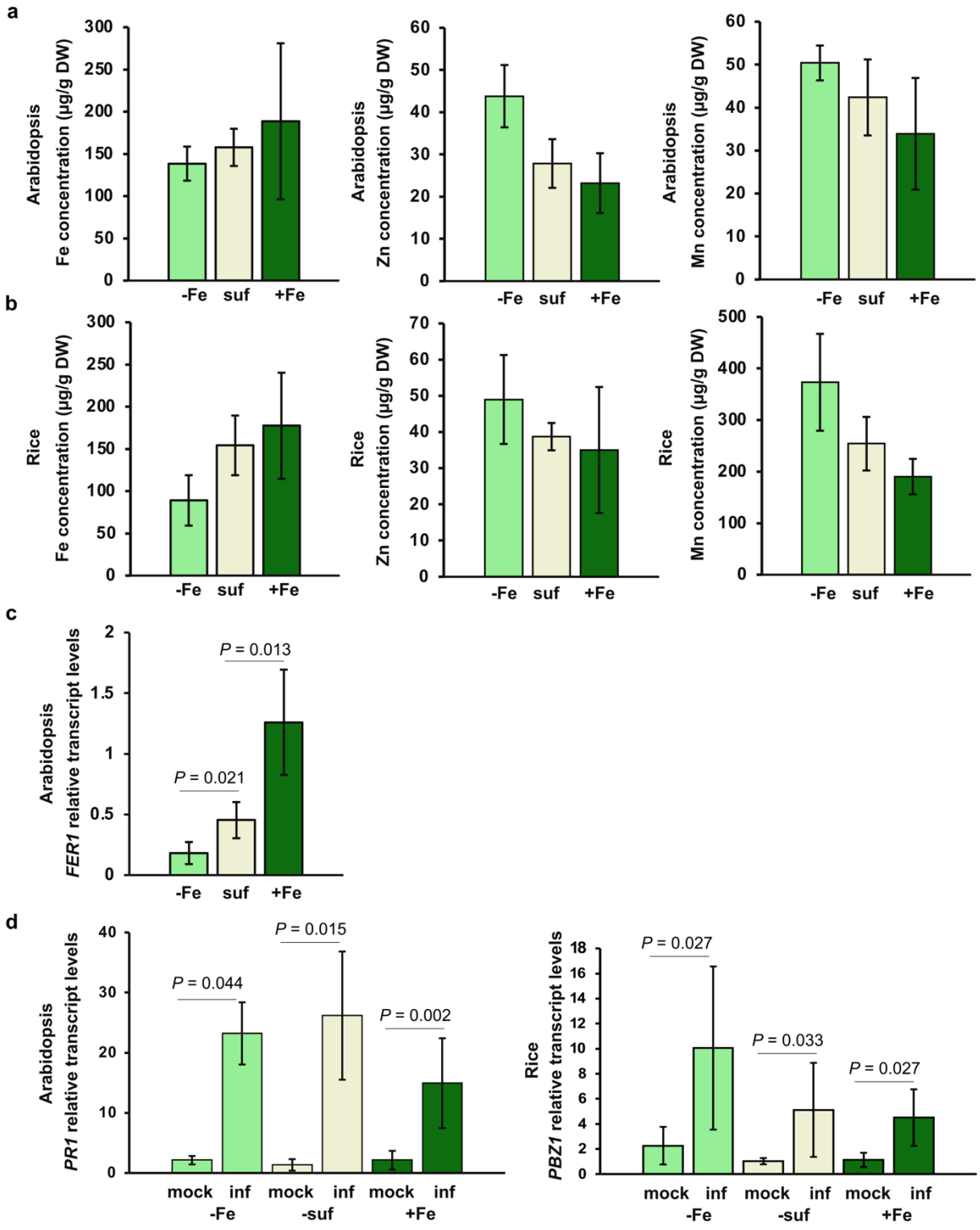
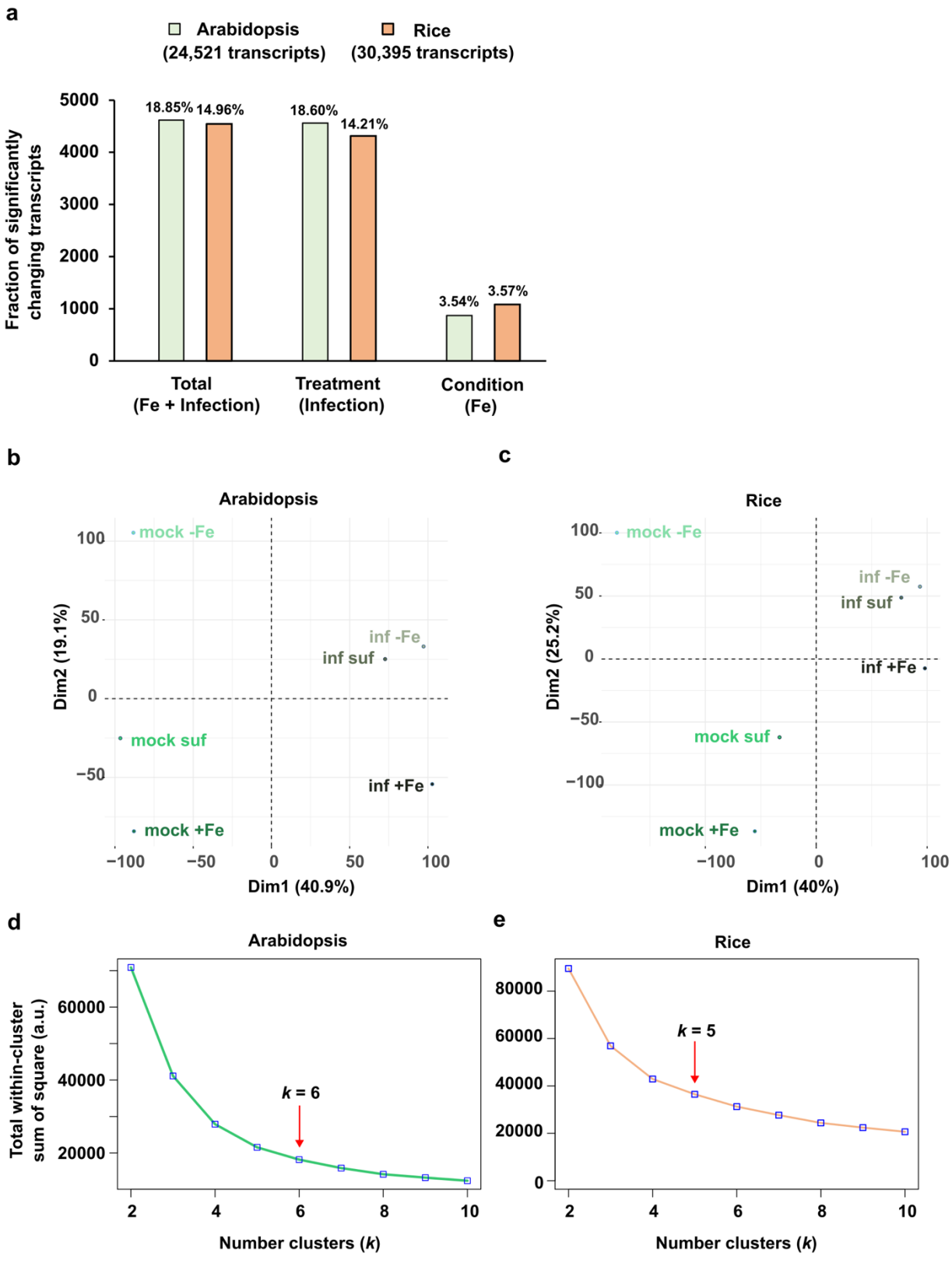
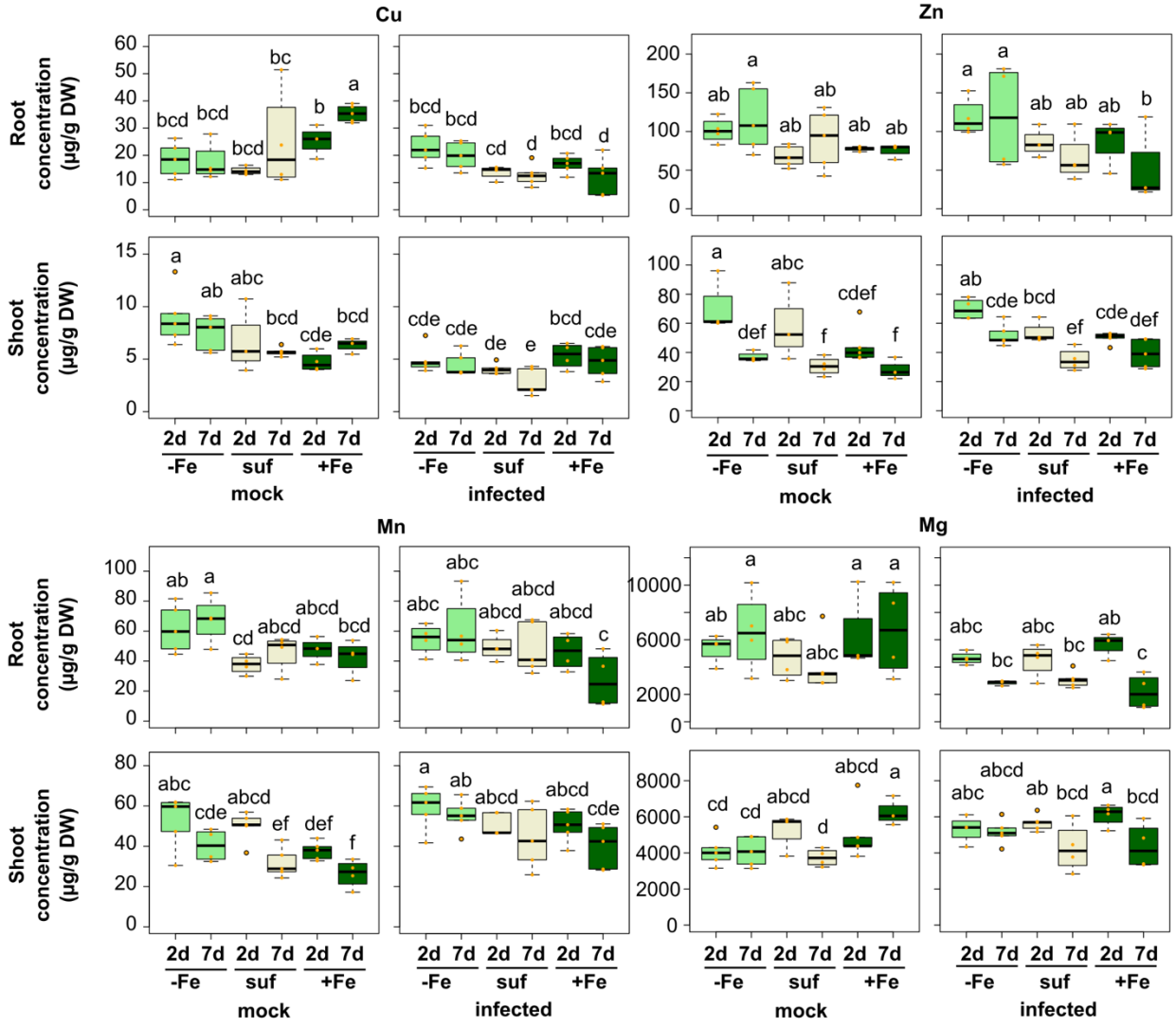


Supplementary Figure 1. Primary characterisation of Arabidopsis and rice responses under different Fe availability conditions. Total concentration of Fe, Zn and Mn in leaves of 18-day-old Arabidopsis (a) and rice (b) cultivated under semi-hydroponic conditions for low (2 µM Fe-EDTA: -Fe),

