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Supporting information

Additional Supporting information may be found in the online version of this article:

Figure S1 Gel image for three samples of 1.5-mm anther proteins. Each lane is one of three technical replicates of sample 293_1F_1.5 mm. The boxes indicate the gel regions recovered for the 3.5–10, 10–15 and 15–20 kDa samples. Size markers in kDa are shown on the right.

Figure S2 68% of all proteins were <25 kDa, as expected. The *x*-axis is molecular weight, the *y*-axis is protein count.

Figure S3 Gene ontology annotation for identified proteins in all four sample types. Percentage of each gene ontology category of expressed proteins in fertile or sterile anthers at different developmental stages. Categories are in alphabetical order, starting from the top of the list.

Figure S4 Protein models for the trans-membrane peptide search.

Figure S5 Peptide start index count.

Table S1 Inter-correlation coefficients between biological triplicates.

Table S2 Intra-correlation coefficients among technical triplicates.

Table S3 Criteria for data filtration.

Table S4 Analysis of potential trans-membrane proteins.

Table S5 GO analysis for 55 proteins that were only identified in the low molecular proteome with more than two assigned peptide, 0.3% peptide FDR and 0.1% protein FDR.

Table S6 GO analysis for 612 proteins that were only identified in the low molecular proteome with at least one assigned peptide, 0.3% peptide FDR and 5.6% protein FDR.

Table S7 GO annotation for the high confidence set of proteins to identify stage-specific and fertile or sterile restricted expression. Note that some proteins are represented in more than one GO category; some proteins identified in this study lacked any GO annotation.

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