

Human-derived content of dust microbiota in athletic facilities reflects building design and operation

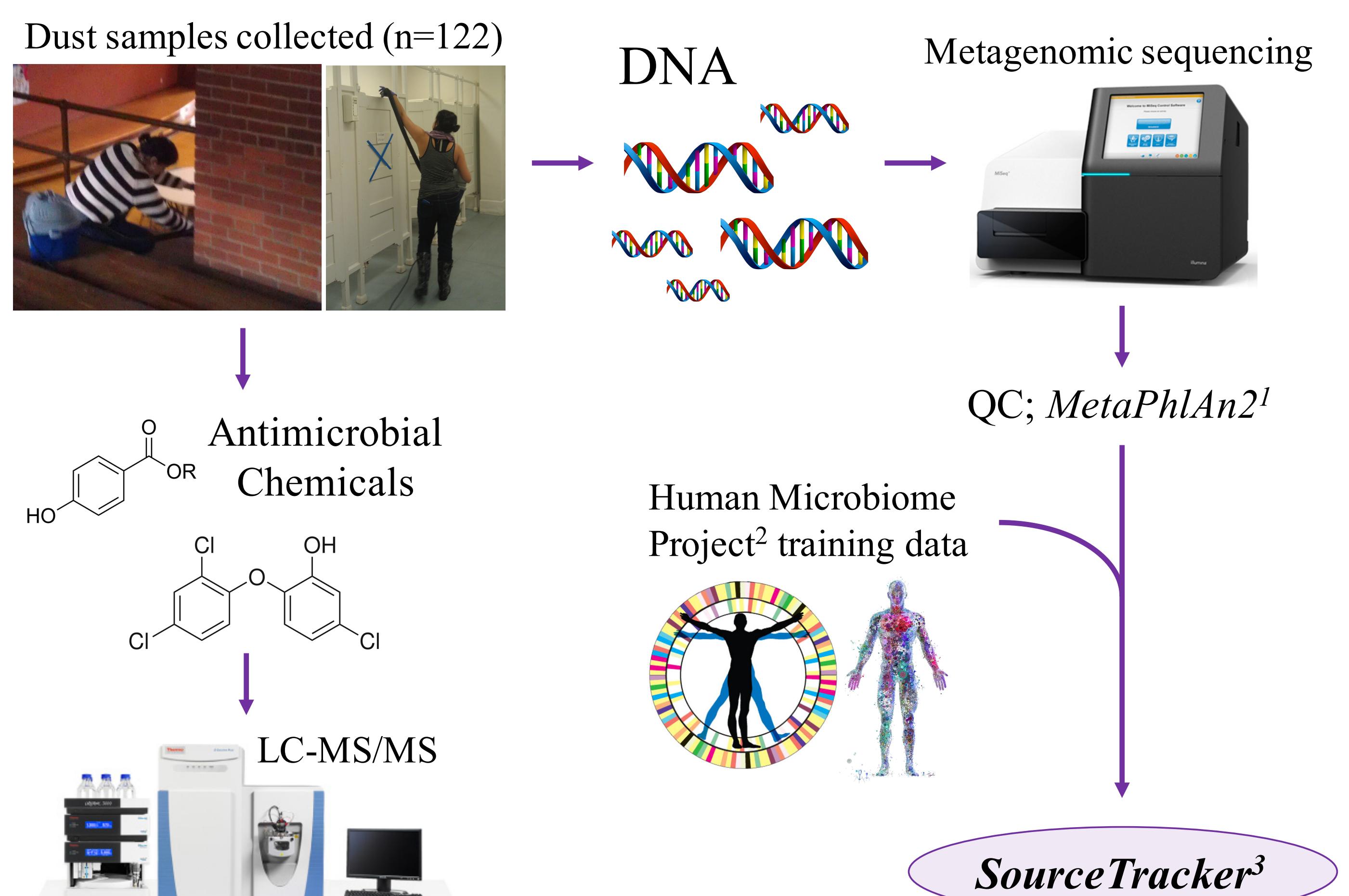
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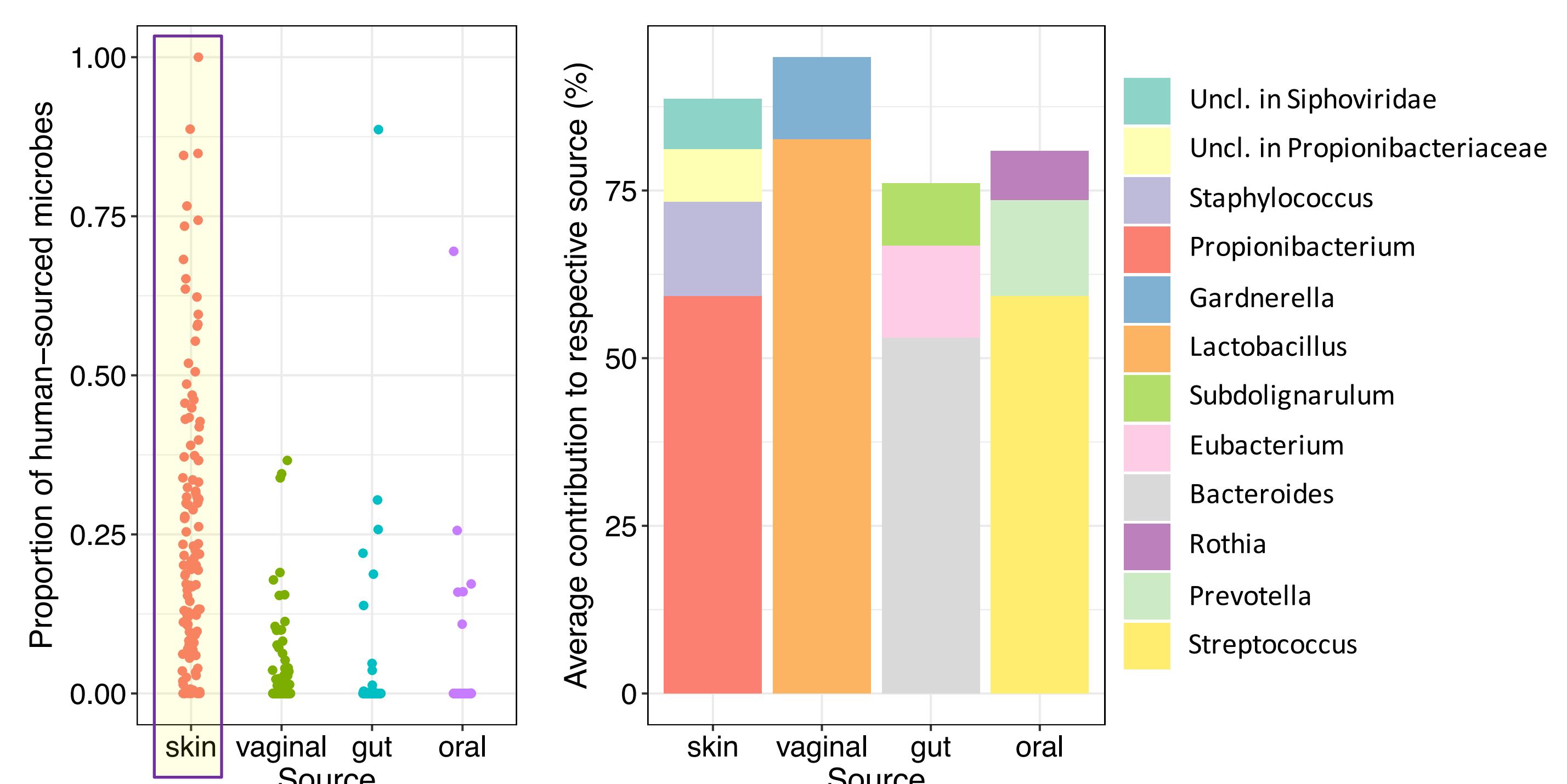
BACKGROUND

- Building design and operation impact the accumulation and survival of microorganisms in indoor spaces.
- These microorganisms, together referred to as the indoor microbiome, have implications for human health and well being.
- Understanding the relative importance of factors that shape the indoor microbiome may inform how to optimize building design and use for human health and safety.
- This study aimed to identify putative sources of microbes found in dust in athletic facilities and determine the building characteristics that most strongly correlate with the human-derived content.