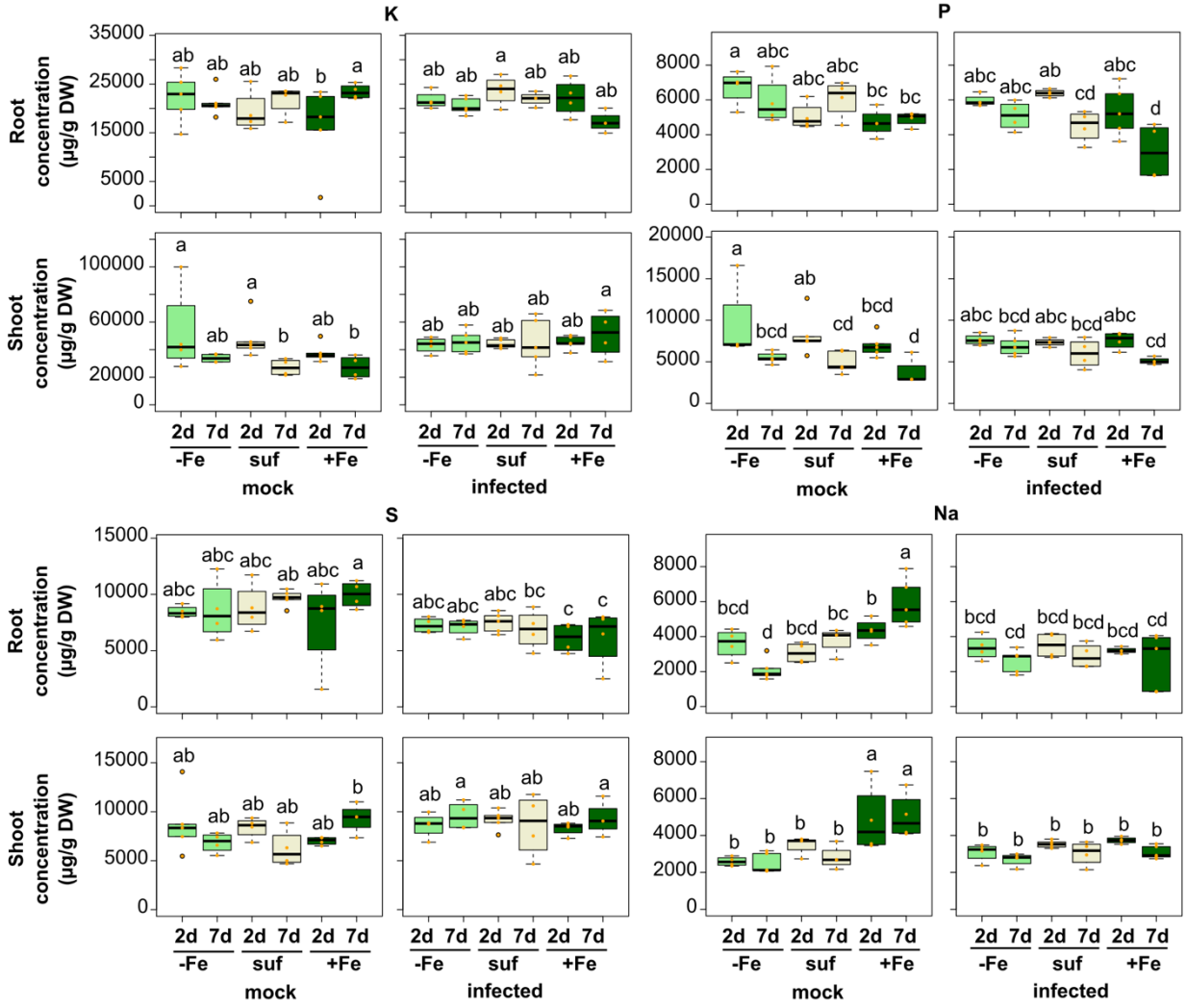
sufficient (20 µM Fe-EDTA: suf), and high (200 µM Fe-EDTA: +Fe) iron availability determined by ICP-OES. Bars represent means ± SD of n = 5 independent plants. Relative transcript levels of *FERRITIN1* (*FER1*) to assess the Fe status in Arabidopsis leaves (c). Relative transcript levels of *PATHOGENESIS RELATED1* (*PR1*) and *PROBENAZOLE-INDUCIBLE PROTEIN* (*PBZ1*) in Arabidopsis and rice plants that were mock treated or infected with *Colletotrichum higginsianum* (Arabidopsis) or *Magnaporthe oryzae* (rice) 2 dpi (d). Transcript levels were determined by qPCR with specific oligonucleotides and referred to *ACT2* (Arabidopsis) or *UBQ10* (rice). Bars represent means ± SD of $n \geq 3$ independent plants. Statistically significant differences are calculated according to the Student's t test.


a
Arabidopsis
(24,521 transcripts)
Rice
(30,395 transcripts)
Fraction of significantly changing transcripts
5000
4000
3000
2000
1000
0
18.85%
14.96%
18.60%
14.21%
3.54%
3.57%
Total
(Fe + Infection)
Treatment
(Infection)
Condition
(Fe)
b
Arabidopsis
mock -Fe
inf -Fe
inf suf
mock suf
inf +Fe
mock +Fe
Dim2 (19.1%)
Dim1 (40.9%)
c
Rice
mock -Fe
inf -Fe
inf suf
inf +Fe
mock suf
mock +Fe
Dim2 (25.2%)
Dim1 (40%)
d
Arabidopsis
Total within-cluster sum of square (a.u.)
