

1 Mycobiota and the contribution of yeasts in floor dust of 50 elementary schools characterized with  
2 sequencing internal transcribed spacer region of ribosomal DNA

3  
4 Ju-Hyeong Park<sup>1\*</sup>, Angela R. Lemons<sup>2</sup>, Tara L. Croston<sup>2</sup>, Yeonmi Park<sup>1</sup>, Jerry Roseman<sup>3</sup>,  
5 Brett J. Green<sup>2</sup>, Jean M. Cox-Ganser<sup>1</sup>

6  
7 <sup>1</sup> National Institute for Occupational Safety and Health, Respiratory Health Division, Morgantown, WV  
8 26505, U.S.A.

9 <sup>2</sup> National Institute for Occupational Safety and Health, Health Effects Laboratory Division,  
10 Morgantown, WV 26505, U.S.A.

11 <sup>3</sup> Philadelphia Federation of Teachers Health & Welfare Fund & Union, Philadelphia, PA 19103, U.S.A.

12  
13  
14 Short title: Fungal community and contribution of yeasts in schools

15 Key words: Schools, Yeasts, Fungal microbiome, Dampness and Mold, Classrooms

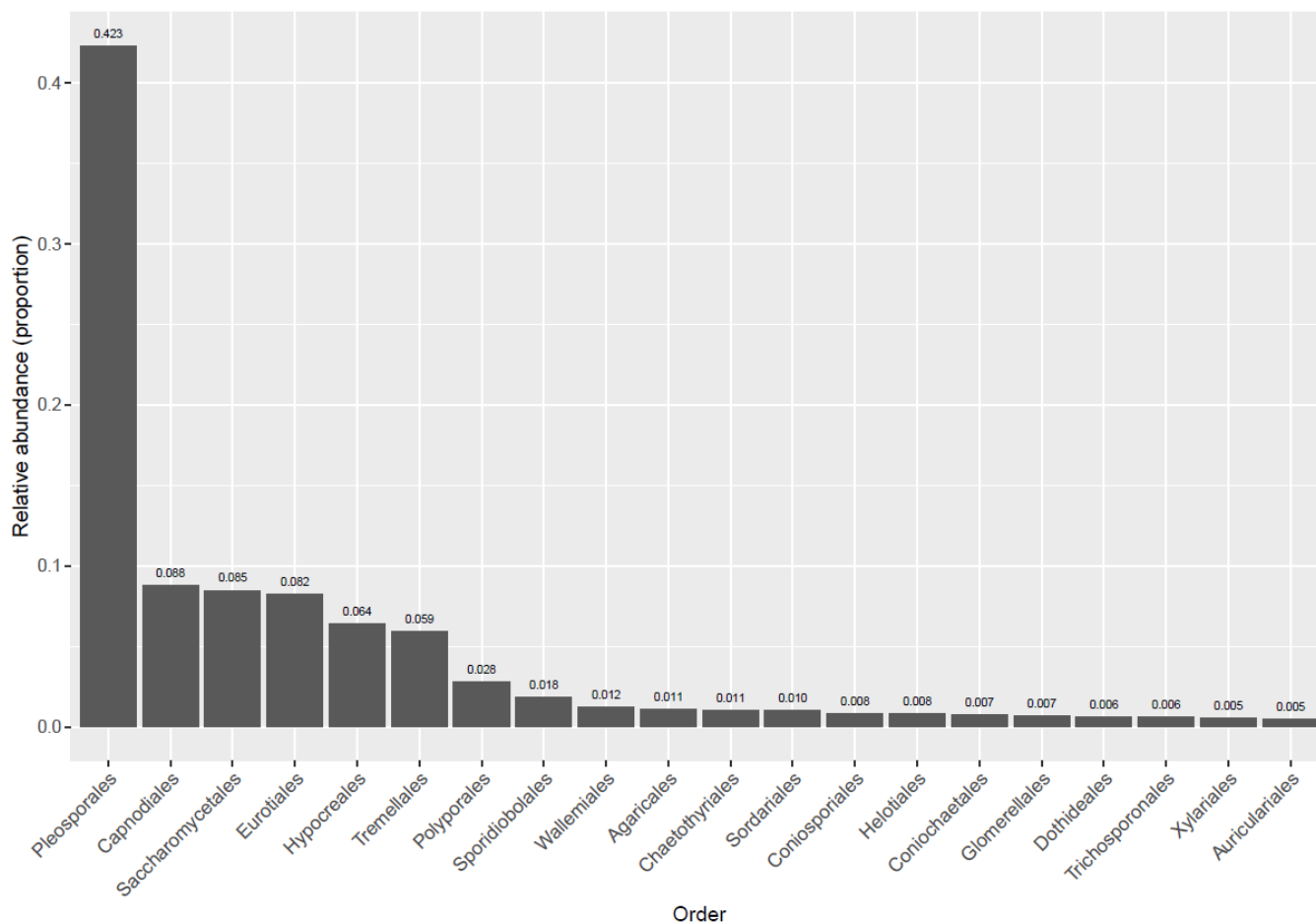
16  
17 **The number of pages: 11**

18 **The number of Figures: 9**

19 **The number of Tables: 1**

20  
21  
22 \* Corresponding author: Dr. Ju-Hyeong Park, 1095 Willowdale Road, Morgantown WV 26505; Email:  
23 [gzp8@cdc.gov](mailto:gzp8@cdc.gov); Tel: 304-285-5967; Fax: 304-285-5820

