



Figure S1. A ground-based brace root phenotyping robot (BRobot) was used for image capture. For the 2020 brace root data, a ground-based BRobot was used to capture RGB images of brace roots. BRobot is a modified Superdroid LT2 Tracked ATR Robot Platform with a custom controller. The red arrow highlights the side-mounted FLIR 3.2 MP Color Blackfly camera that captures images.

RGB Image Acquisition



1434_Plant_10A



1434_Plant_10B

Root Tagging GUI

main.py

Please use fullscreen

Click to draw circles
, place them according to the mode you are in.
hit the enter key to change modes.
you are done with a plant when the text
'done, click next' appears.
Hit 'r' to reset the progress
made for the current plant..

Start

Click through workflow

Previous

Mode: draw_triangles
draw the triangles startnig
with the highest point first and
connect it to the point right
below it (same x value). Then
draw the third to the left or
right of the bottom of the
vertical dots.

12

11

Enter # of brace-roots
lowest level goes in
lowest input box.

Scale
40.79px
Root width
30.08px
Stalk width
95.26px
Triangles
Complete

Next

Pixel Data

process_rootpixel_data.py

Scaled Phenotypes

- Number of roots/whorl (not shown)
- 2 = Single root width
- 3 = Stalk width
- 4 = Height of whorl (*a*)
- 5 = Stalk-to-root grounding (*c*)
- 6 = Root angle (*B*)
- 7 = Spread width
- 8 = Number of whorls in soil

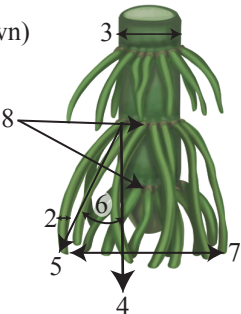


Figure S2. A semi-automated root tagging workflow was developed to optimize image processing. After RGB images are acquired, a python script (*main.py*) launches the root tagging graphical user interface (GUI). A tag of known size (0.5 inches) was placed on the stem prior to image acquisition for scale. First, the tag is selected for a pixel (px) scale, then each additional screen will prompt the user to click and/or record/identify specific regions in the image. The red dots shown on the image highlight the following phenotypes that have been tagged: 1) the number of pixels within a 0.5-inch region, 2) the stalk width, and 3) the single root width. The purple dots shown on the image highlight the right triangle that is used to identify the following phenotypes: 1) the height of the whorl, 2) the stalk-to-root grounding, and 3) the root angle. The number of roots within each whorl was counted and typed into the white boxes (shown on the left). This records the total number of roots per whorl and the number of whorls in the ground. After recording or identifying phenotypes, the user will hit “enter.” After all phenotypes have been recorded, the user will hit “Next” (red bar on the right of the screen) to begin the next image. After completing all images, a python script (*process_rootpixel_data.py*) is used to convert pixel data to scaled phenotype data. All data is exported to a .csv file for processing and analysis.

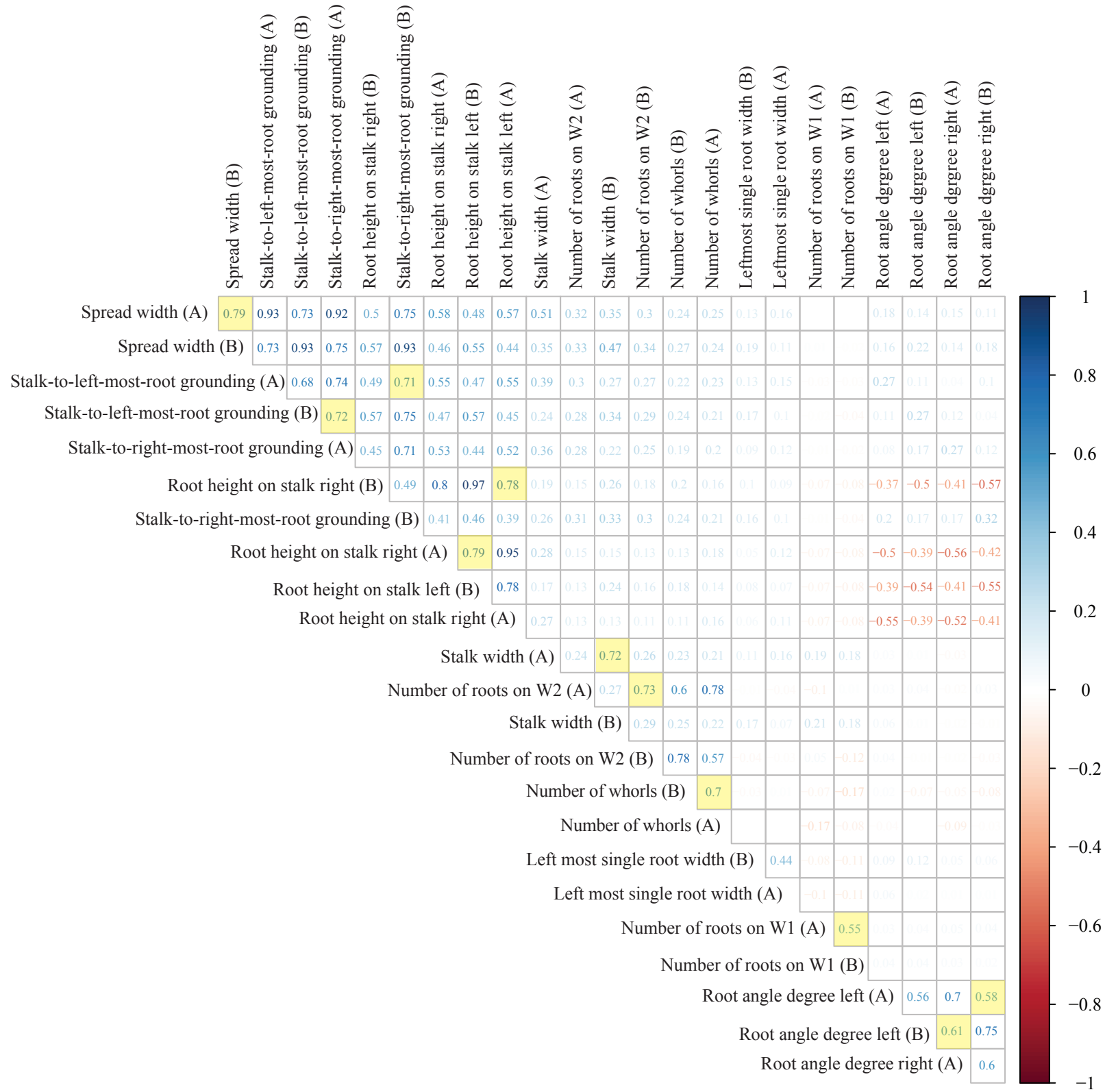


Figure S3. Phenotypes extracted from left and right images were highly correlated. Left and right images (labeled A and B) were acquired for each plant in 2019 and phenotypes were extracted from images with the root tagging GUI. A Pearson correlation analysis was run to determine the precision of our root tagging GUI. Cells highlighted in yellow indicate the same phenotype from both sides of the plant.

