

Figure S1: UML diagram depicting the architecture of the IAP system. Boxes colored with different background represent the main components of the system, which are (1) pipeline definition: defining analysis pipeline templates, (2) image processing: providing block definition, (3) image handling: implementing the image operations, (4) meta-data: describing related information for a given experiment and (5) system extensions: providing the possibility of defining IAP plugins. The relationship of these components is indicated with lines.

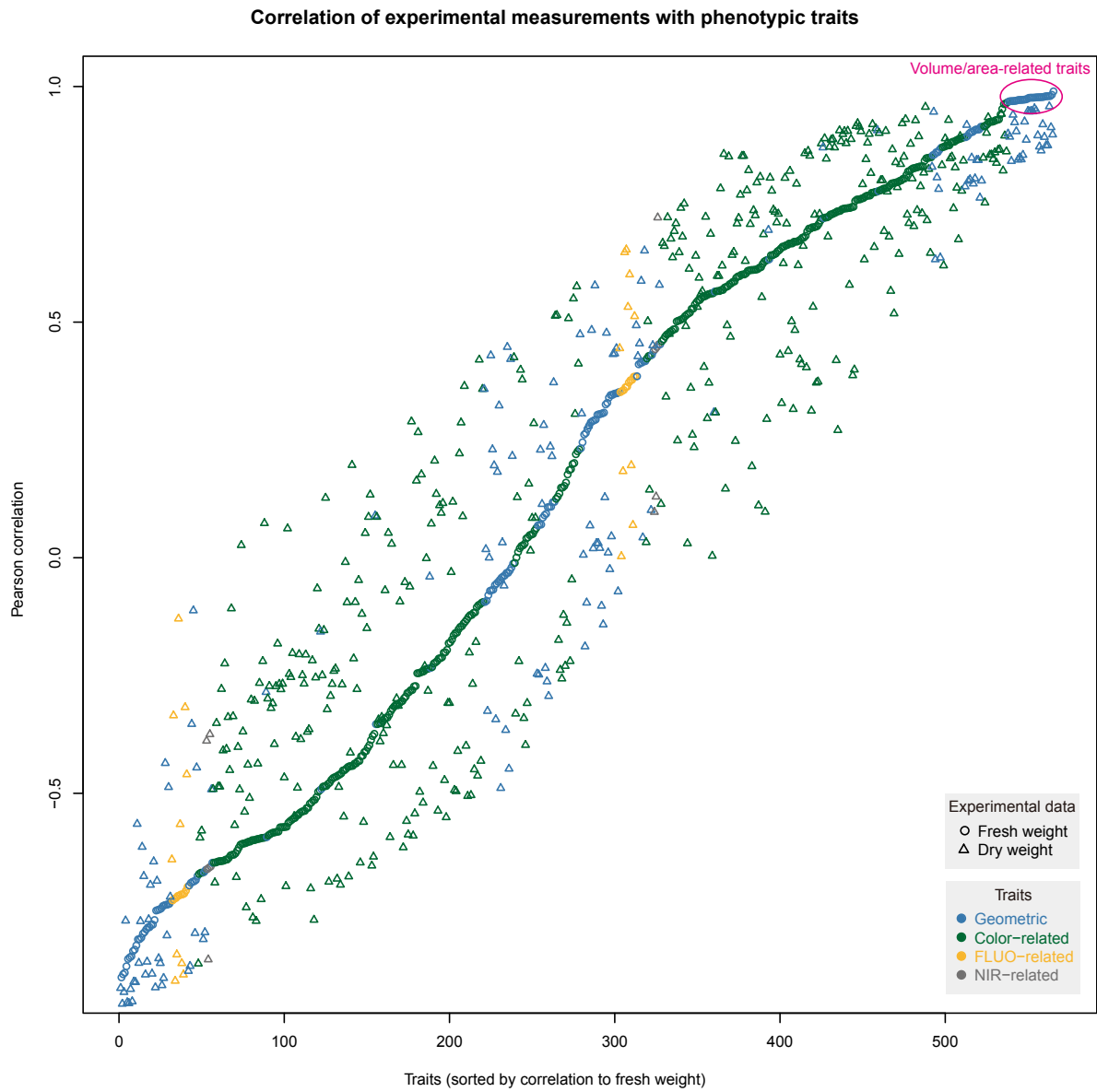


Figure S2: Correlation analysis of phenotypic traits. Experimental measurements (the fresh and dry weight) were correlated to the values of all phenotypic traits. The x-axis indicates the list of traits, which are sorted according to their correlation coefficient to the fresh weight. Traits are colored according to their classification.