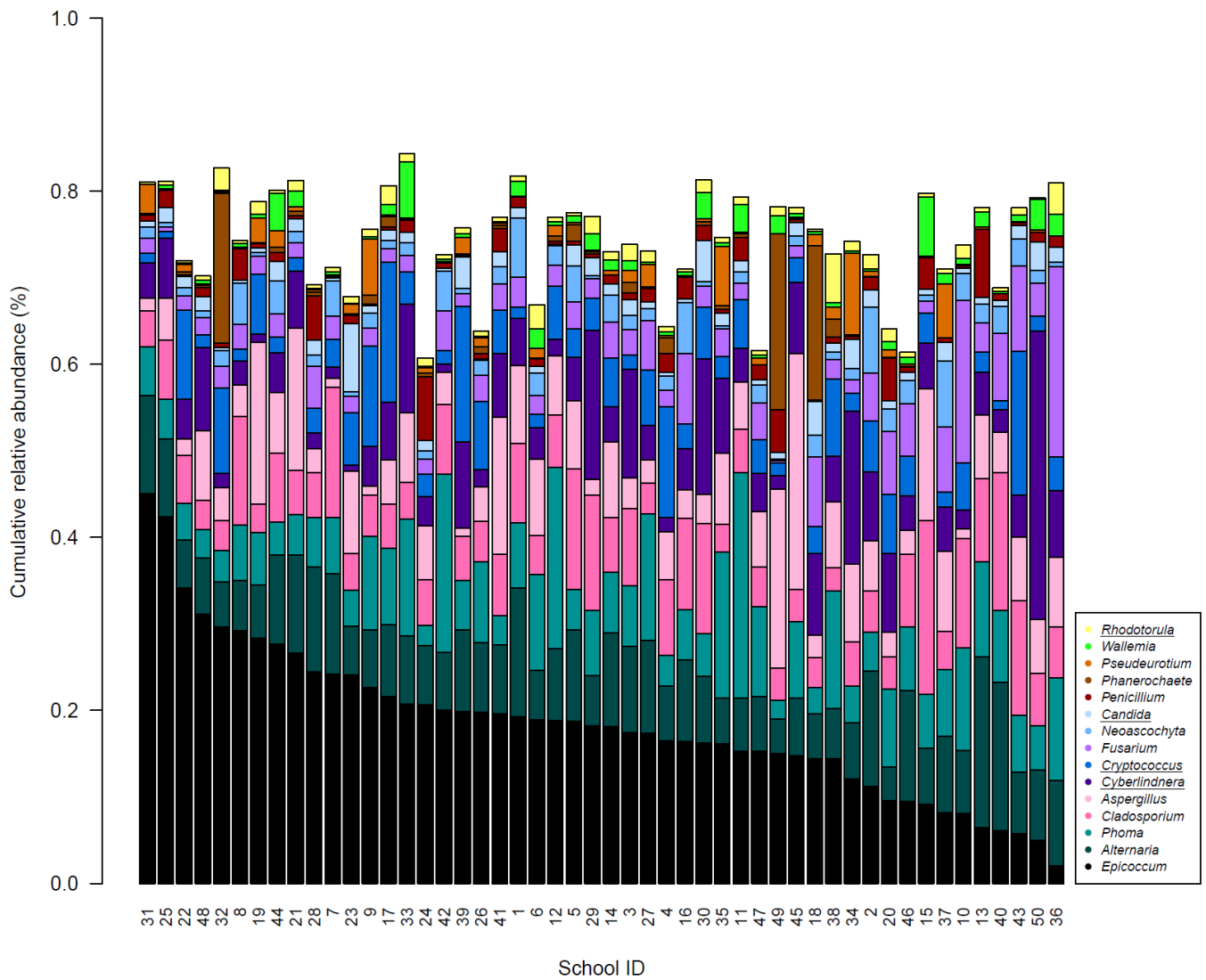
25 **Supplemental Figures and Tables.**



26

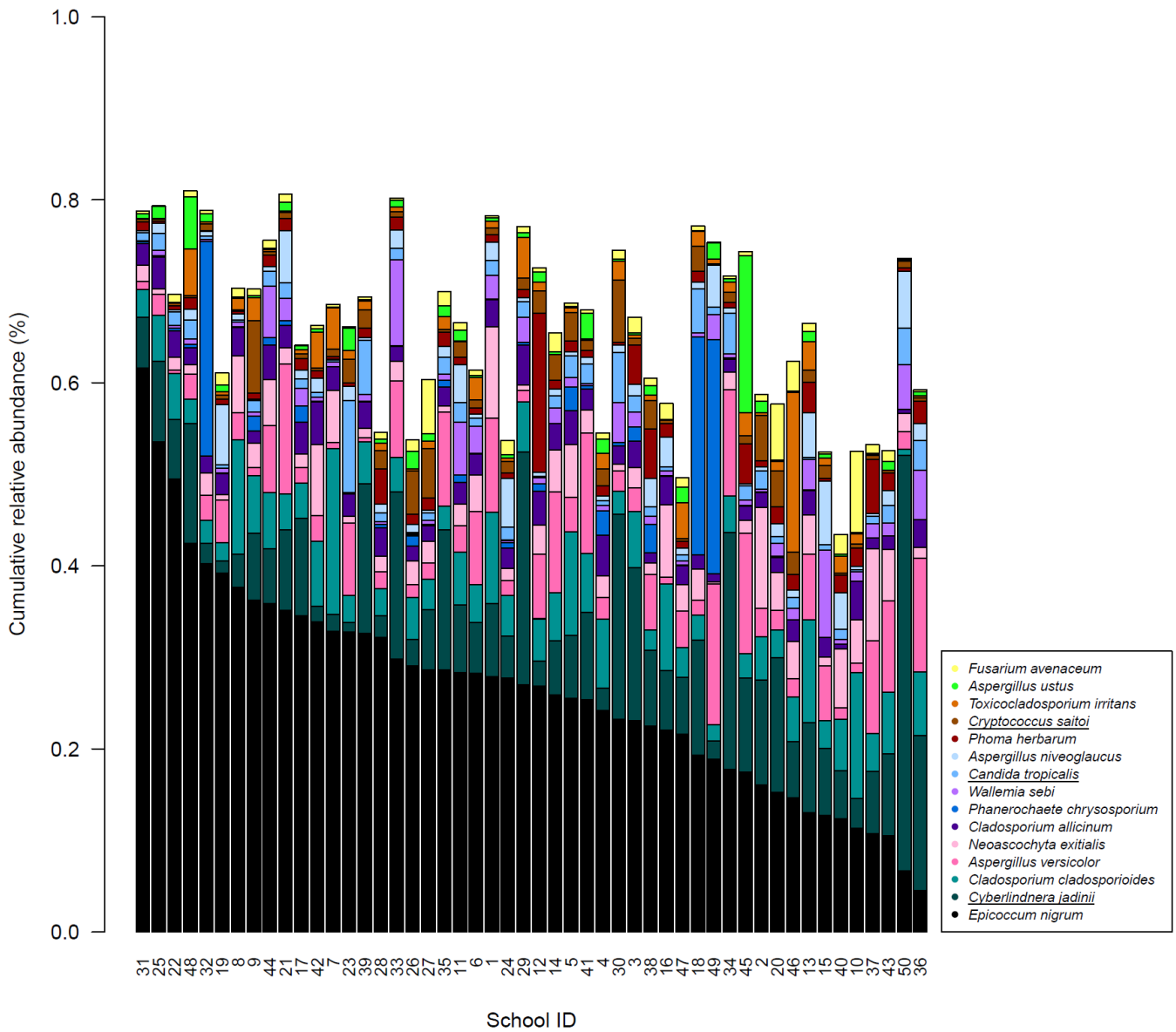
27 Figure S1. Relative abundance of the top 20 most abundant orders of all 89 orders identified. Relative  
28 abundance on y-axis is the overall relative abundance of all 499 samples.

