board participants to facilitate case discussion. When asked how their MTB could be improved, programs suggested adding videoconferencing, having a scribe record minutes, and generating consensus treatment recommendations.

The MTB improves interdisciplinary collaboration while instilling the importance of multidisciplinary care early in training.[4] Our results are limited by potential differences between survey respondents and nonrespondents. Future research is needed to objectively assess if and how the MTB alters clinical outcomes.

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Effect of alcohol-based hand rub on hand microbiome and hand skin health in hospitalized adult stem cell transplant patients: A pilot study

To the Editor: Health care–associated infections cause considerable burden of disease and mortality,[1] and hand hygiene, eg, using alcohol-based hand rub (ABHR), is strongly recommended for infection control and prevention.[2] The effect of hand hygiene on bacterial and fungal microbiomes (the bacteriome and mycobiome, respectively) of patients has not been investigated.

In this prospective pilot clinical study, we used culture assay and Ion-Torrent sequencing (ThermoFisher Scientific, Waltham, MA) to determine the effect of ABHR on hand bacteriome and mycobiome of 20 hospitalized adult (≥18 years old) stem cell transplant patients (enrolled after approval of institutional review board protocol IRB 10-14-11, with written informed consent obtained from all participants). Participants were randomly assigned to 2 groups: group 1 was treatment with ABHR and routine hand hygiene standard-of-care (SOC) over a 7-day period and group 2 was untreated but still given routine hand hygiene SOC. Swabs were obtained from both hands on days 1, 7, and 30 and cultured (on trypticase soy blood agar) or sequenced to identify fungi and bacteria. Amplified sequences included internally transcribed spacer 1 [ITS1] and 16S rDNA V4 region.[3] Skin hydration (moisture) and pH were measured using routine methods.[4]

There were no significant differences in age, sex, and use of concomitant treatments between groups (Supplemental Table I; available at http://www.jaad.org). Colonies of pathogenic bacteria (*Staphylococcus aureus*, *Serratia marcescens*, *Klebsiella oxytoca*, and *Escherichia coli*) were significantly reduced in the ABHR-treated patients compared with the untreated patients on Day 30 ($P = .038$, Supplemental Fig 1; available at http://www.jaad.org).

Principal components analysis showed clustering of the bacteriome varied considerably on days 1 and 7 in the ABHR group, while day 30 samples clustered similar to day 1 (Supplemental Fig 2, *A* and *B*; available at http://www.jaad.org), suggesting the microbiota had recovered by day 30. The bacteriome did not vary in the untreated patient group. There was no significant difference in diversity or core biome between groups. Three bacterial phyla (Actinobacteria, Firmicutes, and Proteobacteria) and 2 fungal phyla (Ascomycota and Basidiomycota) were most abundant (Supplemental Fig 2, *C-F*). Relative abundance of 2 bacterial phyla and 7 bacterial genera were significantly different between the untreated and ABHR-treated groups (Supplemental Table II; available at http://www.jaad.org), while fungal phyla/genera did not differ. We found 572 and 776 unique significant correlations on day 7 in the untreated and ABHR-treated groups, respectively. Interkingdom correlations involving 89 bacterial and 26 fungal species were detected only in the untreated group on day 7 and included pathogenic bacteria

Table I. Bacterial and fungal species with unique interkingdom interactions by treatment groups*