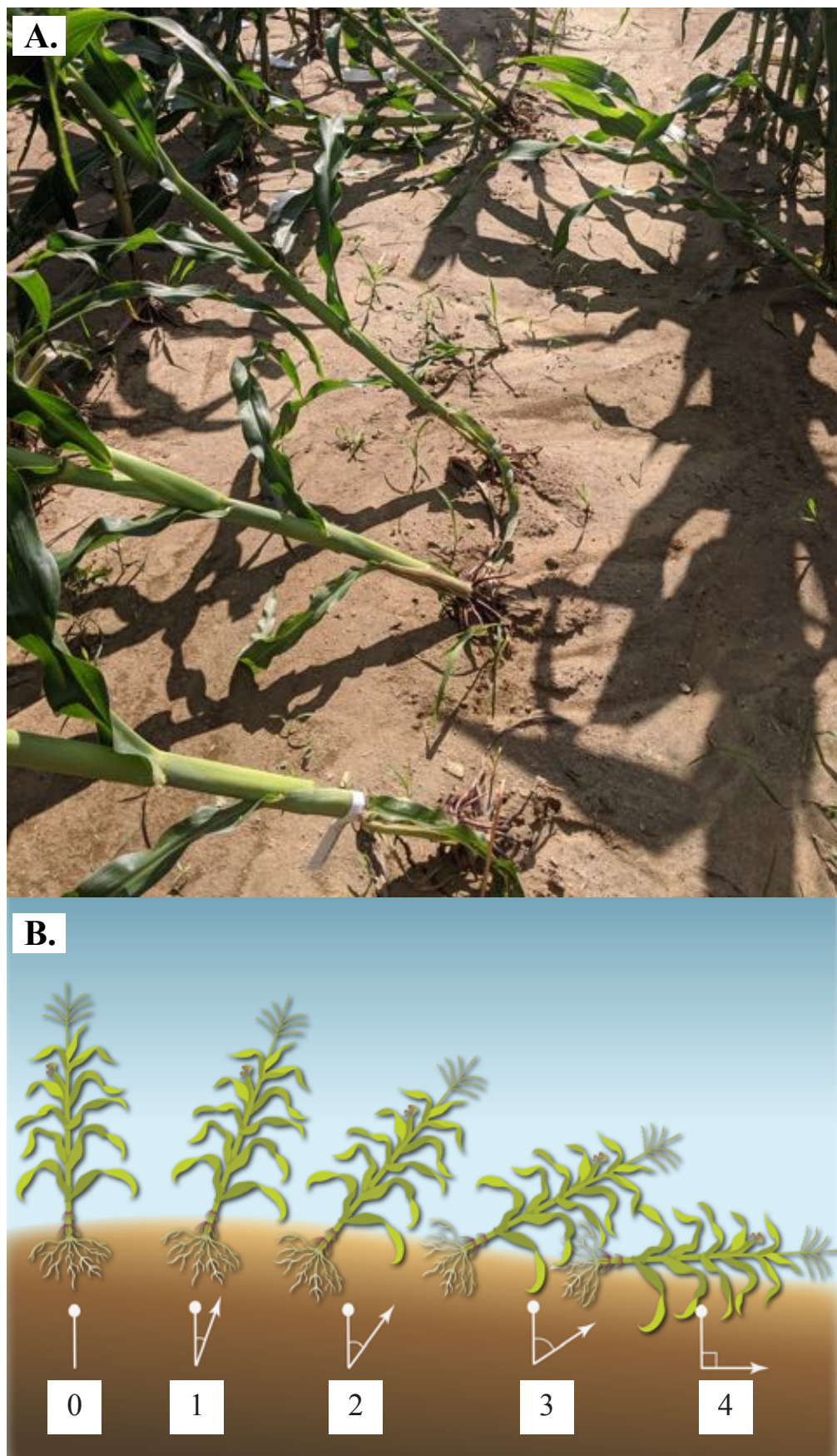
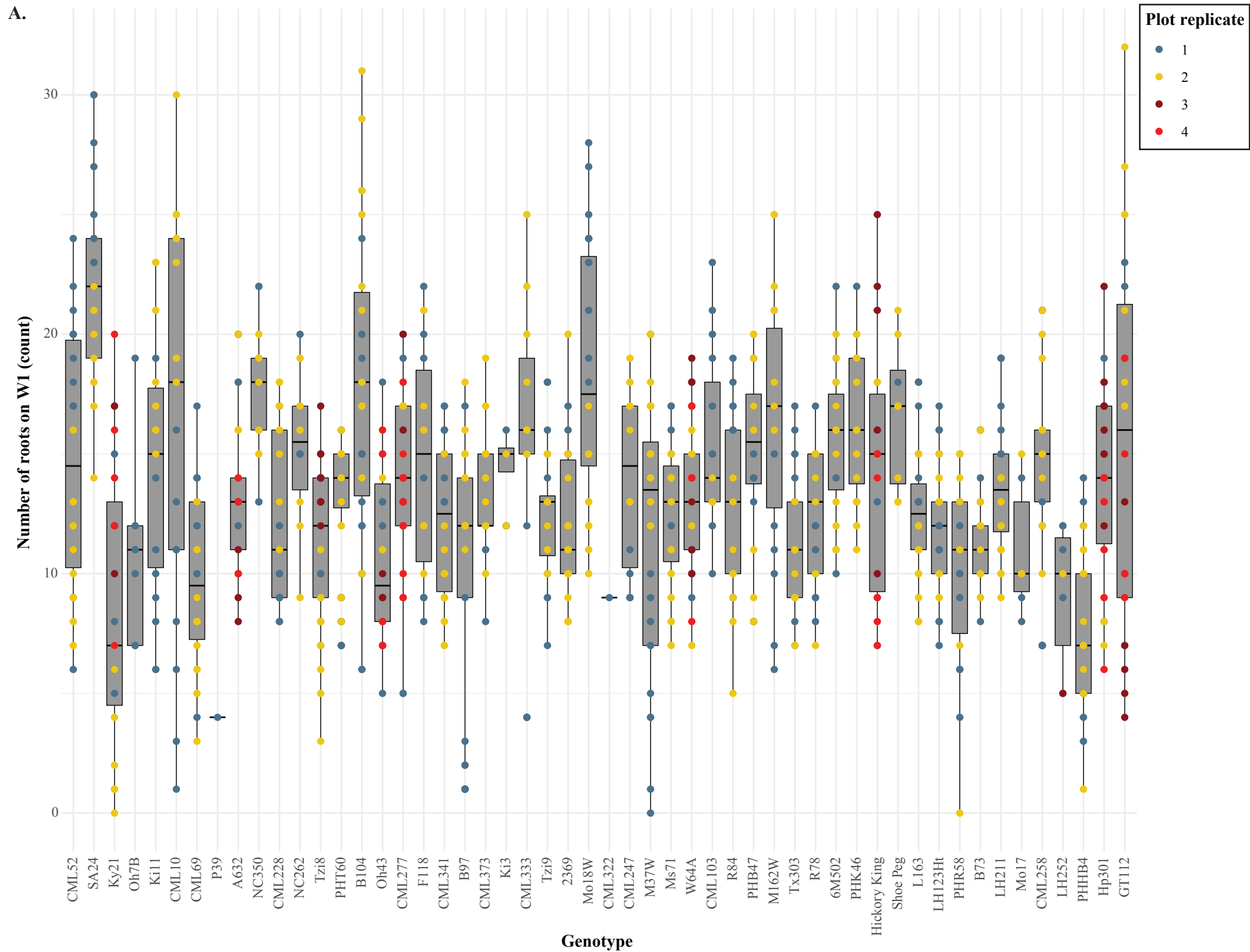


