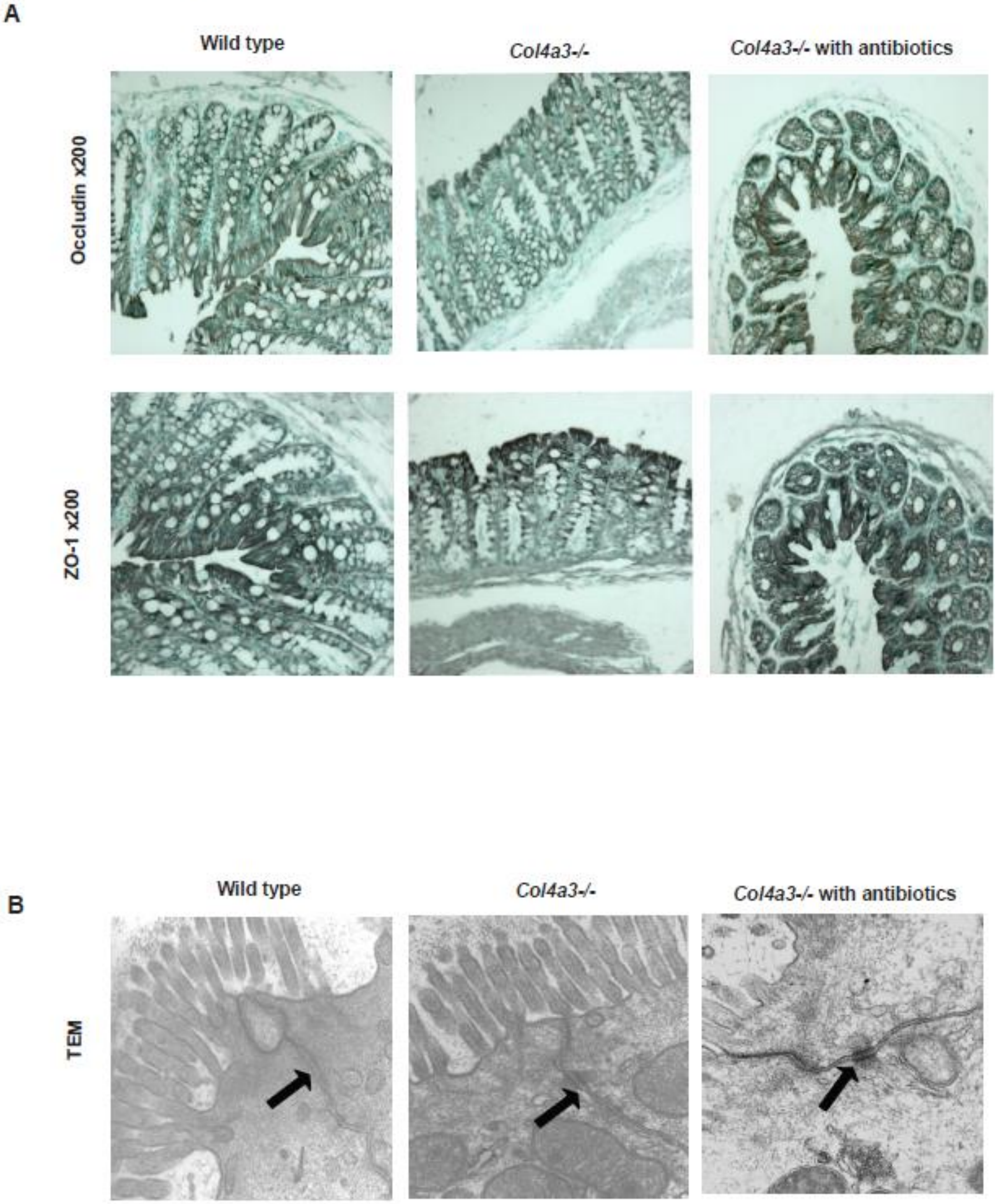