Alcohol-based hand rub–treated				Untreated			
Bacteria	**N**	**Fungi**	**N**	**Bacteria**	**N**	**Fungi**	**N**
Actinomyces yovaginalis	15	uncultured fungus	46	*Actinokineospora iospyrosa*	16	*Emericella nidulans*	26
Afipia elis	15	*Fusarium oxysporum*	40	*Alicyclobacillus olerans*	16	*Candida albicans*	22
Alloiococcus titis	15	*Fusarium oxysporum f cubense*	40	*Arthrobacter eyseri*	16	*Fusarium incarnatum*	22
Arthrobacter ulfureus	15	*Fusarium oxysporum f* sp *carthami*	40	*Arthrobacter olychromogenes*	16	*Fusarium* sp Pr13	22
Bifidobacterium ifidum	15	*Fusarium solani*	40	*Clostridium enationis*	16	*Hebeloma cylindrosporum*	22
Bifidobacterium reve	15	*Fusarium* sp ASR 18	40	*Microbacterium aritypicum*	16	*Monoblepharis polymorpha*	22
Bosea enosp.	15	*Fusarium* sp ASR 258	40	*Microbacterium hocolatum*	16	*Pichia fermentans*	22
Burkholderia lathei	15	*Fusarium* sp ASR 80	40	*Paenibacillus autus*	16	*Trametes versicolor*	22
Capnocytophaga chracea	15	*Gibberella avenacea*	40	*Paenibacillus hondroitinus*	16	*Typhula ishikariensis*	22
Corynebacterium ilosum	15	*Nectria haematococca*	40	*Pannonibacter hragmitetus*	16	*Aureobasidium pullulans*	19
Corynebacterium ubricantis	15	*Nectria haematococca mpVI*	40	*Pseudoclavibacter ifida*	16	*Bullera formosana*	19
Dietzia imorensis	15	*Scleroderma* sp	40	*Salinibacterium murskyense*	16	*Candida dubliniensis*	19
Ehrlichia uminantium	15	*Fusarium* sp ASR 168	38	*Serratia arcescens*	16	*Cryptococcus albidus var diffluens*	19
Eubacterium dolichum	15	uncultured *Fusarium* sp	38	*Streptomyces ureofaciens*	16	*Cryptococcus* sp BF73	19
Halomonas ribbensis	15	*Fusarium* sp EML GYP1	36	*Weeksella irosa*	16	*Epicoccum* sp CHTAM6	19
Helosis ayennensis	15	*Leccinum quercinum*	15	*Williamsia erinedens*	16	*Fusarium* sp A2	19
Hydrogenobacter hermophilus	15	*Candida frijolesensis*	14	*Schumannella uteola*	15	*Fusarium* sp ASR 82	19
Kingella enitrificans	15	*Candida* sp	14	*Carnobacterium iridans*	14	*Fusarium* sp KC 2010ba	19
Lamprocystis urpurea	15	*Candida tropicalis*	14	*Corynebacterium imulans*	14	*Gibberella intermedia*	19
Listeria eihenstephanensis	15	*Hyphoderma praetermissum*	14			*Phaeangium lefebvrei*	19
Oceanobacillus rofundus	15	*Laccaria laccata*	14			*Pichia jadinii*	19
Pelistega uropaea	15	*Rhodotorula cresolica*	14			*Trichophyton fischeri*	19
Plesiomonas higelloides	15	*Tuber indicum*	14			*Rhodotorula mucilaginosa*	18
Porphyromonas ndodontalis	15	*Rhodotorula mucilaginosa*	13			*Epicoccum* sp Co4 ITS14	17
Prevotella anceiensis	15	*Dactylosporina macracantha*	12			*Fusarium* sp ASR 168	17
Prevotella igrescens	15	*Galactomyces geotrichum*	12			*Psathyrella lutensis*	17
Prevotella tercorea	15	*Phaeangium lefebvrei*	12			uncultured *Fusarium* sp	17
Rathayibacter aricis	15						
Roseburia aecis	15						
Salinispora ropica	15						
Salinivibrio osticola	15						
Stenoxybacter cetivorans	15						
Streptomyces adiopugnans	15						
Teredinibacter urnerae	15						

Continued

Table I. Cont'd

Alcohol-based hand rub–treated				Untreated			
Bacteria	**N**	**Fungi**	**N**	**Bacteria**	**N**	**Fungi**	**N**
Corynebacterium roppenstedtii	14						
Corynebacterium urum	14						
Oenothera erteroana	14						
Propionibacterium cnes	14						
Carnobacterium i ridans	13						
Corynebacterium imulans	13						

*Species with ≥10 interactions listed. For complete list of species with unique interkingdom interactions, please see Supplemental Fig 3 (available at http://www.jaad.org).

