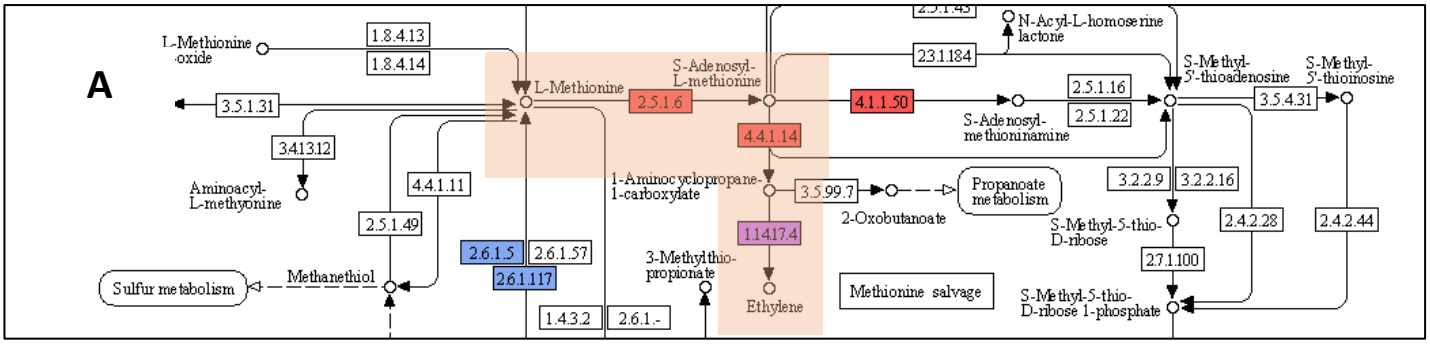

A
L-Methionine oxide
1.8.4.13
1.8.4.14
L-Methionine
S-Adenosyl-L-methionine
2.5.1.6
N-Acyl-L-homoserine lactone
23.1.184
4.1.1.50
S-Methyl-5'-thioadenosine
S-Methyl-5'-thioinosine
3.5.4.31
2.5.1.16
2.5.1.22
S-Adenosyl-methioninamine
3.5.1.31
3.4.13.12
4.4.1.14
Aminoacyl-L-methyonine
4.4.1.11
1-Aminocyclopropane-1-carboxylate
3.5.99.7
2-Oxobutanoate
Propanoate metabolism
3.2.2.9
3.2.2.16
S-Methyl-5-thio-D-ribose
2.4.2.28
2.4.2.44
2.5.1.49
1.14.17.4
2.6.1.5
2.6.1.57
2.6.1.117
3-Methylthio-propionate
Ethylene
Methionine salvage
S-Methyl-5-thio-D-ribose 1-phosphate
Sulfur metabolism
Methanethiol
1.4.3.2
2.6.1.-
B
Baccatin III
2.3.2.-
N-Debenzoyl-deoxytaxol
1.14.-.-
N-Debenzoyl-taxol
2.3.1.-
Taxol
GA14-aldehyde
P450-1
GA12-aldehyde
GA53-aldehyde
11414107
GA14
P450-2
GA12
CYP714B
GA53
1.14.11.12
GA37
GA15
GA44
GA36
GA24
GA19
GA4
1.14.11.15
GA9
GA13ox
GA20
1.14.11.13
DES
1.14.11.-
GA34
GA7
GA51
GA29
2,3-Didehydro-GA9
GA5
GA34-catabolite
GA51-catabolite
GA29-catabolite
GA3
GA1
GA8
GA8-catabolite
4.2.3.183
Nezukol
4.2.3
Abietadiene
Abietinol
Abiet
C
Nitric oxide
1.7.2.5
1.7.1.14
Nitrous oxide
1.7.2.4
Nitrogen
1.18.6.1
1.18.6.2
1.19.6.1
1.7.2.8
Hydrazine
1.7.2.7
Carbon fixation pathways in prokaryotes
Nrt
Nitrate
1.7.7.2
1.7.5.1
NR
1.9.6.1
NtrABCD
Nitrate (extracellular)
1.7.99.-
Nitrite
1.7.2.1
1.7.1.4
1.7.7.1
1.7.1.15
1.7.2.2
Nitrite (extracellular)
1.7.1.10
1.7.99.1
1.7.2.6
1.7.3.6
Hydroxylamine
1.14.99.39
1.13.12.16
1.7.3.1
Nitroalkane
Ammonia
3.5.1.49
Formate
Glyoxylate metabolism
CO2
4.2.1.1
HCO3-
Carbamate
4.2.1.104
Cyanate
2.7.2.2
6.3.4.16
Carbamoyl-P
Arginine biosynthesis
1.4.1.2
1.4.1.3
1.4.1.4
1.4.1.13
1.4.1.14
1.4.7.1
6.3.1.2
L-Glutamine
L-Glutamate
Glutamate metabolism
3.5.5.1
Nitrile
D
Assimilatory nitrate reduction
Nitrate
NarB
NR
NasAB
Nitrite
NIT-6
NirA
Ammonia

Figure S3. Complete KEGG modules reconstructed from differentially expressed genes in *Arabidopsis thaliana* and *Trichoderma atroviride*. Reconstruction of KEGG pathway modules from differentially expressed genes (DEGs) highlights modules that are fully represented by upregulated (red) or downregulated (blue) genes in both organisms. A KEGG module is considered complete when all of its constituent KEGG Orthologs (KOs) are covered by DEGs in each organism-specific dataset. **(A–B)** *A. thaliana*: **(A)** Ethylene biosynthesis pathway "Methionine → Ethylene" (M00368), fully represented by upregulated genes (orange). **(B)** Gibberellin biosynthesis pathway "GA12/GA53 → GA4/GA1" (M00928), fully represented by downregulated genes (blue). **(C–D)** *T. atroviride*: **(C)** Assimilatory nitrate reduction "Nitrate → Ammonia" (M00531) and **(D)** Nitrate assimilation (M00615), both fully reconstructed from upregulated genes (orange), indicating enhanced nitrogen assimilation during interaction.