

The microbiota knows: handling-stress and diet transform the microbial landscape in the gut content of rainbow trout in RAS

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Performance parameters

Specific growth rate (SGR), feed conversion ratio (FCR), daily feed intake (DFI), protein efficiency ratio (PER) and protein retention efficiency (PRE) (performance parameters) were calculated based on group measures by the following equations:

$$\text{SGR} = [\ln(\text{FGW}) - \ln(\text{IGW})] / t * 100$$

$$\text{FCR} = (F_t / 1000) / (\text{FGW} - \text{IGW})$$

$$\text{DFI} = \text{SGR} * \text{FCR}$$

$$\text{PER} = (\text{FGW} - \text{IGW}) * 1000 / \text{CP}_t$$

$$\text{PRE} = \text{CP}_g / \text{CP}_t * 100$$

FWG: final group weight (kg), IGW: initial group weight (kg), t: 59 days, F_t : total feed intake (g), CP_t : total crude protein intake (g), CP_g : total gained body protein (g)

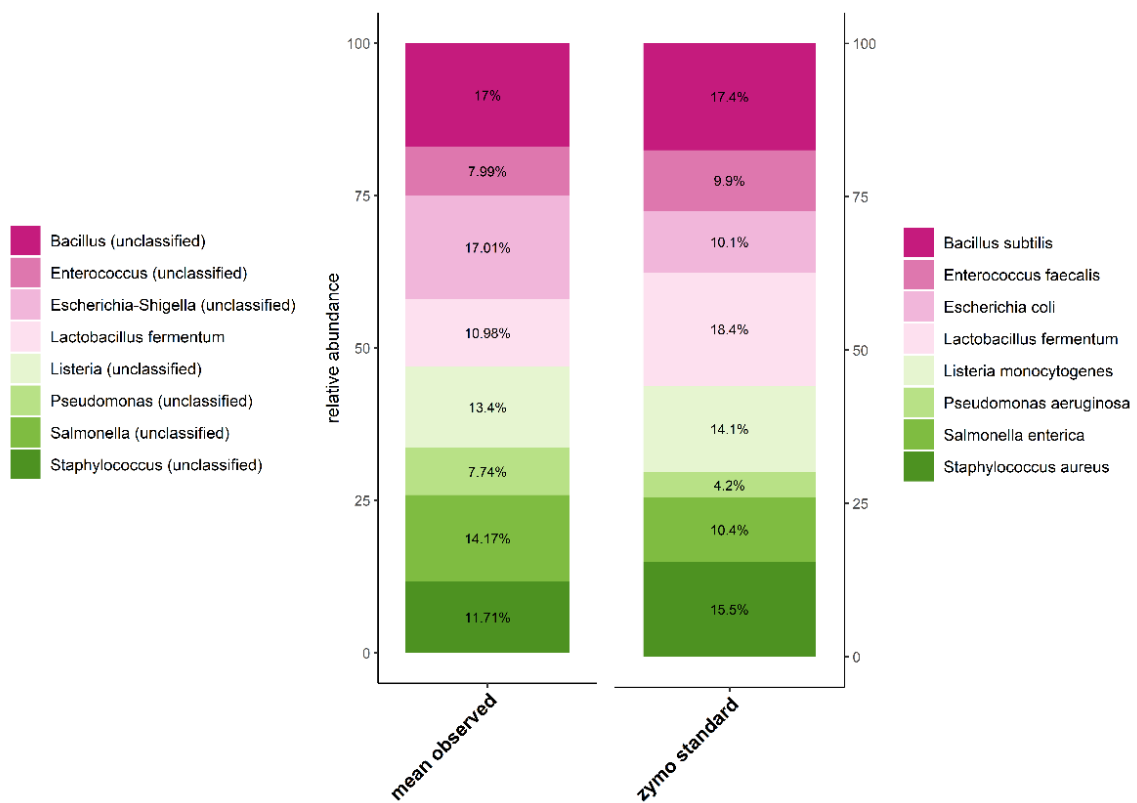


Figure S1 Left barplot (mean observed) shows mean relative abundance of three mock community probes sequenced parallel to the trial samples. Right barplot (zymo standard) shows relative abundance given by the manufacturer (Zymo).

