

Figure S1. The transcripts from three independent biological replicates are highly correlated

Pearson's correlation coefficients are indicated in the figure.

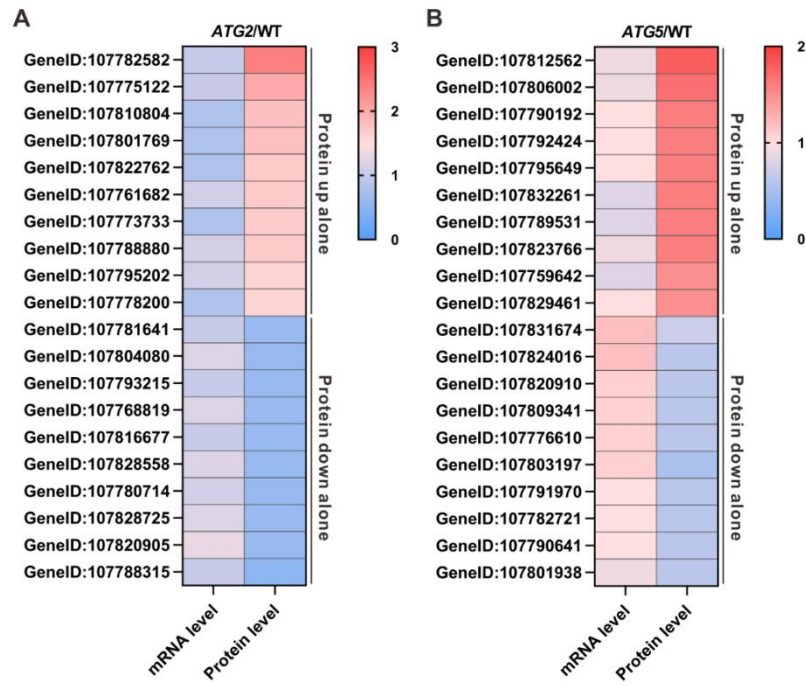


Figure S2. Heat map showing genes that are differentially regulated at mRNA and protein levels

