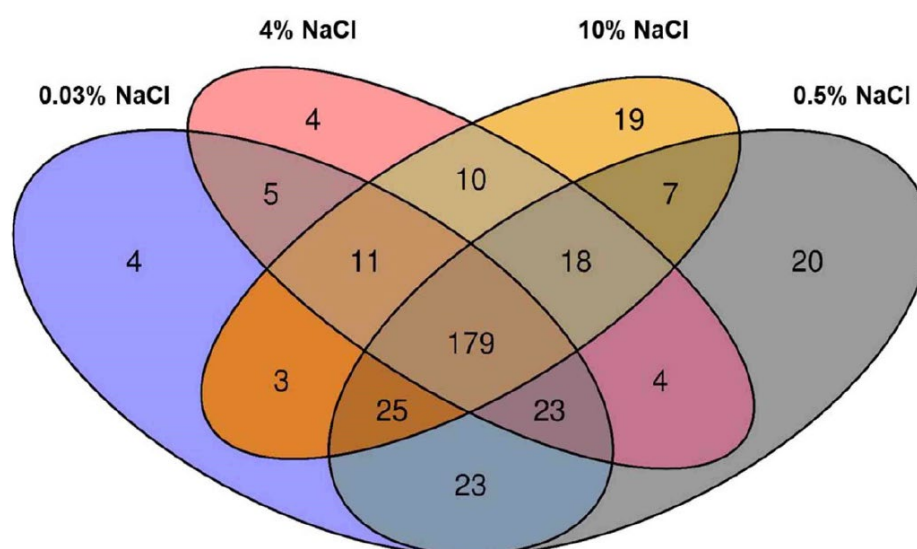
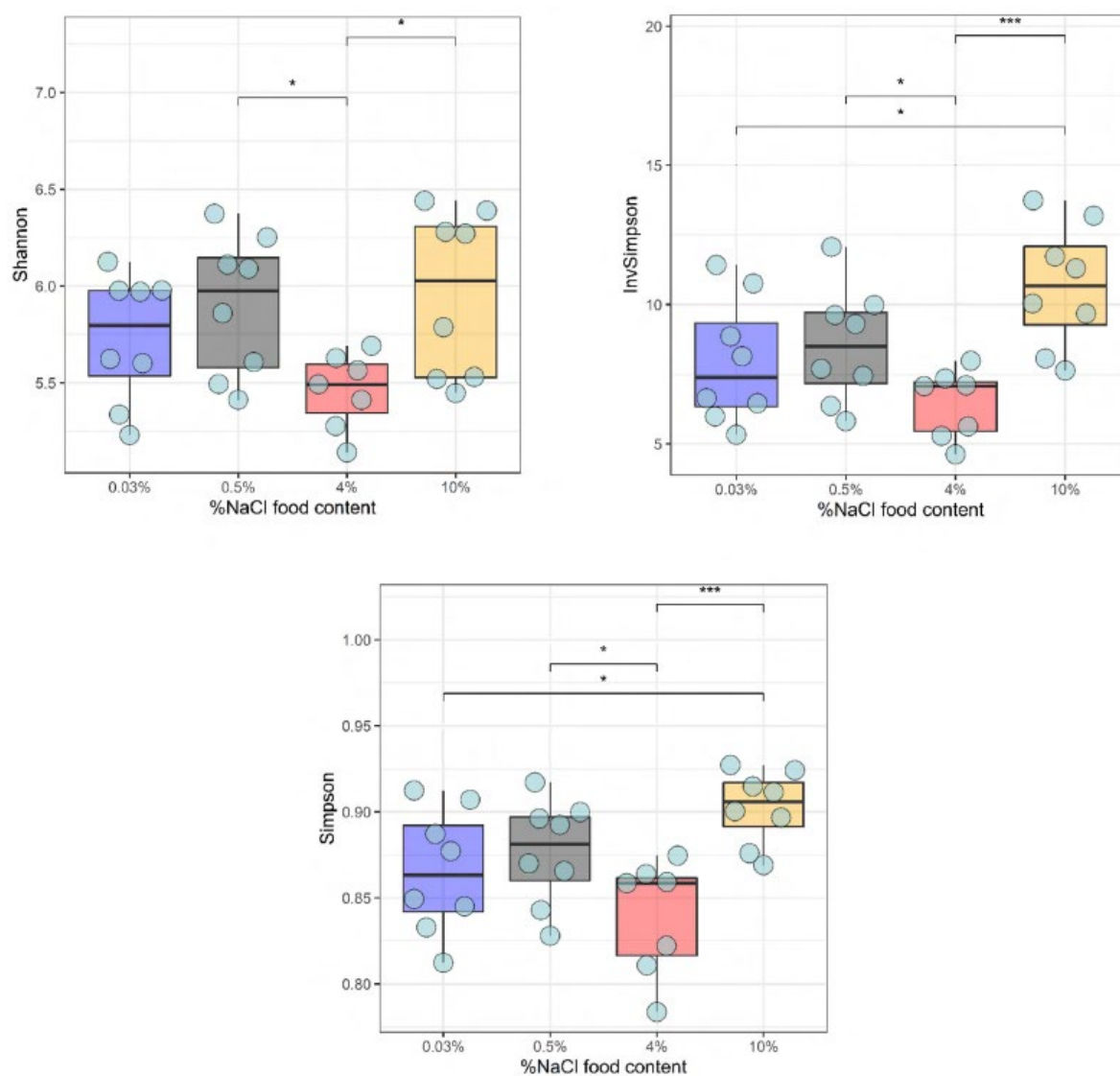


**Figure S1.** Rarefaction curves indicating the observed number of operational taxonomic units (OTUs) within a sample. Rarefaction curves of OTUs clustered and saturated at different levels across exposure groups and indicate the intra-sample diversity.

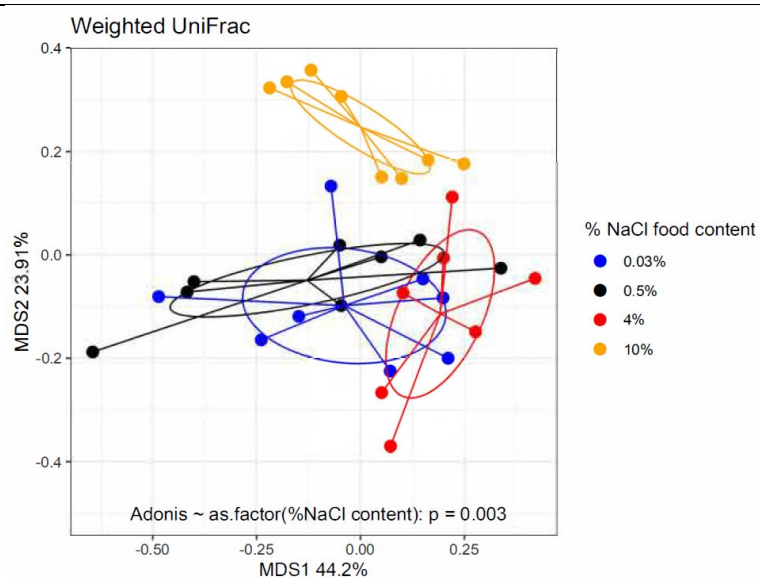


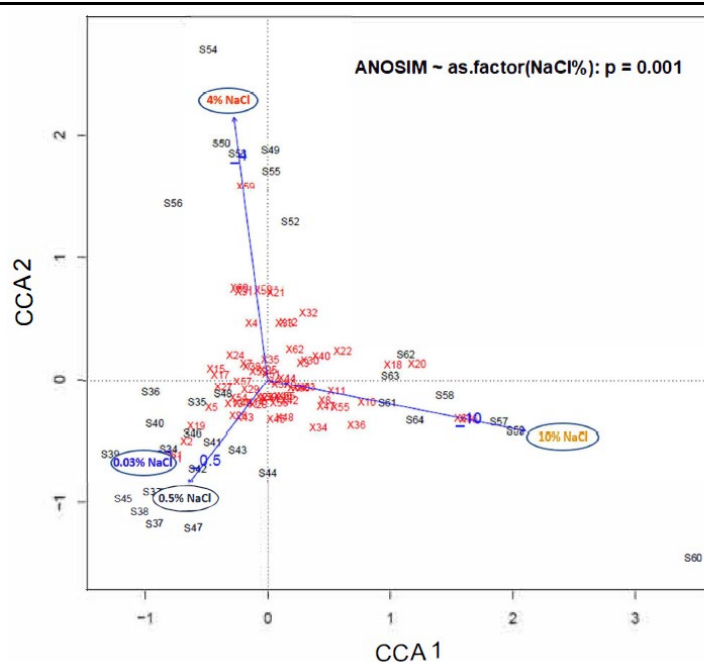
Bacterial OTUs	Type	Food content
p Firmicutes g Blautia otu282	unique	0.03% NaCl
p Firmicutes f Lachnospiraceae otu314	unique	0.03% NaCl
p Firmicutes f Lachnospiraceae otu274	unique	0.03% NaCl
p Actinobacteriota g Bifidobacterium otu183	unique	0.03% NaCl
p Firmicutes g uncultured s unidentified otu395	unique	0.5% NaCl
p Firmicutes g uncultured s unidentified otu260	unique	0.5% NaCl