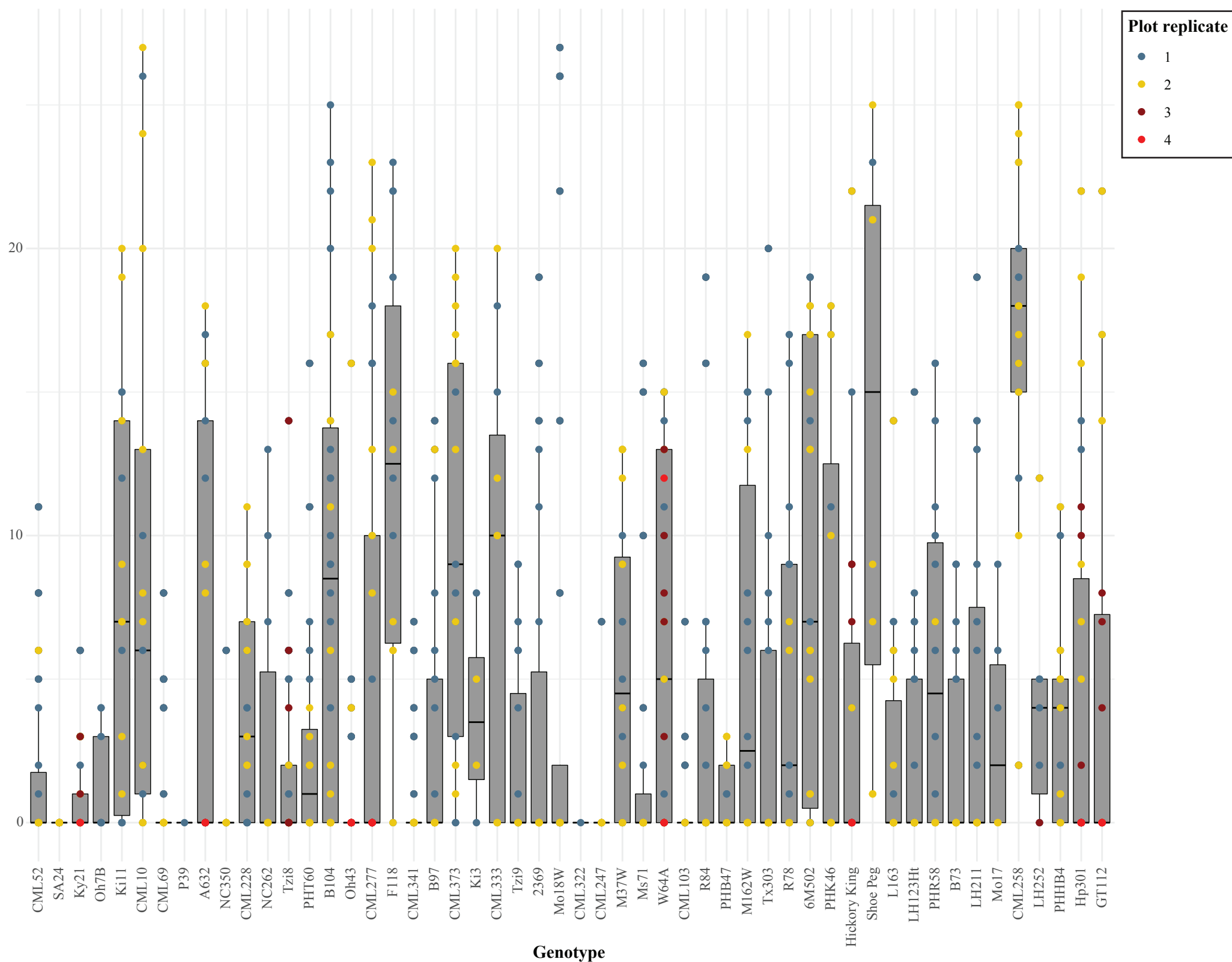
Figure S4. Tropical Storm Isaias caused extensive root lodging to our Newark, DE field site. A) Maize plants were considered root lodged when they were displaced from the vertical position due to roots pulling out of the ground or roots break and/or buckling. B) There was variation in the degree of lodging. An index score was assigned to each plant and was used as a metric for severity. An index score of 0 indicated plants were still vertical (no root lodging), an index score of 1 indicated that plants experienced a 1–30-degree displacement, an index score of 2 indicated plants experienced a 31–60-degree displacement, an index score of 3 indicated plants experienced a 61–80-degree displacement, and an index score of 4 indicated plants were on the ground (90-degree displacement).

A.