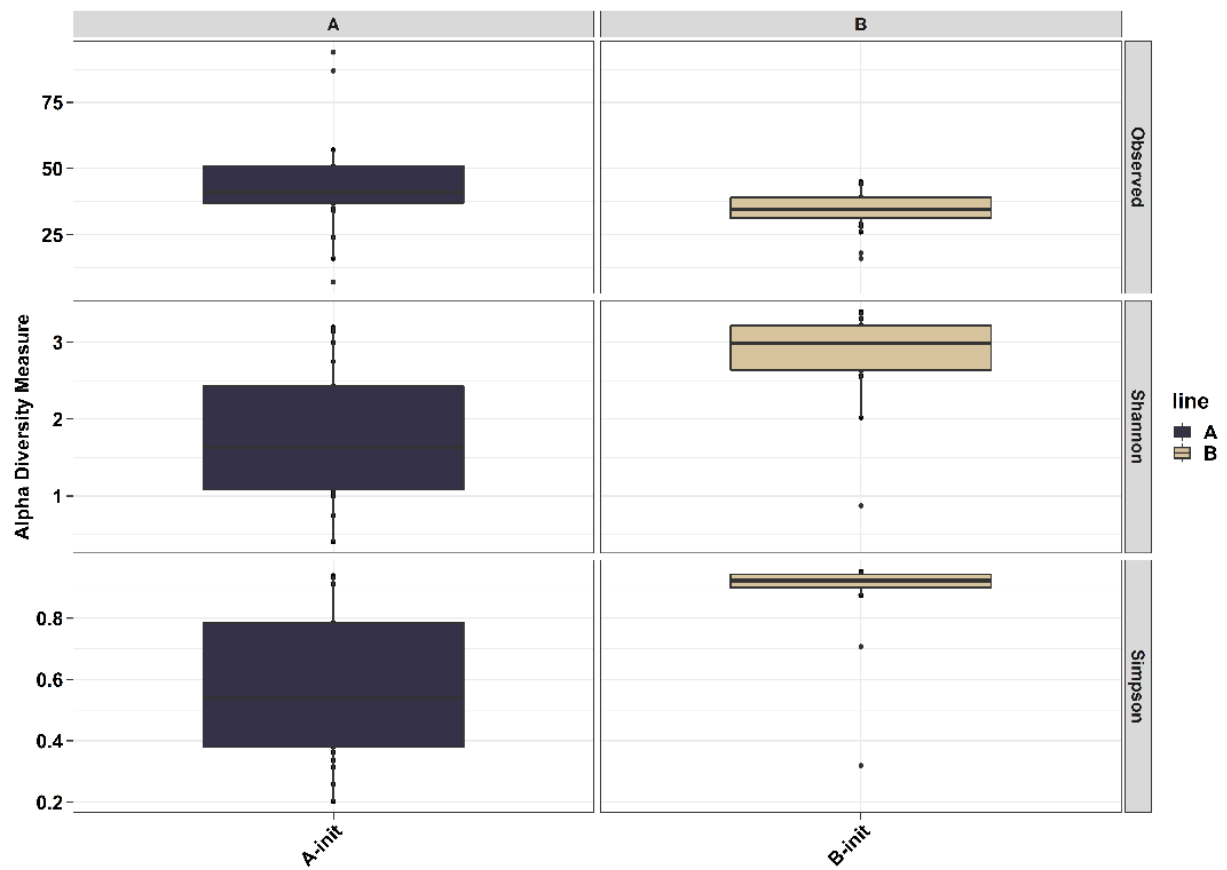


Figure S2 Alpha diversity indices Observed ASVs, Shannon diversity and Simpson of initial sampling from trout line A and B.