METHODS & INITIAL RESULTS



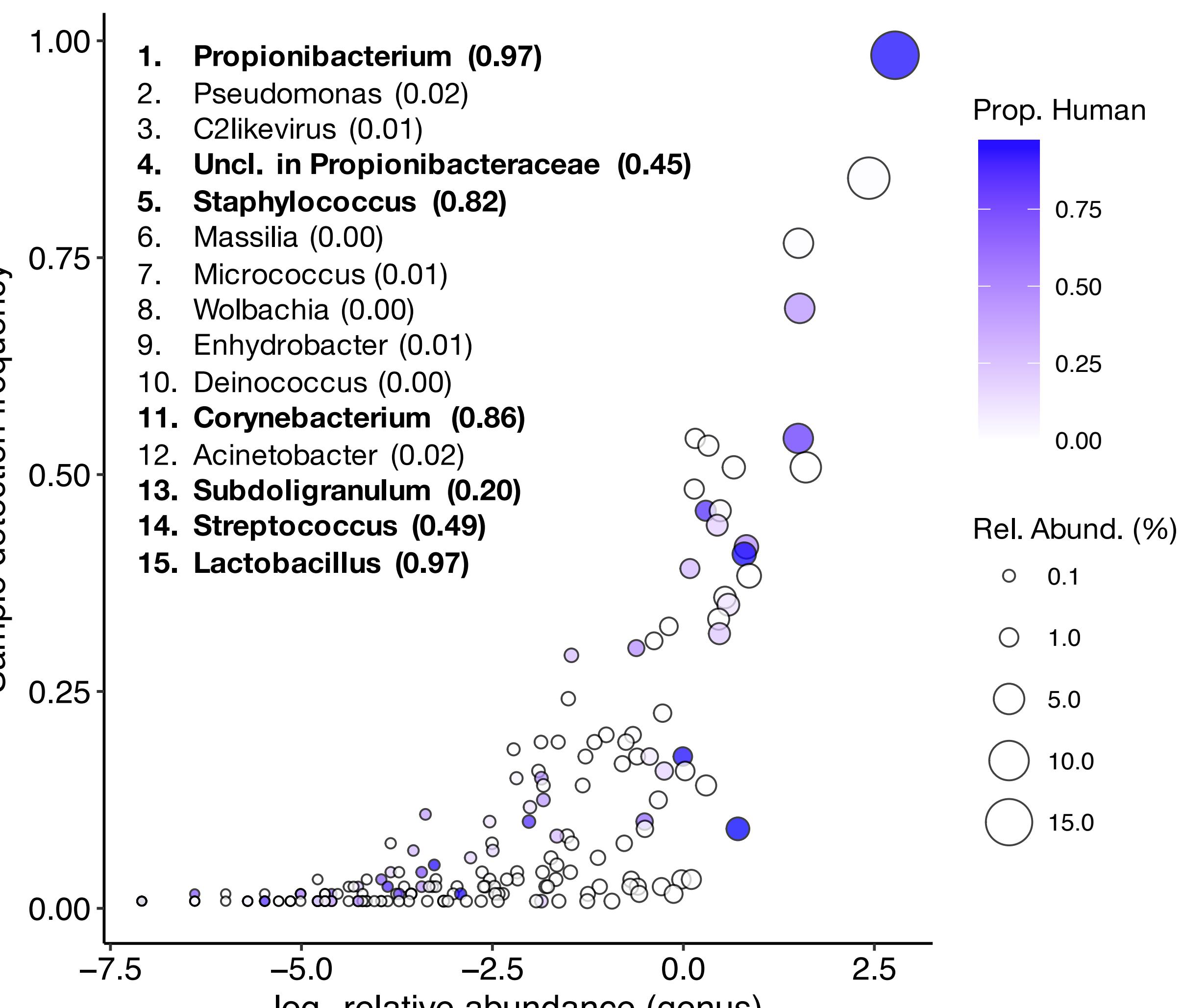
- Associations between estimated proportions of human-derived microbiota and building properties were evaluated with beta regression.
- SourceTracker data were also compared with a culture-dependent assessment of dust microbial diversity.
- Approximately $31.5 \pm 2.2\%$ of the dust microbiota were putatively derived from humans, primarily skin (e.g., *Propionibacterium*, *Staphylococcus*).