k = 6
Number clusters (k)
e
Rice
k = 5
Number clusters (k)

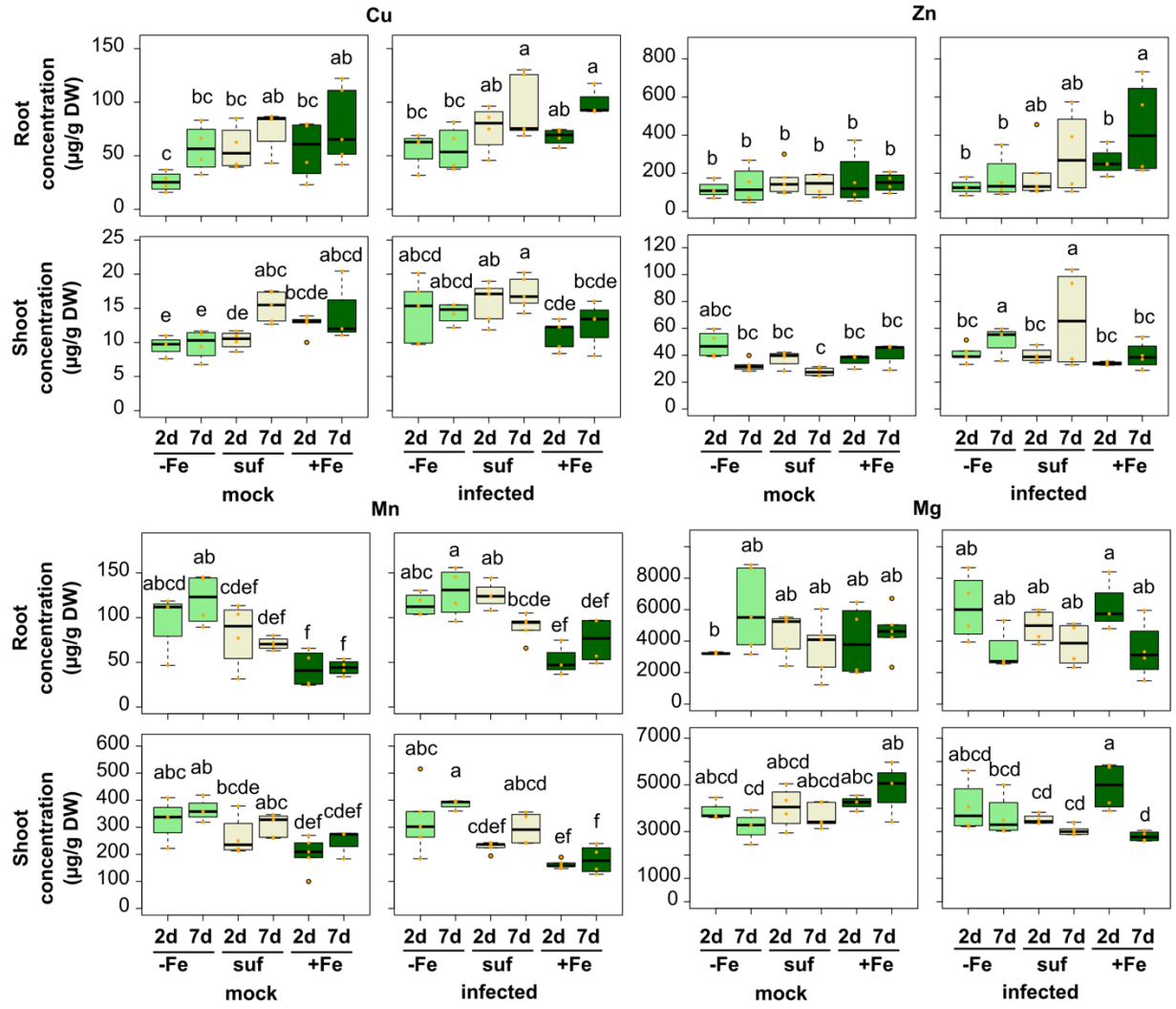
Supplementary Figure 2. Summary of transcriptome changes in Arabidopsis and rice. RNA-Seq was analysed to determine transcripts significantly changing in response to condition (different Fe availability) and treatment (fungal infection) and the totals (responsive to Fe availability and/or fungal infection) (adjusted $P \leq 0.05$, Likelihood ratio test). The percentage of changing transcripts with respect to the total covered transcripts (normalised counts > 0 across all samples) in the RNA-Seq is provided (a). Principal component analysis of transcriptome changes in Arabidopsis (b) and rice (c) were elaborated using the average of normalised counts per condition and treatment. Determination of the optimal number of expression patterns (d, e). The *k*-means method was employed to select the highest number of clusters (*k*) for transcript changes in Arabidopsis (d) and rice (e) that resulted in the minimal total within-cluster sum of square measure.



