

## SUPPLEMENTARY INFORMATION

**Shotgun metagenomics reveals distinct functional diversity and metabolic capabilities between 12 000 year old permafrost and active layers on *Muot da Barba Peider* (Swiss Alps)**

### Authors

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## Supplementary figures legends

**Fig. S1.** Geographic location of *Muot da Barba Peider* with an aerial view of the summit (a), and schematic representation of the soil sample collection (b). The blue fill dot represents the MBP mountain. The aerial photography of MBP was provided by Dr. Marcia Phillips. Pictures overlapping the aerial photography of MBP show the north-facing and south-facing sampling locations at the summit, accompanied with a close visualization of the topsoils. The solid line in (b) represents the permafrost table at a depth of 150 cm b.g.s. N: north-facing, S: south-facing, 10: at a depth of 10 cm, 160: at a depth of 160 cm.

**Fig. S2.** Functional structure of the different soil habitats for the genes assigned to functions. PCoAs computed on Bray-Curtis dissimilarities based on the abundance of selected genes for which the sum of the reads over all soil samples was  $\geq 10$ . N: north-facing, S: south-facing, 10: at a depth of 10 cm, 160: at a depth of 160 cm.

**Fig. S3.** Shannon's diversity of COGs grouped into functional categories for the different soil habitats. Shannon's diversity indexes were calculated on read abundances normalized to transcripts per million (t.p.m.). The represented genes are those for which the sum of the reads over all soil samples was  $\geq 10$ . Mean  $\pm$  SD (n=3). N: north-facing, S: south-facing, 10: at a depth of 10 cm, 160: at a depth of 160 cm.

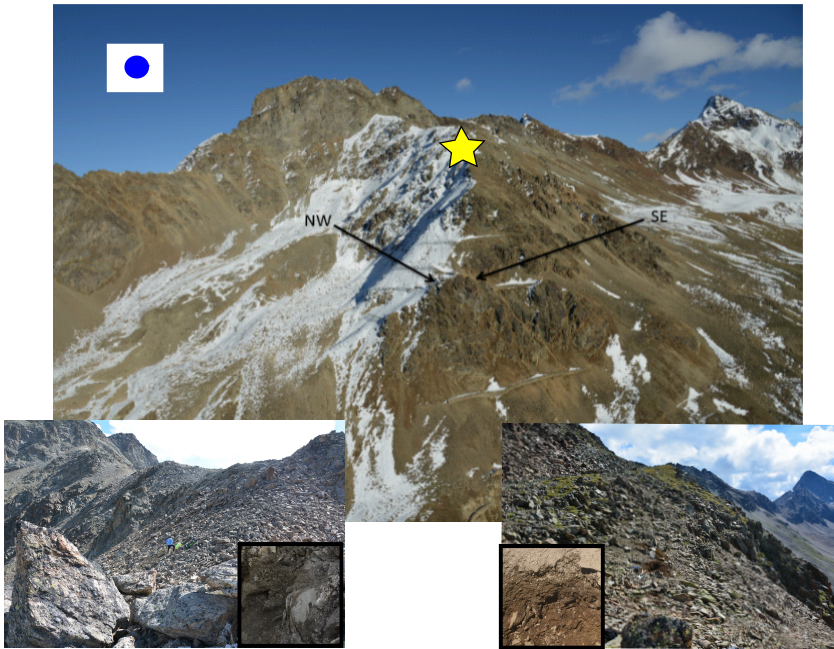
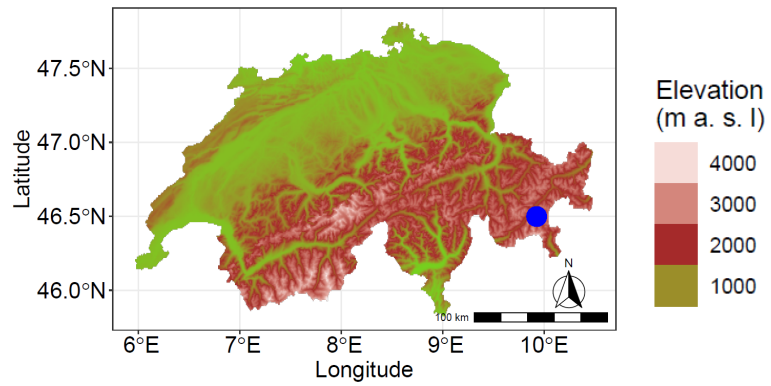
**Fig. S4.** Shannon's diversity of CAZys classes for the different soil habitats. Shannon's diversity indexes were calculated on read abundances normalized to transcripts per million (t.p.m.). The represented genes are those for which the sum of the reads over all soil samples was  $\geq 10$ . Mean  $\pm$  SD (n=3). N: north-facing, S: south-facing, 10: at a depth of 10 cm, 160: at a depth of 160 cm.