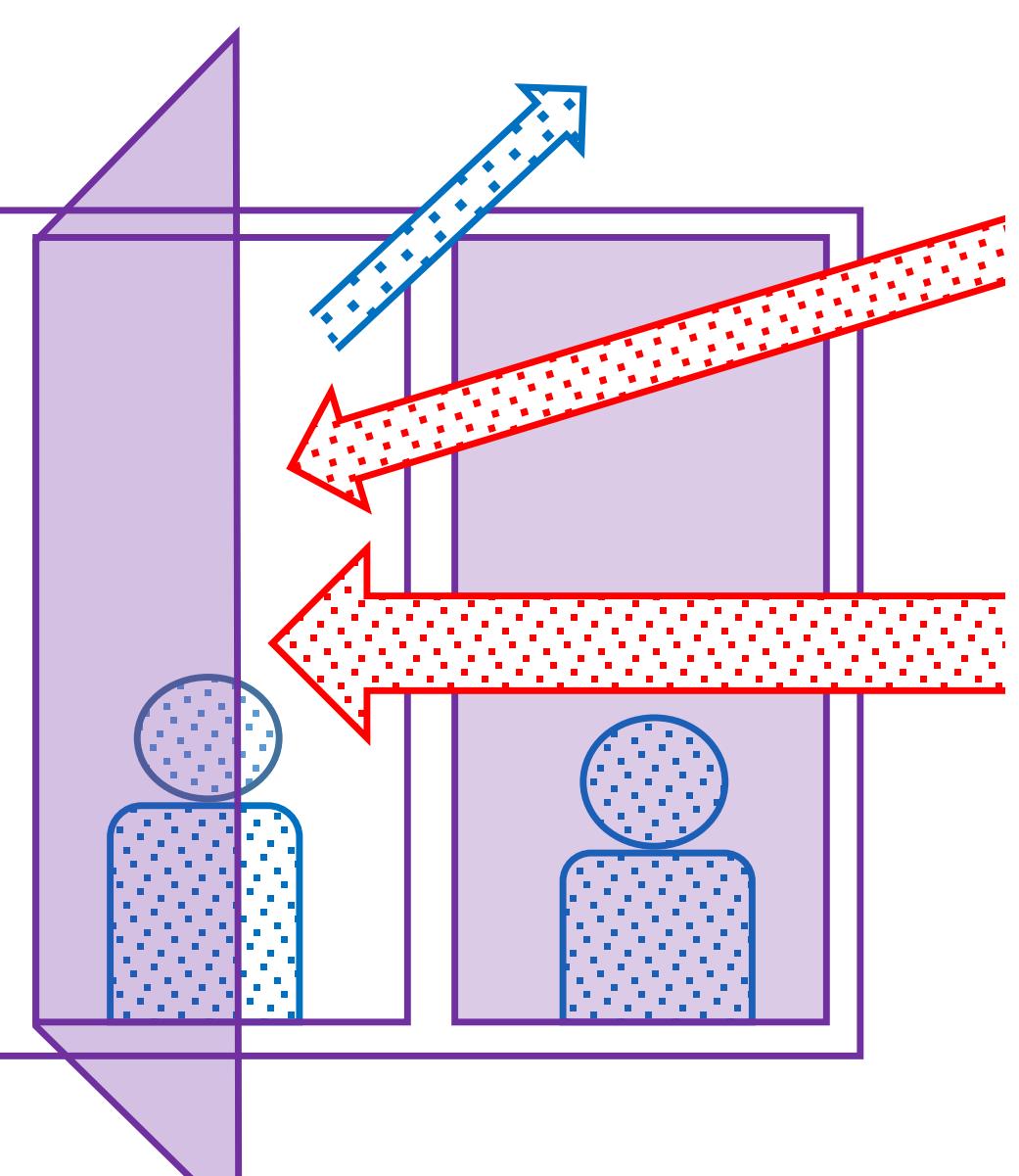
- References:
- Segata et al. 2012. Metagenomic microbial community profiling using unique clade-specific marker genes. *Nature Methods* 9: 811-814.
 - Lloyd-Price et al. 2017. Strains, functions and dynamics in the expanded human microbiome project. *Nature* 550: 61-71.
 - Knights et al. 2011. Bayesian community-wide culture-independent microbial source tracking. *Nature Methods* 8: 761-765.

