

1 Integrated multi-omics analysis reveals Lactobacillus
2 anti-inflammatory process in vaginal tissue

3 A demonstration of Rmarkdown using Herman Bumpus' data

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6 **1 Abstract**

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²³ **2 Introduction**

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troduction Introduction Introduction Introduction (¹), Introduction Introduction Introduction Introduction
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³¹ Introduction Introduction Introduction Introduction Introduction **Introduction Introduction** *Introduc-*
³² *tion* Introduction (^{2,3}) .

³³ Problem / question to answer

34 3 Results

35 Joint analysis of vaginal microbiome reveals distinct patient subgroups

36 To understand the longitudinal and tissue-specific microbiome profile in vaginal samples, 111 adult female
37 sex workers were enrolled in [...]. Among those, 14 were previously tested positive for HIV during the
38 cohort's sampling procedure. [Describe here what was done and when, which samples, which tissues].

39 To be able to better understand the differences in microbiome profile across all datasets collected, we per-
40 formed a joint graph-based clustering analysis in order to identify co-regulated bacterial communities (see
41 "Methods" section for details). A total of 9 bacterial communities were identified.

42 Noticeably, bacterial community NA consisted only of Lactobacillus species (**).

43 Patients were thus subdivided into 5 groups,

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76 **Indentification of bacterial communities metabolic processes linked to Lactobacilli**

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102 Identification of bacterial communities metabolic processes linked to Lactobacilli

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128 4 Discussion

129 I have analysed data collected by Herman Bumpus³ on the relationship between sparrow (*Passer domesticus*)
130 total length and survival following an unusually severe storm. I found that sparrows that died in the storm
131 were longer than sparrows that survived, which suggests that higher sparrow body length decreased survival.
132 Of course, it is not possible to definitively conclude a causal relationship between any aspect of body size and
133 sparrow survival, and even the available data collected by Bumpus would permit a more thoughtful analysis
134 than that conducted in this study (see [Appendix Table 1](#)).

135 Overall, this document demonstrates how high quality, professional looking documents can be written using
136 Rmarkdown. The [underlying code](#) for this manuscript is publicly available, along with [accompanying notes](#)
137 to understand how it was written. By using Rmarkdown to write manuscripts, authors can more easily use
138 version control (e.g., git) throughout the writing process. The ability to easily integrate citations through
139 BibTeX, LaTeX tools, and dynamic R code can also make writing much more efficient and more enjoy-
140 able. Further, obtaining the benefits of using Rmarkdown does not need to come with the cost of isolating
141 colleagues who prefer to work with Word or LaTeX because Rmarkdown can easily be converted to these
142 formats (in the case of Word, with the push of a button). By learning all of the tools used in this manuscript,
143 readers should have all of the necessary knowledge to get started writing and collaborating in Rmarkdown.

¹⁴⁴ **5 Methods**

145 **6 References**

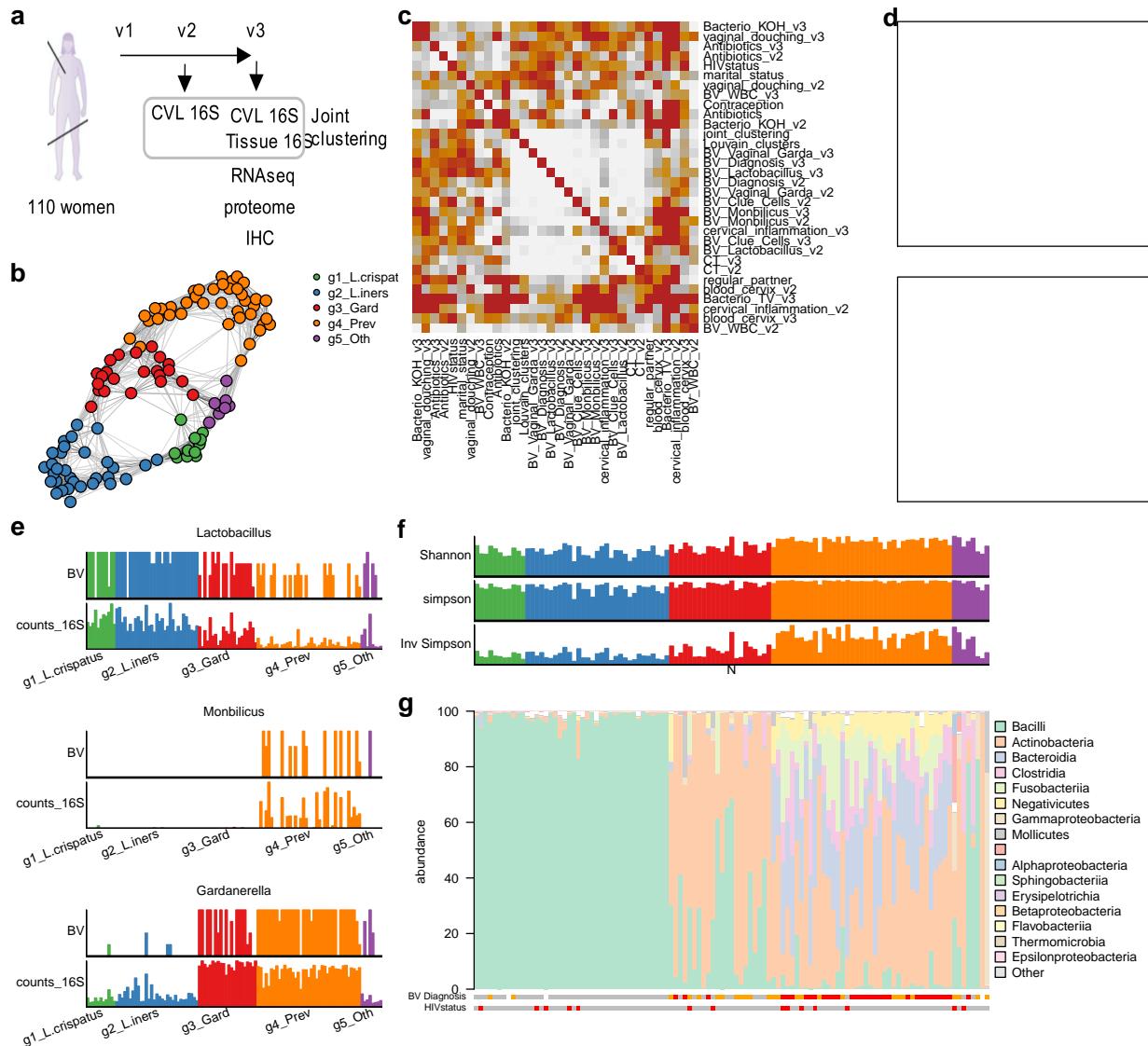
- 146 1. Johnston, R. F., Niles, D. M. & Rohwer, S. A. Hermon bampus and natural selection in the house
147 sparrow *Passer domesticus*. *Evolution* **26**, 20–31 (1972).
- 148 2. Darwin, C. *The origin of species*. 495 (Penguin, 1859).
- 149
- 150 3. Bumpus, H. C. Eleventh lecture. The elimination of the unfit as illustrated by the introduced sparrow,
151 *Passer domesticus*. (A fourth contribution to the study of variation.). *Biological Lectures: Woods
Hole Marine Biological Laboratory* 209–225 (1898).

152 **7 Appendix Table 1**

153 An example table is shown below, which includes all of the variables collected by³ for the first 10 measured
154 sparrows. The full data set can be found online in [GitHub](#).

