

Supplementary Materials:

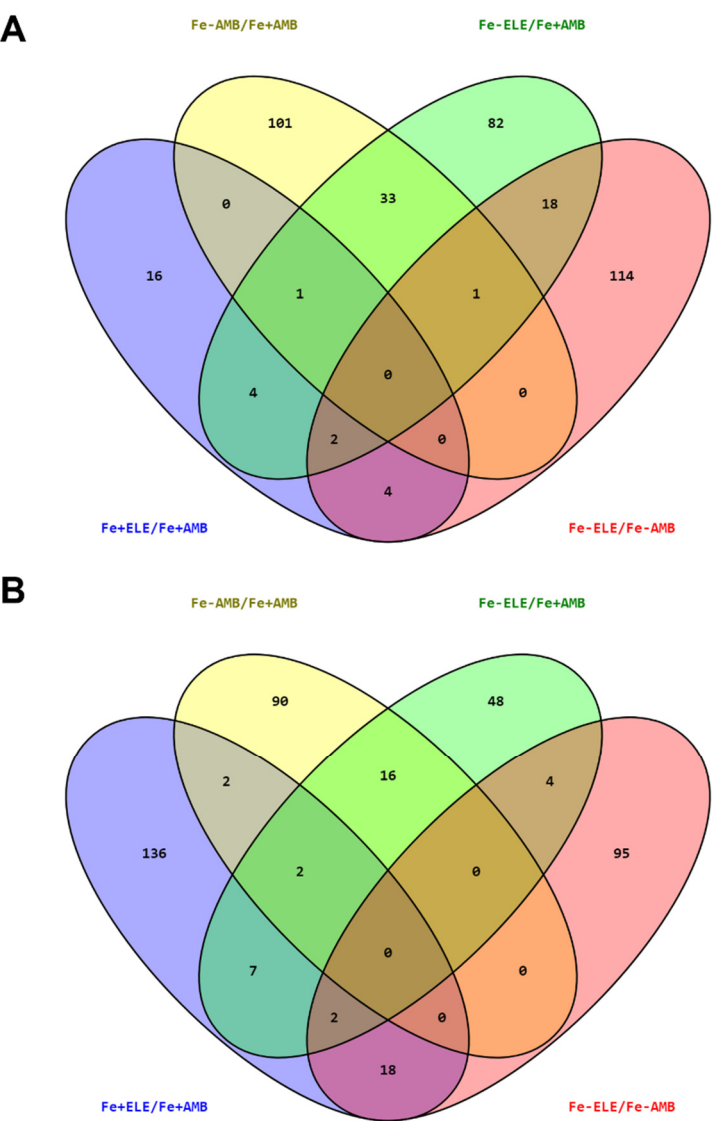


Figure S1. Venn diagram significantly displaying (a) upregulated and (b) downregulated proteins in response to eCO₂ and Fe-limitation in roots. Fe+AMB, Fe-sufficient + aCO₂; Fe+ELE, Fe-sufficient + eCO₂; Fe-AMB, Fe-limitation + aCO₂; Fe-ELE, Fe-limitation + eCO₂.