(eg, *Bacillus cereus*, *Enterobacter cloacae*, and *Enterococcus cecorum*) and fungi (eg, *Fusarium* sp, *Candida albicans*, *C. dubliniensis*, *Cryptococcus* sp, and *Emericella nidulans*) (Table I and Supplemental Fig 3; available at http://www.jaad.org). ABHR treatment had no effect on skin hydration over time but led to a significantly higher change in pH between day 1 and day 7 compared with nontreatment (0.18 vs −0.22, $P = .008$).

ABHR reduced the burden of pathogenic organisms on the hands of transplant patients without affecting skin health or inducing a significant change in the hand microbiome of patients, which agrees with recent studies.[5] Incorporating microbes and microbial products in ABHR may modulate interkingdom microbial interactions and host–microbe interplay. There might be interaction between the hand microbiome and the oral and gut microbiomes, potentially acting as reservoirs of microbes that affect intrinsic and extrinsic variables critical for skin health. Further studies are warranted to validate these findings and ascertain their clinical relevance.

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Generational influence on patient learning preferences in dermatology

To the Editor: Shared decision-making and decision aids can reduce health care utilization while improving patient satisfaction and adherence.[1] Little is known about patient-preferred modalities for education in dermatology to facilitate shared decision-making. Here, we examine the impact of patient characteristics, including generational status, on preferences of learning modality and information sources when making treatment decisions in dermatology.

We surveyed patients >18 years of age at Brigham and Women's Hospital Dermatology during August 2016, asking patients to rate on a 5-point scale preferences for learning modalities and information sources when deciding on treatment for skin growths. Patients were not required to have prior history of any skin condition and participation was optional. Demographic and clinical data were extracted from manual chart review (Table I). Generation groupings were defined as Millennials (born 1981-1997), Generation X (born 1965-1980), Baby Boomers (born 1946-1964), and the Silent Generation (born 1928-1945).[2] Participants born in years outside of these groupings (n = 6) were combined into the closest group. A ranking of 5 on the 5-point scale for learning modalities was considered the most preferred learning preference, and rankings of 4 or 5 on the 5-point scale for information sources were interpreted as the most important information sources on the basis of the distribution of answers. Comparisons were performed by using the chi-squared test, and statistical significance was determined by using Cochran-Armitage trend tests. Analyses were performed using SAS 9.4 (SAS Institute, Cary, NC), and data were stored using Research Electronic Data Capture.[3] This study was approved by the Institutional Review Board of Partners HealthCare.

A total of 458 surveys were administered, of which 375 (82%) were completed. In-person discussion was the most popular learning modality (most preferred by 84.3% of participants, n = 311), followed by diagrams and charts (14.5%, n = 48), short handouts (11.6%, n = 39), short videos (10.4%, n = 35), and phone conversation (8.1%, n = 27) (Table II). Information sources considered important were recommendations from doctors (99.2%, n = 370), patients' past experiences (64.7%, n = 189), patients' personal preferences (55.3%, n = 183), recommendations from friends and family (22.5%, n = 74), and how other patients decide (22.2%, n = 73). Millennials were more likely than other generations to rate personal experiences, personal preferences, recommendations from family and friends, and other patients' experiences as important ($P < .05$).

This study identified patient preferred learning modalities and information sources when deciding about skin growth treatment options. In-person discussion was the most popular learning modality, and phone conversation was the least. Diagrams and charts were favored over short handouts or videos and might serve as useful tools for future decision aids.

There was an age-dependent valuing of nonphysician peer-driven experiences by younger generations (Millennials > Generation X > Baby Boomers and Silent Generation), reflecting emphasis on connectivity (eg, social media) and consumer-driven reviews and experiences (eg, Yelp) by younger generations. Although in-person consultation is currently preferred by patients, these findings suggest that the presence of peer-driven ratings of physicians, hospitals, and even medical procedures available online might increasingly influence patient decision-making over time.[4] Future education efforts could benefit from harnessing social media.

Our findings are limited by a potential lack of generalizability and by differences in demographic and clinical variables between generations that might affect preference differences. However, we believe that our study offers insight into patient decision-making, informing future efforts for decision aids and shared-decision making.

