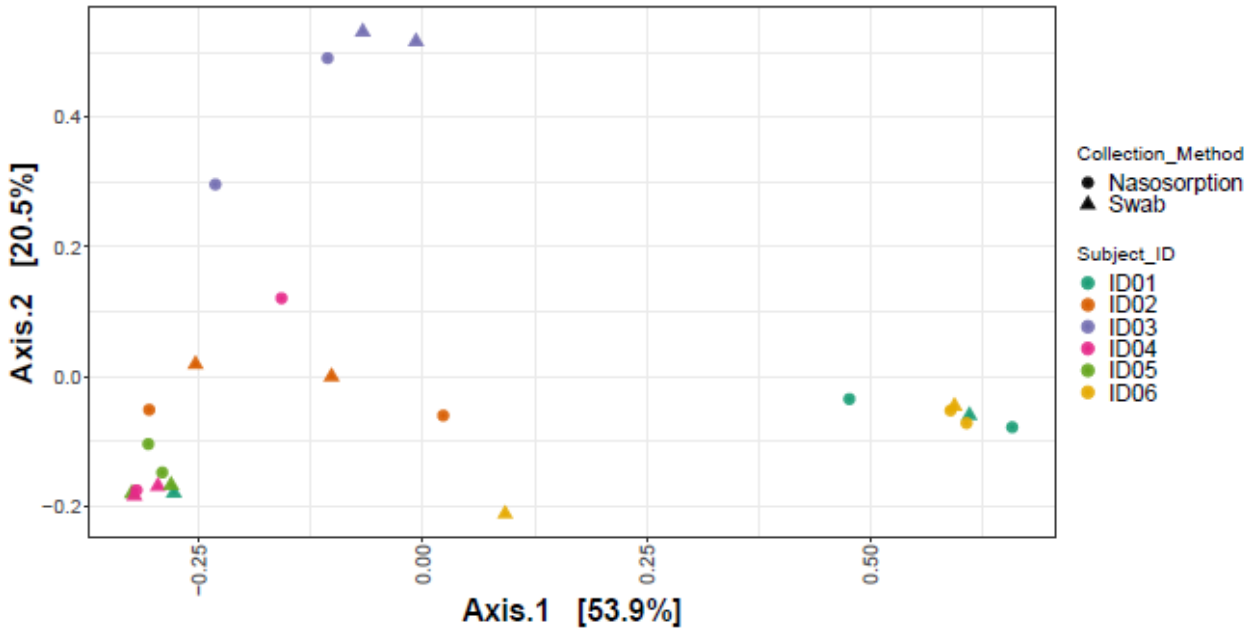
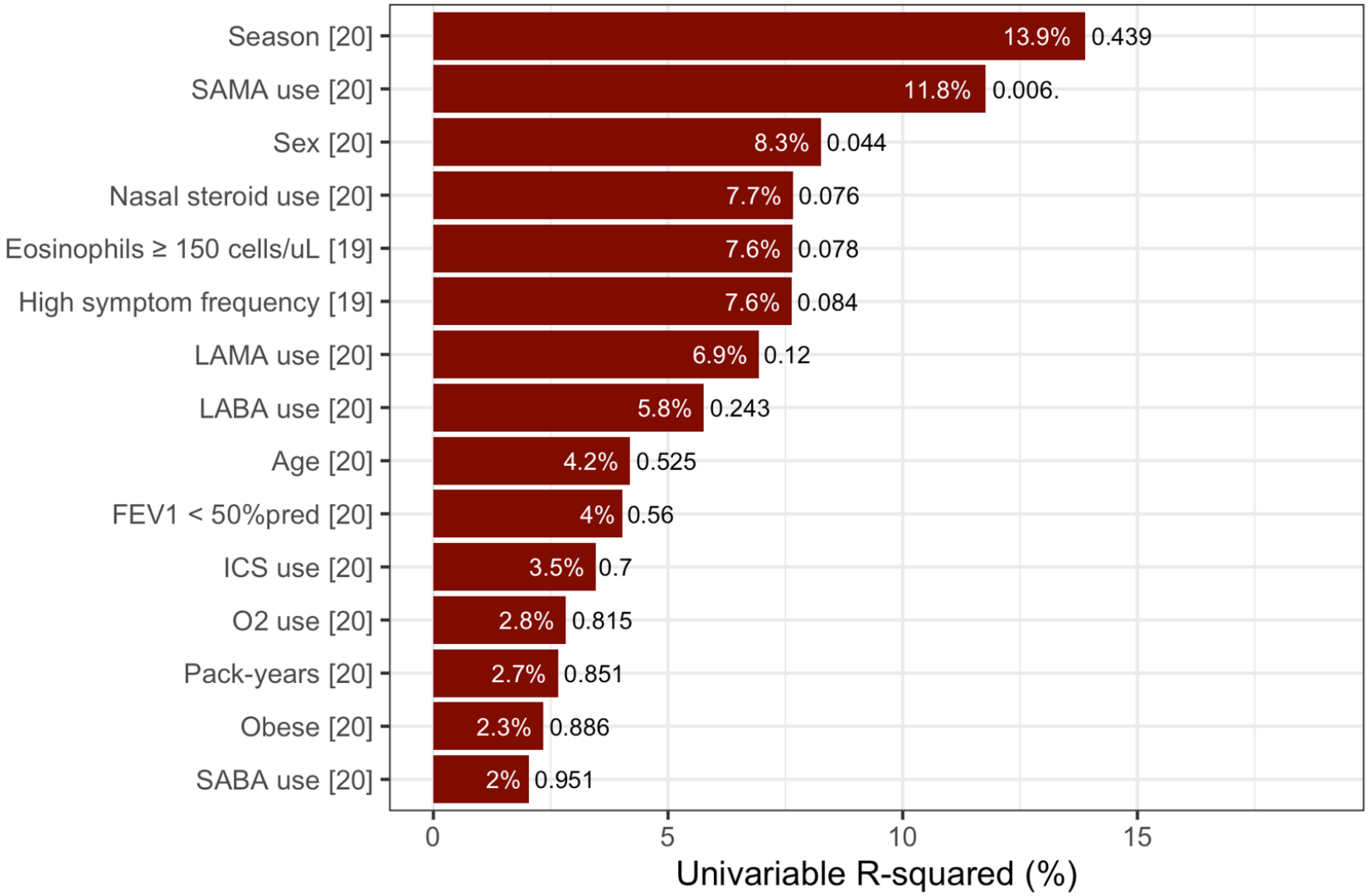
eFigure 1: Heatmap of log10 relative abundances of the top 30 genera in samples, clustered based on similar nasal bacterial compositions, and annotated with sample type. Samples (columns) and taxa (rows) are sorted based on Bray-Curtis dissimilarities and Euclidean distances, respectively. Genera were assigned according to the SILVA reference database.