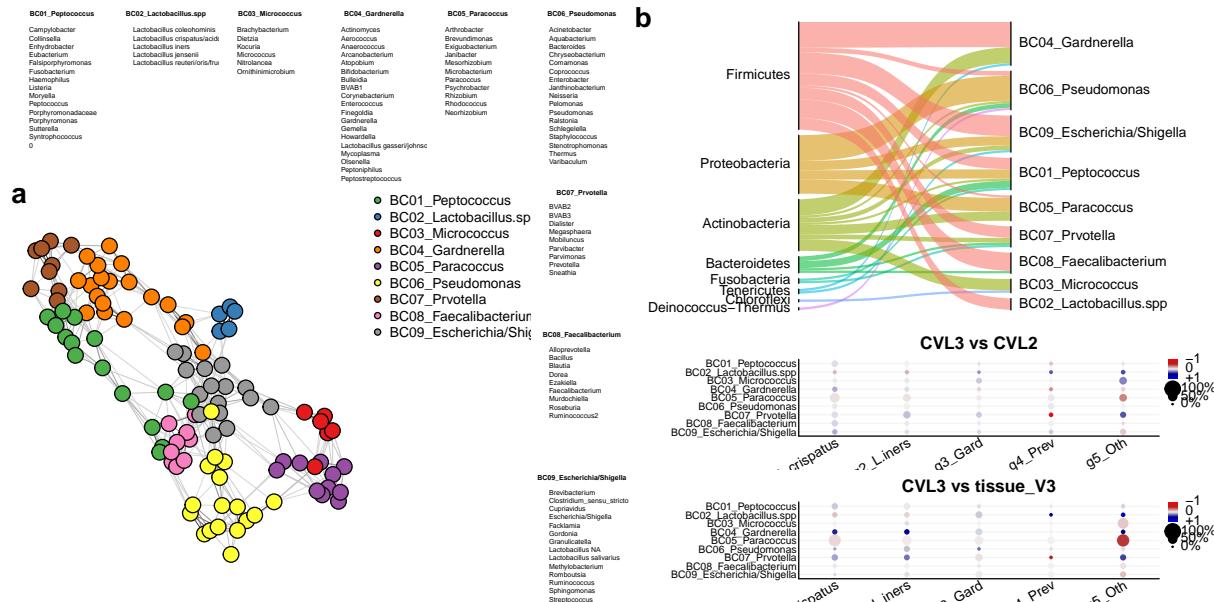
155 **8 FIGURES (MAIN)**

156 **8.1 Figure 1**

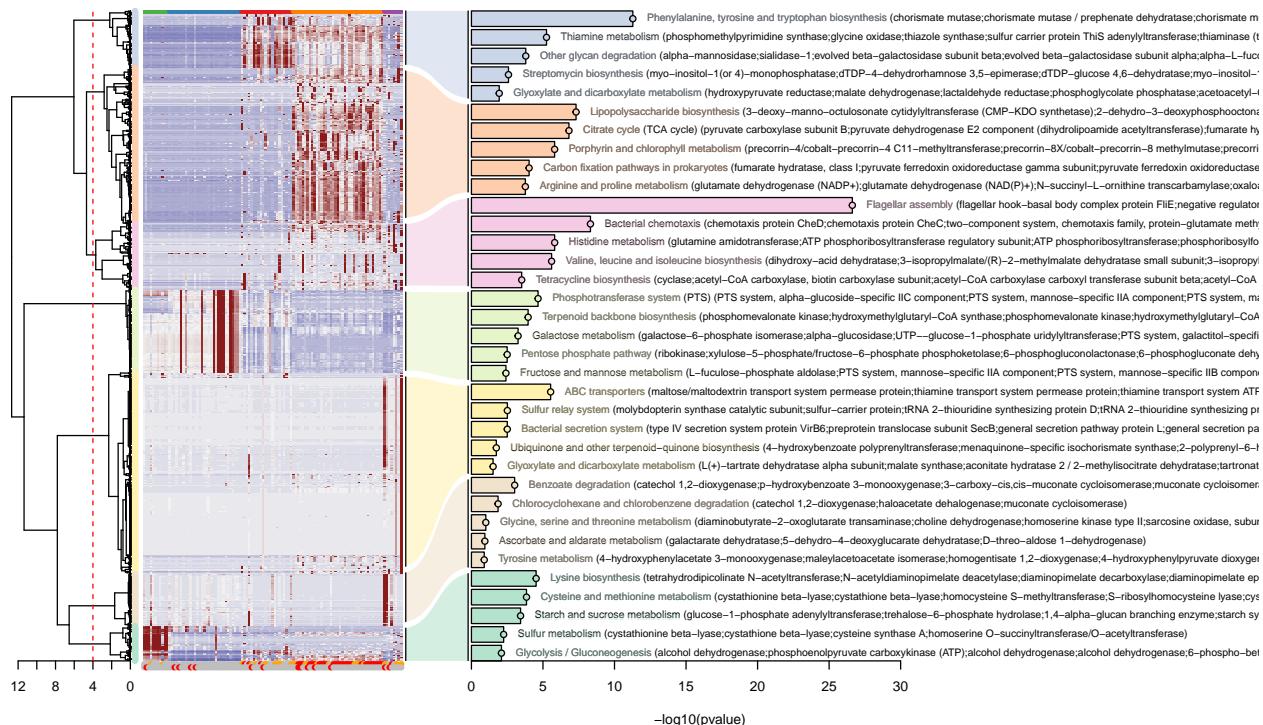


157 **Figure 1. Identification of patient groups.** (a) Schematic representation of #####. (b) Schematic representation of #####. (c) Schematic representation of #####. (d) Schematic representation of #####.

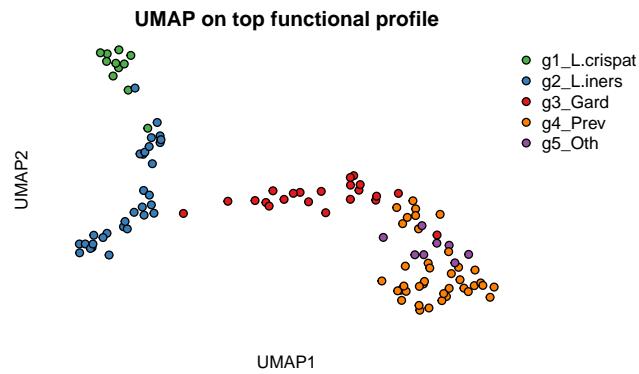
161 8.2 Figure 2



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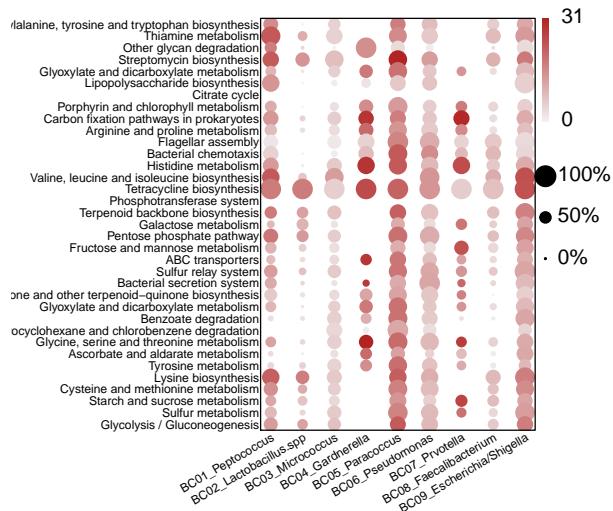


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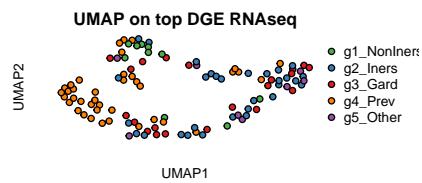
165 **Figure 2. Identification and characterization of vaginal bacterial communities.** (a) Schematic
 166 representation of ##### . (b) Schematic representation of ##### . (c) Schematic
 167 representation of ##### . (d) Schematic representation of ##### .



