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Ramirez, KS and Knight, CG and de Hollander, M and Brearley, Francis and Constantinides, B and Cotton, A and Creer, S and Crowther, TW and Davison, J and Delgado-Baquerizo, M and Dorrepaal, E and Elliott, DR and Fox, G and Griffiths, RI and Hale, C and Hartman, K and Houlden, A and Jones, DL and Krab, EJ and Maestre, FT and McGuire, KL and Monteux, S and Orr, CH and van der Putten, WH and Roberts, IS and Robinson, DA and Rocca, JD and Rowntree, J and Schlaeppi, K and Shepherd, M and Singh, BK and Straathof, AL and Bhatnagar, JM and Thion, C and van der Heijden, MGA and de Vries, FT (2017) Detecting macroecological patterns in bacterial communities across independent studies of global soils. *Nature Microbiology*, 3. pp. 189-196. ISSN 2058-5276

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Supplementary Information Guide

Detecting macroecological patterns in bacterial communities across independent studies of global soils

1. Supplementary Tables and Figures (Ramirez_etal_SupplementaryInfo.docx) (790KB)
2. Summary Datasets: Description of all datasets used - summary_datsets.csv (475KB)
3. Figure generation code: R code to generate figures – Ramirez_etal_final.R (12KB)
4. Figure generation data: Data used to generate figures – Ramirez_etal_data.csv (2MB)
5. ‘Sequence-matched’ sequence merging (De Hollander 2016): Script to combine subset of datasets using sequence data - <https://gitlab.bioinf.nioo.knaw.nl/amplicon-metagenomics/meta-16S>
6. Name-Based merged OTU table: (Rameriz_etal_NameMatched.csv.zip) (6.7MB)
7. Sequence-Based merged OTU table: (Rameriz_etal_SeqMatched.csv.zip) (12MB)