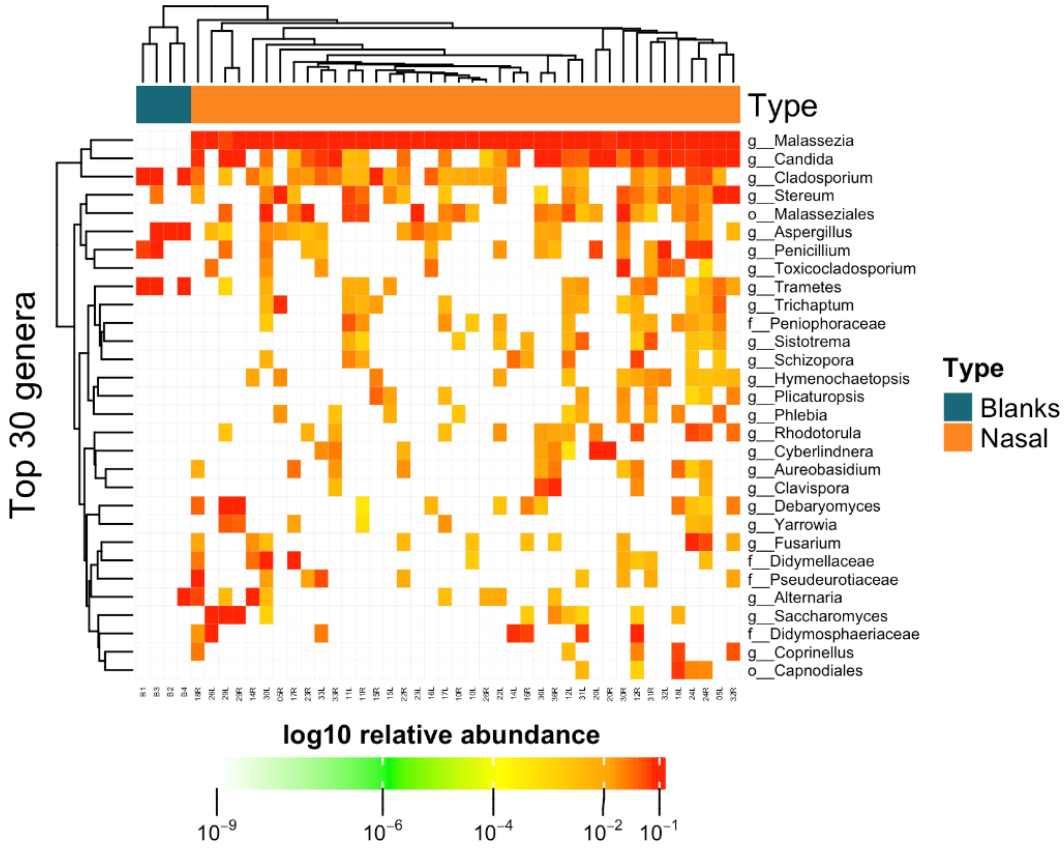
eFigure 2: Bacterial beta diversity comparisons among the 24 samples collected from the 6 volunteers, color coded by Participant # (Subject_ID)and labeled by sampling method (nasosorption vs nasal swab). The proportion of variance explained by each principal coordinate is denoted in the corresponding axis label. In the PERMANOVA on the Bray-Curtis Dissimilarity, individual participant contributed to variation in microbial community structure ($R^2 = 0.676$, $p = 0.001$), but nare (left vs right, $R^2 = 0.05$, $p = 0.894$) and sampling method ($R^2 = 0.015$, $p = 0.366$) did not.



