**Description of supplemental figures.**

**Boxplots** represent the distribution of data. The black dot inside the box indicates the median. The upper part of the box represents the upper quartile (50-75%) of the data. The lower box represents the lower quartile of the data (25-50%). The upper whiskers of the boxplot represent 75-97.5% and the lower whiskers represent 2.5-25% of the data. Any outliers are indicated with circles outlined in blue and are defined as any data point which lies over 97.5% or under 2.5% of the distribution of data.

**Scatter matrix:** Each matrix includes scatterplots (lower diagonals), density plots (diagonals), and correlation values (upper diagonals).

**Scatterplots** identify the relationship (if any) between two variables plotted along two axes. The x and y-axis of scatterplots in matrices are proportions and thus are less than one. **Correlation values** are a statistical measure of the strength of a relationship between two variables, which can be visually represented by a scatterplot. In the scatter plots not found in scatter matrices, colors indicate the treatment type and shapes indicate the explant type used.

**Density plots** represent the distribution of a variable, similar to a histogram. It is important to note that on density plots, the y-axis stands for the value of the density function, not a proportion. Therefore, for the density plots on the diagonals, it is fine to have values larger than 1 on the y-axis.

**Dot plots** are similar to density plots and histograms in that they show the distribution of the data, represented as dots connected with a line. The black dots are the values of the original observations while the blue dots are the mean of the observations. The line crossing a dot implies multiple observations with the same value. For example, a standalone blue dot without a line implies a unique observation, and a blue dot with a line implies multiple observations with the same value.

**Confidence intervals** are a range around the estimated heritability that indicates the precision of the estimated heritability. In these figures, 95% of the confidence intervals computed from random samples will contain the true population value of the heritability. The black dot represents the estimated heritability while the upper and lower limits represent the upper and lower bounds of the confidence intervals.

**Other notes:**

In E4, E5ai, E5aii and E12, some graphs have a code that corresponds to each genotype. Please find the key in the Table S6.

In E13 – cross experiment replication, NP= NAA and 2iP.

When callus size is on an axis, it represents a unit-less score that refers to the 0-3 scoring index detailed in Ma *et al.* 2022.

The entirety of the supporting documents & figures can be found here: <https://www.dropbox.com/sh/7x7vtb2pmb8sdsm/AACbPHeAdTYdlqOzPq0QNP9Ma?dl=0>