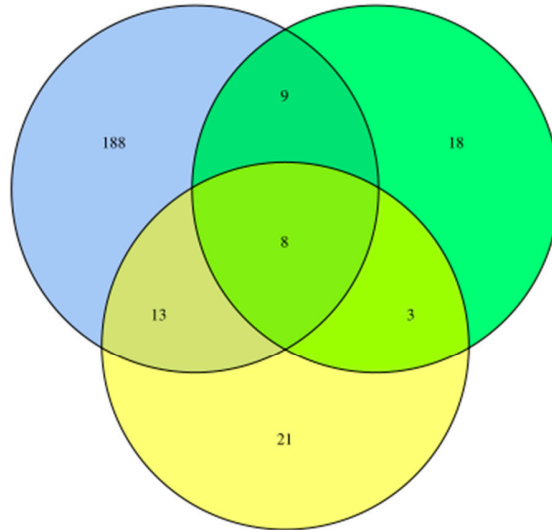


**Supplementary Data:**

BMK\_3\_CONTROL-1\_CONTROL-2\_CONTROL-3\_vs\_BB-1\_BB-2\_BB-3

BMK\_3\_CONTROL-1\_CONTROL-2\_CONTROL-3\_vs\_BB-TH-1\_BB-TH-2\_BB-TH-3



BMK\_3\_CONTROL-1\_CONTROL-2\_CONTROL-3\_vs\_TH-1\_TH-2\_TH-3

**Figure S1.** Venn diagram of differentially expressed genes.

**Table S1.** Summary of reads from *O. furnacalis* transcriptome after fungal inoculation.

| Samples   | Clean reads | Total mapped        | GC (%) | Q30 (%) |
|-----------|-------------|---------------------|--------|---------|
| CONTROL-1 | 47,663,380  | 41,500,043 (87.07%) | 49.05% | 95.98%  |
| CONTROL-2 | 56,855,716  | 49,259,914 (86.64%) | 48.00% | 95.79%  |
| CONTROL-3 | 55,350,190  | 47,655,803 (86.10%) | 48.41% | 95.77%  |
| BB-1      | 49,557,902  | 42,803,307 (86.37%) | 48.91% | 95.90%  |
| BB-2      | 54,617,758  | 47,383,866 (86.76%) | 48.43% | 96.14%  |
| BB-3      | 49,090,076  | 41,044,436 (83.61%) | 48.59% | 95.90%  |
| BB-TH-1   | 44,013,916  | 37,579,113 (85.38%) | 48.99% | 95.09%  |
| BB-TH-2   | 44,801,702  | 38,775,359 (86.55%) | 48.97% | 95.48%  |
| BB-TH-3   | 49,374,034  | 42,763,282 (86.61%) | 49.46% | 95.17%  |
| TH-1      | 63,186,052  | 53,128,376 (84.08%) | 48.70% | 95.79%  |
| TH-2      | 42,901,514  | 36,479,674 (85.03%) | 48.87% | 95.57%  |
| TH-3      | 48,067,818  | 39,696,165 (82.58%) | 48.65% | 95.63%  |

**Table S2.** Primers used for RT-qPCR

| Gene name                                   | Gene I.D          | Direction | Sequence (5'-3')      |
|---------------------------------------------|-------------------|-----------|-----------------------|
| <b>PRPS</b>                                 | gene-LOC114352122 | Forward   | TGCAGAGGTACCACAACAGC  |
|                                             |                   | Reverse   | GCTGACTCCGTTGGCTCTAC  |
| <b>PRPB</b>                                 | gene-LOC114352113 | Forward   | GAAAAATGGCCCGTCTTACA  |
|                                             |                   | Reverse   | CGTCACGAACGGGAAGTTAT  |
| <b>Larval/pupal rigid cuticle protein</b>   | gene-LOC114366353 | Forward   | ATGGCAGCTAAGTTCGTCGT  |
|                                             |                   | Reverse   | CCGTACGAGAAGCTGGTGTAG |
| <b>Larval/pupal rigid cuticle protein 2</b> | gene-LOC114366367 | Forward   | GGGATCAATCATTCGCAGTC  |
|                                             |                   | Reverse   | ACCAGGAGAGCAACAACGAC  |
| <b>Cytochrome P450</b>                      | gene-LOC114353087 | Forward   | AGAGCGACTGGTGAAGGAAA  |
|                                             |                   | Reverse   | CCTCATCAGCTCTGACACCA  |
| <b>ABC transporter 1</b>                    | gene-LOC114354308 | Forward   | AACCACATGACATTGGCTCA  |
|                                             |                   | Reverse   | ACGCGATCGAGCTTCAGTAT  |
| <b>ABC transporter 2</b>                    | gene-LOC114353130 | Forward   | TACCCCCAGAACTCCAGTG   |
|                                             |                   | Reverse   | TTTGGCGGTTTCTCGTATTC  |
| <b>Cadherin</b>                             | gene-LOC114362562 | Forward   | CAACCAACCAGCATTTTGTG  |
|                                             |                   | Reverse   | TCTTTTGACAGCTCGGGTCT  |
| <b>UDP-glucuronosyltransferase</b>          | gene-LOC114350074 | Forward   | GAGTGCCCTTCGAGACTCTG  |
|                                             |                   | Reverse   | AATCGAGGCCGAGTCCTTAT  |
| <b>HSP-70</b>                               | gene-LOC114356221 | Forward   | AAGAACCAGGTCGCTCTCAA  |
|                                             |                   | Reverse   | AAGGGCCAGTGTTTCATGTC  |
| <b>HSP-68</b>                               | gene-LOC114363773 | Forward   | ACATGAAACACTGGCCCTTC  |
|                                             |                   | Reverse   | TACGCCTCTGCAGTTTCCTT  |