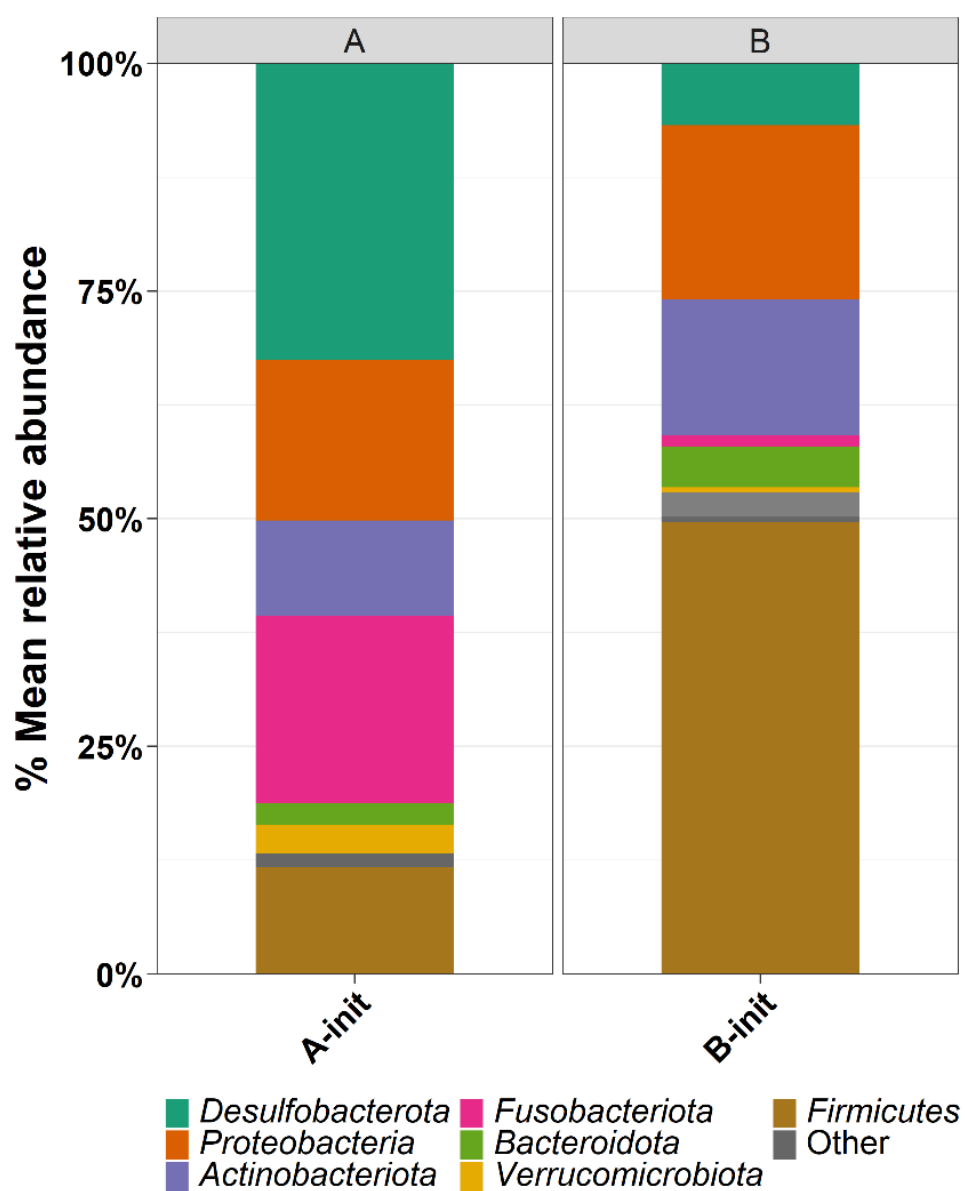


Figure S3 Mean relative abundance (%) at the phylum level of the intestinal microbiota from both trout lines past adaptation time and prior the experiment.

