
Supplementary information

Advanced material modulation of nutritional and phytohormone status alleviates damage from soybean sudden death syndrome

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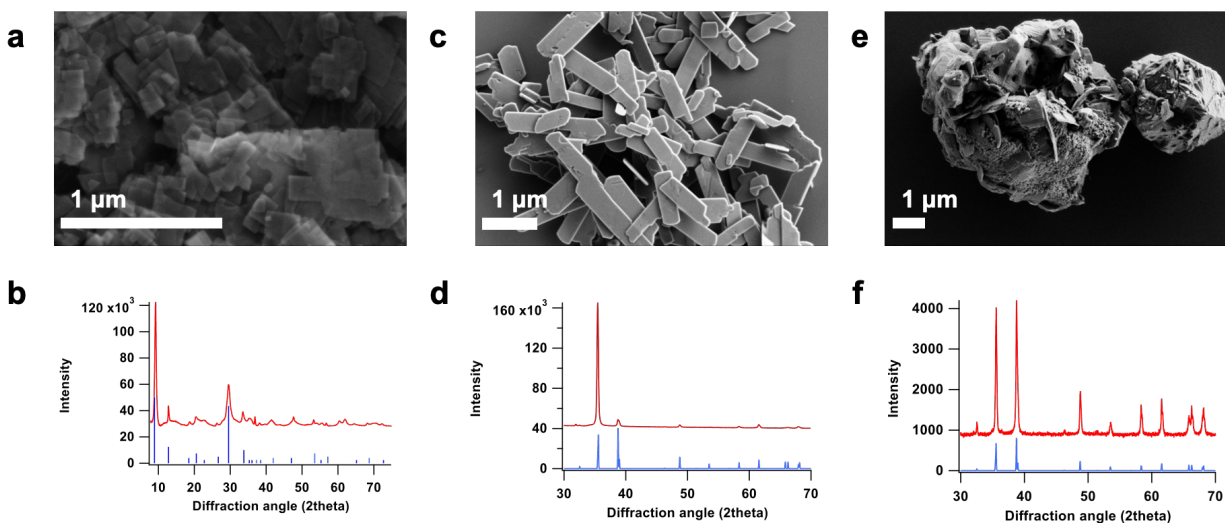
Supplementary Information

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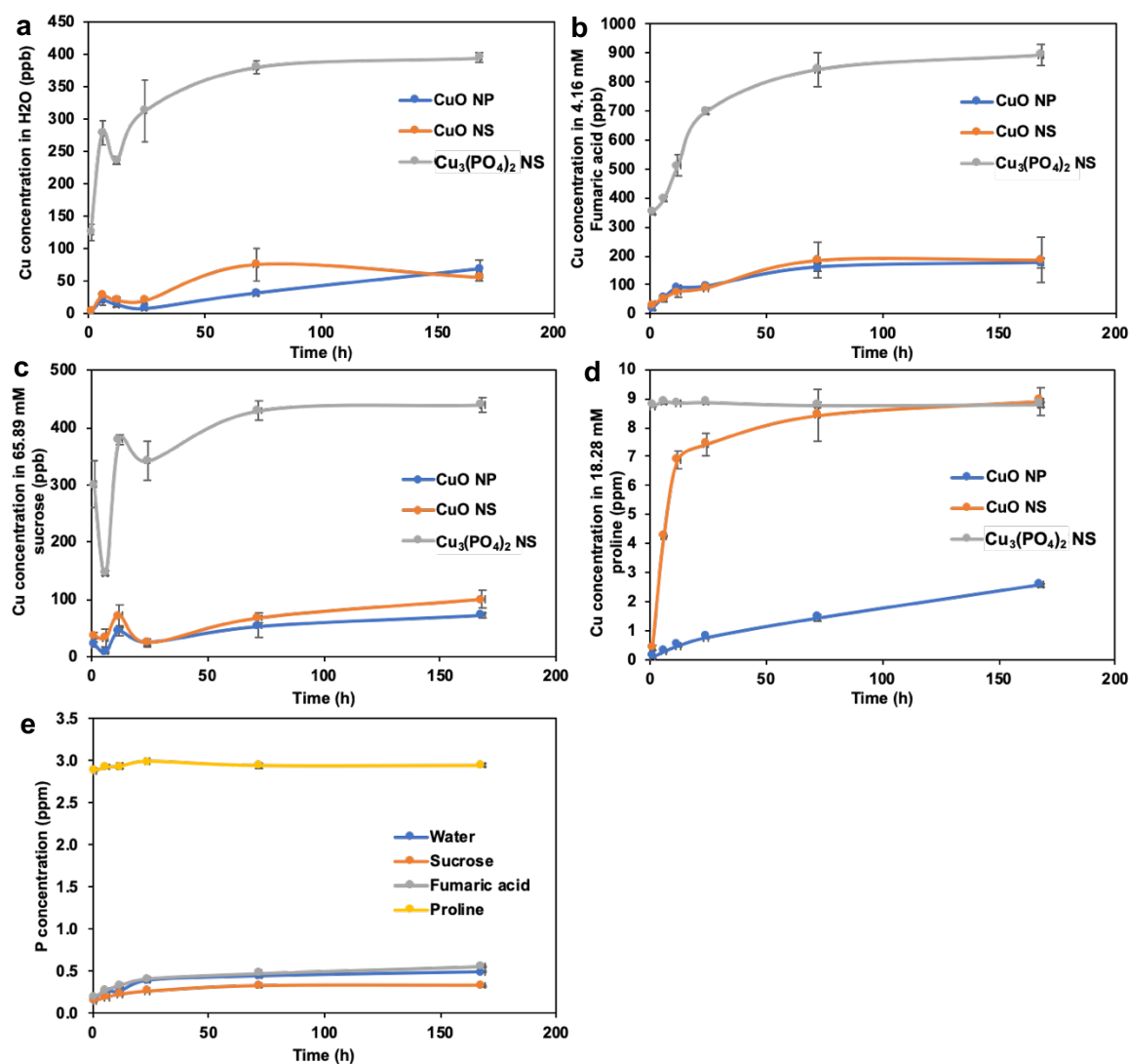
Advance material modulation of nutritional and phytohormone status alleviates damage from soybean sudden death syndrome (SDS) and increases crop growth

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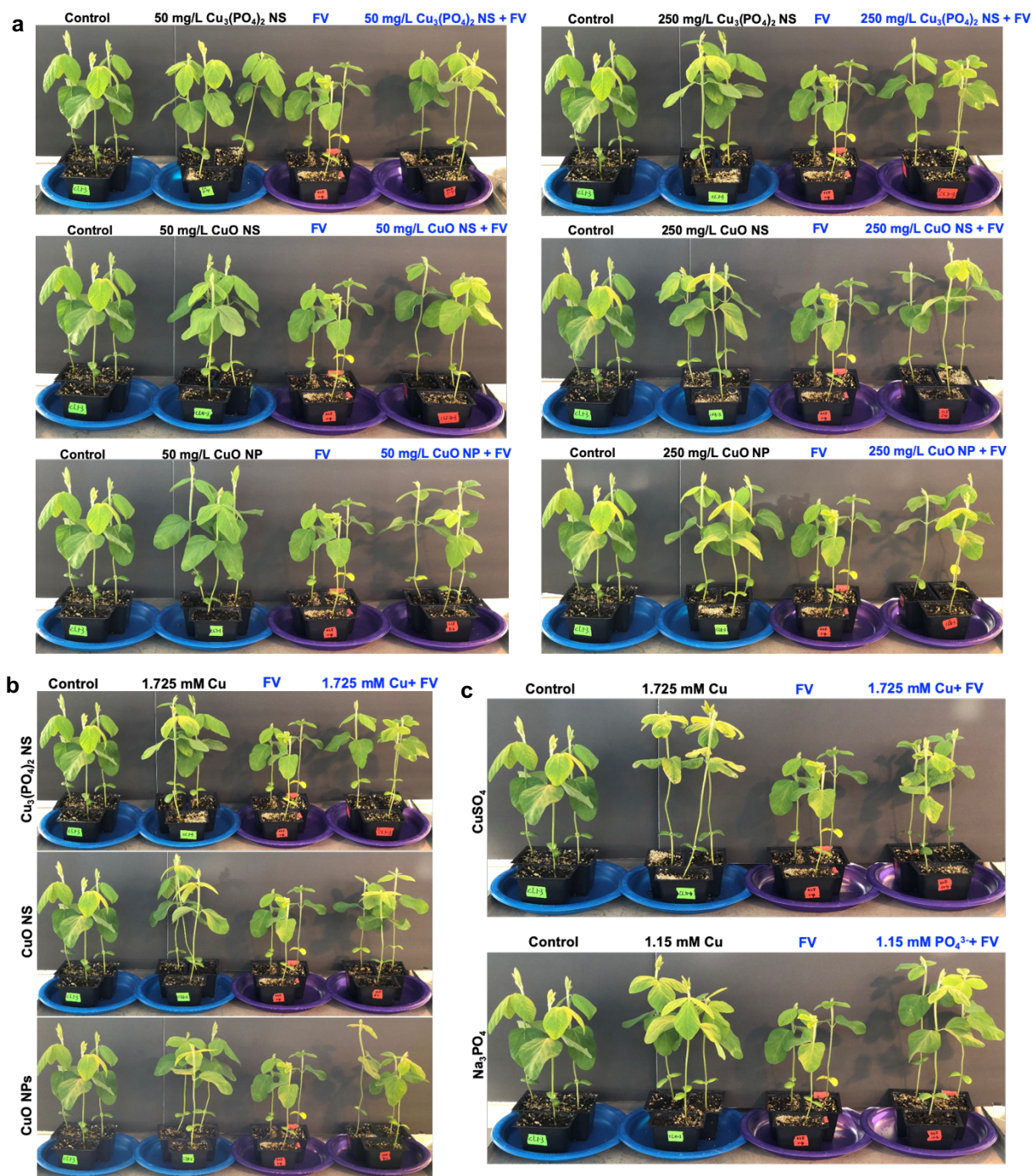
*Corresponding author: Jason.White@ct.gov



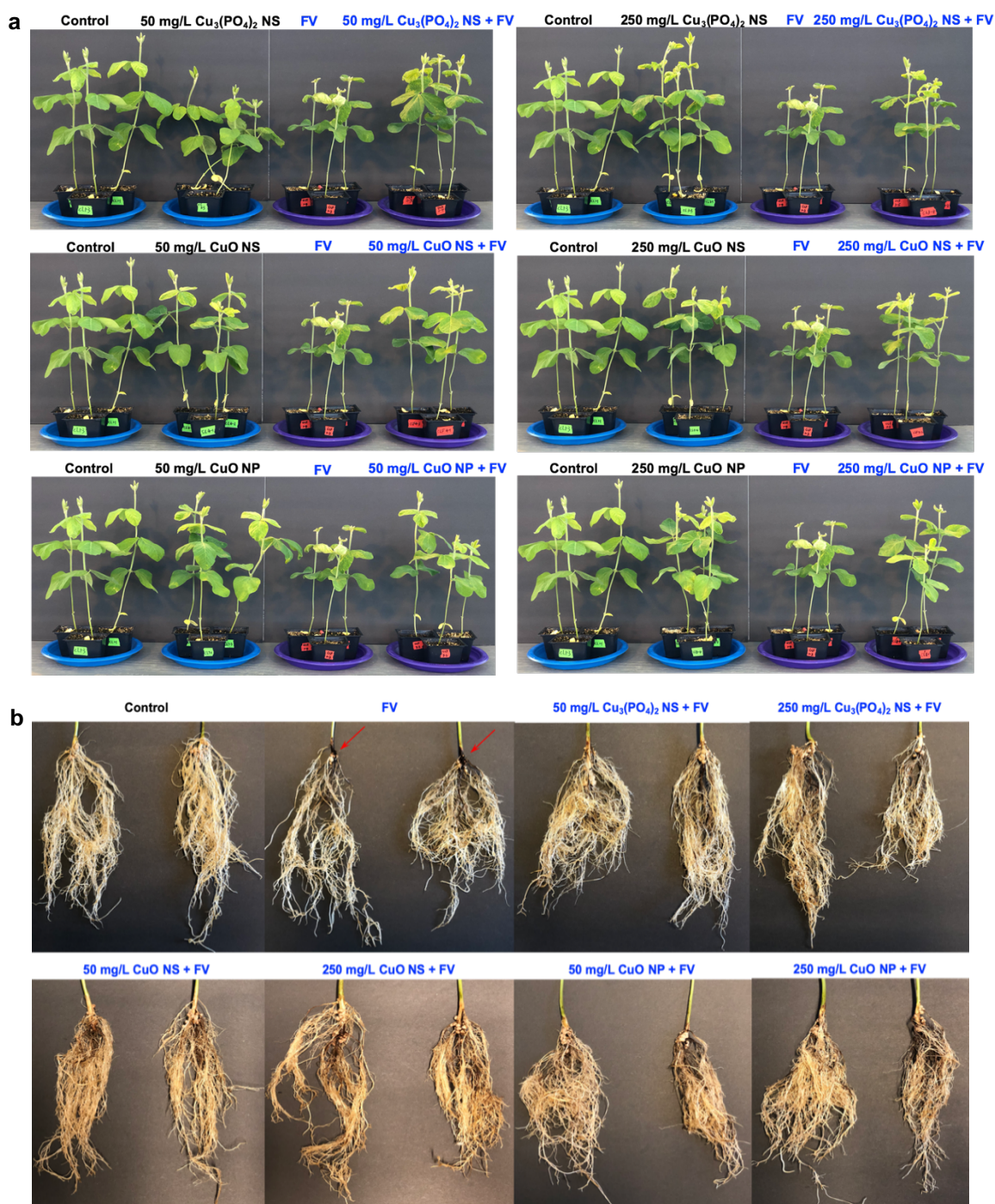
Supplementary Figure 1. SEM image and XRD spectra of in-house synthesized $\text{Cu}_3(\text{PO}_4)_2$ nanosheets (a, b), CuO nanosheets (c, d) and commercial CuO nanoparticles (e, f).



