The raw data for the accepted publication:

Wagg, C., Schlaeppi, K., Banerjee, S., Kuramae, E.E. & van der Heijden, G.G.A. Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. *Nature Communications* (manuscript number NCOMMS-19-08572A, Accepted August 2019).

The file “Wagg\_NatComm2019\_EcpDesgn\_EcosysFunct.csv” contains the experimental design and ecosystem function data. Columns are:

ET: EcoTube number (experimental unit ID)

Block: Experimental block in greenhouse

Treatment: soil diversity sieving treatment where I = sterile, II = 0.01mm, III = 0.025mm, IV = 0.05mm, V = 0.25mm, and VI = 5mm

Decom: The % decomposition of leaf litter

N2O: N2O emission from soil

grNt: Total N in grasses

herbNt: Total Nitrogen in herbs

legNt: Total Nitrogen in legumes

grPt: Total Phosphorous in grasses

herbPt: Total Phosphorous in herbs

legPt: Total Phosphorous in legumes

Pleach: Total P leached per 50 mL

Nleach: Total N leached per 50 mL

aveMF: Averaged Multifunctionality (z-score average of all above response data)

pcaMF: Multivariate Multifunctionality (summed weighted PCA scores using all above response data)

The file “Bacterial\_OTU\_data.csv” contains the number of sequence reads (16S) for each bacterial OTU in each of the samples (EcoTubes = ET).

The file “Bacterial\_OTU\_ID.csv” contains the taxonomy assignment for each bacterial OTU.

The file “Fungal\_OTU\_data.csv” contains the number of sequence reads (ITS) for each fungal OTU in each of the samples (EcoTubes = ET).

The file “Fungal\_OTU\_ID.csv” contains the taxonomy assignment for each fungal OTU.