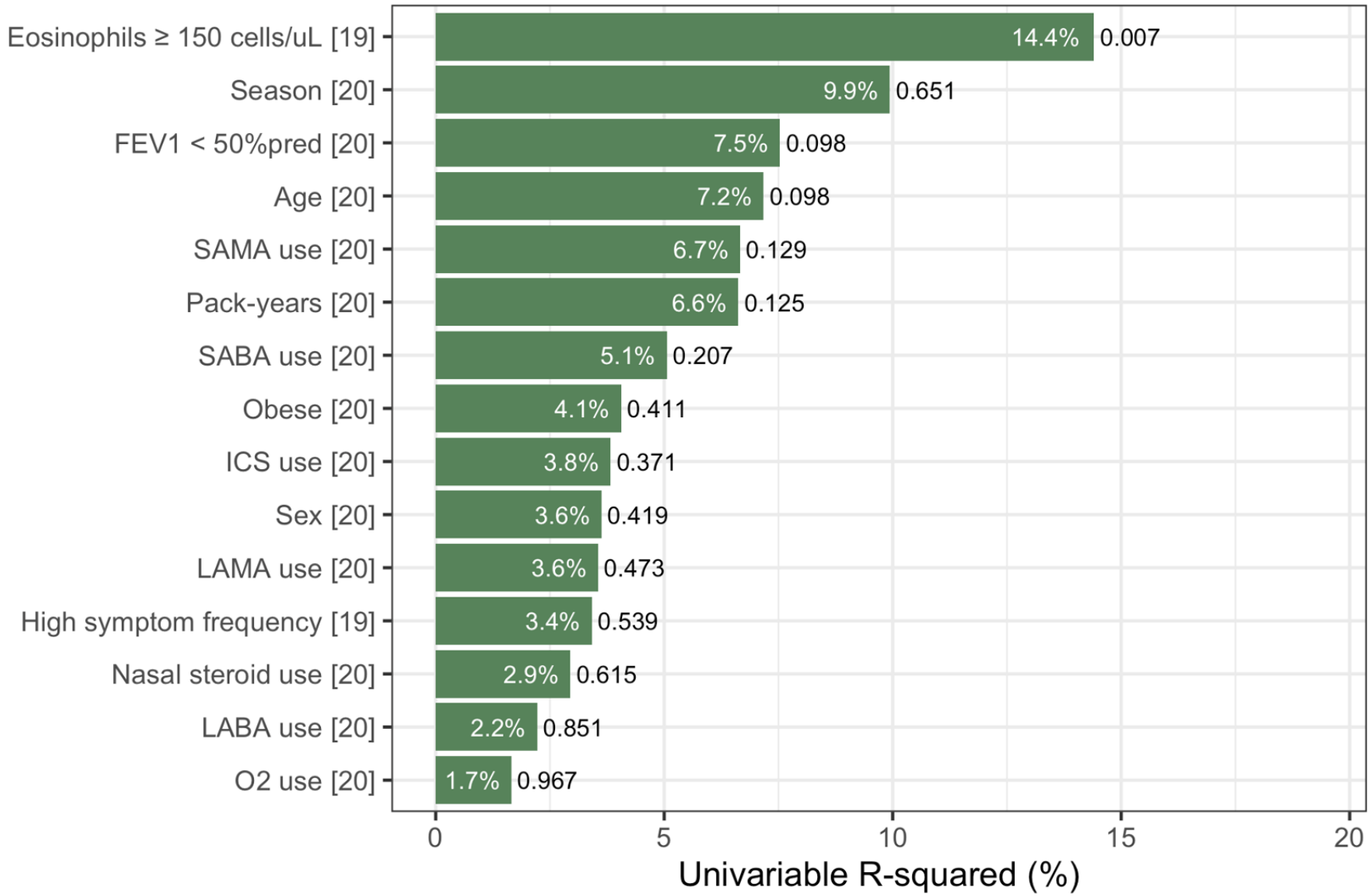
eFigure 3: Percentage of variance in bacterial taxonomy explained by each clinical characteristic, adjusting only for within-participant effects. Each PERMANOVA R^2 is reported in white color text and the number of participants included in each test is shown in square brackets. Individual test statistical significance p-values are listed in black color text. FDR-corrected statistical significance is noted as follows: FDR * $P \leq 0.05$, . $P \leq 0.1$.