FACTORS ASSOCIATED WITH PUTATIVE SOURCES OF DUST MICROBIOTA

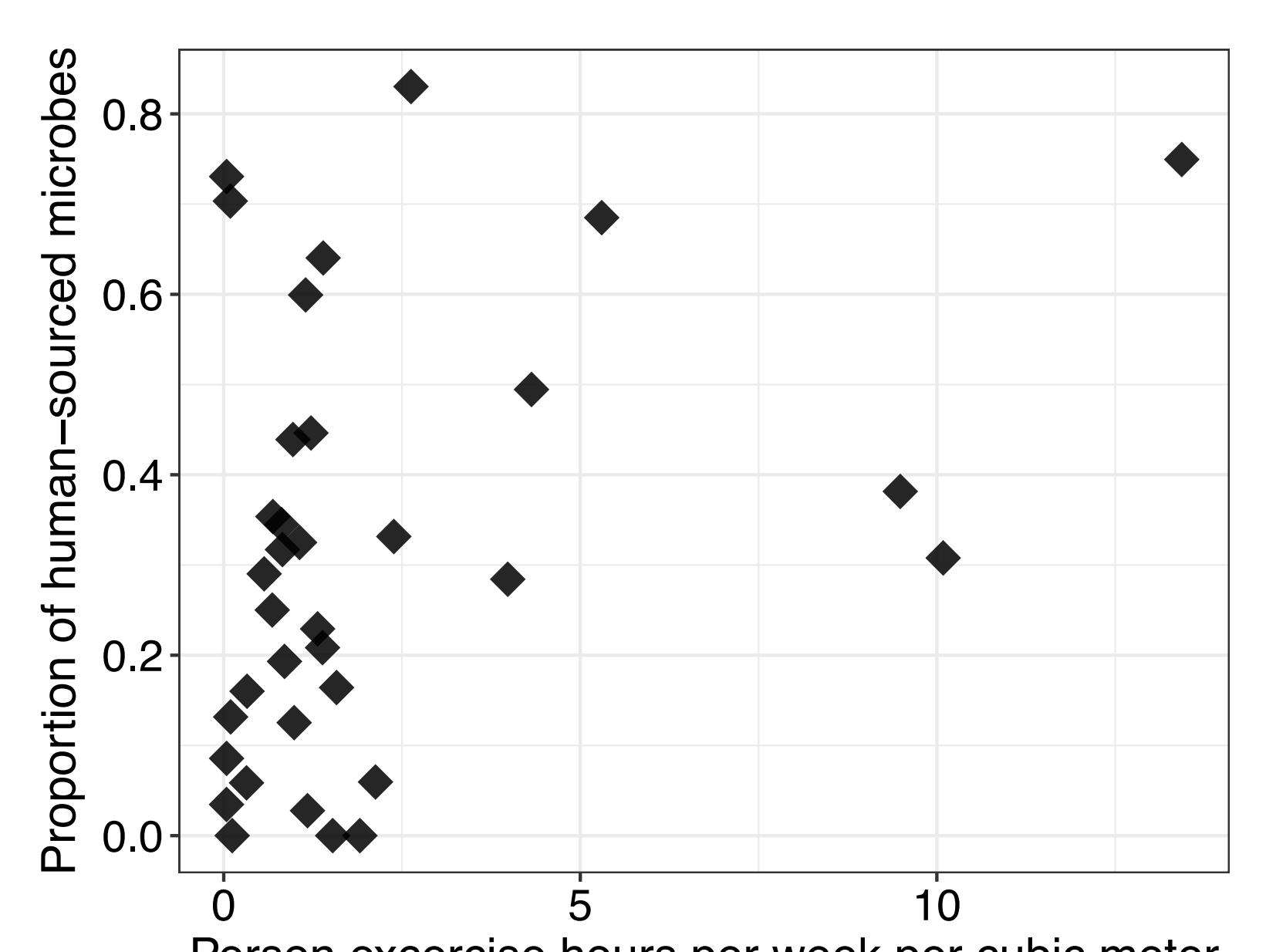
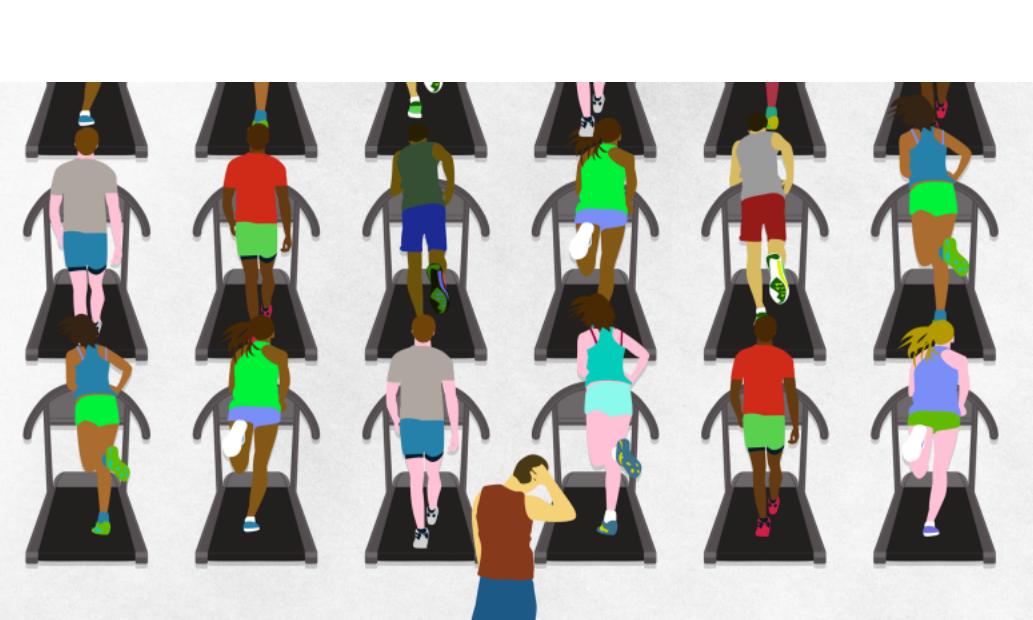
- Dispersal** is a major driver of the indoor microbiome; the heterogeneous microbial communities consisted of few dominant and many low-abundance taxa coming from a mix of sources (19.8 ± 0.8 genera per sample). Bolded genera are human-derived.