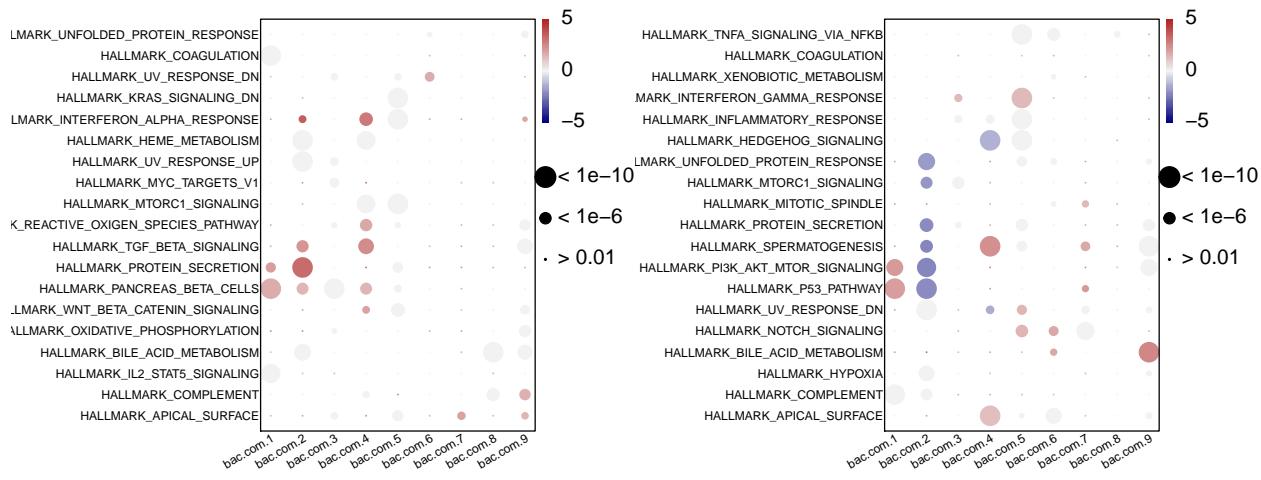
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₁₆₉ **8.3 Figure 3**

₁₇₀ **8.4 individual group comparison DGE**

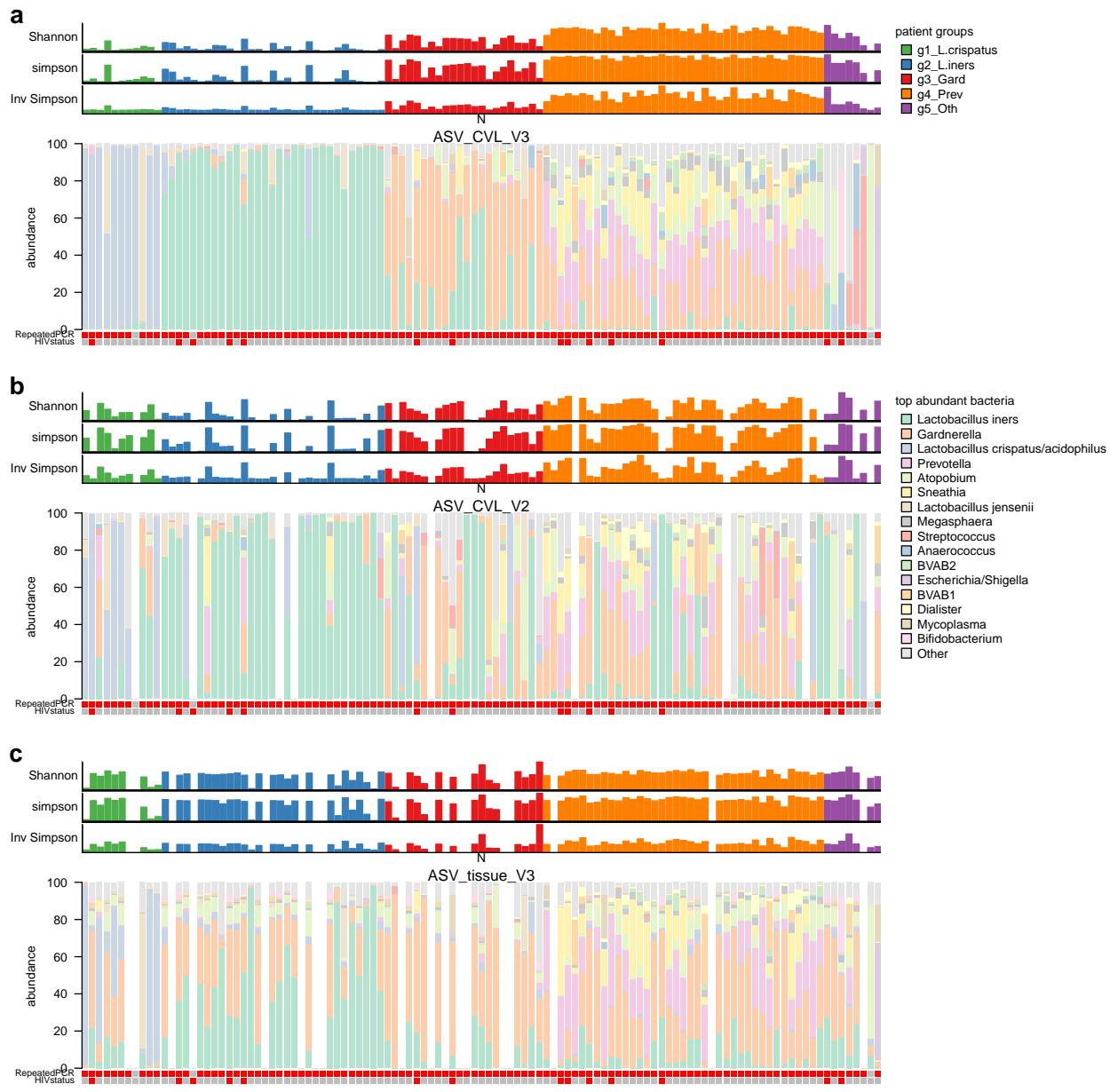


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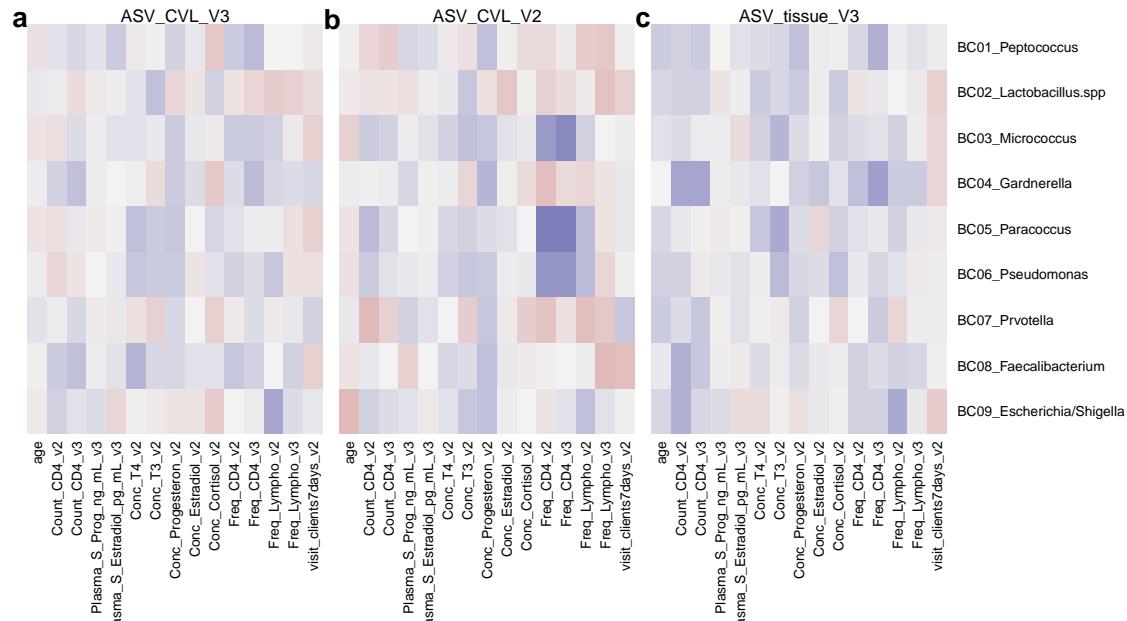


