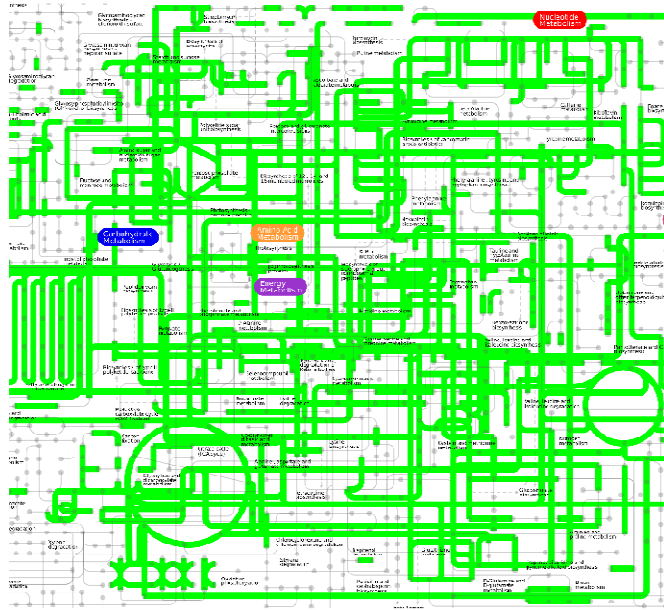
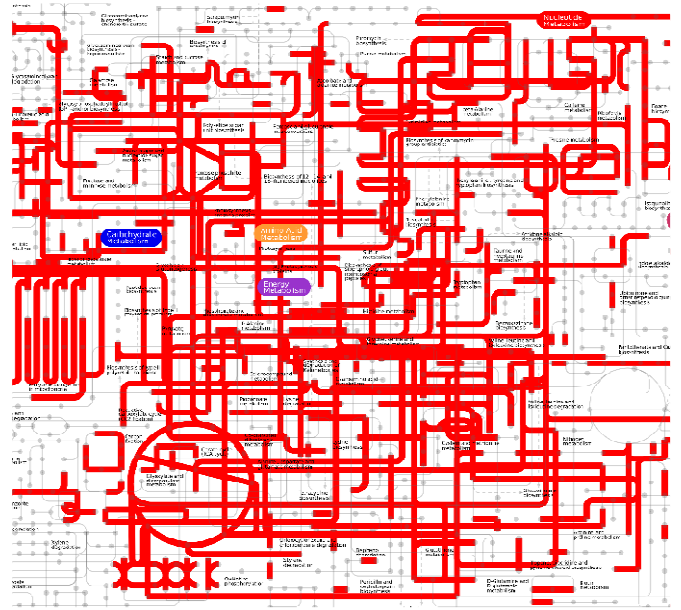


