Supplementary figure captions

Supplementary Figure 1. Principal Component (PC) score plot combined with variable loading plot (i.e., Biplot) representing Vegetation Index data gathered during the 2022 season at 50m (1.18 cm pixel-1resolution) during Haun's stages 7.1 – 7.3. In the header, PC 2 corresponds to the number of PCs used for training the Principal Component Regression model, selected using the Guttman-Kaiser criterion, and the percentage denotes the amount of variability present in the data explained by them. Each data point corresponds to a single plot in the experiment, colored and shaped according to the sowing density (seeds m-2) and Genotype, respectively.

Supplementary Figure 2. Comparison of predicted vs. actual (observed) plant density for the Ridge model trained on 2022 data collected at 50m (1.18 cm pixel-1, cm) during Haun stages 7.1 – 7.3, tested on datasets from the 2023 agronomic season spanning stages 4.4 to 8.4 and various altitudes (resolutions). RGB image data was obtained from ground-level (0.03cm) and UAV at 15m (0.27cm), 30m (0.53cm), and 50m (0.89cm). Each dot represents a plot in the testing set, with colors indicating different sowing density groups in seeds m-2. The upper left corners show coefficient of determination (R2) (*Equation 2*), Mean Absolute Error (*Equation 4*), and Mean Absolute Percentage Error (MAPE) (*Equation 5*) values for each dataset, including plots with 35 and 70 seeds m-2 sowing densities and the outlier outlined in Figure 5 circled in red.

Supplementary Figure 3. Principal Component (PC) score plot combined with variable loading plot (i.e., Biplot) representing Vegetation Index data gathered during the 2023 season during Haun's stages 5.6 – 5.9. Every plot represents a different resolution dataset: A) ground (0.03 cm pixel-1); B) 15m (0.27 cm pixel-1); C) 30m (0.53 cm pixel-1); D) 50m (0.89 cm pixel-1). In the header, PC X corresponds to the number of PCs used for training the Principal Component Regression model, selected using the Guttman-Kaiser criterion, and the percentage denotes the amount of variability present in the data explained by them. Each data point corresponds to a single plot in the experiment, colored and shaped according to the sowing density (seeds m-2) and Genotype, respectively. (-) determines uncharacterized genotype and (MEZCLA) a mix of genotypes.