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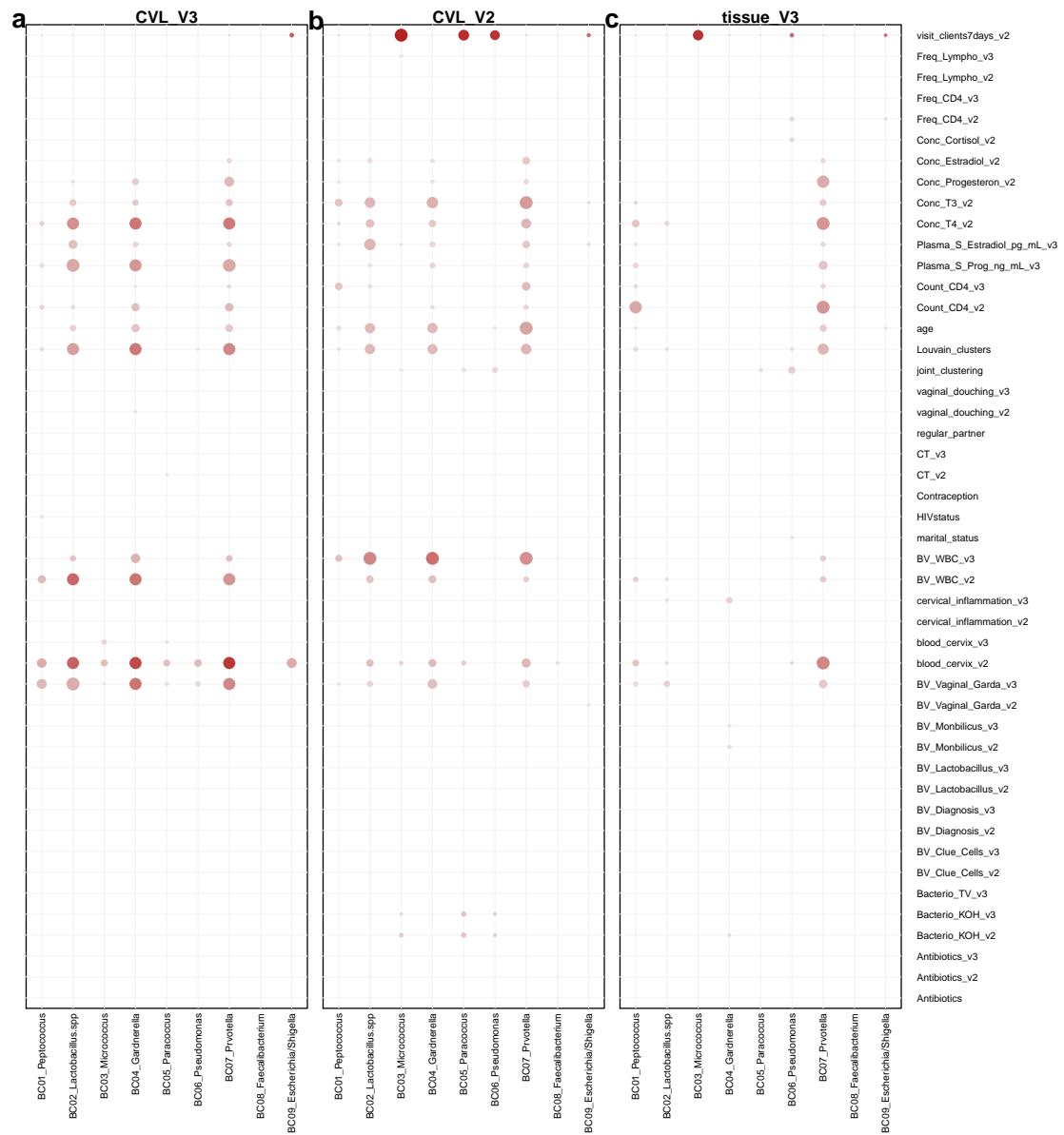
Figure 1. Identification of patient groups. (a) Schematic representation of #####. (b) Schematic representation of #####. (c) Schematic representation of #####. (d) Schematic representation of #####.

176 **9 FIGURES (SUPPL)**177 **9.1 Figure S1**

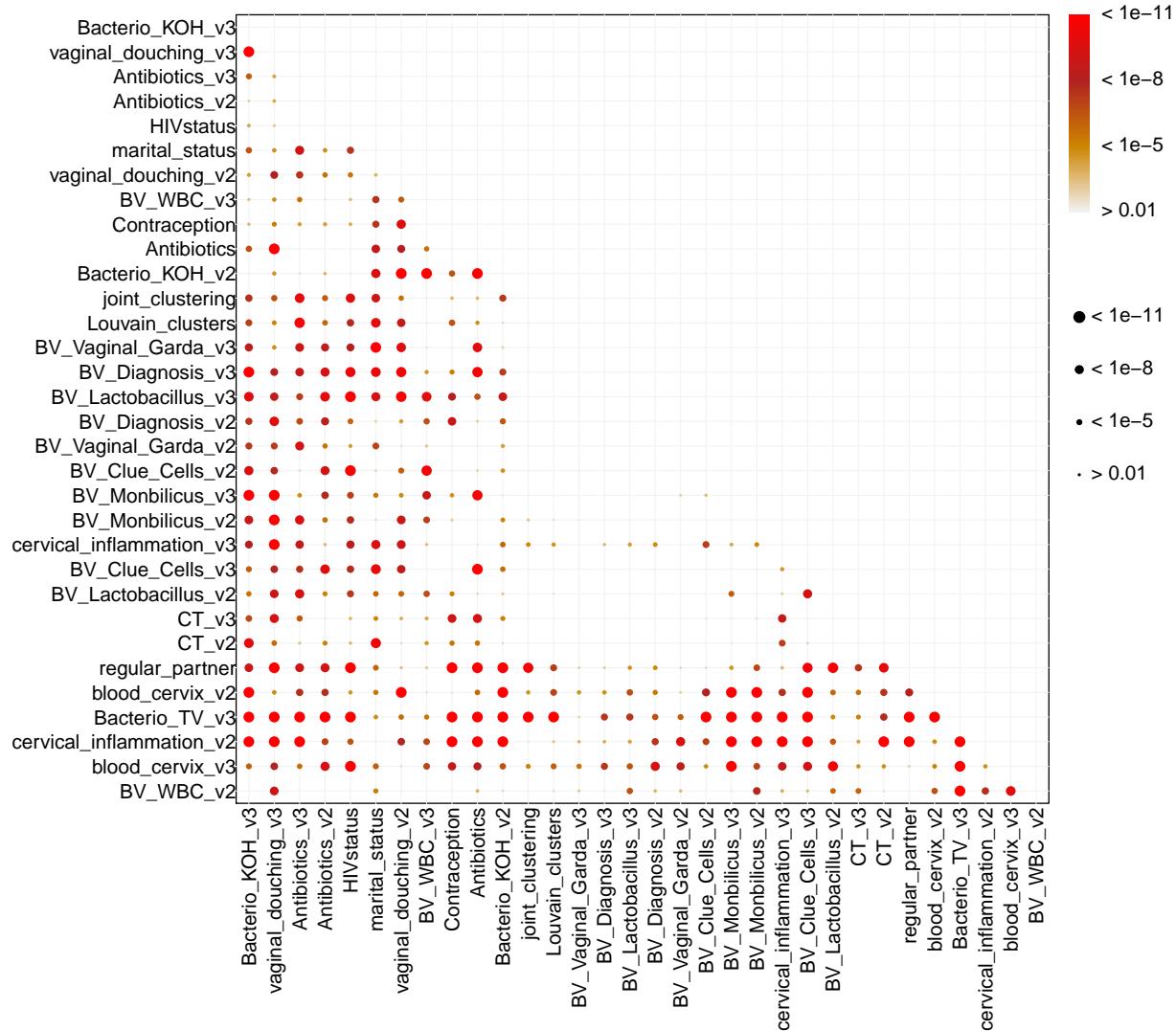
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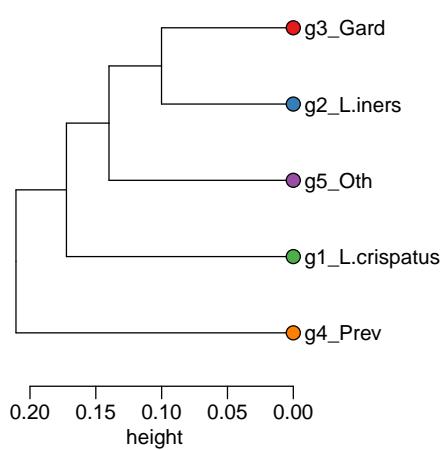
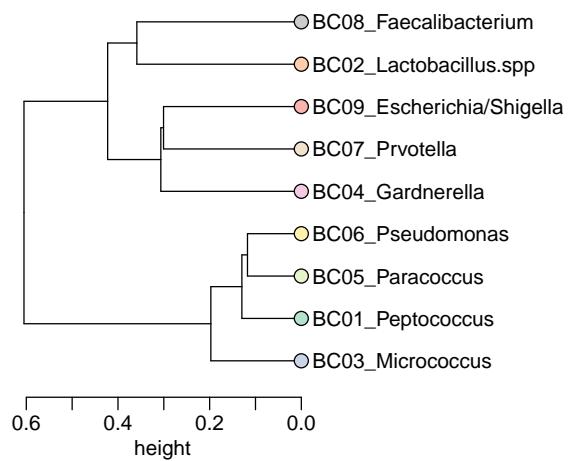
179 **9.2 Figure S2**