**Fig. S5.** Shannon's diversity of N-cycling processes for the different soil habitats. Shannon's diversity indexes were calculated on read abundances normalized to transcripts per million (t.p.m.). The represented genes are those for which the sum of the reads over all soil samples was  $\geq 10$ . ANR: assimilatory nitrogen reduction, DNR: dissimilatory nitrogen reduction. Mean  $\pm$  SD (n=3). N: north-facing, S: south-facing, 10: at a depth of 10 cm, 160: at a depth of 160 cm.

**Fig. S6.** Prokaryotic and eukaryotic composition of the different soil habitats. Taxonomic classification was performed on the contigs larger than 1500 bps, in which SSU regions (> 300 bp) could be identified. Contigs were annotated against the SILVA database. The represented bacterial taxa are those for which the depth of coverage was  $\geq 2\%$  of the total depth of coverage over all bacterial contigs assigned to taxa beyond the kingdom level. Taxa were classified to the deepest taxonomic level possible. N: north-facing, S: south-facing, 10: at a depth of 10 cm, 160: at a depth of 160 cm.

Fig. S1

(a)



(b)

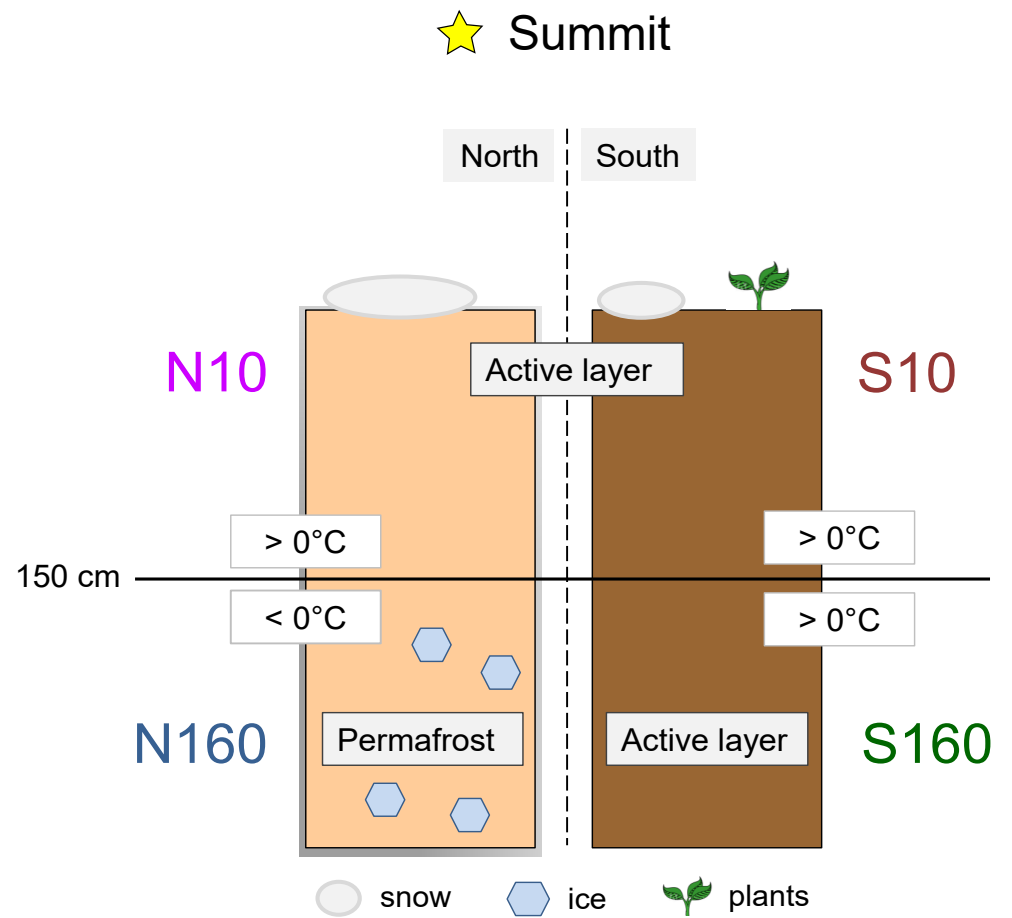


Fig. S2

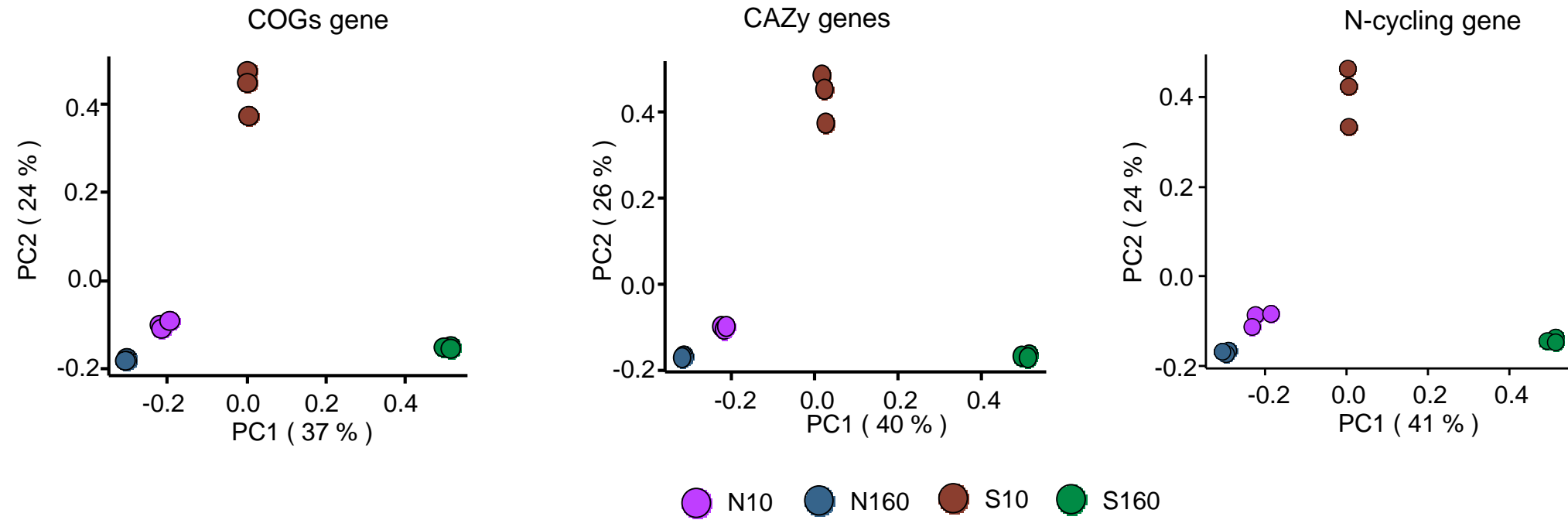


Fig. S3