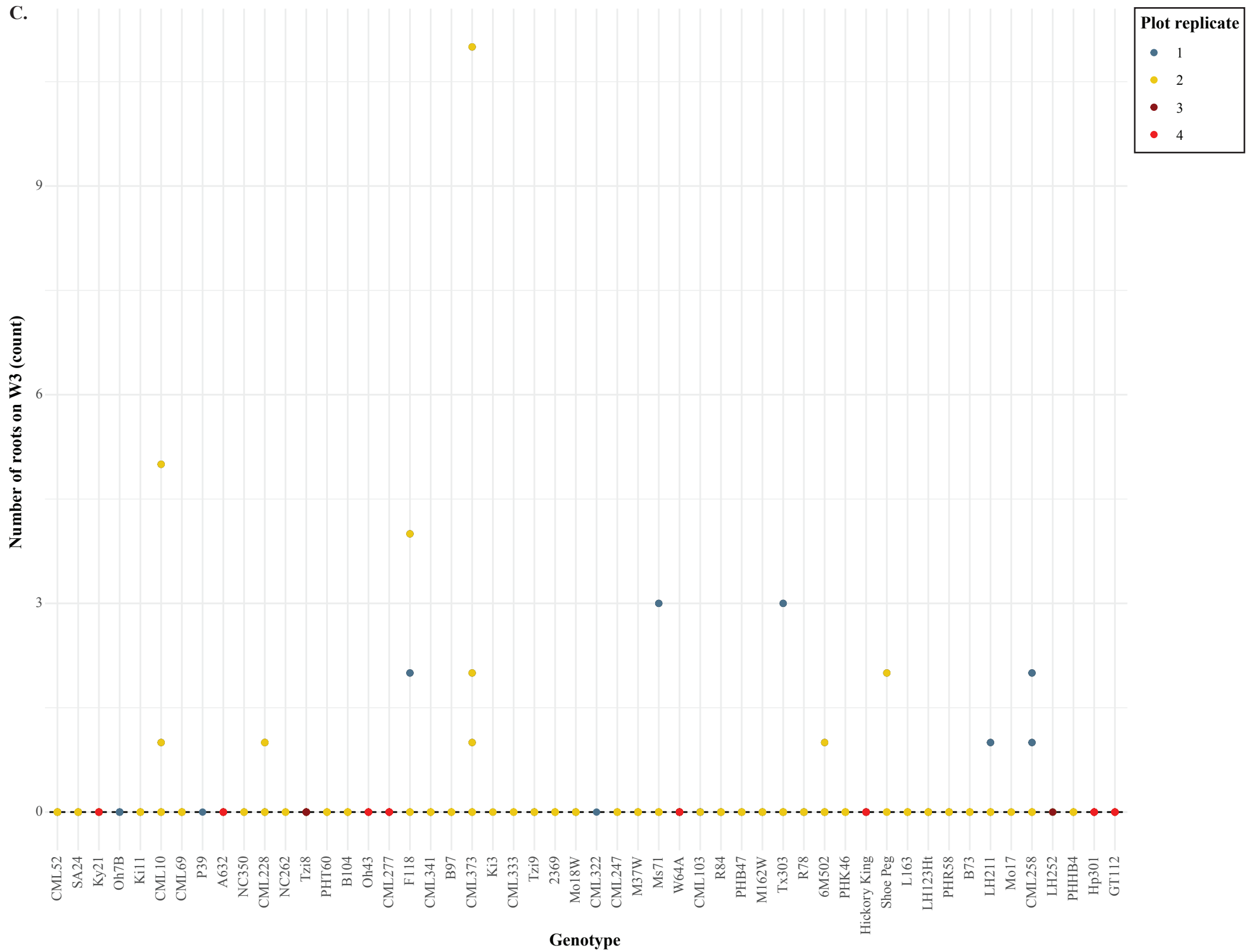


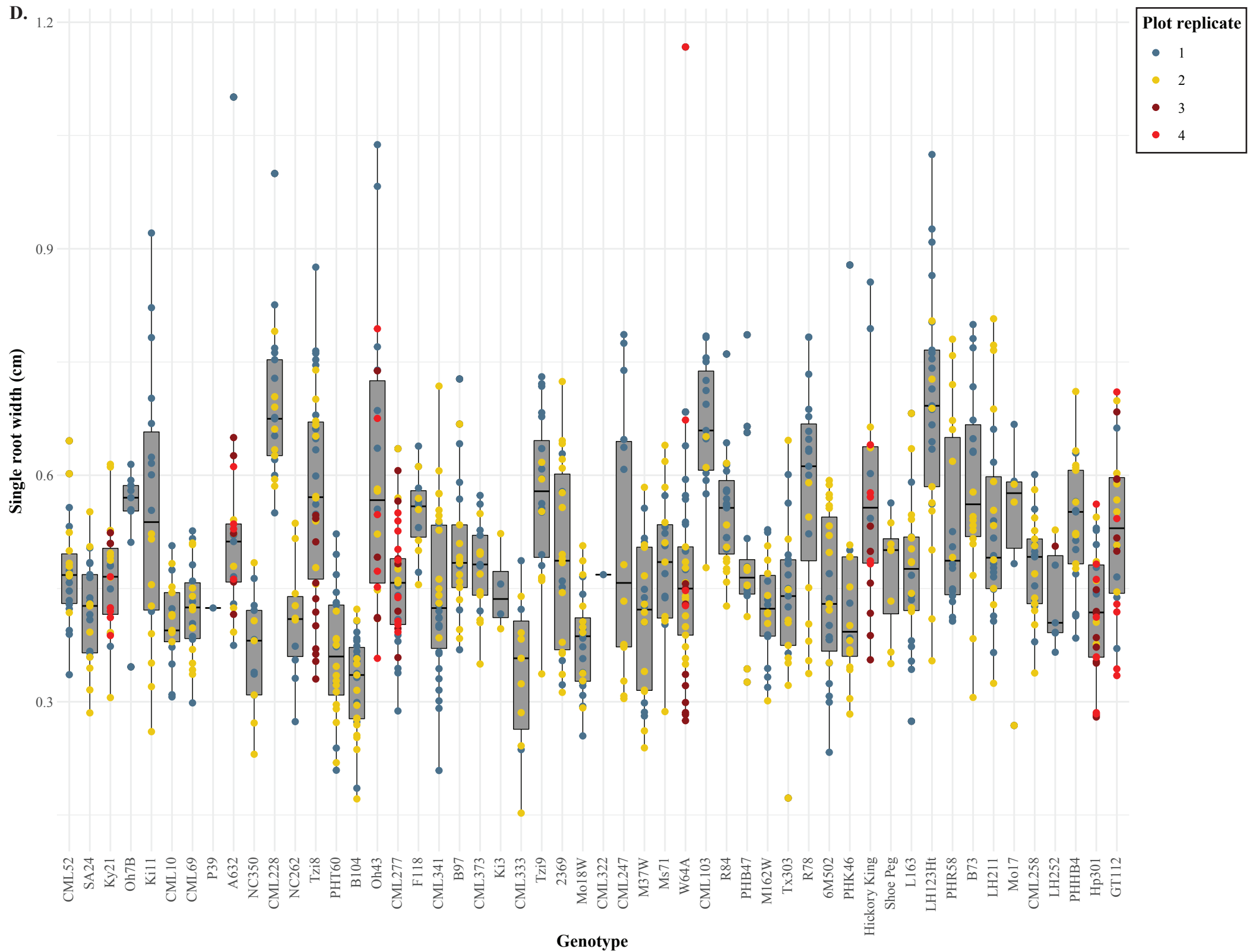
B.

Number of roots on W2 (count)

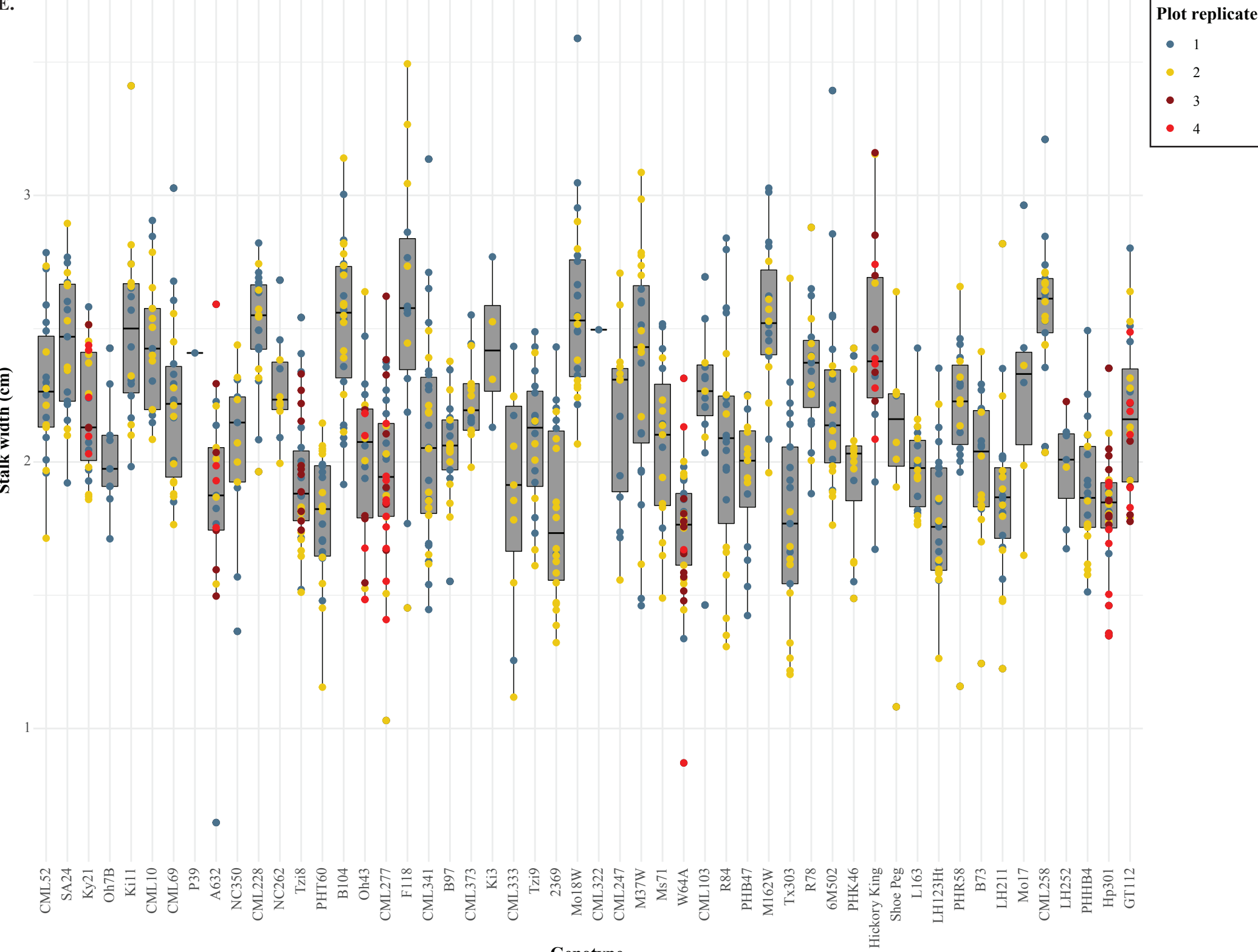


C.