180

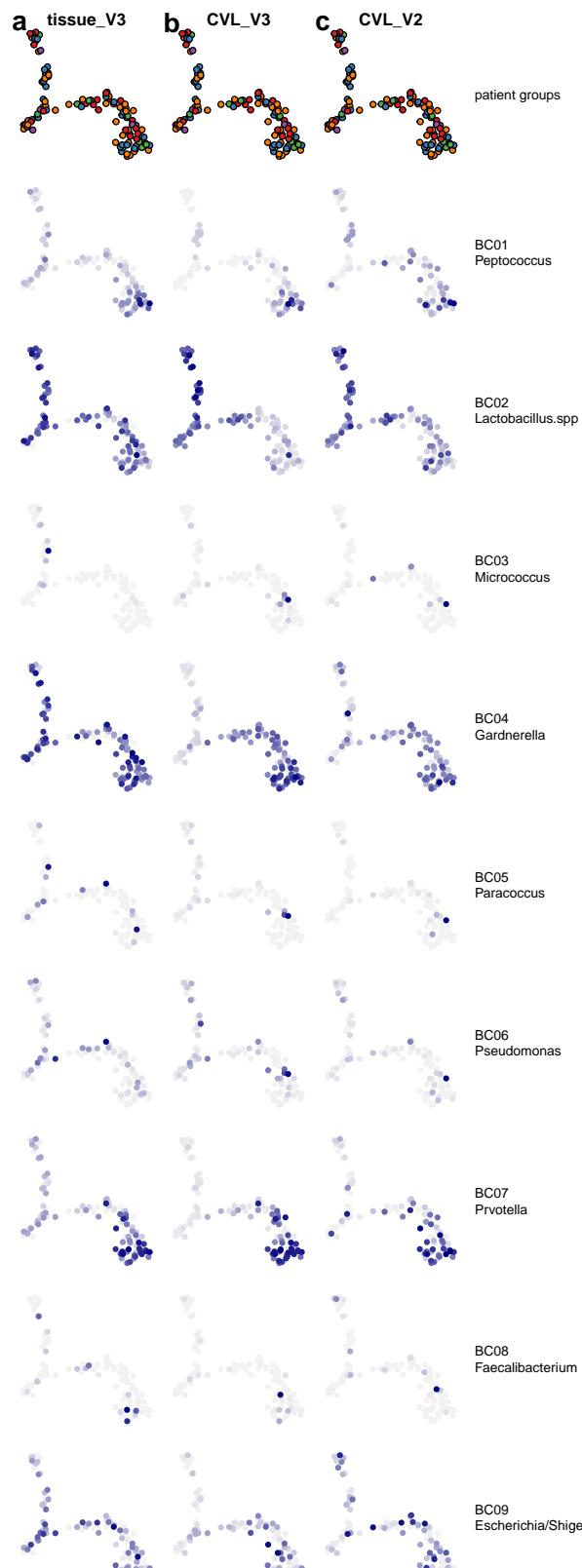
181 **9.3 Figure S2 v2**

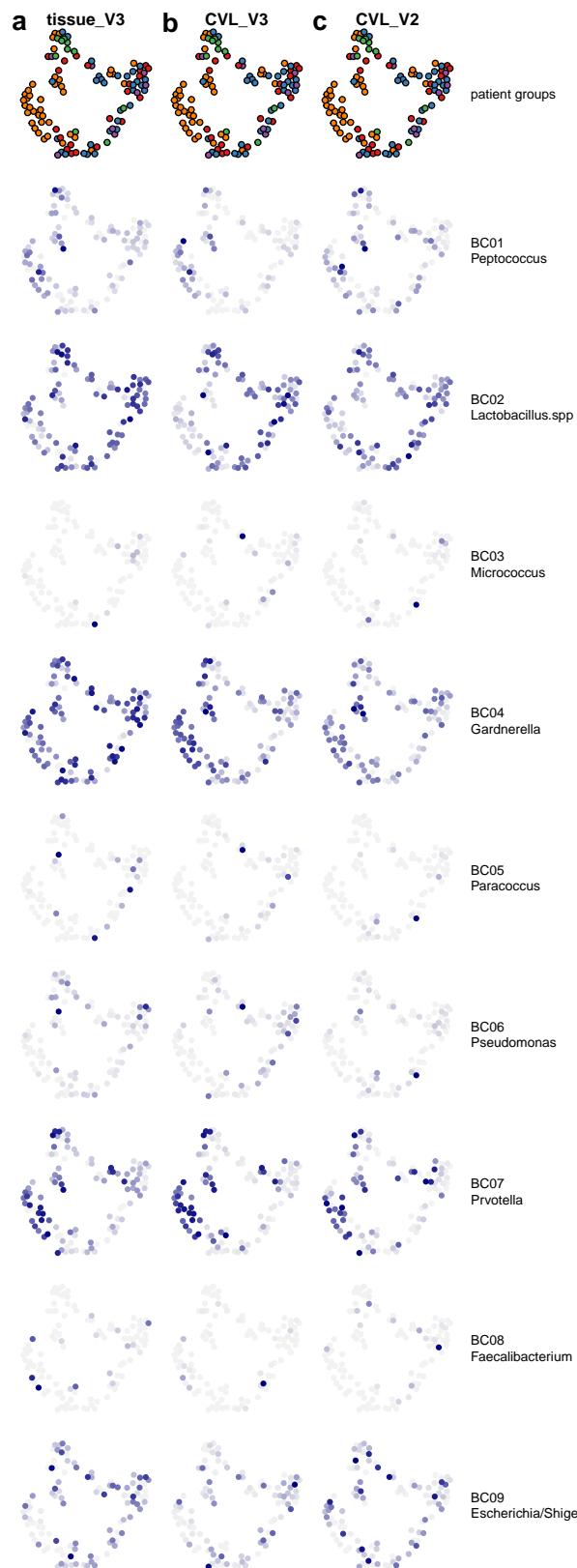
183 9.4 Figure S2 v3



185 **9.5 Figure S3****a****b**

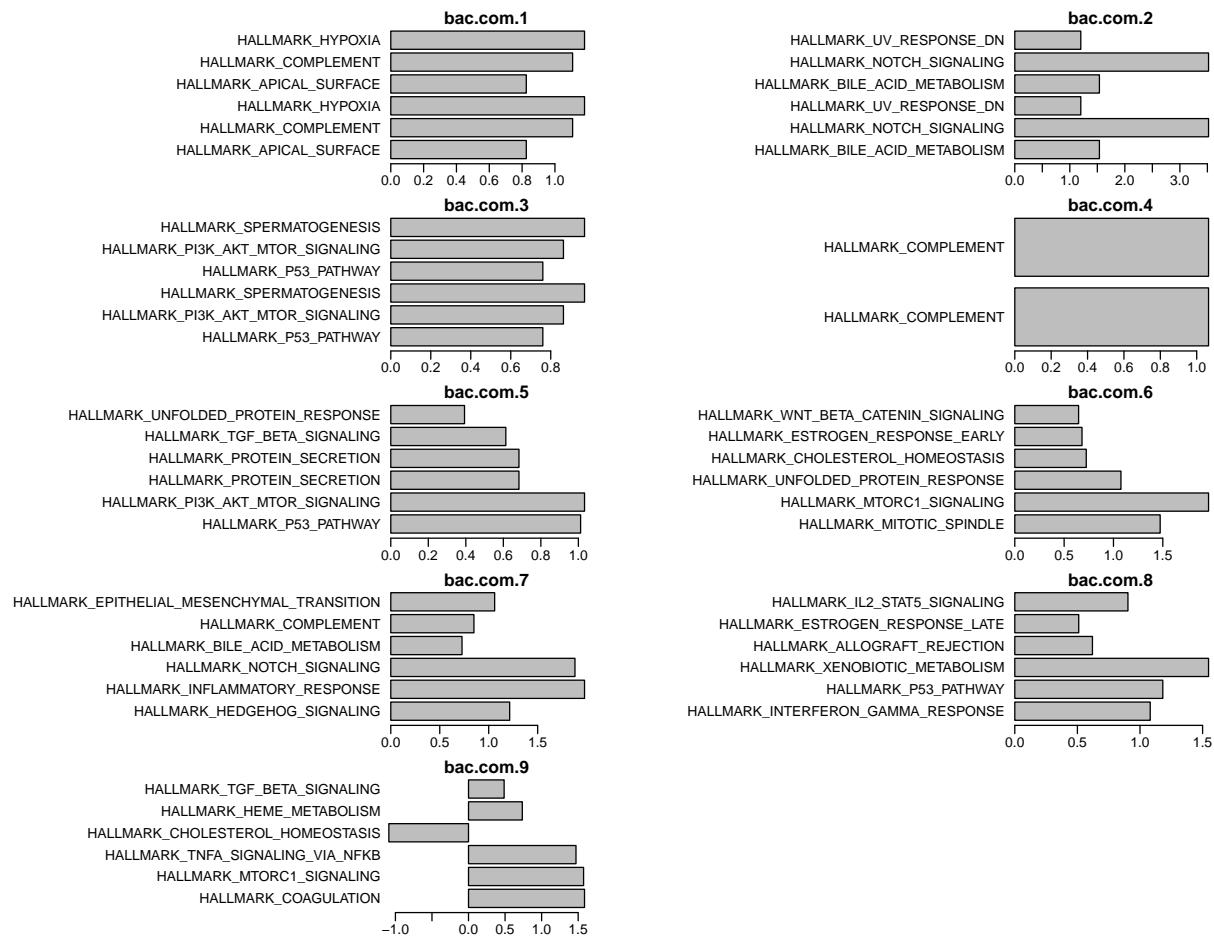