A

Deactivated pathways of cluster 1

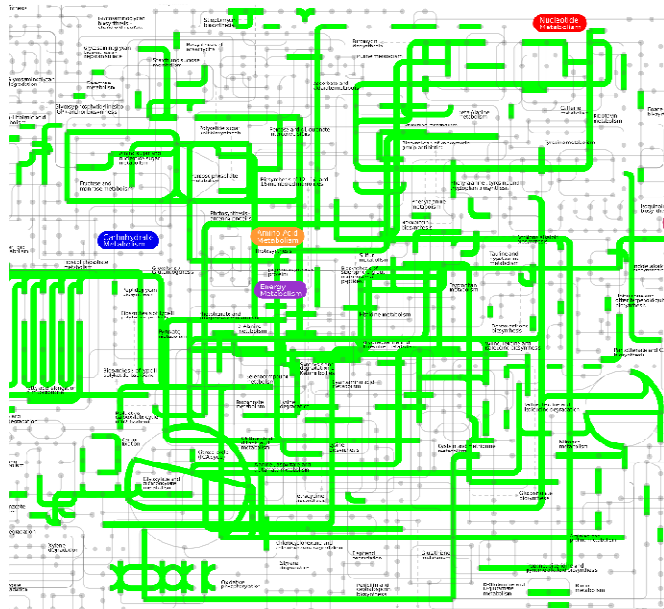


Activated pathways of cluster 1

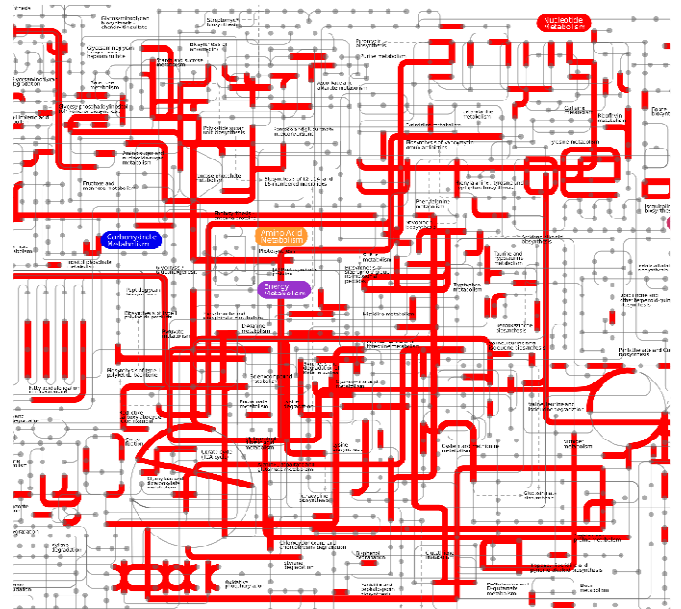


B

Deactivated pathways of cluster 15

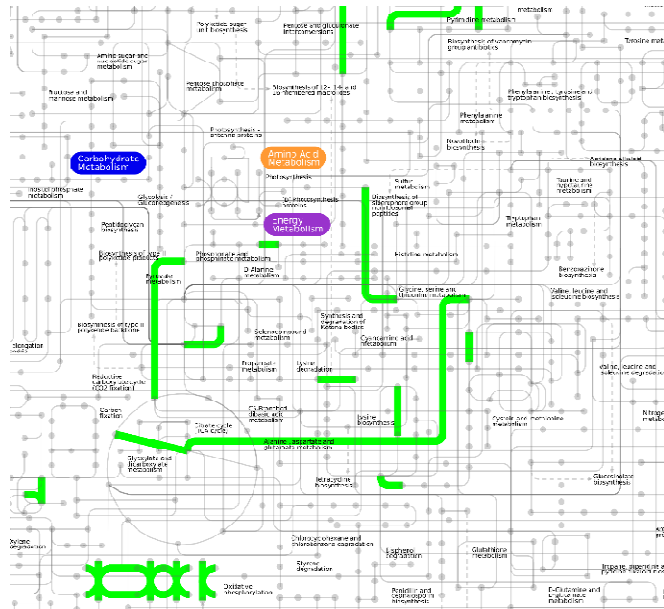


Activated pathways of cluster 15

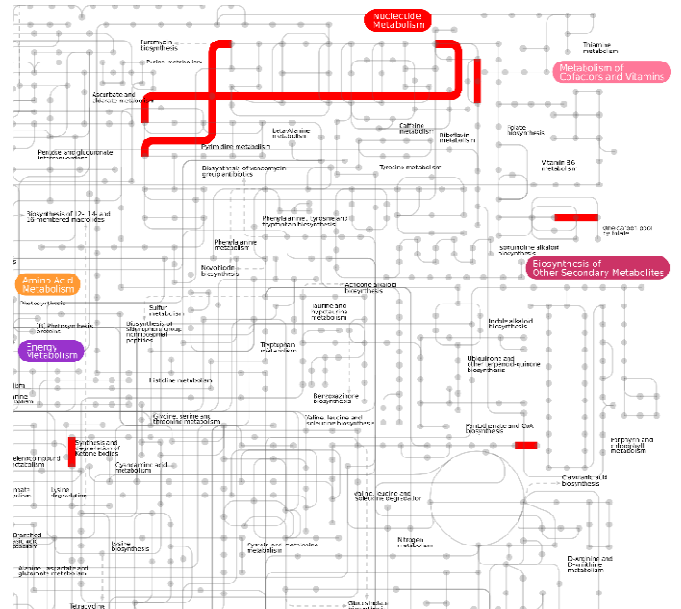


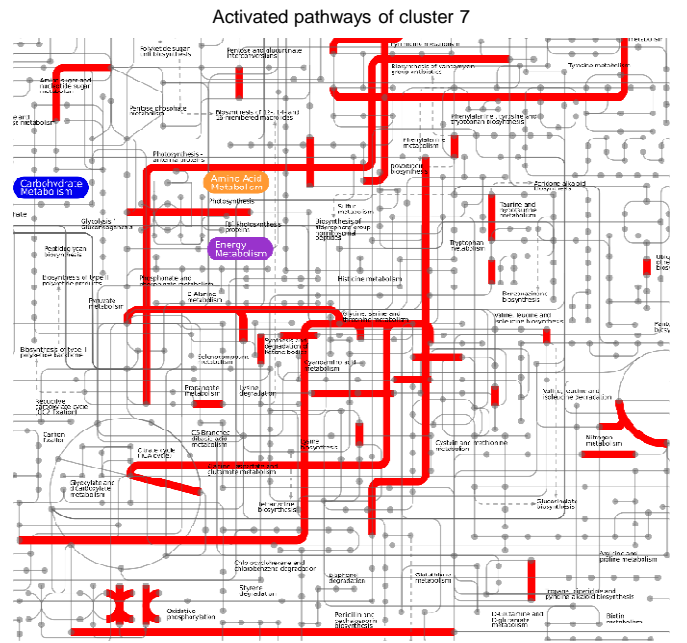
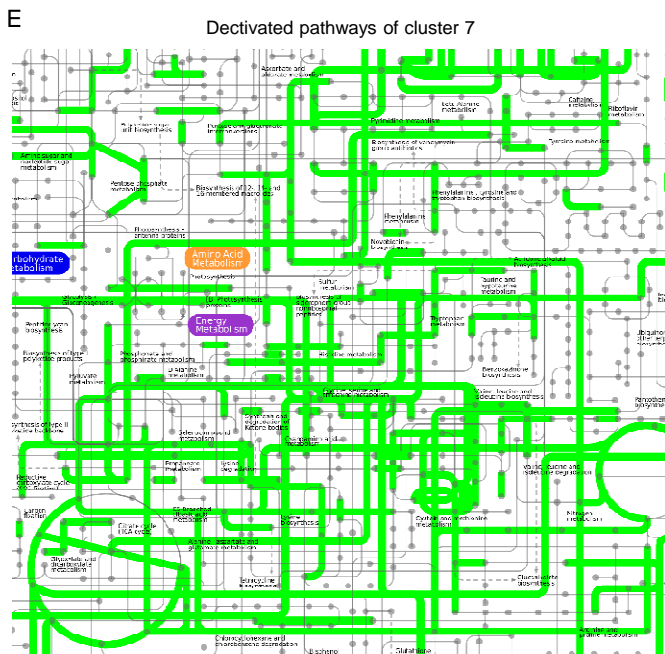
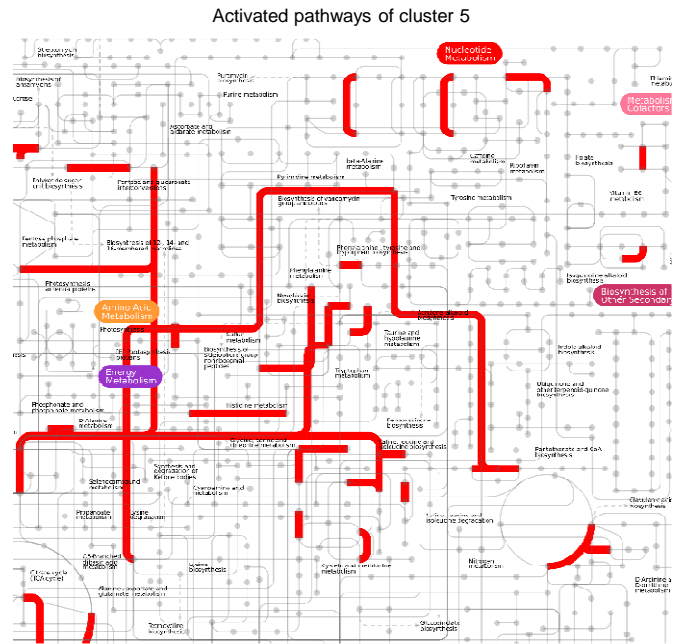
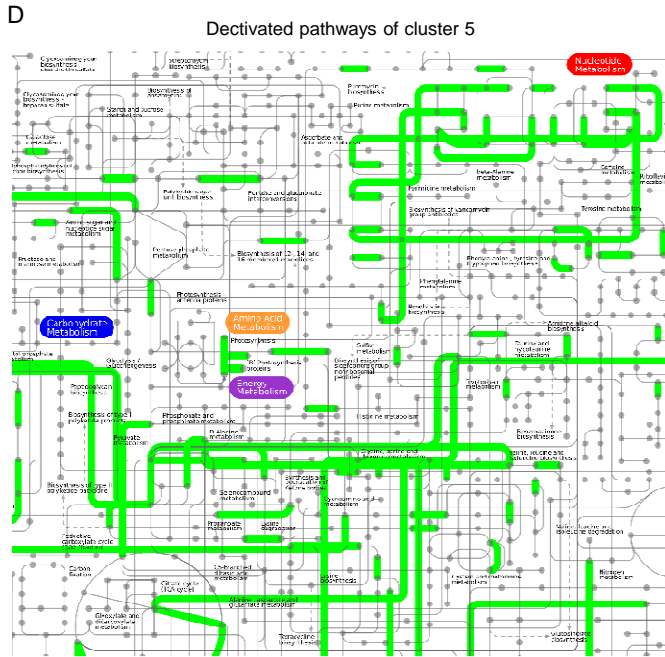
C

Deactivated pathways of cluster 3



Activated pathways of cluster 3





Additional file 10. Metabolic pathways of the simplified soil microcosm, modulated by incubation in the soil matrix. Metabolic pathways deactivated (left panels) and activated (right panels) by 24 h incubation in the soil matrix (A) without reinforced modulation (cluster 1) and (B) with reinforced modulation (cluster 15) in the presence of *Armillaria mellea* and *Trichoderma atroviride* combined. Metabolic pathways modulated by the introduction of (C) *T. atroviride* (cluster 3), (D) *A. mellea* (cluster 5), or (E) both (cluster 7). KEGG pathways were visualised using the iPath2 tool [45], the pathways of upregulated (green) and downregulated (red) genes were highlighted, and a section of the most relevant pathways is reported for each panel.