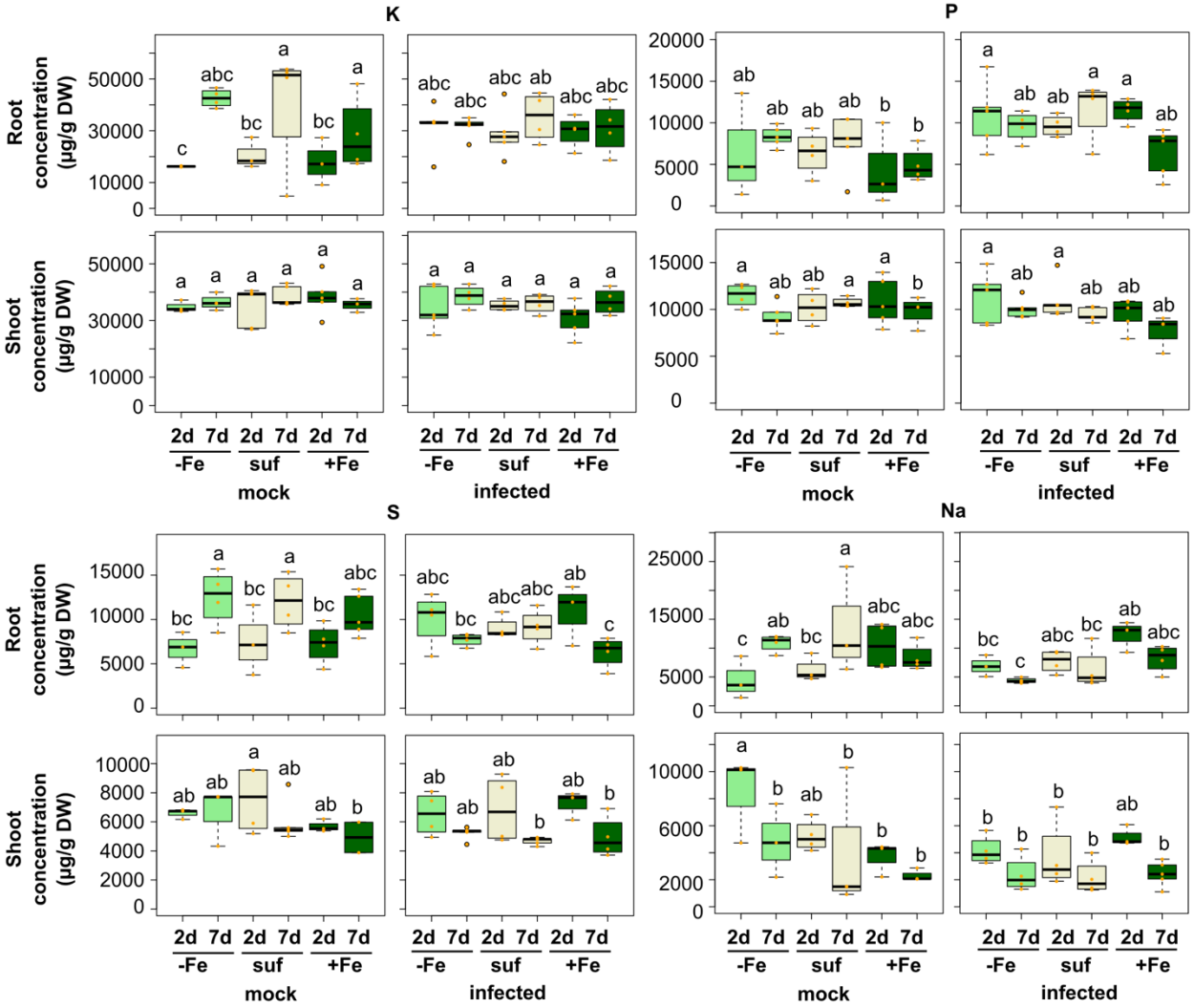
Supplementary Figure 3. Further analysis of the mineral composition of Arabidopsis. Total Cu, Zn, Mn and Mg content in shoots and roots from Arabidopsis cultivated under low, sufficiency, and high Fe (-Fe, suf, +Fe) were determined 2 and 7 days after mock treatment or pathogen infection. Box plots represent data from n = 5 independent experiments.



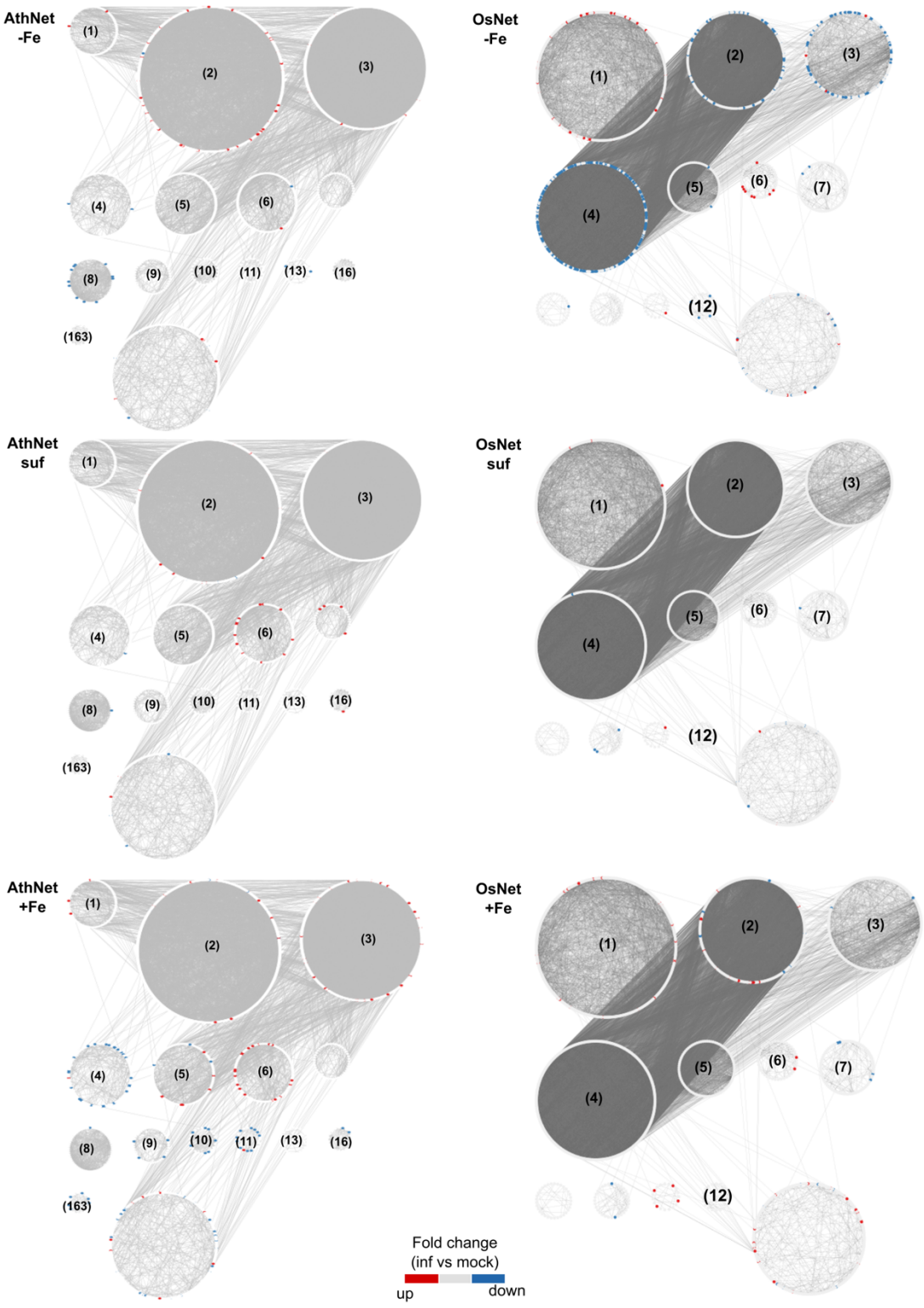
Supplementary Figure 4. Further analysis of the mineral composition of Arabidopsis. Total K, P, S and Na content in shoots and roots from Arabidopsis cultivated under low, sufficiency, and high Fe (-Fe, suf, +Fe) were determined 2 and 7 days after mock treatment or pathogen infection. Box plots represent data from n = 5 independent experiments.



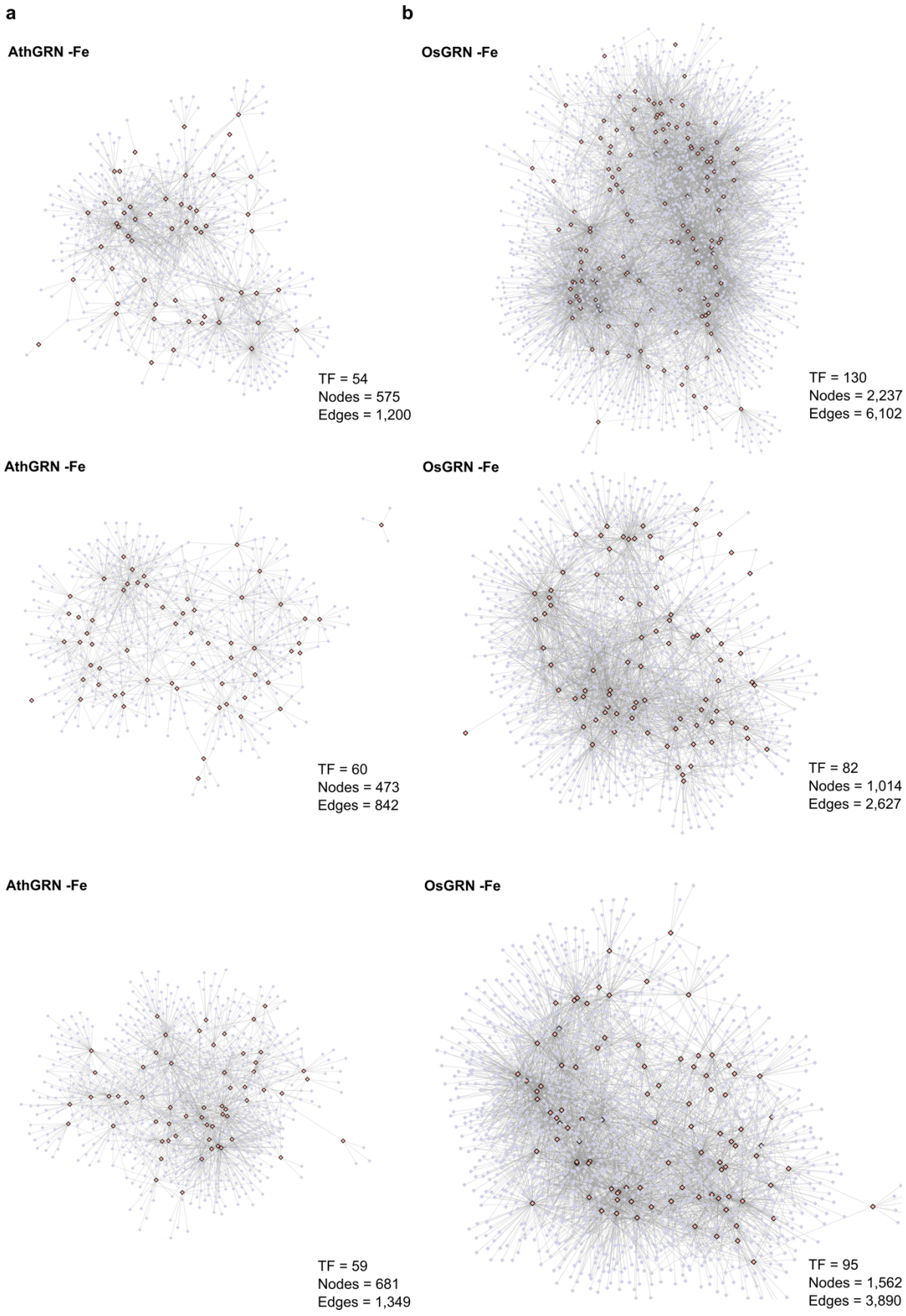
Supplementary Figure 5. Further analysis of the mineral composition of rice. Total Cu, Zn, Mn and Mg content in shoots and roots from rice cultivated