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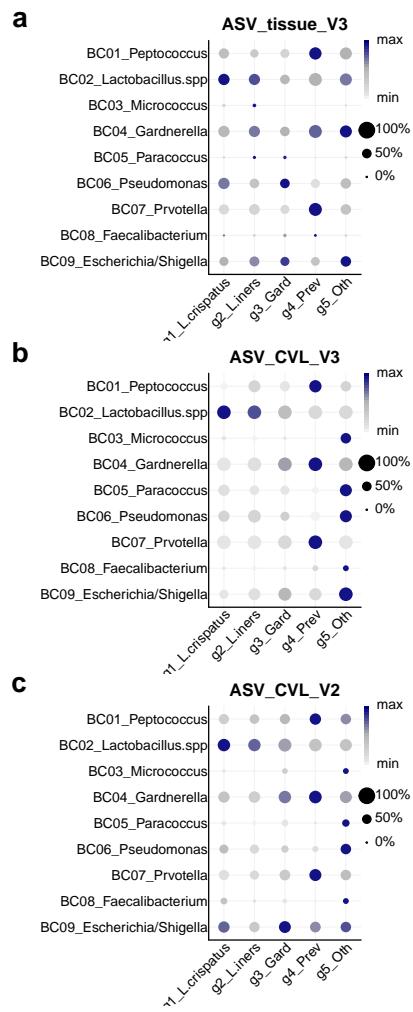
187 **9.6 Figure S4**

189 **9.7 Figure S5**

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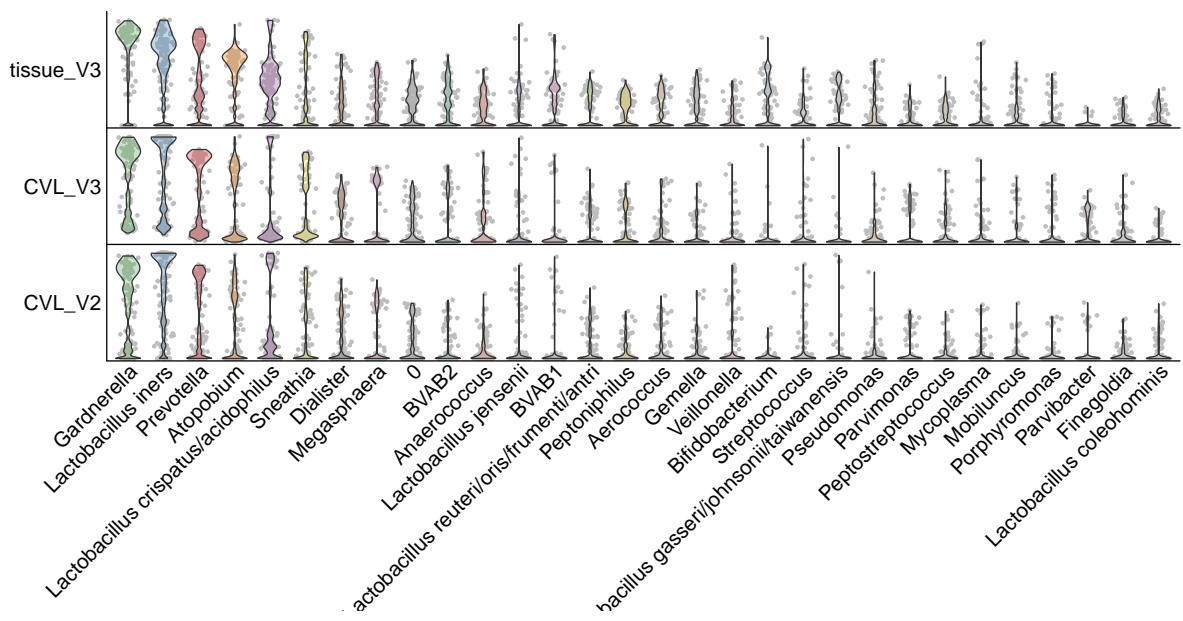
191 9.8 Figure S6