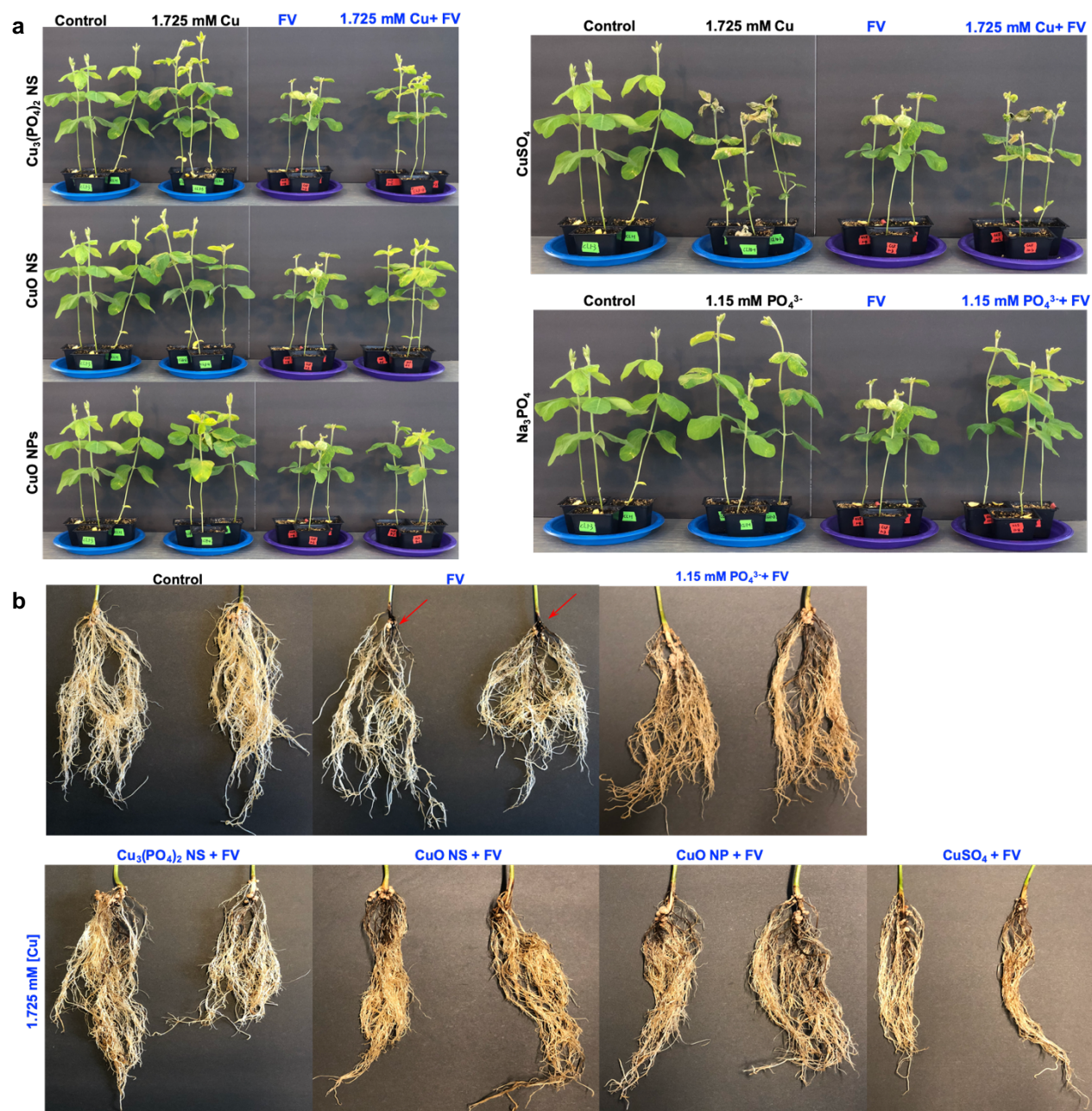
Supplementary Figure 2. Time dependent dissolution of Cu^{2+} from in-house synthesized $\text{Cu}_3(\text{PO}_4)_2$ nanosheets, CuO nanosheets and commercial CuO nanoparticles in deionized water (a), fumaric acid (b), sucrose (c), proline (d) at pH 7.5. P release from the $\text{Cu}_3(\text{PO}_4)_2$ nanosheets in water, sucrose, fumaric acid, and proline was also measured in Figure e.



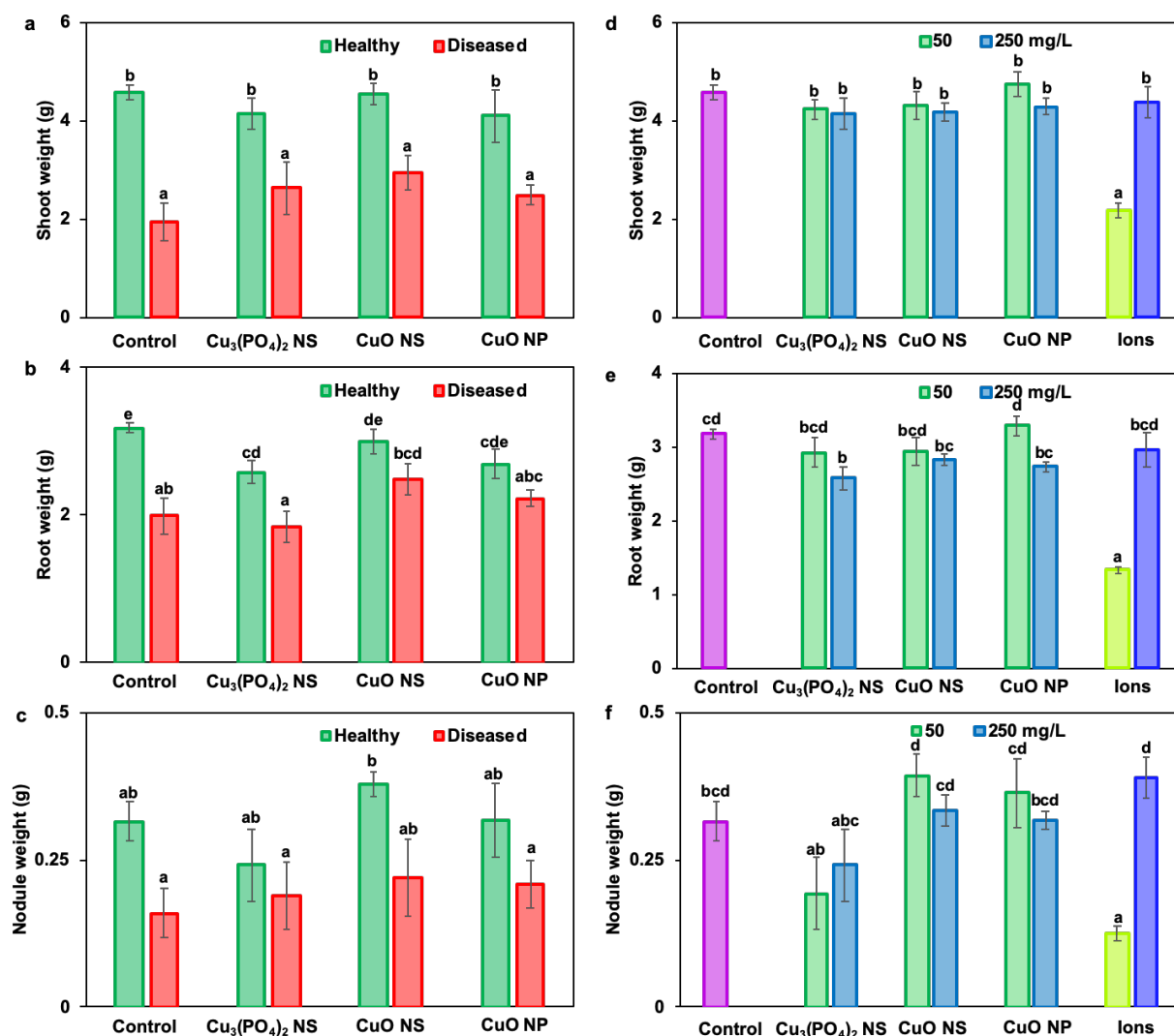
Supplementary Figure 3. Phenotypic images of FV infected soybean foliar treated with different types of Cu-based NMs after the first time NM-exposure. Figure **a** shows plant images of the aboveground part of soybean in the treatments with different types of Cu-based NMs at 50 and 250 mg/L (mass of particles); Figure **b** shows the plant images of the aboveground part of soybean in the treatments with different types of Cu-based NMs at 1.725 mM Cu (different Cu-based NMs were normalized by the equivalent amounts of Cu); Figure **c** shows the plant images of the aboveground part of soybean in the Cu^{2+} and PO_4^{3-} ionic treatment.



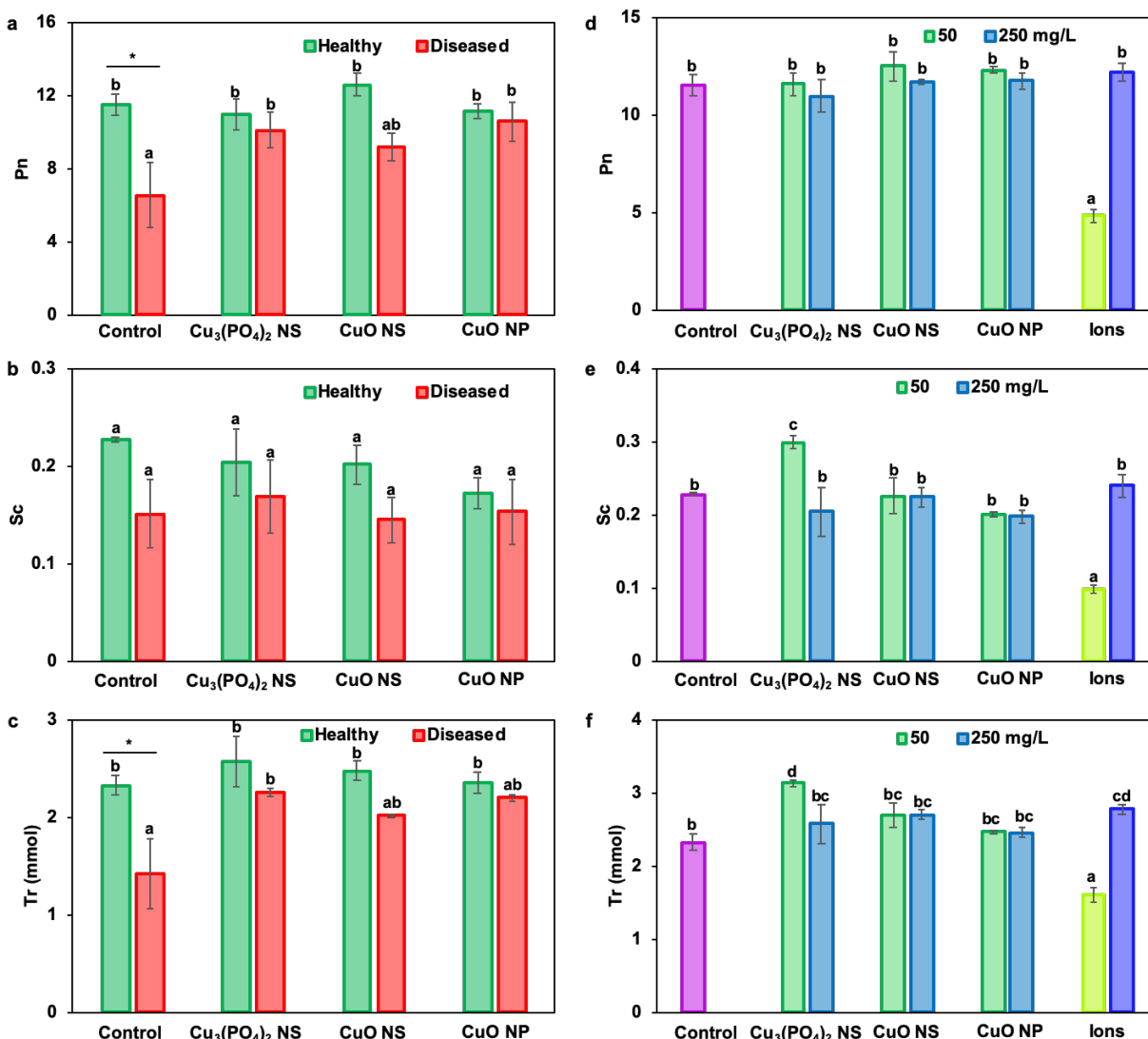
Supplementary Figure 4. Phenotypic images of FV infected soybean foliar treated with different types of Cu-based NMs at 50 and 250 mg/L at harvest. Figure **a** shows plant images of the aboveground part of soybean in the treatments with different types of Cu-based NMs at 50 and 250 mg/L (mass of particles); Figure **b** shows root images of FV infected soybean across all the Cu-based NM treatments. Red arrow point towards the black tissues indicates the FV infection in roots.



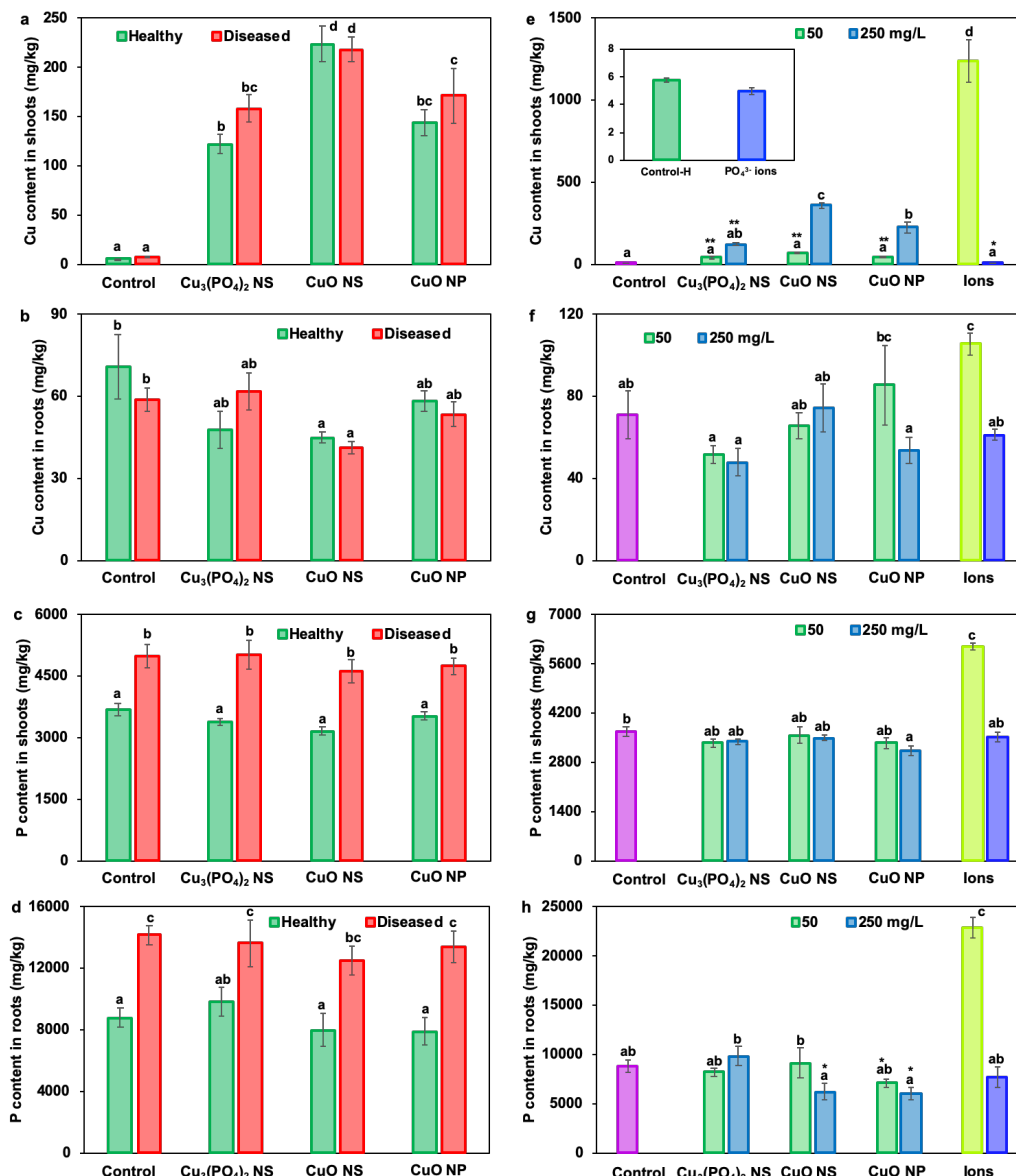
Supplementary Figure 5. Phenotypic images of FV infected soybean foliar treated with different types of Cu-based NMs with the equivalent molar concentration of Cu or the ionic forms of Cu/ PO_4^{3-} at harvest. Figure **a** shows plant images of the aboveground part of soybean in the NM treatments with equivalent amounts of Cu; Figure **b** shows root images of FV infected soybean in the NM treatments with equivalent amounts of Cu. Red arrow point towards the black tissues indicates the FV infection in roots.



Supplementary Figure 6. Fresh weight of different types of Cu-based NM treated soybean infected with or without FV. Figure a-c represents shoot, root, and nodule weight, respectively, in the healthy (■) and diseased (■) treatments with different types of Cu-based NMs at 1.725 mM [Cu]. Figure d-f represents shoot, root, and nodule weight, respectively, in the healthy treatment with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO_4^{3-} . In Figure d-f, purple bar (■) represents the healthy control; light green bar (■) and blue bar (■) represents 1.725 mM [Cu] ionic control and 1.175 mM $[\text{PO}_4^{3-}]$ ionic control, which is the same molar concentration of [Cu] and $[\text{PO}_4^{3-}]$ in 250 mg/L $\text{Cu}_3(\text{PO}_4)_2$ NS, respectively. Error bars correspond to standard error of mean (n=5). Values followed by different letters are significantly different at $p < 0.05$.