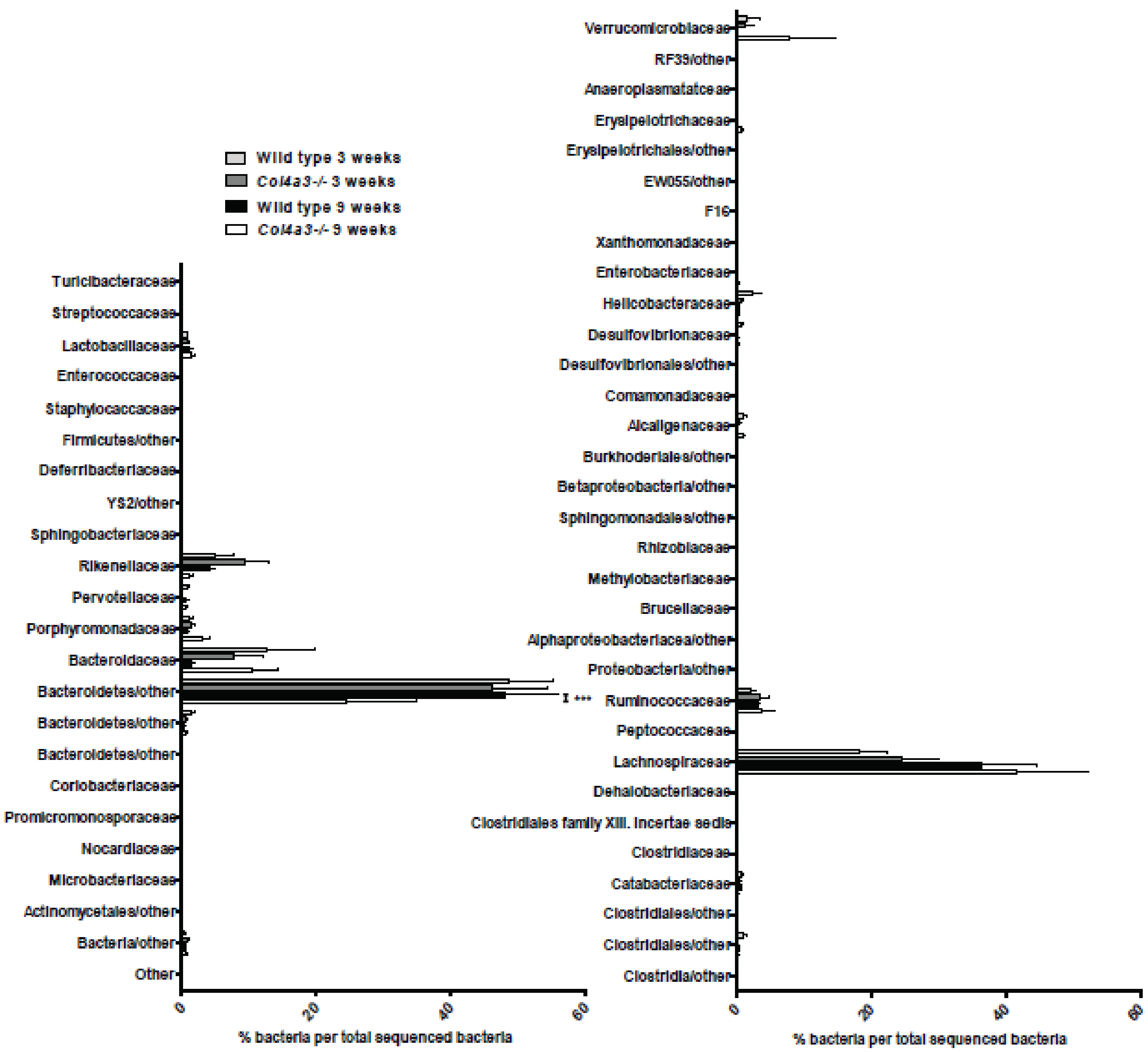
Supplementary figure 1



