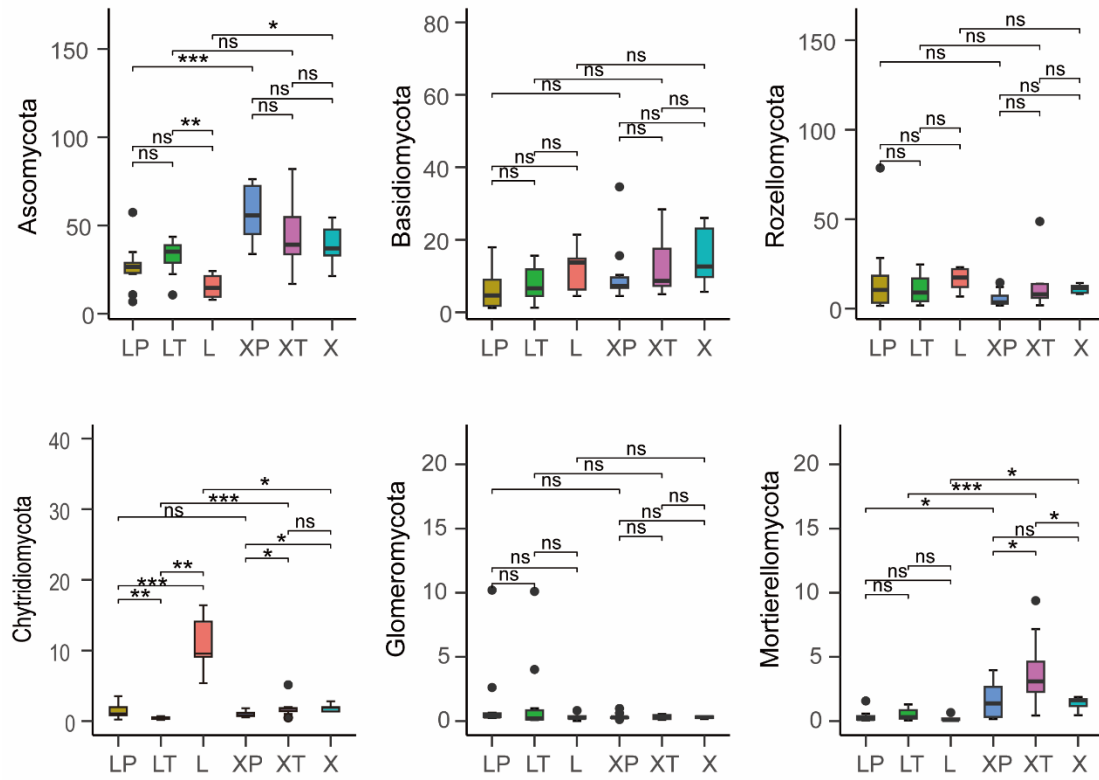


Figure S1 Differences in relative abundance of main bacterial taxa at the phylum level between different habitats. LP = *P. australis*-covered sites in Luohe Constructed Wetland, LT = *T. angustifolia*-covered sites in Luohe Constructed Wetland, L = bare land in Luohe Constructed Wetland, XP = *P. australis*-covered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



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 $p < 0.001$.

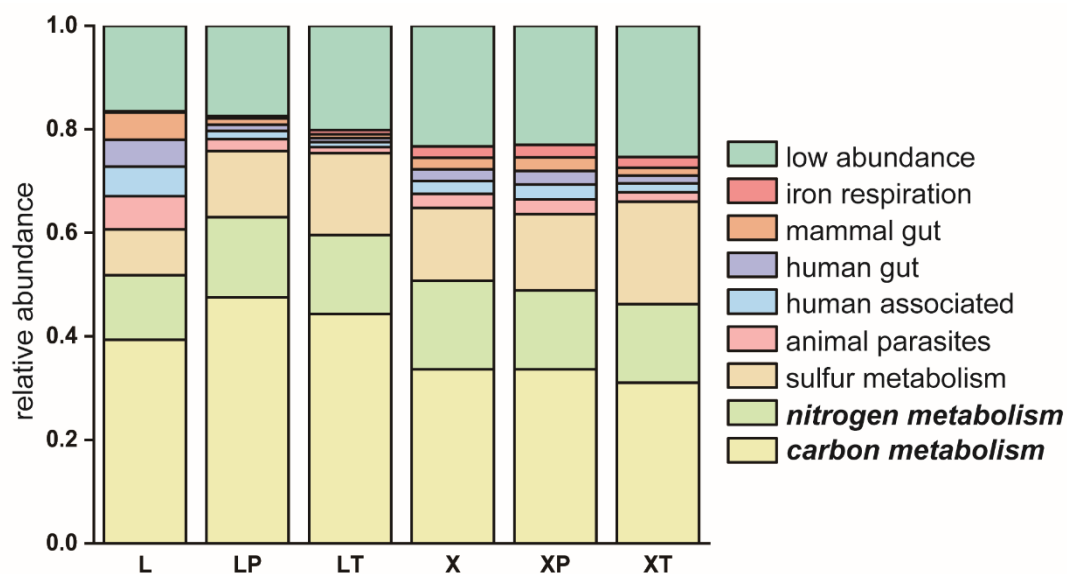


Figure S3 Bacterial functional signature predicted with the FAPROTAX. LP = *P. australis*-covered sites in Luohe Constructed Wetland, LT = *T. angustifolia*-covered sites in Luohe Constructed Wetland, L = bare land in Luohe Constructed Wetland, XP = *P. australis*-covered sites in Xinxue River Constructed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