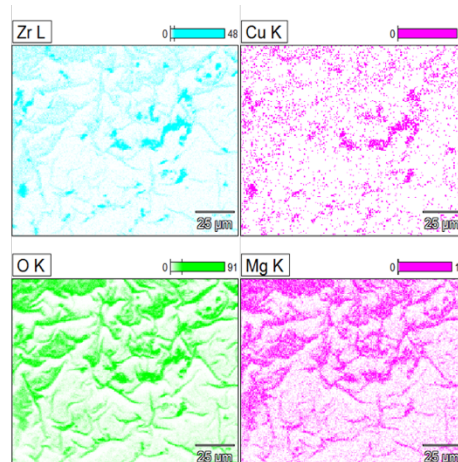
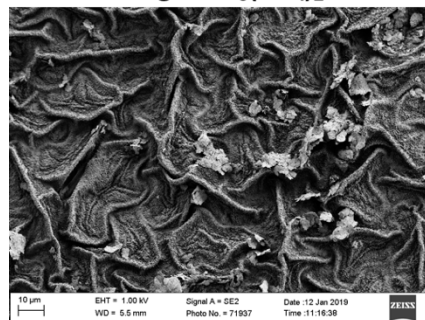


Supplementary Figure 7. Photosynthetic efficiency of different types of Cu-based NM treated soybean infected with or without FV. Figure **a-c** represents net photosynthetic rate, stomatal conductance and transpiration rate, respectively, in the healthy (■) and diseased (■) treatments with different types of Cu-based NMs at 1.725 mM Cu. Figure **d-f** represents net photosynthetic rate, stomatal conductance and transpiration rate, respectively, in the healthy treatment with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO₄³⁻. In Figure **d-f**, purple bar (■) represents the healthy control; light green bar (■) and blue bar (■) represents 1.725 mM [Cu] ionic control and 1.175 mM [PO₄³⁻] ionic control, which is the same molar concentration of [Cu] and [PO₄³⁻] in 250 mg/L Cu₃(PO₄)₂ NS, respectively. Error bars correspond to standard error of mean (n=3). Values followed by different letters are significantly different at p<0.05. Single asterisk “*” indicates significant difference between the diseased control and the healthy control at p<0.05 using a student t-test.

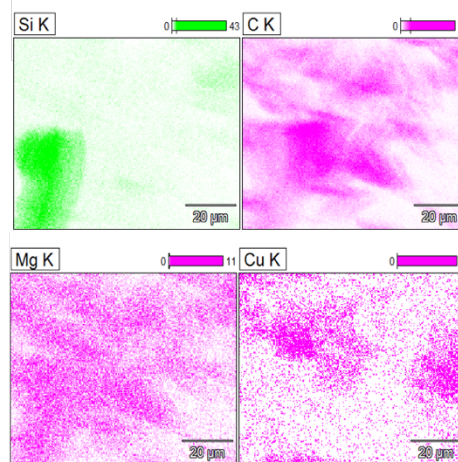
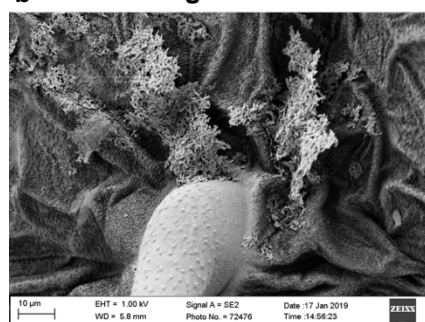


Supplementary Figure 8. Cu and P content in different types of Cu-based NM treated shoots and roots infected with or without FV. Figure **a-b** represents the Cu content in shoots and roots, respectively, in the healthy (green) and diseased (red) treatments with different types of Cu-based NMs at 1.725 mM [Cu]; Figure **c-d** represents the P content in shoots and roots, respectively, in the healthy (green) and diseased (red) treatments with different types of Cu-based NMs at 1.725 mM [Cu]. Figure **e-f** represents the Cu content in shoots and roots, respectively, in the healthy treatment with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO₄³⁻; Figure **g-h** represents the P content in shoots and roots, respectively, in the healthy treatment with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO₄³⁻; in Figure **e-h**, purple bar (pink) represents the healthy control; light green bar (light green) and blue bar (blue) represents 1.725 mM [Cu] ionic control and 1.175 mM [PO₄³⁻] ionic control, which is the same molar concentration of [Cu] and [PO₄³⁻] in 250 mg/L Cu₃(PO₄)₂ NS, respectively. Error bars correspond to standard error of mean (n=4). Values followed by different letters are significantly different at p<0.05. In addition, in Figure **e-h**, single asterisk “*” indicates significant difference between the healthy control and each Cu-based NM treatment at p<0.05; double asterisks “**” indicate significant difference between the healthy control and each Cu-based NM treatment at p<0.01 using a student t-test.

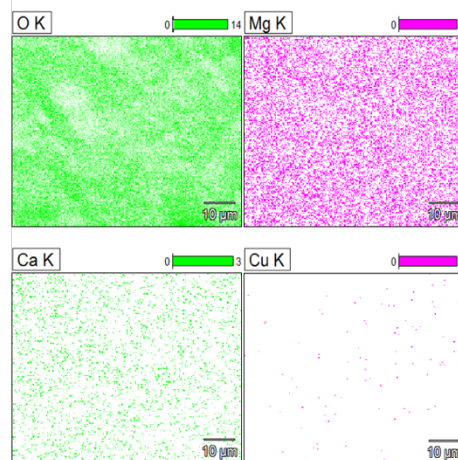
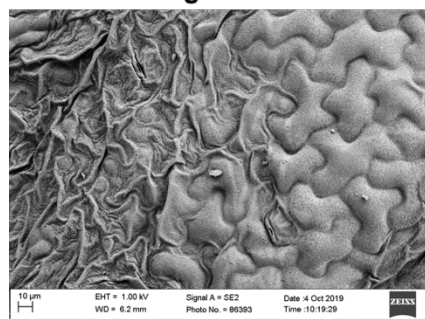
a 250 mg/L $\text{Cu}_3(\text{PO}_4)_2$ NS



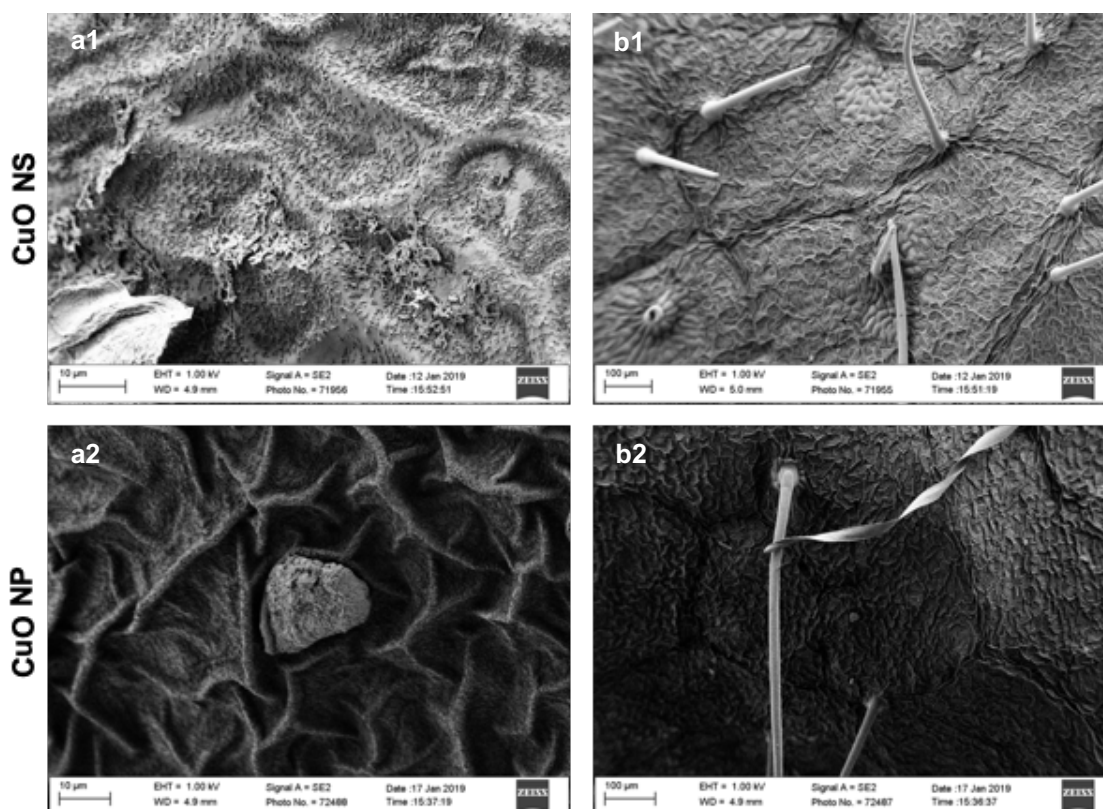
b 250 mg/L CuO NS



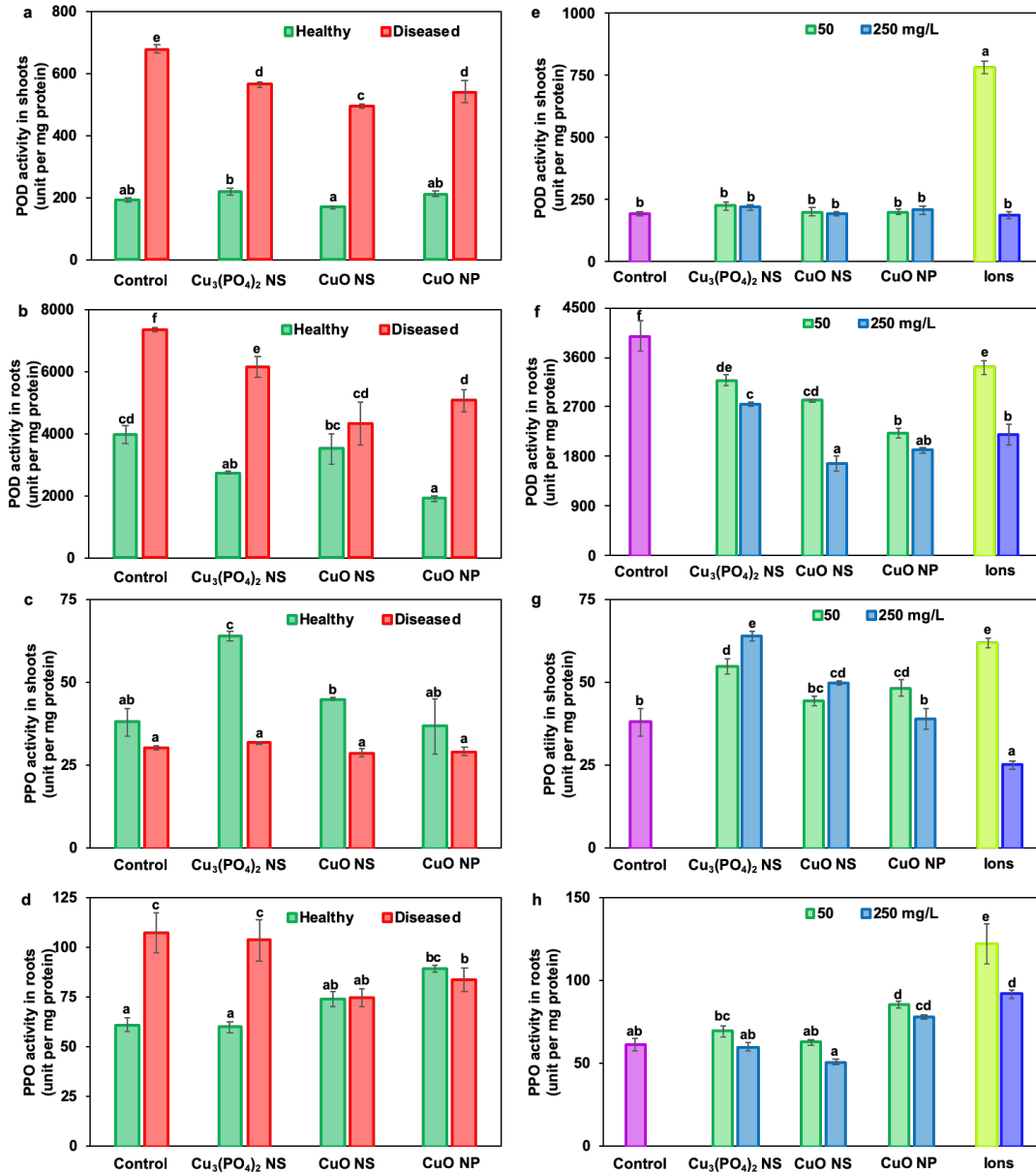
c 250 mg/L CuO NP



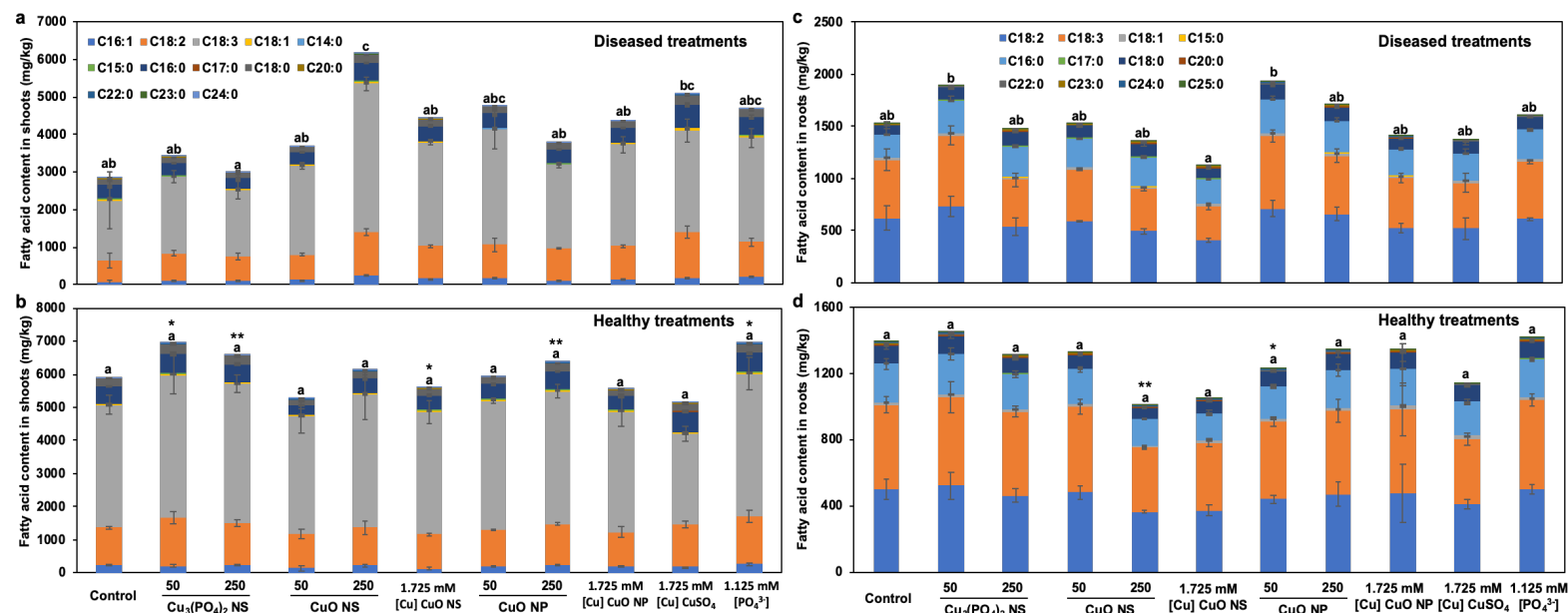
Supplementary Figure 9. Cu-based NM distribution in FV infected soybean foliar treated with 250 mg/L $\text{Cu}_3(\text{PO}_4)_2$ NS (a), CuO NS (b), and CuO NP (c) suspensions. Figure a shows $\text{Cu}_3(\text{PO}_4)_2$ NS distribution on the soybean leaf surface and the corresponding Cu mapping confirms the presence of Cu on the leaf. Figure b shows CuO NS distribution on the leaf surface and the corresponding Cu mapping confirms the presence of Cu on the leaf. Figure c shows CuO NP distribution on the leaf surface and the corresponding Cu mapping confirms the presence of Cu on the leaf. Relative surface coverage analyzed by Image J shows no statistically significant differences.