Supplementary figure 1. *Uremia and intestinal barrier function.* A/B: No alteration of the colon gut barrier in terms of changes in the tight junctions is depicted by Immunohistochemistry stainings for Occludin and ZO-1 (zona occludens protein 1) aswell as in transmission electron microscopy in wild-type, *Col4a3*-deficient or *Col4a3*-deficient mice treated with antibiotics. Colon tissue of 9-week-old mice did not show any correlates for barrier dysfunction in all tested groups. Results are illustrated by representative IHC images. Arrows mark regions of zonula occludens and/or desmosomes.

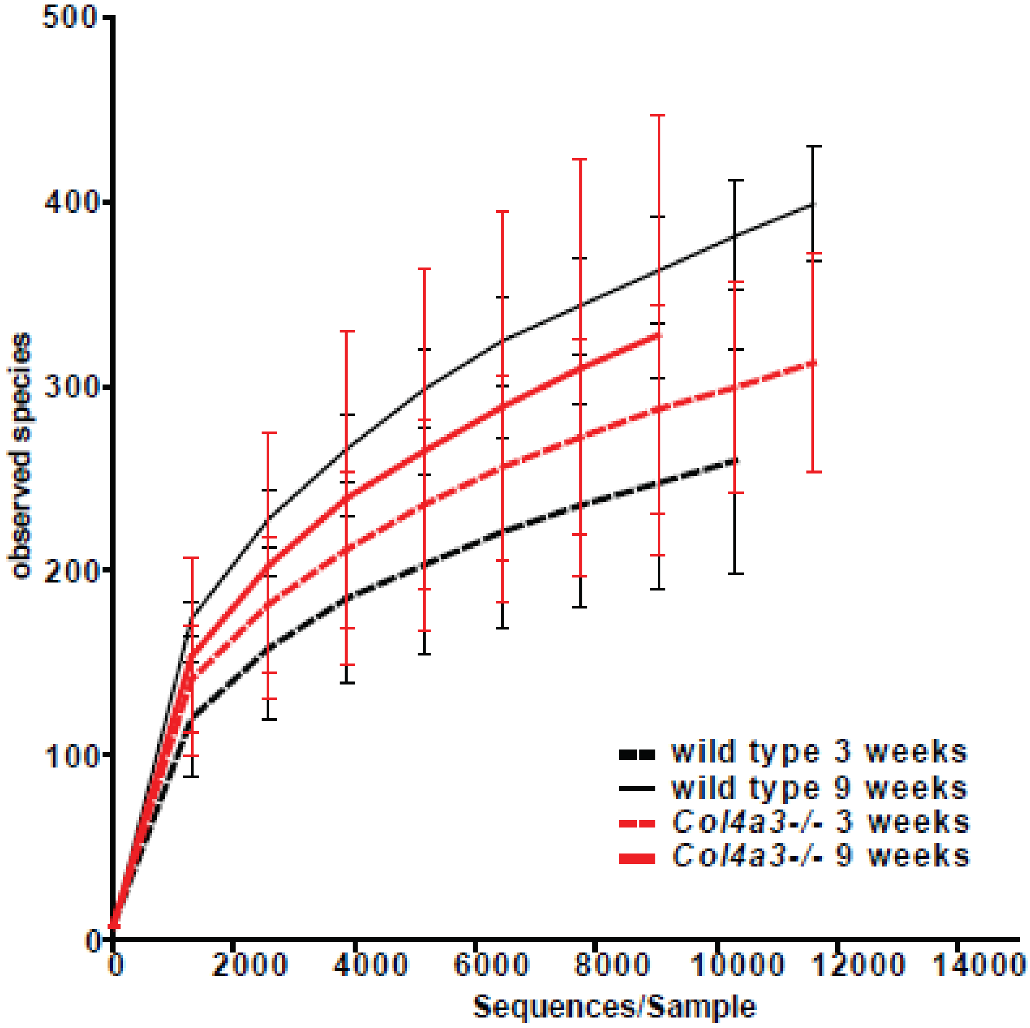
Supplementary figure 2



Supplementary figure 2. *Entire sequencing data of faeces bacteria in wild type and Col4a3-/- mice.* Alterations in the composition of the gut microbiota, which may be accounted for by aging, are detectable in 3 week-old vs. 9 week-old mice in both strains. Comparison of 9 week-old mice show significant changes in the order of Bacteroidales.

