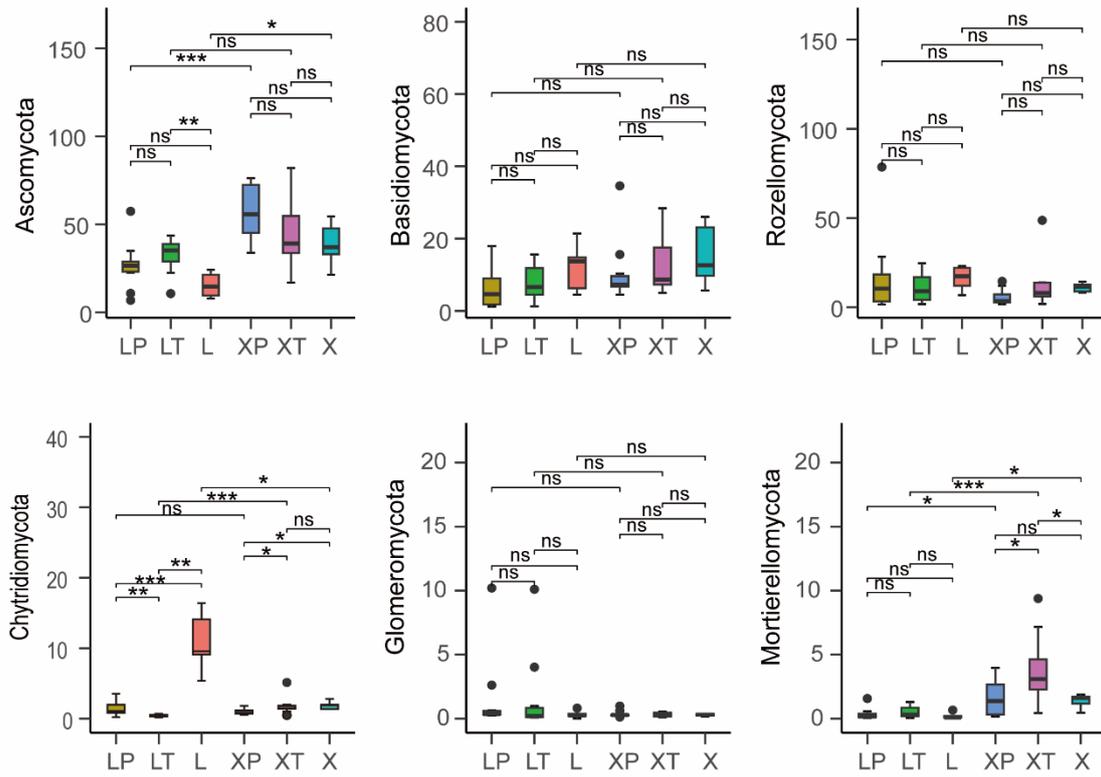


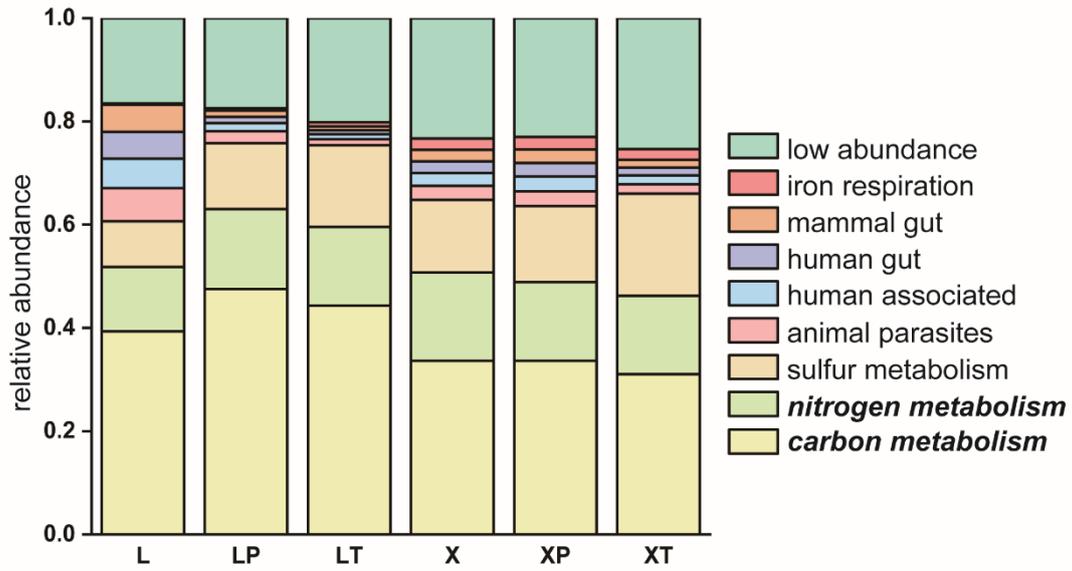
1

2 **Figure S1** Differences in relative abundance of main bacterial taxa at the phylum level between different
3 habitats. LP = *P. australis*-covered sites in Luohe Constructed Wetland, LT = *T. angustifolia*-covered sites
4 in Luohe Constructed Wetland, L = bare land in Luohe Constructed Wetland, XP = *P. australis*-covered
5 sites in Xinxue River Constructed Wetland, XT = *T. angustifolia*-covered sites in Xinxue River
6 Constructed Wetland, X = bare land in Xinxue River Constructed Wetland. * $p < 0.05$, ** $p < 0.01$, ***
7 $p < 0.001$, **** $p < 0.0001$.



8

9 **Figure S2** Differences in relative abundance of main fungal taxa at the phylum level between different
 10 habitats. LP = *P. australis*-covered sites in Luohe Constructed Wetland, LT = *T. angustifolia*-covered sites
 11 in Luohe Constructed Wetland, L = bare land in Luohe Constructed Wetland, XP = *P. australis*-covered
 12 sites in Xinxue River Constructed Wetland, XT = *T. angustifolia*-covered sites in Xinxue River
 13 Constructed Wetland, X = bare land in Xinxue River Constructed Wetland. * $p < 0.05$, ** $p < 0.01$, ***
 14 $p < 0.001$.



15

16 **Figure S3** Bacterial functional signature predicted with the FAPROTAX. LP = *P. australis*-covered sites
 17 in Luohe Constructed Wetland, LT = *T. angustifolia*-covered sites in Luohe Constructed Wetland, L =
 18 bare land in Luohe Constructed Wetland, XP = *P. australis*-covered sites in Xinxue River Constructed
 19 Wetland, XT = *T. angustifolia*-covered sites in Xinxue River Constructed Wetland, X = bare land in
 20 Xinxue River Constructed Wetland.