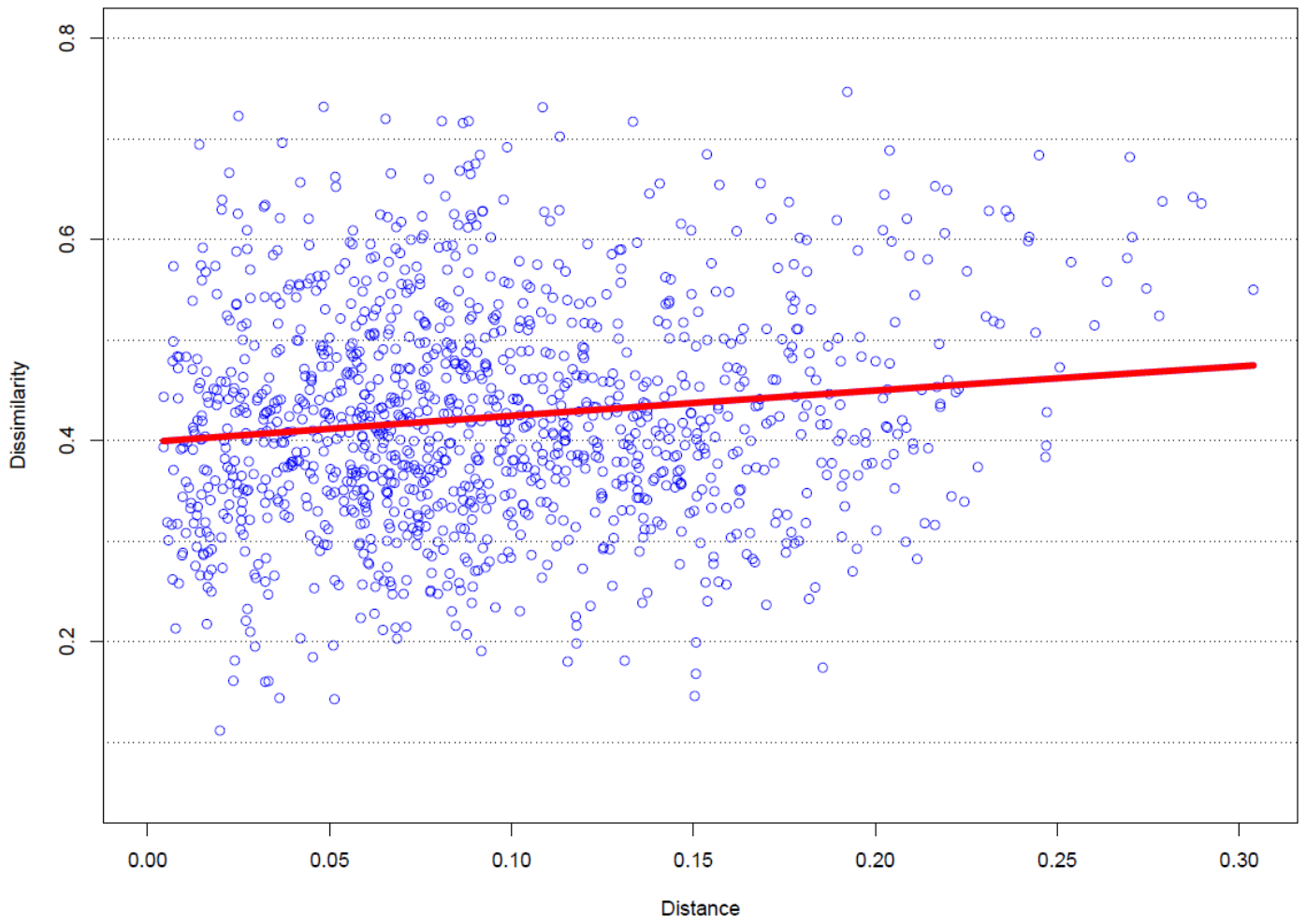
29



30

31 Figure S2. Cumulative relative abundance of the top 15 fungal genera for each school. Yeasts or yeast-  
 32 like fungi are underlined in the list. Relative abundance on y-axis is the overall relative abundance of all  
 33 10 samples within each school.



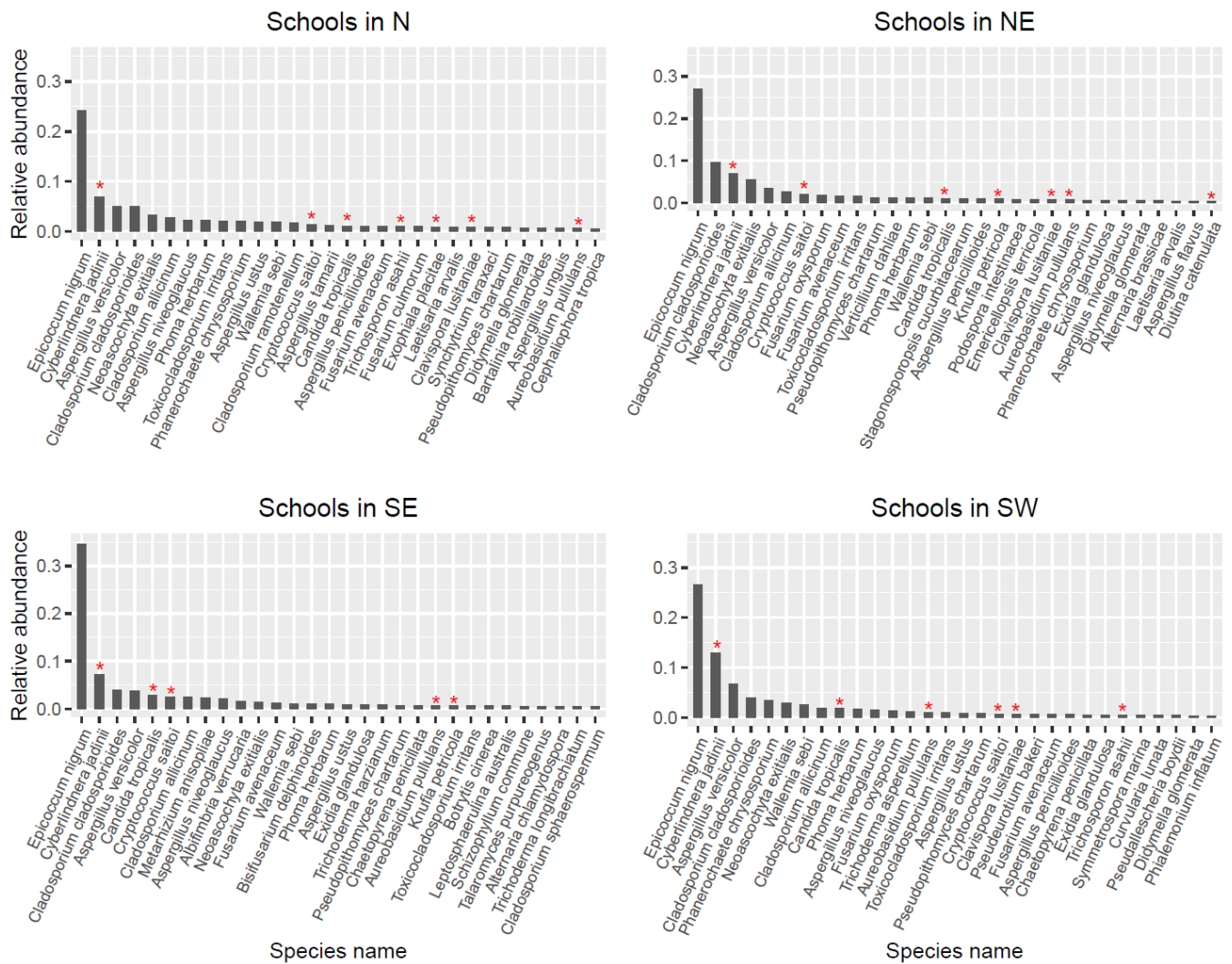


38

39 Figure S4. Distance-decay relationship among all paired schools using Bray-Curtis dissimilarity indices  
40 and the negative exponential function at the species level