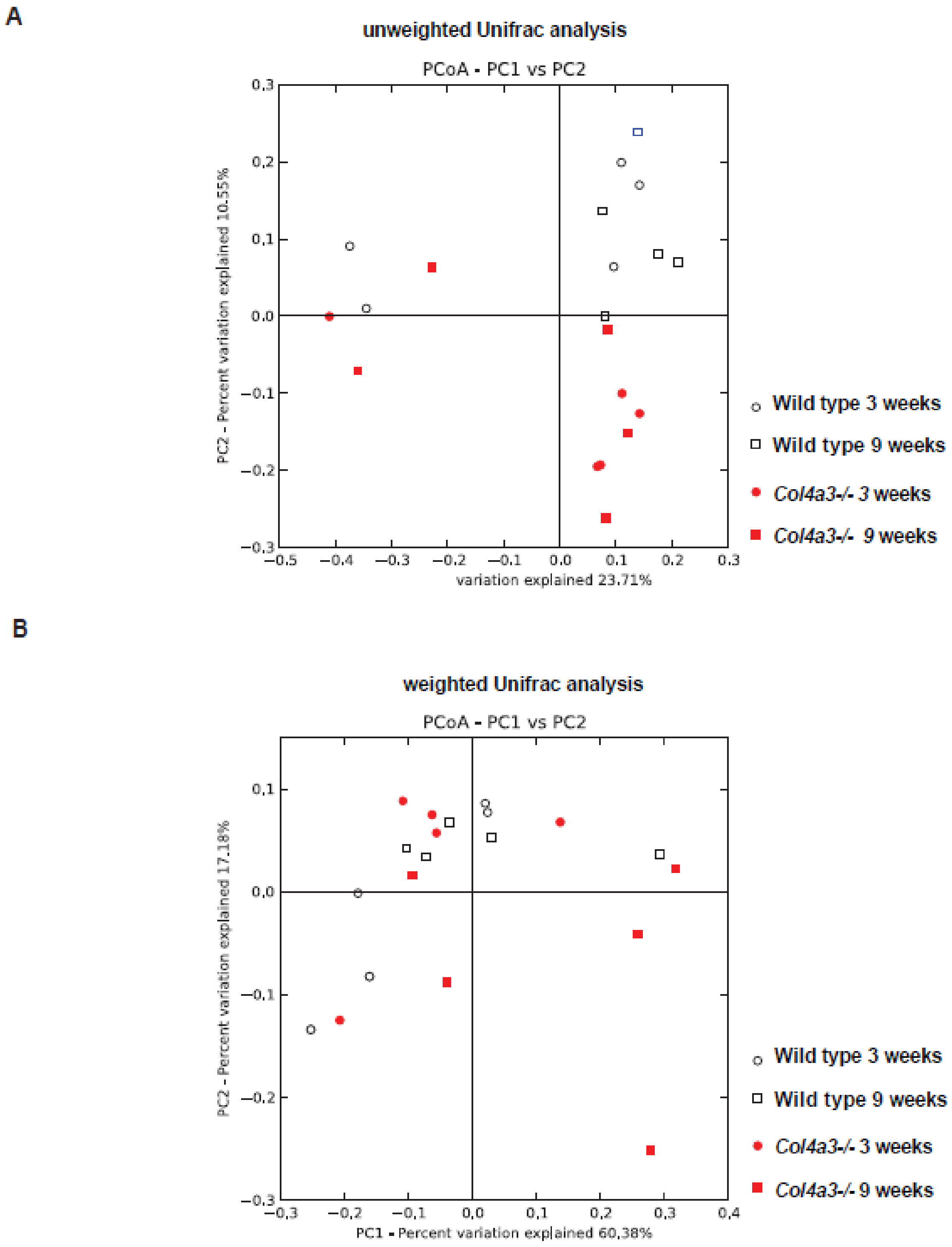
Data represent means±SEM of 5 mice in each group, ***p<0.001 *Col4a3-/-* versus wild type.

Supplementary figure 3



Supplementary figure 3. Alpha-diversity. Alpha diversity (no. of observed species) of fecal microbiota of the different groups of mice was determined.

Supplementary figure 4



Supplementary figure 4. Beta-diversity analysis based on UniFrac distance matrices. Unweighted (A) and weighted UniFrac distance matrices (B) were generated and served as inputs for clustering analyses using PcoA. Statistical significance of factors potentially contributing to compositional differences among microbiota samples was tested using PERMANOVA. P-values < 0.05 were considered significant. **(A)** Unweighted UniFrac distance matrix, PERMANOVA: p= 0.039. (Groups explaining cluster formation: Wild type 9 weeks vs *Col4a3-/-* 9 weeks; p= 0.022; Wild type 9 weeks vs *Col4a3-/-* 3 weeks; p= 0.014; all other groups: p>0.5, not significant) **(B)** Weighted UniFrac distance matrix, PERMANOVA: p>0.05, not significant.

Supplementary Table 1. Bacterial sequencing analysis from faeces of wild type and *Col4a3-/-* at the age of 3 and 9 weeks (calculated via QUIIME). Means are given in percentage terms ± SEM (n=5)

