Characterization of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions

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Supplementary information

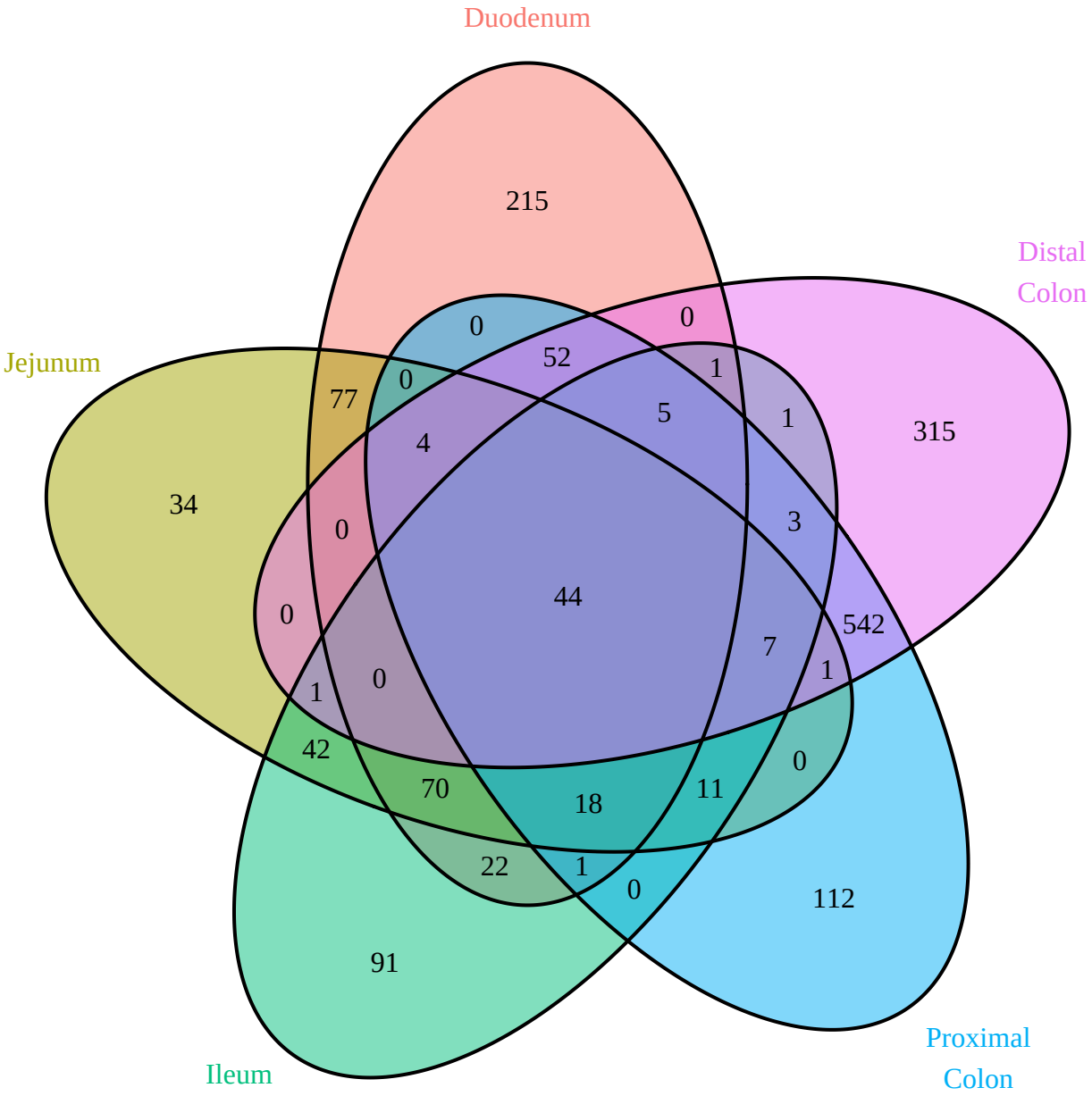
Supplementary Tables

Supplementary Table S1. This table contains the results of the presence/absence analysis at the genus level performed with metagenomeSeq[24]. Each sheet represents one of the four consecutive correlations between the five sections for the 13 pigs. The colour shows which genus is uniquely present in that section when comparing the two sections: red, duodenum; yellow, jejunum; green, ileum; blue, proximal colon and purple, distal colon.