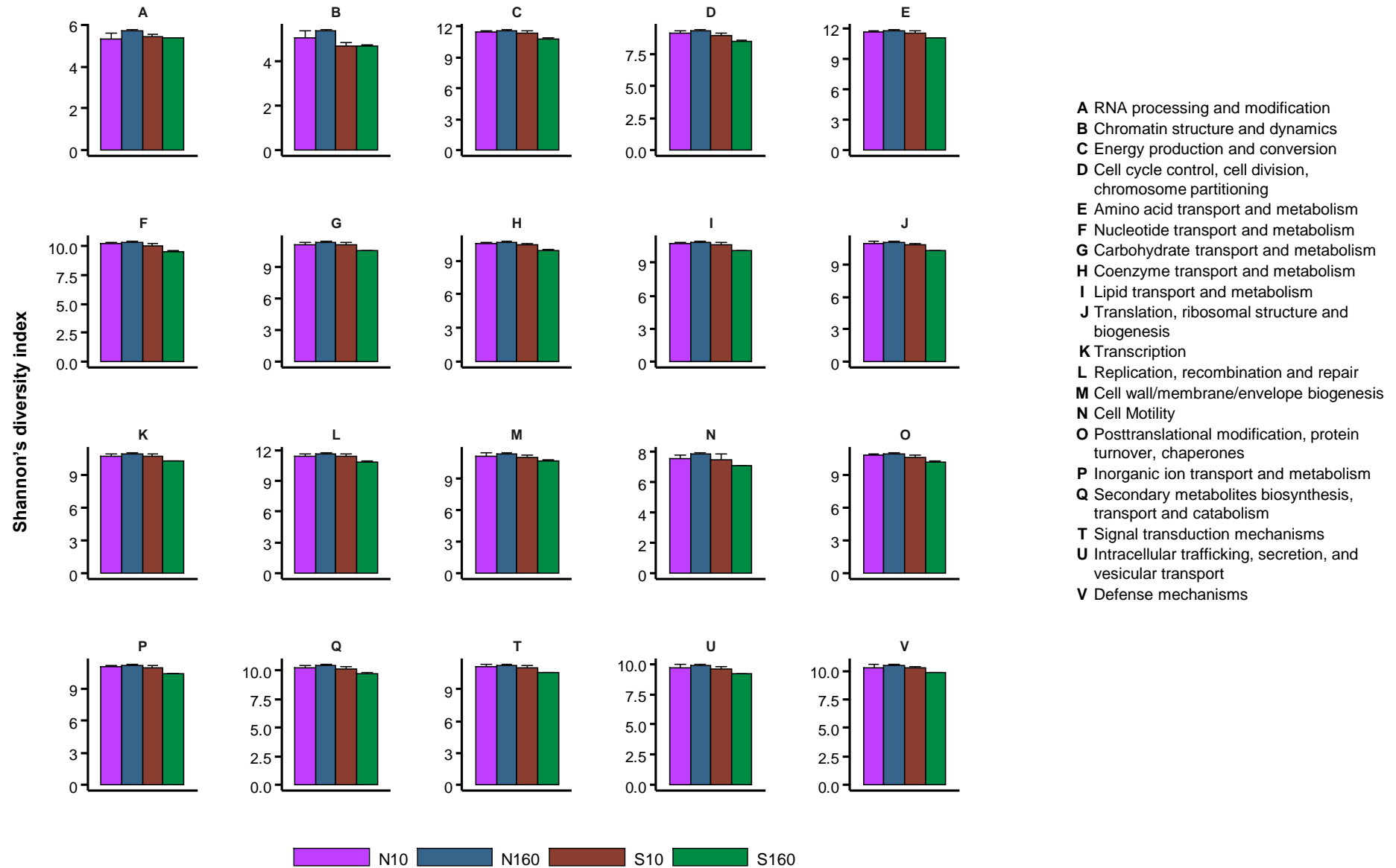


Fig. S4

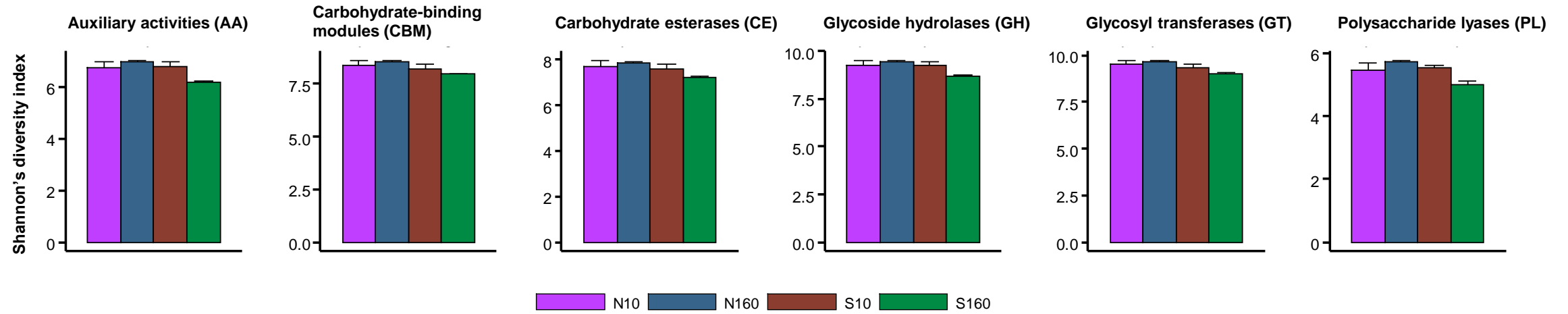


Fig. S5

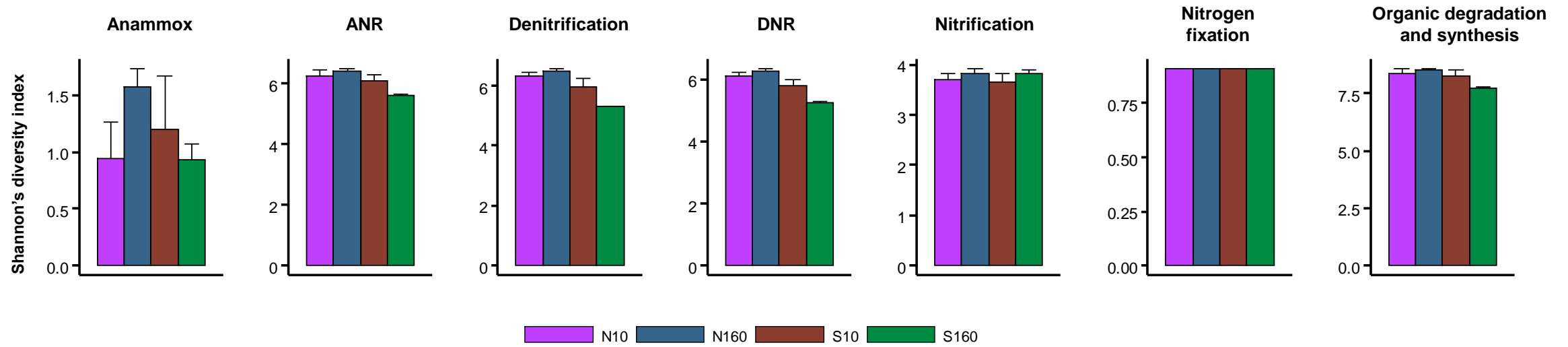
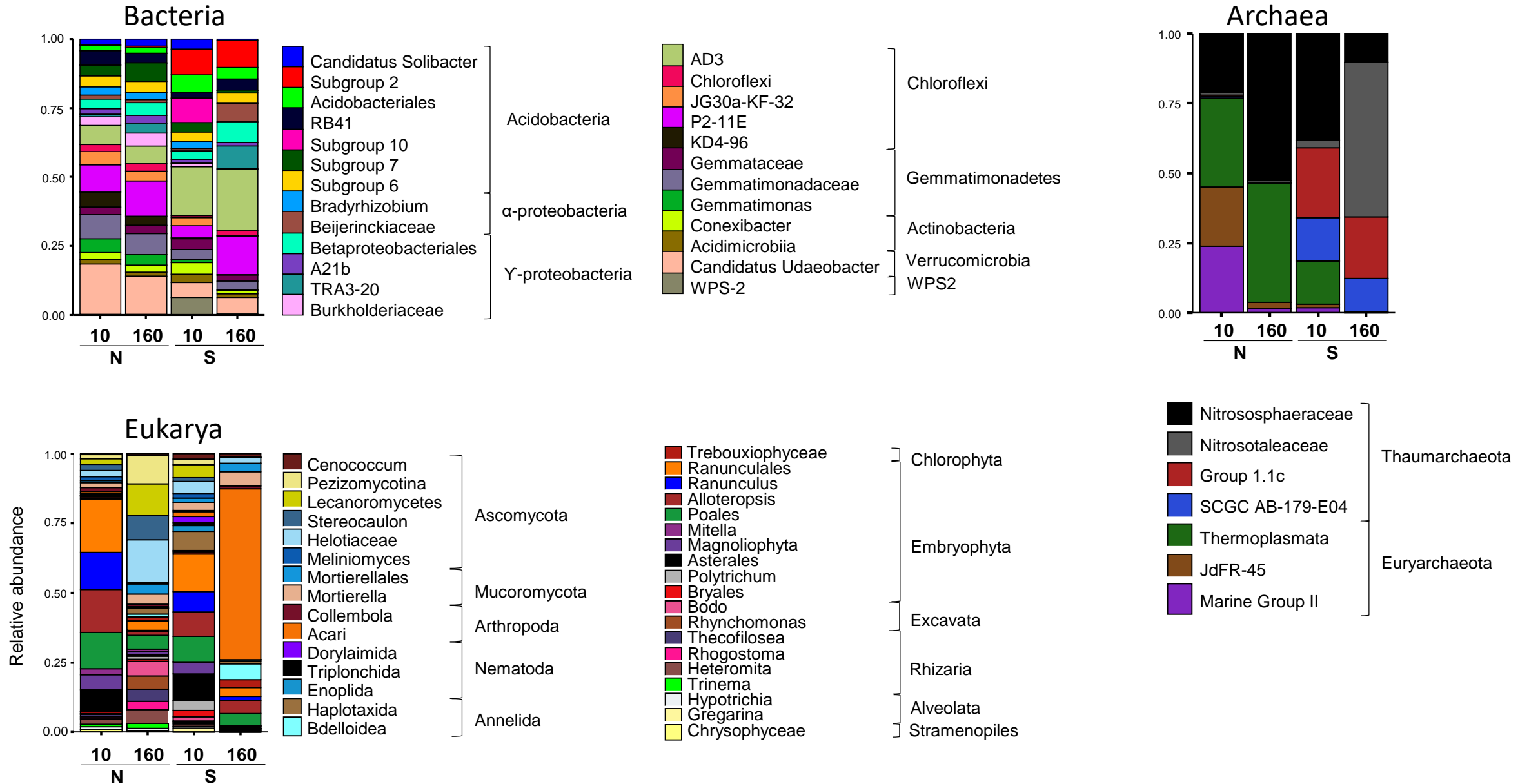


Fig. S6





Supplementary tables (together with its corresponding legend) are provided as single **Sheets** in an unique **xlsx** file.