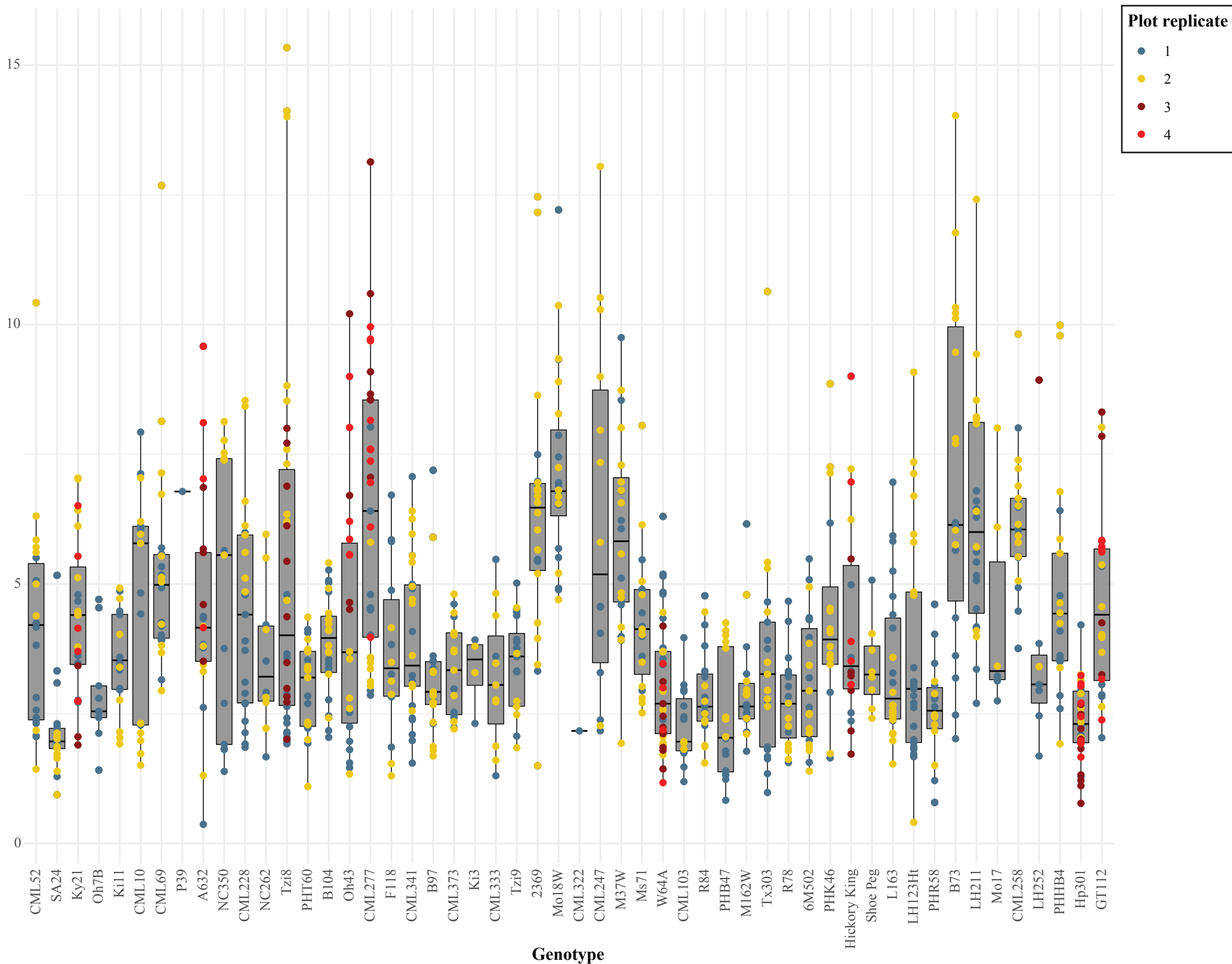
D.

L.

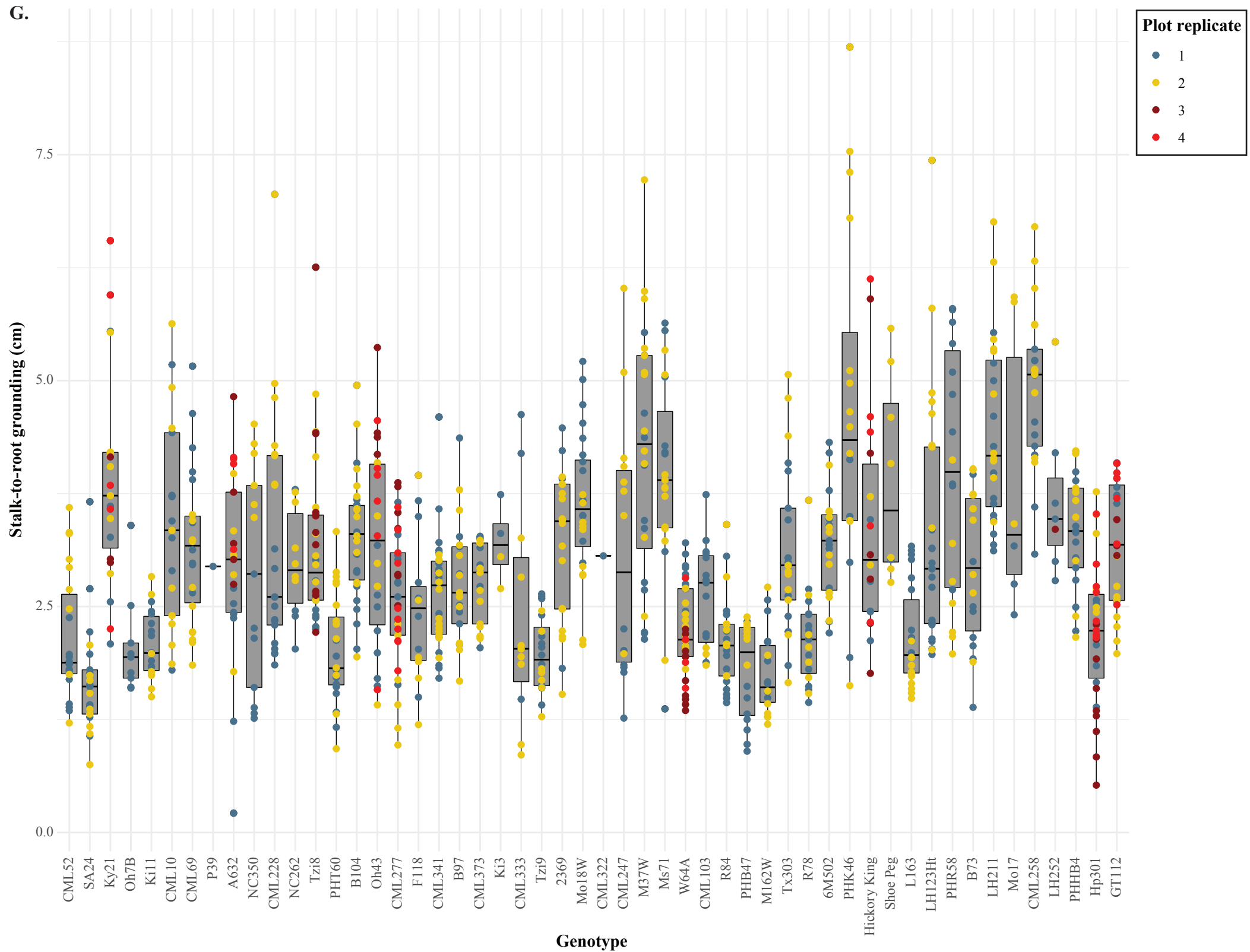


F.

