



**Figure S3.** Synteny analysis of *A. nigrkans*, *P. confluens*, and *T. melanosporum*. **A.** Dot plots of positions of orthologous genes along scaffolds. The three "denser" regions around 0-3 Mb, 8-10 Mb, and 14-15 Mb in *A. nigrkans* comparisons represent the three largest *A. nigrkans* scaffolds. Orthologs of genes on these scaffolds are distributed over a large number of scaffolds in the other two Pezizomycetes, i.e. there is not a high degree of macrosynteny (a dot plot for the highly syntenic genomes of the *Sordariomycetes* *N. crassa* and *S. macrospora* is shown for comparison). Dot plots for *N.crassa*/*S.macrospora* and *P.confluens*/*T.melanosporum* from Traeger et al. (PLoS Genet 2013, 9: e1003820). **B.** Syntenic pairs (20 kb) and syntenic triplets (40 kb) between *A. nigrkans*, *P. confluens*, and *T. melanosporum*. The number of pairs or triplets of orthologous genes within a 20 kb (pairs) or 40 kb (triplets) region was determined for each species pair. The comparison between *P. confluens* and *T. melanosporum* is from Traeger et al. (PLoS Genet 2013, 9: e1003820).