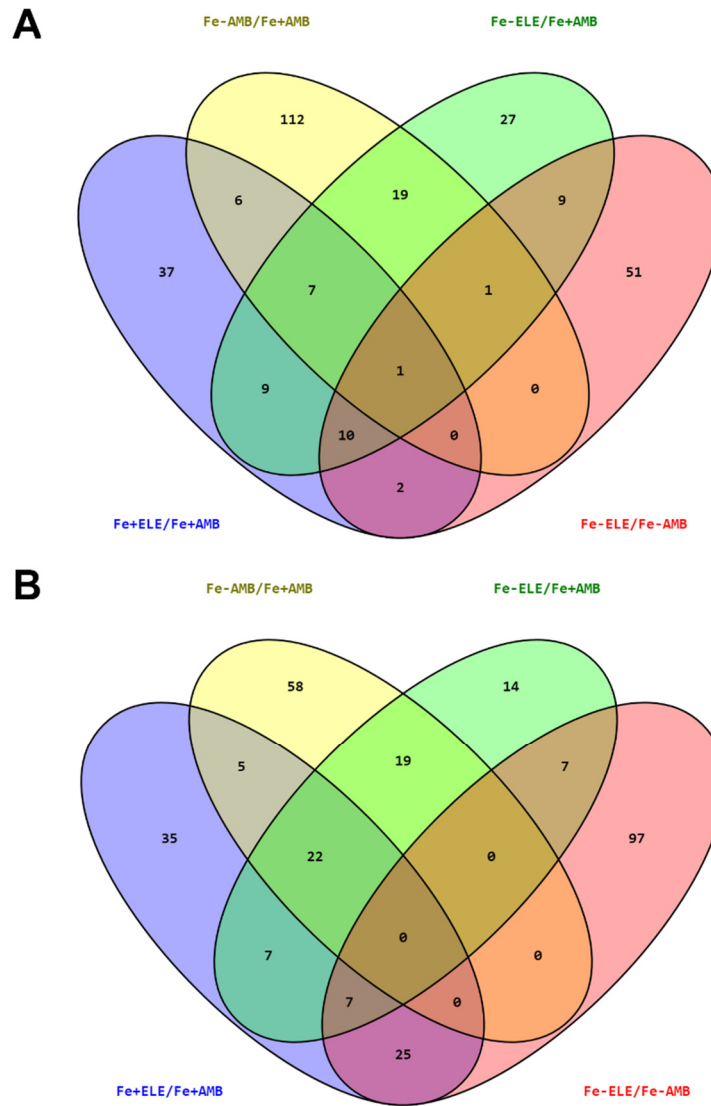


Figure S2. Venn diagram significantly displaying (a) upregulated and (b) downregulated proteins in response to eCO₂ and Fe-limitation in leaves. Fe+AMB, Fe-sufficient + aCO₂; Fe+ELE, Fe-sufficient + eCO₂; Fe-AMB, Fe-limitation + aCO₂; Fe-ELE, Fe-limitation + eCO₂.

[illegible]

GLYCOLYSIS / GLUCONEOGENESIS

Starch and sucrose metabolism

D-Glucose-1P

D-Glucose (extracellular)

D-Glucose-6P

α-D-Glucose

β-D-Glucose

β-D-Glucose-6P

β-D-Fructose-6P

β-D-Fructose-1,6P₂

Glyceraldehyde-3P

Glycerone-P

Glycerate-1,3P₂

Glycerate-2,3P₂

Glycerate-3P

Glycerate-2P

Phosphoenolpyruvate

Pyruvate

2-Hydroxyethyl-ThPP

Acetyl-CoA

Acetate

Acetaldehyde

EutG

Ethanol

L-Lactate

Propanoate metabolism

Pentose phosphate pathway

Carbon fixation in photosynthetic organisms

Citrate cycle

Pyruvate metabolism

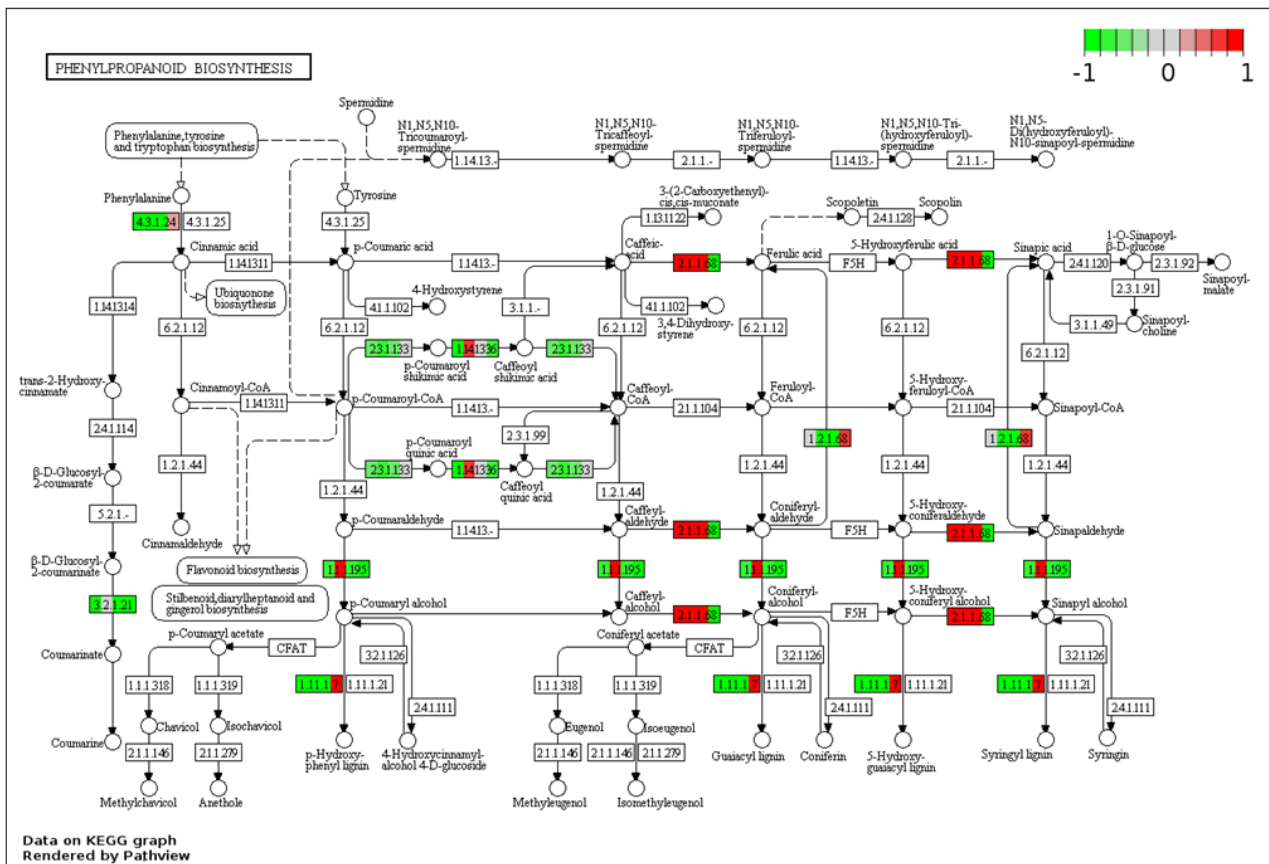
Enzymes (EC numbers):