41

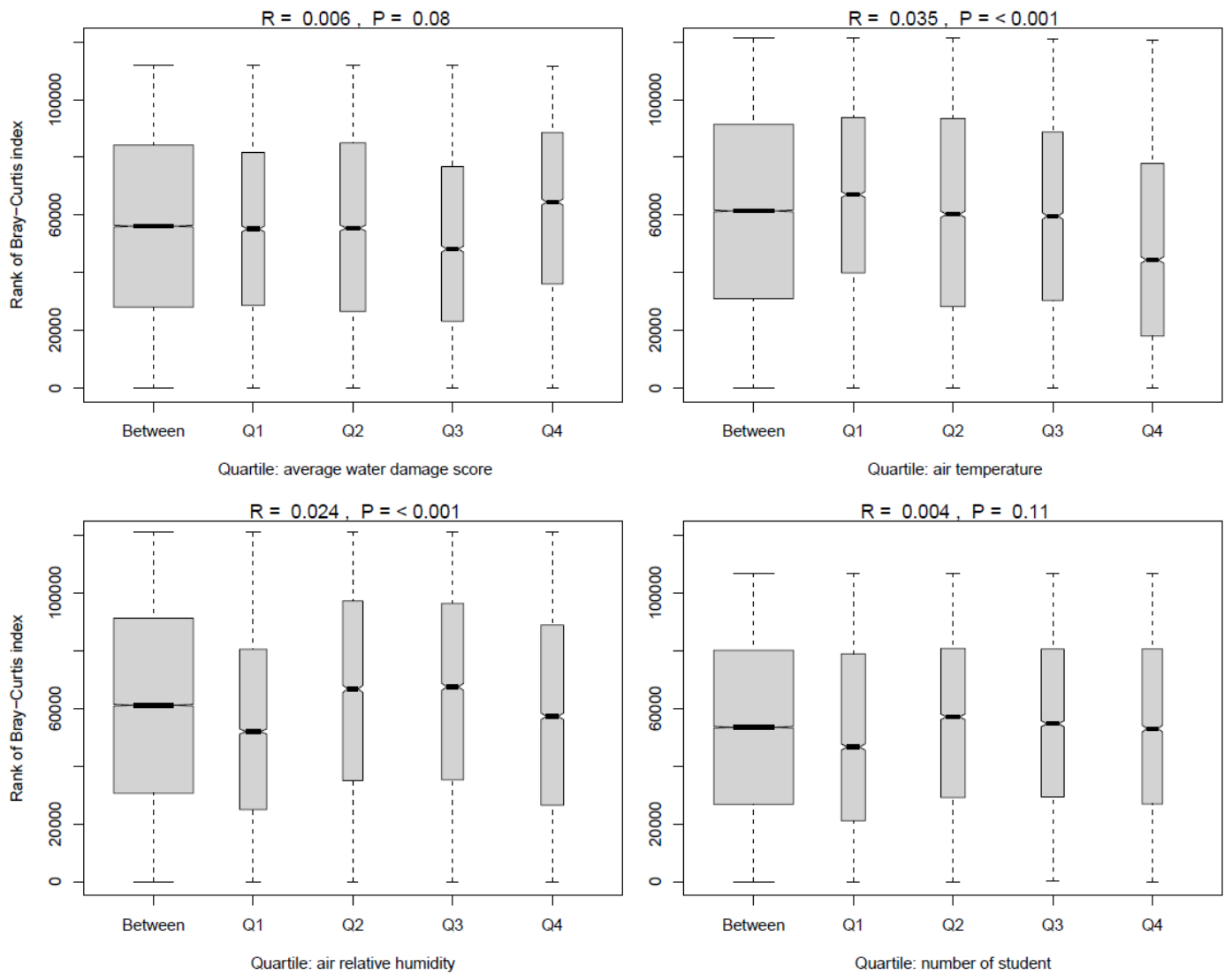
42



43

44 Figure S5. The top 30 most abundant fungal species in the quartile of schools based on school locations.  
 45 Yeasts or yeast-like fungi are denoted with red asterisks. Relative abundance on y-axis is the overall  
 46 relative abundance of all samples within each location group.