p Firmicutes g uncultured s Clostridiales bacterium otu298	unique	0.5% NaCl
p Firmicutes g Oscillibacter s Clostridium leptum otu766	unique	0.5% NaCl
p Firmicutes g Oscillibacter s Clostridiales bacterium otu247	unique	0.5% NaCl
p Firmicutes g Clostridia UCG014 otu71	unique	0.5% NaCl
p Firmicutes g Blautia otu495	unique	0.5% NaCl
p Firmicutes g Blautia otu479	unique	0.5% NaCl
p Firmicutes g Anaeroplasma s uncultured Anaeroplasma otu369	unique	0.5% NaCl
p Firmicutes g Acetatifactor s Acetatifactor muris otu649	unique	0.5% NaCl
p Firmicutes f Peptostreptococcaceae otu663	unique	0.5% NaCl
p Firmicutes f Lachnospiraceae otu598	unique	0.5% NaCl
p Firmicutes f Lachnospiraceae otu370	unique	0.5% NaCl
p Firmicutes f Lachnospiraceae otu354	unique	0.5% NaCl
p Firmicutes f Lachnospiraceae otu336	unique	0.5% NaCl
p Firmicutes f Lachnospiraceae otu276	unique	0.5% NaCl
p Firmicutes f Lachnospiraceae otu272	unique	0.5% NaCl
p Firmicutes f Lachnospiraceae otu193	unique	0.5% NaCl
p Bacteroidota g Muribaculaceae s uncultured bacterium otu208	unique	0.5% NaCl
p Actinobacteriota g Bifidobacterium otu340	unique	0.5% NaCl
p Firmicutes g Clostridia UCG014 s uncultured Escherichia otu236	unique	4% NaCl
p Firmicutes g Blautia s uncultured Clostridiales otu600	unique	4% NaCl
p Firmicutes g Blautia s uncultured Clostridiales otu580	unique	4% NaCl
p Firmicutes g Blautia s uncultured Clostridiales otu519	unique	4% NaCl
p Proteobacteria o Enterobacterales otu92	unique	10% NaCl
p Proteobacteria o Enterobacterales otu62	unique	10% NaCl
p Proteobacteria o Enterobacterales otu301	unique	10% NaCl