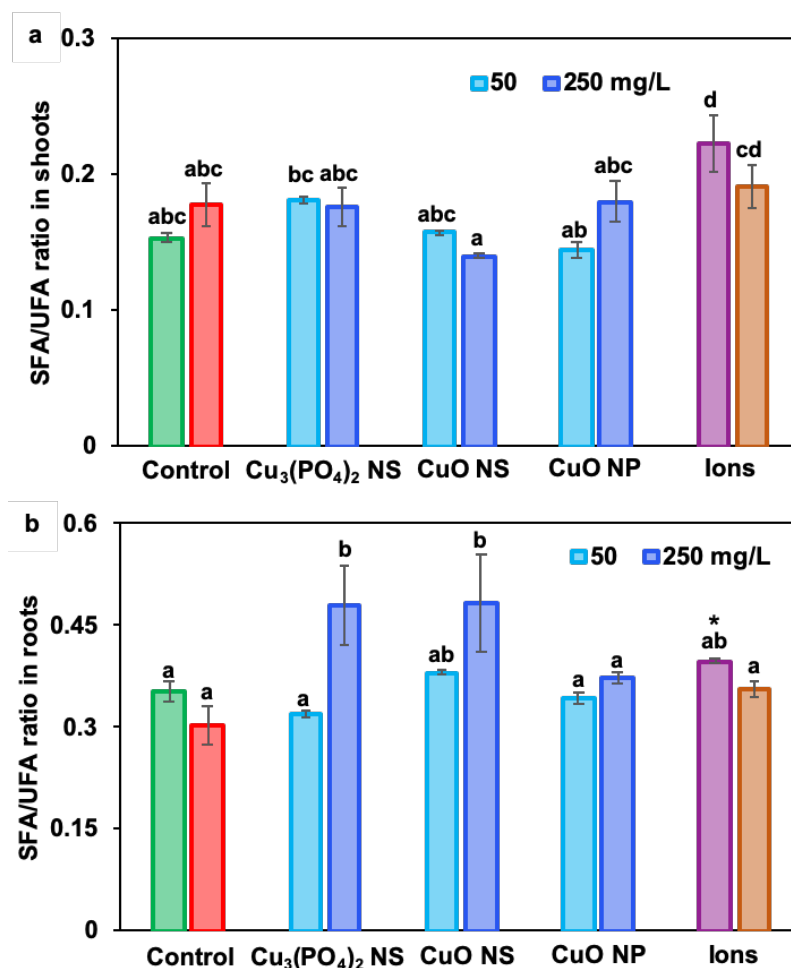
Supplementary Figure 10. Cu-based NM distribution in FV infected soybean foliar treated with different types of NM suspension with the equivalent molar of Cu (1.725 mM) three times with one-week interval. Figure **a1-a2** represents Cu-based NM distribution on the soybean leaf surface in the CuO NS, and CuO NP treatment, respectively. Figure **b1-b2** represents the pattern of Cu-based NM distribution in the area of trichomes in the CuO NS, and CuO NP treatment, respectively. **Note:** The control and $\text{Cu}_3(\text{PO}_4)_2$ NS with 1.725 mM Cu show in **Figure 4a and b**, respectively.



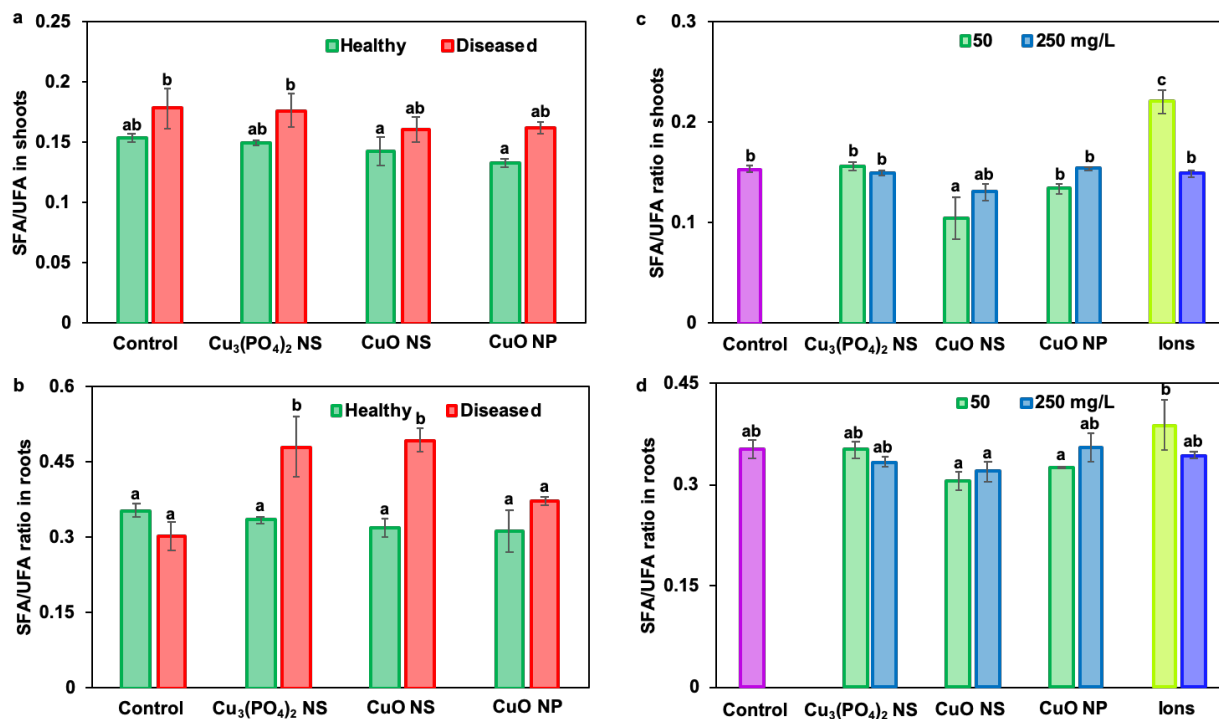
Supplementary Figure 11. POD and PPO activity in different types of Cu-based NM treated shoots and roots infected with or without FV. Figure **a-b** represents the POD activity in shoots and roots, respectively, in the healthy (■) and diseased (■) treatments with different types of Cu-based NMs at 1.725 mM [Cu]; Figure **c-d** represents the PPO activity in shoots and roots, respectively, in the healthy (■) and diseased (■) treatments with different types of Cu-based NMs at 1.725 mM [Cu]. Figure **e-f** represents the POD activity in shoots and roots, respectively, in the healthy treatment with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO_4^{3-} ; Figure **g-h** represents the PPO activity in shoots and roots, respectively, in the healthy treatment with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO_4^{3-} ; in Figure **e-h**, purple bar (■) represents the healthy control; light green bar (■) and blue bar (■) represents 1.725 mM [Cu] ionic control and 1.175 mM $[\text{PO}_4^{3-}]$ ionic control, which is the same molar concentration of [Cu] and $[\text{PO}_4^{3-}]$ in 250 mg/L $\text{Cu}_3(\text{PO}_4)_2$ NS, respectively. Error bars correspond to standard error of mean (n=4). Values followed by different letters are significantly different at $p<0.05$.



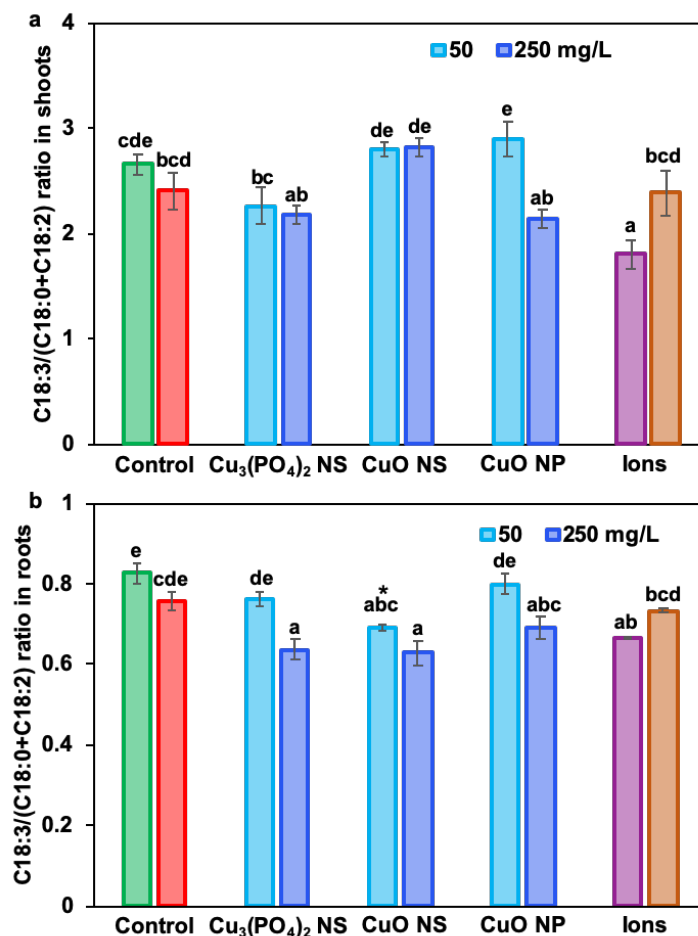
Supplementary Figure 12. Fatty acids profile in different types of Cu-based NM treated soybean shoots and roots w/ or w/o FV infection. Figure **a-b** represents the fatty acids profile in shoots across all the diseased and healthy treatments, respectively. Figure **c-d** represents the fatty acids profile in roots across all the diseased and healthy treatments, respectively. Soybean seedlings were foliar treated with different types of Cu-based NMs at 50 and 250 mg/L (mass of particles) or treated with the equivalent molar of Cu in forms of different types of Cu forms. The equivalent amounts of Cu^{2+} or PO_4^{3-} in form of CuSO_4 and Na_3PO_4 , respective, were set as the ionic controls. Values followed by different letters indicate the significant difference of the total fatty acid content at $p < 0.05$ ($n=3$). In Figure **b** and **d**, a single asterisk “*” indicates significant difference between healthy and diseased treatment with the same Cu-based NMs at $p < 0.05$; double asterisks “**” indicate highly significant difference between healthy and diseased treatment with the same Cu-based NMs at $p < 0.01$ using a student t-test.



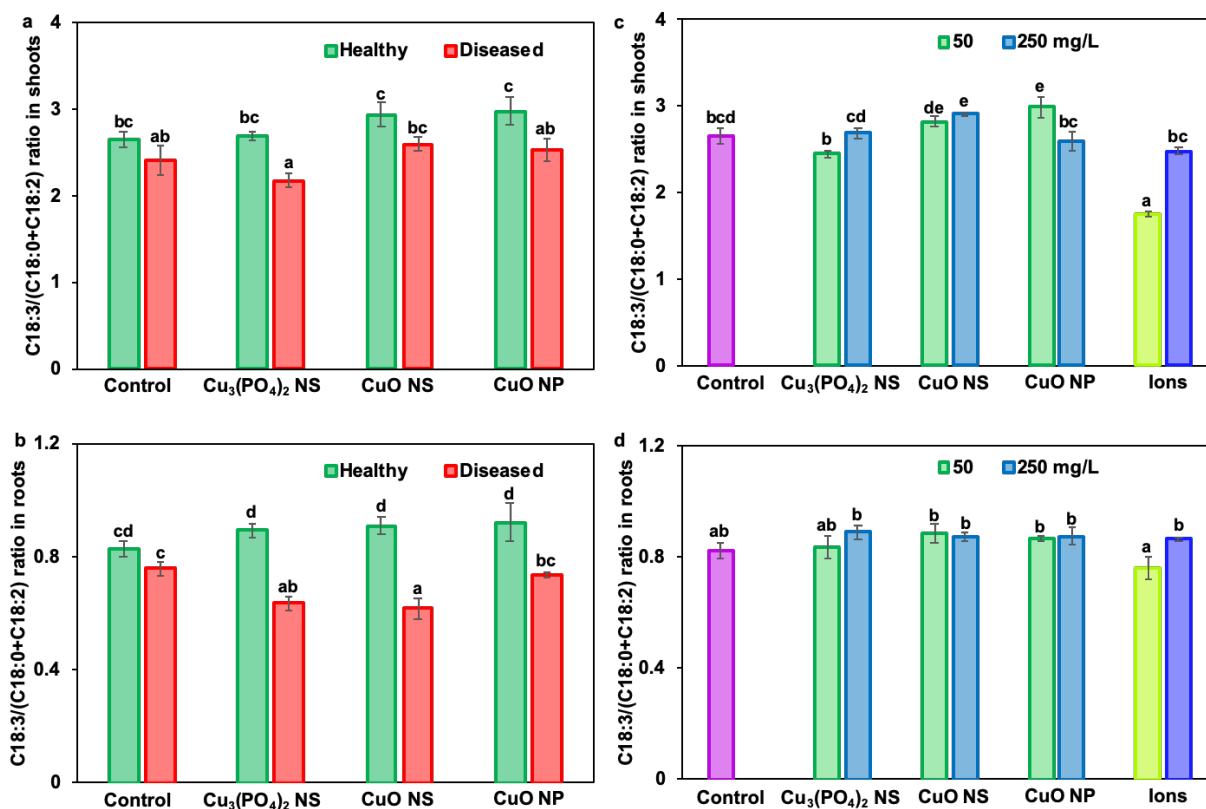
Supplementary Figure 13. The ratio of SFA/UFA in soybean shoots (a) and roots (b) infected with FV. Green bar (■) and red bar (■) represents healthy control and diseased control, respectively; blue bars represent the treatments with different types of Cu-based NMs at 50 and 250 mg particles/L; purple bar (■) and brown bar (■) represents 1.725 mM [Cu] ionic control and 1.175 mM [PO_4^{3-}] ionic control, which is the same molar concentration of [Cu] and [PO_4^{3-}] in 250 mg/L $\text{Cu}_3(\text{PO}_4)_2$ NS, respectively. Error bars correspond to standard error of mean (n=3). Values followed by different letters are significantly different at $p < 0.05$. A single asterisk “*” indicates significant difference between the diseased control and each Cu-based NM treatment at $p < 0.05$.