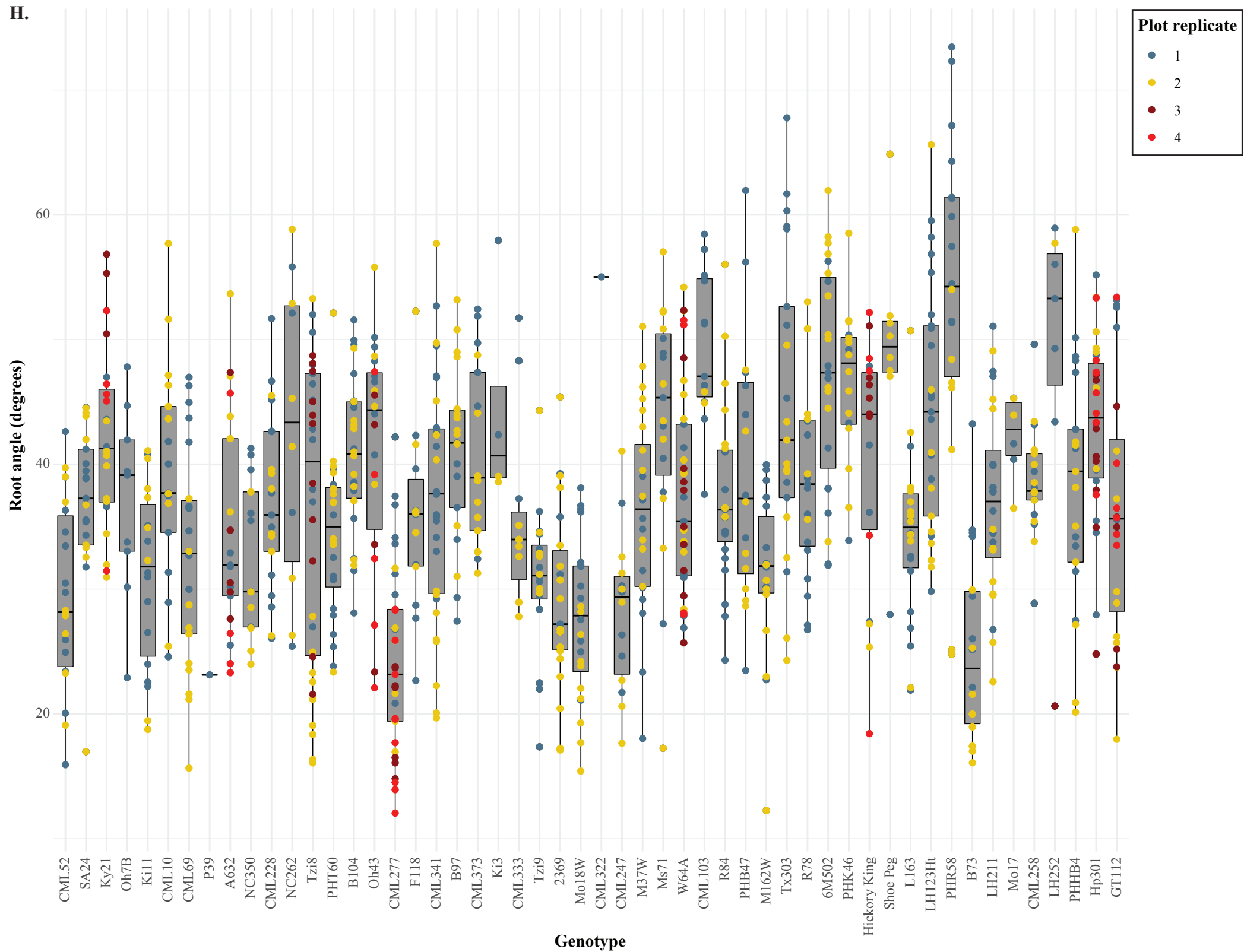
Root height on stalk (cm)

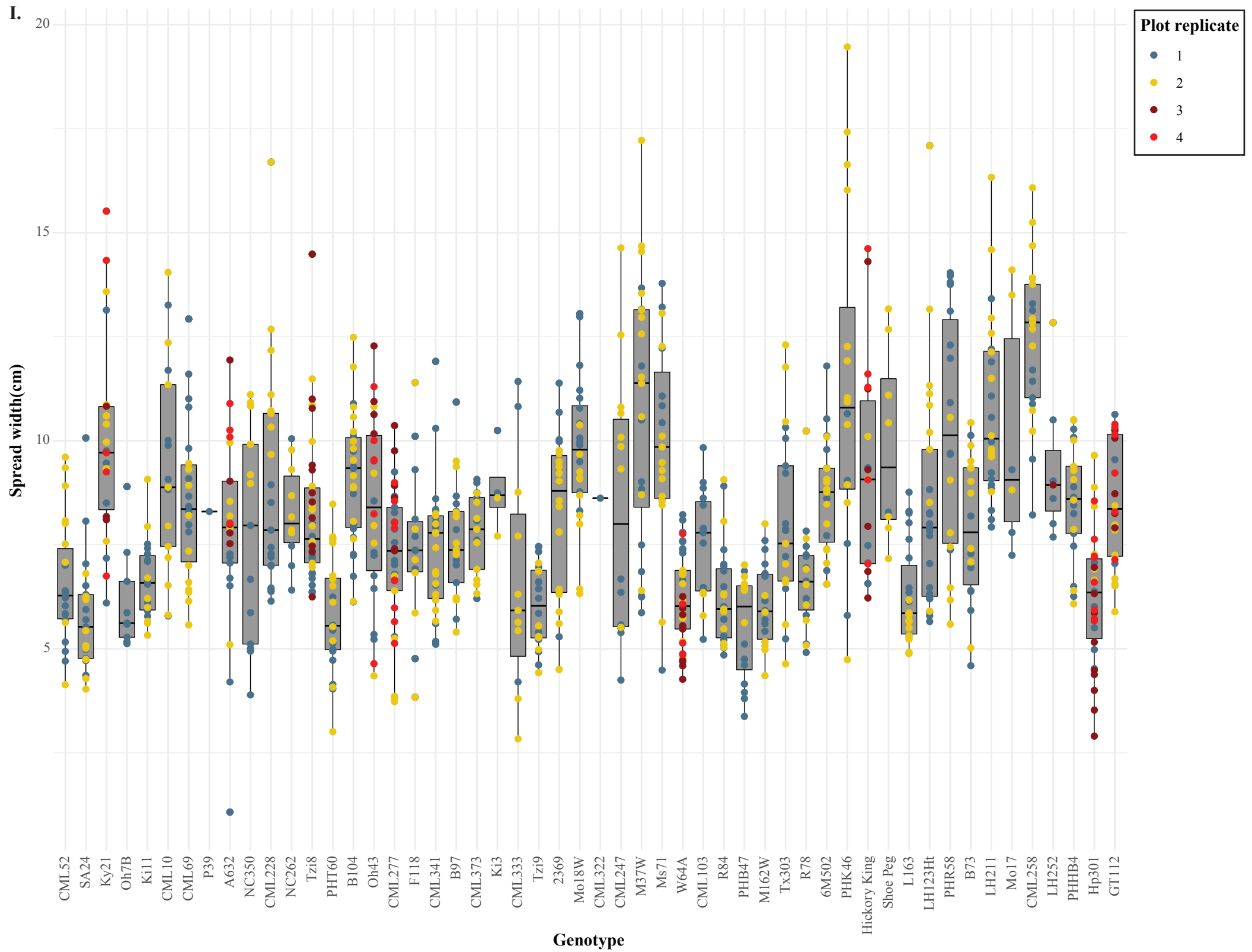


G.