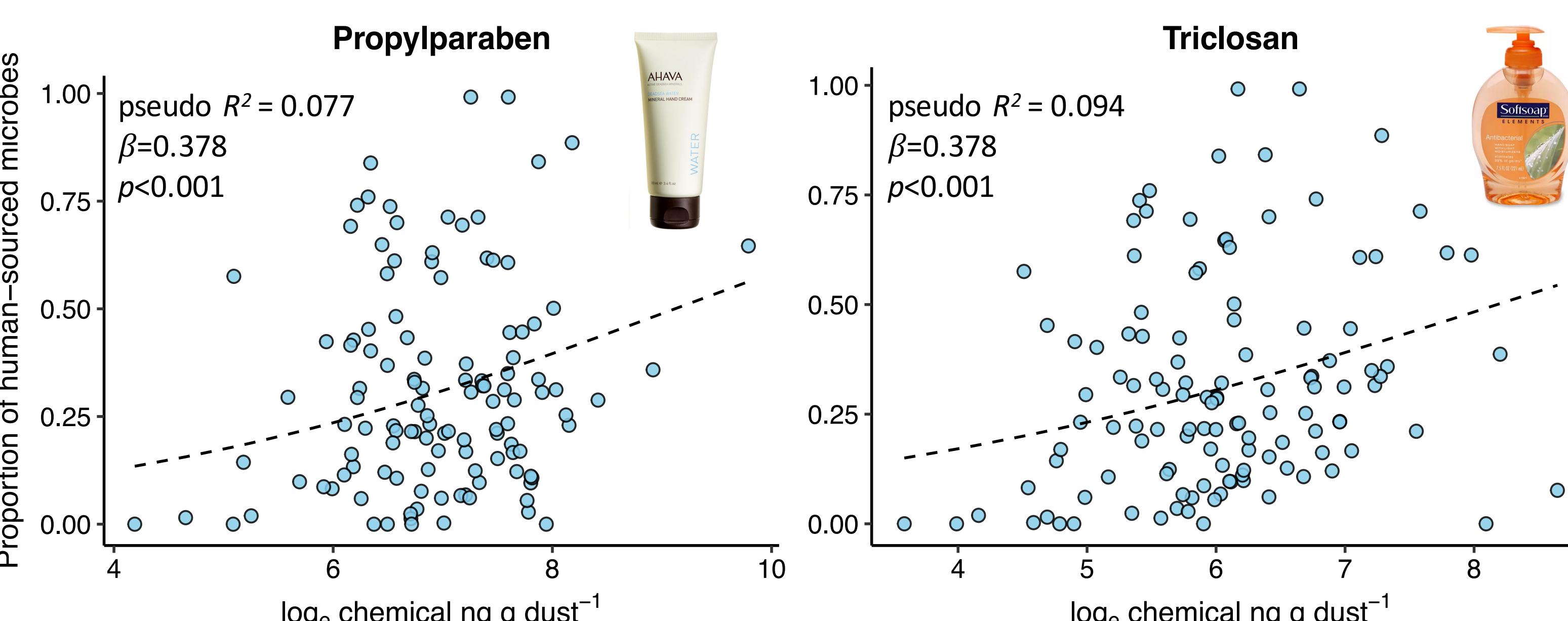
- Spaces with operable windows or exterior doors had significantly lower proportions of human-sourced microbiota ($p=0.013$), suggesting a strong effect of **ventilation**.



- Expectedly, **human occupancy** positively correlated with proportion of human-derived microbiota ($r=0.346, p=0.042$).