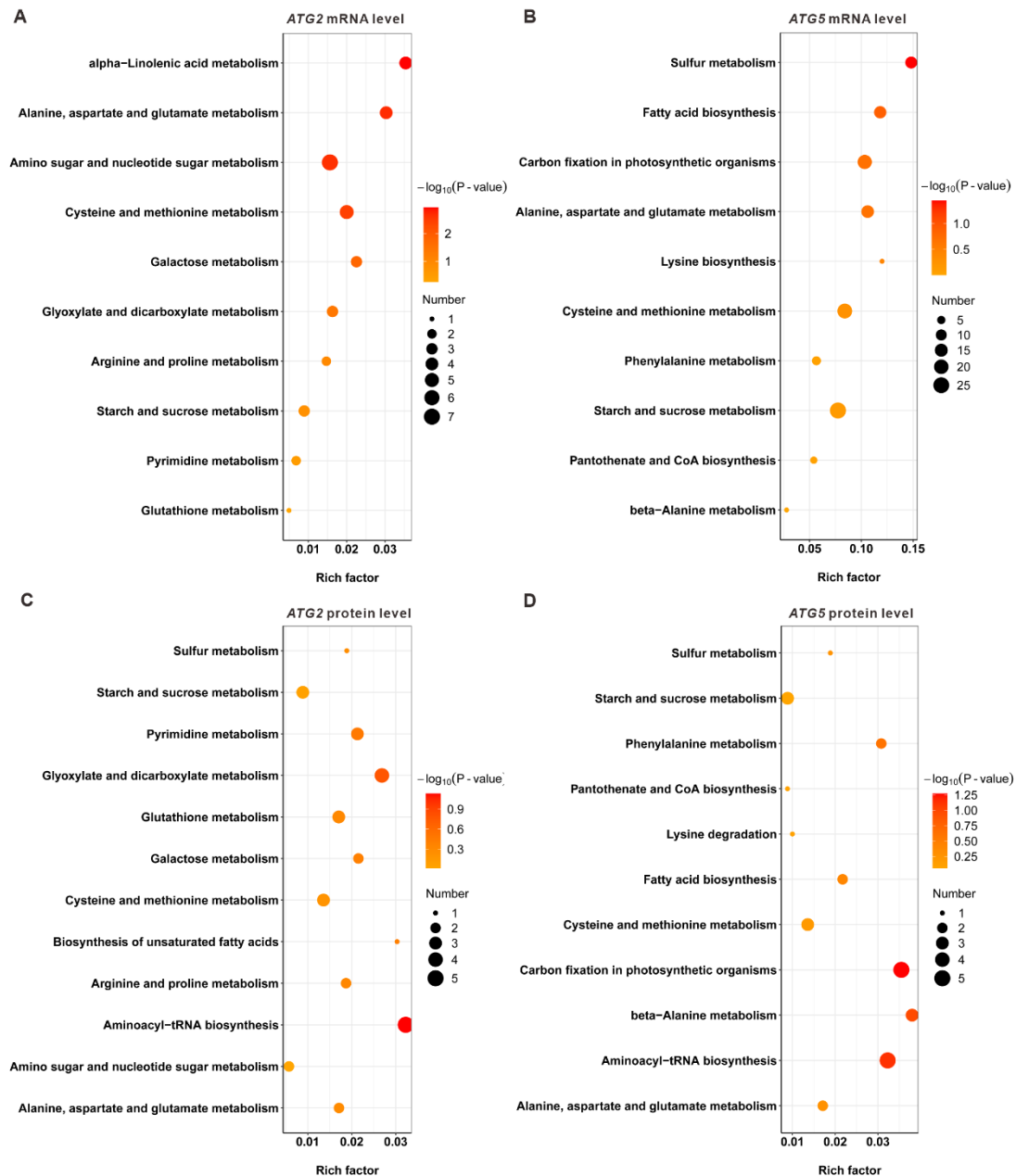


Figure S3. Metabolic pathways identified based on the transcriptomic and proteomic data of *ATG*-silenced pollen.

(A, B). Metabolic pathways affected by the silencing of *ATG2* (A) and *ATG5* (B) during pollen germination were identified based on transcriptomic analysis data. (C, D). Metabolic pathways were identified based on the proteomic analysis data of *ATG2*-silenced (C) and *ATG5*-silenced (D) pollen grains.