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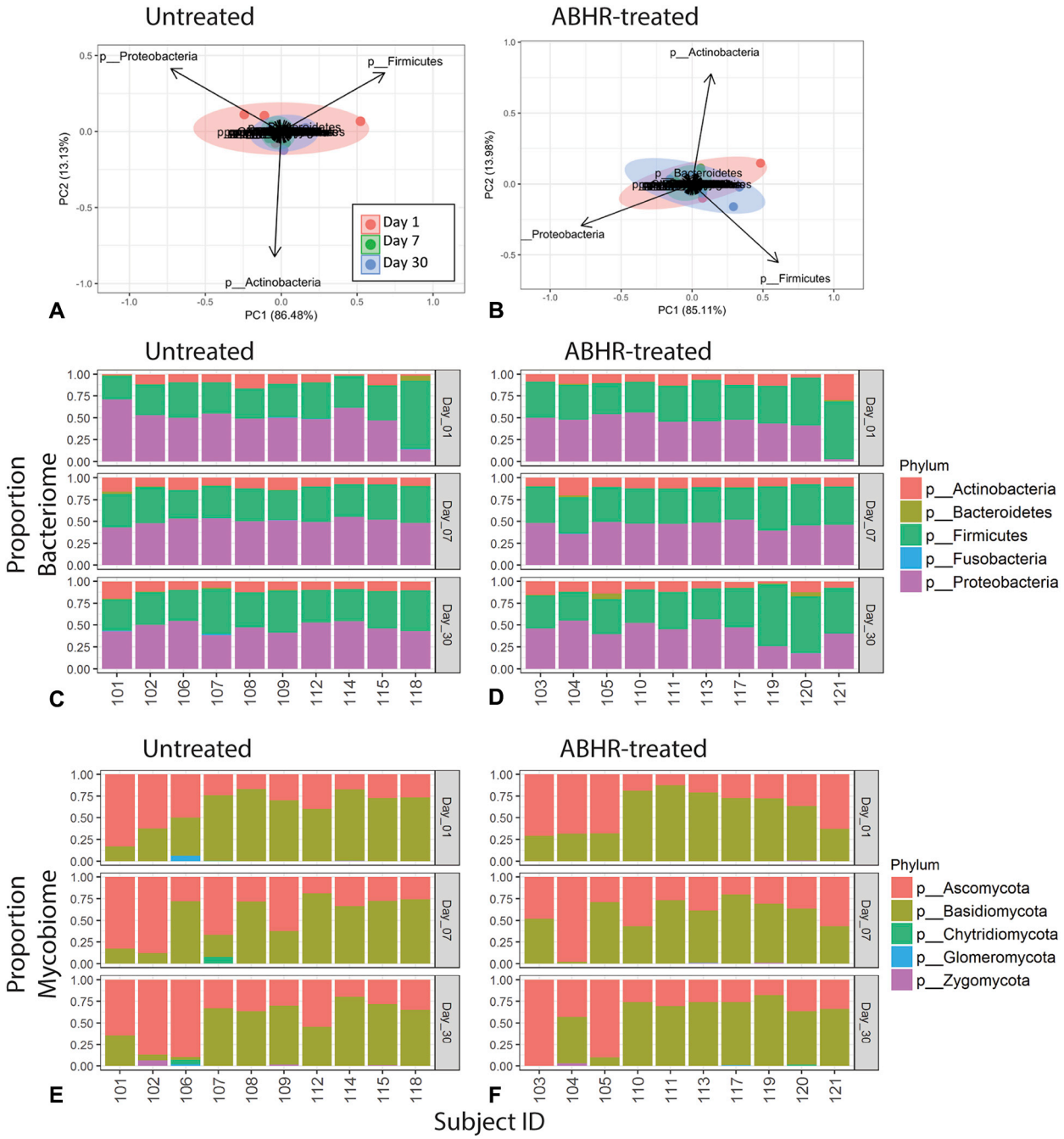
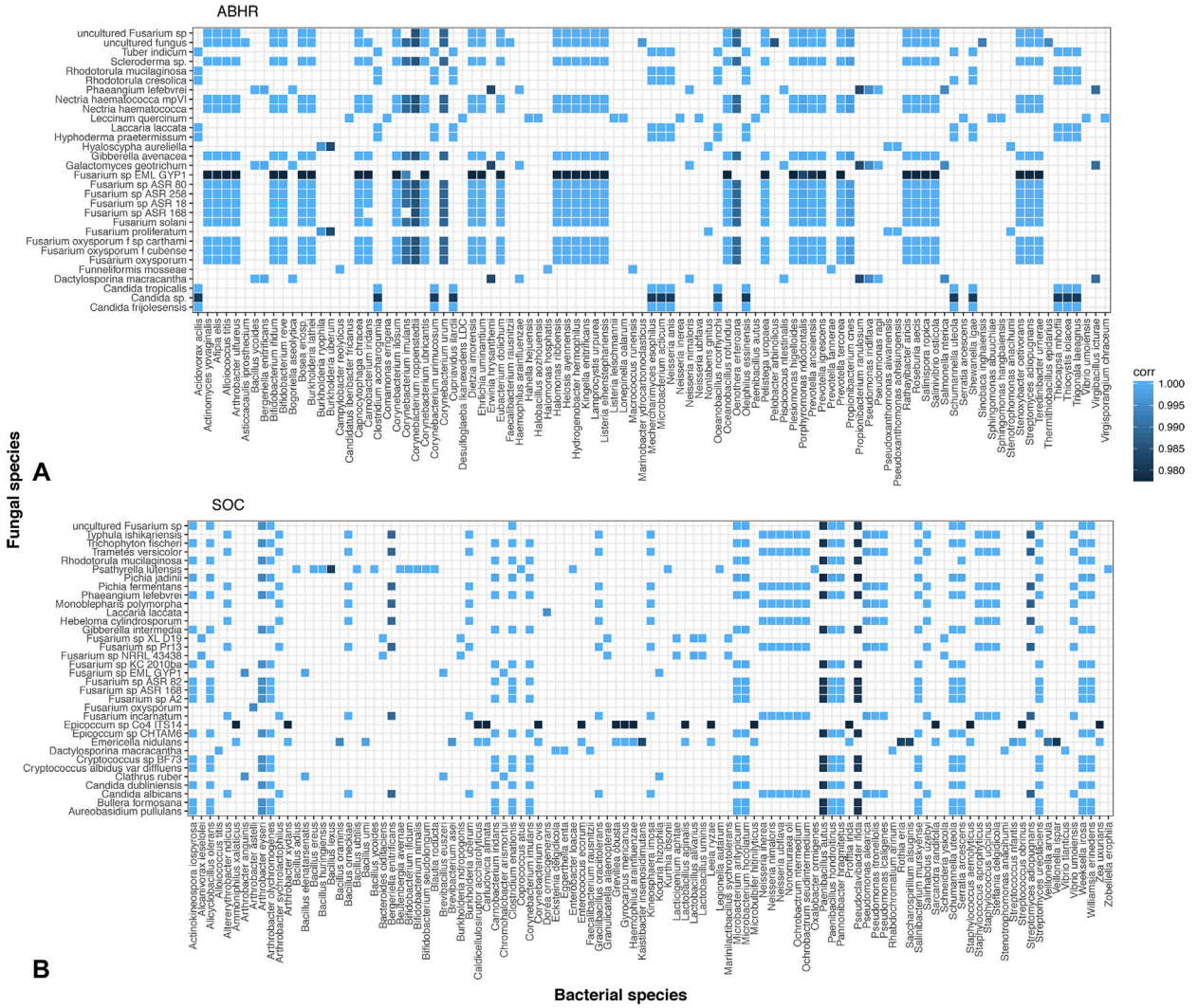
Supplemental Fig 1. Distribution of microbial burden (CFUs/100 μL) in alcohol-based hand rub–treated patients and untreated patients (given standard of care) during study duration. Numbers in panels indicate patient identification numbers. *CNS*, Coagulase-negative staphylococci; *CFU*, colony-forming units.