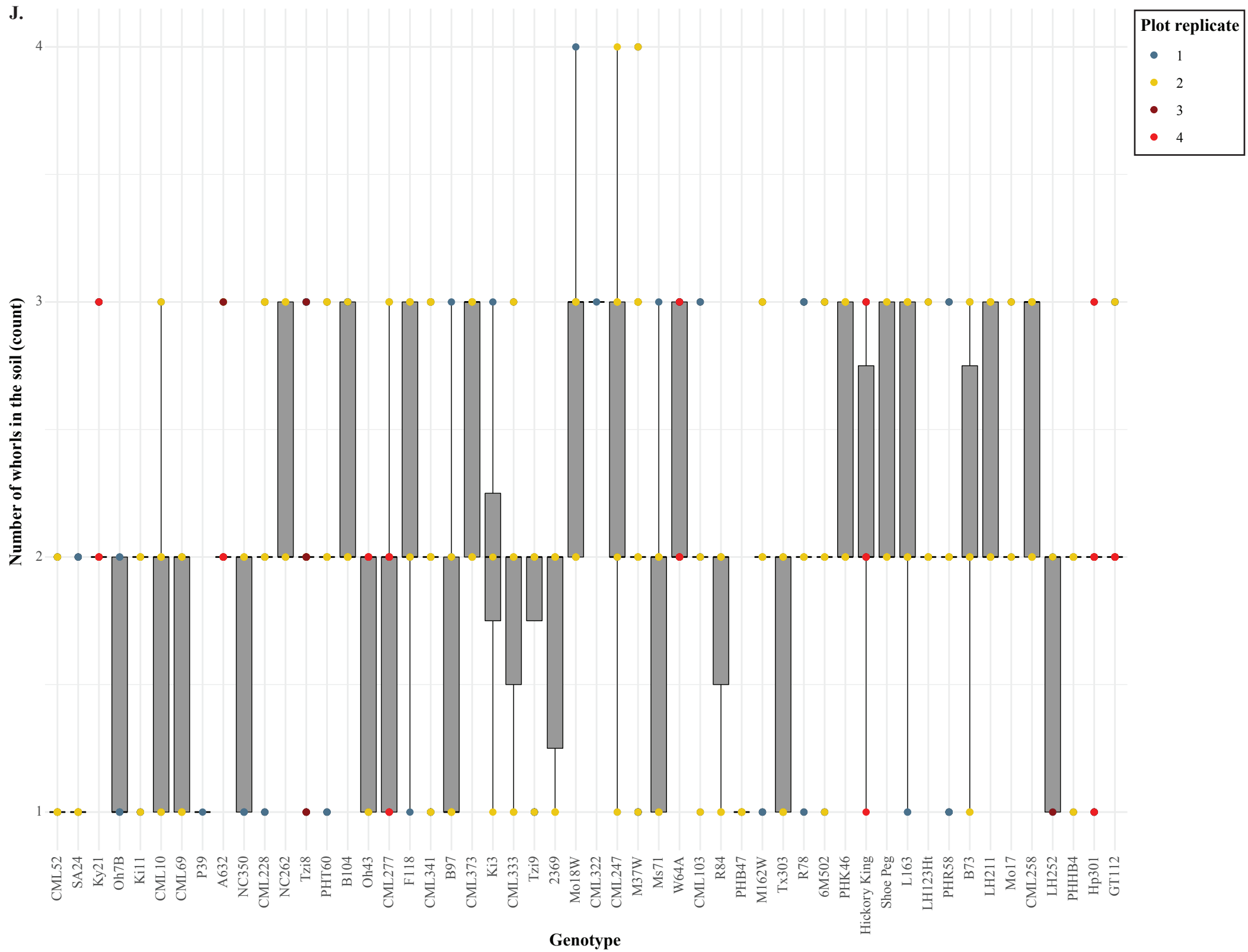


H.





J.



K.

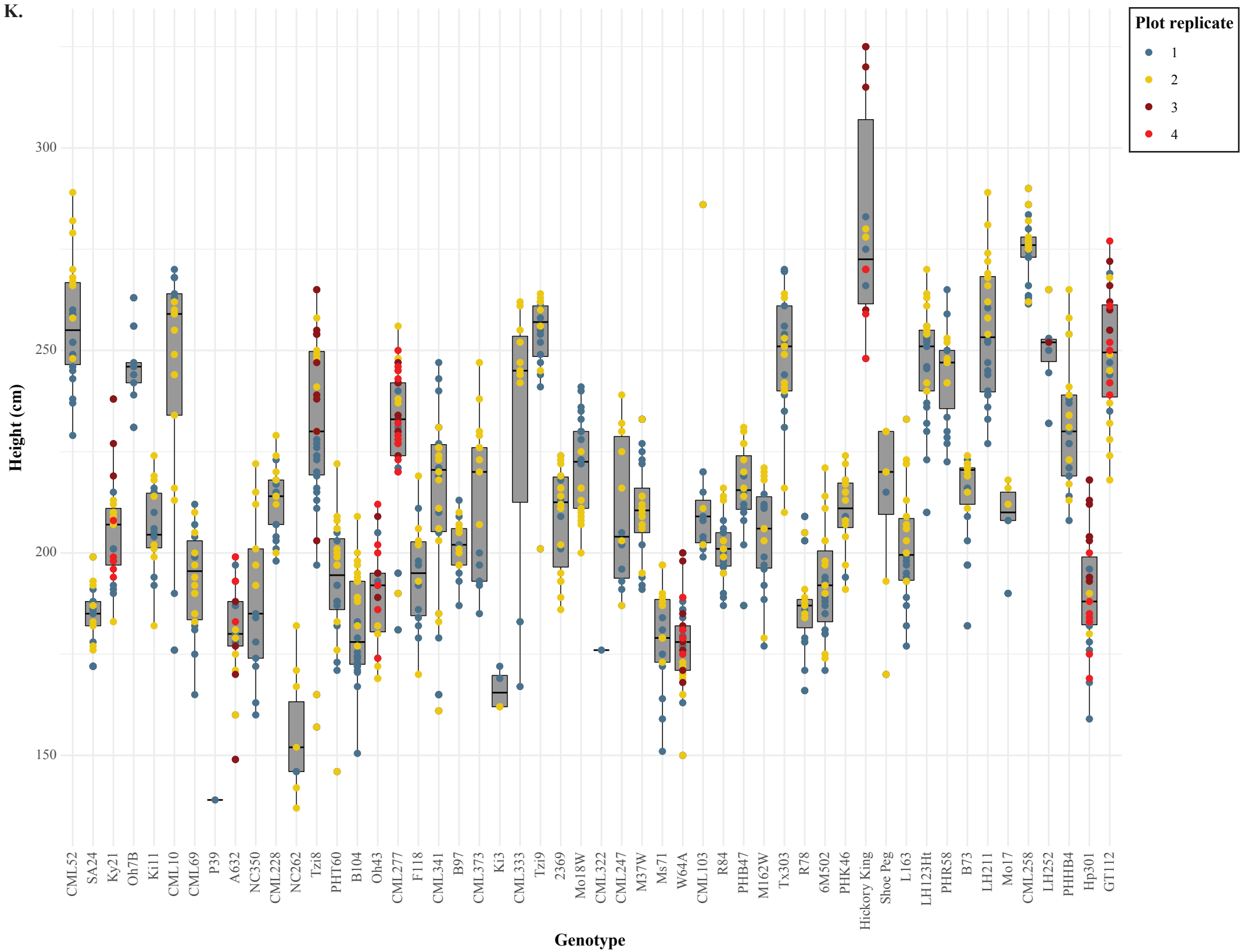


Figure S5. Plant phenotypes vary among genotypes. The following phenotypes vary among genotypes: (A) The number of roots on whorl 1 (the whorl closest to the ground, bottom whorl), (B) the number of roots on whorl 2 (middle whorl), (C) the number of roots on whorl 3 (top whorl), (D) the single root width, (E) the stalk width, (F) the root height on stalk, (G) the stalk-to-root grounding, (H) the root angle, (I) the spread width, (J) the number of whorls in the ground, and (K) plant height. (A-K) Genotypes are ordered by rank (high to low) for the brace root contribution to anchorage according to Figure 1. Each dot represents an individual plant. The color of each dot illustrates the plot replicate. Outliers are outlined in black

