Figure S1: Comparison of human measured and neural network estimated vein lengths on test-set images ($N=85$).
**Figure S2**: Network architecture used in-place of the U-Net structure after the last max pool layer through the first up convolution. The 32x32x512 input tensor represents the output of the last max-pool layer. The 56x56x512 output tensor is the same as the output size of the first up convolution. + represents element-wise addition of the output tensors.
| Dilation | Channels in | Channels out | Kernel | Stride | Padding | Dilation | Activation |
|----------|-------------|--------------|--------|--------|---------|----------|------------|
| 1        | 512         | 1024         | 3x3    | 1      | 0       | 1        | ELU        |
| 2        | 1024        | 1024         | 3x3    | 1      | 2       | 2        | ELU        |
| 4        | 1024        | 1024         | 3x3    | 1      | 4       | 4        | ELU        |
| 8        | 1024        | 1024         | 3x3    | 1      | 8       | 8        | ELU        |
| 16       | 1024        | 1024         | 3x3    | 1      | 16      | 16       | ELU        |
| 32       | 1024        | 1024         | 3x3    | 1      | 32      | 32       | ELU        |
| Transposed Convolution | 1024 | 1024 | 2x2 | 2 | 0 | 2 | ELU |
| Convolution | 1024 | 512 | 5x5 | 1 | 0 | 1 | ELU |
Figure S3: Cross-validated training (red) and validation (black) loss of model with final hyperparameters. Shading indicates standard error.
Figure S4: Bivariate plots for all trait correlations presented in Figure 2. Points represent the estimated marginal means of genotypes. Blue line represents the fitted regression line. Units for all traits are as in Table 1.
\[ y = 63.5 + 0.0164 \times R^2_{adj} = 0.00093 \]

\[ y = 6.93 - 0.00183 \times R^2_{adj} = 0.035 \]

\[ y = 6.33 - 0.00148 \times R^2_{adj} = 0.021 \]

\[ y = 6.63 - 0.00166 \times R^2_{adj} = 0.032 \]

\[ y = 40.2 - 0.0316 \times R^2_{adj} = 0.39 \]

\[ y = 36.7 - 0.0236 \times R^2_{adj} = 0.27 \]
\[ y = 8.95 + 0.0678 \times R_a \]

\[ y = 1.57 + 0.0139 \times R_a \]

\[ y = 1.69 + 0.0169 \times R_a \]

\[ y = 389 - 8.02 \times R_a \]

\[ y = 26.5 - 6.34 \times R_a \]

\[ y = 0.0127 - 0.00509 \times R_a \]
\[ y = 0.0668 - 0.00344 x \quad R^2_{adj} = -0.0041 \]

\[ y = 84.6 - 30.8 x \quad R^2_{adj} = 0.0021 \]

\[ y = 6.64 - 0.194 x \quad R^2_{adj} = -0.004 \]

\[ y = 6.74 - 1.3 x \quad R^2_{adj} = 0.0065 \]

\[ y = 6.69 - 0.746 x \quad R^2_{adj} = -0.00017 \]

\[ y = 31.4 + 3.25 x \quad R^2_{adj} = -0.002 \]
\[ y = 9.4 + 0.151x \quad R^2_{adj} = -0.0042 \]

\[ y = 0.0269 + 0.0698x \quad R^2_{adj} = 0.017 \]

\[ y = 0.0441 + 0.109x \quad R^2_{adj} = 0.017 \]

\[ y = 19.6 + 0.982x \quad R^2_{adj} = -0.0041 \]

\[ y = 5.55 - 2.95x \quad R^2_{adj} = 0.00026 \]

\[ y = 6.07 - 2.79x \quad R^2_{adj} = -0.0012 \]
$y = 6.75 - 0.00125x ~ R_{adj}^2 = 0.05$

$y = 40.6 - 0.0189x ~ R_{adj}^2 = 0.36$

$y = 36.7 - 0.0161x ~ R_{adj}^2 = 0.32$

$y = 38.6 - 0.0175x ~ R_{adj}^2 = 0.39$

$y = 30.9 - 0.0173x ~ R_{adj}^2 = 0.37$

$y = 27.5 - 0.015x ~ R_{adj}^2 = 0.33$
\[ y = 0.903 + 0.00771 \times R^2_{\text{adj}} = 0.14 \]

\[ y = 0.981 + 0.00913 \times R^2_{\text{adj}} = 0.15 \]

\[ y = 0.0024 + 0.000324 \times R^2_{\text{adj}} = 0.11 \]

\[ y = 0.0769 - 0.000529 \times R^2_{\text{adj}} = 0.024 \]

\[ y = 33.9 + 1.45 \times R^2_{\text{adj}} = 0.1 \]

\[ y = 6.96 - 0.0187 \times R^2_{\text{adj}} = 0.013 \]
\[ y = 4.72 - 0.039x \quad R^2_{\text{adj}} = -0.0017 \]

\[ y = 5.78 - 0.0596x \quad R^2_{\text{adj}} = 0.00021 \]

\[ y = 13.7 - 0.126x \quad R^2_{\text{adj}} = 0.019 \]

\[ y = 15.3 - 0.253x \quad R^2_{\text{adj}} = 0.23 \]