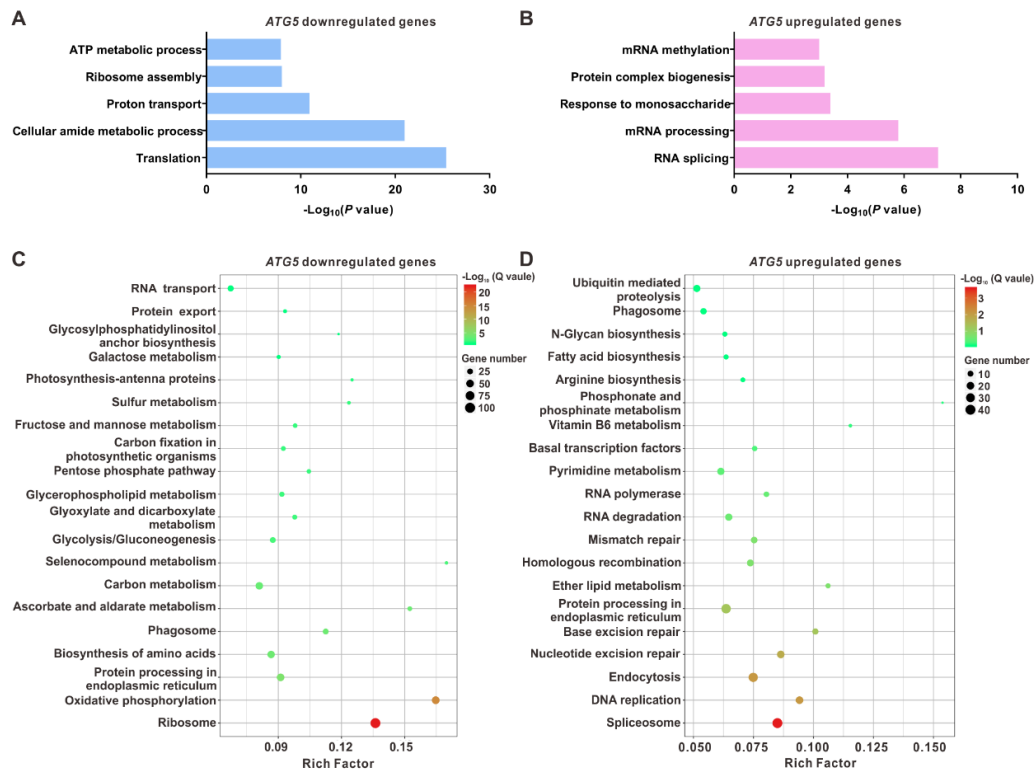


Figure S4. GO and KEGG analysis of differentially expressed genes identified in *ATG5*-silenced pollen.

(A, B). GO enrichment analysis of downregulated (A) and upregulated (B) genes in *ATG5*-silenced pollen. (C, D). KEGG analysis of downregulated (C) and upregulated (D) genes in *ATG5*-silenced pollen.

Table S1. Statistic data of each RNA-seq sample

| Sample | Clean Read Pairs | Clean base (bp) | Total mapped reads (ratio) | Unique mapped reads (ratio) | Expressed Genes (FPKM > 0) |
|---------------|-------------------------|------------------------|-----------------------------------|------------------------------------|--------------------------------------|
| WT-1 | 22,657,803 | 6,797,340,900 | 19,881,228 (87.75%) | 20,444,056 (90.23%) | 41,279 (53.76%) |
| WT-2 | 20,933,724 | 6,280,117,200 | 18,378,841 (87.80%) | 18,965,747 (90.60%) | 40,397 (52.61%) |
| WT-3 | 25,136,102 | 7,540,830,600 | 21,769,750 (86.61%) | 22,551,274 (89.72%) | 41,973 (54.66%) |
| <i>ATG2-1</i> | 29,438,526 | 8,831,557,800 | 25,686,553 (87.25%) | 26,418,422 (89.74%) | 42,527 (55.38%) |
| <i>ATG2-2</i> | 26,600,116 | 7,980,034,800 | 23,234,276 (87.35%) | 23,912,599 (89.90%) | 42,166 (54.91%) |
| <i>ATG2-3</i> | 23,442,799 | 7,032,839,700 | 20,276,792 (86.49%) | 20,988,020 (89.53%) | 41,453 (52.99%) |
| <i>ATG5-1</i> | 29,653,420 | 8,896,026,000 | 25,629,611 (86.43%) | 26,726,843 (90.13%) | 38,341 (49.93%) |
| <i>ATG5-2</i> | 26,579,411 | 7,973,823,300 | 22,765,733 (85.65%) | 23,859,858 (89.77%) | 39,147 (50.98%) |
| <i>ATG5-3</i> | 27,098,056 | 8,129,416,800 | 22,964,257 (84.75%) | 24,109,842 (88.97%) | 39,119 (50.95%) |

Legends for Supplementary Data

Supplementary Data S1. Differentially expressed genes between *ATG2*-silenced and WT pollen or *ATG5*-silenced and WT pollen.

Supplementary Data S2. Gene list used for the comparison of the mRNA and protein levels in *ATG*-silenced pollen.

Supplementary Data S3. Metabolites with different abundances between WT and *ATG2*-silenced pollen or between WT and *ATG5*-silenced pollen.