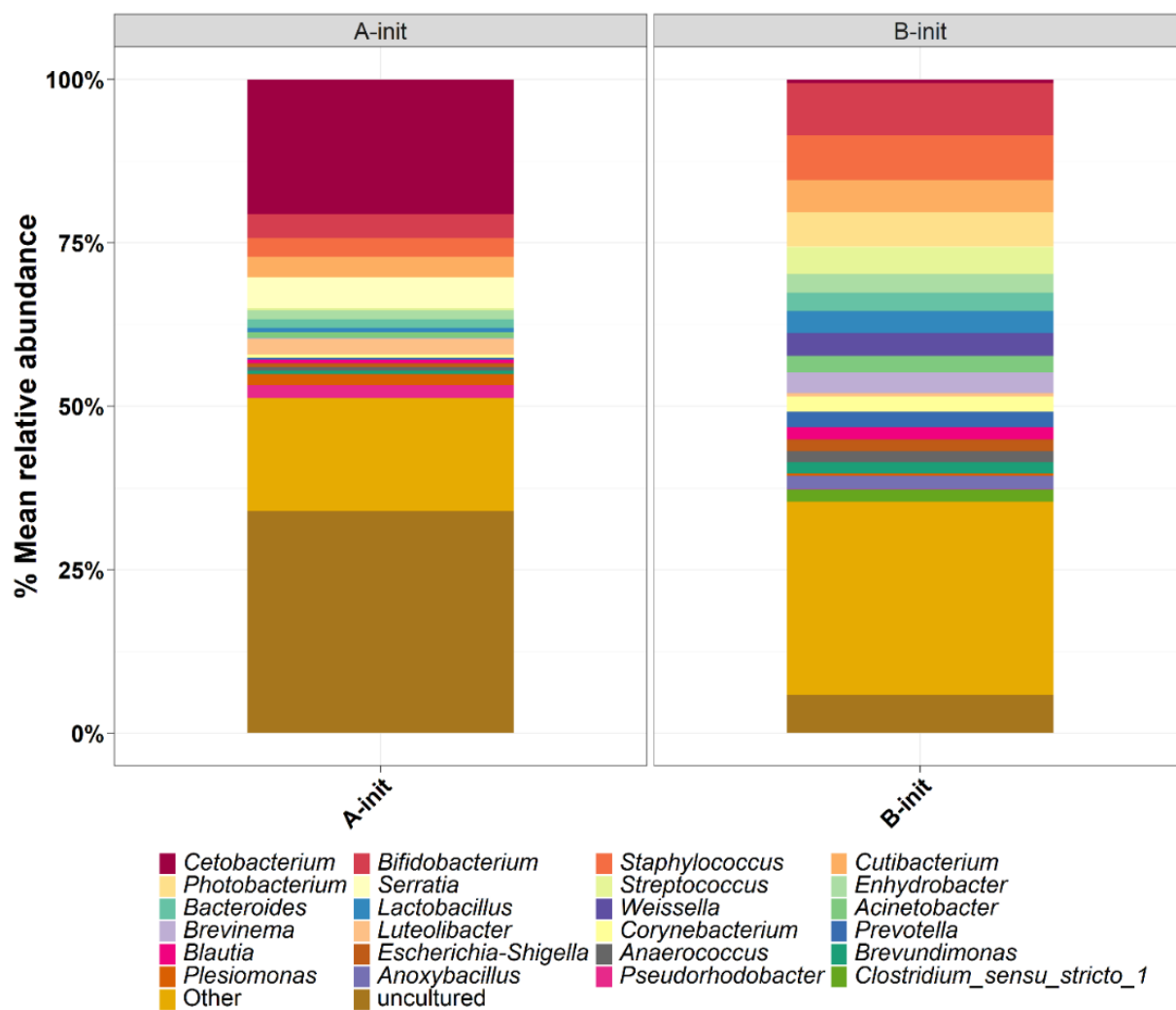


Figure S4 Mean relative abundance (%) at the genus level of the intestinal microbiota from both trout lines past adaptation time and prior the experiment

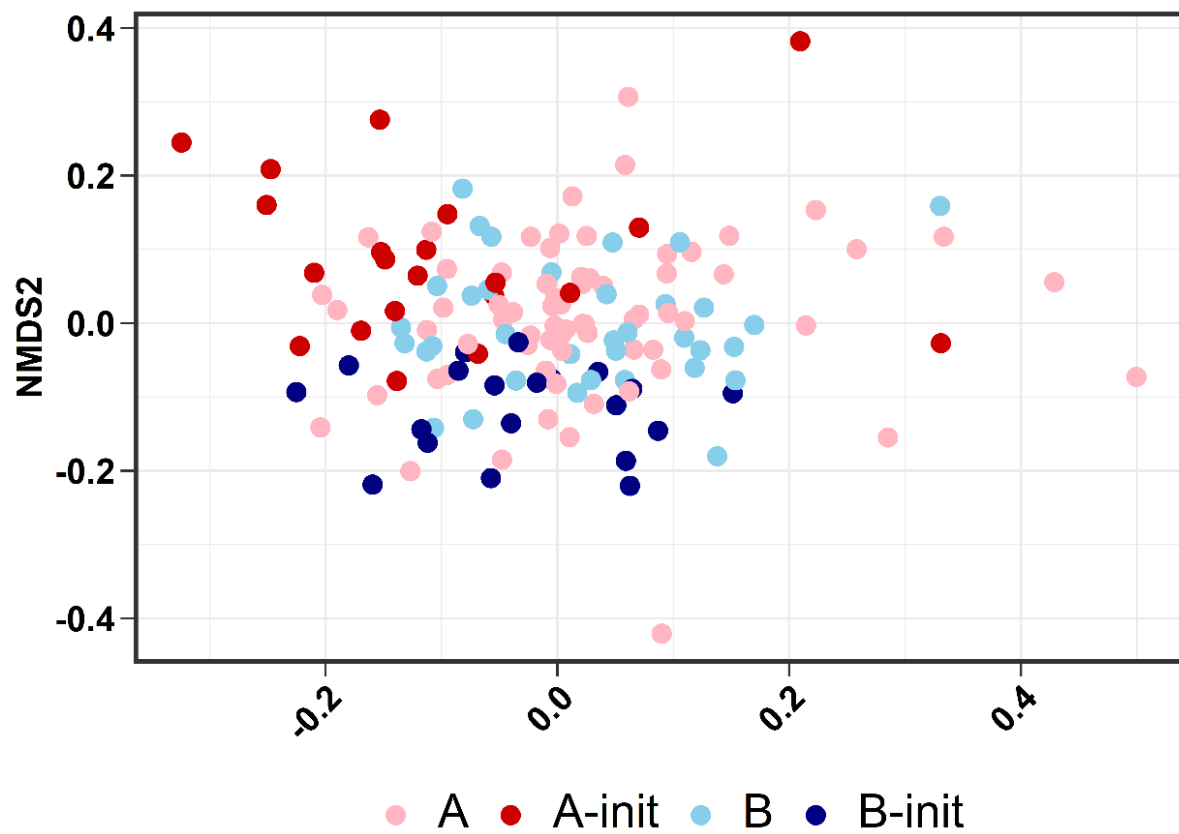


Figure S5 NMDS based on unweighted UniFrac distance using initial samplings and post experiment samples from both trout lines.