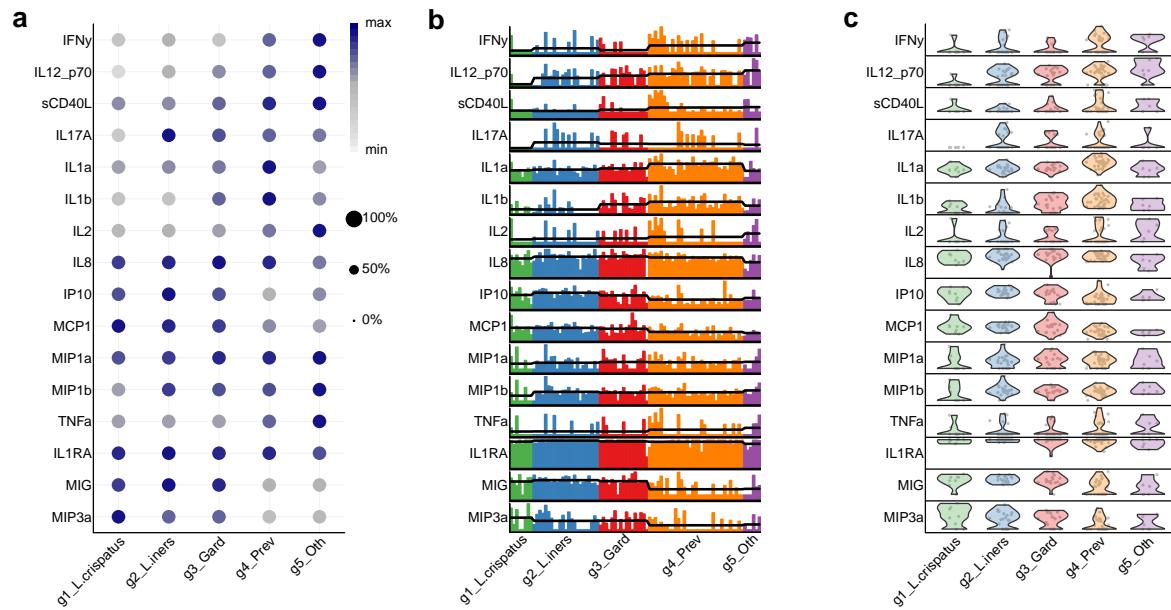
193 **9.9 Figure S7**

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195 9.10 Figure S8

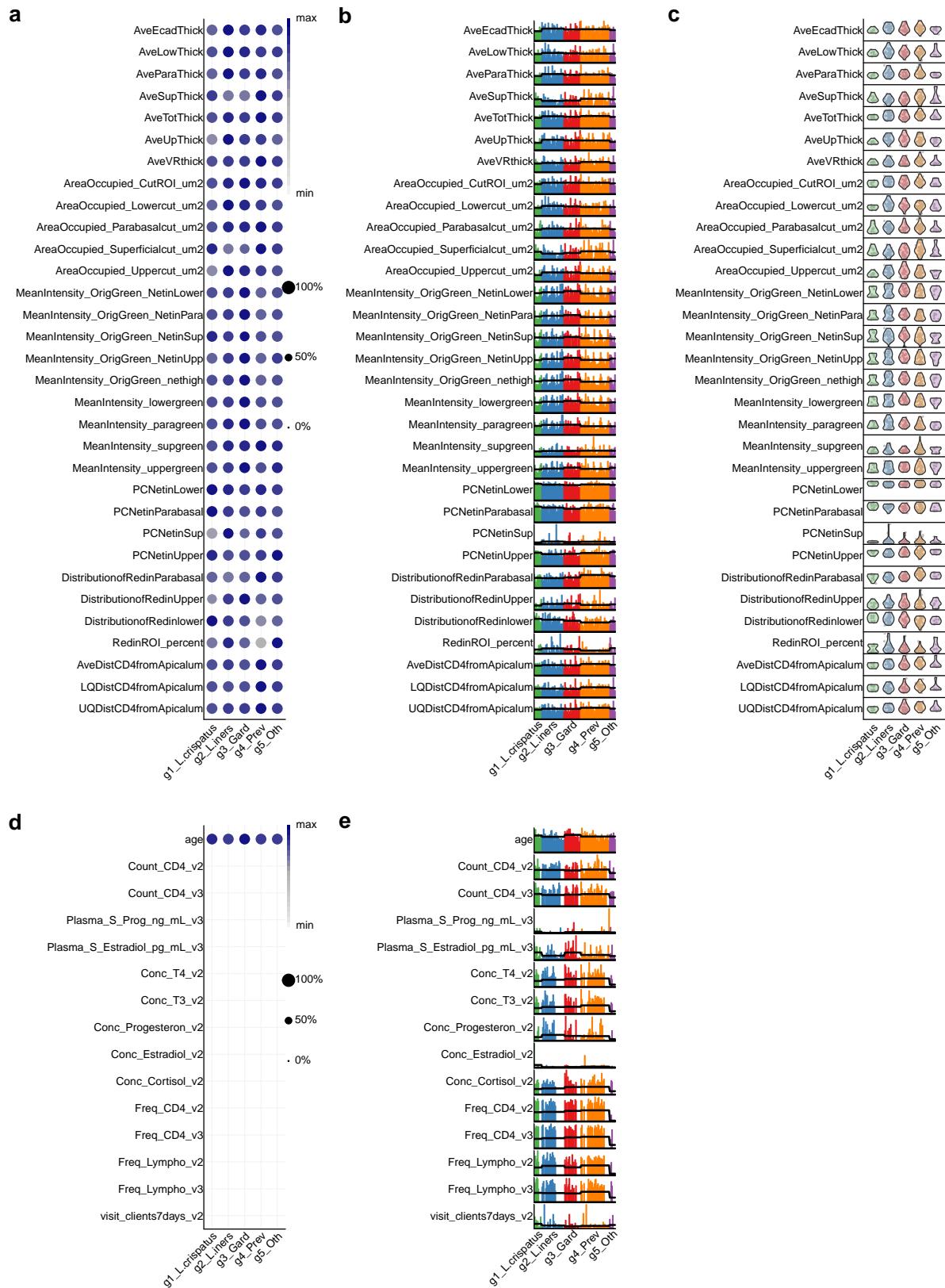


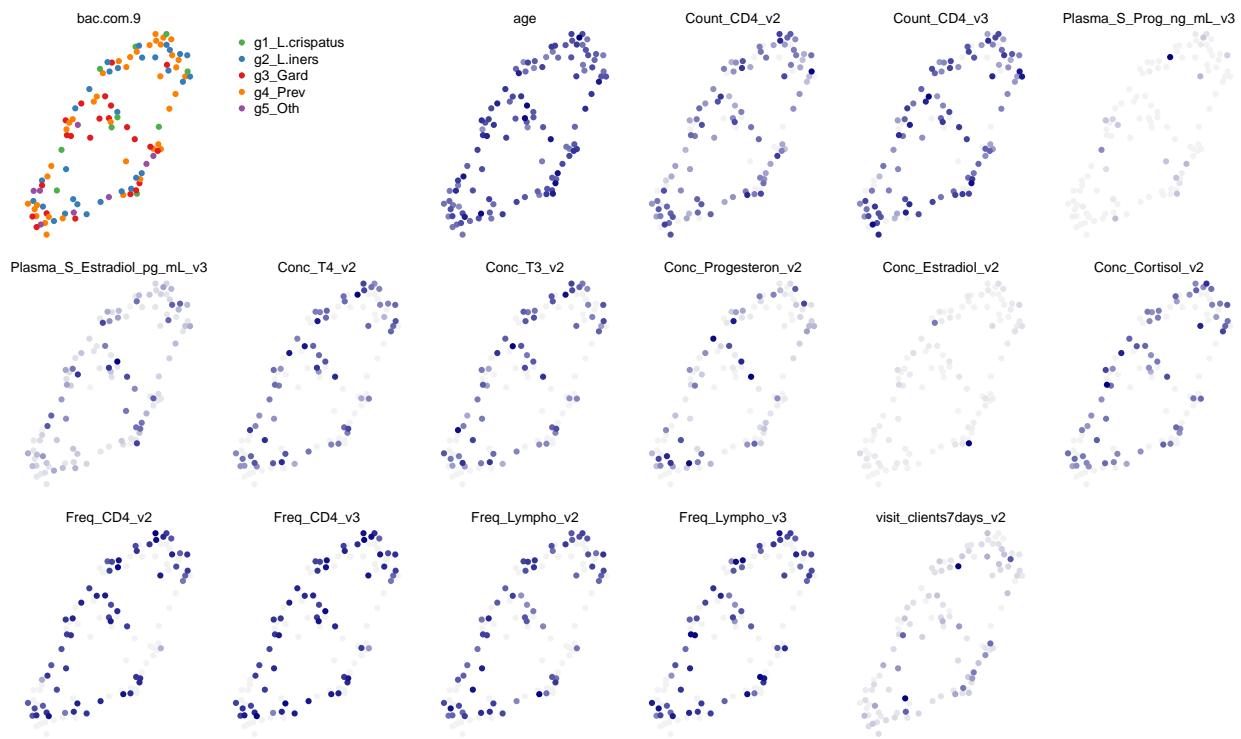
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197 **9.11 Figure S9**

