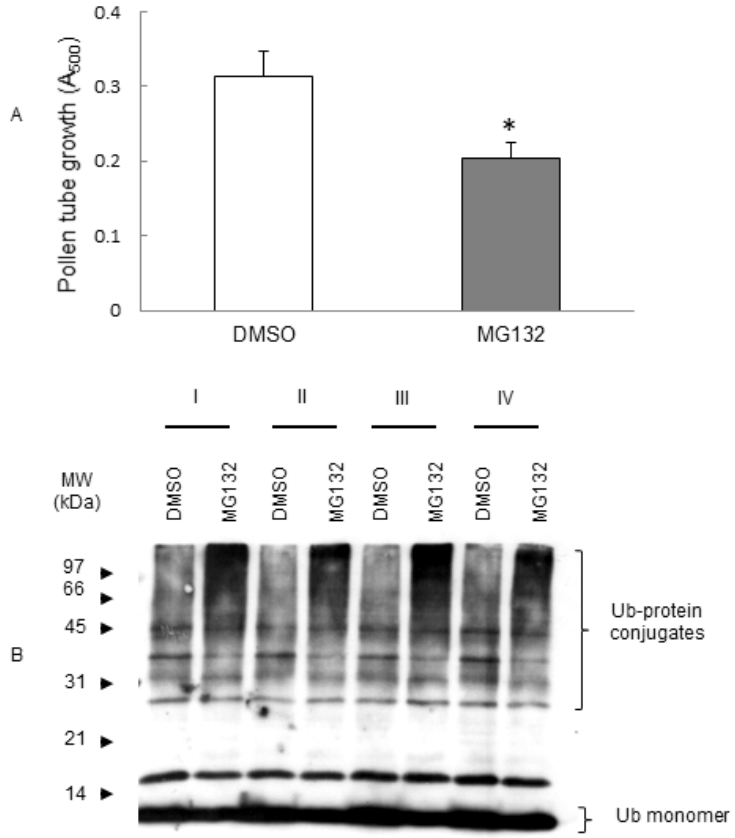

Figure S1. MG132 affects pollen tube growth and induces accumulation of ubiquitin-protein conjugates. (A) Pollen tube growth in the presence and absence of MG132 was determined by the PTG method. Growth is expressed as A_{500} of an aqueous suspension of grains/tubes measured after 90 min of incubation. Data are the means ± S.D. of three different replicates. **(B)** Four µg of total pollen extracts were separated onto 13% polyacrylamide gels, electroblotted and probed with an affinity-purified polyclonal anti-ubiquitin antibody. The positions of molecular mass markers are shown on the left. Roman numbers refer to the 4 different germination experiments.