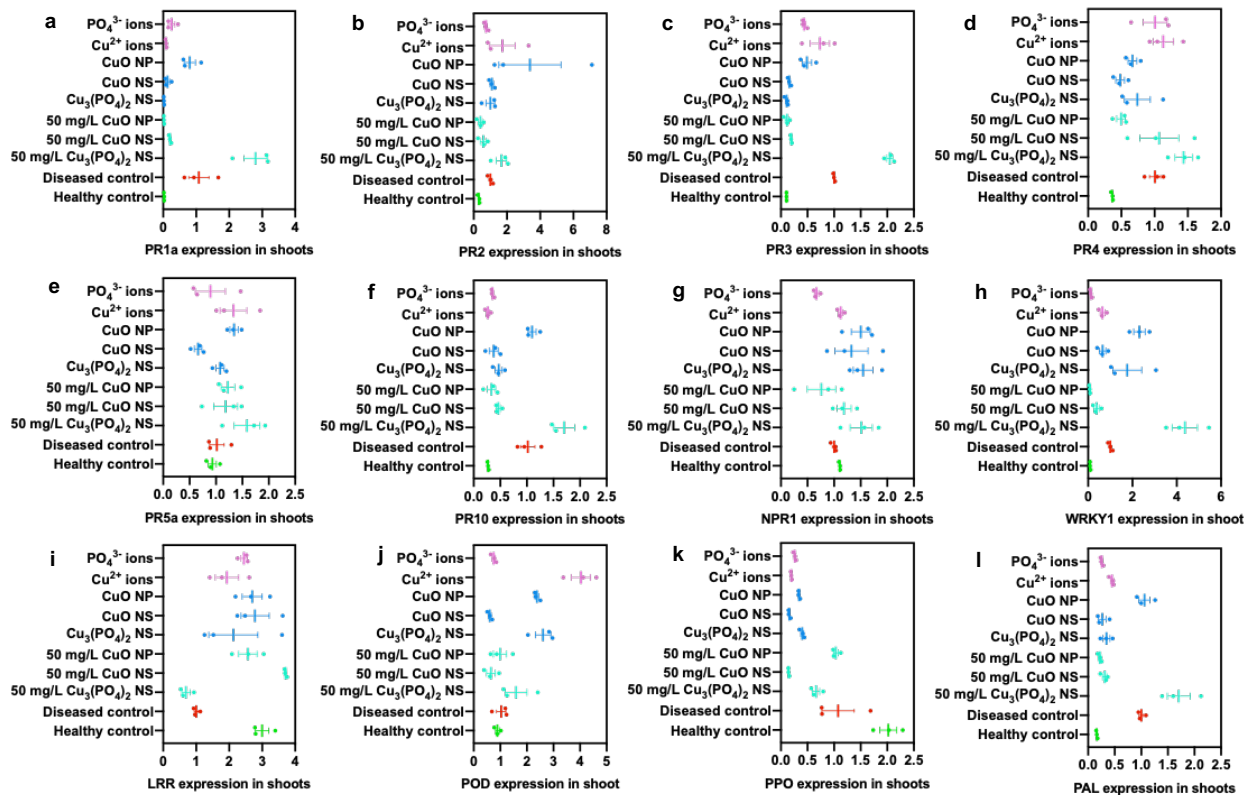
Supplementary Figure 14. The ratio of SFA/UFA in soybean shoots and roots infected with or without FV. Figure **a** and **b** represents SFA/UFA ratio in healthy (green) and diseased (red) shoots and roots treated with different types of Cu-based NMs with equivalent molar concentration of Cu, respectively; Figure **c** and **d** represents SFA/UFA ratio in healthy shoots and roots treated with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO_4^{3-} . In Figure **c** and **d**, purple bar (pink) represents the healthy control; light green bar (light green) and blue bar (blue) represents 1.725 mM $[\text{Cu}]$ ionic control and 1.175 mM $[\text{PO}_4^{3-}]$ ionic control, which is the same molar concentration of $[\text{Cu}]$ and $[\text{PO}_4^{3-}]$ in 250 mg/L $\text{Cu}_3(\text{PO}_4)_2$ NS, respectively. Error bars correspond to standard error of mean ($n=3$). Values followed by different letters are significantly different at $p<0.05$.



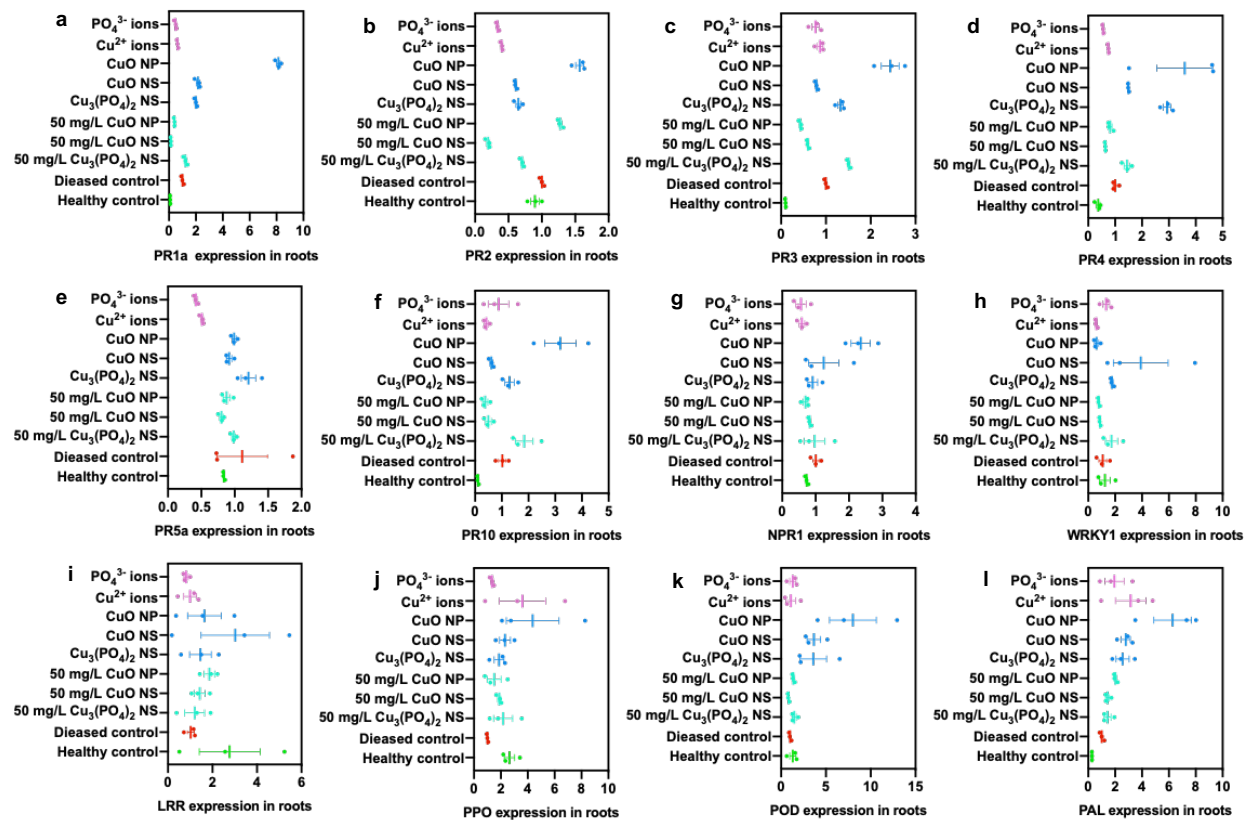
Supplementary Figure 15. The ratio of C18:3/(C18:0+C18:2) in soybean shoots (a) and roots (b) infected with FV. Green bar (■) and red bar (■) represents healthy control and diseased control, respectively; blue bars represent the treatments with different types of Cu-based NMs at 50 and 250 mg particles/L; purple bar (■) and brown bar (■) represents 1.725 mM [Cu] ionic control and 1.175 mM $[\text{PO}_4^{3-}]$ ionic control, which is the same molar concentration of [Cu] and $[\text{PO}_4^{3-}]$ in 250 mg/L $\text{Cu}_3(\text{PO}_4)_2$ NS, respectively. Error bars correspond to standard error of mean (n=3). Values followed by different letters are significantly different at $p < 0.05$. A single asterisk “*” indicates significant difference between the diseased control and each Cu-based NM treatment at $p < 0.05$.



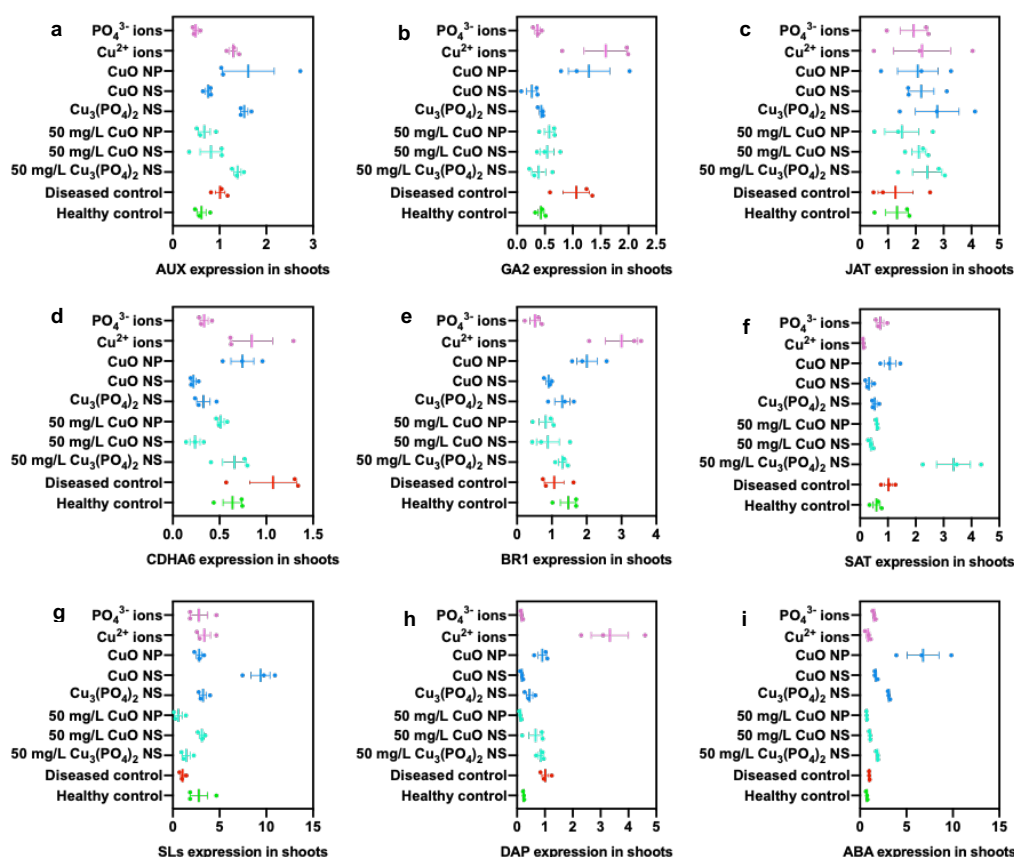
Supplementary Figure 16. The ratio of C18:3/(C18:0+C18:2) in soybean shoots and roots infected with or without FV. Figure **a** and **b** represents the C18:3/(C18:0+C18:2) ratio in healthy (■) and diseased (■) shoots and roots treated with different types of Cu-based NMs with equivalent molar concentration of Cu, respectively; Figure **c** and **d** represents the C18:3/(C18:0+C18:2) ratio in healthy shoots and roots treated with 50 and 250 mg particles/L Cu-based NMs and ionic forms of Cu and PO₄³⁻. In Figure **c** and **d**, purple bar (■) represents the healthy control; light green bar (■) and blue bar (■) represents 1.725 mM [Cu] ionic control and 1.175 mM [PO₄³⁻] ionic control, which is the same molar concentration of [Cu] and [PO₄³⁻] in 250 mg/L Cu₃(PO₄)₂ NS, respectively. Error bars correspond to standard error of mean (n=3). Values followed by different letters are significantly different at p<0.05.



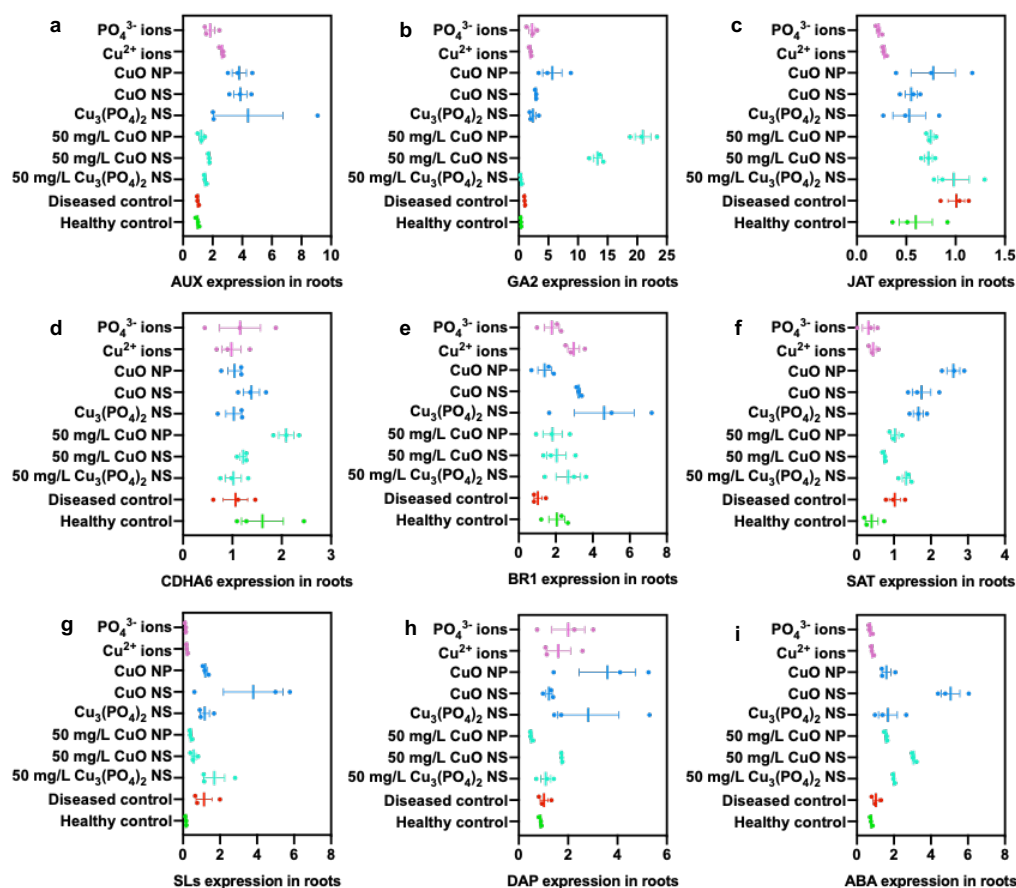
Supplementary Figure 17. Relative expression of disease-related genes in FV infected shoots as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Disease-related genes reported above include pathogenesis-related genes (PR1a, PR2, PR3, PR4, PR5a, PR10; **a-f**), NPR1 protein (**g**), WRKY1 transcription factor (**h**), leucine-rich repeat (LRR; **i**), antioxidant enzymes (POD, PPO and PAL; **j-l**). Gene fold-change was expressed relative to the FV control plants. CuSO_4 and Na_3PO_4 with 1.725 mM Cu^{2+} and 1.15 mM PO_4^{3-} , respectively, was used as the Cu^{2+} and PO_4^{3-} ionic control. Five biological replicates and three technical replicates were used per treatment.



