Figure. S1. The One-way ANOVA test examines fungal abundance at both the genera (a) and phyla (b) levels. Only the taxa that differed between the crop tree densities were shown.
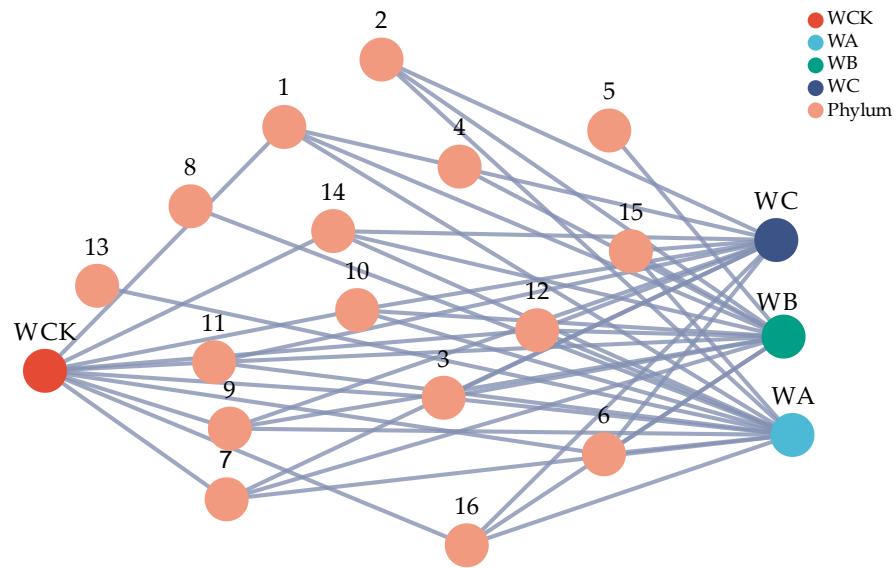
Figure. S2. Collinear networks at the phyla level of the soil fungal communities. The number corresponding to the taxa name: 1: Ascomycota; 2: Basidiobolomycota; 3: Basidiomycota; 4: Blastocladiomycota; 5: Calcarisporiellomycota; 6: Chytridiomycota; 7: Entorrhizomycota; 8: GS01; 9: Glomeromycota; 10: Kickxellomycota; 11: Mortierellomycota; 12: Mucoromycota; 13: Olpidiomycota; 14: Rozellomycota; 15: Zoopagomycota; 16: Unclassified_k__Fungi.
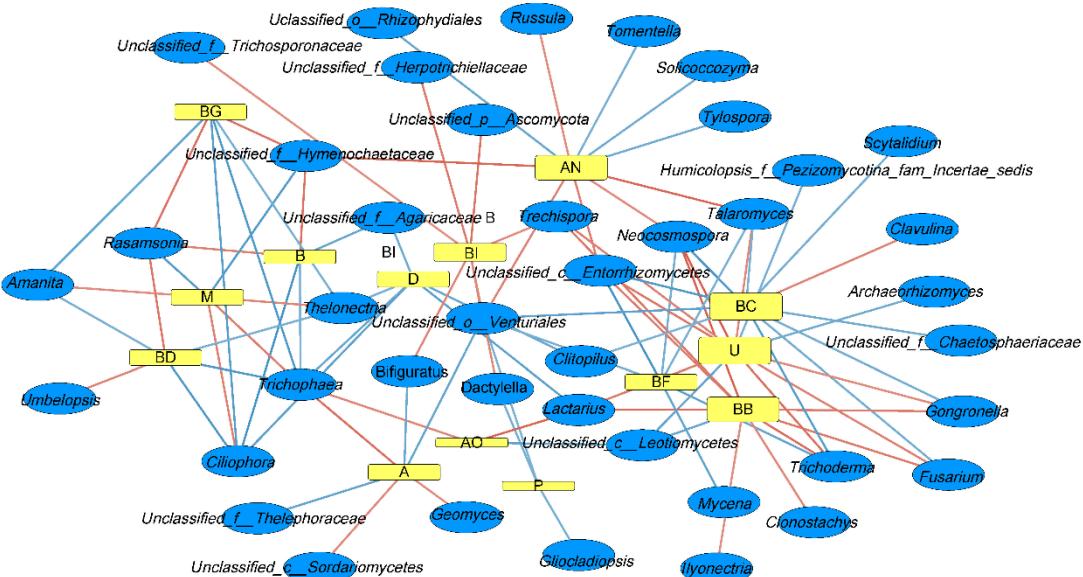

Figure. S3. Network of fungal composition and plant species. Blue and red lines represent negative and positive relationships between plant species (yellow nodes) and fungal composition genera (blue nodes), respectively. The size of each node is proportional to the number of degrees. Only significant fungal genera were shown, and plant species showed plants that existed in every plot. A: *Smilax china* L.; B: *Quercus serrata*; D: *Aralia elata*; M: *Mallotus barbatus (Wall.)*; P: *Callerya congestiflora*; U: *Litsea cubeba*; AN: *Cinnamomum camphora*; AO: *Ardisia japonica*; BB: *Pteridium aquilinum*; BC: *Microlepia hancei*; BD: *Miscanthus sinensis*; BF: *Dicranopteris pedate*; BG: *Odontosoria chinensis*; BI: *Setaria plicata*.