- 2.7.1.41, 3.1.3.10, 3.1.3.9, 5.4.2.3, 2.7.1.199, 2.7.1.1, 2.7.1.63, 2.7.1.2, 2.7.1.147, 5.1.3.3, 5.1.3.13, 5.3.1.9, 3.1.3.11, 2.7.1.146, 2.7.1.90, 4.1.2.13, 5.3.1.1, 1.2.1.12, 1.2.1.59, 1.2.1.9, 1.2.7.6, 1.2.1.90, 5.4.2.4, 2.7.2.3, 3.1.3.13, 5.4.2.11, 5.4.2.12, 3.1.3.80, 4.2.1.11, 2.7.1.40, 1.2.4.1, 4.1.1.1, 1.2.4.1, 2.3.1.12, 1.2.4.1, 1.8.1.4, 1.2.1.13, 6.2.1.1, 6.2.1.13, 1.2.1.5, 1.2.1.-, 1.1.2.7, 1.1.2.8, 1.1.1.2, 1.1.1.2, 1.1.1.2, 1.1.1.2

Data on KEGG graph
Rendered by Pathview

Figure S3. Differential transcript expression in the ‘glycolysis/gluconeogenesis’ KEGG pathway in the response to eCO₂ and Fe- limitation in root (a), and leaf tissues (b). Each enzyme contains four color bars indicating the mean expression of Fe+ELE/Fe+AMB (first), Fe-AMB/Fe+AMB (second), Fe-ELE/Fe+AMB (third), and Fe-ELE/Fe-AMB (fourth) treatments. Red color indicating increased expression, and green indicating decreased expression. 1.1.1.1 - alcohol dehydrogenase; 1.1.1.27 - L-lactate dehydrogenase; 1.2.1.3 - aldehyde dehydrogenase; 1.2.1.9 - NADP-dependent glyceraldehyde-3-phosphate dehydrogenase; 1.2.1.12 - glyceraldehyde 3-phosphate dehydrogenase; 2.7.1.11 - ATP-dependent 6-phosphofructokinase; 2.7.1.40 - pyruvate kinase; 2.7.2.3 - phosphoglycerate kinase; 4.1.1.1 - pyruvate decarboxylase; 4.1.2.13 - fructose-bisphosphate aldolase; 4.2.1.11 - enolase; 5.1.3.15 - glucose-6-phosphate 1-epimerase; 5.4.2.2 - phosphoglucotransferase; 5.4.2.11 - 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; and 6.2.1.1 - acetyl-CoA synthetase.