\[ y = 0.0689 - 1 \times 10^{-4}x \quad R^2_{\text{adj}} = -0.0041 \]

\[ y = 0.101 + 0.000227x \quad R^2_{\text{adj}} = -0.041 \]
\[ y = 23.2 - 28.4 x \quad R^2_{\text{adj}} = 0.049 \]

\[ y = 7.89 - 37.9 x \quad R^2_{\text{adj}} = 0.42 \]

\[ y = 9.2 - 4.5 x \quad R^2_{\text{adj}} = 0.44 \]

\[ y = 0.312 + 0.176 x \quad R^2_{\text{adj}} = 0.14 \]

\[ y = 0.386 + 0.203 x \quad R^2_{\text{adj}} = 0.14 \]

\[ y = 0.0402 + 1.15 x \quad R^2_{\text{adj}} = 0.99 \]
Figure S5: Principal component analysis (PCA) of all measured leaf traits using estimated marginal means for each trait. For stomatal density, length, pore length, and guard cell width, trait values are included separately for the top and bottom of the leaf.
Figure S6: Scree plot showing principal components vs. percent variance explained.
**Figure S7.** Linkage disequilibrium heatmaps for all significant SNPs found on each chromosome. Linkage disequilibrium was estimated as $R^2$ between all significant SNPs per chromosome. Colored blocks represent haplotypic blocks that the SNPs belong to based on the full haplotype map (Figure S10). Block membership is shown for both an analysis based on the full, genome-wide collection of SNPs (“genome”) as well as a re-analysis based on only significant SNPs (“significant”). Colors are arbitrary. For full methodological details, see Temme et al. (2020).
chromosome: 3

Significant Genome

03–01
R2

03–02

3697795
180990739
3697795
180990739

0.000229476
chromosome: 4

Significant Genome

R2

04–01

14897983

1489893

14899893

14897983
chromosome: 5

Genome

Significant

0.943082

R2

05–01

27904105

28035357

28035357

27904105
Genome

Significant

09-01

09-02

Genome

115516275

191930827

R2

0.00172655

chromosome: 9
chromosome: 10
chromosome: 13
chromosome: 17

Significant Genome

17-01
Figure S8: Manhattan plots resulting from GWA analyses for all traits. The red line is the significance threshold based on the modified Bonferroni correction (see text for details) and the blue line is the suggestive threshold based on (i.e., top 0.1% of all SNPs). Colored dots represent SNPs that are significant or suggestive for at least one trait. Color of dots is arbitrary.
**Figure S9**: Distribution of the number of genes per significant region. Points represent the number of genes in each significant block. Note the log scale on the y-axis.
Figure S10: Visualization of haplotypic blocks across the sunflower genome. Blocks are shown for each of the 17 sunflower chromosomes. Blocks are colored in an alternating fashion and colors are arbitrary. Black dots on the x-axis indicate singleton SNPs that did not fall within blocks.
Methods S1: Neural Network Architecture, Training and Prediction.

The neural network followed that of the U-Net (Ronneberger et al., 2015) deep neural network. High-dilation convolutions (Yu and Koltun, 2015) were integrated by replacing the U-Net architecture after the last max-pool through the first up convolution with the structure shown in Figure S1. In addition, all RELU activations were replaced with ELUs (Clevert et al., 2015). The network architecture takes input images of size $572 \times 572 \times 3$ pixels and outputs a segmented target image of $388 \times 388 \times 1$ pixels that corresponds to the center of the $572 \times 572$ image. For training, input images were created by randomly selecting $388 \times 388 \times 3$ regions from the leaf images along with the surrounding 92 pixels to create the $572 \times 572 \times 3$ input image. As in Ronneberger et al. (2015), when surrounding data was missing at the edge of the image, the pixels were extrapolated by mirroring. The $572 \times 572 \times 3$ bright-field leaf input images were independently normalized to have a mean of 0 and a standard deviation of 1. The network was coded using the pytorch (Paszke et al., 2017) framework and trained using backpropagation using the Adam optimizer (Kingma and Ba, 2014). The loss function was weighted binary cross entropy. Non-vein pixels were given a weight of 0.05 and in-vein pixels a weight of 1. The weighting of the non-vein pixels was chosen using 3-fold cross validation of the training set of images using a grid search of 0.01, 0.05, 0.1, and 0.2 for the weight. Cross-validation training was performed out to 3000 batches, but there was no further decrease in the loss on the validation sets past 1900 batches (Figure S3).

Attempts at stitching $388 \times 388$ segmented tiles together to recreate the full size bright-field images resulted in incorrect segmentations at the boundaries between tiles. To avoid the boundary effects, the full-sized images ($2584 \times 1936$ pixels) were mirror padded to $2876 \times 2300$ and passed through the network as one input. The images were normalized as described for the image tiles used in training. The resulting segmented images were cropped back to $2584 \times 1936$ pixels to remove padding pixels. The padding was used to both avoid edge effects – as done during network training – and to ensure all the convolution operations within the network were valid. The network outputs the probability a pixel is within a vein. The in-vein segmentation cutoff of 0.2 maximized the correlation between the number of pixels in the hand drawn vein lines and in that extracted with the network in a 3-way cross validation grid search of values spanning 0.2 to 0.9 with 0.1 increments.