**Supplemental Code S1.** Source data and code used for generating Fig. 1.

**Supplemental Code S2.** Source data and code used for generating Fig. 2.

**Supplemental Code S3.** Source data and code used for generating Fig. 3.

**Supplemental Code S4.** Source data and code used for generating Fig. 4.

**Supplemental Code S5.** Source data and code used for generating Fig. 5.

**Supplemental Code S6.** Source data and code used for generating Supplemental Fig. S2.

**Supplemental Code S7.** Source data and code used for generating Supplemental Fig. S3.

**Supplemental Code S8.** Source data and code used for generating Supplemental Fig. S4.

**Supplemental Code S9.** Source data and code used for generating Supplemental Fig. S7.

**Supplemental Code S10.** Source data and code used for generating Supplemental Fig. S9.

**Supplemental Code S11.** Source data and code used for generating Supplemental Fig. S10.

**Supplemental Code S12.** Source data and code used for generating Supplemental Fig. S11.

**Supplemental Code S13.** Python script used for extracting the 20-nt target recognition sequences of the sgRNAs. In the "combination.txt" file, the 6-nt barcodes in the forward and reverse primers are structured respectively in the first and second columns; the third column shows the well coordinate of each 96-well plate. The first column of the generated file indicates the read counts of the corresponding sgRNAs, followed by the well coordinate in the second column. The sgRNA sequences are given in the third column. Even though noise is presented in the generated results, each plant's exact sgRNA sequence(s) can be easily determined according to the read counts.