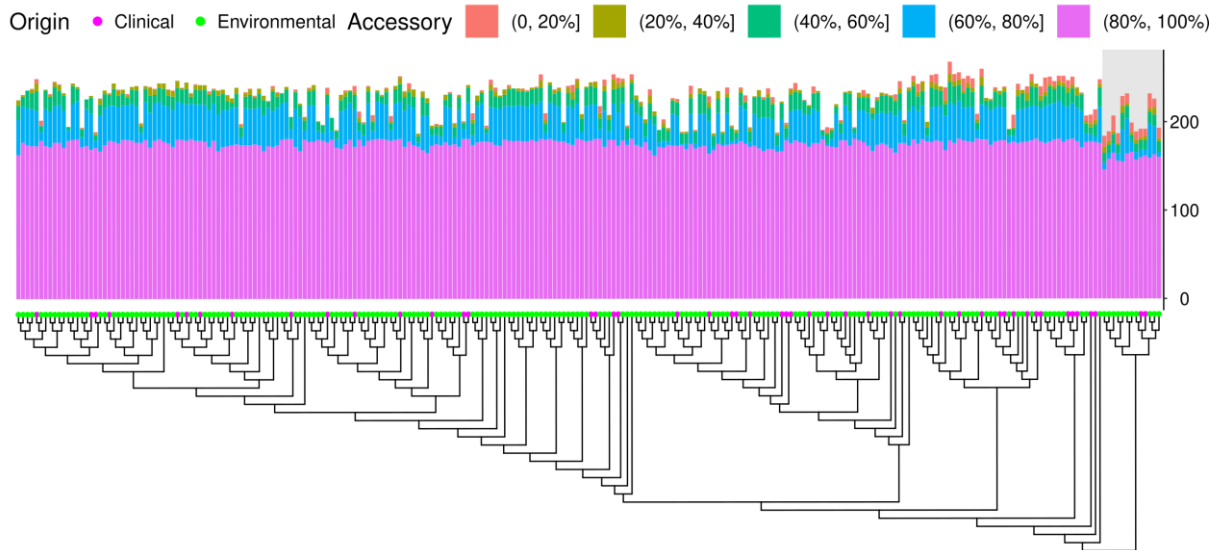


# Supplementary Information

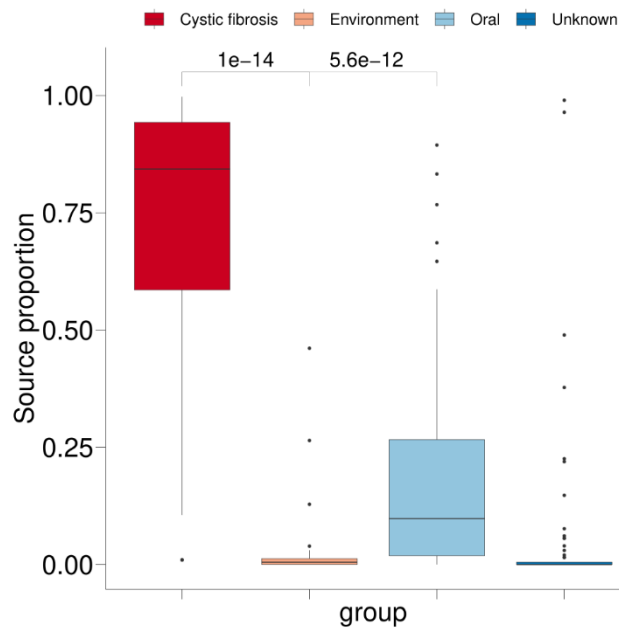
## Supplementary Figures

### Supplementary Figure S1



**Accessory genome conservation among 252 *A. fumigatus* strains.** Indicated percentage ranges denote accessory gene presence across the genomes of all strain-specific GEMs. Cluster with gray background denotes genetic lineage of *A. fumigatus* with significantly fewer accessory genes than other lineages as previously published<sup>1</sup>. Source data for Figure S1 are provided as a Source Data file.

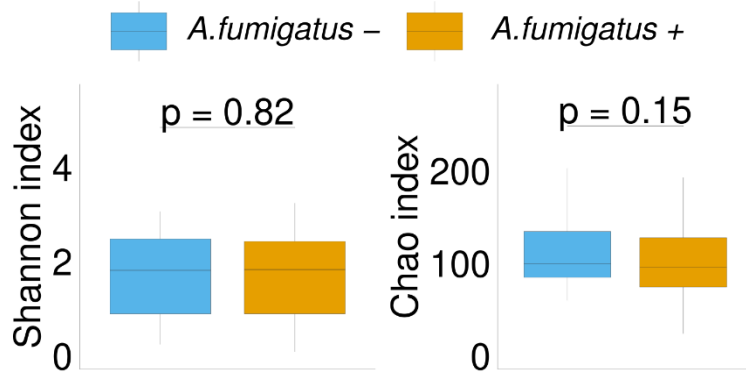
## Supplementary Figure S2



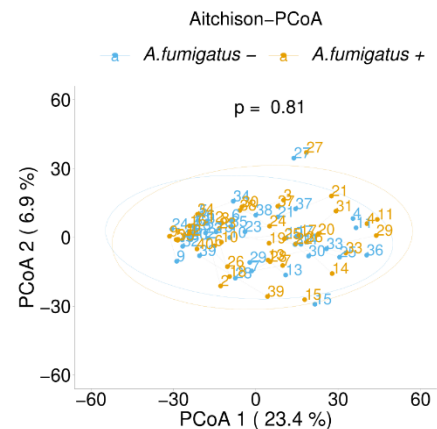
**FEAST result for estimating the contribution of potential source environments by combining three published cystic fibrosis lung microbiome datasets and a clinical environmental dataset (see Methods).** The group “Cystic fibrosis” (n=85) is the contribution of the cystic fibrosis lung microbiome for each sample, and the group “Environment” (n=24) is the contribution of the clinical environment for each sample. “Oral” (n=132) is the contribution of the oral microbiome for each sample. The group “unknown” is the contribution of other environments of unknown origin. The p value was obtained by two-tailed Wilcoxon matched-pairs signed-rank test. Box-plot elements: center line: median, lower/upper bound: 25<sup>th</sup>/75<sup>th</sup> percentile, whiskers: minimum and maximum values within  $1.5 \times$  interquartile range (IQR), outliers: points outside  $\pm 1.5 \times$  IQR. Source data for Figure S2 are provided in the Source Data file.

### Supplementary Figure S3

**a**



**b**



**Alpha and beta diversity of cystic fibrosis lung microbiome.** **a**, Statistical significance according to Shannon and Chao diversity index for alpha diversity ( $n=40$  for samples without (-) and with (+) *A. fumigatus* infection). **b**, Beta diversity (Aitchison distance) based on Kraken-derived taxonomic profiles. Two-tailed Wilcoxon signed-rank test was used for alpha diversity comparisons; PERMANOVA was used to assess the statistical significance of beta diversity comparisons. Box-plot elements: center line: median, lower/upper bound: 25<sup>th</sup>/75<sup>th</sup> percentile, whiskers: minimum and maximum values within  $1.5 \times$  interquartile range. Source data for Figure S3 are provided in the Source Data file.

## References

1. Barber, A. E. *et al.* Aspergillus fumigatus pan-genome analysis identifies genetic variants associated with human infection. *Nature Microbiology* 2021 6:12 **6**, 1526–1536 (2021).