p Firmicutes g uncultured s unidentified otu261	unique	10% NaCl
p Firmicutes g Roseburia otu248	unique	10% NaCl
p Firmicutes g Roseburia otu245	unique	10% NaCl
p Firmicutes g Lachnospiraceae UCG006 s Clostridium sp. otu325	unique	10% NaCl
p Firmicutes g Lachnospiraceae otu306	unique	10% NaCl
p Firmicutes g Incertae Sedis otu321	unique	10% NaCl
p Firmicutes g Colidextribacter otu400	unique	10% NaCl
p Firmicutes g Clostridia UCG014 s uncultured Escherichia otu161	unique	10% NaCl
p Firmicutes g Acetatifactor s Acetatifactor muris otu293	unique	10% NaCl
p Firmicutes f Oscillospiraceae otu327	unique	10% NaCl
p Firmicutes f Oscillospiraceae otu317	unique	10% NaCl
p Firmicutes f Oscillospiraceae otu308	unique	10% NaCl
p Firmicutes f Oscillospiraceae otu228	unique	10% NaCl
p Firmicutes f Lachnospiraceae otu407	unique	10% NaCl
p Bacteroidota g Muribaculum s Muribaculum intestinale otu200	unique	10% NaCl
p Bacteroidota g Muribaculaceae s uncultured bacterium otu190	unique	10% NaCl

**Figure S2.** A Venn diagram depicting the shared and unique bacterial OTUs of the gut microbiome among mice fed on sodium-deficient 0.03% NaCl, 0.5% NaCl (control), high salt 4% NaCl (HSD) and high salt 10% NaCl (HSD).

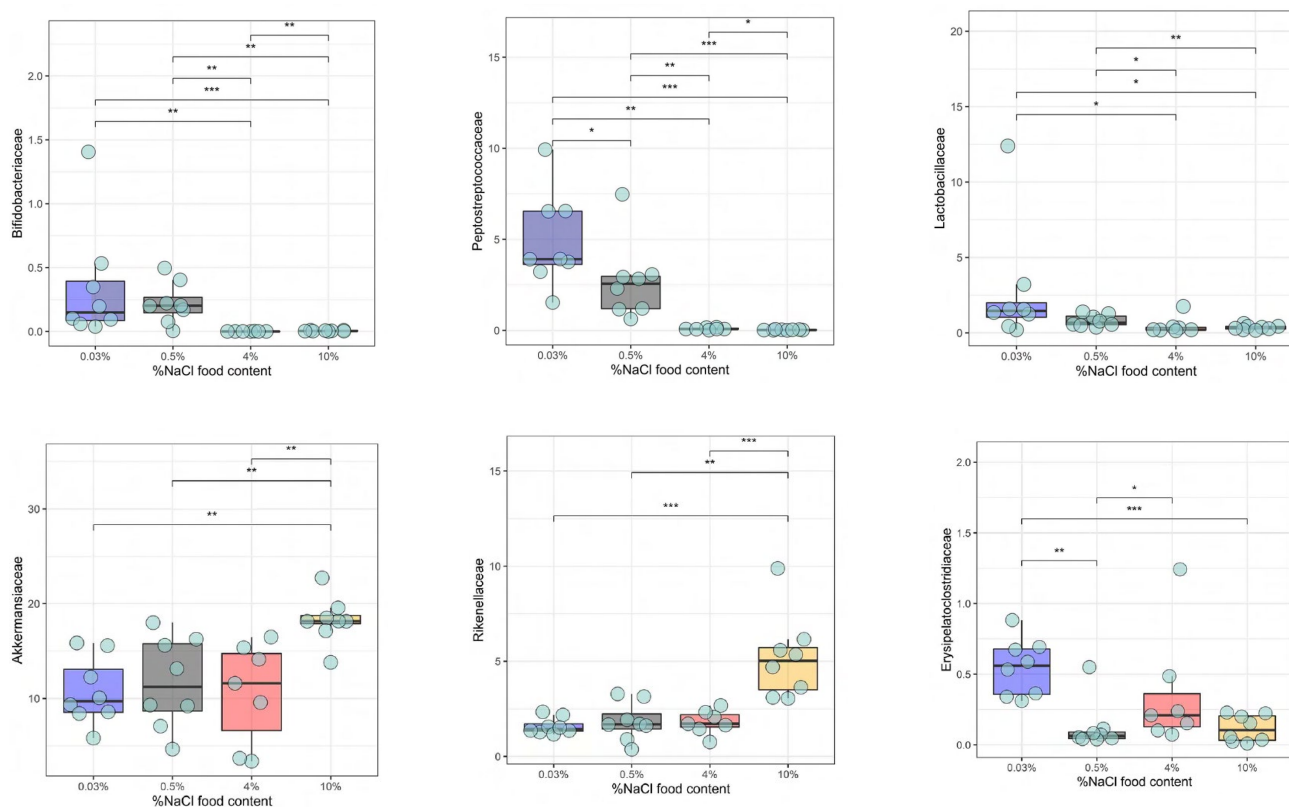


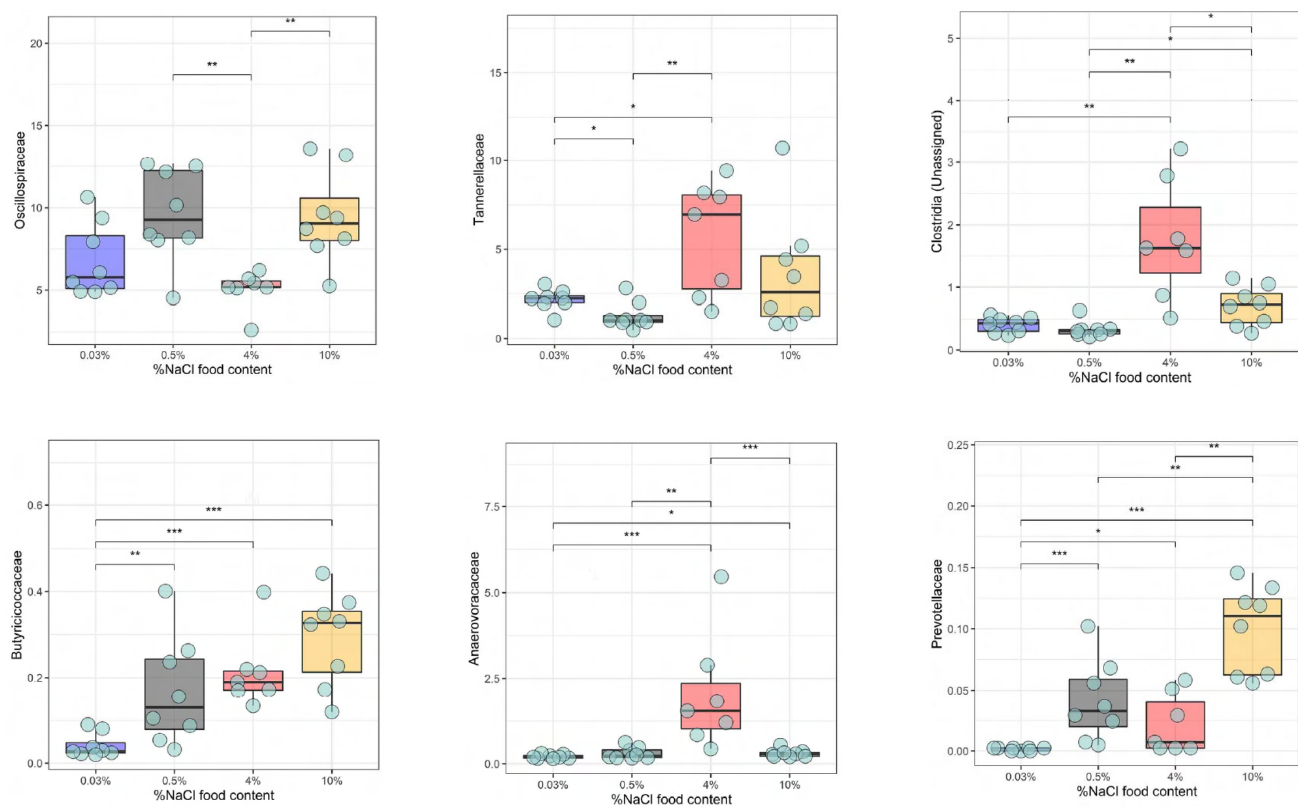
**Figure S3.** Alpha diversity analysis of fecal microbiota, a boxplot depicting the Shannon diversity, InvSimpson and Simpson's diversity index, which is a measure for the diversity of the gut microbiome. \*  $p \leq 0.05$ ; \*\*, \*\*\*  $p \leq 0.001$ .