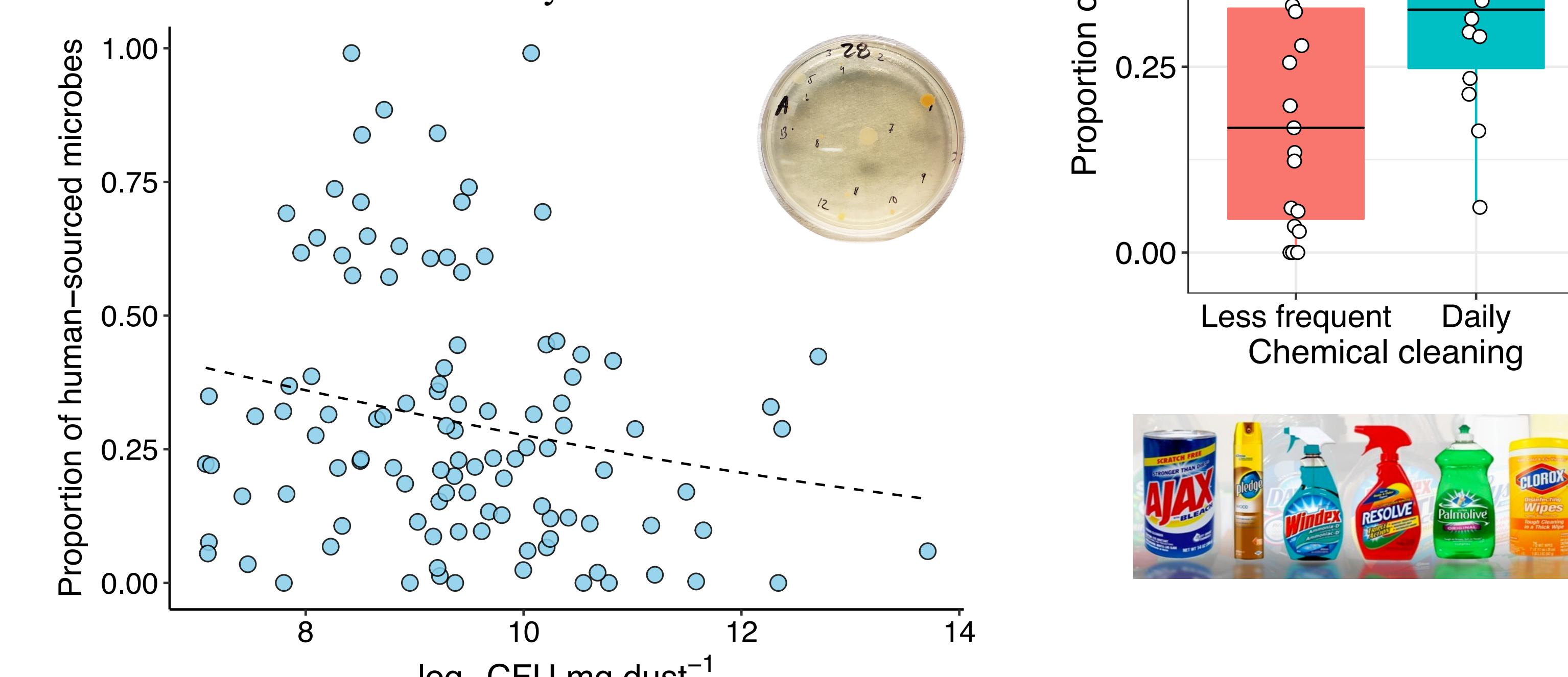


- Weak positive correlations between **consumer product-associated antimicrobials in dust** and putative microbiota sources suggest potential co-transport from human skin.



- Chemical cleaning frequency** correlated with increases as well ($p=0.001$). This may suggest that human-associated microbes are more tolerant of cleaning chemicals than environmental-sourced (e.g., soil, water) microbes. Alternatively, maybe spaces that are cleaned more frequently are also used more often, thus allowing for deposition of more human-derived microbes.

- We found a weak negative correlation between human-associatedness and culture richness ($\beta=-0.194, p=0.017$), suggesting that **environmental taxa are more viable** or that our culture methods may have been biased.



CONCLUSIONS

- Formation of the indoor microbiome involves passive transport of microbes and potential interaction with chemicals from human skin.
- This process is dominated by dispersal, though potential impacts of cleaning and personal hygiene products may increase in spaces with limited windows and exterior doors, especially as spaces become more crowded.
- Future studies will focus on specific mechanisms for adaptations in the indoor microbiome and implications for human health (e.g., antibiotic resistance dissemination).

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