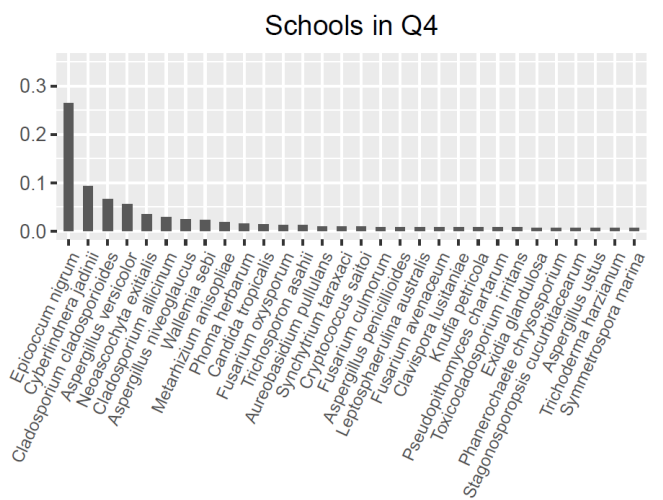
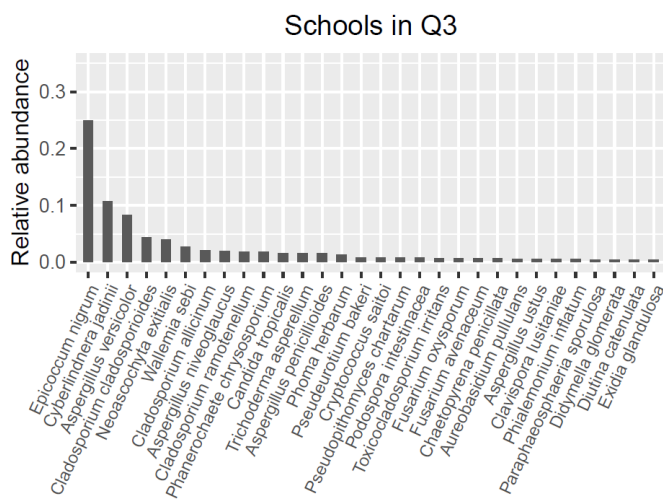
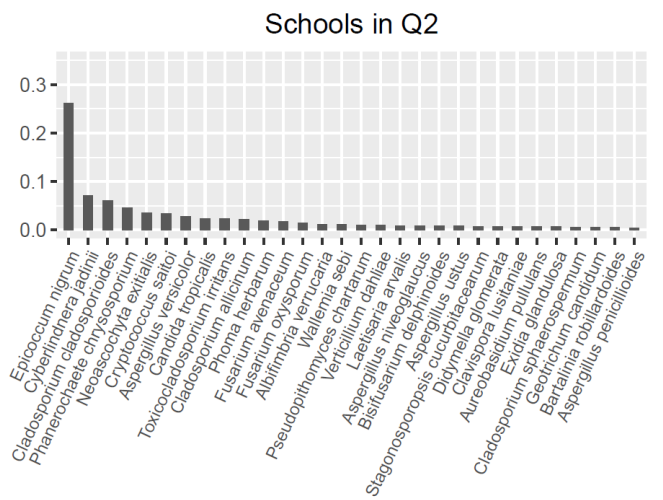
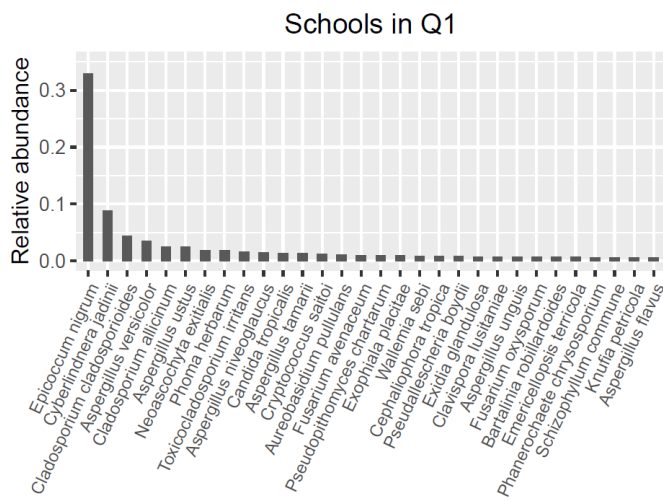
47



48

49 Figure S6. ANOSIM at the species level for the water-damage score, air temperature, RH, and number  
 50 of students in a classroom. Classroom average water damage score: minimum = 0; 1<sup>st</sup> quartile = 0.053;  
 51 median = 0.108; 3<sup>rd</sup> quartile: 0.188; maximum = 0.595. Classroom air temperature: minimum = 64.0°F;  
 52 1<sup>st</sup> quartile = 77.0; median = 83.0; 3<sup>rd</sup> quartile: 85.0; maximum = 91.0. Classroom air RH: minimum =  
 53 26.0 %; 1<sup>st</sup> quartile = 43.0; median = 50.0; 3<sup>rd</sup> quartile: 58.0; maximum = 78.0. Number of students per  
 54 classroom: minimum = 0; 1<sup>st</sup> quartile = 17; median = 23; 3<sup>rd</sup> quartile: 28; maximum = 45.