Supplemental Fig 2. Clustering and abundance profile of hand microbiome in ABHR-treated or untreated patients. Principal components analysis of hand bacteriome (phylum level) of ABHR-treated (**A**) or untreated (given standard of care) (**B**) patients. **C-F**, Distribution of bacterial (**C** and **D**) and fungal (**E** and **F**) phyla across tested samples at 3 different time points: day 1, 7, and 28. *ABHR*, Alcohol-based hand rub.



Supplemental Fig 3. Unique interkingdom (bacterial–fungal) correlations at species level in ABHR-treated (**A**) and untreated (given SOC) (**B**) patient groups at the end of treatment (day 7). Blue tiles indicate positive correlations. *ABHR*, Alcohol-based hand rub; *SOC*, standard of care.

Supplemental Table I. Demographics and characteristics of hospitalized stem cell transplant patients enrolled in study

	Treatment group	
Characteristics	**Untreated**	**ABHR-treated**
No. enrolled	10	10
Age, y, mean ± SD	58.9 ± 13.95	59.9 ± 8.39*
Sex, n		
Male	5	4
Female	5	6
Transplant type, n		
Allogeneic	5	4
Autologous	5	6
Concomitant treatment, n		
Radiation therapy	0	1
Anti-infectives	4	6
Steroids	4	7
Other	8	7

ABHR, Alcohol-based hand rub; *SD*, standard deviation.
*$P = .32$ for the treated versus untreated comparison (Kruskal-Wallis rank sum test).

Supplemental Table II. Mean relative abundance of bacterial phyla and genera in alcohol-based hand rub–treated and untreated patients during study period

		Day 1					Day 7					Day 30				
		ABHR-treated, %		Untreated, %			ABHR-treated, %		Untreated, %			ABHR-treated, %		Untreated, %		
Taxon	Bacteria	Mean	SD	Mean	SD	*P*	Mean	SD	Mean	SD	*P*	Mean	SD	Mean	SD	*P*
Phylum	p__Firmicutes	44.5	9.4	40.7	13.6	.082	42.4	4.0	38.2	3.1	.041	46.1	12.8	41.2	5.8	.496
	p__Proteobacteria	43.3	15.0	49.8	14.7	.082	45.9	4.9	50.3	3.5	.028	42.5	12.5	47.1	5.8	.545
Genus	p__Actinobacteria.c__Actinobacteria.o__ Actinomycetales.f__Corynebacteriaceae.g__ *Corynebacterium*	0.8	0.6	0.2	0.2	.004	0.5	0.4	0.4	0.3	.496	0.6	0.5	0.5	0.4	.705
	p__Firmicutes.c__Bacilli.o__Bacillales.f__ Bacillaceae	2.6	1.0	3.2	1.3	.174	2.8	0.6	3.3	0.9	.226	2.4	0.6	3.3	0.8	.013
	p__Firmicutes.c__Bacilli.o__Bacillales.f__ Bacillaceae.g__*Virgibacillus*	0.2	0.1	0.3	0.2	.450	0.3	0.1	0.3	0.3	.940	0.2	0.1	0.3	0.1	.028
	p__Firmicutes.c__Bacilli.o__Gemellales.f__ Gemellaceae.	0.1	0.2	0	0.1	.049	0.2	0.7	0	0.1	.820	0	0	0.1	0.1	.650
	p__Firmicutes.c__Clostridia.o__Clostridiales.f__ Lachnospiraceae.g__*Blautia*	0.4	0.9	0.2	0.3	.024	0.2	0.3	0.1	0.2	.600	0.1	0.3	0.1	0.1	.730
	p__Proteobacteria.c__Gammaproteobacteria.o__ Oceanospirillales.f__Halomonadaceae	6.4	2.3	7.4	2.2	.131	6.8	1.1	7.6	0.6	.028	6.0	1.9	7.1	1.2	.174
	p__Proteobacteria.c__Gammaproteobacteria.o__ Oceanospirillales.f__Halomonadaceae.g__ *Halomonas*	32.1	11.4	35.8	10.5	.131	33.6	4.8	37.5	2.6	.008	31.5	10.2	34.7%	5.7	.545

ABHR, Alcohol-based hand rub; *c*, class; *f*, family; *g*, genus; *o*, order; *p*, phylum; *SD*, standard deviation.