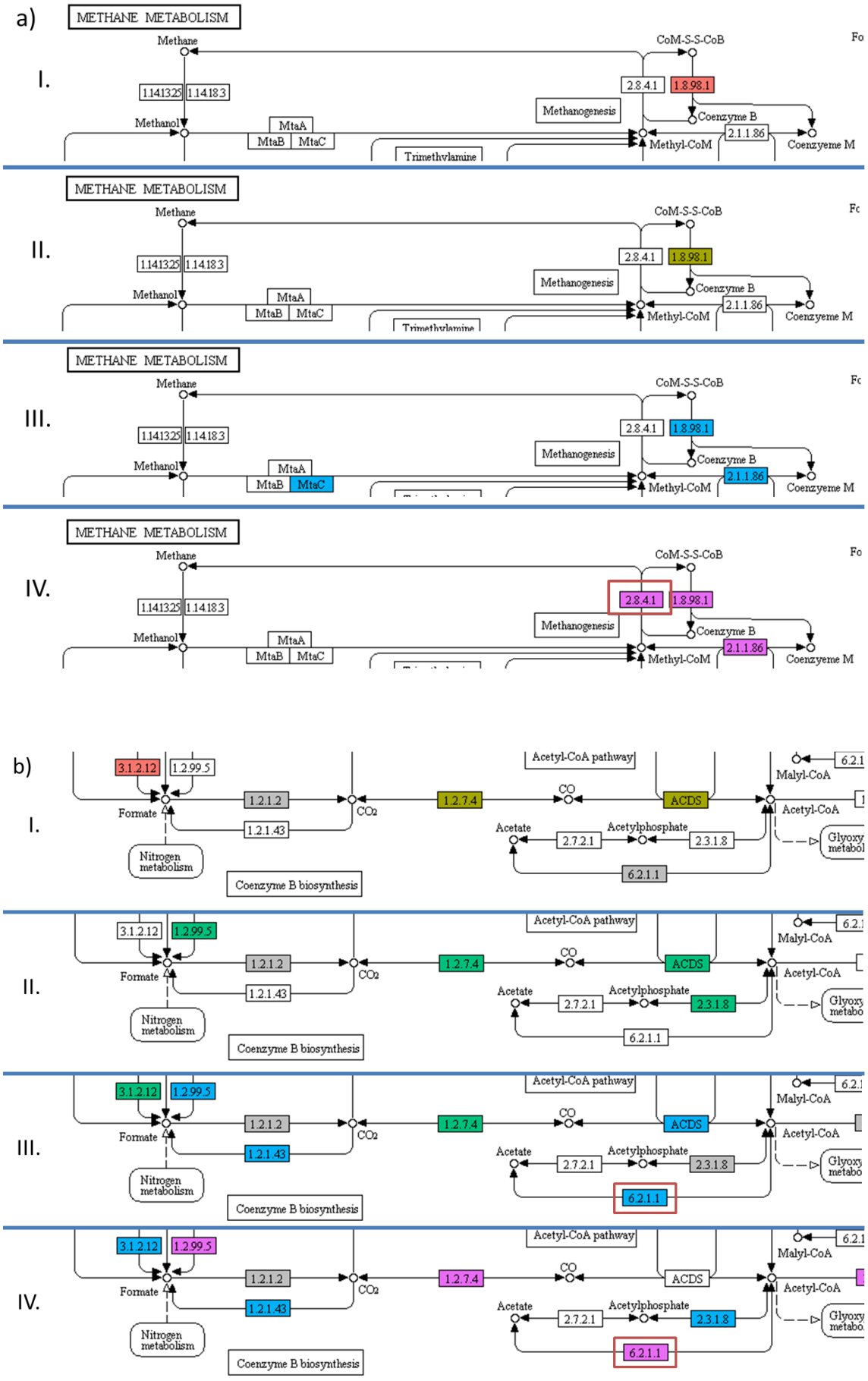
Supplementary Table S2. This table contains the results of the differential abundance analysis at the genus level performed with metagenomeSeq[24]. Each sheet represents one of the four consecutive correlations between the five sections for the 13 pigs. The colour shows which genus is more abundant in that section when comparing the two sections: red, duodenum; yellow, jejunum; green, ileum; blue, proximal colon and, purple, distal colon.

Supplementary Table S3. This table contains the results of the differential abundance analysis performed with DESeq2[27] for the KEGG[26] orthologies (KOs) predicted with PICRUSt[25] at the pathway level. Each sheet represents one of the four consecutive correlations between the five sections for the 13 pigs. The colour shows which pathway is more abundant in that section when comparing the two sections: red, duodenum; yellow, jejunum; green, ileum; blue, proximal colon and purple, distal colon.

Supplementary Figures



Supplementary Figure S1. Five-part Venn diagram performed for the OTUs shared among sections when combining the datasets from all subjects: duodenum (red), jejunum (yellow), ileum (green), proximal colon (blue), and distal colon (purple).


a)
I.
II.
III.
IV.
METHANE METABOLISM
Methane
Methanol
1.14.13.25
1.14.18.3
MtaA
MtaB
MtaC
Trimethylamine
CoM-S-S-CoB
2.8.4.1
1.8.98.1
Methanogenesis
Coenzyme B
2.1.1.86
Methyl-CoM
Coenzyme M
b)
I.
II.
III.
IV.
3.1.2.12
1.2.99.5
Formate
1.2.1.2
1.2.1.43
CO2
Nitrogen metabolism
Coenzyme B biosynthesis
1.2.7.4
CO
Acetyl-CoA pathway
ACDS
Acetyl-CoA
Malyl-CoA
Acetate
2.7.2.1
Acetylphosphate
2.3.1.8
6.2.1.1

Supplementary Figure S2. DESeq2[27] results below a padj≤0.01 cut-off for the four comparisons between each pair of consecutive sections of the KEGG[26] orthologies (KOs) predicted by PICRUSt[25] represented over the KEGG[26] methane metabolism pathway (map00680): **I.** duodenum vs jejunum; **II.** jejunum vs ileum; **III.** ileum vs proximal colon; **IV.** proximal colon vs distal colon. The colour shows which KO was more abundant in that section when comparing the two sections: white, non-significant; red, duodenum; yellow, jejunum; green, ileum; blue, proximal colon and purple, distal colon. Ambiguous KOs were coloured grey. For clarity of presentation, the methane metabolism pathway was divided into two parts: **a)** The red rectangle shows how the production of methane was more abundant in the distal colon than in the rest of the comparisons. **b)** The two red rectangles represent how the production of acetate was more abundant in the proximal colon than in the ileum and more abundant in the distal colon than in the proximal colon.