**Supplemental material included with this manuscript.**

Supplemental Figure S1. Number of differentially expressed genes as compared to the overall number of pairwise comparisons, and to the number of transcripts in the treatment and control samples across all 10 potato stress conditions.

Supplemental Figure S2. Heat map of module eigengenes representing each gene co-expression module. (A) Abiotic stress. (B) Biotic stress. (C) Hormone treatments. Rows correspond to eigengenes for each of the gene modules. Columns represent control and treatment samples. The color scale indicates the relative expression levels of all genes in the module.

Supplemental Figure S3. Trend plots of the normalized gene expression values for each gene from thirteen identified gene coexpression modules in Abiotic treatments.

Supplemental Figure S4. Trend plots of the normalized gene expression values for each gene from thirteen identified gene coexpression modules in Biotic treatments.

Supplemental Figure S5. Trend plots of the normalized gene expression values for each gene from thirteen identified gene coexpression modules in Hormone treatments.

Supplemental Figure S6. Cross-species comparison of gene expression between *S. tuberosum* Group Phureja clone DM1-3 516R44 (DM) and *Arabidopsis thaliana* (AT) tissues under abiotic stress and ABA treatments (↑ up and ↓ down regulated). DE: differentially expressed.

Supplemental Table S1. Statistically significant DE up-regulated genes under Abiotic, Biotic, and Hormone treatments with FPKM value ≥ 1 and a log2 fold change cutoff ≥ 1.

Supplemental Table S2. Statistically significant DE down-regulated genes under Abiotic, Biotic and Hormone treatments with FPKM value ≥ 1 and a log2 fold change cutoff ≥ 1.

Supplemental Table S3. Assignment of Gene Ontology (GO) molecular function terms to DE up-regulated genes with a FPKM value ≥ 1 and a log2 fold change ≥ 1.

Supplemental Table S4. Assignment of Gene Ontology (GO) molecular function terms to DE down-regulated genes with a FPKM value ≥ 1 and a log2 fold change ≥ 1.

Supplemental Table S5. DE up-regulated genes associated to GO molecular function terms with statistically significant enrichment in Abiotic, Biotic, and Hormone treatments.
Supplemental Table S6. DE down-regulated genes associated to GO molecular function terms with statistically significant enrichment in Abiotic, Biotic, and Hormone treatments.

Supplemental Table S7. Significantly enriched Gene Ontology (GO) molecular function terms to a subset of DE down-regulated genes.

Supplemental Table S8. Assignment of Gene Ontology (GO) molecular function terms to a subset of DE up-regulated genes overlapping between Abiotic and Hormone treatments.

Supplemental Table S9. Matrix of differentially expressed genes. Each value in the matrix represents the overlap between two profiling experiments as defined by the number of differentially expressed genes (and percentage). The up- and down-regulated expression profiles are plotted in the upper-left and lower-right triangles, respectively in Fig. 2. The main diagonal displays the total number of up- and down-regulated genes.

Supplemental Table S10. Transcription factor families with domains and Pfam IDs identified in the 39,031 DM predicted proteome.

Supplemental Table S11. Abiotic stress modules (A1 to A13) with their corresponding gene ID and putative function as determined by BLASTX searches against UniRef100 (E-value cutoff of 1e-5).

Supplemental Table S12. Biotic stress modules (B1 to B8) with their corresponding gene ID and putative function as determined by BLASTX searches against UniRef100 (E-value cutoff of 1e-5).

Supplemental Table S13. Hormones modules (C1 to A13) with their corresponding gene ID and putative function as determined by BLASTX searches against UniRef100 (E-value cutoff of 1e-5).

Supplemental Table S14. Gene ontology terms and annotations that were overrepresented in stress-related module genes.

Supplemental Table S15. List of common differentially expressed (DE) orthologous, up-regulated potato genes, putative function, and Pfam domain/s ID/s.

Supplemental Table S16. List of common differentially expressed (DE) orthologous, down-regulated potato genes, putative function, and Pfam domain/s ID/s.

Supplemental Table S17. List of common differentially expressed (DE) orthologous, up-regulated *A. thaliana* genes and putative function.
Supplemental Table S18. List of common differentially expressed (DE) orthologous, down-regulated *A. thaliana* genes and putative function.

Supplemental Table S19. RNA-Seq of potato (*S. tuberosum* Group Phureja clone DM1-3 516R44) Illumina Fragment libraries with NCBI-SRA accession numbers.
Figure S6

DM

Overall DE genes ↑3,098 ↓2,677

Potato singletons + lineage specific gene families 1,305

DE orthologous genes ↑2,357 ↓2,113

OrthoMCL clusters containing potato DE genes ↑2,023 ↓1,448

Common OrthoMCL clusters

Common DE orthologous genes ↑356 ↓258

OrthoMCL clusters containing DM and AT genes 10,547

OrthoMCL clusters 13,708

OrthoMCL

A. thaliana

Overall DE genes ↑2,071 ↓2,311

Arabidopsis singletons + lineage specific gene families 1,833

DE orthologous genes ↑1,199 ↓1,350

OrthoMCL clusters containing Arabidopsis DE genes ↑1,026 ↓1,079

Common DE orthologous genes ↑346 ↓267