Season [20]
SAMA use [20]
Sex [20]
Nasal steroid use [20]
Eosinophils ≥ 150 cells/uL [19]
High symptom frequency [19]
LAMA use [20]
LABA use [20]
Age [20]
FEV1 < 50%pred [20]
ICS use [20]
O2 use [20]
Pack-years [20]
Obese [20]
SABA use [20]
13.9%
0.439
11.8%
0.006.
8.3%
0.044
7.7%
0.076
7.6%
0.078
7.6%
0.084
6.9%
0.12
5.8%
0.243
4.2%
0.525
4%
0.56
3.5%
0.7
2.8%
0.815
2.7%
0.851
2.3%
0.886
2%
0.951
0
5
10
15
Univariable R-squared (%)

eFigure 4: Heatmap of log10 relative abundances of the top 30 genera in samples, clustered based on similar nasal fungal compositions, and annotated with sample type. Samples (columns) and taxa (rows) are sorted based on Bray-Curtis dissimilarities and Euclidean distances, respectively. Genera were assigned according to the UNITE reference database.



eFigure 5: Percentage of variance in fungal taxonomy explained by each clinical characteristic, adjusting only for within-participant effects. Each PERMANOVA R^2 is reported in white color text and the number of participants included in each test is shown in square brackets. Individual test statistical significance p-values are listed in black color text. FDR-corrected statistical significance is noted as follows: FDR * $P \leq 0.05$, . $P \leq 0.1$.


Eosinophils ≥ 150 cells/uL [19]
Season [20]
FEV1 < 50%pred [20]
Age [20]
SAMA use [20]
Pack-years [20]
SABA use [20]
Obese [20]
ICS use [20]
Sex [20]
LAMA use [20]
High symptom frequency [19]
Nasal steroid use [20]
LABA use [20]
O2 use [20]
14.4%
0.007
9.9%
0.651
7.5%
0.098
7.2%
0.098
6.7%
0.129
6.6%
0.125
5.1%
0.207
4.1%
0.411
3.8%
0.371
3.6%
0.419
3.6%
0.473
3.4%
0.539
2.9%
0.615
2.2%
0.851
1.7%
0.967
0
5
10
15
20
Univariable R-squared (%)

eTable 1: Bacterial Genera Identified on both Blank and Nasal Samples
(among top 30 genera in nasal samples)

Bacterial Taxa	Evidence of presence in nasal cavity
g__Corynebacterium_1	1–4,6
g__Staphylococcus	1-4,6
g__Streptococcus	1-4,6
g__Acinetobacter	1,3,5
g__Klebsiella	1
g__Lawsonella	6
c__Oxyphotobacteria	*

* Oxyphotobacteria has been reported in samples taken from the indoor environment, soil and air (7-9). We did not identify published studies reporting its presence in the nasal cavity.

References for eTable 1:

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