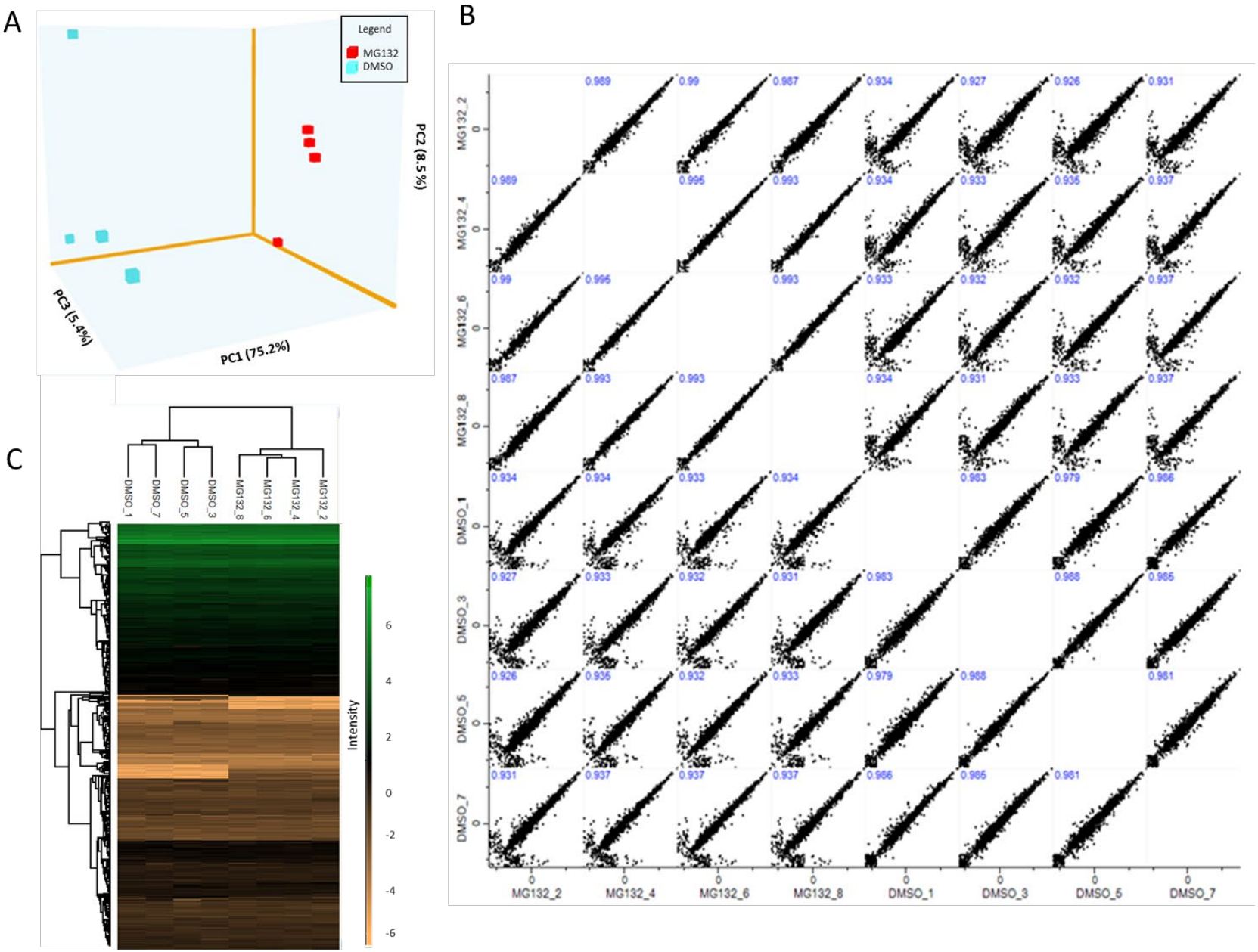

Figure S2. Principal component analysis (PCA), scatter plot, and hierarchical clustering of proteomic data. Analysis were performed onto the phosphosite intensities centered as described in materials and methods. **(A)** Principal component analysis (PCA) plot. The first principal component (PC1) describes the largest variation in the dataset in which the samples spread the most in the variable space. The second (PC2) and the third (PC3) components describe the next largest variations and are orthogonal to each other. **(B)** Multi scatter plot. Each sample was compared with each other sample present in the analysis. For each pairwise comparison Pearson correlation distribution was indicated. **(C)** Heat map for hierarchical Euclidean clustering of LFQ intensities of the experimental groups (MG132-treated and DMSO-treated samples).

