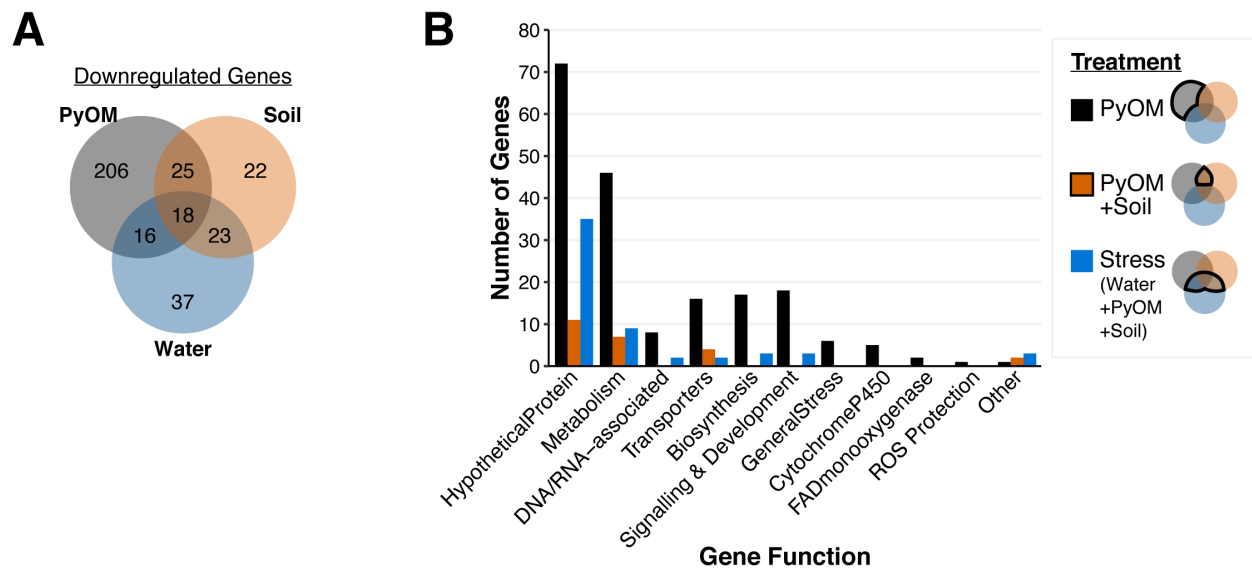


Supplemental Figure 1. *P. domesticum* biomass wet weight on agar media treatments.

Prior to Methylene Blue staining, *P. domesticum* biomass was harvested and immediately weighed. Error bars indicate standard deviation (n = 5).



Supplemental Figure 2. Down-regulated genes on pyrolyzed substrates in *P. domesticum*.

(A) Venn diagram showing the number of significantly downregulated genes in each treatment compared to sucrose (adjusted p-value < 0.01, fold change < -4, n = 3). (B) Number of significantly downregulated genes compared to expression on sucrose in each functional gene category (adjusted p-value < 0.01, fold change < -4, n = 3). Functional gene categories were determined via KEGG, GO, and pfam annotations. Black bars indicate the number of genes downregulated on PyOM alone (total = 206). Orange bars indicate the number of genes downregulated in both PyOM and soil (total = 25). Blue bars indicate the number of genes downregulated on water that also overlap with soil and/or PyOM (total = 57).