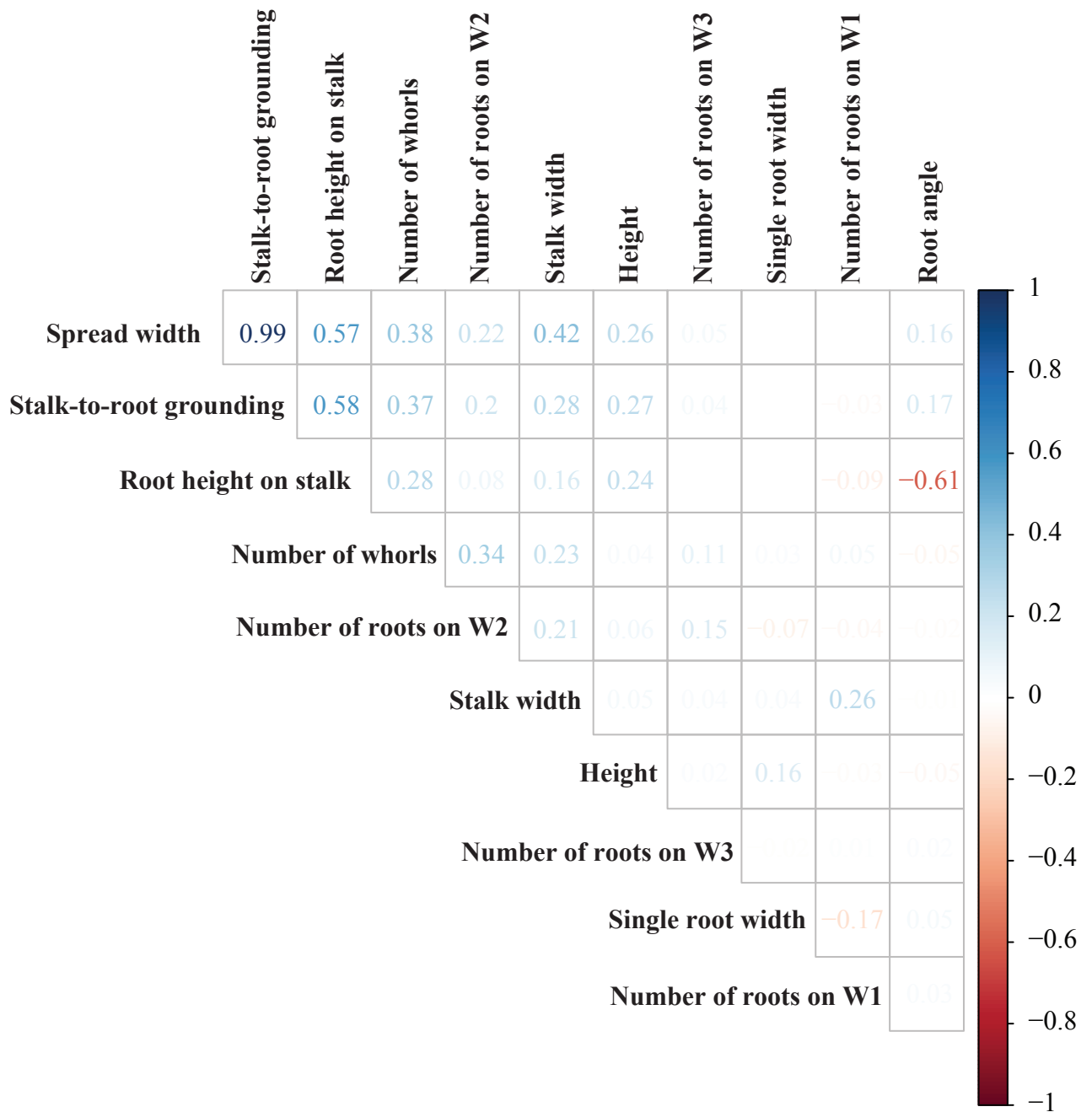


Figure S6. Brace root phenotypes are correlated with each other. A Pearson correlation analysis shows which phenotypes are highly correlated.

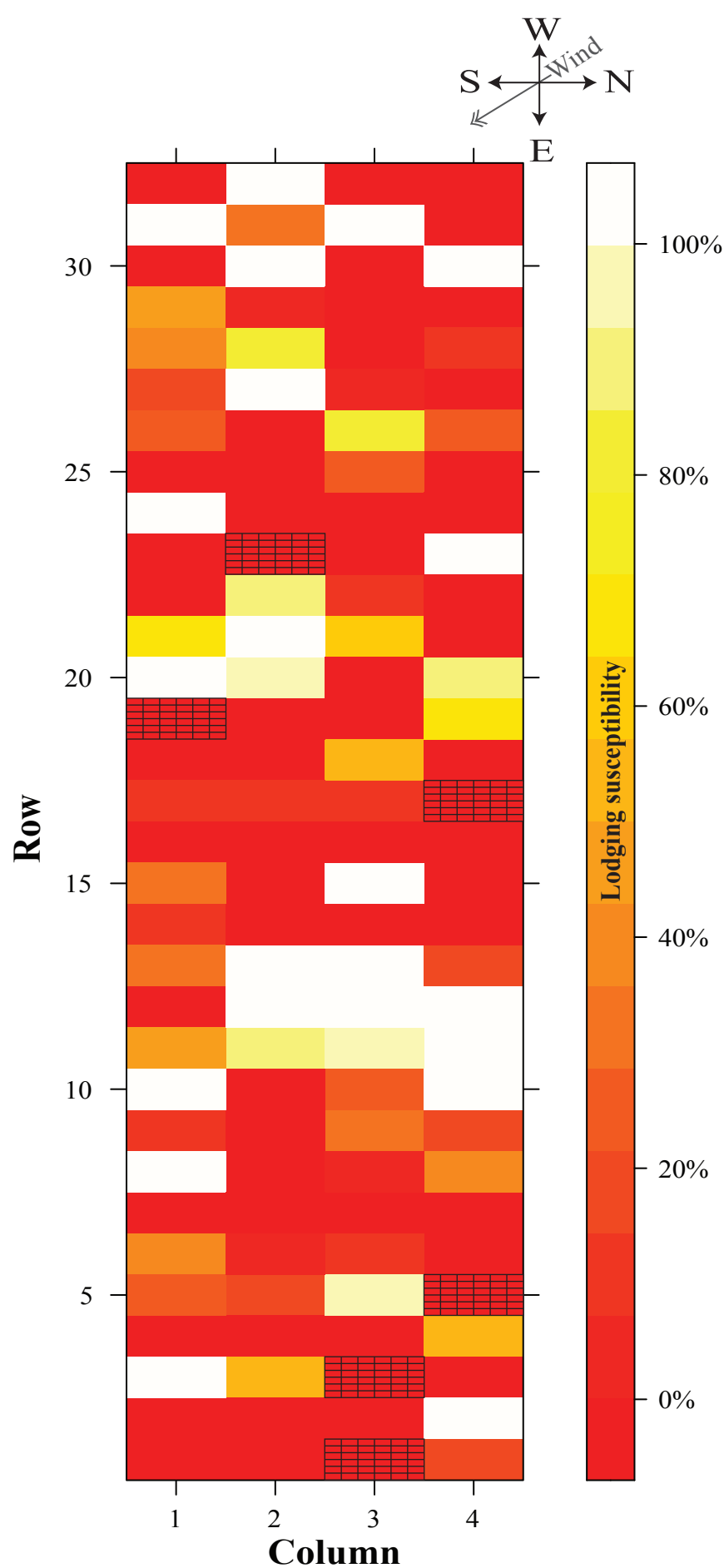


Figure S7. Root lodging was not related to field position. Winds from the West and North-West induced root lodging. Plots were colored according to the susceptibility of root lodging within each plot. Plots with 100% root lodging were highlighted with white, whereas plots that had 0% root lodging were highlighted with dark red. Plots with a grid overlaid indicate plots that did not germinate.