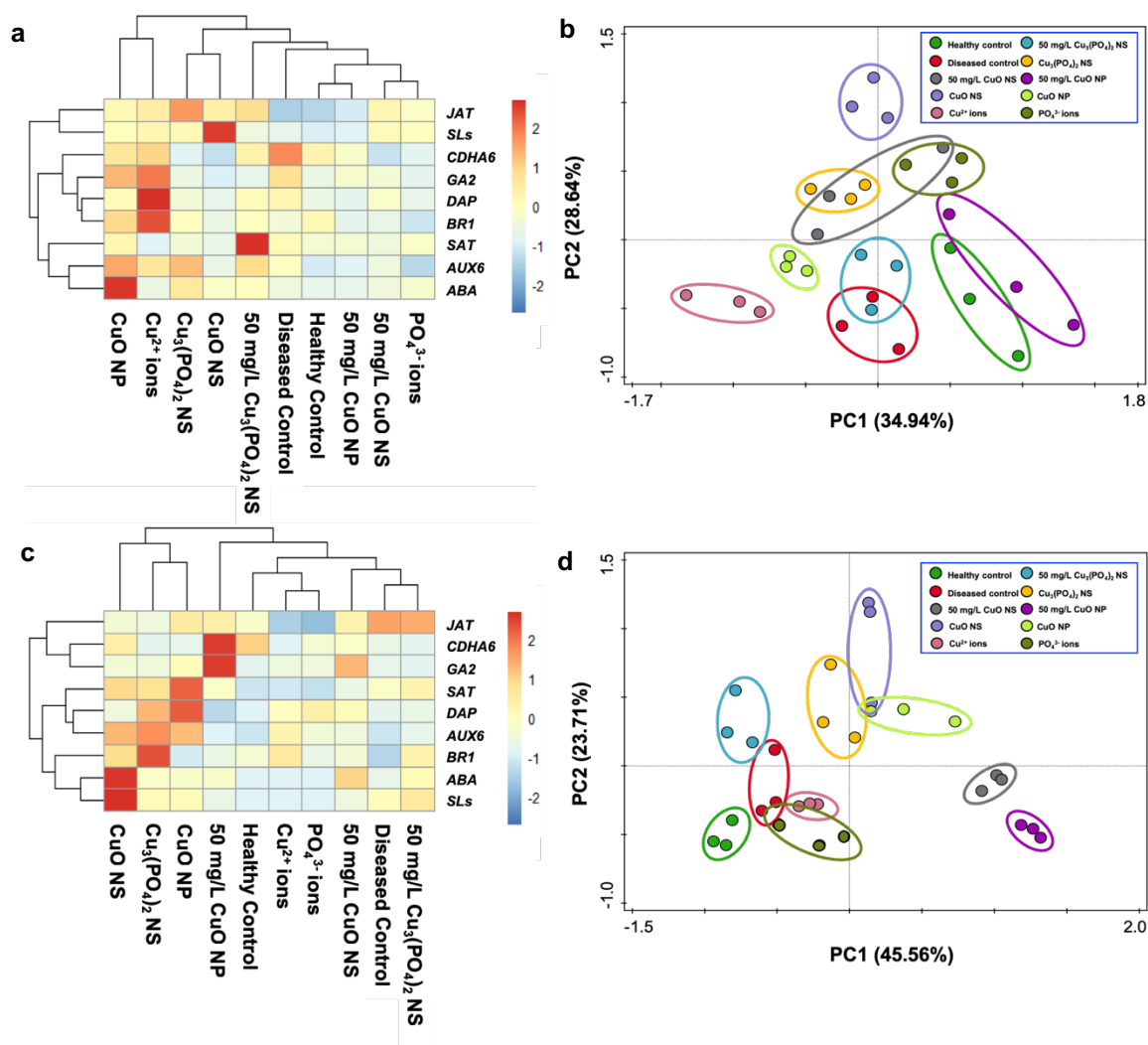
Supplementary Figure 18. Relative expression of disease-related genes in FV infected roots as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Disease-related genes reported above include pathogenesis-related genes (PR1a, PR2, PR3, PR4, PR5a, PR10; **a-f**), NPR1 protein (**g**), WRKY1 transcription factor (**h**), leucine-rich repeat (LRR; **i**), antioxidant enzymes (POD, PPO and PAL; **j-l**). Gene fold-change was expressed relative to the FV control plants. $CuSO_4$ and Na_3PO_4 with 1.725 mM Cu^{2+} and 1.15 mM PO_4^{3-} , respectively, was used as the Cu^{2+} and PO_4^{3-} ionic control. Five biological replicates and three technical replicates were used per treatment.



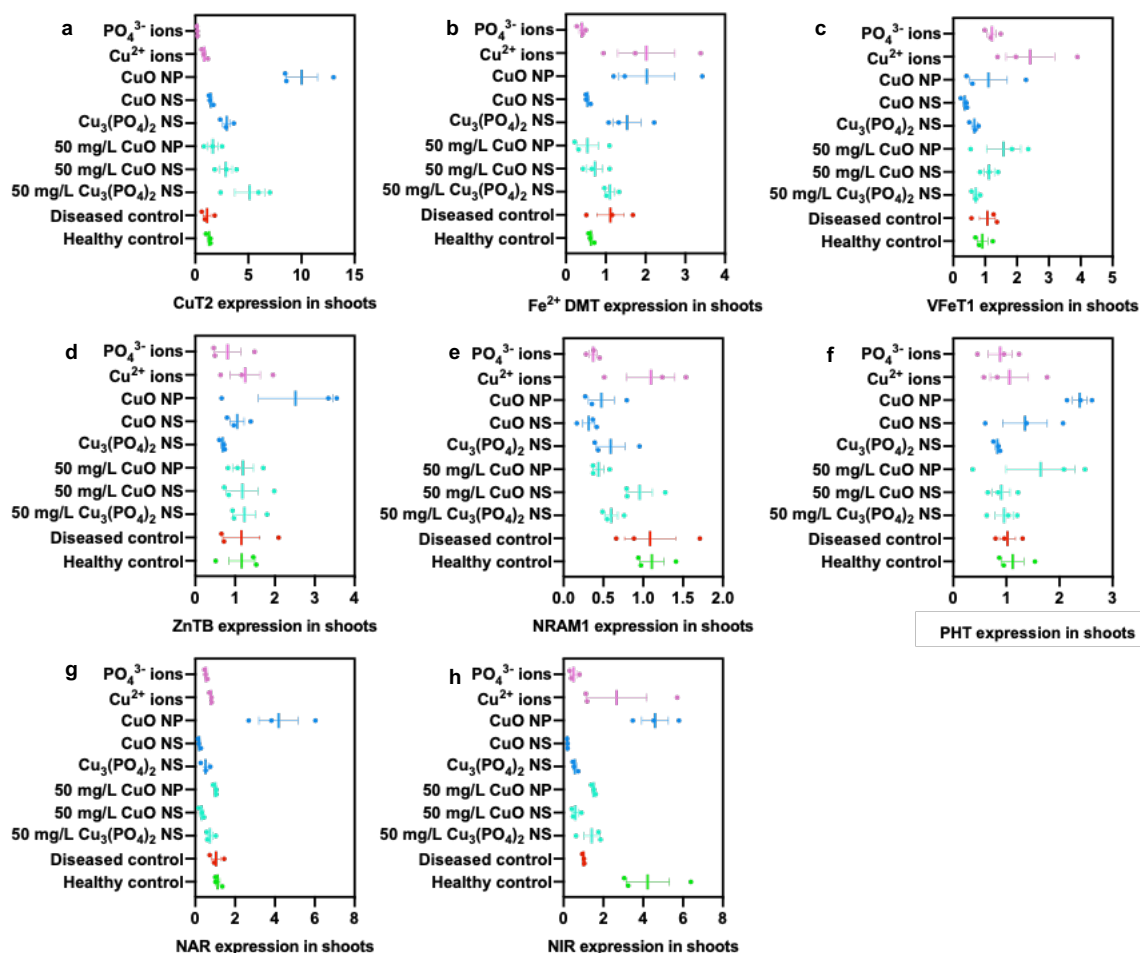
Supplementary Figure 19. Relative expression of phytohormone-related genes in FV infected shoots as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Phytohormone-related genes reported above include auxin (AUX; **a**), gibberellin-regulated protein2 (GA2; **b**), jasmonate O-methyltransferase (JAT; **c**), cytokinin dehydrogenase 6 (CDHA6; **d**), brassinosteroid receptor (BR1; **e**), salicylic acid methyltransferase like protein (SAT; **f**), strigolactone esterase (SLs; **g**), dormancy-associated protein (DAP; **h**), and abscisic acid receptor (ABA; **i**). Gene fold-change was expressed relative to the FV control plants. $CuSO_4$ and Na_3PO_4 with 1.725 mM Cu^{2+} and 1.15 mM PO_4^{3-} , respectively, was used as the Cu^{2+} and PO_4^{3-} ionic control. Five biological replicates and three technical replicates were used per treatment.



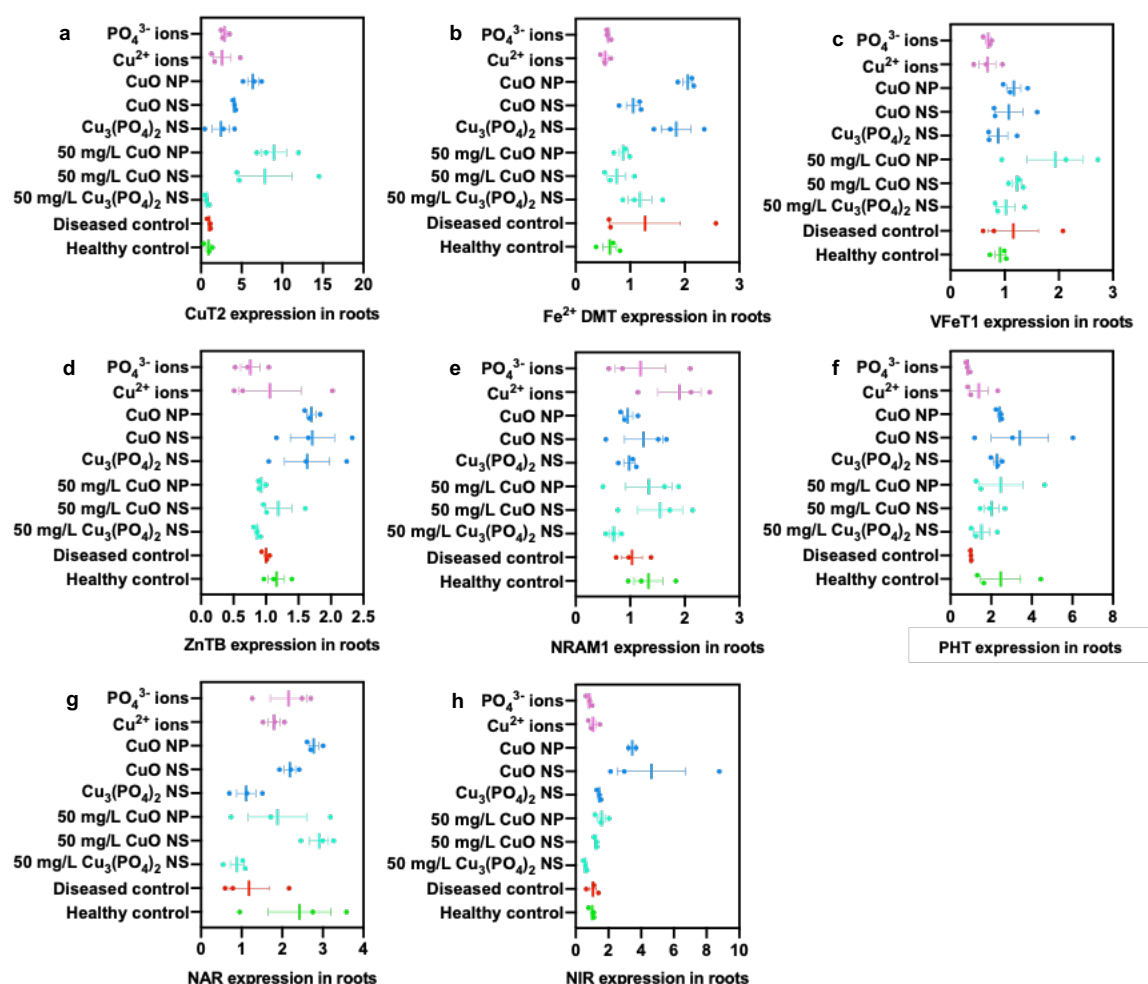
Supplementary Figure 20. Relative expression of phytohormone-related genes in FV infected roots as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Phytohormone-related genes reported above include auxin (AUX; **a**), gibberellin-regulated protein2 (GA; **b**), jasmonate O-methyltransferase (JAT; **c**), cytokinin dehydrogenase 6 (CDHA6; **d**), brassinosteroid receptor (BR1; **e**), salicylic acid methyltransferase like protein (SAT; **f**), strigolacton esterase (SLs; **g**), dormancy-associated protein (DAP; **h**), and abscisic acid receptor (ABA; **i**). Gene fold-change was expressed relative to the FV control plants. CuSO_4 and Na_3PO_4 with 1.725 mM Cu^{2+} and 1.15 mM PO_4^{3-} , respectively, was used as the Cu^{2+} and PO_4^{3-} ionic control. Five biological replicates and three technical replicates were used per treatment.



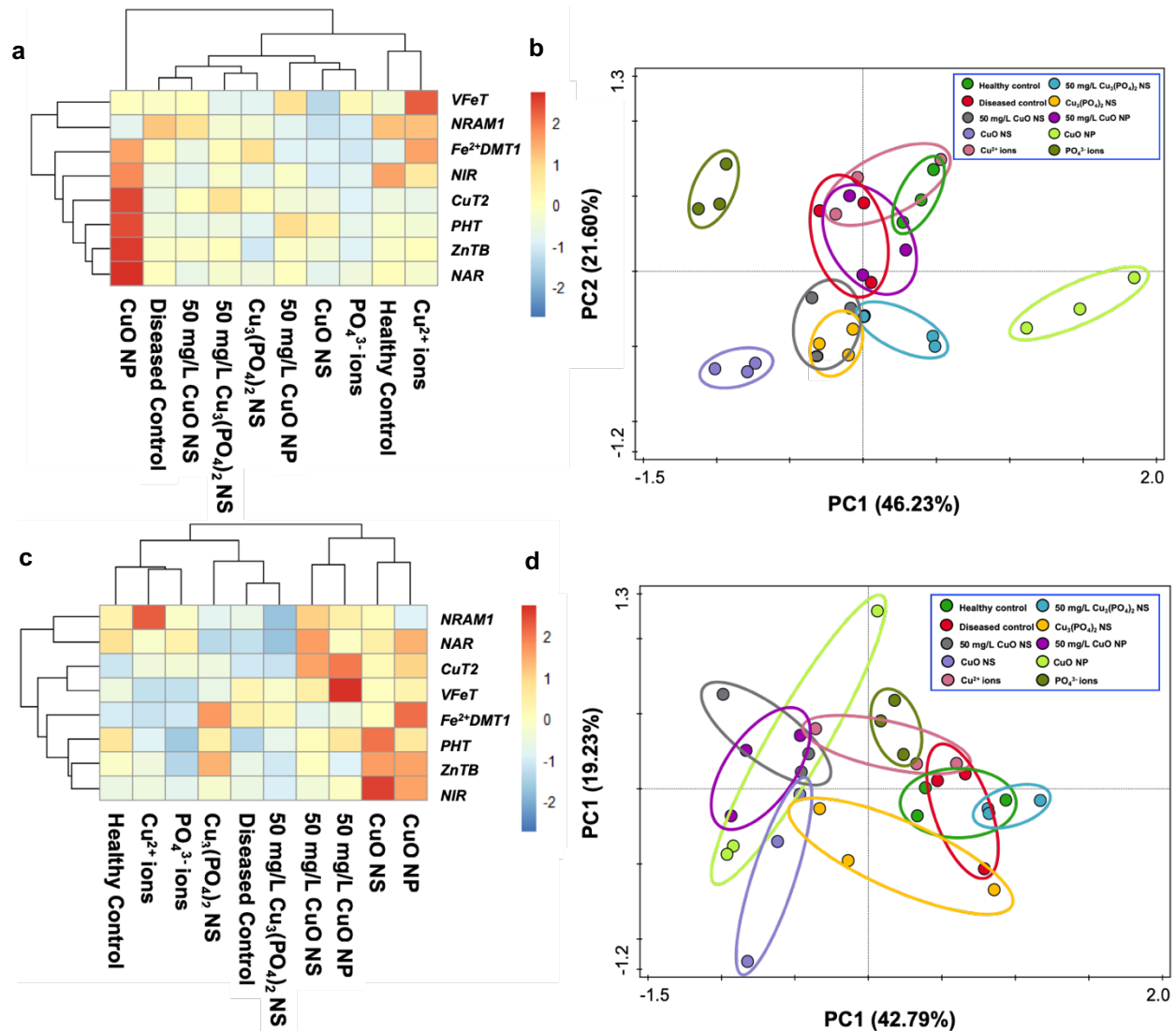
Supplementary Figure 21. Heatmap and PCA analysis of the relative expression of phytohormone-related genes in FV infected shoots (**a, b**) and roots (**c, d**) as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Phytohormone-related genes reported above include auxin (AUX), gibberellin-regulated protein2 (GA2), jasmonate O-methyltransferase (JAT), cytokinin dehydrogenase 6 (CDHA6), brassinosteroid receptor (BR1), salicylic acid methyltransferase like protein (SAT), strigolacton esterase (SLs), dormancy-associated protein (DAP), and abscisic acid receptor (ABA). Gene fold-change was expressed relative to the FV control plants. CuSO₄ and Na₃PO₄ with 1.725 mM Cu²⁺ and 1.15 mM PO₄³⁻, respectively, was used as the Cu²⁺ and PO₄³⁻ ionic control.



