

## Supplementary Figure and Tables

Suppl. Figure 1 Relative abundance of proteins in 35 groups obtained by kmeans clustering. NSAF scores were averaged over three biological replicates and were normalized for each protein to represent their proportion of the total abundance over all eight stages. A, microsporocytes; B, meiotic cells; C, tetrads; D, microspores; F, binuclear pollen; G, desiccated pollen; H, pollen tubes.

Suppl. Table 1 Peptide list. List of all peptides identified in all samples.

Suppl. Table 2 Pollen proteins.

Suppl. Table 3 Pollen and leaf proteins.

Suppl. Table 4 PCA analysis of proteins from eight stages of pollen development.

Suppl. Table 5 PCA analysis of proteins from eight stages of pollen development, leaves and roots.

Suppl. Table 6 Kmean clustering of proteins from eight stages of pollen development.

Suppl. Table 7 Functional clustering of proteins from stages of pollen development, leaves and roots.

Suppl. Table 8 Comparison of tobacco transcript levels and protein abundances.

Suppl. Table 9 Comparison of *Arabidopsis* transcript levels and tobacco protein abundances.

Suppl. Table 10 Arabidopsis genes and their corresponding tobacco protein homologues identified in this study.

Suppl. Table 12 Literature survey of Arabidopsis genes affected in pollen development or pollen tube growth. Genes were blasted against tobacco proteins identified in this study. The cut-off of the E-value was  $1e-010$ .

Suppl. Table 12 Peptides harboring post translational modifications.

Suppl. Figure 1