A



B

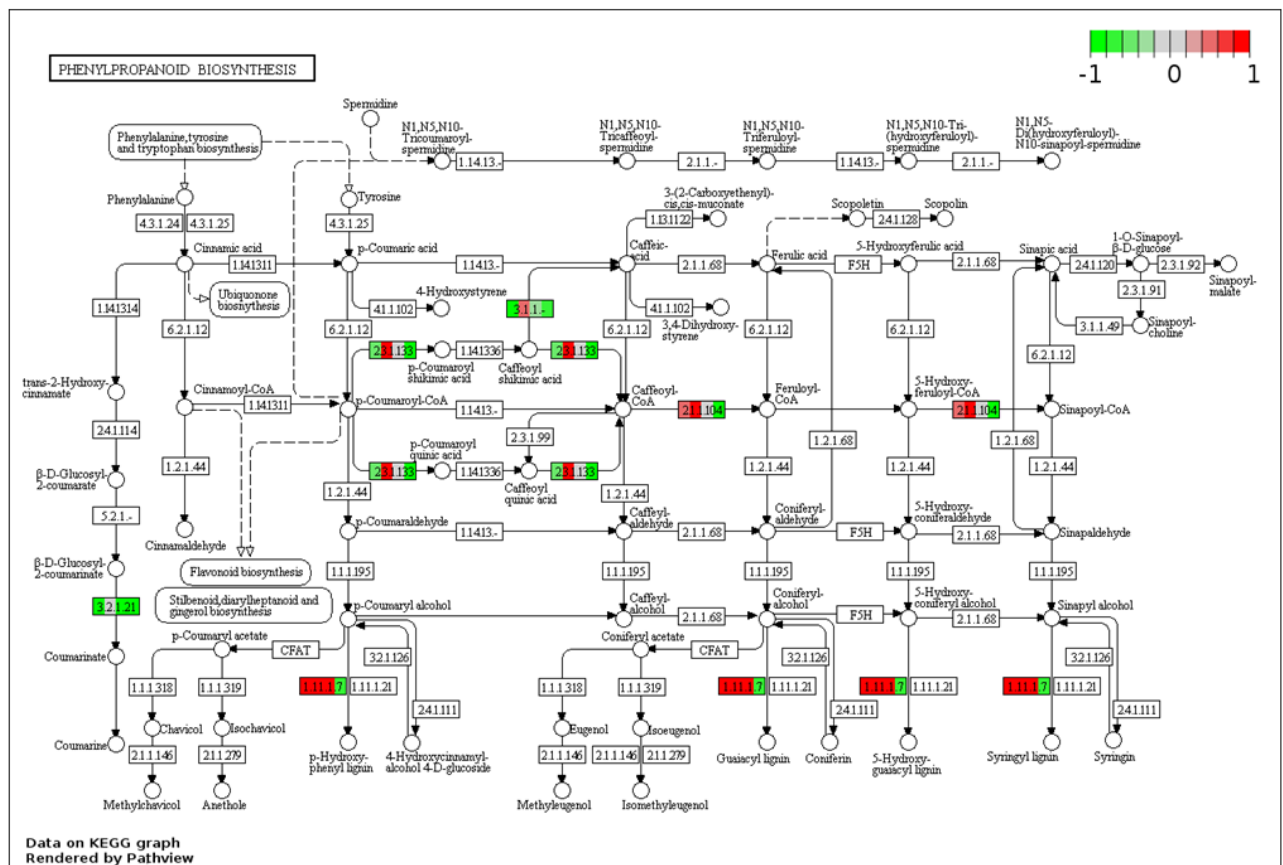


Figure S4. Differential transcript expression in the 'phenylpropanoid biosynthesis' KEGG pathway in the response to eCO₂ and Fe- limitation in root (a), and leaf tissues (b). Each pathway component contains four color bars indicating the mean expression of Fe+ELE/Fe+AMB (first), Fe-AMB/Fe+AMB (second), Fe-ELE/Fe+AMB (third), and Fe-ELE/Fe-AMB (fourth) treatments. Red color indicating increased expression, and green indicating decreased expression. 1.1.1.195 - cinnamyl-alcohol dehydrogenase; 1.2.1.68 - aldehyde dehydrogenase; 1.1.1.17 - peroxidase; 1.14.14.96 - cytochrome P450; 2.1.1.68 - caffeic acid 3-O-methyltransferase; 2.1.1.104 - caffeoyl-CoA O-methyltransferase; 2.3.1.133 - shikimate O-hydroxycinnamoyltransferase; 3.1.1.- - caffeoyl shikimate esterase; 3.2.1.21 - vicianin beta-glucosidase; and 4.3.1.24 - phenylalanine ammonia-lyase.