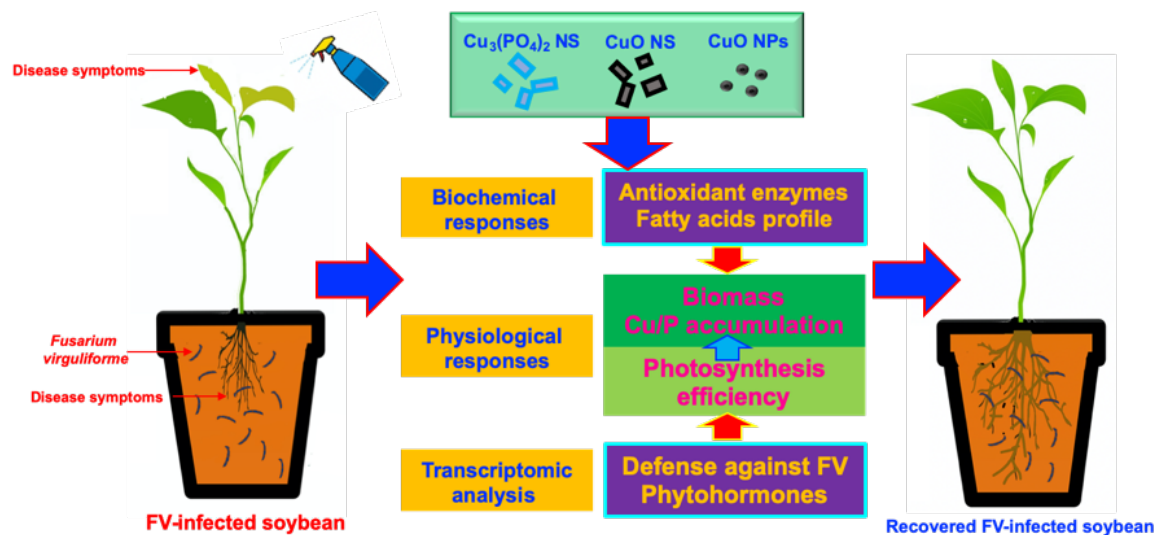
Supplementary Figure 22. Relative expression of genes involved in metal and phosphate transport and nitrogen assimilation in FV infected shoots as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Genes reported above include copper transporter (CuT2; **a**), ferrous ion membrane transporter (Fe^{2+} DMT; **b**), vacuolar iron transporter (VFeT1; **c**), zinc transporter (ZnTB; **d**), iron transporter (NRAM1; **e**), phosphate transporter (PHT; **f**), nitrate reductase (NAR; **g**) and nitrite reductase (NIR; **h**). Gene fold-change was expressed relative to the FV control plants. CuSO_4 and Na_3PO_4 with 1.725 mM Cu^{2+} and 1.15 mM PO_4^{3-} , respectively, was used as the Cu^{2+} and PO_4^{3-} ionic control. Five biological replicates and three technical replicates were used per treatment.



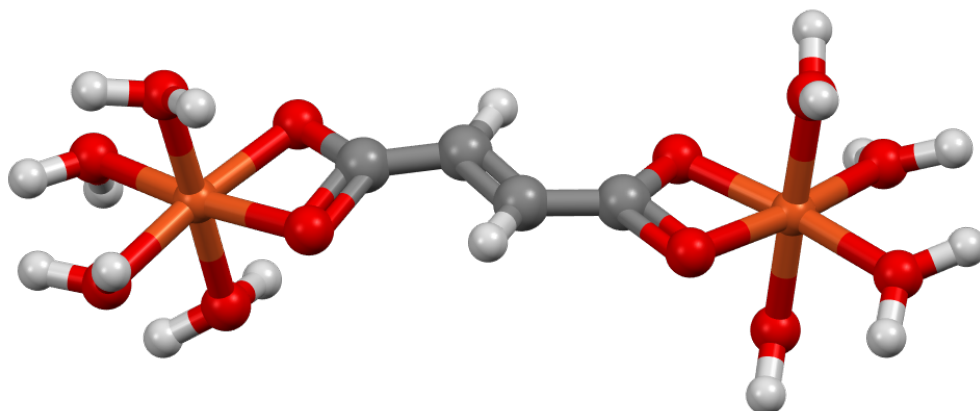
Supplementary Figure 23. Relative expression of genes involved in metal and phosphate transport and nitrogen assimilation in FV infected roots as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Genes reported above include copper transporter (CuT2 ; **a**), ferrous ion membrane transporter (Fe^{2+} DMT; **b**), vacuolar iron transporter (VFeT1 ; **c**), zinc transporter (ZnTB ; **d**), iron transporter (NRAM1 ; **e**), phosphate transporter (PHT ; **f**), nitrate reductase (NAR ; **g**) and nitrite reductase (NIR ; **h**). Gene fold-change was expressed relative to the FV control plants. CuSO_4 and Na_3PO_4 with 1.725 mM Cu^{2+} and 1.15 mM PO_4^{3-} , respectively, was used as the Cu^{2+} and PO_4^{3-} ionic control. Five biological replicates and three technical replicates were used per treatment.



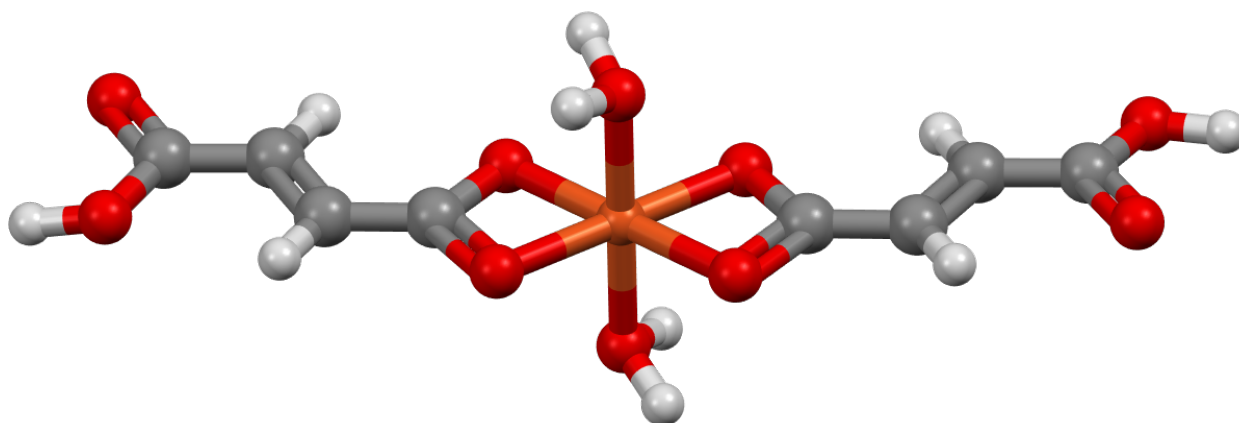
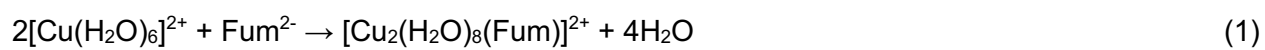
Supplementary Figure 24. Heatmap and PCA analysis of the relative expression of genes involved in metal and phosphate transport and nitrogen assimilation in FV infected shoots (a, b) and roots (c, d) as affected by different types of Cu-based NMs at 50 mg/L (mass of particles) or the equivalent amount of Cu (1.725 mM). Genes reported above include copper transporter (CuT2), ferrous ion membrane transporter (Fe²⁺ DMT), vacuolar iron transporter (VFeT1), zinc transporter (ZnTB), iron transporter (NRAM1), phosphate transporter (PHT), nitrate reductase (NAR) and nitrite reductase (NIR). Gene fold-change was expressed relative to the FV control plants. CuSO₄ and Na₃PO₄ with 1.725 mM Cu²⁺ and 1.15 mM PO₄³⁻, respectively, was used as the Cu²⁺ and PO₄³⁻ ionic control.



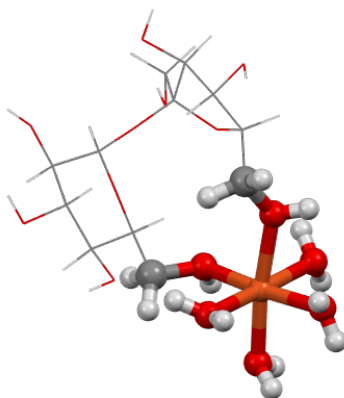
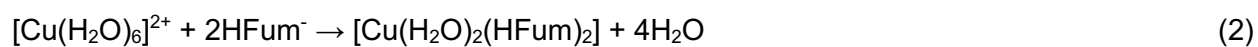
Supplementary Figure 25. Overview of the responses of FV-infected interaction upon foliar-exposure of different types of Cu-based NMs.



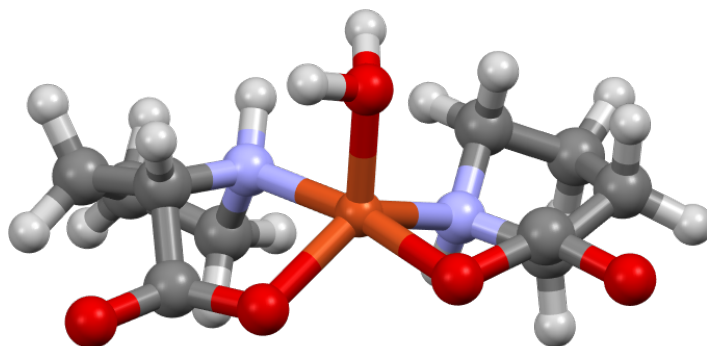
Supplementary Figure 26a. Structural representation of $\text{Cu}_2(\text{H}_2\text{O})_8(\text{Fu})$ modeled by Equation (1).



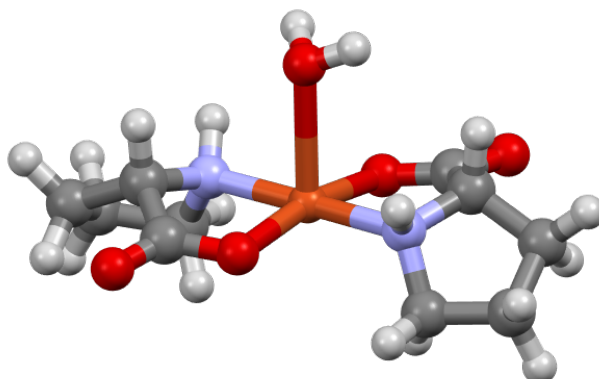
Supplementary Figure 26b. Structural representation of $\text{Cu}(\text{H}_2\text{O})_2(\text{HFu})_2$ modeled by Equation (2).



Supplementary Figure 26c. Structural representation of $[\text{Cu}(\text{H}_2\text{O})_4(\text{Su})]^{2+}$ modeled by Equation (3).



Supplementary Figure 26d. Structural representation of *cis*- $\text{Cu}(\text{H}_2\text{O})(\text{Pr})_2$ modeled by Equation (4).



Supplementary Figure 26e. Structural representation of *trans*- $\text{Cu}(\text{H}_2\text{O})(\text{Pr})_2$ modeled by Equation (4).



Supplementary Table 1. The content of macronutrients in soybean shoots w/ or w/o FV infection

Treatment (mg/kg)	Ca		Mg		P		K		S	
	H	D	H	D	H	D	H	D	H	D
Control	12155 ±500	12393 ±100	3179.0 ±70	3239.0 ±100	3678.0 ±100	4990.0 ±300 ⁺⁺	24584 ±1000	27769 ±700 ⁺	2492.0 ±100	3229.0 ±200 ⁺⁺
50 mg/L Cu₃(PO₄)₂ NS	11036 ±400	11383 ±200 ^{**}	3048.0 ±100	3178.0 ±90	3347.0 ±100	4075.0 ±100 ^{***}	22553 ±2000	26753 ±1000 ⁺	2579.0 ±100	2964.0 ±50 ⁺
250 mg/L Cu₃(PO₄)₂ NS	11012 ±1000	11509 ±400 [*]	2955.0 ±200	3104.0 ±100	3393.0 ±80	5026.0 ±300 ⁺⁺	21863 ±1000	27668 ±1000 ⁺	2322.0 ±200	2866.0 ±100 ⁺
50 mg/L CuO NS	11571 ±400	10862 ±30 ^{**}	3077.0 ±200	2760.0 ±60 ^{**}	3573.0 ±200	4026.0 ±300 [*]	22906 ±2000	22007 ±300 ^{**}	2755.0 ±200.0	2492.0 ±90 ^{**}
250 mg/L CuO NS	12532 ±400	11377 ±600	3581.0 ±200 [*]	3053.0 ±100 ⁺	3494.0 ±80	4098.0 ±200 ⁺⁺	24496 ±800	25452 ±2000	2571.0 ±200	2810.0 ±90 [*]
1.725 mM [Cu] CuO NS	11149 ±200	11475 ±300 [*]	3181.0 ±100	2815.0 ±50 ^{***}	3158.0 ±100 [*]	4606.0 ±300 ⁺⁺	21097 ±700	25280 ±2000 ⁺	2583.0 ±30	2958.0 ±200
50 mg/L CuO NP	11897 ±300	12521 ±200	3328.0 ±200	3130.0 ±70	3344.0 ±100	4863.0 ±300 ⁺⁺	21292 ±800	25855 ±2000 ⁺	2645.0 ±100	3127.0 ±80 ⁺⁺
250 mg/L CuO NP	11642 ±400	12582 ±400	3310.0 ±60	3283.0 ±100	3129.0 ±100 [*]	4730.0 ±300 ⁺⁺	20262 ±1000	26620 ±1000 ⁺⁺	2619.0 ±80	3048.0 ±90 ⁺⁺
1.725 mM [Cu] CuO NP	13013 ±500	11815 ±300	3477.0 ±200	3080.0 ±60	3527.0 ±100	4739.0 ±200 ⁺⁺	22667 ±900	26581 ±2000	2587.0 ±200	3067.0 ±200
1.725 mM [Cu] CuSO₄	12196 ±400	11918 ±500	3585.0 ±100 [*]	3404.0 ±100	6072.0 ±100 ^{**}	7494.0 ±400 ^{***}	36978 ±300	36860 ±900 ^{**}	3921.0 ±200 ^{**}	4888.0 ±200 ^{***+}
1.125 mM [PO₄³⁻] Na₃PO₄	11096 ±400	11072 ±200 ^{**}	2989.0 ±100	2944.0 ±200	3523.0 ±100	4241.0 ±300 ⁺	19988 ±800	24581 ±1000 ⁺⁺	2460 ±50	2688.0 ±100 [*]

Note: Student t-test is used to calculate significance between control and each treatment. Single asterisk indicates the significant difference between each Cu treatment and the respective control at p<0.05; Double asterisks indicate the significant difference between each Cu treatment and the respective control at p<0.01. In addition, single cross indicates the significant difference of each element content between healthy and diseased treatment at p<0.05; double crosses indicate the significant difference of each element content between healthy and diseased treatment at p<0.01.