55

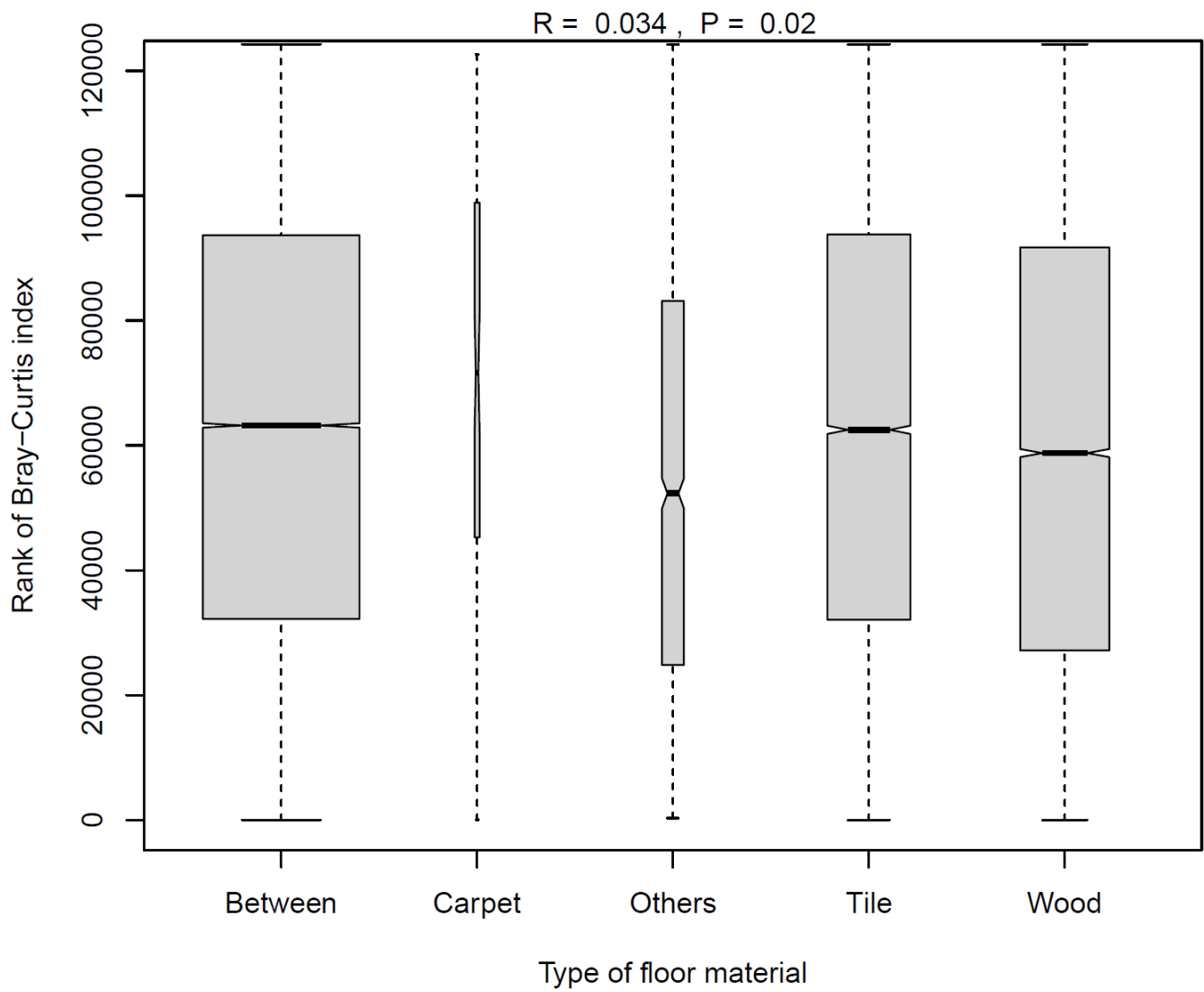


56

57 Figure S7. The top 30 most abundant fungal species in the quartile of schools based on average RH of  
 58 sampled classrooms. Relative abundance on y-axis is the overall relative abundance of all samples  
