

Figure S6: Average relative abundance (%) in the metagenomic libraries ($n = 30$) of glycoside hydrolase genes targeting various substrates among the bacteria (white bars) and fungi (grey bars). Substrate codes are as follows: CE, cellulose; CH, chitin; D, dextran; F, fructan; LY, lysozyme; M, mixed; O, oligosaccharides; OAP, other animal polysaccharides; OPP, other plant polysaccharides; ST, starch/glycogen; X, xylan.

