



Figure S1. Comparisons between PC9_AS and PC15 genome of *P. ostreatus* strains. Circos plot showing regions of similarity shared between PC9_AS (scaffolds 1-17) and PC15 (scaffolds 1-12) (identity>95%, length>10-kb). Tracks (outer to inner) represent the distribution of genomic features in each assembly: 1) sizes (in Mb) of scaffolds, with numbers prefixed by the letter “C” indicating the order of scaffold size; 2) distribution of telomere repeats with 1-kb sliding windows, ranging between 10-30 repeats