under low, sufficiency, and high Fe (-Fe, suf, +Fe) were determined 2 and 7 days after mock treatment or pathogen infection. Box plots represent data from n= 5 independent experiments.



Supplementary Figure 6. Further analysis of the mineral composition of rice. Total K, P, S and Na content in shoots and roots from rice cultivated under low, sufficiency, and high Fe (-Fe, suf, +Fe) were determined 2 and 7 days after mock treatment or pathogen infection. Box plots represent data from n= 5 independent experiments.


AthNet
-Fe
(1)
(2)
(3)
(4)
(5)
(6)
(8)
(9)
(10)
(11)
(13)
(16)
(163)
OsNet
-Fe
(1)
(2)
(3)
(4)
(5)
(6)
(7)
(12)
AthNet
suf
(1)
(2)
(3)
(4)
(5)
(6)
(8)
(9)
(10)
(11)
(13)
(16)
(163)
OsNet
suf
(1)
(2)
(3)
(4)
(5)
(6)
(7)
(12)
AthNet
+Fe
(1)
(2)
(3)
(4)
(5)
(6)
(8)
(9)
(10)
(11)
(13)
(16)
(163)
OsNet
+Fe
(1)
(2)
(3)
(4)
(5)
(6)
(7)
(12)
Fold change
(inf vs mock)
up
down

Supplementary Figure 7. Position of differentially expressed genes in transcriptome correlation networks. Specific Arabidopsis and rice DEGs for comparisons between mock and infected plants under each Fe availability were mapped in the corresponding correlation networks. Colours indicate the sign of change to mock conditions. The identifiers of the communities are indicated in brackets.


a
b
AthGRN -Fe
TF = 54
Nodes = 575
Edges = 1,200
OsGRN -Fe
TF = 130
Nodes = 2,237
Edges = 6,102
AthGRN -Fe
TF = 60
Nodes = 473
Edges = 842
OsGRN -Fe
TF = 82
Nodes = 1,014
Edges = 2,627
AthGRN -Fe
TF = 59
Nodes = 681
Edges = 1,349
OsGRN -Fe
TF = 95
Nodes = 1,562
Edges = 3,890

Supplementary Figure 8. Gene Regulatory Networks operating in the response to fungal infection depending on Fe availability. Arabidopsis and rice transcription factors and DEGs lists were used to infer the Gene Regulatory Networks (GRNs) operating in response to fungal infection using the GENIE3 method. The number of transcription factors (TF), nodes, and edges in each network are provided.