CLUSTAL O(1.2.4) multiple sequence alignment

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jgi|Pyrdom1|124492|gene_2648      MDPATIIASVKAMTPIQLGA--VGLIG-----FYILASLFTSIQTSIKSRSL---      45
AN1884                             -----MAPIPWGMLYVSVVGYSVLTSNLFVFLATALTALKIVYASFLYPEY      48
                                   *:* * * *:* * *:* * *:* * *
jgi|Pyrdom1|124492|gene_2648      ----GC-QSPWAWDPLGLRRVYMM---RYALNHQLPLYSVKLFKDFNTKVPPIIDFG      96
AN1884                             LTPIKHIPTPKRPSWVRGN-TDTYVVISPFEGLNWTKSPNNGLLRYIIIGNI-----      101
                                   * : * . * : . * * : . * : : . :
jgi|Pyrdom1|124492|gene_2648      KPGYLTCDPRNIQAALATNFKDWGF-GSARYPMLPIL-GDGIFTQDGEAWAHSRSMIRPS      154
AN1884                             -EQVLVTPPKALSELLVQNAYDYQKPE SIRISLARIAGEHGILLVEGQEHKRHRKNLMPA      160
                                   * . * : . * . * * : * * : * . * : * : * : * : * :
jgi|Pyrdom1|124492|gene_2648      FTKSQIADFE-----SLEEHMQEFFTTLEMTTKSDGAVSLKPLFSDLTMDFAS      202
AN1884                             FSYRHIKDLYPTFWAKSVEMVKCIEKDLQDRR-----DTGDITVTVRPWASRATLDIIG      214
                                   * : * * : . * : * : . * : * : * : * : * : * : * :
jgi|Pyrdom1|124492|gene_2648      EF----LFGETA---NSLKQRREGIAETGMAHWF-----AGMHVVTMSFNMGRHLHN      247
AN1884                             LAGMDRDFGSLADPQNELAAQYHRILE-DPPLWLKLLFAAAFVLGNEELVMALPVK----      269
                                   ** . * * . * : . * * . * : . * . . . * : :
jgi|Pyrdom1|124492|gene_2648      FWRPKEYRQSIKVFREFVDGVRHRALEERLAIGDIKEKERAKMNGGRYVFLNALTDNITD      307
AN1884                             --RNRDIAEGAKYVRQVAQLISEK---RERIKHNPE-KAEGGGGKILSVALSNGNFT      323
                                   * : : . * : * : : : . * * * * : * : * : * : * : * : * :
jgi|Pyrdom1|124492|gene_2648      PIVLRNQVLNIMLAGRDTAALLSWVLNLRARRPEVLERLKQVEAETIGVAENA--TLPT      365
AN1884                             DIEIDQMMTFLAAGHETSSALQWSVYALCKHPDIQTRLRQEIRSNLPSVSSNDPKPIT      383
                                   * * * : : : * : * : * : * : * : * : * : * : * : * : * : * :
jgi|Pyrdom1|124492|gene_2648      WQVLKDMRYLQAVIHETLRLFPSPVFSNRIATRDVLPYGGGSDGNAPLFAPKDTQLIYS      425
AN1884                             AEAVDLSPYLHAFCEVLRFHPSVPIFRTRTTRDTTLA-----GTLLEPKGTQLTIS      434
                                   : . . . : * : * . : * . * : * : * : * : * : * : * : * : * :
jgi|Pyrdom1|124492|gene_2648      IYAMQRRPEIWGADAAEFSPDRWLRADAGKM-LREVGWGNMPSFGGPRICPGQGFALTET      484
AN1884                             PEVINHDPDLWGPDAHIFNPDRWLGPRANTGGASSNYALMTFLHGPRSCIGGFAKAEL      494
                                   . : : * : * * * * . * : * : . . . * * * * * * * * * * :
jgi|Pyrdom1|124492|gene_2648      SYVVSRLQLRYQWVEKAPGESDVPSEASLVTPPADMVEMFTKY---      529
AN1884                             ACLVAAMVGRFEMELADPGKKLAVRRRTAT-IS-PVDGVVARLTPLDGW      540
                                   : : * : : * : : * : . . * : : * . * * . : *

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Supplemental Figure 3. Protein sequence alignment of the *A. nidulans* bapA gene (AN1884) and *P. domesticum* gene_2648. Alignment performed using the EMBL-EBI Clustal Omega web tool (Madeira et al., 2019). Yellow highlights indicate broadly conserved motifs (Ostrem Loss et al., 2019).