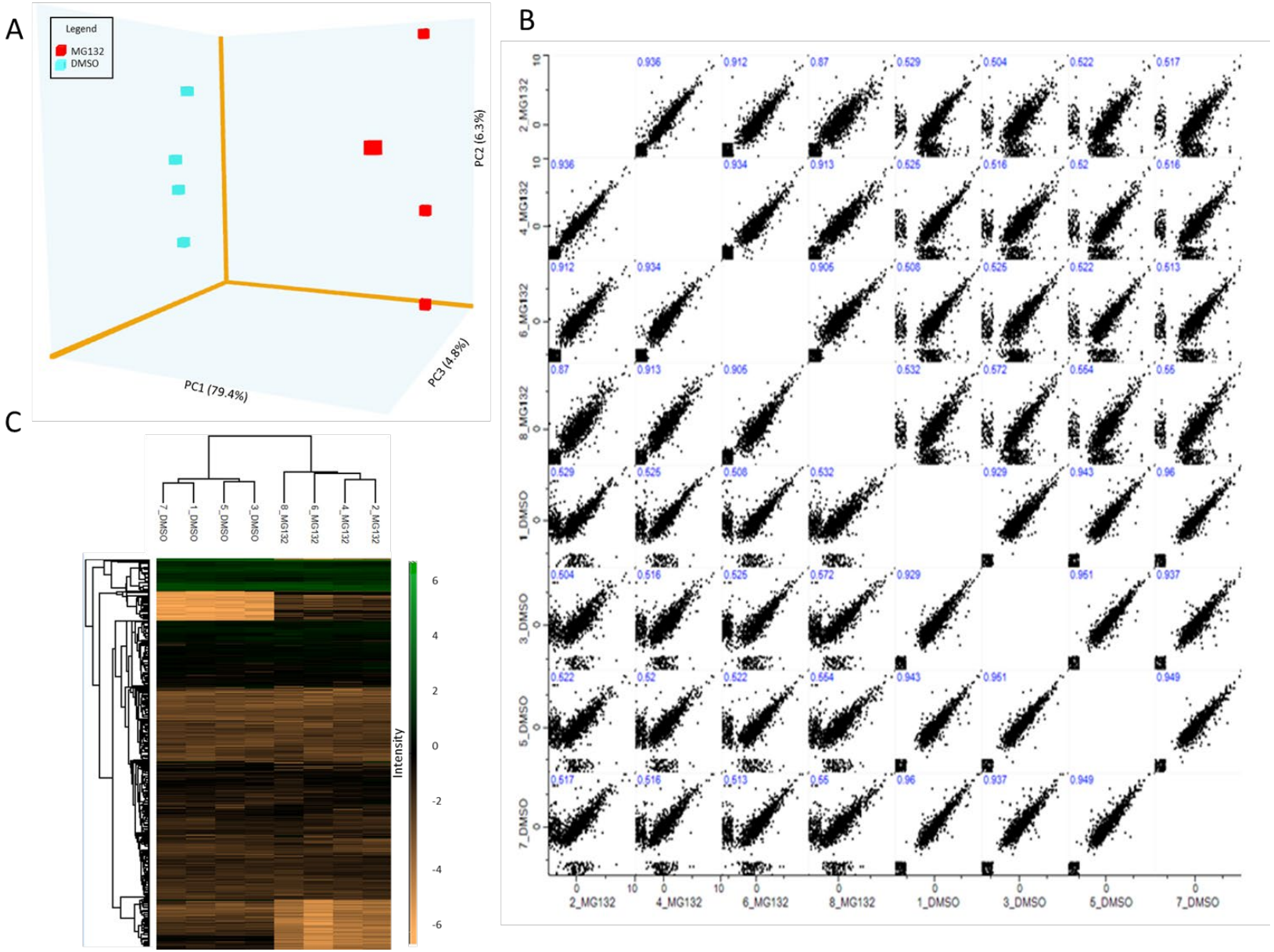

Figure S3. Principal component analysis (PCA), scatter plot, and hierarchical clustering of phosphoproteomic data. Analysis were performed onto the phosphosite intensities centered as described in materials and methods. **(A)** Principal component analysis (PCA) plot. The first principal component (PC1) describes the largest variation in the dataset in which the samples spread the most in the variable space. The second (PC2) and the third (PC3) components describe the next largest variations and are orthogonal to each other. **(B)** Multi scatter plot. Each sample was compared with each other sample present in the analysis. For each pairwise comparison Pearson correlation distribution was indicated. **(C)** Heat map for hierarchical Euclidean clustering of phosphosites intensities of the experimental groups (MG132-treated and DMSO-treated samples).