 59 within each RH quartile group.

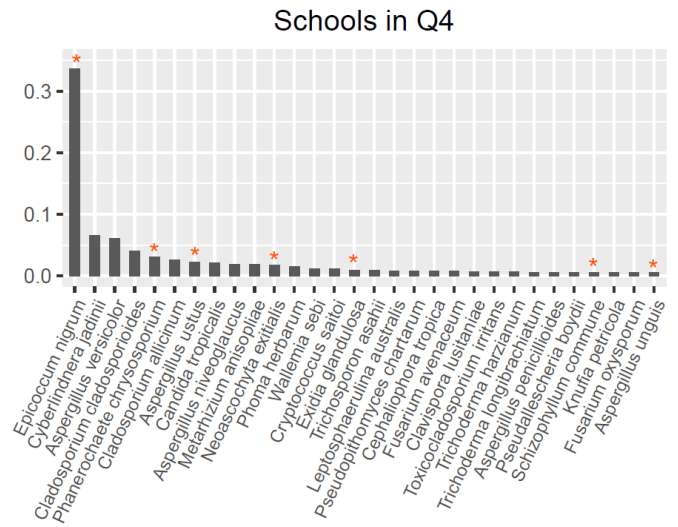
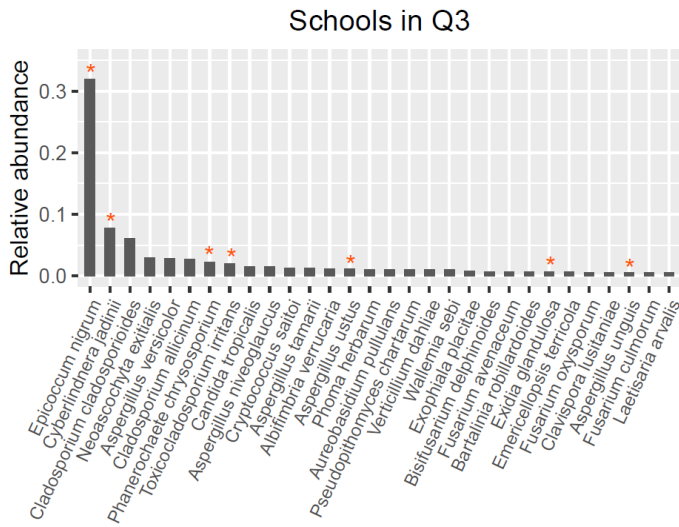
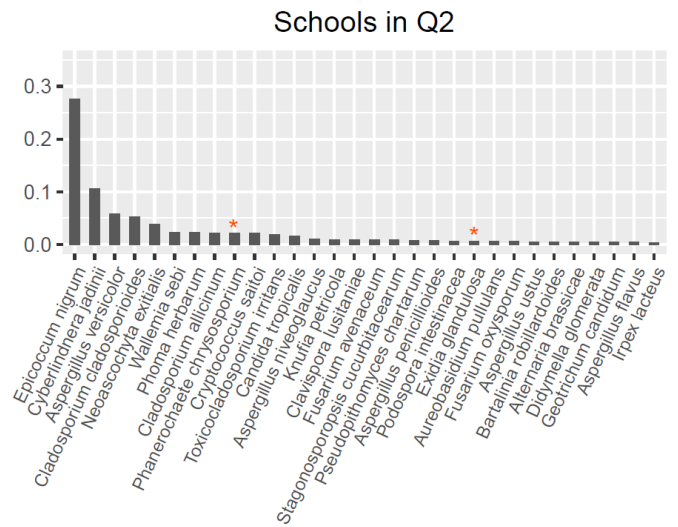
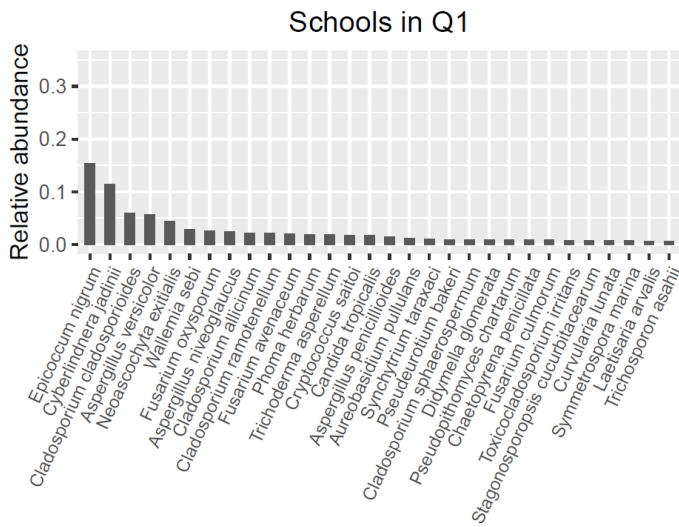
60





