|  |  |  |
| --- | --- | --- |
| **AUTHOR** | **CHANGE** | **ACTION** |
| Lindsey Edwards | Wording | Done |
| Mathieu Almeida | 1. Not necessary here if you provide the associated BioProject ID in the data availability section. If the BioProject is not already created you can create one without giving access to the samples until paper release.  2. I think this will raise a lot of question at this stage as it is a little more complex than rarefying to 10M reads. You should probably refer to the method section instead.  3. does this mean that the micro-organisms dominant in westernized countries are dominant in all human microbiota ? Or that the dominant micro-organisms in westernized country produce antimicrobial peptides and homoserine lactone that potentially explain their dominance ?  4. Really ? I remember an old figure clearly showing association between F. nucleatum and CRC. Do you mean that F. nucleatum is not always associated with CRC? Maybe I am wrong sorry | 1. Removed all mentions of the wellness and integrated into the main number of samples. Might need to get a BioProject ID in time.  2. Agreed, removed.  3. Removed that sentence and replaced with the amr functions that are enriched between western/non-western countries  4. Clarified that ES was able to predict Fuso but RF was not |
| Emmanuelle Le Chatelier | Sample number | Changed to 5708 on lines 38, 89, 119, 880 |
| Gomez Cabrero Lopez, David | 1. Add SHAP full name  2. Maybe this is a bit picky: monocle is for setting trajectories, while what is shown in the Fig 1E is the projection. In the original monocle they used ICA (independent component analysis); maybe that is enough. | 1. Done  2. I have not seen the phrase ‘projection’ in other studies that use monacle, they just refer to the analysis as ‘monocle analysis’ or ‘monocle generated plots’ https://www.researchgate.net/publication/341077236\_Single-cell\_resolution\_analysis\_of\_the\_human\_pancreatic\_ductal\_progenitor\_cell\_niche/figures?lo=1 |
| Cheng Zhang | Sample number | See Emmanuelle |
| Jens B Nielsen | Grammar | Done |
| Florian Plaza-Onate |  |  |
| Neelu Begum |  |  |
| Ceri Proffitt |  |  |
| Dorinês Simões Rosário |  |  |
| Stefania Vaga |  |  |
| junseok park |  |  |
| Kalle von Feilitzen |  |  |
| Vincent Lombard |  |  |
| Bernard Henrissat | Reference change and CAZYME addition to regional enrichment | Made those changes |
| Fredric Johansson |  |  |
| Azadeh Harzandi |  |  |
| Franck Gauthier |  |  |
| Doheon Lee |  |  |
| Debbie Shawcross |  |  |
| Gordon Proctor | Figure legend change | Done |
| Lars Engstrand |  |  |
| Adil Mardinoglu | Wording change | Done |
| David Moyes | Sorted | sorted |
| Claire Steves |  |  |
| Mathias Uhlen |  |  |
| Dusco ehrlich | In which cluster? If in patho, it may be useful for the host – perhaps comment. AUC of 0.68 is not viewed as high ptecision | Clarified cluster section. Also we never mentioned that the precision was high, only that it was relatively consistent across cohorts. |