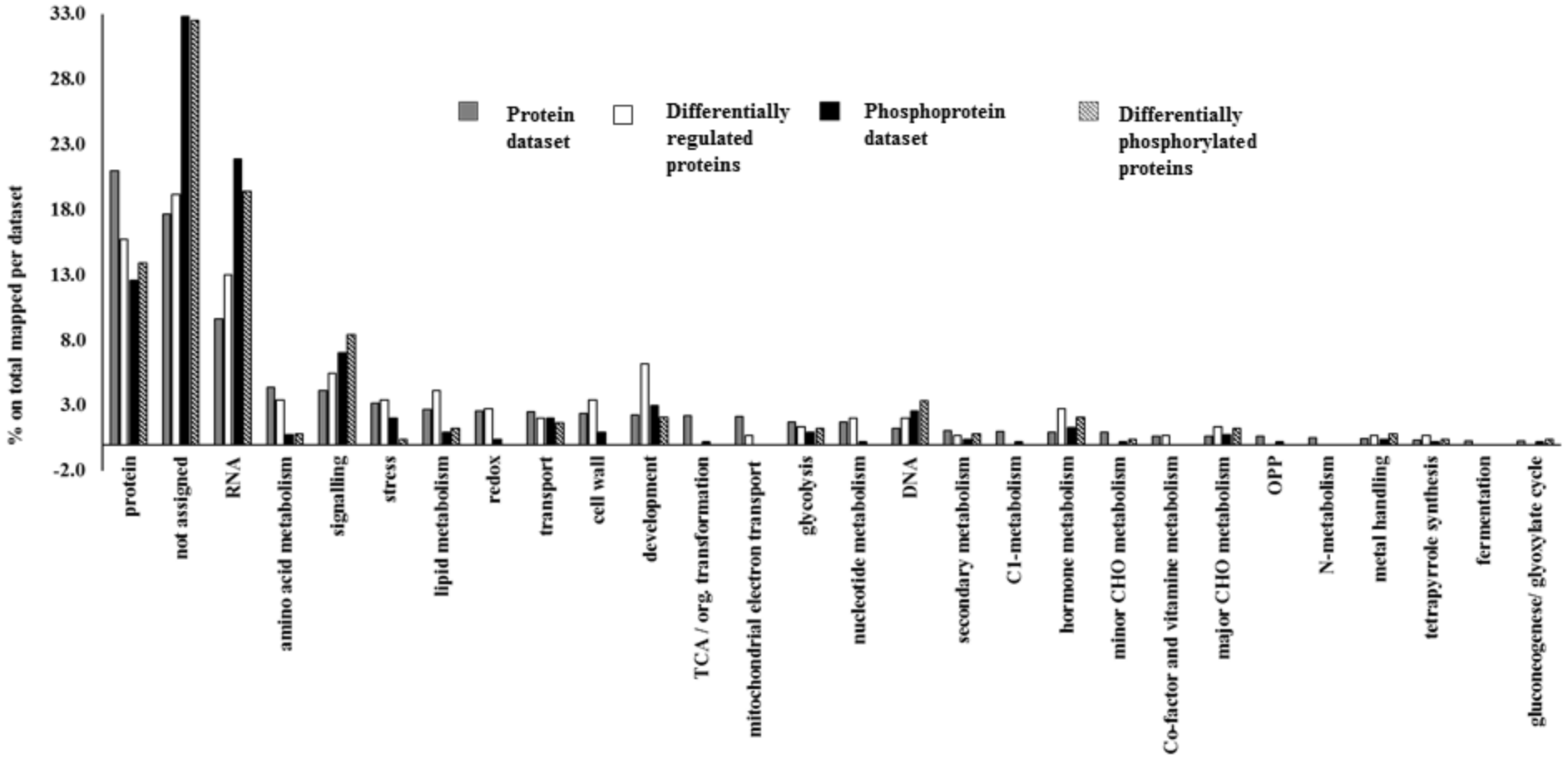

Figure S4. Overview of MapMan functional categories. *Arabidopsis thaliana* homologues to the kiwifruit pollen protein datasets were binned to MapMan categories. Y axis values represent the percent of proteins assigned to each categories calculated with respect to the total mapped proteins