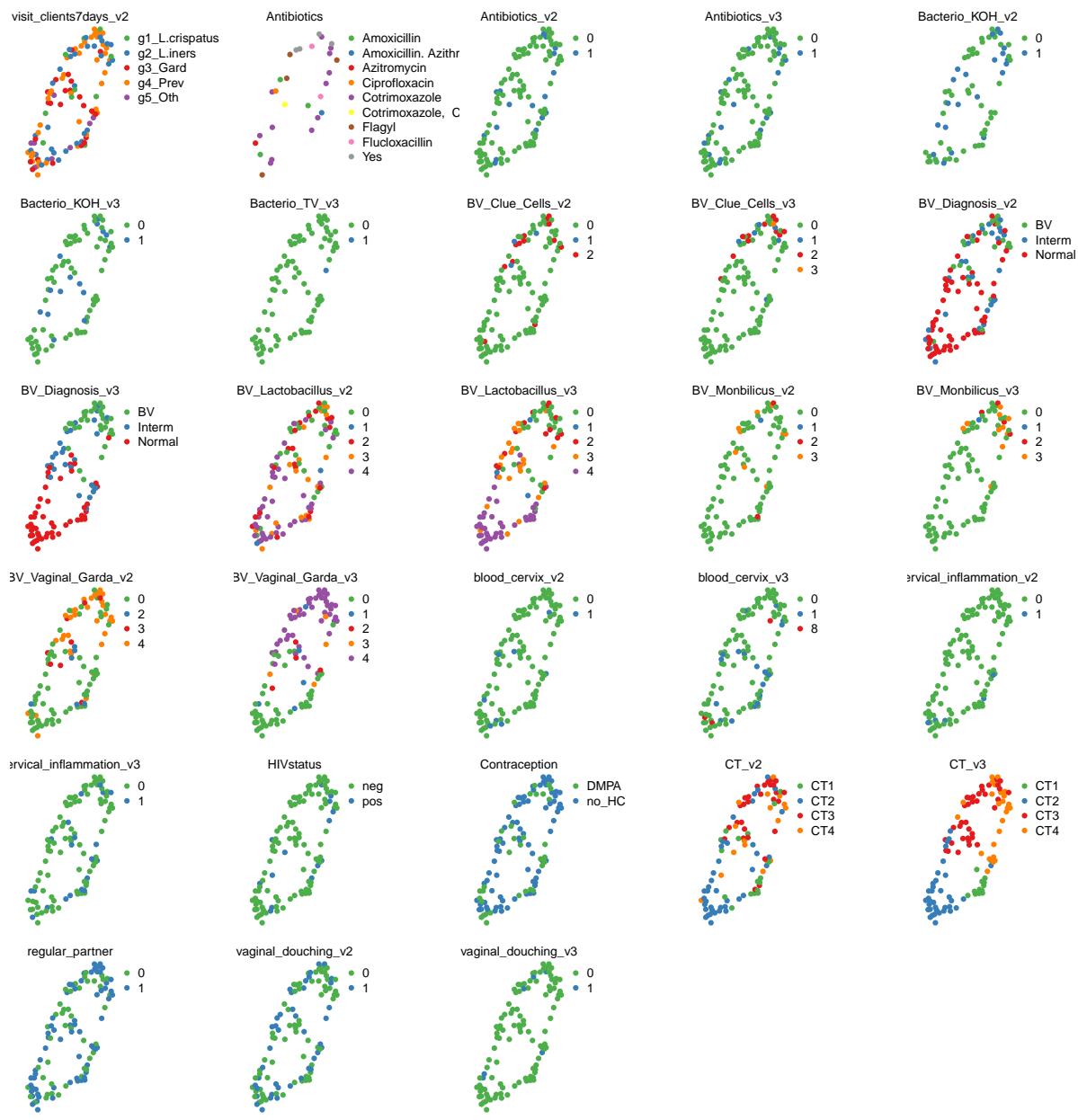
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199 9.12 Figure S10

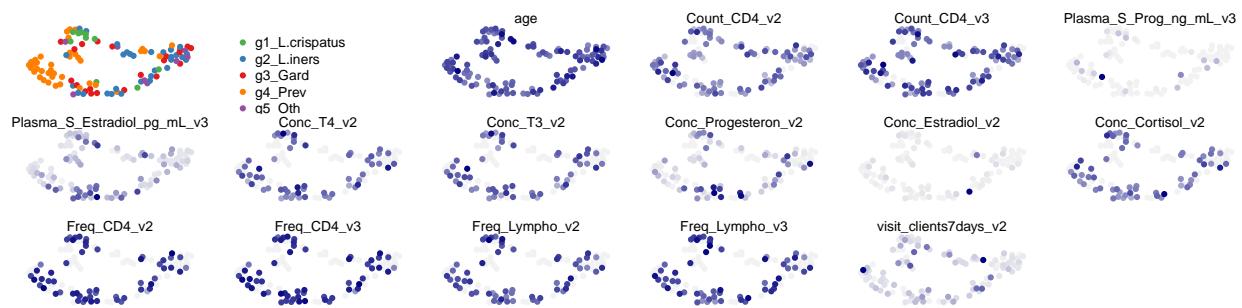


202 **9.13 Figure S11**

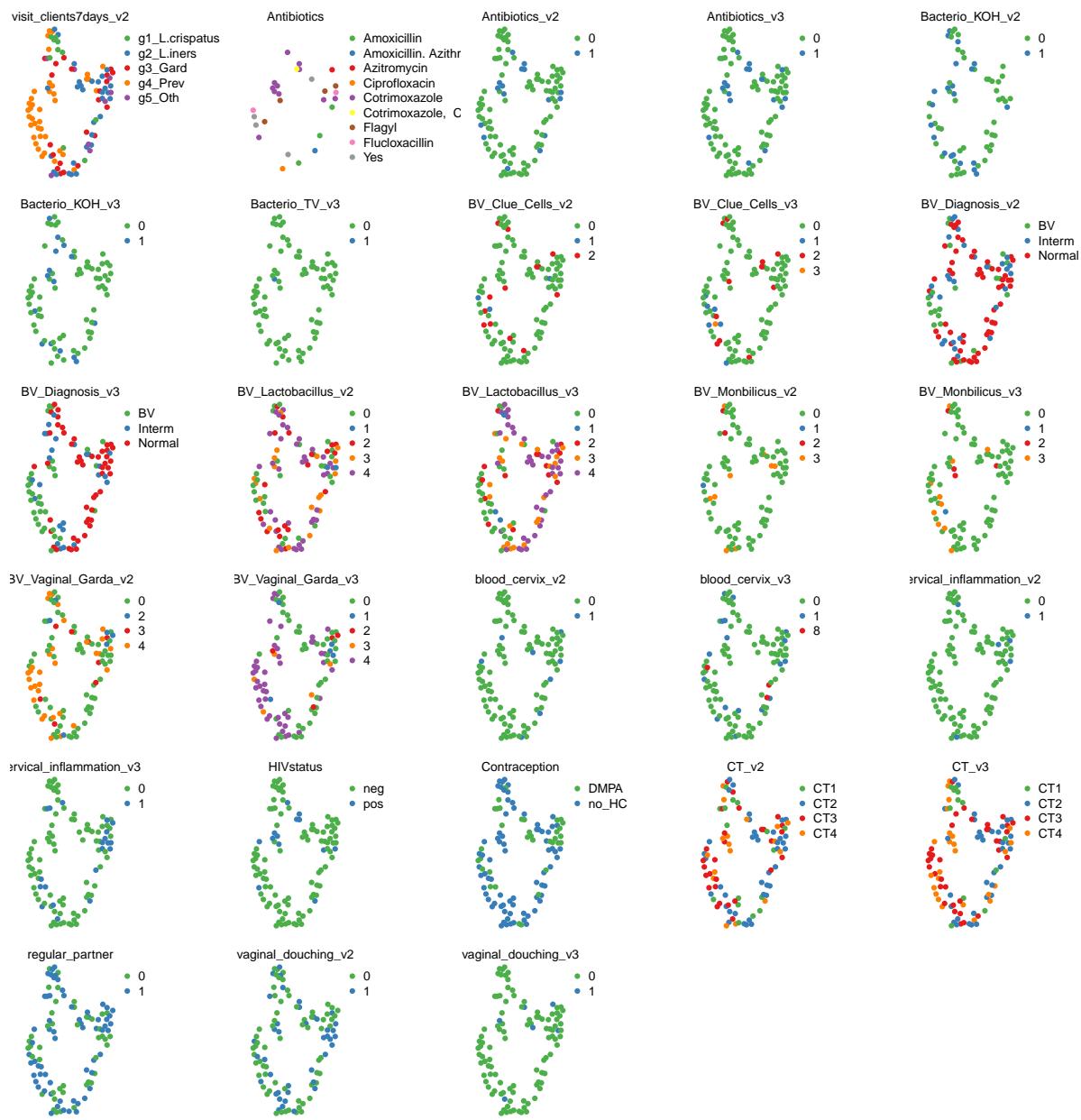
204 9.14 Figure S12



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206 **9.15 Figure S13**

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208 **9.16 Figure S14**

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210 **9.17 Figure S15**

211 **Supp. Figure 10. Rarefaction curves.** **A** Boston 1 sequencing run, **B** Sthlm sequencing run and **C** and
212 **D** shows Boston sequencing run 2 split in two plots showing the CVL visit 2 samples and the TISSUE
213 visit 3 samples respectively

₂₁₄ **10 TABLES (MAIN)**

₂₁₅ **10.1 Table 1**

²¹⁶ **10.2 Table 2**

²¹⁷ **10.3 Table 3**

²¹⁸ **11 TABLES (SUPPL)**

²¹⁹ **11.1 Table S1**

220 **11.2 Table S2**

221 **11.3 Table S3**