Taxon	Wild type 3 weeks	Col4a3-/- 3 weeks	Wild type 9 weeks	Col4a3-/- 9 weeks
Other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Bacteria/other	0.52±0.07	0.93±0.23	0.67±0.08	0.65±0.16
Actinomycetales/other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Microbacteriaceae	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Nocardiaceae	0.00±0.00	0.01±0.00	0.00±0.00	0.00±0.00
Promicromonosporaceae	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Coriobacteriaceae	0.04±0.02	0.09±0.03	0.12±0.01	0.09±0.05
Bacteroidetes/other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Bacteroidetes/other	1.57±0.60	0.72±0,35	0.46±0.31	0.58±0.35
Bacteroidetes/other	48.51±6.72	46.27±8.03	48.05±7.97	**24.57±10.46*****
Bacteroidaceae	12.81±6.93	7.79±4.27	1.45±0.72	10.65±3.72
Porphyromonadaceae	1.27±0.54	1.40±0.67	0.92±0.25	3.05±1.05
Pervotellaceae	0.99±0.27	0.07±0.07	0.74±0.60	0.61±0.47
Rikenellaceae	5.13±2,57	9.33±3.59	4.27±0.90	1.32±0.47
Sphingobacteriaceae	0.00±0.00	0.01±0.01	0.00±0.00	0.00±0.00
YS2/other	0.02±0.02	0.01±0.01	0.00±0.00	0.00±0.00
Deferribacteriaceae	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Firmicutes/other	0,00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Staphylocaccaceae	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Enterococcaceae	0.00±0.00	0.00±0.00	0.00±0.00	0.01±0.01
Lactobacillaceae	0.81±0.09	1.02±0.20	1.29±0.39	1.53±0.60
Streptococcaceae	0.00±0.00	0.00±0.00	0.01±0.00	0.01±0.01
Turicibacteraceae	0.00±0.00	0.00±0.00	0.03±0.02	0.00±0.00
Clostridia/other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Clostridiales/other	1.01±0.59	0.20±0.06	0.39±0.10	0.29±0.13

Taxon	Wild type 3 weeks	Col4a3-/- 3 weeks	Wild type 9 weeks	Col4a3-/- 9 weeks
Clostridiales/other	0.02±0.02	0.17±0.11	0.00±0.00	0.07±0.03
Catabacteriaceae	0.67±0.36	0.50±0.23	0.66±0.20	0.28±0.11
Clostridiaceae	0.00±0.00	0.00±0.00	0.00±0.00	0.08±0.06
Clostridiales family XIII. incertae sedis	0.01±0.00	0.00±0.00	0.01±0.01	0.00±0.00
Dehalobacteriaceae	0.07±0.00	0.07±0.02	0.10±0.03	0.06±0.03
Lachnospiraceae	18.21±4.28	24.64±5.48	36.52±8.18	41.53±10.77
Peptococcaceae	0.00±0.00	0.04±0.02	0.01±0.01	0.01±0.000
Ruminococcaceae	2.12±0.91	3.58±1.18	3.15±0.50	3.71±1.94
Proteobacteria/other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Alphaproteobacteria/other	0.07±0.06	0.04±0.04	0.00±0.00	0.09±0.07
Brucellaceae	0.00±0.00	0.01±0.00	0.00±0.00	0.00±0.00
Methylobacteriaceae	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Rhizobiaceae	0.00±0.00	0.01±0.00	0.01±0.01	0.00±0.00
Sphingomonadales/other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Betaproteobacteria/other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Burkhoderiales/other	0.02±0.01	0.02±0.01	0.00±0.00	0.01±0.00
Alcaligenaceae	1.09±0.49	0.45±0.32	0.09±0.03	0.94±0.42
Comamonadaceae	0.02±0.01	0.03±0.01	0.01±0.01	0.01±0.01
Desulfovibrionales/other	0.00±0.00	0.00±0.00	0.00±0.00	0.01±0.01
Desulfovibrionaceae	0.72±0.39	0.22±0.08	0.32±0.11	0.32±0.13
Helicobacteraceae	2.43±1.29	0.83±0.22	0.40±0.04	0.44±0.14
Enterobacteriaceae	0.04±0.03	0.02±0.02	0.00±0.00	0.31±0.23
Xanthomonadaceae	0.00±0.00	0.01±0.00	0.00±0.00	0.00±0.00
F16	0.01±0.01	0.10±0.04	0.11±0.05	0.01±0.01
EW055/other	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Erysipelotrichales/other	0.00±0.00	0.00±0.00	0.01±0.01	0.05±0.05
Erysipelotrichaceae	0.08±0.03	0.06±0.03	0.10±0.04	0.78±0.39
Anaeroplasmatatceae	0.00±0.00	0.00±0.00	0.04±0.02	0.04±0.03
RF39/other	0.00±0.00	0.00±0.00	0.01±0.01	0.00±0.00
Verrucomicrobiaceae	1.73±1.72	1.36±1.35	0.04±0.01	7.90±6.95

*** $p < 0.001$ wild type vs. *Col4a3-/-* (ANOVA, Bonferroni post-test)