Supplementary Table 2. The content of macronutrients in soybean roots w/ or w/o FV infection

Treatment (mg/kg)	Ca		Mg		P		K		S	
	H	D	H	D	H	D	H	D	H	D
Control	5259.0 ±80	6343.0 ±200 ⁺⁺	13821 ±1000	5336.0 ±700 ⁺⁺	8790.0 ±600	14133 ±600	36863 ±4000	44562 ±3000	8095.0 ±80	7497.0 ±100 ⁺⁺
50 mg/L Cu₃(PO₄)₂ NS	5131.0 ±100	6944.0 ±200 ⁺⁺⁺	12694 ±400	10361 ±2000 [*]	8208.0 ±400	12051 ±2000	35213 ±2000	33534 ±3000 [*]	8683.0 ±200 [*]	8358.0 ±900 [*]
250 mg/L Cu₃(PO₄)₂ NS	5325.0 ±100	6829.0 ±300 ⁺⁺	14983 ±1000	6506.0 ±1000 ⁺⁺	9810.0 ±1000	13605 ±2000	33907 ±4000	44224 ±6000	8767.0 ±600	8340.0 ±300
50 mg/L CuO NS	5899.0 ±200 [*]	6532.0 ±500	15353 ±700	8135.0 ±2000 ⁺⁺	9141.0 ±2000	11604 ±1000	29498 ±5000	36578 ±4000	9579.0 ±1000	6985.0 ±400 ⁺
250 mg/L CuO NS	5715.0 ±40 ^{**}	6809.0 ±200 ⁺⁺⁺	15764 ±1000	9614.0 ±700 ^{****}	6214.0 ±800 [*]	11597 ±1000	25607 ±2000 [*]	28982 ±2000 ^{**}	6969.0 ±700	6978.0 ±300
1.725 mM [Cu] CuO NS	6048.0 ±200 [*]	6411.0 ±100	15764 ±1000	7269.0 ±400 ⁺⁺⁺	7969.0 ±1000	12506 ±900	24688 ±3000 [*]	39773 ±3000 ⁺⁺	7849.0 ±500	7528.0 ±700
50 mg/L CuO NP	5585.0 ±80 [*]	6713.0 ±400 ⁺	15326 ±700	7846.0 ±2000 ⁺⁺	7070.0 ±400 [*]	12460 ±1000	26726 ±2000 [*]	28636 ±4000 ⁺	8901.0 ±100 ^{**}	7894.0 ±500
250 mg/L CuO NP	5679.0 ±100 [*]	6768.0 ±200 ⁺⁺	16468 ±1000	6987.0 ±1000 ⁺	6046.0 ±600 [*]	13071 ±1000	21542 ±2000 [*]	39797 ±3000 ⁺⁺	8383.0 ±800	7312.0 ±400
1.725 mM [Cu] CuO NP	5824.0 ±200 [*]	7734.0 ±300 ^{****}	15782 ±2000	7403.0 ±1000 ⁺⁺	7883.0 ±900	13369 ±1000	30646 ±4000	41154 ±3000 ⁺	9374.0 ±400 [*]	8082.0 ±800
1.725 mM [Cu] CuSO₄	6492.0 ±90 ^{**}	8100.0 ±200 ^{****}	7651.0 ±600 [*]	3137.0 ±400 ⁺⁺⁺	22878 ±1000 [*]	21973 ±300 ^{**}	59899 ±2000 ^{**}	57264 ±2000 ^{**}	10947 ±200 ^{**}	9187.0 ±400 ⁺⁺⁺
1.125 mM [PO₄³⁻] Na₃PO₄	5243.0 ±100	6407.0 ±200 ⁺⁺	15793 ±600	9375.0 ±1000 ⁺⁺⁺	7670.0 ±1000	10526 ±900 ^{**}	23975 ±3000 [*]	30343 ±2000 ^{****}	7880.0 ±300	6986.0 ±600

Note: Student t-test is used to calculate significance between control and each treatment. Single asterisk indicates the significant difference between each Cu treatment and the respective control at p<0.05; Double asterisks indicate the significant difference between each Cu treatment and the respective control at p<0.01. In addition, single cross indicates the significant difference of each element content between healthy and diseased treatment at p<0.05; double crosses indicate the significant difference of each element content between healthy and diseased treatment at p<0.01.

Supplementary Table 3. The content of micronutrients in soybean shoots w/ or w/o FV infection

Treatment (mg/kg)	Cu		Fe		Mn		Zn	
	H	D	H	D	H	D	H	D
Control	5.760 ±0.2	7.710 ±0.9 ⁺⁺	66.98 ±2	81.80 ±10	63.96 ±4	66.80 ±5	41.06 ±3	47.94 ±3
50 mg/L Cu₃(PO₄)₂ NS	41.25 ±6 ^{**}	34.36 ±2 ^{**}	74.34 ±8	77.92 ±6	55.60 ±5	51.15 ±5 [*]	39.12 ±3	41.73 ±1
250 mg/L Cu₃(PO₄)₂ NS	121.9 ±10 ^{**}	158.2 ±10 ^{***+}	68.42 ±5	68.31 ±9	52.29 ±8	60.67 ±0.9	32.55 ±2 [*]	46.18 ±1 ⁺⁺
50 mg/L CuO NS	68.58 ±6 ^{**}	68.71 ±4 ^{**}	68.19 ±4	47.99 ±5 ⁺⁺	50.60 ±2 [*]	44.18 ±2 ^{***}	35.03 ±3	36.42 ±1 [*]
250 mg/L CuO NS	359.2 ±20 ^{**}	361.7 ±30 ^{**}	68.53 ±4	81.17 ±20	53.55 ±2 [*]	54.69 ±5	37.15 ±1	41.89 ±3
1.725 mM [Cu] CuO NS	223.3 ±20 ^{**}	217.6 ±10 ^{**}	73.03 ±4	55.39 ±10	47.19 ±3 ^{**}	55.98 ±7	33.15 ±1 [*]	38.24 ±2 ^{**}
50 mg/L CuO NP	47.18 ±4 ^{**}	45.40 ±8 ^{**}	110.2 ±30	64.73 ±7	55.96 ±3	56.15 ±3	36.18 ±0.9	40.83 ±2 ⁺
250 mg/L CuO NP	225.1 ±40 ^{**}	230.0 ±30 ^{**}	75.52 ±7	70.86 ±10	45.23 ±2 ^{**}	61.74 ±2 ⁺⁺	33.67 ±2 [*]	45.79 ±2 ⁺⁺
1.725 mM [Cu] CuO NP	143.6 ±10 ^{**}	170.7 ±30 ^{**}	71.54 ±6	62.07 ±6	60.65 ±3	52.59 ±3 [*]	3.863 ±1	41.37 ±2
1.725 mM [Cu] CuSO₄	1237 ±100 ^{**}	1047 ±100 ^{**}	93.40 ±9 [*]	83.91 ±5	71.78 ±3	75.62 ±6	57.83 ±5 [*]	60.33 ±3 [*]
1.125 mM [PO₄³⁻] Na₃PO₄	4.980 ±0.3 [*]	5.76 ±0.3 ^{***}	59.02 ±1 [*]	57.40 ±2	46.96 ±2 ^{**}	53.53 ±0.7 ⁺⁺	30.80 ±1 [*]	37.04 ±2 ^{**}

Note: Student t-test is used to calculate significance between control and each treatment. Single asterisk indicates the significant difference between each Cu treatment and the respective control at p<0.05; Double asterisks indicate the significant difference between each Cu treatment and the respective control at p<0.01. In addition, single cross indicates the significant difference of each element content between healthy and diseased treatment at p<0.05; double crosses indicate the significant difference of each element content between healthy and diseased treatment at p<0.01.

Supplementary Table 4. The content of micronutrients in soybean roots w/ or w/o FV infection

Treatment (mg/kg)	Cu		Fe		Mn		Zn	
	H	D	H	D	H	D	H	D
Control	70.75 ±10	58.79 ±4	120.1 ±1	174.2 ±30	412.3 ±60	246.2 ±20	96.77 ±5	79.75 ±6 ⁺
50 mg/L Cu₃(PO₄)₂ NS	51.41 ±4	59.88 ±9	115.6 ±4	143.5 ±10	286.2 ±30	271.1 ±30	90.85 ±10	84.40 ±10
250 mg/L Cu₃(PO₄)₂ NS	47.74 ±7	61.88 ±7	121.6 ±2	140.0 ±9	364.3 ±90	320.4 ±90	79.44 ±8	70.74 ±5
50 mg/L CuO NS	65.66 ±6	56.26 ±6	123.2 ±6	115.4 ±8	321.7 ±40	199.0 ±7 ⁺	126.9 ±5 ^{**}	75.23 ±3 ⁺⁺
250 mg/L CuO NS	74.21 ±10	59.87 ±4	120.1 ±4	122.1 ±8	333.1 ±20	313.0 ±100	95.35 ±9	75.14 ±5
1.725 mM [Cu] CuO NS	44.88 ±2	41.20 ±2 ^{**}	151.5 ±5 ^{**}	126.9 ±10	285.7 ±20	272.4 ±90	92.55 ±4	66.26 ±3 ⁺⁺
50 mg/L CuO NP	85.38 ±20	66.66 ±2	133.5 ±10	192.4 ±30	287.0 ±30	279.0 ±30	123.2 ±20	90.6 ±8
250 mg/L CuO NP	53.49 ±6	46.97 ±4 [*]	117.5 ±7	122.7 ±8	228.7 ±20 [*]	331.0 ±50	90.45 ±5	94.21 ±4
1.725 mM [Cu] CuO NP	58.36 ±4	53.35 ±5	125.4 ±8	151.8 ±10	337.8 ±50	246.5 ±40	106.8 ±20	83.29 ±7
1.725 mM [Cu] CuSO₄	105.4 ±5 [*]	82.46 ±10	139.7 ±10	188.9 ±20	635.8 ±60 [*]	539.6 ±200	113.0 ±2 [*]	101.5 ±8 [*]
1.125 mM [PO₄³⁻] Na₃PO₄	61.06 ±3	43.48 ±4 [*]	108.7 ±7	110.9 ±5	285.9 ±30	308.2 ±50	94.79 ±2	69.45 ±4 ⁺⁺

Note: Student t-test is used to calculate significance between control and each treatment. Single asterisk indicates the significant difference between each Cu treatment and the respective control at p<0.05; Double asterisks indicate the significant difference between each Cu treatment and the respective control at p<0.01. In addition, single cross indicates the significant difference of each element content between healthy and diseased treatment at p<0.05; double crosses indicate the significant difference of each element content between healthy and diseased treatment at p<0.01.

Supplementary Table 5. A list of genes tested in this study

Gene function	Gene	Primer
Housekeeping gene	GmEF1b-F	CCA CTG CTG AAG AAG ATG ATG ATG
	GmEF1b-R	AAG GAC AGA AGA CTT GCC ACT C
Disease-related genes*	GmPR1a-F	TGA AAA TGT GGG TTG ATG AGA AAT
	GmPR1a-R	AAG TGA TGA AAG TGC CTC CGT T
	GmPR2-F	GTT CGG AAT GTG AAG CAA GGA
	GmPR2-R	ATA GGA GAA AAG AGC CGC CAA
	GmPR3-F	AAC ACC AAC TCC AAC AAC ACC TA
	GmPR3-R	TGC CAA AGC CAT TGA AAG A
	GmPR4-F	AAC GCC GTG AGT GCT TAT TGT
	GmPR4-R	TTT GCT CCT GTT CCT GTA TTT GTC
	GmPR5a-F	CCC TCG CCT CCA CTT CTT C
	GmPR5a-R	TTG GTG CTC ATC TTG CCT CTA
	GmPR10-F	TAG CAT CCA CAG CAT TGT TTT C
	GmPR10-R	CAA GGC AGT GCC CTC AGT TA
	GmNPR1-F	TGC TCG GAA GTG TTG GAT AAG
	GmNPR1-R	GAA ATC CCA GAG CGG CTA AA
	GmWRKY1-F	GAG ACG ATG AGT GCA GCT ATT
	GmWRKY1-R	TGT CCC ATT AAG AGG AAG ATC AC
	GmLRR-F	CTC GAT AAG GCT ACC GTC TTT G
	GmLRR-R	TCT CAG GAA CCT CTC CGT AAA
	GmPOD-F	CTC CTG GTG CTG ATA CCA TTC
	GmPOD-R	TCC AAA CGA GTC TCC ATT CAC
	GmPPO-F	GCT CCT CAT AAC ACG GTT CAT A
	GmPPO-R	GTC CTT TCT TCC TTC TCC CAA T
	GmPAL-F	GTT TGT GAG GGA GGA GTT AGA G
	GmPAL-R	ATG GGA GAC CCT TTC CAA TC

***Note:** PR1a, PR2, PR3, PR4, PR5a, PR10 and EF1 primers were from *Frontiers in Plant Science* 8 (2017):781. Primers for the rest of genes were designed based on the coding sequence from NCBI by using Realtime PCR Tool in Integrated DNA Technologies.

Continued Supplementary Table 5. A list of genes tested in this study

Gene function	Gene	Primer
Phytohormone-related genes	GmDAP-F	ACC ATT GTT CGC TCC CAA TC
	GmDAP-R	CAC TCT CCA CTG TTG ACG ATT T
	GmAUX6-F	CTA CCA CAG GCA CTG ATT CTT
	GmAUX6-R	CTT CCA AAG GAC CCT GAC TTA T
	GmCDHA6-F	GTC GTC TTC GGG AAT ATC CTT AC
	GmCDHA6-R	CCG TCA GTT CCA GTT GAA GAT
	GmSAT-F	TTT GGG AAG AAG AAG CGA TGA
	GmSAT-R	GGA TGG AGT GTA TTG AGG GAT G
	GmJAT-F	GCT CTT GGA GGG TTT GAT TGA
	GmJAT-R	CCT TCA TCC CAA GGC AAG ATT A
	GmGA2-F	GGA GGA ACG TAA TGT GCC TAA G
	GmGA2-R	CTT GAG ATG TCC TCC ATG TGT G
	GmABA-F	TCG AGT CCT ACG TCG TTG A
	GmABA-R	TCG TTG ATG GAG TTT GGT TAG G
	GmBR1-F	CAT TCC CTC TGG GCT TGT T
	GmBR1-R	CGG CCG GAG AAA GAG TTA TT
	GmSLs-F	GTG CCA GCT TCC ACC ATA AT
	GmSLs-R	GCT TGC AAC AAC GAA CGA TAA G

Continued Supplementary Table 5. A list of genes tested in this study

Gene function	Gene	Primer
Metal transporters	GmPHT-F	TTG TGT CTC ATC CTG CTG ATA AT
	GmPHT-R	GGC TCC AGT AAG AGT TCC AAT C
	GmCuT2-F	GGC TCA AGC AAC CTT CTA TGT
	GmCuT2-R	CGA GGA GGA CTC TTG TTC TCT A
	GmVFeT1-F	GGT TGT TCC TCT CCT TCC TTA C
	GmVFeT1-R	GCG CCA ATT AGA GCT GTT TC
	GmNRAM1-F	AAG TGG ATG AGG GCA TTG ATA A
	GmNRAM1-R	GCA AGG GAA CAA GTG CAA AG
	GmFe2+DMT1-F	GCT GCT CTG GTG ATA GTG ATT
	GmFe2+DMT1-R	GGT GAT GGC TTG CCA AAT AAG
	GmZnTB-F	GCC CAT GGA GAG CAA GTA TAT C
	GmZnTB-R	CTG TCT AGA CCA GCC TGA ATT G
Nitrogen assimilation	GmNAR-F	TGG ATG AGT TGG CTC GTT TAG
	GmNAR-R	CAA TAG AGA AGG TTC GGG TGA G
	GmNIR-F	GAG AGA GCA TCT GAG GAA GAA C
	GmNIR-R	GCG CCA ACT CAT CCA TAT CA