61

62 Figure S8. ANOSIM at the species level for the type of floor material. The number of classrooms by the  
 63 type of floor material: carpet (N=13), tile (208), wood (223), and others (N=55).



64

65 Figure S9. The top 30 most abundant fungal species in the quartile of schools based on average  
 66 temperature. Red-colored asterisks indicate species that are significantly different in abundance  
 67 compared to schools in Q1. Relative abundance on y-axis is the overall relative abundance of all  
 68 samples within each temperature quartile group.

69

70 Table S1. Yeasts or yeast-like fungal genera identified in our study by the descending order of relative  
 71 abundance as percentage

Genus name	%*	Genus name	%*	Genus name	%*
<i>Cyberlindnera</i>	6.1	<i>Sporidiobolus</i>	0.06	<i>Cutaneotrichosporon</i>	< 0.01
<i>Cryptococcus</i>	5.2	<i>Meyerozyma</i>	0.05	<i>Phialophora</i>	< 0.01
<i>Candida</i>	1.5	<i>Veronaea</i>	0.03	<i>Xanthophyllomyces</i>	< 0.01
<i>Rhodotorula</i>	1.1	<i>Cystobasidium</i>	0.03	<i>Zygoascus</i>	< 0.01
<i>Coniochaeta</i>	0.7	<i>Pichia</i>	0.03	<i>Rhodosporidium</i>	< 0.01
<i>Exophiala</i>	0.6	<i>Cladophialophora</i>	0.02	<i>Tremella</i>	< 0.01
<i>Trichosporon</i>	0.6	<i>Wickerhamomyces</i>	0.02	<i>Torula</i>	< 0.01
<i>Aureobasidium</i>	0.6	<i>Scytalidium</i>	0.02	<i>Hyphopichia</i>	< 0.01
<i>Clavispora</i>	0.5	<i>Lodderomyces</i>	0.02	<i>Malassezia</i>	< 0.01
<i>Knufia</i>	0.5	<i>Phaeococcomyces</i>	0.02	<i>Erythrobasidium</i>	< 0.01
<i>Papiliotrema</i>	0.3	<i>Bullera</i>	0.02	<i>Ochroconis</i>	< 0.01
<i>Sporobolomyces</i>	0.2	<i>Leucosporidium</i>	0.01	<i>Hanseniaspora</i>	< 0.01
<i>Sterigmatomyces</i>	0.2	<i>Blastobotrys</i>	0.01	<i>Kluyveromyces</i>	< 0.01
<i>Filobasidium</i>	0.2	<i>Debaryomyces</i>	0.01	<i>Citeromyces</i>	< 0.01
<i>Vishniacozyma</i>	0.2	<i>Apiotrichum</i>	0.01	<i>Kazachstania</i>	< 0.01
<i>Cystofilobasidium</i>	0.2	<i>Kockovaella</i>	0.01	<i>Ustilago</i>	< 0.01
<i>Diutina</i>	0.2	<i>Saccharomyces</i>	< 0.01	<i>Yarrowia</i>	< 0.01
<i>Geotrichum</i>	0.1	<i>Naganishia</i>	< 0.01	<i>Lipomyces</i>	< 0.01
<i>Rhinocladiella</i>	0.1	<i>Itersonilia</i>	< 0.01	<i>Saccharomycopsis</i>	< 0.01
<i>Dipodascus</i>	0.1	<i>Metschnikowia</i>	< 0.01	<i>Pseudozyma</i>	< 0.01
<i>Rhodosporidiobolus</i>	0.09	<i>Issatchenkia</i>	< 0.01	–	–

72 \* Percent of DNA sequences for each genus.

73

74