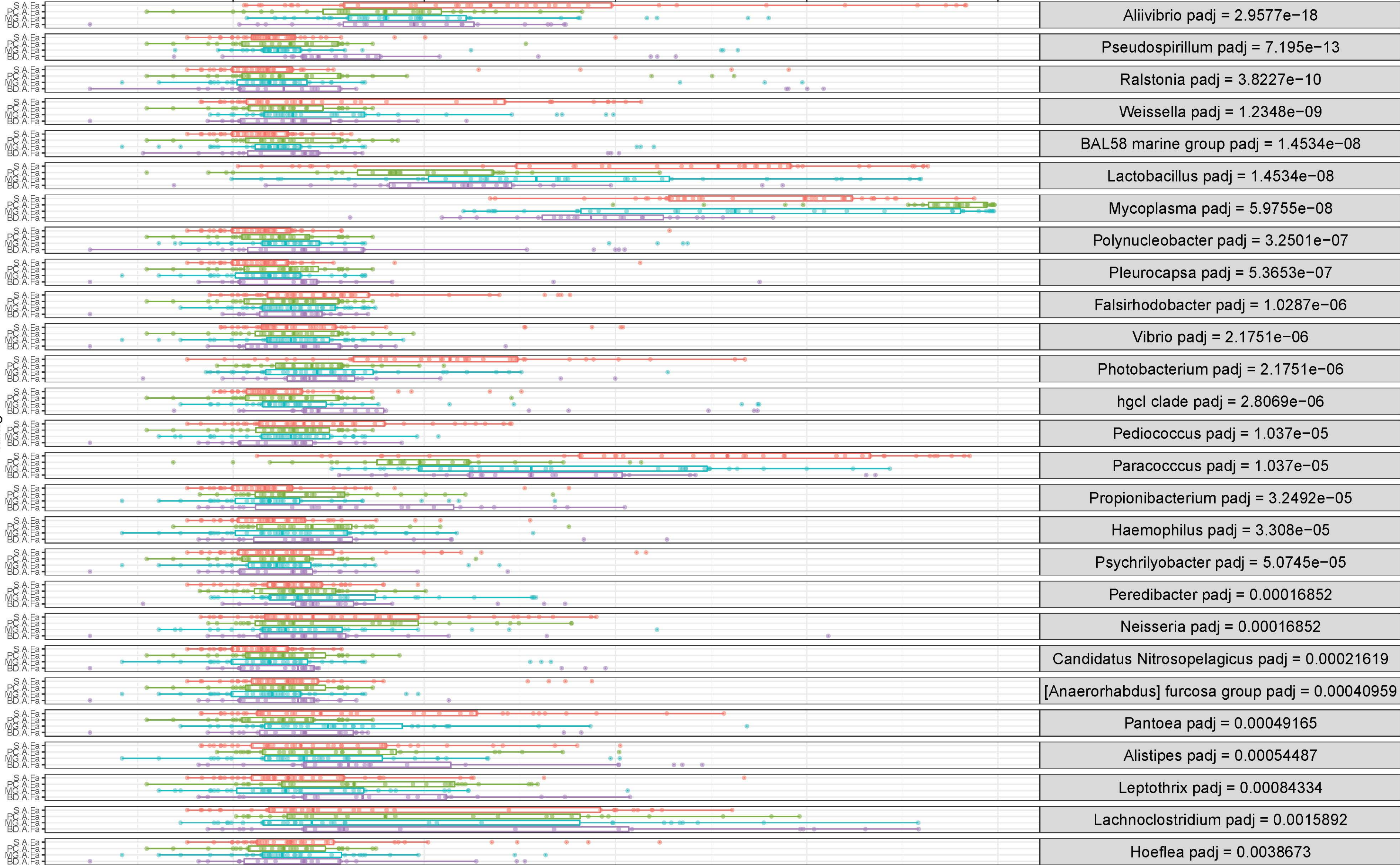


Log-relative normalised

-10.0 -7.5 -5.0 -2.5 0.0



Groups

Groups
 S.A.Fa
 PC.A.Fa
 MG.A.Fa
 BD.A.Fa

Supplementary material

Figure S1: Microbial genera that showed significant differential abundance between lifecycle stages. Samples include smolt (MG.S.Fr), parr (MG.P.Fr), returning adult (MG.R.Fr) and marine adult (MG.A.SI).

Figure S2: Microbial genera that showed significant differential abundance between gut compartments of farmed fish. Samples include stomach (S.A.Fa), pyloric caecum (PC.A.Fa), mid-gut (MG.A.Fa) and bile duct (BD.A.Fa).

Table S1: Full list of OTUs that accounted for those that did not fit the neutral model.