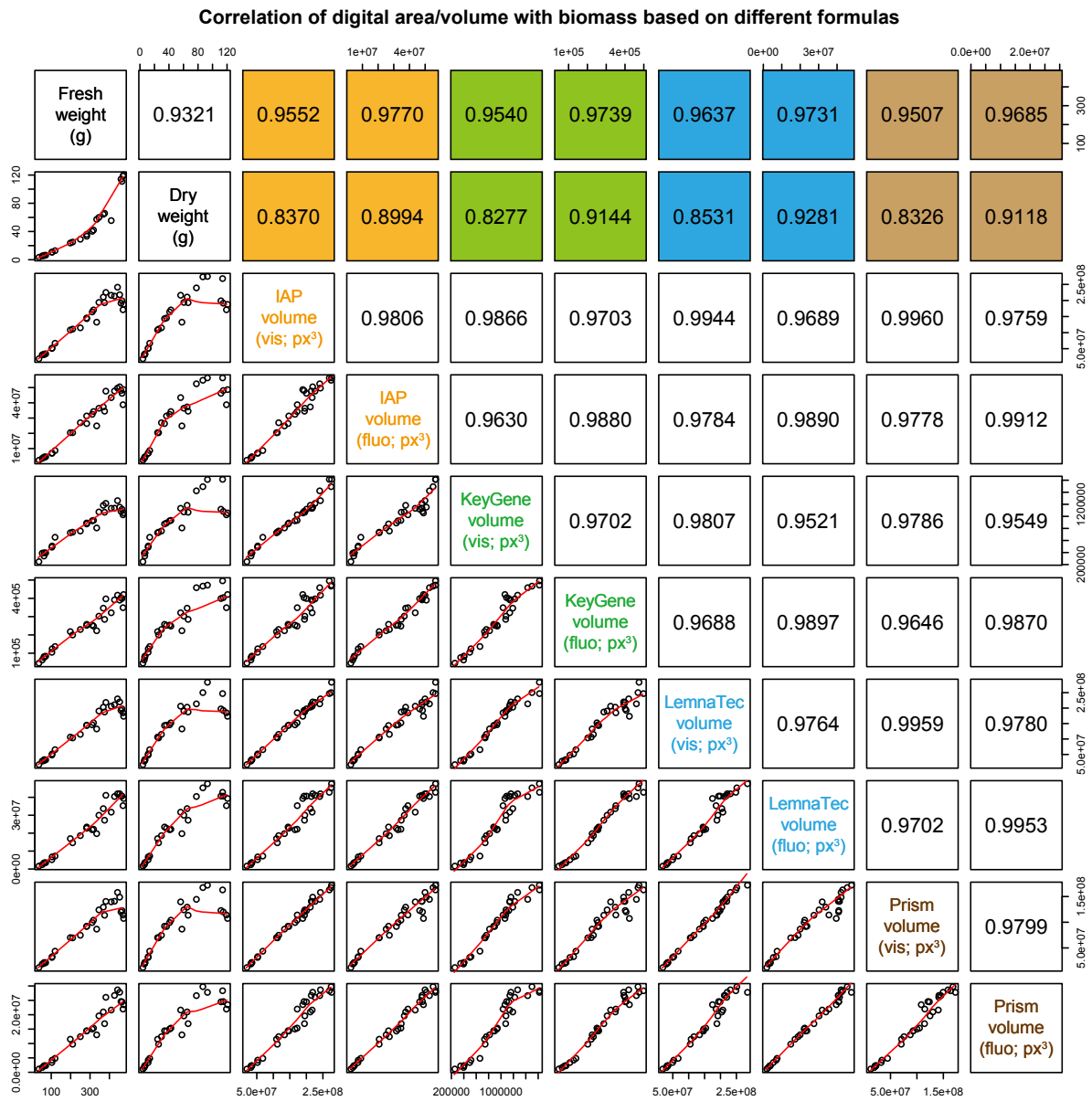


Figure S3: Correlation of the digital volume with experimental measurements of biomass (fresh and dry weight). The volume was calculated by four different formulas (IAP, KeyGene, LemnaTec and Prism) from visible (vis) and fluorescence (fluo) images. Shown values represent Pearson correlation coefficients (r).