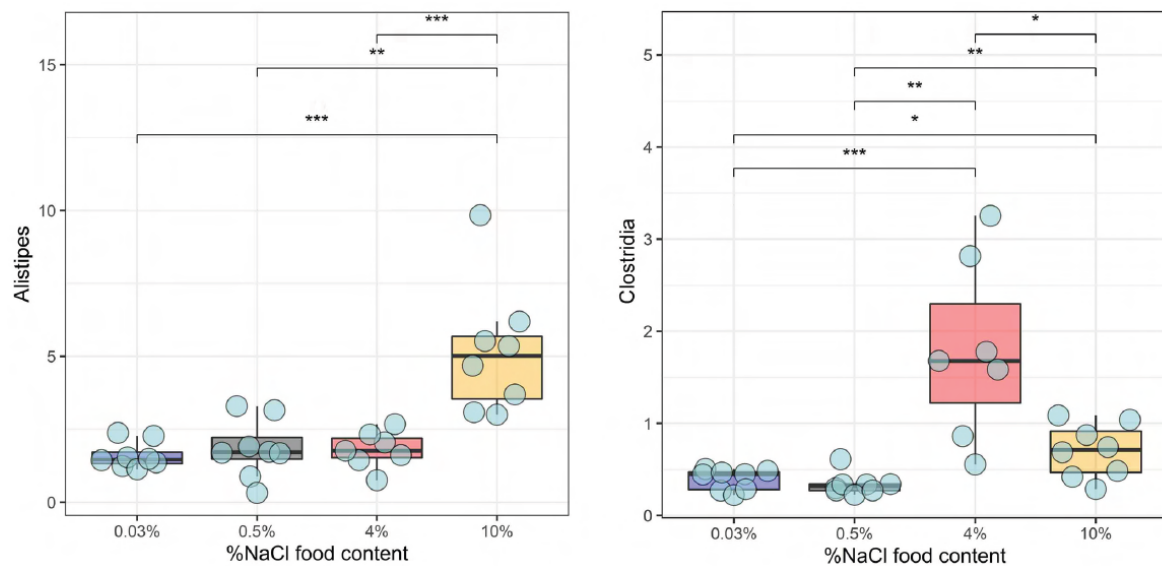


**Figure S4.** PCoA of unweighted and weighted UniFrac distances (upper and middle). PCoA results calculated with unweighted UniFrac distances depicting the beta diversity of gut microbiota among mice fed on sodium-deficient 0.03% NaCl, 0.5% NaCl (control), high salt 4% NaCl (HSD) and high salt 10% NaCl (HSD). Conditional correspondence analysis constrained by %NaCl content (bottom), the analysis of similarity was performed by the anosim function from “vegan” package of R,  $p$  value = 0.001.





**Figure S5.** Bacterial families differentially represented in feces of mice fed on sodium-deficient 0.03% NaCl, 0.5% NaCl (control), high salt 4% NaCl (HSD) and high salt 10% NaCl (HSD). \*  $p \leq 0.05$ ; \*\*  $p \leq 0.01$ ; \*\*\*  $p \leq 0.001$ .



**Figure S6.** Bacterial genera differentially represented in feces of mice fed on sodium-deficient 0.03% NaCl, 0.5% NaCl (control), high salt 4% NaCl (HSD) and high salt 10% NaCl (HSD). \*  $p \leq 0.05$ ; \*\*  $p \leq 0.01$ ; \*\*\*  $p \leq 0.001$ .